(19) DANMARK

(10) **DK/EP 3570885 T3**

Patent- og Varemærkestyrelsen

(12) Oversættelse af europæisk patentskrift

(51) Int.Cl.: ***A 61 K 39/395 (2006.01)*** ***A 61 P 3/10 (2006.01)*** ***C 07 K 16/28 (2006.01)***

(45) Oversættelsen bekendtgjort den: **2024-12-16**

(80) Dato for Den Europæiske Patentmyndigheds bekendtgørelse om meddelelse af patentet: **2024-09-18**

(86) Europæisk ansøgning nr.: **18714635.2**

(86) Europæisk indleveringsdag: **2018-01-16**

(87) Den europæiske ansøgnings publiceringsdag: **2019-11-27**

(86) International ansøgning nr.: **US2018013918**

(87) Internationalt publikationsnr.: **WO2018136440**

(30) Prioritet: **2017-01-17 US 201762447332 P**

(84) Designerede stater: **AL AT BE BG CH CY CZ DE DK EE ES FI FR GB GR HR HU IE IS IT LI LT LU LV MC MK MT NL NO PL PT RO RS SE SI SK SM TR**

(73) Patenthaver: **Amgen Inc., One Amgen Center Drive , Thousand Oaks, California 91320, USA**

(72) Opfinder: **CHENG, Yuan, 5329 Via Jacinto, Newbury Park, California 91320, USA**
NETIROJJANAKUL, Chawita, 4631 Kester Ave., Apt. 103, Sherman Oaks, California 91403, USA
HOLDER, Jerry Ryan, 1102 Waltham Road, Simi Valley, California 93065, USA
WU, Bin, 3090 Hollycrest Avenue, Thousand Oaks, California 91362, USA
FALSEY, James R., 13209 Peach Hill Road, Moorpark, California 93021, USA
HERBERICH, Bradley J., 1746 Hays Drive, Newbury Park, California 91320, USA
SHAM, Kelvin, 3111 La Casa Court, Thousand Oaks, California 91362, USA
MIRANDA, Leslie P., 3586 Mapleknoll Place, Thousand Oaks, California 91362, USA
LU, Shu-Chen, 2356 Rutland Place, Thousand Oaks, California 91362, USA
VENIANT-ELLISON, Murielle M., 645 Camino Manzanas, Thousand Oaks, California 91360, USA
STANISLAUS, Shanaka, 4196 Minnecota Drive, Thousand Oaks, California 91360, USA
YIE, Junming, 4 Sugarwood Way, Warren, New Jersey 07059, USA
XU, Jing, 67 Bishops Forest Drive, Waltham, Massachusetts 02452, USA

(74) Fuldmægtig i Danmark: **RWS Group, Europa House, Chiltern Park, Chiltern Hill, Chalfont St Peter, Bucks SL9 9FG, Storbritannien**

(54) Benævnelse: **FREMGANGSMÅDE TIL BEHANDLING ELLER BEDRING AF METABOLISKE FORSTYRRELSER VED ANVENDELSE AF GLP-1-RECEPTORAGONISTER KONJUGERET TIL ANTAGONISTER FOR GASTRISK INHIBITORISK PEPTID-RECEPTOR (GIPR)**

(56) Fremdragne publikationer:
WO-A2-2007/028633
WO-A2-2017/112824
J T LEWIS ET AL: "Glucose-dependent insulinotropic polypeptide confers early phase insulin release to oral glucose in rats: demonstration by a receptor antagonist", ENDOCRINOLOGY, vol. 141, no. 10, 1 October 2000

Fortsættes ...

(2000-10-01), pages 3710 - 3716, XP055174431, ISSN: 0013-7227, DOI: 10.1210/en.141.10.3710
DAISUKE SHINMI ET AL: "One-Step Conjugation Method for Site-Specific Antibody-Drug Conjugates through Reactive Cysteine-Engineered Antibodies", BIOCONJUGATE CHEMISTRY, vol. 27, no. 5, 18 May 2016 (2016-05-18), US, pages 1324 - 1331, XP055299626, ISSN: 1043-1802, DOI: 10.1021/acs.bioconjchem.6b00133
CHRISTOPHER R BEHRENS ET AL: "Methods for site-specific drug conjugation to antibodies", MABS, vol. 6, no. 1, 20 January 2014 (2014-01-20), US, pages 46 - 53, XP055293357, ISSN: 1942-0870, DOI: 10.4161/mabs.26632
SCHUMACHER DOMINIK ET AL: "Current Status: Site-Specific Antibody Drug Conjugates", JOURNAL OF CLINICAL IMMUNOLOGY, KLUWER ACADEMIC PUBLISHERS, NEW YORK, vol. 36, no. 1, 22 March 2016 (2016-03-22), pages 100 - 107, XP035837954, ISSN: 0271-9142, [retrieved on 20160322], DOI: 10.1007/S10875-016-0265-6
SULEIMAN AL-SABAH: "Molecular Pharmacology of the Incretin Receptors", MEDICAL PRINCIPLES AND PRACTICE, vol. 25, no. 1, 20 June 2015 (2015-06-20), CH, pages 15 - 21, XP055475051, ISSN: 1011-7571, DOI: 10.1159/000433437
PETER RAVN ET AL: "Structural and Pharmacological Characterization of Novel Potent and Selective Monoclonal Antibody Antagonists of Glucose-dependent Insulinotropic Polypeptide Receptor", JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 288, no. 27, 5 July 2013 (2013-07-05), US, pages 19760 - 19772, XP055355497, ISSN: 0021-9258, DOI: 10.1074/jbc.M112.426288
MCCLEAN P L ET AL: "GIP receptor antagonism reverses obesity, insulin resistance, and associated metabolic disturbances induced in mice by prolonged consumption of high -fat diet", AMERICAN JOURNAL OF PHYSIOLOGY: ENDOCRINOLOGY AND METABOL, AMERICAN PHYSIOLOGICAL SOCIETY, BETHESDA, MD, US, vol. 293, no. 6, 1 January 2007 (2007-01-01), pages E1746 - E1755, XP008099009, ISSN: 0193-1849, DOI: 10.1152/AJPENDO.00460.2007

DESCRIPTION

FIELD OF THE INVENTION

[0001] The present disclosure relates to the treatment or amelioration of a metabolic disorder, such as type 2 diabetes, elevated glucose levels, elevated insulin levels, obesity, non-alcoholic fatty liver disease, cardiovascular diseases or diabetic nephropathy, using GLP-1 receptor agonists conjugated to an antigen binding protein specific for the gastric inhibitory peptide receptor (GIPR).

BACKGROUND OF THE INVENTION

[0002] Glucose-dependent insulinotropic polypeptide (GIP) is a single 42-amino acid peptide secreted from K-cells in the small intestine (duodenum and jejunum). Human GIP is derived from the processing of proGIP, a 153-amino acid precursor that is encoded by a gene localized to chromosome 17q (Inagaki et al., Mol Endocrinol 1989; 3:1014-1021; Fehmann et al. Endocr Rev. 1995; 16:390-410). GIP was formerly called gastric inhibitory polypeptide.

[0003] GIP secretion is induced by food ingestion. GIP has a number of physiological effects in tissues, including promotion of fat storage in adipocytes and promotion of pancreatic islet β-cell function and glucose-dependent insulin secretion. GIP and glucagon like polypeptide-1 (GLP-1) are known insulinotropic factors ("incretins"). Intact GIP is rapidly degraded by DPPIV to an inactive form. The insulinotropic effect of GIP is lost in type 2 diabetic patients while GLP-1's incretin effect remains intact (Nauck et al. J. Cline. 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] Collectively, these links to obesity and insulin resistance imply GIPR inhibition is a useful approach for therapeutic intervention.

[0007] Glucagon-like peptide-1 is a 31-amino acid peptide derived from the proglucagon gene. It is secreted by intestinal L-cells and released in response to food ingestion to induce insulin secretion from pancreatic β-cells (Diabetes 2004, 53:S3, 205-214). In addition to the incretin effects, GLP-1 also decreases glucagon secretion, delays gastric emptying and reduces caloric intake (Diabetes Care, 2003, 26(10): 2929-2940). GLP-1 exerts its effects by activation of the GLP-1 receptor, which belongs to a class B G-protein-coupled receptor (Endocrinology. 1993, 133(4):1907-10). The function of GLP-1 is limited by rapid degradation by the DPP-IV enzyme, resulting in a half-life of approximately 2 minutes. Recently, long-lasting GLP-1 receptor agonists (GLP-1 RAs) such as exenatide, liraglutide, dulaglutide have been developed and are now being used clinically to improve glycemic control in patients with type 2 diabetes. Furthermore, GLP-1RAs also promote body weight reduction as well as reduction in blood pressure and plasma cholesterol levels in patients (Bioorg. Med. Chem.Lett 2013, 23:4011-4018).

[0008] Peter Ravn et al., "Structural and pharmacological characterization of novel potent and selective monoclonal antibody antagonists of glucose-dependent insulinotropic polypeptide receptor", The Journal of Biological Chemistry, Vol. 288, No. 27 (2013), concerns an antibody to the GIP receptor.

[0009] Suleiman Al-Sabah, "Molecular Pharmacology of the Incretin Receptors", Medical Principles and Practice, Vol. 25, No. 1 (2015), concerns signaling mechanisms and regulation of GIP and GLP-1.

[0010] Paula L. McClean et al., "GIP receptor antagonism reverses obesity, insulin resistance, and associated metabolic disturbances induced in mice by prolonged consumption of high-fat diet", American Journal of Physiology: Endocrinology and Metabolism 293 (2007) concerns studies on the effects of the administration of a GIP receptor antagonist.

[0011] Dominik Schumacher et al., "Current Status: Site-Specific Antibody Drug Conjugates", Journal of Clinical immunology, Volume 36, No. 1 (2016), concerns the site-directed attachment of drugs for second generation antibody drug conjugates.

[0012] Christopher R Behrens and Bin Liu, "Methods for site-specific drug conjugation to antibodies", MABS, Volume 6, Issue 1 (2014), concerns methods for site-specific drug conjugation to antibodies.

[0013] Jamie T. Lewis et al., "Glucose dependent Insulinotropic Polypeptide Confers Early Phase Insulin Release to

Oral Glucose in Rats: Demonstration by a Receptor Antagonist", Endocrinology, Vol. 141, No. 10 (2000), concerns a GIP receptor antagonist.

SUMMARY OF THE INVENTION

[0014] The protected invention is defined in the claims.

[0015] References to methods of treatment in this description are not to be interpreted as being protected by the present claims as such. Rather, some of the present claims are directed to the compositions of the present invention for use in the treatment of a metabolic disorder.

[0016] In one aspect, the present invention provides a composition comprising a) an antibody or functional fragment thereof that specifically binds to human GIPR, wherein the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid substitution at one or more conjugation site(s); and b) a GLP-1 receptor agonist, wherein the GLP-1 receptor agonist is conjugated to the antibody or functional fragment thereof through the side-chain of the cysteine residue or non-canonical amino acid residue substituted at the one or more conjugation site(s), wherein the antibody or functional fragment thereof is an antagonist of GIPR, for use in a method of treating a subject with a metabolic disorder. In one embodiment, the metabolic disorder is a disorder of glucose metabolism. In another embodiment, the glucose metabolism disorder comprises hyperglycemia and administering the antigen binding protein reduces plasma glucose. In another embodiment, the glucose metabolism disorder comprises hyperinsulinemia and administering the antigen binding protein reduces plasma insulin. In another embodiment, the glucose metabolism disorder comprises glucose intolerance and administering the antigen binding protein reduces increases glucose tolerance. In another embodiment, the glucose metabolism disorder comprises insulin resistance and administering the antigen binding protein reduces insulin resistance. In another embodiment, the glucose metabolism disorder comprises diabetes mellitus. In another embodiment, the subject is obese. In another embodiment, administering the composition reduces body weight in an obese subject. In another embodiment, administering the composition reduces body weight gain in an obese subject. In another embodiment, administering the composition reduces fat mass in an obese subject. In another embodiment, the glucose metabolism disorder comprises insulin resistance and administering the composition reduces insulin resistance in an obese subject. In another embodiment, administering the composition reduces liver steatosis in an obese subject having increased liver steatosis. In another embodiment, administering the composition reduces liver fat content in an obese subject having increased liver fat content.

[0017] In one aspect, the composition comprises an antibody or functional fragment thereof that specifically binds to human GIPR, wherein the antibody or functional fragment thereof is an antagonist of GIPR and comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s) selected from the group consisting of D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455; E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, and T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612; and a GLP-1 receptor agonist, wherein the GLP-1 receptor agonist is conjugated to the antibody or functional fragment thereof through the side-chain of the cysteine residue or non-canonical amino acid residue substituted at the one or more conjugation site(s).

[0018] In one embodiment, the human GIPR has a sequence comprising a sequence selected from the group consisting of SEQ ID NO: 3141, SEQ ID NO: 3143, and SEQ ID NO: 3145. In one embodiment, the antibody is a monoclonal antibody, a recombinant antibody, a human antibody, a humanized antibody, a chimeric antibody, a multispecific antibody, or the functional fragment thereof is a functional fragment of a monoclonal antibody, a recombinant antibody, a human antibody, a humanized antibody, a chimeric antibody, or a multispecific antibody. In one embodiment, the antibody fragment is a Fab fragment, a Fab' fragment, or a F(ab')2 fragment. In one embodiment, the antibody or functional fragment thereof is of the IgG1-, IgG2- IgG3- or IgG4-type. In one embodiment, the antibody or functional fragment thereof inhibits binding of GIP to the extracellular portion of human GIPR.

[0019] In one embodiment, the GLP-1 receptor agonist is GLP-1(7-37) or a GLP-1(7-37) analog. In one embodiment, the GLP-1 receptor agonist is selected from the group consisting of exenatide, liraglutide, lixisenatide, albiglutide, dulaglutide, semaglutide, and taspoglutide. In one embodiment, the GLP-1 receptor agonist is selected from the group consisting of GLP-1(7-37) (SEQ ID NO: 3184); GLP-1(7-36)-NH_2 (SEQ ID NO: 3185); liraglutide; albiglutide; taspoglutide, dulaglutide, seniaglutide; LY2428757, Exendin-4 (SEQ ID NO: 3163); Exendin-3 (SEQ ID NO: 3164); Leu^{14}-exendin-4 (SEQ ID NO: 3165); Leu^{14},Phe^{25}-exendin-4 (SEQ ID NO: 3166); Leu^{14},Ala^{19},Phe^{25}-exendin-4 (SEQ ID NO: 3167); exendin-4(1-30) (SEQ ID NO: 3168); Leu^{14}-exendin-4(1-30) (SEQ ID NO: 3169); Leu^{14},Phe^{25}-exonditi-4(1-30) (SEQ ID NO: 3170); Leu^{14},Ala^{19},Phe^{25}-exendin-4(1-30) (SEQ ID NO: 3171); exendin-4(1-28) (SEQ ID NO: 3172); Leu^{14}-exendin-4(1-28) (SEQ ID NO: 3173); Leu^{14},Phe^{25}-exendin-4(1-28) (SEQ ID NO: 3174); Leu^{14},Ala^{19},Phe^{25}-exendin-4 (1-28) (SEQ ID NO: 3175); Leu^{14},$Lys^{17,20}$,Ala^{19},Glu^{21},Phe^{25},Gln^{28}-exendin-4 (SEQ ID NO: 3176); Leu^{14},$Lys^{17,20}Ala^{19}$,$Glu^{21}Gln^{28}$-exendin-4 (SEQ ID NO: 3177); octylGly^{14},Gln^{28}-exendin-4 (SEQ ID NO: 3178); Leu^{14},Gln^{28},octylGly^{34}-exendin-4 (SEQ ID NO: 3179); Phe^{4},Leu^{J4},Gln^{28},Lys^{3}3,Glu^{34}, $Ile^{35,36}$,Ser^{37}-exendin-4(1-37) (SEQ ID NO: 3180); Phe^{4},Leu^{14},$Lys^{17,20}$,Ala^{19},Glu^{21},Gln^{28}-exendin-4 (SEQ ID NO: 3181);

Val^{11},Ile^{13},Leu^{14},Ala^{16},Lys^{21},Phe^{23}-exendin-4 (SEQ ID NO: 3182); exendin-4-Lys^{40} (SEQ ID NO: 3183); GLP-1(7-37) (SEQ ID NO: 3184); GLP-1(7-36)-NH_2 (SEQ ID NO: 3185); $Aib^{8,35}$,$Arg^{26,34}$,Phe^{31}-GLP-1(7-36)) (SEQ ID NO: 3186); $HXaa_8EGTFTSDVSSYLEXaa_{22}Xaa_{23}AAKEFIXaa_{30}WLXaa_{33}Xaa_{34}G\ Xaa_{36}Xaa_{37}$; wherein Xaa_8 is A, V, or G; Xaa_{22} is G, K, or E; Xaa_{23} is Q or K; Xaa_{30} is A or E; Xaa_{33} is V or K; Xaa_{34} is K, N, or R; Xaa_{36} is R or G; and Xaa_{37} is G, H, P, or absent (SEQ ID NO: 3187); Arg^{34}-GLP-1(7-37) (SEQ ID NO: 3188); Glu^{30}-GLP-1(7-37) (SEQ ID NO: 3189); Lys^{22}-GLP-1(7-37) (SEQ ID NO: 3190); $Gly^{8,36}$,Glu^{22}-GLP-1(7-37) (SEQ ID NO: 3191); Val^{8},Glu^{22},Gly^{36}-GLP-1(7-37) (SEQ ID NO: 3192); $Gly^{8,36}$,Glu^{22},Lys^{33},Asn^{34}-GLP-1(7-37) (SEQ ID NO: 3193); Val^{8},Glu^{22},Lys^{33},Asn^{34},Gly^{36}-GLP-1(7-37) (SEQ ID NO: 3194); $Gly^{8,36}$,Glu^{22},Pro^{37}-GLP-1(7-37) (SEQ ID NO: 3195); Val^{8},Glu^{22},Gly^{36},Pro^{37}-GLP-1(7-37) (SEQ ID NO: 3196); $Gly^{8,36}$,Glu^{22},Lys^{33}, $Asn3^{4}$,Pro^{37}-GLP-1(7-37) (SEQ ID NO: 3197); Val^{8},Glu^{22},Lys^{33},Asn^{34},Gly^{36},Pro^{37}-GLP-1(7-37) (SEQ ID NO: 3198); $Gly^{8,36}$,Glu^{22}-GLP-1(7-36) (SEQ ID NO: 3199); Val^{8},Glu^{22},Gly^{36}-GLP-1(7-36) (SEQ ID NO: 3200); Val^{8},Glu^{22},Asn^{34},Gly^{36}-GLP-1(7-36) (SEQ ID NO: 3201); $Gly^{8,36}$,Glu^{22},Asn^{34}-GLP-1(7-36) (SEQ ID NO: 3202); GLP-1 analog (SEQ ID NO: 3206); GLP-1 analog (SEQ ID NO: 3207); [N^{e}-(17-carboxyheptadecanoic acid)Lys^{20}]exendin-4-NH_2 (SEQ ID NO: 3208); [N^{e}-(17-carboxyhepta-decanoyl)Lys^{32}]exendin-4-NH_2 (SEQ ID NO: 3209); [desaiino-His^{1},N^{e}-(17-carboxyheptadecanoyl)Lys^{20}]exendin-4-NH_2 (SEQ ID NO: 3210); [$Arg^{12,27}$,NLe^{14},N^{e}-(17-carboxy-heptadecanoyl)Lys^{32}]exendin-4-NH_2 (SEQ ID NO: 3211); [N^{e}-(19-carboxy-nonadecanoylamino)Lys^{20}]-exendin-4-NH_2 (SEQ ID NO: 3212); [N^{e}-(15-carboxypentadecanoylamino)Lys^{20}]-exendin-4-NH_2 (SEQ ID NO: 3213); [N^{e}-(13-carboxytridecanoylamino)Lys^{20}]exendin-4-NH_2 (SEQ ID NO: 3214); [N^{e}-(11-carboxy-undecanoyl-amino)Lys^{20}]exendin-4-NH_2 (SEQ ID NO: 3215); exendin-4-Lys^{40}(e-MPA)-NH_2 (SEQ ID NO: 3216); exendin-4-Lys^{40}(e-AEEA-AEEA-MPA)-NH_2 (SEQ ID NO: 3217); exendin-4-Lys^{40}(e-AEEA-MPA)-NH_2 (SEQ ID NO: 3218); exendin-4-Lys^{40}(e-MPA)-albumin (SEQ ID NO: 3219); exendin-4-Lys^{40}(e-AEEA-AEEA-MPA)-albumin (SEQ ID NO: 3220); exendin-4-Lys^{40}(e-AEEA-MPA)-albumin (SEQ ID NO: 3221); desamino-His^{7}, Ar^{26},Lys^{34}(N^{ε}-(γ-Glu(N-a-hexadecanoyl)))-GLP-1(7-37) (core peptide disclosed as SEQ ID NO: 3222) (SEQ ID NO: 3222); desamino-His^{7},Arg^{26},Lys^{34}(N^{ε}-octanoyl)-GLP-1(7-37) (SEQ ID NO: 3223); $Arg^{26,34}$,Lys^{38}(N^{ε}-((o-carboxypentadecanoyl))-GLP-1(7-38) (SEQ ID NO: 3224); $Arg^{26,34}$,Lys^{36}(N^{ε}-(γ-Glu(N-a-hexadecanoyl)))-GLP-1(7-36) (core peptide disclosed as SEQ ID NO: 3225) (SEQ ID NO: 3225); [Aib^{8};Lys^{37}]GLP-1_(7-37) (SEQ ID NO: 3226); [Aib^{8}, Lys^{26}]GLP-1_(7-37) (SEQ ID NO: 3227); [$Aib^{8,22}$;Lys^{36}]GLP-1(7-36)-Amide (SEQ ID NO: 3228); [$Aib^{8,22}$;$BLeu^{32}$;Lys^{36}]GLP-17-36)-Amide (SEQ ID NO: 3229); [$Aib^{8,22}$;Lys^{37}]GLP-1(7-37)-Amide (SEQ ID NO: 3230); [$Aib^{8,22}$;$BLeu^{32}$;Lys^{37}]GLP-1(7-37)-Amide (SEQ ID NO: 3231); [$Aib^{8,22}$;$aMeLeu^{32}$;Lys^{37}]GLP-1(7-37)-Amide (SEQ ID NO: 3232); [$Aib^{8,22}$;$AMEF^{12}$;Lys^{37}]GLP-1(7-37)-Amide (SEQ ID NO: 3233); [$Aib^{8,22}$;$BLeu^{16}$;Lys^{37}]GLP-1(7-37)-Amide (SEQ ID NO: 3234); [$Aib^{8,22}$;Gly^{36};Lys^{37}]GLP-1(7-37)-Amide (SEQ ID NO: 3235); [$Aib^{8,22}$;$Lys^{33,37}$;Asn^{34};Gly^{36}]GLP-1(7-37)-Amide (SEQ ID NO: 3236); [$Aib^{8,22}$;Lys^{33};Asn^{34};Gly^{36};$Aeea^{37}$]GLP-1(7-37)-Aeea-Lys-Amide (SEQ ID NO: 3237); [$Aib^{8,22}$;$Gly3^{6}$]GLP-1(7-37) (SEQ ID NO: 3238); cyclo[E^{23}-K^{27}][Aib^{8};Gly^{36}]GLP-1(7-37) (SEQ ID NO: 3239); cyclo[E^{22}-K^{26}][Aib^{8};Gly^{36};Lys^{37}]GLP-1(7-37)-Amide (SEQ ID NO: 3240); [$Aib^{8,22}$]-GLP-1(7-22)-Ex4(17-39) (SEQ ID NO: 3241); [$Gly^{8,36}$;Glu^{22}]GLP-1(7-37) (SEQ ID NO: 3242); [Aib^{8};Glu^{22};Gly^{36}]GLP-1(7-37)-Amide (SEQ ID NO: 3243); [Aib^{8};$Tyr1^{6}$;Glu^{22};Gly^{36}]GLP-1_(7-37) (SEQ ID NO: 3244); [Aib^{8};$Lys^{18,33}$;$Glu^{22,23,30}$;Val^{25};Arg^{26};Leu^{27};Asn^{34};Gly^{36}]GLP-1(7-37) (SEQ ID NO: 3245); [Aib^{8};$Lys^{18,33}$;$Glu^{22,23,30}$;Leu^{27};Asn^{34};Gly^{36}]GLP-1(7-37) (SEQ ID NO: 3246); [Aib^{8};Lys^{18};$Glu^{22,23,30}$;Leu^{27};Gly^{36}]GLP-1(7-37) (SEQ ID NO: 3247); [$Aib^{8,22}$;Ile^{9};Gly^{36}]GLP-1_(7-36) (SEQ ID NO: 3248); and [$Aib^{8,22}$;Glu^{15};Gly^{36}]GLP-1_(7-36) (SEQ ID NO: 3249).

[0020] In one embodiment, the GLP-1(7-37) or GLP-1(7-37) analog is conjugated to the antibody or fragment thereof at a residue that corresponds to K26, K36, K37, K39 or a C-terminal amine group of said analog.

[0021] In one embodiment, the GLP-1 receptor agonist if conjugated to the antibody or fragment thereof via a peptide linker comprising a sequence selected from the group consisting of $(Gly_3Ser)_2$, $(Gly_4Ser)_2$, $(Gly_3Ser)_3$, $(Gly_4Ser)_3$, $(Gly_3Ser)_4$, $(Gly_4Ser)_4$, $(Gly_3Ser)_5$, $(Gly_4Ser)_5$, $(Gly_3Ser)_6$, and $(Gly_4Ser)_6$.

BRIEF DESCRIPTION OF THE DRAWINGS

[0022]

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

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

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

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

FIGS. 5A-5D. GLP-1 receptor agonist and GIPR Antagonist In vivo Activity of SG12 and 2G10 Chemical Conjugates in C57B16 mice (glucose tolerance test)

FIGS. 6A-6B. GLP-1 receptor agonist and GIPR Antagonist In vivo Activity of SG12 and 2G10 Chemical Conjugates in DIO mice (plasma glucose and change in body weight)

FIG. 7. GLP-1R-GIPR bispecific conjugate 1273 reduces body weight in male spontaneously obese cynomolgus monkeys (% change from baseline)
FIG. 8. GLP-1R-GIPR bispecific conjugate 1273 reduces total energy intake in male spontaneously obese cynomolgus monkeys (% change from baseline)
FIG. 9. GLP-1R-GIPR bispecific conjugate 1273 reduces fasting insulin in male spontaneously obese cynomolgus monkeys (% change from baseline)
FIG. 10. GLP-1R-GIPR bispecific conjugate 1273 reduces fasting triglycerides in male spontaneously obese cynomolgus monkeys (% change from baseline)
FIG. 11. GLP-1R-GIPR bispecific conjugate 1273 reduces fasting total cholesterol in male spontaneously obese cynomolgus monkeys (% change from baseline)
FIG. 12. GLP-1R-GIPR bispecific conjugate 1264 reduces body weight in male spontaneously obese cynomolgus monkeys (% change from baseline)
FIG. 13. GLP-1R-GIPR bispecific conjugate 1264 reduces total energy intake in male spontaneously obese cynomolgus monkeys (% change from baseline)
FIG. 14. GLP-1R-GIPR bispecific conjugate 1264 reduces fasting insulin in male spontaneously obese cynomolgus monkeys (% change from baseline)
FIG. 15. GLP-1R-GIPR bispecific conjugate 1264 reduces fasting triglycerides in male spontaneously obese cynomolgus monkeys (% change from baseline)
FIG. 16. GLP-1R-GIPR bispecific conjugate 1264 reduces fasting total cholesterol in male spontaneously obese cynomolgus monkeys (% change from baseline)
FIG. 17. GLP-1R-GIPR bispecific conjugates 1248 and 1257 reduce body weight in male spontaneously obese cynomolgus monkeys (% change from baseline)
FIG. 18. GLP-1R-GIPR bispecific conjugates 1248 and 1257 reduce total energy intake in male spontaneously obese cynomolgus monkeys (% change from baseline)
FIG. 19. GLP-1R-GIPR bispecific conjugates 1248 and 1257 reduce fasting insulin in male spontaneously obese cynomolgus monkeys (% change from baseline)
FIG. 20. GLP-1R-GIPR bispecific conjugates 1248 and 1257 reduce fasting triglycerides in male spontaneously obese cynomolgus monkeys (% change from baseline)
FIG. 21. GLP-1R-GIPR bispecific conjugates 1248 and 1257 reduce fasting cholesterol in male spontaneously obese cynomolgus monkeys (% change from baseline)
FIGS. 22A-22B. Binding affinity of anti-GIPR/GLP-1R bispecific conjugates
FIG. 23. Anti-GIPR/GLP-1R bispecific conjugate 1248 promotes strong GLP-1R and GIPR internalization in cells expressing both GLP-1R and GIPR
FIGS. 24A-24B. Time course and dose response of anti-GIPR/GLP-1R bispecific conjugates in GLP-1R internalization assay
FIGS. 25A-25D. GLP-1R, GIPR and bispecific conjugate are co-localized upon internalization
FIGS. 26A-26B. Inhibition of receptor internalization reduces 1248-induced cAMP generation
FIGS. 27A-27C. Bispecific conjugates show binding to GLP-1R and GIPR in FACS analysis
FIG. 28. Anti-GIPR/GLP-1R bispecific conjugates stimulate calcium flux
FIGS. 29A-29B. Anti-GIPR/GLP-1R bispecific conjugate 1248 promotes beta-arrestin recruitments through both GLP-1R and GIPR pathways
FIG. 30. Anti-GIPR/GLP-1R bispecific conjugate 1248 stimulates insulin secretion in human pancreatic microislets

DETAILED DESCRIPTION OF THE INVENTION

[0023] The present invention provides a composition comprising a) an antibody or functional fragment thereof that specifically binds to human GIPR, wherein the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid substitution at one or more conjugation site(s); and a GLP-1 receptor agonist, wherein the GLP-1 receptor agonist is conjugated to the antibody or functional fragment thereof through the side-chain of the cysteine residue or non-canonical amino acid residue substituted at the one or more conjugation site(s), wherein the antibody or functional fragment thereof is an antagonist of GIPR, for use in a method of treating a metabolic disorder, such as a disorder of glucose metabolism (e.g. Type 2 diabetes, elevated glucose levels, elevated insulin levels, dyslipidemia, metabolic syndrome (Syndrome X or insulin resistance syndrome), glucosuria, metabolic acidosis, diabetic neuropathy, diabetic nephropathy, diabetic retinopathy, diabetic cardiomyopathy, Type 1 diabetes, obesity and conditions exacerbated by obesity) by blocking or interfering with the biological activity of GIP. Methods of administration and delivery are also provided.

[0024] 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).

[0025] The section headings used herein are for organizational purposes only and are not to be construed as limiting the subject matter described.

[0026] 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.

[0027] 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). 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.

[0028] 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.

[0029] 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%.

[0030] Following convention, as used herein "a" and "an" mean "one or more" unless specifically indicated otherwise.

[0031] 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.

[0032] 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.

[0033] An "amino acid mimetic" is a chemical compound that has a structure that is different from the general chemical structure of an amino acid, but that functions in a manner similar to a naturally occurring amino acid. Examples include a methacryloyl or acryloyl derivative of an amide, β-, γ-, δ-imino acids (such as piperidine-4-carboxylic acid) and the like.

[0034] 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), Nα-methylcitrulline (NMeCit), Nα-methylhomocitrulline (Nα-MeHoCit), ornithine (Orn), Nα-Methylornithine (Nα-MeOrn or NMeOrn), sarcosine (Sar), homolysine (hLys or hK), homoarginine (hArg or hR), homoglutamine (hQ), Nα-methylarginine (NMeR), Nα-methylleucine (Nα-MeL or NMeL), N-methylhomolysine (NMeHoK), Nα-methylglutamine (NMeQ), norleucine (Nle), norvaline (Nva), 1,2,3,4-tetrahydroisoquinoline (Tic), Octahydroindole-2-carboxylic acid (Oic), 3-(1-naphthyl)alanine (1-Nal), 3-(2-naphthyl)alanine (2-Nal), 1,2,3,4-tetrahydroisoquinoline (Tic), 2-indanylglycine (Igl), para-iodophenylalanine (pI-Phe), para-aminophenylalanine (4AmP or 4-Amino-Phe), 4-guanidino phenylalanine (Guf), glycyllysine (abbreviated "K(Nε-glycyl)" or "K(glycyl)" or "K(gly)"), nitrophenylalanine (nitrophe), aminophenylalanine (aminophe or Amino-Phe), benzylphenylalanine (benzylphe), γ-carboxyglutamic acid (y-carboxyglu), hydroxyproline (hydroxypro), p-carboxyl-phenylalanine (Cpa), α-aminoadipic acid (Aad), Nα-methyl valine (NMeVal), N-α-methyl leucine (NMeLeu), Nα-methylnorleucine (NMeNle), cyclopentylglycine (Cpg), cyclohexylglycine (Chg), acetylarginine (acetylarg), α, β-diaminopropionoic acid (Dpr), α, γ-diaminobutyric acid (Dab), diaminopropionic acid (Dap),

cyclohexylalanine (Cha), 4-methyl-phenylalanine (MePhe), β, β-diphenyl-alanine (BiPhA), aminobutyric acid (Abu), 4-phenyl-phenylalanine (or biphenylalanine; 4Bip), α-amino-isobutyric acid (Aib), beta-alanine, beta-aminopropionic acid, piperidinic acid, aminocaprioic acid, aminoheptanoic acid, aminopimelic acid, desmosine, diaminopimelic acid, N-ethylglycine, N-ethylaspargine, hydroxylysine, allo-hydroxylysine, isodesmosine, alloisoleucine, 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.

[0035] 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.

[0036] 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.

[0037] A composition of the present invention that includes a GLP-1 receptor agonist of the invention covalently linked, attached, or bound, either directly or indirectly through a linker moiety, to another an anti-GIPR antigen binding protein of the invention or is a "conjugate" or "conjugated" molecule, whether conjugated by chemical means (e.g., post-translationally or post-synthetically).

[0038] The term "encoding" refers to a polynucleotide sequence encoding one or more amino acids. The term does not require a start or stop codon.

[0039] 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.

[0040] 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.

[0041] Recommended parameters for determining percent identity for polypeptides or nucleotide sequences using the GAP program are the following:

Algorithm: Needleman et al., 1970, J. Mol. Biol. 48:443-453;
Comparison matrix: BLOSUM 62 from Henikoff et al., 1992, supra;
Gap Penalty: 12 (but with no penalty for end gaps)
Gap Length Penalty: 4
Threshold of Similarity: 0

[0042] 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.

[0043] 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 resides and which is encoded by the nucleic acid sequence of SEQ ID NO: 3146, or SEQ ID NO. 3147, which consists of 460 amino acids residues and which is encoded by the nucleic acid sequence of SEQ ID NO: 3148, or SEQ ID NO. 3149, which consists of 230 amino acids residues and which is encoded by the nucleic acid sequence of SEQ ID NO: 3150.

[0044] 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.

[0045] In various embodiments, a GIPR polypeptide comprises an amino acid sequence that is at least about 90 percent identical to a naturally-occurring GIPR polypeptide (e.g., SEQ ID NOs: 3141, 3143 or 3145). In other embodiments, a GIPR polypeptide comprises an amino acid sequence that is at least about 95, 96, 97, 98, or 99 percent identical to a naturally-occurring GIPR polypeptide amino acid sequence (e.g., SEQ ID NOs: 3141, 3143 or 3145). Such GIPR polypeptides preferably, but need not, possess at least one activity of a wild-type GIPR polypeptide, such as the ability to bind GIP. The present invention also encompasses nucleic acid molecules encoding such GIPR polypeptide sequences.

[0046] 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).

[0047] 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).

[0048] The terms "GIP", "Gastric inhibitory polypeptide", "glucose-dependent insulinotropic peptide" and "GIP ligand" are used interchangeably and mean a naturally-occurring wild-type polypeptide expressed in a mammal, such as a human or a mouse, and includes naturally occurring alleles (e.g., naturally occurring allelic forms of human GIP protein). For purposes of this disclosure, the term "GIP" can be used interchangeably to refer to any mature GIP polypeptide.

[0049] The 42 amino acid sequence of mature human GIP is:

YAEGTFISDY SIAMDKIHQQ DFVNWLLAQK GKKNDWKHNI TQ (SEQ ID NO: 3151)

and is encoded by the DNA sequence:

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

[0050] The 42 amino acid sequence of mature murine GIP is:

YAEGTFISDY SIAMDKIRQQ DFVNWLLAQR GKKSDWKHNI TQ (SEQ ID NO: 3153)

and is encoded by the DNA sequence:

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

[0051] The 42 amino acid sequence of mature rat GIP is:

YAEGTFISDY SIAMDKIRQQ DFVNWLLAQK GKKNDWKHNL TQ (SEQ ID NO: 3155)
and is encoded by the DNA sequence:

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

[0052] A "GIPR antagonist" refers to compounds that reduce or inhibit GIP activation of GIPR. Such antagonists include chemically synthesized small molecules and antigen binding proteins.

[0053] 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.

[0054] In general, a GIPR antigen binding protein is said to "specifically bind" its target antigen GIPR when the antigen binding protein exhibits essentially background binding to non-GIPR molecules. An antigen binding protein that specifically binds GIPR may, however, cross-react with GIPR polypeptides from different species. Typically, a GIPR antigen binding protein specifically binds human GIPR when the dissociation constant (KD) is $\leq 10^{-7}$ M as measured via a surface plasma resonance technique (e.g., BIACore, GE-Healthcare Uppsala, Sweden) or Kinetic Exclusion Assay (KinExA, Sapidyne, Boise, Idaho). A GIPR antigen binding protein specifically binds human GIPR with "high affinity" when the KD is $\leq 5\times 10^{-9}$ M, and with "very high affinity" when the KD is $\leq 5\times 10^{-10}$ M, as measured using methods described.

[0055] "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.

[0056] 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.

[0057] 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.

[0058] 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.

[0059] 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.

[0060] 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.

[0061] 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.

[0062] In another embodiment, Fvs, domain antibodies and scFvs, and may be derived from an antibody of the present invention.

[0063] 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.

[0064] 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.

[0065] 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.

[0066] 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.

[0067] 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.

[0068] The "Fv region" comprises the variable regions from both the heavy and light chains, but lacks the constant regions.

[0069] "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.

[0070] 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.

[0071] 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.

[0072] A multispecific antigen binding protein" or "multispecific antibody" is one that targets more than one antigen or epitope.

[0073] 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.

[0074] The term "compete" when used in the context of antigen binding proteins (e.g., antibodies) means competition between antigen binding proteins is determined by an assay in which the antigen binding protein (e.g., antibody or immunologically functional fragment thereof) under test prevents or inhibits specific binding of a reference antigen binding protein to a common antigen (e.g., GIPR or a fragment thereof). Numerous types of competitive binding assays can be

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

[0075] 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.

[0076] 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.

[0077] 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.

[0078] 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.

[0079] 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.

[0080] 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.

[0081] 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, phoshoraniladate and phosphoroamidate.

[0082] 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.

[0083] 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.

[0084] 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."

[0085] 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.

[0086] 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.

[0087] 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.

[0088] 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.

[0089] 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.

[0090] 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 glyc-

oproteins, 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.

[0091] 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.

[0092] 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.

[0093] 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.

[0094] 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.

[0095] A "subject" or "patient" as used herein can be any mammal. In a typical embodiment, the subject or patient is a human.

[0096] 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.

[0097] 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.

[0098] The 466 amino acid sequence of human GIPR is (Volz et al., FEBS Lett. 373:23-29 (1995); NCBI Reference Sequence: NP_0001555):

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

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

ggcagcggtg gcaggggctg caggagcaag tgaccaggag caggactggg
gacaggcctg atcgcccctg cacgaaccag acccttcgcc gccctcacga
tgactacctc tccgatcctg cagctgctgc tgcggctctc actgtgcggg
ctgctgctcc agagggcgga gacaggctct aaggggcaga cggcgggga
gctgtaccag cgctgggaac ggtaccgcag ggagtgccag gagaccttgg
cagccgcgga accgccttca ggcctcgcct gtaacgggtc cttcgatatg
tacgtctgct gggactatgc tgcacccaat gccactgccc gtgcgtcctg
cccctggtac ctgccctggc accaccatgt ggctgcaggt ttcgtcctcc
gccagtgtgg cagtgatggc caatggggac tttggagaga ccatacacaa
tgtgagaacc cagagaagaa tgaggccttt ctggaccaaa ggctcatctt
ggagcggttg caggtcatgt acactgtcgg ctactccctg tctctcgcca
cactgctgct agccctgctc atcttgagtt tgttcaggcg gctacattgc

actagaaact atatccacat caacctgttc acgtctttca tgctgcgagc
tgcggccatt ctcagccgag accgtctgct acctcgacct ggcccctacc
ttggggacca ggcccttgcg ctgtggaacc aggccctcgc tgcctgccgc
acggcccaga tcgtgaccca gtactgcgtg ggtgccaact acacgtggct
gctggtggag ggcgtctacc tgcacagtct cctggtgctc gtgggaggct
ccgaggaggg ccacttccgc tactacctgc tcctcggctg gggggccccc
gcgcttttcg tcattccctg ggtgatcgtc aggtacctgt acgagaacac
gcagtgctgg gagcgcaacg aagtcaaggc catttggtgg attatacgga
cccccatcct catgaccatc ttgattaatt tcctcatttt tatccgcatt
cttggcattc tcctgtccaa gctgaggaca cggcaaatgc gctgccggga
ttaccggctg aggctggctc gctccacgct gacgctggtg cccctgctgg
gtgtccacga ggtggtgttt gctcccgtga cagaggaaca ggcccggggc
gccctgcgct tcgccaagct cggctttgag atcttcctca gctccttcca
gggcttcctg gtcagcgtcc tctactgctt catcaacaag gaggtgcagt
cggagatccg ccgtggctgg caccactgcc gcctgcgccg cagcctgggc
gaggagcaac gccagctccc ggagcgcgcc ttccgggccc tgccctccgg
ctccggcccg ggcgaggtcc ccaccagccg cggcttgtcc tcggggaccc
tcccagggcc tgggaatgag gccagccggg agttggaaag ttactgctag
ggggcgggat ccccgtgtct gttcagttag catggattta ttgagtgcca
actgcgtgcc aggcccagta cggaggacgc tggggaaatg gtgaaggaaa
cagaaaaaag gtccctgccc ttctggagat gacaactgag tggggaaaac
agaccgtgaa cacaaaacat caagttccac acacgctatg gaatggttat
gaagggaagc gagaaggggg cctagggtgg tctgggaggc gtctccaagg
aggtgacact taagccatcc ccgaaagagg tgaaagagat cactttgggg
agagctggag aacaggattc taggcggaag cgatagcata ggcaaaggcc
cttgggcagg aaggcgctca gccttggctg gagtagaatt aagtcagagc
caacaggtgg ggagagacag agaagtgggc aggggcaccc aagttgggat
ttcatttcag gtgcattgga gattcttagg agtgtctctt gggggtaata
ttttattttt taaaaaatga ggat (SEQ ID NO: 3142).

[0099] A 430 amino acid isoform of human GIPR (isoform X1), predicted by automated computational analysis, has the sequence (NCBI Reference Sequence XP_005258790):

MTTSPILQLL LRLSLCGLLL QRAETGSKGQ TAGELYQRWE RYRRECQETL
AAAEPPSVAA GFVLRQCGSD GQWGLWRDHT QCENPEKNEA FLDQRLILER
LQVMYTVGYS LSLATLLLAL LILSLFRRLH CTRNYIHINL FTSFMLRAAA

ILSRDRLLPR PGPYLGDQAL ALWNQALAAC RTAQIVTQYC VGANYTWLLV
EGVYLHSLLV LVGGSEEGHF RYYLLLGWGA PALFVIPWVI VRYLYENTQC
WERNEVKAIW WIIRTPILMT ILINFLIFIR ILGILLSKLR TRQMRCRDYR
LRLARSTLTL VPLLGVHEVV FAPVTEEQAR GALRFAKLGF EIFLSSFQGF
LVSVLYCFIN KEVQSEIRRG WHHCRLRRSL GEEQRQLPER AFRALPSGSG
PGEVPTSRGL SSGTLPGPGN EASRELESYC (SEQ ID NO: 3143)

and is encoded by the DNA sequence:

atgaccacca gcccgattct gcagctgctg ctgcgcctga gcctgtgcgg
cctgctgctg cagcgcgcgg aaaccggcag caaaggccag accgcgggcg
aactgtatca gcgctgggaa cgctatcgcc gcgaatgcca ggaaaccctg
gcggcggcgg aaccgccgag cgtggcggcg ggctttgtgc tgcgccagtg
cggcagcgat ggccagtggg gcctgtggcg cgatcatacc cagtgcgaaa
acccggaaaa aaacgaagcg tttctggatc agcgcctgat tctggaacgc
ctgcaggtga tgtataccgt gggctatagc ctgagcctgg cgaccctgct
gctggcgctg ctgattctga gcctgtttcg ccgcctgcat tgcacccgca
actatattca tattaacctg tttaccagct ttatgctgcg cgcggcggcg
attctgagcc gcgatcgcct gctgccgcgc ccgggcccgt atctgggcga
tcaggcgctg gcgctgtgga accaggcgct ggcggcgtgc cgcaccgcgc
agattgtgac ccagtattgc gtgggcgcga actatacctg gctgctggtg
gaaggcgtgt atctgcatag cctgctggtg ctggtgggcg gcagcgaaga
aggccatttt cgctattatc tgctgctggg ctggggcgcg ccggcgctgt
ttgtgattcc gtgggtgatt gtgcgctatc tgtatgaaaa cacccagtgc
tgggaacgca acgaagtgaa agcgatttgg tggattattc gcaccccgat
tctgatgacc attctgatta actttctgat ttttattcgc attctgggca
ttctgctgag caaactgcgc acccgccaga tgcgctgccg cgattatcgc
ctgcgcctgg cgcgcagcac cctgaccctg gtgccgctgc tgggcgtgca
tgaagtggtg tttgcgccgg tgaccgaaga acaggcgcgc ggcgcgctgc
gctttgcgaa actgggcttt gaaatttttc tgagcagctt tcagggcttt
ctggtgagcg tgctgtattg ctttattaac aaagaagtgc agagcgaaat
tcgccgcggc tggcatcatt gccgcctgcg ccgcagcctg ggcgaagaac
agcgccagct gccggaacgc gcgtttcgcg cgctgccgag cggcagcggc
ccgggcgaag tgccgaccag ccgcggcctg agcagcggca ccctgccggg
cccgggcaac gaagcgagcc gcgaactgga aagctattgc (SEQ ID NO: 3144).

[0100] 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):

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

and is encoded by the DNA sequence:

atgaccacca gcccgattct gcagctgctg ctgcgcctga gcctgtgcgg
cctgctgctg cagcgcgcgg aaaccggcag caaaggccag accgcgggcg
aactgtatca gcgctgggaa cgctatcgcc gcgaatgcca ggaaaccctg
gcggcggcgg aaccgccgag cggcctggcg tgcaacggca gctttgatat
gtatgtgtgc tgggattatg cggcgccgaa cgcgaccgcg cgcgcgagct
gcccgtggta tctgccgtgg catcatcatg tggcggcggg ctttgtgctg
cgccagtgcg gcagcgatgg ccagtggggc ctgtggcgcg atcataccca
gtgcgaaaac ccggaaaaaa acgaagcgtt tctggatcag cgcctgattc
tggaacgcct gcaggtgatg tataccgtgg gctatagcct gagcctggcg
accctgctgc tggcgctgct gattctgagc ctgtttcgcc gcctgcattg
cacccgcaac tatattcata ttaacctgtt taccagcttt atgctgcgcg
cggcggcgat tctgagccgc gatcgcctgc tgccgcgccc gggcccgtat
ctgggcgatc aggcgctggc gctgtggaac caggcgctgg cggcgtgccg
caccgcgcag attgtgaccc agtattgcgt gggcgcgaac tatacctggc
tgctggtgga aggcgtgtat ctgcatagcc tgctggtgct ggtgggcggc
agcgaagaag gccattttcg ctattatctg ctgctgggct ggggcgcgcc
ggcgctgttt gtgattccgt gggtgattgt gcgctatctg tatgaaaaca
cccagtgctg ggaacgcaac gaagtgaaag cgatttggtg gattattcgc
accccgattc tgatgaccat tctgattaac tttctgattt ttattcgcat
tctgggcatt ctgctgagca aactgcgcac ccgccagatg cgctgccgcg

attatcgcct gcgcctggcg cgcagcaccc tgaccctggt gccgctgctg
ggcgtgcatg aagtggtgtt tgcgccggtg accgaagaac aggcgcgcgg
cgcgctgcgc tttgcgaaac tgggctttga aatttttctg agcagctttc
agggctttct ggtgagcgtg ctgtattgct ttattaacaa agaagtgggc
cgcgatccgg cggcggcgcc ggcgctgtgg cgccgccgcg gcaccgcgcc
gccgctgagc gcgattgtga gccaggtgca gagcgaaatt cgccgcggct
ggcatcattg ccgcctgcgc cgcagcctgg gcgaagaaca gcgccagctg
ccggaacgcg cgtttcgcgc gctgccgagc ggcagcggcc cgggcgaagt
gccgaccagc cgcggcctga gcagcggcac cctgccgggc ccgggcaacg
aagcgagccg cgaactggaa agctattgct aa (SEQ ID NO: 3146)

[0101] 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.

MPLRLLLLLL WLWGLQWAET DSEGQTTTGE LYQRWEHYGQ ECQKMLETTE
PPSGLACNGS FDMYACWNYT AANTTARVSC PWYLPWFRQV SAGFVFRQCG
SDGQWGSWRD HTQCENPEKN GAFQDQTLIL ERLQIMYTVG YSLSLTTLLL
ALLILSLFRR LHCTRNYIHM NLFTSFMLRA AAILTRDQLL PPLGPYTGDQ
APTPWNQALA ACRTAQIMTQ YCVGANYTWL LVEGVYLHHL LVIVGRSEKG
HFRCYLLLGW GAPALFVIPW VIVRYLRENT QCWERNEVKA IWWIIRTPIL
ITILINFLIF IRILGILVSK LRTRQMRCPD YRLRLARSTL TLVPLLGVHE
VVFAPVTEEQ VEGSLRFAKL AFEIFLSSFQ GFLVSVLYCFINKEVQSEIRQ
GWRHRRLRLS LQEQRPRPHQ ELAPRAVPLS SACREAAVGN ALPSGMLHVP
GDEVLESYC (SEQ ID NO: 3147)

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

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

tattcatatg aacctgttta ccagctttat gctgcgcgcg gcggcgattc
tgacccgcga tcagctgctg ccgccgctgg gcccgtatac cggcgatcag
gcgccgaccc cgtggaacca ggcgctggcg gcgtgccgca ccgcgcagat
tatgacccag tattgcgtgg gcgcgaacta tacctggctg ctggtggaag
gcgtgtatct gcatcatctg ctggtgattg tgggccgcag cgaaaaaggc
cattttcgct gctatctgct gctgggctgg ggcgcgccgg cgctgtttgt
gattccgtgg gtgattgtgc gctatctgcg cgaaaacacc cagtgctggg
aacgcaacga agtgaaagcg atttggtgga ttattcgcac cccgattctg
attaccattc tgattaactt tctgattttt attcgcattc tgggcattct
ggtgagcaaa ctgcgcaccc gccagatgcg ctgcccggat tatcgcctgc
gcctggcgcg cagcaccctg accctggtgc cgctgctggg cgtgcatgaa
gtggtgtttg cgccggtgac cgaagaacag gtggaaggca gcctgcgctt
tgcgaaactg gcgtttgaaa tttttctgag cagctttcag ggctttctgg
tgagcgtgct gtattgcttt attaacaaag aagtgcagag cgaaattcgc
cagggctggc gccatcgccg cctgcgcctg agcctgcagg aacagcgccc
gcgcccgcat caggaactgg cgccgcgcgc ggtgccgctg agcagcgcgt
gccgcgaagc ggcggtgggc aacgcgctgc cgagcggcat gctgcatgtg
ccgggcgatg aagtgctgga aagctattgc taa (SEQ ID NO: 3148)

[0102] 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):

MPLRLLLLLL WLWGLQWAET DSEGQTTTGE LYQRWEHYGQ ECQKMLETTE
PPSGLACNGS FDMYACWNYT AANTTARVSC PWYLPWFRQV SAGFVFRQCG
SDGQWGSWRD HTQCENPEKN GAFQDQTLIL ERLQIMYTVG YSLSLTTLLL
ALLILSLFRR LHCTRNYIHM NLFTSFMLRA AAILTRDQLL PPLGPYTGDQ
APTPWNQVLH RLLPGGTKTF PIYFRTFPHH (SEQ ID NO: 3149)

and is encoded by the DNA sequence:

atgccgctgc gcctgctgct gctgctgctg tggctgtggg gcctgcagtg
ggcggaaacc gatagcgaag gccagaccac caccggcgaa ctgtatcagc
gctgggaaca ttatggccag gaatgccaga aaatgctgga aaccaccgaa
ccgccgagcg gcctggcgtg caacggcagc tttgatatgt atgcgtgctg
gaactatacc gcggcgaaca ccaccgcgcg cgtgagctgc ccgtggtatc
tgccgtggtt tcgccaggtg agcgcgggct ttgtgtttcg ccagtgcggc
agcgatggcc agtggggcag ctggcgcgat catacccagt gcgaaaaccc

ggaaaaaaac ggcgcgtttc aggatcagac cctgattctg gaacgcctgc
agattatgta taccgtgggc tatagcctga gcctgaccac cctgctgctg
gcgctgctga ttctgagcct gtttcgccgc ctgcattgca cccgcaacta
tattcatatg aacctgttta ccagctttat gctgcgcgcg gcggcgattc
tgacccgcga tcagctgctg ccgccgctgg gcccgtatac cggcgatcag
gcgccgaccc cgtggaacca ggtgctgcat cgcctgctgc cgggcggcac
caaaaccttt ccgatttatt ttcgcacctt tccgcatcat taa (SEQ ID NO: 3150).

[0103] As stated herein, the term "GIPR polypeptide" encompasses naturally occurring GIPR polypeptide sequences, e.g., human amino acid sequences SEQ ID NOs: 3141, 3143 or 3145. The term "GIPR polypeptide," however, also encompasses polypeptides comprising an amino acid sequence that differs from the amino acid sequence of a naturally occurring GIPR polypeptide sequence, e.g., SEQ ID NOs: 3141, 3143 or 3145, by one or more amino acids, such that the sequence is at least 90% identical to SEQ ID NOs: 3141, 3143 or 3145. GIPR polypeptides can be generated by introducing one or more amino acid substitutions, either conservative or non-conservative and using naturally or non-naturally occurring amino acids, at particular positions of the GIPR polypeptide.

[0104] 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.

[0105] Naturally occurring residues can be divided into classes based on common side chain properties:

(1) hydrophobic: norleucine, Met, Ala, Val, Leu, Ile;
(2) neutral hydrophilic: Cys, Ser, Thr;
(3) acidic: Asp, Glu;
(4) basic: Asn, Gln, His, Lys, Arg;

(5) residues that influence chain orientation: Gly, Pro; and
(6) aromatic: Trp, Tyr, Phe.

[0106] 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).

[0107] 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.

[0108] 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).

[0109] 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.

[0110] 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.

[0111] 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.

[0112] 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.

[0113] 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.

[0114] 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.

[0115] 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.

[0116] 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.

[0117] 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.

[0118] 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 is it naturally expressed or it can be isolated from a cell that has been engineered to express GIPR, for example a cell that does not naturally express GIPR.

[0119] 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.

[0120] 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.

[0121] In one aspect the present invention is directed to a composition comprising an antibody or functional fragment thereof that specifically binds to human GIPR, wherein the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s), and wherein the antibody or functional fragment thereof is an antagonist of GIPR; and a GLP-1 receptor agonist, wherein the GLP-1 receptor agonist is conjugated to the antibody or functional fragment thereof through the side-chain of the cysteine residue or non-canonical amino acid residue substituted at the one or more conjugation site(s).

[0122] 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.

[0123] 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.

[0124] 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.

[0125] 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.

[0126] 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.

[0127] 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.

[0128] 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:

(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.
(b) ability to decrease blood glucose;
(c) ability to increase glucose tolerance;
(d) ability to increase insulin sensitivity;
(e) ability to decrease body weight or reduce body weight gain;
(f) ability to decrease fat mass or decrease inflammation in fat tissue;
(g) ability to decrease fasting insulin levels;
(h) ability to decrease circulating cholesterol levels;
(i) ability to decrease circulating triglyceride levels;
(j) ability to decrease liver steatosis or reduce triglyceride level in liver;
(k) decrease AST, ALT, and/or ALP levels.

[0129] In one embodiment, a GIPR antigen binding protein has one or more of the following activities:

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

[0130] Some antigen binding proteins that are provided have an on-rate (ka) for GIPR of at least 10^4/ M × seconds, at least 10^5/M × seconds, or at least 10^6/M × 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 kd (off-rate) of 1×10^{-2} s^{-1} , or 1×10^{-3} s^{-1} , or 1×10^{-4} s^{-1} , or 1×10^{-5} s^{-1} . In certain embodiments, the antigen binding protein has a KD (equilibrium binding affinity) of less than 25 pM, 50 pM, 100 pM, 500 pM, 1 nM, 5 nM, 10 nM, 25 nM or 50 nM.

[0131] 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.

[0132] 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.

[0133] 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. The variable regions of each light/heavy chain pair typically form the antigen binding site.

[0134] 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.

[0135] 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.

[0136] 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.

[0137] 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

(continued)

Identifier	Construct	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
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

(continued)

Identifier	Construct	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
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

(continued)

Identifier	Construct	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
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

(continued)

Identifier	Construct	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
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

(continued)

Identifier	Construct	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
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

(continued)

Identifier	Construct	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
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

(continued)

Identifier	Construct	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
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

(continued)

Identifier	Construct	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
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

(continued)

Identifier	Construct	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
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

(continued)

Identifier	Construct	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
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

(continued)

Identifier	Construct	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
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 GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT CTGGAAGTAGCTCCAACATCGGAAGTAATACTG TAAACTGGTACCAGCACCTCCCAGGAACGGCCC CCAAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATGACAGCCTGAATGGTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT	CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCCGGATACACCTTCACCGGCTACTAT ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG CTTGAGTGGATGGGATGGATCAACCCTAACAGT GGTGGCACAAACTATGCACAGAAGTTTCAGGGC AGGGTCACCATGACCAGGGACACGTCCATCAGT ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT GACGACACGGCCGTGTATTACTGTGCGAGAGGG GGGGATTACGTTTGGGGGACTTATCGGCCTCAC TACTACTACGGTATGGACGTCTGGGGCCAAGGG ACCACGGTCACCGTCTCCTCA
			SEQ ID NO: 1571	SEQ ID NO: 1728
		AA	QSVLTQPPSASGTPGQRVTISCSGSSNIGSNTVNW YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDDSLNGPVFGGGTK LTVLG	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG GDYVWGTYRPHYYYGMDVWGQGTTVTVSS
			SEQ ID NO: 1	SEQ ID NO: 158
iPS:335914	4B1	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCGCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGGAA GTAATGAAAACTATGCAGACTCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAATA CGCTGTATCTGCACATGAACAGCCTGAGAGTCG CGGACACGGCTGTGTATTATTGTGCGCGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1572	SEQ ID NO: 1729

iPS:335938	6H1	AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR
			SEQ ID NO: 2
		NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCGCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGA
			SEQ ID NO: 1573
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR
			SEQ ID NO: 3
iPS:335941	2F11	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTAGCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTACGATGCATCCAATTTGGAAA CAGGGGTCCCATCAAGGTTCAGTGGAAGTGGAT CTGGGACAGATTTTAGTTTCACCATCAGCAGCCT GCAGCCTGAAGATATTGCAACATATTACTGTCA ACAGTATGATATTCTCCTCACTTTCGGCGGAGG GACCAAGGTGGAGATCAAGCGA
			SEQ ID NO: 1574
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDGSNENYADSVKG RFTISRDNSKNTLYLHMNSLRVADTAVYYCARDG TIFGVVLGDYWGQGTLVTVSS
			SEQ ID NO: 159
		NA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCCGGATTCACCTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGGAA GTAATAAATACTATGCAGACTCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTTGGAGTGCTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1730
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAVIWYDGSNKYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGTLVTVSS
			SEQ ID NO: 160
		NA	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGTTATATGGTATGATGGA AGTAATAAATACTATGCAGACTCCGTGAAGGGC CGATTCACCATCTCCAGCGACAATTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT AGGACGATTTTTGGAGTGGTTCTTGACTACTGG GGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1731

iPS:333970	5C2	AA	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW YQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTD FSFTISSLQPEDIATYYCQQYDILLTFGGGTKVEIKR
			SEQ ID NO: 4
		NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAGCAG CAACCAGGACATCCTCCTAAGCTGCTCATTTACT GGGCATCTACCCGGGAATCCGGGTCCCTGACC GATTCAGTGGCAGCGGGTCTGGGACAGATTTCA CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCGGCCAAGGGACCAAGGTGGA AATCAAACGA
			SEQ ID NO: 1575
		AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK NYIAWYQQPGHPPKLLIYWASTRESGVPDRFSGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKR
			SEQ ID NO: 5
iPS:333978	13H12	NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAGCAG AAACCAGGACATCCTCCTCCTAAGCTGCTCATTTACT GGGCATCTACCCGGGAATCCGGGTCCCTGACC GATTCAGTGGCAGCGGGTCTGGGACAGATTTCA CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCGGCCAAGGGACCAAGGTGGA AATCAAACGA
			SEQ ID NO: 1576

			QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGM HWVRQAPGKGLEWVAVIWYDGSNKYYADSVKG RFTISSDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLDYWGQGTLVTVSS
			SEQ ID NO: 161
			CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCGGCTACTAT ATCCACTGGGTGCGACAGGCCCCTGGACAAGGG CTTGAGTGGATGGGGTGGATCAACCCTGACAGT GGTGGCACAGACTATTCACAGAGGTTTCAGGGC AGGTTCACCATGACCAGGGACACGTCCATCAGC ACAGCCTACATGGAACTGAACAGGCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAG GCCACGATTTTTTGGAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT CCTCA
			SEQ ID NO: 1732
			QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWINPDSGGTDYSQRFQGR FTMTRDTSISTAYMELNRLRSDDTAVYYCAREATI FGMVIVPFDYWGQGTLVTVSS
			SEQ ID NO: 162
			CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCGGCTACTAT ATCCACTGGGTGCGACAGGCCCCTGGACAAGGA CTTGAGTGGATGGGGTGGATCAACCCTGACAGT GGTGGCACAGACTATTCACAGAGGTTTCAGGGC AGGTTCACCATGACCAGGGACACGTCCATCAGC ACAGCCTACATGGAACTGAGCAGGCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAG GCCACGATTTTTTGGAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT CCTCA
			SEQ ID NO: 1733

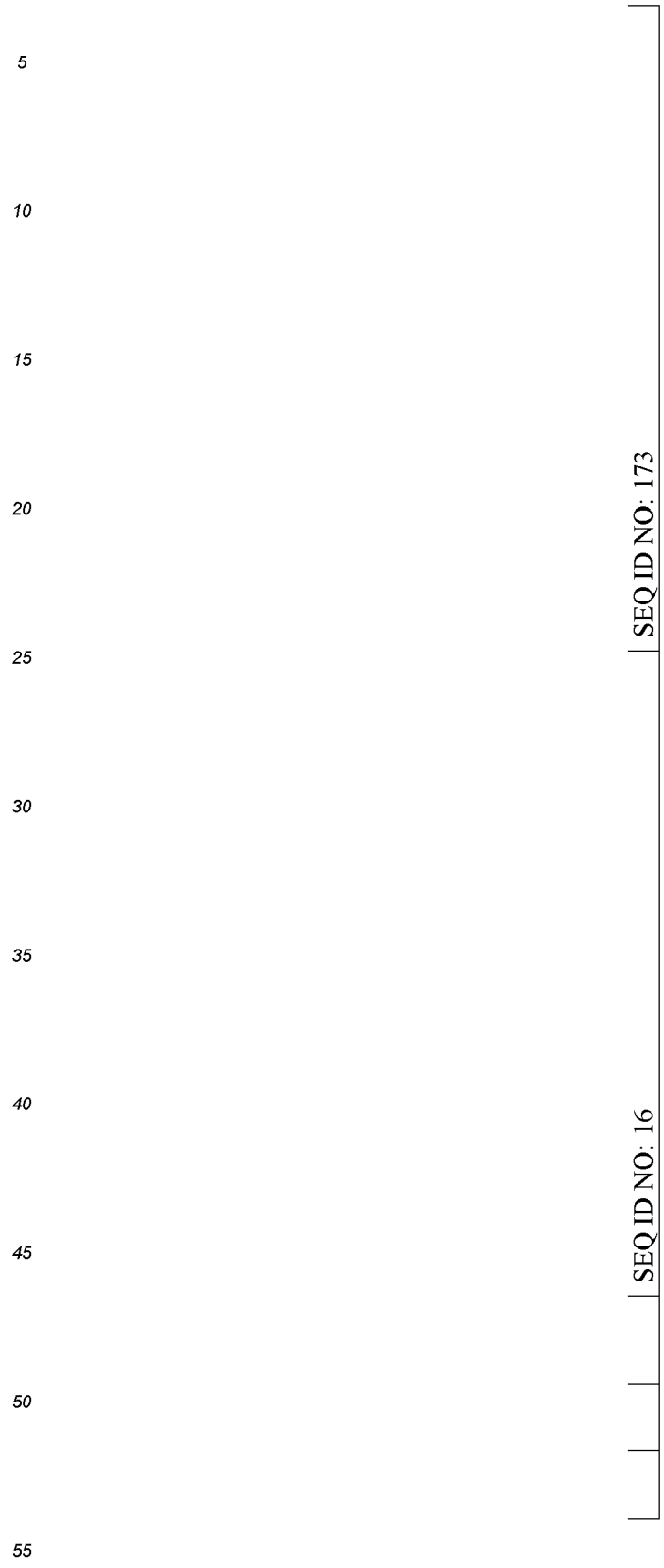
iPS:335986	11C1	AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK NYIAWYQQKPGHPPKLLIYWASTRESGVPDRFSGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKR
			SEQ ID NO: 6
		NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC AACAATAAGAACTACTTAGCTTGGTACCAACAG AAACCAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTCAGCAATATTATCGTA CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG AAATCAAACGA
			SEQ ID NO: 1577
		AA	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK NYLAWYQQKPGQPPNLLIYWTSTRDSGVPDRFSG SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR
			SEQ ID NO: 7
iPS:335994	12H11	NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC AACAATAAGAACTACTTAGCTTGGTACCAGCAG AAACCAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTCAGCAATATTATCGTA CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG AAATCAAACGA	CAGGTGCCGCTGGTACAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCGGCTACTAT ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG CTTGAGTGGATGGGGTGGATAAGCCCTAACAAT GGTGACACAAACTATGCACAGAAGTTTCAGGAC AGGGTCACCATGACCAGGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGACTGAGATCT GACGACACGGCCGTGTATTTCTGTACGAGAG GCCACGATTTTTGGAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT CCTCA
			SEQ ID NO: 1734
		AA	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLVWMGWISPNSGDTSYAQKFQDR VTMTRDTSISTAYMELSRLRSDDTAVYFCTREATI FGMLIVPFDYWGQGTLVTVSS
			SEQ ID NO: 164
		NA	CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCGGCTACTAT ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG CTTGAGTGGATGGGGTGGATAAGCCCTAACAAT GGTGACACAAACTATGCACAGAAGTTTCAGGAC AGGGTCACCATGACCAGGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGACTGAGATCT GACGACACGGCCGTGTATTACTGTACGAGAGAG GCCACGATTTTTGGAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT CCTCA
			SEQ ID NO: 1735

IPS:336024	18E3	AA	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK NYLAWYQQKPGQPPNLLIYWTSTRDSGVPDRFSG SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR
		NA	SEQ ID NO: 8 GAAATTGTGTTGACGCAGTCTCCAGGCACCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG GGTCTGGGACAGACTTCACTCTCACCATCAGCA GACAGGAGCCTGATGATTTTGCAGTGTATTACT GTCAGCAGTATGGTAGTTCACCGCTCACTTTCGG CGGAGGGACCAAGGTGGAGATCAAACGA
		AA	SEQ ID NO: 1579 EIVLTQSPGTLSLSPGERATLSCRASQSISYSYLAW YQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF TLTISRQEPDDFAVYYCQQYGSSPLTFGGGTKVEI KR
		NA	SEQ ID NO: 9 GAAATAGTGATGACGCAGTCTCCAGCCACCCTG TCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCC TGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGCAGCCACCAGGGCC ACTGGTATCCCAGCCAGGGTCAGTGGCAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGCAGTCTGAAGATTTTGCAGTTTATTACTGTC AGCAGTATAATAACTGGCCTCTCACTTTCGGCG GAGGGACCAAGGTGGAGATCAAACGA
IPS:336041	2G10_LC1	AA	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWISPNNGDTNYAQKFQD RVTMTRDTSISTAYMELSRLRSDDTAVYYCTREA TIFGMLIVPFDYWGQGTLVTVSS
		NA	SEQ ID NO: 165 CAGGTGCAGTTGCAGGAGTCGGGCCCAGGACTG GTGAAGCCTTCACAGACCCTGTCCCTCACCTGC ACTGTCTCTGGTGACTCCATCAGCAGTGGTGGTTT ACTACTGGAGCTGGATCCGCCAGCACCCAGGGA AGGGCCTGGAGTGGATTGGGTACATCTATTACA GTGGGAGCACCTACTACAACCCGTCCCTCAAGA GTCGAGTTACCATATCAGTAGACACGTCTAAGA ACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC CGCGGACACGGCCGTGTATTACTGTGCGAGAGA TCGTATTACGATTTTTGGAGTGGTTATGGGGGGC GGTATGGACGTCTGGGGCCAAGGGACCACGGTC ACCGTCTCCTCA
		AA	SEQ ID NO: 1736 QVQLQESGPGLVKPSQTLSLTCTVSGDSISSGGYY WSWIRQHPGKGLEWIGYIYYSGSTYYNPSLKSRVT ISVDTSKNQFSLKLSSVTAADTAVYYCARDRITIFG VVMGGGMDVWGQGTTVTVSS
		NA	SEQ ID NO: 166 CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACCTTCAGTAACTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCGAGGGG CTGGAGTGGGTGGCAGCTATATGGTTTGATGGA AGTGATAAATACTATGCAGACTCCGTGAAGGGC CGATTCACCATCTCCAGAGACAACTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGGCGATTTTTGGAGTGGTCCCCGACTACTGG GGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1737

		AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGM HWVRQAPGEGLEWVAAIWFDGSDKYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGTLVTVSS
		NA	SEQ ID NO: 167 CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGGAA GTAATAAATACTATGCAGACTCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTTGGAGTGCTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
		AA	SEQ ID NO: 168 QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAVIWYDGSNKYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGTLVTVSS
		NA	SEQ ID NO: 169 CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCTCCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGCTATATGGTGATGGAA ATAATAAATACTATGCAGACTCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATC GGACGATTTTTGGAGTGGTCCTTGAGTACCTCG GCCAGGGAACCCTGGTCACCGTCTCCTCA
		AA	SEQ ID NO: 170 QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAAIWYDGNNKYYADSVKG

		FTFTISSLQPEDIATYYCQQYDDLFTFGPGTKVDIK R	RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYLGQGTLVTVSS
		SEQ ID NO: 12	SEQ ID NO: 169
iPS:336099	17H11.004	NA	GACATCCAGATGACCCAGTCTCCATCTTCCGTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GTCGGGCGAGTCAGGGTCTTATCATCTGGTTAG CCTGGTATCAGCAGAAACCGGGGAAAGCCCCTA AACTCCTGATCTATGCTGCATCCAGTTTGCAAAG TGGGGTCCCATCAAGGTTCAGCGGCAGTGGCTC TGGGACAGATTTCACTCTCACCATCAGCAGCCT ACAGCCTGAAGATTTTGCAACTTACTATTGTCAA CAGACTAACAGTTTCCCTCCGACGTTCGGCCAA GGGACCAAGGTGGAAATCAAACGA
		AA	DIQMTQSPSSVSASVGDRVTITCRASQGLIIWLAW YQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTD FTLTISSLQPEDFATYYCQQTNSFPPTFGQGTKVEI KR
		SEQ ID NO: 13	SEQ ID NO: 170
iPS:359621	17H11.004.001	NA	GACATCCAGATGACCCAGTCTCCATCTTCCGTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GTCGGGCGAGTCAGGGTCTTATCATCTGGTTAG CCTGGTATCAGCAGAAACCGGGGAAAGCCCCTA AACTCCTGATCTATGCTGCATCCAGTTTGCAAAG TGGGGTCCCATCAAGGTTCAGCGGCAGTGGCTC TGGGACAGATTTCACTCTCACCATCAGCAGCCT ACAGCCTGAAGATTTTGCAACTTACTATTGTCAA CAGACTAACAGTTTCCCTCCGACGTTCGGCCAA GGGACCAAGGTGGAAATCAAACGA
		AA	DIQMTQSPSSVSASVGDRVTITCRASQGLIIWLAW YQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTD
		SEQ ID NO: 1584	SEQ ID NO: 1741
			QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWS WIRQPAGKGLEWIGRIYTSGSTNYNPSLKSRVTMS

		FTLTISSLQPEDFATYYCQQTNSFPPTFGQGTKVEI KR	IDTSKNQFSLKLNSVTAADTAVYYCARDVAVAGF DYWGQGTLVTVSS
iPS:359781	4H9.004.001	SEQ ID NO: 14	SEQ ID NO: 171
	NA	GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGGCATTAGAAATGAGTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCATCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAGTTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTTGTAACTTATTACTGTCT ACAGCATAATAGTTACCCATTCACTTTCGGCCA AGGGACCAAAGTGGATGTCAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTTGGAGTGCTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
	AA	SEQ ID NO: 1585	SEQ ID NO: 1742
		DIQMTQSPSSLSASVGDRVTITCRASQGIRNELGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFVTYYCLQHNSYPFTFGQGTKVD VKR	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGTLVTVSS
iPS:360929	4H9.004.002	SEQ ID NO: 15	SEQ ID NO: 172
	NA	GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGGCATTAGAAATGAGTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCATCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAGTTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTTGTAACTTATTACTGTCT ACAGCATAATAGTTACCCATTCACTTTCGGCCA AGGGACCAAAGTGGATGTCAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATAAATACTATGCAGACTCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTTGGAGTGCTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
	AA	SEQ ID NO: 1586	SEQ ID NO: 1743
		DIQMTQSPSSLSASVGDRVTITCRASQGIRNELGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFVTYYCLQHNSYPFTFGQGTKVD VKR	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAVIWYDASNKYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGTLVTVSS


SEQ ID NO: 173
SEQ ID NO: 16

IPS:360936	4H9.004.003	
	NA	GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGGCATTAGAAATGAGTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCATCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAGTTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTTGTAACTTATTACTGTCT ACAGCATAATAGTTACCCATTCACTTTCGGCCA AGGGACCAAAGTGGATGTGTCAAACGA
		SEQ ID NO: 1587
	AA	DIQMTQSPSSLSASVGDRVTITCRASQGIRNELGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFVTYYCLQHNSYPFTFGQGTKVD VKR
		SEQ ID NO: 17
IPS:360943	4H9.004.004	
	NA	GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGGCATTAGAAATGAGTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCATCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAGTTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTTGTAACTTATTACTGTCT ACAGCATAATAGTTACCCATTCACTTTCGGCCCT GGGACCAAAGTGGATGTGTCAAACGA
		SEQ ID NO: 1588
	AA	DIQMTQSPSSLSASVGDRVTITCRASQGIRNELGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFVTYYCLQHNSYPFTFGPGTKVDV KR
		SEQ ID NO: 1745
		CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGGAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTTGGAGTGCTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
		SEQ ID NO: 1744
		QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAVIWYDGSNKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGTLVTVSS

IPS:360949	4H9.004.005	NA	SEQ ID NO: 18
			GACATTCAGATGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTGTAGGAGACAGAGTCACCATCACTT
			GCCGGGCAAGTCAGGGCATTAGAAATGAGTTAG
			GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA
			AACGCCTGATCTATGGTGCATCCAGTTTGCAAA
			GTGGGGTCCCATCAAGGTTCAGCGGCAGTGGAT
			CTGGGACAGAGTTCACTCTCACAATCAGCAGCC
			TGCAGCCTGAAGATTTTGTAACTTATTACTGTCT
			ACAGCATAATAGTTACCCATTCACTTTCGGCCA
			AGGGACCAAAGTGGATGTGTCAAACGA
		AA	SEQ ID NO: 1589
			DIQMTQSPSSLSASVGDRVTITCRASQGIRNELGW
			YQQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTE
			FTLTISSLQPEDFVTYYCLQHNSYPFTFGQGTKVD
			VKR
IPS:359761	4H9.004.006	NA	SEQ ID NO: 19
			GACATTCAGATGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTGTAGGAGACAGAGTCACCATCACTT
			GCCGGGCAAGTCAGGGCATTAGAAATGAGTTAG
			GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA
			AACTCCTGATCTATGGTGCATCCAGTTTGCAAA
			GTGGGGTCCCATCAAGGTTCAGCGGCAGTGGAT
			CTGGGACAGAGTTCACTCTCACAATCAGCAGCC
			TGCAGCCTGAAGATTTTGTAACTTATTACTGTCT
			ACAGCATAATAGTTACCCATTCACTTTCGGCCA
			AGGGACCAAAGTGGATGTCAAACGA
		AA	SEQ ID NO: 1590
			DIQMTQSPSSLSASVGDRVTITCRASQGIRNELGW
			YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE
			FTLTISSLQPEDFVTYYCLQHNSYPFTFGQGTKVD
			VKR
			SEQ ID NO: 175
			CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
			GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA
			TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC
			TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
			GTAATAAATACTATGCAGACGCCGTGAAGGGCC
			GCTTCACCATCTCCAGAGACAATTCCAAGAACA
			CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
			AGGACACGGCTGTGTATTACTGTGCGCGAGATG
			GGACGATTTTTGGAGTGCTCTTGGGGGACTACT
			GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1746
			QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM
			HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG
			RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG
			TIFGVLLGDYWGQGTLVTVSS
			SEQ ID NO: 176
			CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
			GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA
			TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC
			TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
			GTAATAAATACTATGCAGACGCCGTGAAGGGCC
			GCTTCACCATCTCCAGAGACAATTCCAAGAACA
			CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
			AGGACACGGCTGTGTATTACTGTGCGCGAGATA
			GGACGATTTTTGGAGTGCTCTTGGGGGACTACT
			GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1747
			QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM
			HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG
			RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR
			TIFGVLLGDYWGQGTLVTVSS

iPS:360955	4B1.010	NA	SEQ ID NO: 20
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTATAGGAGACAGAGTCACCATCACTT
			GCCGGGCAAGTCAGGACATTAGAGATTATTTAG
			GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA
			AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA
			GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT
			CTGGGACAGAATTCACTCTCACAATCAGCAGCC
			TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT
			ACAGCATAATAATACCCCTTCACTTTCGGCCAA
			GGGACCAAAGTGGATATCAAACGA
			SEQ ID NO: 1591
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY
			QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFT
			LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK
			R
			SEQ ID NO: 21
iPS:360962	4B1.011	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTATAGGAGACAGAGTCACCATCACTT
			GCCGGGCAAGTCAGGACATTAGAGATTATTTAG
			GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA
			AGCGCCTGATCTATGGTGCATCCAGTTTGCAAA
			GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT
			CTGGGACAGAATTCACTCTCACAATCAGCAGCC
			TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT
			ACAGCATAATAATTACCCCTTCACTTTCGGCCAA
			GGGACCAAAGTGGATATCAAACGA
			SEQ ID NO: 1592
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY
			QQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTEFT
			LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK
			R
			SEQ ID NO: 177
			CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
			GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA
			TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC
			TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
			GTAATGAAAACTATGCAGACGCCGTGAAGGGCC
			GATTCACCATCTCCAGAGACAATTCCAAGAATA
			CGCTGTATCTGCAAATGAACAGCCTGAGAGTCG
			CGGACACGGCTGTGTATTATTGTGCGCGAGATG
			GGACGATCTTTGGAGTGGTCTTGGGGGACTACT
			GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1748
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM
			HWVRQAPGKGLEWVAVIWYDASNENYADAVKG
			RFTISRDNSKNTLYLQMNSLRVADTAVYYCARDG
			TIFGVVLGDYWGQGTLVTVSS
			SEQ ID NO: 178
		NA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
			GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA
			TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC
			TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
			GTAATGAAAACTATGCAGACGCCGTGAAGGGCC
			GATTCACCATCTCCAGAGACAATTCCAAGAATA
			CGCTGTATCTGCAAATGAACAGCCTGAGAGTCG
			CGGACACGGCTGTGTATTATTGTGCGCGAGATG
			GGACGATCTTTGGAGTGGTCTTGGGGGACTACT
			GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1749
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM
			HWVRQAPGKGLEWVAVIWYDASNENYADAVKG
			RFTISRDNSKNTLYLQMNSLRVADTAVYYCARDG
			TIFGVVLGDYWGQGTLVTVSS

IPS:360968	4B1.012	NA	SEQ ID NO: 22
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTATAGGAGACAGAGTCACCATCACTT
			GCCGGGCAAGTCAGGACATTAGAGATTATTTAG
			GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA
			AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA
			GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT
			CTGGGACAGAATTCACTCTCACAATCAGCAGCC
			TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT
			ACAGCATAATAATACCCCTTCACTTTCGGCCCT
			GGGACCAAAGTGGATATCAAACGA
			SEQ ID NO: 1593
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY
			QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFT
			LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR
			SEQ ID NO: 23
IPS:360974	4B1.013	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTATAGGAGACAGAGTCACCATCACTT
			GCCGGGCAAGTCAGGACATTAGAGATTATTTAG
			GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA
			AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA
			GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT
			CTGGGACAGAATTCACTCTCACAATCAGCAGCC
			TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT
			ACAGCATAATAATTACCCCTTCACTTTCGGCCAA
			GGGACCAAAGTGGATATCAAACGA
			SEQ ID NO: 1594
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY
			QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFT
			LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK
			R
			SEQ ID NO: 179
			CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
			GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA
			TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC
			TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
			GTAATGAAAACTATGCAGACGCCGTGAAGGGCC
			GATTCACCATCTCCAGAGACAATTCCAAGAATA
			CGCTGTATCTGCAAATGAACAGCCTGAGAGTCG
			CGGACACGGCTGTGTATTATTGTGCGCGAGATG
			GGACGATCTTTGGAGTGGTCTTGGGGGACTACT
			GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1750
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM
			HWVRQAPGKGLEWVAVIWYDASNENYADAVKG
			RFTISRDNSKNTLYLQMNSLRVADTAVYYCARDG
			TIFGVVLGDYWGQGTLVTVSS
			SEQ ID NO: 180
		NA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
			GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA
			TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC
			TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
			GTAATGAAAACTATGCAGACTCCGTGAAGGGCC
			GATTCACCATCTCCAGAGACAATTCCAAGAATA
			CGCTGTATCTGCACATGAACAGCCTGAGAGTCG
			CGGACACGGCTGTGTATTATTGTGCGCGAGATG
			GGACGATCTTTGGAGTGGTCTTGGGGGACTACT
			GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1751
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM
			HWVRQAPGKGLEWVAVIWYDASNENYADSVKG
			RFTISRDNSKNTLYLHMNSLRVADTAVYYCARDG
			TIFGVVLGDYWGQGTLVTVSS

iPS:360978	4B1.014	NA	SEQ ID NO: 24
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTATAGGAGACAGAGTCACCATCACTT
			GCCGGGCAAGTCAGGACATTAGAGATTATTTAG
			GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA
			AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA
			GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT
			CTGGGACAGAATTCACTCTCACAATCAGCAGCC
			TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT
			ACAGCATAATAATACCCCTTCACTTTCGGCCAA
			GGGACCAAAGTGGATATCAAACGA
			SEQ ID NO: 1595
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY
			QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFT
			LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK
			R
			SEQ ID NO: 25
iPS:359785	4B1.015	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTATAGGAGACAGAGTCACCATCACTT
			GCCGGGCAAGTCAGGACATTAGAGATTATTTAG
			GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA
			AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA
			GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT
			CTGGGACAGAATTCACTCTCACAATCAGCAGCC
			TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT
			ACAGCATAATAATACCCCTTCACTTTCGGCCAA
			GGGACCAAAGTGGATATCAAACGA
			SEQ ID NO: 1596
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY
			QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFT
			LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK
			R
			SEQ ID NO: 181
			CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
			GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA
			TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC
			TGGAGTGGGTGGCAGTTATATGGTATGATGGAA
			GTAATGAAAACTATGCAGACGCCGTGAAGGGCC
			GATTCACCATCTCCAGAGACAATTCCAAGAATA
			CGCTGTATCTGCACATGAACAGCCTGAGAGTCG
			CGGACACGGCTGTGTATTATTGTGCGCGAGATG
			GGACGATCTTTGGAGTGGTCTTGGGGGACTACT
			GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1752
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM
			HWVRQAPGKGLEWVAVIWYDGSNENYADAVKG
			RFTISRDNSKNTLYLHMNSLRVADTAVYYCARDG
			TIFGVVLGDYWGQGTLVTVSS
			SEQ ID NO: 182
		NA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
			GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA
			TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC
			TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
			GTAATGAAAACTATGCAGACGCCGTGAAGGGCC
			GATTCACCATCTCCAGAGACAATTCCAAGAATA
			CGCTGTATCTGCAAATGAACAGCCTGAGAGTCG
			AGGACACGGCTGTGTATTATTGTGCGCGAGATA
			GGACGATCTTTGGAGTGGTCTTGGGGGACTACT
			GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1753
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM
			HWVRQAPGKGLEWVAVIWYDASNENYADAVKG
			RFTISRDNSKNTLYLQMNSLRVEDTAVYYCARDR
			TIFGVVLGDYWGQGTLVTVSS

iPS:360982	4B1.016	NA	SEQ ID NO: 26
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTATAGGAGACAGAGTCACCATCACTT
			GCCGGGCAAGTCAGGACATTAGAGATTATTTAG
			GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA
			AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA
			GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT
			CTGGGACAGAATTCACTCTCACAATCAGCAGCC
			TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT
			ACAGCATAATAATACCCCTTCACTTTCGGCCAA
			GGGACCAAAGTGGATATCAAACGA
			SEQ ID NO: 1597
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY
			QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFT
			LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK
			R
			SEQ ID NO: 27
iPS:335922	18F2	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTATAGGAGACAGAGTCACCATCACTT
			GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG
			GCTGGTATCACCAGAAACCAGGGAAAGCCCCTA
			AGCGCCTGATCTATGGTGCATCCAGTTTGCAAA
			GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT
			CTGGGACAGAATTCACTCTCACAATCAGCAGCC
			TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT
			ACAGCATAATAATTACCCCTTCACTTTCGGCCCT
			GGGACCAAAGTGGATATCAAACGA
			SEQ ID NO: 1598
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW
			YHQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTE
			FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI
			KR

			SEQ ID NO: 183
			CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
			GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA
			TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC
			TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
			GTAATGAAAACTATGCAGACGCCGTGAAGGGCC
			GATTCACCATCTCCAGAGACAATTCCAAGAATA
			CGCTGTATCTGCAAATGAACAGCCTGAGAGTCG
			AGGACACGGCTGTGTATTATTGTGCGCGAGATG
			GGACGATCTTTGGAGTGGTCTTGGGGGACTACT
			GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1754
			QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM
			HWVRQAPGKGLEWVAVIWYDASNENYADAVKG
			RFTISRDNSKNTLYLQMNSLRVEDTAVYYCARDG
			TIFGVVLGDYWGQGTLVTVSS
			SEQ ID NO: 184
			CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
			GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA
			TGCACTGGGTCCGCCAGGCCCCAGGGCAAGGGGC
			TGGAGTGGGTGGCAGTTATATGGTATGATGGAA
			GTAATGAAAACTATGCAGACTCCGTGAAGGGCC
			GATTCACCATCTCCAGAGACAATTCCAAGAACA
			CGCTGTATCTCCAGAGCCTGAGAGCCG
			CGGACACGGCTGTGTATTACTGTGCGAGAGATG
			GGACGATCTTTGGAGTGGTCTTGGGGGACTACT
			GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1755
			QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM
			HWVRQAPGKGLEWVAVIWYDGSNENYADSVKG
			RFTISRDNSKNTLYLHMNSLRAADTAVYYCARDG
			TIFGVVLGDYWGQGTLVTVSS

iPS:360986	18F2.002	NA	SEQ ID NO: 28
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTATAGGAGACAGAGTCACCATCACTT
			GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG
			GCTGGTATCAACAGAAACCAGGGAAAGCCCCTA
			AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA
			GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT
			CTGGGACAGAATTCACTCTCACAATCAGCAGCC
			TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT
			ACAGCATAATAATTACCCCTTCACTTTCGGCCCT
			GGGACCAAAGTGGATATCAAACGA
		AA	SEQ ID NO: 1599
			DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW
			YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE
			FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI
			KR
iPS:360995	18F2.003	NA	SEQ ID NO: 29
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTATAGGAGACAGAGTCACCATCACTT
			GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG
			GCTGGTATCAACAGAAACCAGGGAAAGCCCCTA
			AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA
			GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT
			CTGGGACAGAATTCACTCTCACAATCAGCAGCC
			TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT
			ACAGCATAATAATTACCCCTTCACTTTCGGCCCT
			GGGACCAAAGTGGATATCAAACGA
		AA	SEQ ID NO: 1600
			DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW
			YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE
			FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI
			KR

			SEQ ID NO: 185
			CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
			GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA
			TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC
			TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
			GTAATGAAAACTATGCAGACGCCGTGAAGGGCC
			GATTCACCATCTCCAGAGACAATTCCAAGAACA
			CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
			CGGACACGGCTGTGTATTACTGTGCGAGATG
			GGACGATCTTTGGAGTGGTCTTGGGGACTACT
			GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1756
			QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM
			HWVRQAPGKGLEWVAVIWYDASNENYADAVKG
			RFTISRDNSKNTLYLQMNSLRAADTAVYYCARDG
			TIFGVVLGDYWGQGTLVTVSS
			SEQ ID NO: 186
			CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
			GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA
			TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC
			TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
			GTAATGAAAACTATGCAGACGCCGTGAAGGGCC
			GATTCACCATCTCCAGAGACAATTCCAAGAACA
			CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
			CGGACACGGCTGTGTATTACTGTGCGAGATG
			GGACGATCTTTGGAGTGGTCTTGGGGACTACT
			GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1757
			QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM
			HWVRQAPGKGLEWVAVIWYDASNENYADAVKG
			RFTISRDNSKNTLYLHMNSLRAADTAVYYCARDG
			TIFGVVLGDYWGQGTLVTVSS

iPS:360999	18F2.004	NA	SEQ ID NO: 30
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCACCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGA
			SEQ ID NO: 1601
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YHQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI KR
			SEQ ID NO: 31
iPS:361005	18F2.005	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCAACAGAAACCAGGGAAAGCCCCTA AGCGCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGA
			SEQ ID NO: 1602
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YQQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI KR
			SEQ ID NO: 187
			CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTCATGATGCAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG CGGACACGGCTGTGTATTACTGTGCGAGATG GGACGATCTTTGGAGTGGTCTTGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1758
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDASNENYADAVKG RFTISRDNSKNTLYLQMNSLRAADTAVYYCARDG TIFGVVLGDYWGQGTLVTVSS
			SEQ ID NO: 188
		NA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTCATGATGCAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG CGGACACGGCTGTGTATTACTGTGCGAGATG GGACGATCTTTGGAGTGGTCTTGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1759
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDASNENYADAVKG RFTISRDNSKNTLYLQMNSLRAADTAVYYCARDG TIFGVVLGDYWGQGTLVTVSS

iPS:361009	18F2.006	NA	SEQ ID NO: 32
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCAACAGAAACCAGGGAAAGCCCCTA AGCGCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGA
		AA	SEQ ID NO: 1603
			DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YQQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI KR
iPS:361013	18F2.007	NA	SEQ ID NO: 33
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCACCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGA
		AA	SEQ ID NO: 1604
			DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YHQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI KR

			SEQ ID NO: 189
			CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTGATGCAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCACATGAACAGCCTGAGAGCCG CGGACACGGCTGTGTATTACTGTGCGAGATG GGACGATCTTTGGAGTGGTCTTGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1760
			QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDASNENYADAVKG RFTISRDNSKNTLYLHMNSLRAADTAVYYCARDG TIFGVVLGDYWGQGTLVTVSS
			SEQ ID NO: 190
			CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTGATGCAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCACATGAACAGCCTGAGAGCCG CGGACACGGCTGTGTATTACTGTGCGAGATG GGACGATCTTTGGAGTGGTCTTGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1761
			QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDASNENYADAVKG RFTISRDNSKNTLYLHMNSLRAADTAVYYCARDG TIFGVVLGDYWGQGTLVTVSS

iPS:361017	18F2.008	NA	SEQ ID NO: 34
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCACCAGAAACCAGGGAAAGCCCCTA AGCGCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGA
		AA	SEQ ID NO: 1605
			DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YHQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI KR
iPS:361021	18F2.009	NA	SEQ ID NO: 35
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCAACAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGA
		AA	SEQ ID NO: 1606
			DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI KR

			SEQ ID NO: 191
			CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG CGGACACGGCTGTGTATTACTGTGCGAGATG GGACGATCTTTGGAGTGGTCTTGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1762
			QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDASNENYADAVKG RFTISRDNSKNTLYLQMNSLRAADTAVYYCARDG TIFGVVLGDYWGQGTLVTVSS
			SEQ ID NO: 192
			CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGGAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG CGGACACGGCTGTGTATTACTGTGCGAGATG GGACGATCTTTGGAGTGGTCTTGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1763
			QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDGSNENYADAVKG RFTISRDNSKNTLYLQMNSLRAADTAVYYCARDG TIFGVVLGDYWGQGTLVTVSS

iPS:361028	18F2.010	NA	SEQ ID NO: 36
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTATAGGAGACAGAGTCACCATCACTT
			GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG
			GCTGGTATCAACAGAAACCAGGGAAAGCCCCTA
			AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA
			GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT
			CTGGGACAGAATTCACTCTCACAATCAGCAGCC
			TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT
			ACAGCATAATAATACCCCTTCACTTTCGGCCCT
			GGGACCAAAGTGGATATCAAACGA
		AA	SEQ ID NO: 1607
			DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW
			YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE
			FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI
			KR
		NA	SEQ ID NO: 37
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTATAGGAGACAGAGTCACCATCACTT
			GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG
			GCTGGTATCAACAGAAACCAGGGAAAGCCCCTA
			AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA
			GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT
			CTGGGACAGAATTCACTCTCACAATCAGCAGCC
			TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT
			ACAGCATAATAATACCCCTTCACTTTCGGCCAA
			GGGACCAAAGTGGATATCAAACGA
		AA	SEQ ID NO: 1608
			DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW
			YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE
			FTLTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDI
			KR
iPS:360535	18F2.011	NA	SEQ ID NO: 193
			CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
			GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA
			TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC
			TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
			GTAATGAAAACTATGCAGACTCCGTGAAGGGCC
			GATTCACCATCTCCAGAGACAATTCCAAGAACA
			CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
			CGGACACGGCTGTGTATTACTGTGCGAGATG
			GGACGATCTTTGGAGTGGTCTTGGGGGACTACT
			GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
		AA	SEQ ID NO: 1764
			QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM
			HWVRQAPGKGLEWVAVIWYDASNENYADSVKG
			RFTISRDNSKNTLYLQMNSLRAADTAVYYCARDG
			TIFGVVLGDYWGQGTLVTVSS
		NA	SEQ ID NO: 194
			CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
			GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA
			TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC
			TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
			GTAATGAAAACTATGCAGACGCCGTGAAGGGCC
			GATTCACCATCTCCAGAGACAATTCCAAGAACA
			CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
			AGGACACGGCTGTGTATTACTGTGCGAGATA
			GGACGATCTTTGGAGTGGTCTTGGGGGACTACT
			GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
		AA	SEQ ID NO: 1765
			QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM
			HWVRQAPGKGLEWVAVIWYDASNENYADAVKG
			RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR
			TIFGVVLGDYWGQGTLVTVSS

iPS:361035	18F2.012	NA	SEQ ID NO: 38
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCAACAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGA
			SEQ ID NO: 1609
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI KR
			SEQ ID NO: 39
iPS:359940	2F11.002	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCAGGGCGAGTCAGGACATTAGCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTACGATGCATCCAATTTGGAAA CAGGGGTCCCATCAAGGTTCAGTGGAAGTGGAT CTGGGACAGATTTTAGTCTCACCATCAGCAGCC TGCAGCCTGAAGATTTTGCAACATATTACTGTCA ACAGTATGATATTCTCCTCACTTTCGGCGGAGG GACCAAGGTGGAGATCAAGCGA
			SEQ ID NO: 1610
		AA	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW YQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTD FSLTISSLQPEDFATYYCQQYDILLTFGGGTKVEIK R

			SEQ ID NO: 195
			CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGATG GGACGATCTTTGGAGTGGTCTTGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1766
			QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDASNENYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVVLGDYWGQGTLVTVSS
			SEQ ID NO: 196
			CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGTTATATGGTATGATGCA AGTAATAAATACTATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGGGACAATTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT AGGACGATTTTTGGAGTGGTTCTTGACTACTGG GGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1767
			QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGM HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLDYWGQGTLVTVSS

iPS:361039	2F11.003	NA	SEQ ID NO: 40
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTGTAGGAGACAGAGTCACCATCACTT
			GCCAGGCGAGTCAGGACATTAGCAACTATTTAA
			ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA
			AGCTCCTGATCTACGATGCATCCAATTTGGAAA
			CAGGGGTCCCATCAAGGTTCAGTGGAAGTGGAT
			CTGGGACAGATTTTAGTCTCACCATCAGCAGCC
			TGCAGCCTGAAGATTTTTGCAACATATTACTGTCA
			ACAGTATGATATTCTCCTCACTTTCGGCGGAGG
			GACCAAGGTGGAGATCAAGCGA
			SEQ ID NO: 1611
		AA	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW
			YQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTD
			FSLTISSLQPEDFATYYCQQYDILLTFGGGTKVEIK
			R
			SEQ ID NO: 41
iPS:361043	2F11.004	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTGTAGGAGACAGAGTCACCATCACTT
			GCCAGGCGAGTCAGGACATTAGCAACTATTTAA
			ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA
			AGCTCCTGATCTACGATGCATCCAATTTGGAAA
			CAGGGGTCCCATCAAGGTTCAGTGGAAGTGGAT
			CTGGGACAGATTTTAGTCTCACCATCAGCAGCC
			TGCAGCCTGAAGATATTGCAACATATTACTGTC
			AACAGTATGATATTCTCCTCACTTTCGGCGGAG
			GGACCAAGGTGGAGATCAAGCGA
			SEQ ID NO: 1612
		AA	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW
			YQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTD
			FSLTISSLQPEDIATYYCQQYDILLTFGGGTKVEIKR
			SEQ ID NO: 197
			CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG
			GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC
			ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG
			CTGGAGTGGGTGGCAGTTATATGGTATGATGCA
			AGTAATAAATACTATGCAGACGCCGTGAAGGGC
			CGATTCACCATCTCCAGCGACAATTCCAAGAAC
			ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC
			GAGGACACGGCTGTGTATTACTGTGCGAGAGAT
			AGGACGATTTTTGGAGTGGTTCTTGACTACTGG
			GGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1768
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGM
			HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG
			RFTISSDNSKNTLYLQMNSLRAEDTAVYYCARDR
			TIFGVVLDYWGQGTLVTVSS
			SEQ ID NO: 198
		NA	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG
			GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC
			ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG
			CTGGAGTGGGTGGCAGTTATATGGTATGATGCA
			AGTAATAAATACTATGCAGACGCCGTGAAGGGC
			CGATTCACCATCTCCAGGGACAATTCCAAGAAC
			ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC
			GAGGACACGGCTGTGTATTACTGTGCGAGAGAT
			AGGACGATTTTTGGAGTGGTTCTTGACTACTGG
			GGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1769
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGM
			HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG
			RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR
			TIFGVVLDYWGQGTLVTVSS

iPS:361049	2F11.005	NA	SEQ ID NO: 42
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTAGCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTACGATGCATCCAATTTGGAAA CAGGGGTCCCATCAAGGTTCAGTGGAAGTGGAT CTGGGACAGATTTTAGTTTCACCATCAGCAGCCT GCAGCCTGAAGATTTTTGCAACTATTACTGTCA ACAGTATGATATTCTCCTCACTTTCGGCGGAGG GACCAAGGTGGAGATCAAGCGA
			SEQ ID NO: 1613
		AA	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW YQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTD FSFTISSLQPEDFATYYCQQYDILLTFGGGTKVEIK R
			SEQ ID NO: 43
iPS:361055	2F11.006	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTAGCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTACGATGCATCCAATTTGGAAA CAGGGGTCCCATCAAGGTTCAGTGGAAGTGGAT CTGGGACAGATTTTAGTCTCACCATCAGCAGCC TGCAGCCTGAAGATATTGCAACATATTACTGTC AACAGTATGATATTCTCCTCACTTTCGGCGGAG GGACCAAGGTGGAGATCAAGCGA
			SEQ ID NO: 1614
		AA	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW YQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTD FSLTISSLQPEDIATYYCQQYDILLTFGGGTKVEIKR

			SEQ ID NO: 199
		NA	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGTTATATGGTATGATGCA AGTAATAAATACTATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGGGACAATTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT AGGACGATTTTTGGAGTGGTTCTTGACTACTGG GGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1770
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGM HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLDYWGQGTLVTVSS
			SEQ ID NO: 200
		NA	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGTTATATGGTATGATGCA AGTAATAAATACTATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGCGACAATTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT AGGACGATTTTTGGAGTGGTTCTTGACTACTGG GGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1771
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGM HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG RFTISSDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLDYWGQGTLVTVSS

iPS:361059	2F11.007	NA	SEQ ID NO: 44
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTAGCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTACGATGCATCCAATTTGGAAA CAGGGGTCCCATCAAGGTTCAGTGGAAGTGGAT CTGGGACAGATTTTAGTTTCACCATCAGCAGCCT GCAGCCTGAAGATTTTTGCAACATATTACTGTCA ACAGTATGATATTCTCCTCACTTTCGGCGGAGG GACCAAGGTGGAGATCAAGCGA
			SEQ ID NO: 1615
		AA	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW YQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTD FSFTISSLQPEDFATYYCQQYDILLTFGGGTKVEIK R
			SEQ ID NO: 45
iPS:361063	2F11.008	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTAGCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTACGATGCATCCAATTTGGAAA CAGGGGTCCCATCAAGGTTCAGTGGAAGTGGAT CTGGGACAGATTTTAGTTTCACCATCAGCAGCCT GCAGCCTGAAGATATTTGCAACATATTACTGTCA ACAGTATGATATTCTCCTCACTTTCGGCGGAGG GACCAAGGTGGAGATCAAGCGA
			SEQ ID NO: 1616
		AA	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW YQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTD FSFTISSLQPEDIATYYCQQYDILLTFGGGTKVEIKR
			SEQ ID NO: 201
			CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGTTATATGGTATGATGCA AGTAATAAATACTATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGCGACAATTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT AGGACGATTTTTGGAGTGGTTCTTGACTACTGG GGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1772
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGM HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG RFTISSDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLDYWGQGTLVTVSS
			SEQ ID NO: 202
		NA	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGTTATATGGTATGATGCA AGTAATAAATACTATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGGGACAATTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT AGGACGATTTTTGGAGTGGTTCTTGACTACTGG GGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1773
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGM HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLDYWGQGTLVTVSS

iPS:359949	2F11.009	NA	SEQ ID NO: 46
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTAGCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTACGATGCATCCAATTTGGAAA CAGGGGTCCCATCAAGGTTCAGTGGAAGTGGAT CTGGGACAGATTTTAGTCTCACCATCAGCAGCC TGCAGCCTGAAGATTTTTGCAACATATTACTGTCA ACAGTATGATATTCTCCTCACTTTCGGCGGAGG GACCAAGGTGGAGATCAAGCGA
			SEQ ID NO: 1617
		AA	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW YQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTD FSLTISSLQPEDFATYYCQQYDILLTFGGGTKVEIK R
			SEQ ID NO: 47
iPS:359956	2F11.010	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTAGCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTACGATGCATCCAATTTGGAAA CAGGGGTCCCATCAAGGTTCAGTGGAAGTGGAT CTGGGACAGATTTTAGTCTCACCATCAGCAGCC TGCAGCCTGAAGATTTTTGCAACATATTACTGTCA ACAGTATGATATTCTCCTCACTTTCGGCGGAGG GACCAAGGTGGAGATCAAGCGA
			SEQ ID NO: 1618
		AA	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW YQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTD FSLTISSLQPEDFATYYCQQYDILLTFGGGTKVEIK R

			SEQ ID NO: 203
		NA	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGTTATATGGTATGATGCA AGTAATAAATACTATGCAGACTCCGTGAAGGGC CGATTCACCATCTCCAGGGACAATTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT AGGACGATTTTTGGAGTGGTTCTTGACTACTGG GGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1774
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGM HWVRQAPGKGLEWVAVIWYDASNKYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLDYWGQGTLVTVSS
			SEQ ID NO: 204
		NA	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGTTATATGGTATGATGGA AGTAATAAATACTATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGGGACAATTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT AGGACGATTTTTGGAGTGGTTCTTGACTACTGG GGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1775
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGM HWVRQAPGKGLEWVAVIWYDGSNKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLDYWGQGTLVTVSS

iPS:359865	6H1.002	NA	SEQ ID NO: 48
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTATAGGAGACAGAGTCACCATCACTT
			GCCGGGCAAGTCAGGACATTAGAGATTATTTAG
			GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA
			AGCGCCTGATCTATGGTGCATCCAGTTTGCAAA
			GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT
			CTGGGACAGAATTCACTCTCACAATCAGCAGCC
			TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT
			ACAGCATAATAATACCCCTTCACTTTCGGCCCT
			GGGACCAAAGTGGATATCAAACGA
			SEQ ID NO: 1619
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY
			QQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTEFT
			LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR
			SEQ ID NO: 49
iPS:359869	6H1.003	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTATAGGAGACAGAGTCACCATCACTT
			GCCGGGCAAGTCAGGACATTAGAGATTATTTAG
			GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA
			AGCGCCTGATCTATGGTGCATCCAGTTTGCAAA
			GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT
			CTGGGACAGAATTCACTCTCACAATCAGCAGCC
			TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT
			ACAGCATAATAATACCCCTTCACTTTCGGCCCT
			GGGACCAAAGTGGATATCAAACGA
			SEQ ID NO: 1620
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY
			QQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTEFT
			LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR

			SEQ ID NO: 205
			CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
			GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA
			TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC
			TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
			GTAATAAATACTATGCAGACGCCGTGAAGGGCC
			GCTTCACCATCTCCAGAGACAATTCCAAGAACA
			CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
			AGGACACGGCTGTGTATTACTGTGCGCGAGATG
			GGACGATTTTTGGAGTGCTCTTGGGGGACTACT
			GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1776
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM
			HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG
			RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG
			TIFGVLLGDYWGQGTLVTVSS
			SEQ ID NO: 206
		NA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
			GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA
			TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC
			TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
			GTAATAAATACTATGCAGACGCCGTGAAGGGCC
			GCTTCACCATCTCCAGAGACAATTCCAAGAACA
			CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
			AGGACACGGCTGTGTATTACTGTGCGCGAGATA
			GGACGATTTTTGGAGTGCTCTTGGGGGACTACT
			GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1777
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM
			HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG
			RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR
			TIFGVLLGDYWGQGTLVTVSS

iPS:359873	6H1.004	NA	SEQ ID NO: 50
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCAA GGGACCAAAGTGGATATCAAACGA
		AA	SEQ ID NO: 1621
			DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK R
			SEQ ID NO: 208
iPS:359877	6H1.005	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCAA GGGACCAAAGTGGATATCAAACGA
			SEQ ID NO: 1622
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK R
			SEQ ID NO: 207
		NA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTTGGAGTGCTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
		AA	SEQ ID NO: 1778
			QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGTLVTVSS
			SEQ ID NO: 209
		NA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATA GGACGATTTTTGGAGTGCTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
		AA	SEQ ID NO: 1779
			QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVLLGDYWGQGTLVTVSS

iPS;361067	6H1.006	NA	SEQ ID NO: 52
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTATAGGAGACAGAGTCACCATCACTT
			GCCGGGCAAGTCAGGACATTAGAGATTATTTAG
			GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA
			AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA
			GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT
			CTGGGACAGAATTCACTCTCACAATCAGCAGCC
			TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT
			ACAGCATAATAATTACCCCTTCACTTTCGGCCCT
			GGGACCAAAGTGGATATCAAACGA
			SEQ ID NO: 1623
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY
			QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFT
			LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR
			SEQ ID NO: 53
iPS;361071	6H1.007	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTATAGGAGACAGAGTCACCATCACTT
			GCCGGGCAAGTCAGGACATTAGAGATTATTTAG
			GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA
			AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA
			GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT
			CTGGGACAGAATTCACTCTCACAATCAGCAGCC
			TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT
			ACAGCATAATAATTACCCCTTCACTTTCGGCCCT
			GGGACCAAAGTGGATATCAAACGA
			SEQ ID NO: 1624
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY
			QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFT
			LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR
			SEQ ID NO: 54

			SEQ ID NO: 209
			CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
			GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA
			TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC
			TGGAGTGGGTGGCAGTTATATGGTATGATGGAA
			GTAATAAATACTATGCAGACTCCGTGAAGGGCC
			GCTTCACCATCTCCAGAGACAATTCCAAGAACA
			CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
			AGGACACGGCTGTGTATTACTGTGCGCGAGATG
			GGACGATTTTTGGAGTGCTCTTGGGGGACTACT
			GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1780
			QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM
			HWVRQAPGKGLEWVAVIWYDGSNKYYADSVKG
			RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG
			TIFGVLLGDYWGQGTLVTVSS
			SEQ ID NO: 210
			CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
			GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA
			TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC
			TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
			GTAATAAATACTATGCAGACTCCGTGAAGGGCC
			GCTTCACCATCTCCAGAGACAATTCCAAGAACA
			CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
			AGGACACGGCTGTGTATTACTGTGCGCGAGATG
			GGACGATTTTTGGAGTGCTCTTGGGGGACTACT
			GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1781
			QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM
			HWVRQAPGKGLEWVAVIWYDASNKYYADSVKG
			RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG
			TIFGVLLGDYWGQGTLVTVSS
			SEQ ID NO: 211

iPS:361075	6HI.008		
	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGA	SEQ ID NO: 1625
	AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	SEQ ID NO: 55
iPS:361079	6AS.004.001		
	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTACGATGCTTCCAATTTGGAGCC AGGGGTCCCATCAAGGTTCAGTGGAAGTGGATC TGGGACAGATTTTACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACATATTACTGTCA ACAGTATGATGATCTATTCACTTTCGGCCCTGGG ACCAAAGTGGATATCAAACGA	SEQ ID NO: 1626
	AA	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGSGTD FTLTISSLQPEDFATYYCQQYDDLFTFGPGTKVDIK R	SEQ ID NO: 1783
		QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAAIWYDANNKYYADAVKG RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYWGQGTLVTVSS	

IPS:361085	6A5.004.002	NA	SEQ ID NO: 56
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTACGATGCTTCCAATTTGGAGCC AGGGGTCCCATCAAGGTTCAGTGGAAGTGGATC TGGGACAGATTTTACTCTCACCATCAGCAGCCT GCAGCCTGAAGATATTGCAACATATTACTGTCA ACAGTATGATGATCTATTCACTTTCGGCCCTGGG ACCAAAGTGGATATCAAACGA
		AA	SEQ ID NO: 1627
			DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGSGTD FTLTISSLQPEDIATYYCQQYDDLFTFGPGTKVDIK R
			SEQ ID NO: 57
IPS:361091	6A5.004.003	NA	SEQ ID NO: 213
			CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCTCCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGCCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGCTATATGGTATGATGCAA ATAATAAATACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATC GGACGATTTTTGGAGTGGTCCTTGAGTACTGGG GCCAGGGAACCCTGGTCACCGTCTCCTCA
		AA	SEQ ID NO: 1784
			QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAAIWYDANNKYYADAVKG RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYWGQGTLVTVSS
			SEQ ID NO: 214
		NA	SEQ ID NO: 58
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTACGATGCTTCCAATTTGGAGCC AGGGGTCCCATCAAGGTTCAGTGGAAGTGGATC TGGGACAGATTTTACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACATATTACTGTCA ACAGTATGATGATCTATTCACTTTCGGCCCTGGG ACCAAAGTGGATATCAAACGA
		AA	SEQ ID NO: 1628
			DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGSGTD FTLTISSLQPEDFATYYCQQYDDLFTFGPGTKVDIK R
			SEQ ID NO: 215
		NA	SEQ ID NO: 59
			CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCTCCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGCCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGCTATATGGTATGATGCAA ATAATAAATACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATC GGACGATTTTTGGAGTGGTCCTTGAGTACCTCG GCCAGGGAACCCTGGTCACCGTCTCCTCA
		AA	SEQ ID NO: 1785
			QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAAIWYDANNKYYADAVKG RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYLGQGTLVTVSS
			SEQ ID NO: 216

		SEQ ID NO: 58	SEQ ID NO: 215
iPS:361095	6A5.004.004	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTACGATGCTTCCAATTTGGAGCC AGGGGTCCCATCAAGGTTCAGTGGAAGTGGATC TGGGACAGATTTTACTTTCACCATCAGCAGCCTG CAGCCTGAAGATTTTGCAACATATTACTGTCAA CAGTATGATCTATTCACTTTCGGCCCTGGGA CCAAAGTGGATATCAAACGA	GCCAGGGAACCCTGGTCACCGTCTCCTCA
		AA	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGSGTD FTFTISSLQPEDFATYYCQQYDDLFTFGPGTKVDIK R	TIFGVVLEYWGQGTLVTVSS
			SEQ ID NO: 1629	SEQ ID NO: 1786
			SEQ ID NO: 59	SEQ ID NO: 216
iPS:361101	6A5.004.005	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTACGATGCTTCCAATTTGGAGCC AGGGGTCCCATCAAGGTTCAGTGGAAGTGGATC TGGGACAGATTTTACTCTCACCATCAGCAGCCT GCAGCCTGAAGATATTGCAACATATTACTGTCA ACAGTATGATGATCTATTCACTTTCGGCCCTGGG ACCAAAGTGGATATCAAACGA	GCCAGGGAACCCTGGTCACCGTCTCCTCA
		AA	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGSGTD FTLTISSLQPEDIATYYCQQYDDLFTFGPGTKVDIK R	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAAIWYDANNKYYADAVKG RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYLGQGTLVTVSS
			SEQ ID NO: 1630	SEQ ID NO: 1787

		SEQ ID NO: 60	SEQ ID NO: 217
IPS:361105	6AS.004.006	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTACGATGCTTCCAATTTGGAGCC AGGGGTCCCATCAAGGTTCAGTGGAAGTGGATC TGGGACAGATTTTACTTTCACCATCAGCAGCCTG CAGCCTGAAGATTTTGCAACTATTACTGTCAA CAGTATGATGATCTATTCACTTTCGGCCCTGGGA CCAAAGTGGATATCAAACGA
		SEQ ID NO: 1631	SEQ ID NO: 1788
		AA	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGSGTD FTFTISSLQPEDFATYYCQQYDDLFTFGPGTKVDIK R
		SEQ ID NO: 61	SEQ ID NO: 218
IPS:361109	6AS.004.007	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTACGATGCTTCCAATTTGGAGCC AGGGGTCCCATCAAGGTTCAGTGGAAGTGGATC TGGGACAGATTTTACTTTCACCATCAGCAGCCTG CAGCCTGAAGATATTGCAACATATTACTGTCAA CAGTATGATGATCTATTCACTTTCGGCCCTGGGA CCAAAGTGGATATCAAACGA
		SEQ ID NO: 1632	SEQ ID NO: 1789
		AA	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGSGTD FTFTISSLQPEDIATYYCQQYDDLFTFGPGTKVDIK R
		SEQ ID NO: 60	SEQ ID NO: 217

iPS:361113	6A5.004.008	NA	SEQ ID NO: 62
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTGTGGGGGACAGAGTCACCATCACTT
			GCCAGGCGAGTCAGGACATTACCAACTATTTAA
			ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA
			AACTCCTGATCTACGATGCTTCCAATTTGGAGCC
			AGGGGTCCCATCAAGGTTCAGTGGAAGTGGATC
			TGGGACAGATTTTACTCTCACCATCAGCAGCCT
			GCAGCCTGAAGATTTTGCAACATATTACTGTCA
			ACAGTATGATGATCTATTCACTTTCGGCCCTGGG
			ACCAAAGTGGATATCAAACGA
			SEQ ID NO: 1633
		AA	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW
			YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGSGTD
			FTLTISSLQPEDFATYYCQQYDDLFTFGPGTKVDIK
			R
			SEQ ID NO: 63
iPS:361120	6A5.004.009	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTGTGGGGGACAGAGTCACCATCACTT
			GCCAGGCGAGTCAGGACATTACCAACTATTTAA
			ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA
			AACTCCTGATCTACGATGCTTCCAATTTGGAGCC
			AGGGGTCCCATCAAGGTTCAGTGGAAGTGGATC
			TGGGACAGATTTTACTCTCACCATCAGCAGCCT
			GCAGCCTGAAGATTTTGCAACATATTACTGTCA
			ACAGTATGATGATCTATTCACTTTCGGCCCTGGG
			ACCAAAGTGGATATCAAACGA
			SEQ ID NO: 1634
		AA	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW
			YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGSGTD
			FTLTISSLQPEDFATYYCQQYDDLFTFGPGTKVDIK
			R

SEQ ID NO: 219	
	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
	GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
	GCAGCGTCTGGATTCTCCTTCAGTAGCTATGGCA
	TGCACTGGGTCCGCCAGCCTCCAGGCAAGGGGC
	TGGAGTGGGTGGCAGCTATATGGTATGATGGAA
	ATAATAAATACTATGCAGACGCCGTGAAGGGCC
	GATTCACCATCTCCAGAGACAGTTCCAAGAACA
	CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
	AGGACACGGCTGTGTATTACTGTGCGAGATC
	GGACGATTTTTGGAGTGGTCCTTGAGTACTGGG
	GCCAGGGAACCCTGGTCACCGTCTCCTCA
SEQ ID NO: 1790	
	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM
	HWVRQPPGKGLEWVAAIWYDGNNKYYADAVKG
	RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR
	TIFGVVLEYWGQGTLVTVSS
SEQ ID NO: 220	
	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
	GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
	GCAGCGTCTGGATTCTCCTTCAGTAGCTATGGCA
	TGCACTGGGTCCGCCAGCCTCCAGGCAAGGGGC
	TGGAGTGGGTGGCAGCTATATGGTATGATGCAA
	ATAATAAATACTATGCAGACTCCGTGAAGGGCC
	GATTCACCATCTCCAGAGACAGTTCCAAGAACA
	CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
	AGGACACGGCTGTGTATTACTGTGCGAGATC
	GGACGATTTTTGGAGTGGTCCTTGAGTACTGGG
	GCCAGGGAACCCTGGTCACCGTCTCCTCA
SEQ ID NO: 1791	
	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM
	HWVRQPPGKGLEWVAAIWYDANNKYYADSVKG
	RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR
	TIFGVVLEYWGQGTLVTVSS

		SEQ ID NO: 64	SEQ ID NO: 221
iPS:35896	6A5.004.010	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTACGATGCTTCCAATTTGGAGCC AGGGGTCCCATCAAGGTTCAGTGGAAGTGGATC TGGGACAGATTTTACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACTATTACTGTCA ACAGTATGATGATCTATTCACTTTCGGCCAAGG GACCAAAGTGGATATCAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCTCCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGCCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGCTATATGGTATGATGCAA ATAATAAATACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATC GGACGATTTTTGGAGTGGTCCTTGAGTACTGGG GCCAGGGAACCCTGGTCACCGTCTCCTCA
		SEQ ID NO: 1635	SEQ ID NO: 1792
	AA	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGSGTD FTLTISSLQPEDFATYYCQQYDDLFTFGQGTKVDI KR	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAAIWYDANNKYYADAVKG RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYWGQGTLVTVSS
		SEQ ID NO: 65	SEQ ID NO: 222
iPS:35890	6A5.004.011	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTACGATGCTTCCAATTTGGAGCC AGGGGTCCCATCAAGGTTCAGTGGAAGTGGATC TGGGACAGATTTTACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACTATTACTGTCA ACAGTATGATGATCTATTCACTTTCGGCCAAGG GACCAAAGTGGATATCAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCTCCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGCCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGCTATATGGTATGATGCAA ATAATAAATACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATC GGACGATTTTTGGAGTGGTCCTTGAGTACCTCG GCCAGGGAACCCTGGTCACCGTCTCCTCA
		SEQ ID NO: 1636	SEQ ID NO: 1793
	AA	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGSGTD FTLTISSLQPEDFATYYCQQYDDLFTFGQGTKVDI KR	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAAIWYDANNKYYADAVKG RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYLGQGTLVTVSS

		SEQ ID NO: 66	SEQ ID NO: 223
iPS:359567	2A11.002	NA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT GCAGGGCCAGTCAGATTTTTACCAGCACCTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCAGGCTCCTCATCTATGGTGCATCCAGCAGGG CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG GGTCTGGGACAGACTTCACTCTCACCATCAGCA GATTGGAGCCTGAAGATTTTTGCAGTGTATTACT GTCAGCAGTATGGTAGCTCACCTCGCTTCGGCC AAGGGACACGACTGGAGATTAAACGA
		SEQ ID NO: 1637	SEQ ID NO: 1794
		AA	EIVLTQSPGTLSLSPGERATLSCRASQIFTSTYLAW YQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF TLTISRLEPEDFAVYYCQQYGSSPRFGQGTRLEIKR
		SEQ ID NO: 67	SEQ ID NO: 224
iPS:333965	2A11.003	NA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT GCAGGGCCAGTCAGATTTTTACCAGCACCTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCAGGCTCCTCATCTATGGTGCATCCAGCAGGG CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG GGTCTGGGACAGACTTCACTCTCACCATCAGCA GATTGGAGCCTGAAGATTTTTGCAGTGTATTACT GTCAGCAGTATGGTAGCTCACCTCGCTTCGGCC AAGGGACACGACTGGAGATTAAACGA
		SEQ ID NO: 1638	SEQ ID NO: 1795
		AA	EIVLTQSPGTLSLSPGERATLSCRASQIFTSTYLAW YQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF TLTISRLEPEDFAVYYCQQYGSSPRFGQGTRLEIKR

			QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQAPGKGLEWVAVIWYDGSNKYYEDSVKG RFTISRDNSKNTLFLQVNSLRAEDTAVYYCARGITI FGHGFEYWGQGTLVTVSS
			SEQ ID NO: 1795
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQAPGKGLEWVAVIWYDGSNKYYEDSVKG RFTISRDNSKNTLFLQVNSLRAEDTAVYYCARGITI FGHGFEYWGQGTLVTVSS

IPS:361158	2A11.004	NA	SEQ ID NO: 68
			GAAATTGTGTTGACGCAGTCTCCAGGCACCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT GCAGGGCCAGTCAGATTTTTACCAGCACCTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCAGGCTCCTCATCTATGGTGCATCCAGCAGGG CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG GGTCTGGGACAGACTTCACTCTCACCATCAGCA GATTGGAGCCTGAAGATTTTTGCAGTGTATTACT GTCAGCAGTATGGTAGCTCACCTCGCTTCGGCC AAGGGACACGACTGGAGATTAAACGA
			SEQ ID NO: 1639
		AA	EIVLTQSPGTLSLSPGERATLSCRASQIFTSTYLAW YQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF TLTISRLEPEDFAVYYCQQYGSSPRFGQGTRLEIKR
			SEQ ID NO: 69
IPS:361165	2A11.005	NA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT GCAGGGCCAGTCAGATTTTTACCAGCACCTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCAGGCTCCTCATCTATGGTGCATCCAGCAGGG CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG GGTCTGGGACAGACTTCACTCTCACCATCAGCA GATTGGAGCCTGAAGATTTTTGCAGTGTATTACT GTCAGCAGTATGGTAGCTCACCTCGCTTCGGCC AAGGGACACGACTGGAGATTAAACGA
			SEQ ID NO: 1640
		AA	EIVLTQSPGTLSLSPGERATLSCRASQIFTSTYLAW YQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF TLTISRLEPEDFAVYYCQQYGSSPRFGQGTRLEIKR
			SEQ ID NO: 225
			CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCAGTTTCAGTAGCTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGA CTGGAGTGGGTGGCAGTTATATGGTATGATGGA AGTAATAAATACTATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGAGACAATTCCAAGAAC ACGCTGTTTCTGCAAGTGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGGG ATTACGATTTTTGGTCATGGGTTTGAATATTGGG GCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1796
			QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQAPGKGLEWVAVIWYDGSNKYYEDAVKG RFTISRDNSKNTLFLQVNSLRAEDTAVYYCARGITI FGHGFEYWGQGTLVTVSS
			SEQ ID NO: 226
			CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCAGTTTCAGTAGCTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGA CTGGAGTGGGTGGCAGTTATATGGTATGATGCA AGTAATAAATACTATGCAGACTCCGTGAAGGGC CGATTCACCATCTCCAGAGACAATTCCAAGAAC ACGCTGTTTCTGCAAGTGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGGG ATTACGATTTTTGGTCATGGGTTTGAATATTGGG GCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1797
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQAPGKGLEWVAVIWYDASNKYYEDSVKG RFTISRDNSKNTLFLQVNSLRAEDTAVYYCARGITI FGHGFEYWGQGTLVTVSS

iPS:361172	2G10_LC1.003	NA	SEQ ID NO: 70
			GAAATAGTGATGACGCAGTCTCCAGCCACCCTG TCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCC TGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGCAGCCACCAGGGCC ACTGGTATCCCAGCCAGGTTCAGTGGCAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGCAGTCTGAAGATTTTGCAGTTTATTACTGTC AGCAGTATAATAACTGGCCTCTCACTTTCGGCG GAGGGACCAAGGTGGAGATCAAACGA
			SEQ ID NO: 1641
		AA	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGAATRATGIPARFSGSGSGTE FTLTISSLQSEDFAVYYCQQYNNWPLTFGGGTKVE IKR
			SEQ ID NO: 71
iPS:361178	2G10_LC1.004	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTG TCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCC TGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGCAGCCACCAGGGCC ACTGGTATCCCAGCCAGGTTCAGTGGCAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGCAGTCTGAAGATTTTGCAGTTTATTACTGTC AGCAGTATAATAACTGGCCTCTCACTTTCGGCG GAGGGACCAAGGTGGAGATCAAACGA
			SEQ ID NO: 1642
		AA	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGAATRATGIPARFSGSGSGTE FTLTISSLQSEDFAVYYCQQYNNWPLTFGGGTKVE IKR
			SEQ ID NO: 227
		NA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACCTTCAGTAACTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCGAGGGG CTGGAGTGGGTGGCAGCTATATGGTTTGATGCA AGTGATAAATACTATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGAGACAACTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGGCGATTTTTGGAGTGGTCCCCGACTACTGG GGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1798
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGM HWVRQAPGEGLEWVAAIWFDASDKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGTLVTVSS
			SEQ ID NO: 228
		NA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACCTTCAGTAACTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCGAGGGG CTGGAGTGGGTGGCAGCTATATGGTTTGATGCA AGTGATAAATACTATGCAGACTCCGTGAAGGGC CGATTCACCATCTCCAGAGACAACTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGGCGATTTTTGGAGTGGTCCCCGACTACTGG GGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1799
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGM HWVRQAPGEGLEWVAAIWFDASDKYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGTLVTVSS

		SEQ ID NO: 72	SEQ ID NO: 229
iPS:361185	2G10_LC1.005	GAAATAGTGATGACGCAGTCTCCAGCCACCCTG TCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCC TGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGCAGCCACCAGGGCC ACTGGTATCCCAGCCAGGTTCAGTGGCAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGCAGTCTGAAGATTTTGCAGTTTATTACTGTC AGCAGTATAATAACTGGCCTCTCACTTTCGGCG GAGGGACCAAGGTGGAGATCAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACCTTCAGTAACTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCGAGGGG CTGGAGTGGGTGGCAGCTATATGGTTTGATGGA AGTGATAAATACTATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGAGACAACTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGGCGATTTTTGGAGTGGTCCCCGACTACTGG GGCCAGGGAACCCTGGTCACCGTCTCCTCA
		SEQ ID NO: 1643	SEQ ID NO: 1800
	AA	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGAATRATGIPARFSGSGSGTE FTLTISSLQSEDFAVYYCQQYNNWPLTFGGGTKVE IKR	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGM HWVRQAPGEGLEWVAAIWFDGSDKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGTLVTVSS
		SEQ ID NO: 73	SEQ ID NO: 230
iPS:361192	2G10_LC1.006	GAAATAGTGATGACGCAGTCTCCAGCCACCCTG TCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCC TGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGCAGCCACCAGGGCC ACTGGTATCCCAGCCAGGGTCAGTGGCAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGCAGTCTGAAGATTTTGCAGTTTATTACTGTC AGCAGTATAATAACTGGCCTCTCACTTTCGGCG GAGGGACCAAGGTGGAGATCAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACCTTCAGTAACTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCGAGGGG CTGGAGTGGGTGGCAGCTATATGGTTTGATGCA AGTGATAAATACTATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGAGACAACTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGGCGATTTTTGGAGTGGTCCCCGACTACTGG GGCCAGGGAACCCTGGTCACCGTCTCCTCA
		SEQ ID NO: 1644	SEQ ID NO: 1801
	AA	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGAATRATGIPARVSGSGSGTE FTLTISSLQSEDFAVYYCQQYNNWPLTFGGGTKVE IKR	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGM HWVRQAPGEGLEWVAAIWFDASDKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGTLVTVSS

		SEQ ID NO: 74	SEQ ID NO: 231
iPS:359609	2G10_LC1.007	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTG TCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCC TGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGCAGCCACCAGGGCC ACTGGTATCCCAGCCAGGTTCAGTGGCAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGGAGCCTGAAGATTTTGCAGTTTATTACTGTC AGCAGTATAATAACTTCCCTCTCACTTTCGGCGG AGGGACCAAGGTGGAGATCAAACGA
		SEQ ID NO: 1645	SEQ ID NO: 1802
		AA	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGAATRATGIPARFSGSGSGTE FTLTISSLEPEDFAVYYCQQYNNFPLTFGGGTKVEI KR
		SEQ ID NO: 75	SEQ ID NO: 232
iPS:359615	2G10_LC1.008	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTG TCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCC TGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGCAGCCACCAGGGCC ACTGGTATCCCAGCCAGGTTCAGTGGCAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGGAGCCTGAAGATTTTGCAGTTTATTACTGTC AGCAGTATAATAACTATCCTCTCACTTTCGGCGG AGGGACCAAGGTGGAGATCAAACGA
		SEQ ID NO: 1646	SEQ ID NO: 1803
		AA	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGAATRATGIPARFSGSGSGTE FTLTISSLEPEDFAVYYCQQYNNYPLTFGGGTKVEI KR	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGM HWVRQAPGKGLEWVAAIWFDASDKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGTLVTVSS

		SEQ ID NO: 76	SEQ ID NO: 233
iPS:361196	2G10_LC1.009	GAAATAGTGATGACGCAGTCTCCAGCCACCCTG TCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCC TGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGCAGCCACCAGGGCC ACTGGTATCCCAGCCAGGTTCAGTGGCAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGGAGCCTGAAGATTTTGCAGTTTATTACTGTC AGCAGTATAATAACTGGCCTCTCACTTTCGGCG GAGGGACCAAGGGTGGAGATCAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACCTTCAGTAACTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCGAGGGG CTGGAGTGGGTGGCAGCTATATGGTTTGATGCA AGTGATAAATACTATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGAGACAACTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGGCGATTTTTGGAGTGGTCCCCGACTACTGG GGCCAGGGAACCCTGGTCACCGTCTCCTCA
		SEQ ID NO: 1647	SEQ ID NO: 1804
	AA	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGAATRATGIPARFSGSGSGTE FTLTISSLEPEDFAVYYCQQYNNWPLTFGGGTKVE IKR	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGM HWVRQAPGEGLEWVAAIWFDASDKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGTLVTVSS
		SEQ ID NO: 77	SEQ ID NO: 234
iPS:361202	2G10_LC1.010	GAAATAGTGATGACGCAGTCTCCAGCCACCCTG TCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCC TGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGCAGCCACCAGGGCC ACTGGTATCCCAGCCAGGTTCAGTGGCAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGGAGCCTGAAGATTTTGCAGTTTATTACTGTC AGCAGTATAATAACTGGCCTCTCACTTTCGGCG GAGGGACCAAGGGTGGAGATCAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACCTTCAGTAACTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGCTATATGGTTTGATGCA AGTGATAAATACTATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGAGACAACTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGGCGATTTTTGGAGTGGTCCCCGACTACTGG GGCCAGGGAACCCTGGTCACCGTCTCCTCA
		SEQ ID NO: 1648	SEQ ID NO: 1805
	AA	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGAATRATGIPARFSGSGSGTE FTLTISSLEPEDFAVYYCQQYNNWPLTFGGGTKVE IKR	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGM HWVRQAPGKGLEWVAAIWFDASDKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGTLVTVSS

iPS:359644	18E3.002	NA	SEQ ID NO: 78
			GAAATTGTGTTGACGCAGTCTCCAGGCACCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG GGTCTGGGACAGACTTCACTCTCACCATCAGCA GACTGGAGCCTGATGATTTTTGCAGTGTATTACTG TCAGCAGTATGGTAGTTCACCGCTCACTTTCGGC GGAGGGACCAAGGTGGAGATCAAACGA
			SEQ ID NO: 1649
		AA	EIVLTQSPGTLSLSPGERATLSCRASQSISYSYLAW YQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF TLTISRLEPDDFAVYYCQQYGSSPLTFGGGTKVEIK R
			SEQ ID NO: 79
iPS:361206	18E3.003	NA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG GGTCTGGGACAGACTTCACTCTCACCATCAGCA GACAGGAGCCTGATGATTTTTGCAGTGTATTACT GTCAGCAGTATGGTAGTTCACCGCTCACTTTCGG CGGAGGGACCAAGGTGGAGATCAAACGA
			SEQ ID NO: 1650
		AA	EIVLTQSPGTLSLSPGERATLSCRASQSISYSYLAW YQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF TLTISRQEPDDFAVYYCQQYGSSPLTFGGGTKVEI KR
			SEQ ID NO: 235
		NA	CAGGTGCAGTTGCAGGAGTCGGGCCCAGGACTG GTGAAGCCTTCAGAGACCCTGTCCCTCACCTGC ACTGTCTCTGGTGACTCCATCAGCAGTGGTGGTTT ACTACTGGAGCTGGATCCGCCAGCCCCCAGGGA AGGGCCTGGAGTGGATTGGGTACATCTATTACA GTGGGAGCACCTACTACAACCCGTCCCTCAAGA GTCGAGTTACCATATCAGTAGACACGTCTAAGA ACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC CGCGGACACGGCCGTGTATTACTGTGCGAGAGA TCGTATTACGATTTTTGGAGTGGTTATGGGGGGC GGTATGGACGTCTGGGGCCAAGGGACCACGGTC ACCGTCTCCTCA
			SEQ ID NO: 1806
		AA	QVQLQESGPGLVKPSETLSLTCTVSGDSISSGGYY WSWIRQPPGKGLEWIGYIYYSGSTYYNPSLKSRVT ISVDTSKNQFSLKLSSVTAADTAVYYCARDRITIFG VVMGGGMDVWGQGTTVTVSS
			SEQ ID NO: 236
		NA	CAGGTGCAGTTGCAGGAGTCGGGCCCAGGACTG GTGAAGCCTTCAGAGACCCTGTCCCTCACCTGC ACTGTCTCTGGTGACTCCATCAGCAGTGGTGGTTT ACTACTGGAGCTGGATCCGCCAGCCCCCAGGGA AGGGCCTGGAGTGGATTGGGTACATCTATTACA GTGGGAGCACCTACTACAACCCGTCCCTCAAGA GTCGAGTTACCATATCAGTAGACACGTCTAAGA ACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC CGCGGACACGGCCGTGTATTACTGTGCGAGAGA TCGTATTACGATTTTTGGAGTGGTTATGGGGGGC GGTATGGACGTCTGGGGCCAAGGGACCACGGTC ACCGTCTCCTCA
			SEQ ID NO: 1807
		AA	QVQLQESGPGLVKPSETLSLTCTVSGDSISSGGYY WSWIRQPPGKGLEWIGYIYYSGSTYYNPSLKSRVT ISVDTSKNQFSLKLSSVTAADTAVYYCARDRITIFG VVMGGGMDVWGQGTTVTVSS

iPS:359628	18E3.004	NA	SEQ ID NO: 80
			GAAATTGTGTTGACGCAGTCTCCAGGCACCCTG
			TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT
			GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT
			TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC
			CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG
			CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG
			GGTCTGGGACAGACTTCACTCTCACCATCAGCA
			GACTGGAGCCTGATGATTTTGCAGTGTATTACTG
			TCAGCAGTATGGTAGTTCACCGCTCACTTTCGGC
			GGAGGGACCAAGGTGGAGATCAAACGA
			SEQ ID NO: 1651
		AA	EIVLTQSPGTLSLSPGERATLSCRASQSISYSYLAW
			YQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF
			TLTISRLEPDDFAVYYCQQYGSSPLTFGGGTKVEIK
			R
			SEQ ID NO: 81
iPS:359637	18E3.005	NA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTG
			TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT
			GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT
			TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC
			CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG
			CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG
			GGTCTGGGACAGACTTCACTCTCACCATCAGCA
			GACTGGAGCCTGATGATTTTGCAGTGTATTACTG
			TCAGCAGTATGGTAGTTCACCGCTCACTTTCGGC
			GGAGGGACCAAGGTGGAGATCAAACGA
			SEQ ID NO: 1652
		AA	EIVLTQSPGTLSLSPGERATLSCRASQSISYSYLAW
			YQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF
			TLTISRLEPDDFAVYYCQQYGSSPLTFGGGTKVEIK
			R

			SEQ ID NO: 237
			CAGGTGCAGTTGCAGGAGTCGGGCCCAGGACTG
			GTGAAGCCTTCACAGACCCTGTCCCTCACCTGC
			ACTGTCTCTGGTGACTCCATCAGCAGTGGTGGTT
			ACTACTGGAGCTGGATCCGCCAGCCCCCAGGGA
			AGGGCCTGGAGTGGATTGGGTACATCTATTACA
			GTGGGAGCACCTACTACAACCCGTCCCTCAAGA
			GTCGAGTTACCATATCAGTAGACACGTCTAAGA
			ACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC
			CGCGGACACGGCCGTGTATTACTGTGCGAGAGA
			TCGTATTACGATTTTTGGAGTGGTTATGGGGGGC
			GGTATGGACGTCTGGGGCCAAGGGACCACGGTC
			ACCGTCTCCTCA
			SEQ ID NO: 1808
			QVQLQESGPGLVKPSQTLSLTCTVSGDSISSGGYY
			WSWIRQPPGKGLEWIGYIYYSGSTYYNPSLKSRVT
			ISVDTSKNQFSLKLSSVTAADTAVYYCARDRITIFG
			VVMGGGMDVWGQGTTVTVSS
			SEQ ID NO: 238
			CAGGTGCAGTTGCAGGAGTCGGGCCCAGGACTG
			GTGAAGCCTTCAGAGACCCTGTCCCTCACCTGC
			ACTGTCTCTGGTGACTCCATCAGCAGTGGTGGTT
			ACTACTGGAGCTGGATCCGCCAGCACCCAGGGA
			AGGGCCTGGAGTGGATTGGGTACATCTATTACA
			GTGGGAGCACCTACTACAACCCGTCCCTCAAGA
			GTCGAGTTACCATATCAGTAGACACGTCTAAGA
			ACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC
			CGCGGACACCGGCCGTGTATTACTGTGCGAGAGA
			TCGTATTACGATTTTTGGAGTGGTTATGGGGGGC
			GGTATGGACGTCTGGGGCCAAGGGACCACGGTC
			ACCGTCTCCTCA
			SEQ ID NO: 1809
			QVQLQESGPGLVKPSETLSLTCTVSGDSISSGGYY
			WSWIRQHPGKGLEWIGYIYYSGSTYYNPSLKSRVT
			ISVDTSKNQFSLKLSSVTAADTAVYYCARDRITIFG
			VVMGGGMDVWGQGTTVTVSS

iPS:361210	18E3.006	NA	SEQ ID NO: 82
			GAAATTGTGTTGACGCAGTCTCCAGGCACCCTG
			TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT
			GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT
			TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC
			CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG
			CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG
			GGTCTGGGACAGACTTCACTCTCACCATCAGCA
			GACTGGAGCCTGATGATTTTGCAGTGTATTACTG
			TCAGCAGTATGGTAGTTCACCGCTCACTTTCGGC
			GGAGGGACCAAGGTGGAGATCAAACGA
			SEQ ID NO: 1653
		AA	SEQ ID NO: 1810
			EIVLTQSPGTLSLSPGERATLSCRASQSISYSYLAW
			YQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF
			TLTISRLEPDDFAVYYCQQYGSSPLTFGGGTKVEIK
			R
			SEQ ID NO: 83
iPS:361214	18E3.007	NA	SEQ ID NO: 240
			GAAATTGTGTTGACGCAGTCTCCAGGCACCCTG
			TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT
			GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT
			TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC
			CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG
			CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG
			GGTCTGGGACAGACTTCACTCTCACCATCAGCA
			GACAGGAGCCTGATGATTTTGCAGTGTATTACT
			GTCAGCAGTATGGTAGTTCACCGCTCACTTTCGG
			CGGAGGGACCAAGGTGGAGATCAAACGA
			SEQ ID NO: 1654
		AA	SEQ ID NO: 1811
			EIVLTQSPGTLSLSPGERATLSCRASQSISYSYLAW
			YQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF
			TLTISRQEPDDFAVYYCQQYGSSPLTFGGGTKVEI
			KR

			SEQ ID NO: 239
			CAGGTGCAGTTGCAGGAGTCGGGCCCAGGACTG
			GTGAAGCCTTCACAGACCCTGTCCCTCACCTGC
			ACTGTCTCTGGTGACTCCATCAGCAGTGGTGGTT
			ACTACTGGAGCTGGATCCGCCAGCACCCAGGGA
			AGGGCCTGGAGTGGATTGGGTACATCTATTACA
			GTGGGAGCACCTACTACAACCCGTCCCTCAAGA
			GTCGAGTTACCATATCAGTAGACACGTCTAAGA
			ACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC
			CGCGGACACGGCCGTGTATTACTGTGCGAGAGA
			TCGTATTACGATTTTTGGAGTGGTTATGGGGGGC
			GGTATGGACGTCTGGGGCCAAGGGACCACGGTC
			ACCGTCTCCTCA
			SEQ ID NO: 1810
			QVQLQESGPGLVKPSQTLSLTCTVSGDSISSGGYY
			WSWIRQHPGKGLEWIGYIYYSGSTYYNPSLKSRVT
			ISVDTSKNQFSLKLSSVTAADTAVYYCARDRITIFG
			VVMGGGMDVWGQGTTVTVSS
			SEQ ID NO: 240
			CAGGTGCAGTTGCAGGAGTCGGGCCCAGGACTG
			GTGAAGCCTTCAGAGACCCTGTCCCTCACCTGC
			ACTGTCTCTGGTGACTCCATCAGCAGTGGTGGTT
			ACTACTGGAGCTGGATCCGCCAGCACCCAGGGA
			AGGGCCTGGAGTGGATTGGGTACATCTATTACA
			GTGGGAGCACCTACTACAACCCGTCCCTCAAGA
			GTCGAGTTACCATATCAGTAGACACGTCTAAGA
			ACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC
			CGCGGACACGGCCGTGTATTACTGTGCGAGAGA
			TCGTATTACGATTTTTGGAGTGGTTATGGGGGGC
			GGTATGGACGTCTGGGGCCAAGGGACCACGGTC
			ACCGTCTCCTCA
			SEQ ID NO: 1811
			QVQLQESGPGLVKPSETLSLTCTVSGDSISSGGYY
			WSWIRQHPGKGLEWIGYIYYSGSTYYNPSLKSRVT
			ISVDTSKNQFSLKLSSVTAADTAVYYCARDRITIFG
			VVMGGGMDVWGQGTTVTVSS

iPS:361218	18E3.008	NA	SEQ ID NO: 84
			GAAATTGTGTTGACGCAGTCTCCAGGCACCCTG
			TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT
			GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT
			TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC
			CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG
			CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG
			GGTCTGGGACAGACTTCACTCTCACCATCAGCA
			GACAGGAGCCTGATGATTTTGCAGTGTATTACT
			GTCAGCAGTATGGTAGTTCACCGCTCACTTTCGG
			CGGAGGGACCAAGGTGGAGATCAAACGA
			SEQ ID NO: 1655
		AA	SEQ ID NO: 1812
			EIVLTQSPGTLSLSPGERATLSCRASQSISYSYLAW
			YQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF
			TLTISRQEPDDFAVYYCQQYGSSPLTFGGGTKVEI
			KR
			SEQ ID NO: 85
iPS:361222	5C2.006	NA	SEQ ID NO: 241
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACATAGCTTGGTACCAGCAG
			CAACCAGGACATCCTCCTCTAAGCTGCTCATTTACT
			GGGCATCTACCCGGGAATCCGGGTCCCTGACC
			GATTCAGTGGCAGCGGGTCTGGGACAGATTTCA
			CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG
			TGGCAGTTTTTTACTGTCAACAATATTATAGTAC
			TCCGTGGACGTTCGGCCAAGGGACCAAGGTGGA
			AATCAAACGA
			SEQ ID NO: 1656
		AA	SEQ ID NO: 1813
			DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK
			NYIAWYQQPGHPPKLLIYWASTRESGVPDRFSGS
			GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ
			GTKVEIKR
			CAGGTGCAGTTGCAGGAGTCGGGCCCAGGACTG
			GTGAAGCCTTCACAGACCCTGTCCCTCACCTGC
			ACTGTCTCTGGTGACTCCATCAGCAGTGGTGGTT
			ACTACTGGAGCTGGATCCGCCAGCCCCCAGGGA
			AGGGCCTGGAGTGGATTGGGTACATCTATTACA
			GTGGGAGCACCTACTACAACCCGTCCCTCAAGA
			GTCGAGTTACCATATCAGTAGACACGTCTAAGA
			ACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC
			CGCGGACACGGCCGTGTATTACTGTGCGAGAGA
			TCGTATTACGATTTTTGGAGTGGTTATGGGGGGC
			GGTATGGACGTCTGGGGCCAAGGGACCACGGTC
			ACCGTCTCCTCA
			SEQ ID NO: 1812
		AA	QVQLQESGPGLVKPSQTLSLTCTVSGDSISSGGYY
			WSWIRQPPGKGLEWIGYIYYSGSTYYNPSLKSRVT
			ISVDTSKNQFSLKLSSVTAADTAVYYCARDRITIFG
			VVMGGGMDVWGQGTTVTVSS
			SEQ ID NO: 242
		NA	CAGGTGCAGCTGGTGCAGTCTGGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATCCACTGGGTGCGACAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGGTGGATCAACCCTGAAAGT
			GGTGGCACAGACTATTCACAGAGGTTTCAGGGC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTACATGGAACTGAACAGGCTGAGATCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGAG
			GCCACGATTTTTGGAATGGTTATTGTACCGTTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1813
		AA	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLEWMGWINPESGGTDYSQRFQGR
			VTMTRDTSISTAYMELNRLRSDDTAVYYCAREATI
			FGMVIVPFDYWGQGTLVTVSS

iPS:361229	5C2.007	NA	SEQ ID NO: 86
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACATAGCTTGGTACCAGCAG
			CAACCAGGACATCCTCCTCAAGCTGCTCATTTACT
			GGGCATCTACCCGGGAATCCGGGTCCCTGACC
			GATTCAGTGGCAGCGGGTCTGGGACAGATTTTCA
			CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG
			TGGCAGTTTTTTACTGTCAACAATATTATAGTAC
			TCCGTGGACGTTCGGCCAAGGGACCAAGGTGGA
			AATCAAACGA
			SEQ ID NO: 1657
		AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK
			NYIAWYQQQPGHPPKLLIYWASTRESGVPDRFSGS
			GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ
			GTKVEIKR
			SEQ ID NO: 87
iPS:361236	5C2.008	NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACATAGCTTGGTACCAGCAG
			CAACCAGGACATCCTCCTCAAGCTGCTCATTTACT
			GGGCATCTACCCGGGAATCCGGGTCCCTGACC
			GATTCAGTGGCAGCGGGTCTGGGACAGATTTTCA
			CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG
			TGGCAGTTTTTTACTGTCAACAATATTATAGTAC
			TCCGTGGACGTTCGGCCAAGGGACCAAGGTGGA
			AATCAAACGA
			SEQ ID NO: 1658
		AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK
			NYIAWYQQQPGHPPKLLIYWASTRESGVPDRFSGS
			GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ
			GTKVEIKR
			SEQ ID NO: 243
			CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATCCACTGGGTGCGACAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGGTGGATCAACCCTGAAAGT
			GGTGGCACAGACTATTTCACAGAGGTTTCAGGGC
			AGGTTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTACATGGAACTGAACAGGCTGAGATCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGAG
			GCCACGATTTTTGGAATGGTTATTGTACCGTTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1814
		AA	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLEWMGWINPESGGTDYSQRFQGR
			FTMTRDTSISTAYMELNRLRSDDTAVYYCAREATI
			FGMVIVPFDYWGQGTLVTVSS
			SEQ ID NO: 244
		NA	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATCCACTGGGTGCGACAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGGTGGATCAACCCTGACGCT
			GGTGGCACAGACTATTTCACAGAGGTTTCAGGGC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTACATGGAACTGAACAGGCTGAGATCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGAG
			GCCACGATTTTTGGAATGGTTATTGTACCGTTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1815
		AA	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLEWMGWINPDAGGTDYSQRFQG
			RVTMTRDTSISTAYMELNRLRSDDTAVYYCAREA
			TIFGMVIVPFDYWGQGTLVTVSS

iPS:359685	5C2.009	NA	SEQ ID NO: 88
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACATAGCTTGGTACCAGCAG
			CAACCAGGACATCCTCCTCAAGCTGCTCATTTACT
			GGGCATCTACCCGGGAATCCGGGTCCCTGACC
			GATTCAGTGGCAGCGGGTCTGGGACAGATTTTCA
			CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG
			TGGCAGTTTTTTACTGTCAACAATATTATAGTAC
			TCCGTGGACGTTCGGCCAAGGGACCAAGGTGGA
			AATCAAACGA
			SEQ ID NO: 1659
		AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK
			NYIAWYQQQPGHPPKLLIYWASTRESGVPDRFSGS
			GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ
			GTKVEIKR
			SEQ ID NO: 89
iPS:361240	5C2.010	NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACATAGCTTGGTACCAGCAG
			CAACCAGGACATCCTCCTCAAGCTGCTCATTTACT
			GGGCATCTACCCGGGAATCCGGGTCCCTGACC
			GATTCAGTGGCAGCGGGTCTGGGACAGATTTTCA
			CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG
			TGGCAGTTTTTTACTGTCAACAATATTATAGTAC
			TCCGTGGACGTTCGGCCAAGGGACCAAGGTGGA
			AATCAAACGA
			SEQ ID NO: 1660
		AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK
			NYIAWYQQQPGHPPKLLIYWASTRESGVPDRFSGS
			GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ
			GTKVEIKR
			SEQ ID NO: 245
			CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATCCACTGGGTGCGACAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGGTGGATCAACCCTGACGCT
			GGTGGCACAGACTATTTCACAGAGGTTTCAGGGC
			AGGTTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTACATGGAACTGAACAGGCTGAGATCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGAG
			GCCACGATTTTTGGAATGGTTATTGTACCGTTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1816
		AA	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLEWMGWINPDAGGTDYSQRFQG
			RFTMTRDTSISTAYMELNRLRSDDTAVYYCAREA
			TIFGMVIVPFDYWGQGTLVTVSS
			SEQ ID NO: 246
		NA	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATCCACTGGGTGCGACAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGGTGGATCAACCCTGACAGT
			GGTGGCACAGACTATTTCACAGAGGTTTCAGGGC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTACATGGAACTGAACAGGCTGAGATCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGAG
			GCCACGATTTTTGGAATGGTTATTGTACCGTTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1817
		AA	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLEWMGWINPDSGGTDYSQRFQGR
			VTMTRDTSISTAYMELNRLRSDDTAVYYCAREATI
			FGMVIVPFDYWGQGTLVTVSS

IPS:361247	SC2.011	NA	SEQ ID NO: 90
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACATAGCTTGGTACCAGCAG
			CAACCAGGACATCCTCCTCAAGCTGCTCATTTACT
			GGGCATCTACCCGGGAATCCGGGTCCCTGACC
			GATTCAGTGGCAGCGGGTCTGGGACAGATTTTCA
			CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG
			TGGCAGTTTTTTACTGTCAACAATATTATAGTAC
			TCCGTGGACGTTCGGCCAAGGGACCAAGGTGGA
			AATCAAACGA
			SEQ ID NO: 1661
		AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK
			NYIAWYQQQPGHPPKLLIYWASTRESGVPDRFSGS
			GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ
			GTKVEIKR
			SEQ ID NO: 91
IPS:361254	SC2.012	NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACATAGCTTGGTACCAGCAG
			CAACCAGGACATCCTCCTCAAGCTGCTCATTTACT
			GGGCATCTACCCGGGAATCCGGGTCCCTGACC
			GATTCAGTGGCAGCGGGTCTGGGACAGATTTTCA
			CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG
			TGGCAGTTTTTTACTGTCAACAATATTATAGTAC
			TCCGTGGACGTTCGGCCAAGGGACCAAGGTGGA
			AATCAAACGA
			SEQ ID NO: 1662
		AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK
			NYIAWYQQQPGHPPKLLIYWASTRESGVPDRFSGS
			GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ
			GTKVEIKR
			SEQ ID NO: 247
			CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATCCACTGGGTGCGACAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGGTGGATCAACCCTGACAGT
			GGTGGCACAGACTATTTCACAGAGGTTTCAGGGC
			AGGTTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTACATGGAACTGAACAGGCTGAGATCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGAG
			GCCACGATTTTTGGAATGGTTATTGTACCGTTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1818
		AA	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLEWMGWINPDSGGTDYSQRFQGR
			FTMTRDTSISTAYMELNRLRSDDTAVYYCAREATI
			FGMVIVPFDYWGQGTLVTVSS
			SEQ ID NO: 248
		NA	CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATCCACTGGGTGCGACAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGGTGGATCAACCCTGACAGT
			GGTGGCACAGACTATTTCACAGAGGTTTCAGGGC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTACATGGAACTGAACAGGCTGAGATCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGAG
			GCCACGATTTTTGGAATGGTTATTGTACCGTTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1819
		AA	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLEWMGWINPDSGGTDYSQRFQGR
			VTMTRDTSISTAYMELNRLRSDDTAVYYCAREATI
			FGMVIVPFDYWGQGTLVTVSS

iPS:361261	5C2.013	NA	SEQ ID NO: 92
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACATAGCTTGGTACCAGCAG
			CAACCAGGACATCCTCCTCAAGCTGCTCATTTACT
			GGGCATCTACCCGGGAATCCGGGTCCCTGACC
			GATTCAGTGGCAGCGGGTCTGGGACAGATTTTCA
			CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG
			TGGCAGTTTTTTACTGTCAACAATATTATAGTAC
			TCCGTGGACGTTCGGCCAAGGGACCAAGGTGGA
			AATCAAACGA
			SEQ ID NO: 1663
		AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK
			NYIAWYQQQPGHPPKLLIYWASTRESGVPDRFSGS
			GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ
			GTKVEIKR
			SEQ ID NO: 93
iPS:361268	5C2.014	NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACATAGCTTGGTACCAGCAG
			CAACCAGGACATCCTCCTCAAGCTGCTCATTTACT
			GGGCATCTACCCGGGAATCCGGGTCCCTGACC
			GATTCAGTGGCAGCGGGTCTGGGACAGATTTTCA
			CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG
			TGGCAGTTTTTTACTGTCAACAATATTATAGTAC
			TCCGTGGACGTTCGGCCAAGGGACCAAGGTGGA
			AATCAAACGA
			SEQ ID NO: 1664
		AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK
			NYIAWYQQQPGHPPKLLIYWASTRESGVPDRFSGS
			GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ
			GTKVEIKR
			SEQ ID NO: 249
			CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATCCACTGGGTGCGACAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGGTGGATCAACCCTGACGCT
			GGTGGCACAGACTATTCACAGAGGTTTCAGGGC
			AGGTTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTACATGGAACTGAACAGGCTGAGATCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGAG
			GCCACGATTTTTGGAATGGTTATTGTACCGTTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1820
		AA	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLEWMGWINPDAGGTDYSQRFQG
			RFTMTRDTSISTAYMELNRLRSDDTAVYYCAREA
			TIFGMVIVPFDYWGQGTLVTVSS
			SEQ ID NO: 250
		NA	CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATCCACTGGGTGCGACAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGGTGGATCAACCCTGACGCT
			GGTGGCACAGACTATTCACAGAGGTTTCAGGGC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTACATGGAACTGAACAGGCTGAGATCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGAG
			GCCACGATTTTTGGAATGGTTATTGTACCGTTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1821
		AA	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLEWMGWINPDAGGTDYSQRFQG
			RVTMTRDTSISTAYMELNRLRSDDTAVYYCAREA
			TIFGMVIVPFDYWGQGTLVTVSS

iPS:359669	5C2.015	NA	SEQ ID NO: 94
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACATAGCTTGGTACCAGCAG
			AAACCAGGACAACCTCCTAAGCTGCTCATTTAC
			TGGGCATCTACCCGGGAATCCGGGGTCCCTGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC
			ACTCTCACCATCAGCAGCCTGCAGGCTGAAGAT
			GTGGCAGTTTTTTACTGTCAACAATATTATAGTA
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG
			AAATCAAACGA
			SEQ ID NO: 1665
		AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK
			NYIAWYQQKPGQPPKLLIYWASTRESGVPDRFSGS
			GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ
			GTKVEIKR
			SEQ ID NO: 95
iPS:359678	5C2.016	NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACATAGCTTGGTACCAGCAG
			AAACCAGGACAACCTCCTAAGCTGCTCATTTAC
			TGGGCATCTACCCGGGGAATCCGGGGTCCCTGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC
			ACTCTCACCATCAGCAGCCTGCAGGCTGAAGAT
			GTGGCAGTTTTTTACTGTCAACAATATTATAGTA
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG
			AAATCAAACGA
			SEQ ID NO: 1666
		AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK
			NYIAWYQQKPGQPPKLLIYWASTRESGVPDRFSGS
			GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ
			GTKVEIKR
			SEQ ID NO: 251
			CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATCCACTGGGTGCGACAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGGTGGATCAACCCTGACGCT
			GGTGGCACAGACTATTTCACAGAGGTTTCAGGGC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTACATGGAACTGAACAGCCTGAGATCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGAG
			GCCACGATTTTTGGAATGGTTATTGTACCGTTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1822
		AA	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLEWMGWINPDAGGTDYSQRFQG
			RVTMTRDTSISTAYMELNSLRSDDTAVYYCAREA
			TIFGMVIVPFDYWGQGTLVTVSS
			SEQ ID NO: 252
		NA	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATCCACTGGGTGCGACAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGGTGGATCAACCCTGAAAGT
			GGTGGCACAGACTATTTCACAGAGGTTTCAGGGC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTACATGGAACTGAACAGCCTGAGATCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGAG
			GCCACGATTTTTGGAATGGTTATTGTACCGTTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1823
		AA	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLEWMGWINPESGGTDYSQRFQGR
			VTMTRDTSISTAYMELNSLRSDDTAVYYCAREATI
			FGMVIVPFDYWGQGTLVTVSS

iPS:361275	11C1.002	NA	SEQ ID NO: 253
			CAGGTGCCGCTGGTACAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
			CTTGTGTGGATGGGGTGGATCAGCCCTAACAGT
			GGTGAAACAAGCTATGCACAGAAGTTTCAGGAC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTATATGGAGCTGAGCAGACTGAGATCT
			GACGACACGGCCGTGTATTTCTGTGCGAGAGAG
			GCCACGATTTTTGGAATGCTTATTGTACCATTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1824
		AA	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLVWMGWISPNSGETSYAQKFQDR
			VTMTRDTSISTAYMELSRLRSDDTAVYFCAREATI
			FGMLIVPFDYWGQGTLVTVSS
			SEQ ID NO: 254
iPS:361282	11C1.003	NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACTTAGCTTGGTACCAACAG
			AAACCAGGACAGCCTCCTAACCTGCTCATTTAC
			TGGACTTCTACCCGAGAATCCGGGGTCCCTGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC
			ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT
			GTGGCTGTTTATTACTGTCAGCAATATTATCGTA
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG
			AAATCAAACGA
			SEQ ID NO: 1667
		AA	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK
			NYLAWYQQKPGQPPNLLIYWTSTRESGVPDRFSG
			SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF
			GQGTKVEIKR
			SEQ ID NO: 97
		NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACTTAGCTTGGTACCAACAG
			AAACCAGGACAGCCTCCTAACCTGCTCATTTAC
			TGGACTTCTACCCGAGAATCCGGGGTCCCTGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC
			ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT
			GTGGCTGTTTATTACTGTCAGCAATATTATCGTA
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG
			AAATCAAACGA
			SEQ ID NO: 1668
		AA	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK
			NYLAWYQQKPGQPPNLLIYWTSTRESGVPDRFSG
			SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF
			GQGTKVEIKR
			SEQ ID NO: 255
		NA	CAGGTGCCGCTGGTACAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
			CTTGTGTGGATGGGGTGGATCAGCCCTAACAGT
			GGTGAAACAAGCTATGCACAGAAGTTTCAGGAC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTATATGGAGCTGAGCAGACTGAGATCT
			GACGACACGGCCGTGTATTTCTGTGCGAGAGAG
			GCCACGATTTTTGGAATGCTTATTGTACCATTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1825
		AA	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLVWMGWISPNSGDTSYAQKFQDR
			VTMTRDTSISTAYMELSRLRSDDTAVYFCAREATI
			FGMLIVPFDYWGQGTLVTVSS

iPS:361289	11C1.004	NA	SEQ ID NO: 98
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACTTAGCTTGGTACCAACAG
			AAACCAGGACAGCCTCCTAACCTGCTCATTTAC
			TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC
			ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT
			GTGGCTGTTTATTACTGTCAGCAATATTATCGTA
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG
			AAATCAAACGA
			SEQ ID NO: 1669
		AA	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK
			NYLAWYQQKPGQPPNLLIYWTSTRDSGVPDRFSG
			SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF
			GQGTKVEIKR
			SEQ ID NO: 99
iPS:359712	11C1.005	NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACTTAGCTTGGTACCAACAG
			AAACCAGGACAGCCTCCTAACCTGCTCATTTAC
			TGGACTTCTACCCGAGAATCCGGGGTCCCTGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC
			ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT
			GTGGCTGTTTATTACTGTCAGCAATATTATCGTA
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG
			AAATCAAACGA
			SEQ ID NO: 1670
		AA	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK
			NYLAWYQQKPGQPPNLLIYWTSTRESGVPDRFSG
			SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF
			GQGTKVEIKR
			SEQ ID NO: 255
			CAGGTGCCGCTGGTACAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
			CTTGTGTGGATGGGGGTGGATCAGCCCTAACAGT
			GGTGAAACAAGCTATGCACAGAAGTTTCAGGAC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTATATGGAGCTGAGCAGACTGAGATCT
			GACGACACGGCCGTGTATTTCTGTGCGAGAGAG
			GCCACGATTTTTGGAATGCTTATTGTACCATTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1826
		AA	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLVWMGWISPNSGETSYAQKFQDR
			VTMTRDTSISTAYMELSRLRSDDTAVYFCAREATI
			FGMLIVPFDYWGQGTLVTVSS
			SEQ ID NO: 256
		NA	CAGGTGCCGCTGGTACAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
			CTTGTGTGGATGGGGGTGGATCAGCCCTAACAGT
			GGTGAAACAAGCTATGCACAGAAGTTTCAGGAC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTATATGGAGCTGAGCAGACTGAGATCT
			GACGACACGGCCGTGTATTTCTGTACGAGAGAG
			GCCACGATTTTTGGAATGCTTATTGTACCATTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1827
		AA	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLVWMGWISPNSGETSYAQKFQDR
			VTMTRDTSISTAYMELSRLRSDDTAVYFCTREATI
			FGMLIVPFDYWGQGTLVTVSS

iPS:361293	11C1.006	NA	SEQ ID NO: 100
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACTTAGCTTGGTACCAACAG
			AAACCAGGACAGCCTCCTAACCTGCTCATTTAC
			TGGACTTCTACCCGAGAATCCGGGGTCCCTGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC
			ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT
			GTGGCTGTTTATTACTGTCAGCAATATTATCGTA
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG
			AAATCAAACGA
			SEQ ID NO: 1671
		AA	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK
			NYLAWYQQKPGQPPNLLIYWTSTRESGVPDRFSG
			SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF
			GQGTKVEIKR
			SEQ ID NO: 101
iPS:361297	11C1.007	NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACTTAGCTTGGTACCAACAG
			AAACCAGGACAGCCTCCTAACCTGCTCATTTAC
			TGGACTTCTACCCGAGAATTCCGGGGTCCCTGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC
			ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT
			GTGGCTGTTTATTACTGTCAGCAATATTATCGTA
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG
			AAATCAAACGA
			SEQ ID NO: 1672
		AA	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK
			NYLAWYQQKPGQPPNLLIYWTSTRDSGVPDRFSG
			SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF
			GQGTKVEIKR
			SEQ ID NO: 257
			CAGGTGCCGCTGGTACAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
			CTTGTGTGGATGGGGGTGATCAGCCCTAACAGT
			GGTGACACAAGCTATGCACAGAAGTTTCAGGAC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTATATGGAGCTGAGCAGACTGAGATCT
			GACGACACGGCCGTGTATTTCTGTACGAGAGAG
			GCCACGATTTTTGGAATGCTTATTGTACCATTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1828
		AA	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLVWMGWISPNSGDTSYAQKFQDR
			VTMTRDTSISTAYMELSRLRSDDTAVYFCTREATI
			FGMLIVPFDYWGQGTLVTVSS
			SEQ ID NO: 258
		NA	CAGGTGCCGCTGGTACAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
			CTTGTGTGGATGGGGGTGATCAGCCCTAACAGT
			GGTGAAACAAGCTATGCACAGAAGTTTCAGGAC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTATATGGAGCTGAGCAGACTGAGATCT
			GACGACACGGCCGTGTATTTCTGTACGAGAGAG
			GCCACGATTTTTGGAATGCTTATTGTACCATTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1829
		AA	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLVWMGWISPNSGETSYAQKFQDR
			VTMTRDTSISTAYMELSRLRSDDTAVYFCTREATI
			FGMLIVPFDYWGQGTLVTVSS

iPS:361301	11C1.008	NA	SEQ ID NO: 259
			CAGGTGCCGCTGGTACAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
			CTTGTGTGGATGGGGTGGATCAGCCCTAACAGT
			GGTGACACAAGCTATGCACAGAAGTTTCAGGAC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTATATGGAGCTGAGCAGACTGAGATCT
			GACGACACGGCCGTGTATTTCTGTGCGAGAGAG
			GCCACGATTTTTGGAATGCTTATTGTACCATTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1673
		AA	SEQ ID NO: 1830
			QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLVWMGWISPNSGDTSYAQKFQDR
			VTMTRDTSISTAYMELSRLRSDDTAVYFCAREATI
			FGMLIVPFDYWGQGTLVTVSS
			SEQ ID NO: 103
iPS:359703	11C1.009	NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACTTAGCTTGGTACCAACAG
			AAACCAGGACAGCCTCCTAAACTGCTCATTTAC
			TGGACTTCTACCCGAGAATCCGGGGTCCCTGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC
			ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT
			GTGGCTGTTTATTACTGTCAGCAATATTATCGTA
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG
			AAATCAAACGA
			SEQ ID NO: 1674
		AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK
			NYLAWYQQKPGQPPKLLIYWTSTRESGVPDRFSG
			SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF
			GQGTKVEIKR

iPS:361305	11C1.010	NA	SEQ ID NO: 104
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACTTAGCTTGGTACCAACAG
			AAACCAGGACAGCCTCCTAACCTGCTCATTTAC
			TGGACTTCTACCCGAGAATCCGGGGTCCCTGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC
			ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT
			GTGGCTGTTTATTACTGTCAGCAATATTATCGTA
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG
			AAATCAAACGA
			SEQ ID NO: 1675
		AA	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK
			NYLAWYQQKPGQPPNLLIYWTSTRESGVPDRFSG
			SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF
			GQGTKVEIKR
			SEQ ID NO: 105
iPS:361312	13H12.002	NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACATAGCTTGGTACCAGCAG
			AAACCAGGACATCCTCCTCTAAGCTGCTCATTTACT
			GGGCATCTACCCGGGGAATCCGGGGTCCCTGACC
			GATTCAGTGGCAGCGGGTCTGGGACAGATTTCA
			CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG
			TGGCAGTTTTTTACTGTCAACAATATTATAGTAC
			TCCGTGGACGTTCGGCCAAGGGACCAAGGTGGA
			AATCAAACGA
			SEQ ID NO: 1676
		AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK
			NYIAWYQQKPGHPPKLLIYWASTRESGVPDRFSGS
			GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ
			GTKVEIKR
			SEQ ID NO: 261
			CAGGTGCAGCTGGTACAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGGGTGGATCAGCCCTAACAGT
			GGTGAAACAAGCTATGCACAGAAGTTTCAGGAC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTATATGGAGCTGAGCAGACTGAGATCT
			GACGACACGGCCGTGTATTTCTGTGCGAGAGAG
			GCCACGATTTTTGGAATGCTTATTGTACCATTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1832
		AA	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLEWMGWISPNSGETSYAQKFQDR
			VTMTRDTSISTAYMELSRLRSDDTAVYFCAREATI
			FGMLIVPFDYWGQGTLVTVSS
			SEQ ID NO: 262
		NA	CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATCCACTGGGGTGCGACAGGCCCCTGGACAAGGA
			CTTGAGTGGATGGGGGTGGATCAACCCTGAAAGT
			GGTGGCACAGACTATTCACAGAGGTTTCAGGGC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTACATGGAACTGAGCAGGCTGAGATCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGAG
			GCCACGATTTTTGGAATGGTTATTGTACCGTTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1833
		AA	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLEWMGWINPESGGTDYSQRFQGR
			VTMTRDTSISTAYMELSRLRSDDTAVYYCAREATI
			FGMVIVPFDYWGQGTLVTVSS

iPS:359744	13H12.003	NA	SEQ ID NO: 106
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACATAGCTTGGTACCAGCAG
			AAACCAGGACATCCTCCTAAGCTGCTCATTTACT
			GGGCATCTACCCGGGAATCCGGGTCCCTGACC
			GATTCAGTGGCAGCGGGTCTGGGACAGATTTTCA
			CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG
			TGGCAGTTTTTTACTGTCAACAATATTATAGTAC
			TCCGTGGACGTTCGGCCAAGGGACCAAGGTGGA
			AATCAAACGA
			SEQ ID NO: 263
		AA	SEQ ID NO: 1677
			DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK
			NYIAWYQQKPGHPPKLLIYWASTRESGVPDRFSGS
			GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ
			GTKVEIKR
			SEQ ID NO: 1834
iPS:361319	13H12.004	NA	SEQ ID NO: 264
			CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATCCACTGGGTGCGACAGGCCCCTGGACAAGGA
			CTTGAGTGGATGGGGTGGATCAACCCTGACAGT
			GGTGGCACAGACTATTTCACAGAGGTTTCAGGGC
			AGGTTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTACATGGAACTGAGCAGGCTGAGATCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGAG
			GCCACGATTTTTGGAATGGTTATTGTACCGTTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1835
		AA	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLEWMGWINPDSGGTDYSQRFQGR
			VTMTRDTSISTAYMELSRLRSDDTAVYYCAREATI
			FGMVIVPFDYWGQGTLVTVSS

iPS:359737	13H12.005	NA	SEQ ID NO: 108
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACATAGCTTGGTACCAGCAG
			AAACCAGGACAACCTCCTAAGCTGCTCATTTAC
			TGGGCATCTACCCGGGAATCCGGGGTCCCTGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC
			ACTCTCACCATCAGCAGCCTGCAGGCTGAAGAT
			GTGGCAGTTTTTTACTGTCAACAATATTATAGTA
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG
			AAATCAAACGA
			SEQ ID NO: 1679
		AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK
			NYIAWYQQKPGQPPKLLIYWASTRESGVPDRFSGS
			GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ
			GTKVEIKR
			SEQ ID NO: 109
iPS:361326	13H12.006	NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACATAGCTTGGTACCAGCAG
			AAACCAGGACAACCTCCTAAGCTGCTCATTTAC
			TGGGCATCTACCCGGGAATCCGGGGTCCCTGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC
			ACTCTCACCATCAGCAGCCTGCAGGCTGAAGAT
			GTGGCAGTTTTTTACTGTCAACAATATTATAGTA
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG
			AAATCAAACGA
			SEQ ID NO: 1680
		AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK
			NYIAWYQQKPGQPPKLLIYWASTRESGVPDRFSGS
			GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ
			GTKVEIKR
			SEQ ID NO: 265
			CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATCCACTGGGTGCGACAGGCCCCTGGACAAGGA
			CTTGAGTGGATGGGGTGGATCAACCCTGAAAGT
			GGTGGCACAGACTATTTCACAGAGGTTTCAGGGC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTACATGGAACTGAGCAGCCTGAGATCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGAG
			GCCACGATTTTTGGAATGGTTATTGTACCGTTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1836
		AA	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLEWMGWINPESGGTDYSQRFQGR
			VTMTRDTSISTAYMELSSLRSDDTAVYYCAREATI
			FGMVIVPFDYWGQGTLVTVSS
			SEQ ID NO: 266
		NA	CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATCCACTGGGTGCGACAGGCCCCTGGACAAGGA
			CTTGAGTGGATGGGGTGGATCAACCCTGAAAGT
			GGTGGCACAGACTATTTCACAGAGGTTTCAGGGC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTACATGGAACTGAGCAGGCTGAGATCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGAG
			GCCACGATTTTTGGAATGGTTATTGTACCGTTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1837
		AA	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLEWMGWINPESGGTDYSQRFQGR
			VTMTRDTSISTAYMELSRLRSDDTAVYYCAREATI
			FGMVIVPFDYWGQGTLVTVSS

iPS:361330	12H11.002	NA	SEQ ID NO: 110
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACTTAGCTTGGTACCAGCAG
			AAACCAGGACAGCCTCCTAACCTGCTCATTTAC
			TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC
			ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT
			GTGGCTGTTTATTACTGTCAGCAATATTATCGTA
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG
			AAATCAAACGA
		AA	SEQ ID NO: 1681
			DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK
			NYLAWYQQKPGQPPNLLIYWTSTRDSGVPDRFSG
			SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF
			GQGTKVEIKR
iPS:361337	12H11.003	NA	SEQ ID NO: 111
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACTTAGCTTGGTACCAGCAG
			AAACCAGGACAGCCTCCTAACCTGCTCATTTAC
			TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC
			ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT
			GTGGCTGTTTATTACTGTCAGCAATATTATCGTA
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG
			AAATCAAACGA
		AA	SEQ ID NO: 1682
			DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK
			NYLAWYQQKPGQPPNLLIYWTSTRDSGVPDRFSG
			SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF
			GQGTKVEIKR

	SEQ ID NO: 267
	CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG
	AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
	AAGGCTTCTGGATACACCTTCACCGGCTACTAT
	ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
	CTTGAGTGGATGGGGGTGGATAAGCCCTAACCAA
	GGTGAAACAAACTATGCACAGAAGTTTCAGGAC
	AGGGTCACCATGACCAGGGACACGTCCATCAGC
	ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT
	GACGACACGGCCGTGTATTACTGTGCGAGAGAG
	GCCACGATTTTTGGAATGCTTATTGTACCATTTG
	ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
	CCTCA
	SEQ ID NO: 1838
	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
	HWVRQAPGQGLEWMGWISPNQGETNYAQKFQD
	RVTMTRDTSISTAYMELSRLRSDDTAVYYCAREA
	TIFGMLIVPFDYWGQGTLVTVSS
	SEQ ID NO: 268
	CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG
	AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
	AAGGCTTCTGGATACACCTTCACCGGCTACTAT
	ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
	CTTGAGTGGATGGGGGTGGATAAGCCCTAACCAA
	GGTGACACAAACTATGCACAGAAGTTTCAGGAC
	AGGGTCACCATGACCAGGGACACGTCCATCAGC
	ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT
	GACGACACGGCCGTGTATTACTGTGCGAGAGAG
	GCCACGATTTTTGGAATGCTTATTGTACCATTTG
	ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
	CCTCA
	SEQ ID NO: 1839
	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
	HWVRQAPGQGLEWMGWISPNQGDTNYAQKFQD
	RVTMTRDTSISTAYMELSRLRSDDTAVYYCAREA
	TIFGMLIVPFDYWGQGTLVTVSS

iPS:361344	12H11.004	NA	SEQ ID NO: 269
			CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGGGTGGATAAGCCCTAACCAA
			GGTGAAACAAACTATGCACAGAAGTTTCAGGAC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT
			GACGACACGGCCGTGTATTACTGTACGAGAGAG
			GCCACGATTTTTGGAATGCTTATTGTACCATTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
		AA	SEQ ID NO: 1683
			DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK
			NYLAWYQQKPGQPPNLLIYWTSTRDSGVPDRFSG
			SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF
			GQGTKVEIKR
iPS:361351	12H11.005	NA	SEQ ID NO: 270
			CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGGGTGGATAAGCCCTAACAAT
			GGTGAAACAAACTATGCACAGAAGTTTCAGGAC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGAG
			GCCACGATTTTTGGAATGCTTATTGTACCATTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
		AA	SEQ ID NO: 1684
			DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK
			NYLAWYQQKPGQPPNLLIYWTSTRDSGVPDRFSG
			SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF
			GQGTKVEIKR

			SEQ ID NO: 271
			CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGGGTGGATAAGCCCTAACCAA
			GGTGAAACAAACTATGCACAGAAGTTTCAGGAC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGAG
			GCCACGATTTTTGGAATGCTTATTGTACCATTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 272
			DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK
			NYLAWYQQKPGQPPNLLIYWTSTRDSGVPDRFSG
			SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF
			GQGTKVEIKR

iPS:361358	12H11.006	NA	SEQ ID NO: 271
			CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGGGTGGATAAGCCCTAACAAT
			GGTGACACAAACTATGCACAGAAGTTTCAGGAC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGAG
			GCCACGATTTTTGGAATGCTTATTGTACCATTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
		AA	SEQ ID NO: 1842
			QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLEWMGWISPNNGDTNYAQKFQD
			RVTMTRDTSISTAYMELSRLRSDDTAVYYCAREA
			TIFGMLIVPFDYWGQGTLVTVSS
		NA	SEQ ID NO: 272
			CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGGGTGGATAAGCCCTAACCAA
			GGTGACACAAACTATGCACAGAAGTTTCAGGAC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT
			GACGACACGGCCGTGTATTACTGTACGAGAGAG
			GCCACGATTTTTGGAATGCTTATTGTACCATTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
	12H11.007	AA	SEQ ID NO: 1843
			QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLEWMGWISPNQGDTNYAQKFQD
			RVTMTRDTSISTAYMELSRLRSDDTAVYYCTREA
			TIFGMLIVPFDYWGQGTLVTVSS
		NA	SEQ ID NO: 1685
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACTTAGCTTGGTACCAGCAG
			AAACCAGGACAGCCTCCTAACCTGCTCATTTAC
			TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC
			ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT
			GTGGCTGTTTATTACTGTCAGCAATATTATCGTA
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG
			AAATCAAACGA
		AA	SEQ ID NO: 1685
			DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK
			NYLAWYQQKPGQPPNLLIYWTSTRDSGVPDRFSG
			SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF
			GQGTKVEIKR
		NA	SEQ ID NO: 115
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACTTAGCTTGGTACCAGCAG
			AAACCAGGACAGCCTCCTAACCTGCTCATTTAC
			TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC
			ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT
			GTGGCTGTTTATTACTGTCAGCAATATTATCGTA
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG
			AAATCAAACGA
		AA	SEQ ID NO: 1686
			DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK
			NYLAWYQQKPGQPPNLLIYWTSTRDSGVPDRFSG
			SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF
			GQGTKVEIKR

IPS:361372	12H11.008	NA	SEQ ID NO: 116
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACTTAGCTTGGTACCAGCAG
			AAACCAGGACAGCCTCCTAACCTGCTCATTTAC
			TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC
			ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT
			GTGGCTGTTTATTACTGTCAGCAATATTATCGTA
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG
			AAATCAAACGA
		AA	SEQ ID NO: 1687
			DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK
			NYLAWYQQKPGQPPNLLIYWTSTRDSGVPDRFSG
			SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF
			GQGTKVEIKR
IPS:361379	12H11.009	NA	SEQ ID NO: 117
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACTTAGCTTGGTACCAGCAG
			AAACCAGGACAGCCTCCTAACCTGCTCATTTAC
			TGGACTTCTACCCGAGAATCCGGGGTCCCTGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC
			ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT
			GTGGCTGTTTATTACTGTCAGCAATATTATCGTA
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG
			AAATCAAACGA
		AA	SEQ ID NO: 1688
			DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK
			NYLAWYQQKPGQPPNLLIYWTSTRESGVPDRFSG
			SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF
			GQGTKVEIKR

			SEQ ID NO: 273
			CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGGGTGATAAGCCCTAACAAT
			GGTGAAACAAACTATGCACAGAAGTTTCAGGAC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT
			GACGACACGGCCGTGTATTACTGTACGAGAGAG
			GCCACGATTTTTGGAATGCTTATTGTACCATTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1844
			QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLEWMGWISPNNGETNYAQKFQD
			RVTMTRDTSISTAYMELSRLRSDDTAVYYCTREA
			TIFGMLIVPFDYWGQGTLVTVSS
			SEQ ID NO: 274
			CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGGGTGATAAGCCCTAACCAA
			GGTGAAACAAACTATGCACAGAAGTTTCAGGAC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGAG
			GCCACGATTTTTGGAATGCTTATTGTACCATTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1845
			QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLEWMGWISPNQGETNYAQKFQD
			RVTMTRDTSISTAYMELSRLRSDDTAVYYCAREA
			TIFGMLIVPFDYWGQGTLVTVSS

iPS:361383	12H11.010	NA	SEQ ID NO: 118
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACTTAGCTTGGTACCAGCAG
			AAACCAGGACAGCCTCCTAACCTGCTCATTTAC
			TGGACTTCTACCCGAGAATCCGGGGTCCCTGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC
			ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT
			GTGGCTGTTTATTACTGTCAGCAATATTATCGTA
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG
			AAATCAAACGA
		AA	SEQ ID NO: 1689
			DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK
			NYLAWYQQKPGQPPNLLIYWTSTRESGVPDRFSG
			SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF
			GQGTKVEIKR
iPS:361387	12H11.011	NA	SEQ ID NO: 119
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACTTAGCTTGGTACCAGCAG
			AAACCAGGACAGCCTCCTAACCTGCTCATTTAC
			TGGACTTCTACCCGAGAATCCGGGGTCCCTGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC
			ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT
			GTGGCTGTTTATTACTGTCAGCAATATTATCGTA
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG
			AAATCAAACGA
		AA	SEQ ID NO: 1690
			DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK
			NYLAWYQQKPGQPPNLLIYWTSTRESGVPDRFSG
			SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF
			GQGTKVEIKR
		NA	SEQ ID NO: 275
			CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGGGTGATAAGCCCTAACAAT
			GGTGACACAAACTATGCACAGAAGTTTCAGGAC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGAG
			GCCACGATTTTTGGAATGCTTATTGTACCATTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
		AA	SEQ ID NO: 1846
			QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLEWMGWISPNNGDTNYAQKFQD
			RVTMTRDTSISTAYMELSRLRSDDTAVYYCAREA
			TIFGMLIVPFDYWGQGTLVTVSS
		NA	SEQ ID NO: 276
			CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGGGTGATAAGCCCTAACCAA
			GGTGACACAAACTATGCACAGAAGTTTCAGGAC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGAG
			GCCACGATTTTTGGAATGCTTATTGTACCATTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
		AA	SEQ ID NO: 1847
			QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLEWMGWISPNQGDTNYAQKFQD
			RVTMTRDTSISTAYMELSRLRSDDTAVYYCAREA
			TIFGMLIVPFDYWGQGTLVTVSS

iPS:361391	12H11.012	NA	SEQ ID NO: 120
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACTTAGCTTGGTACCAGCAG
			AAACCAGGACAGCCTCCTAACCTGCTCATTTAC
			TGGACTTCTACCCGAGAATCCGGGGTCCCTGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC
			ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT
			GTGGCTGTTTATTACTGTCAGCAATATTATCGTA
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG
			AAATCAAACGA
			SEQ ID NO: 1691
		AA	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK
			NYLAWYQQKPGQPPNLLIYWTSTRESGVPDRFSG
			SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF
			GQGTKVEIKR
			SEQ ID NO: 121
iPS:361395	12H11.013	NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACTTAGCTTGGTACCAGCAG
			AAACCAGGACAGCCTCCTAAACTGCTCATTTAC
			TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC
			ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT
			GTGGCTGTTTATTACTGTCAGCAATATTATCGTA
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG
			AAATCAAACGA
			SEQ ID NO: 1692
		AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK
			NYLAWYQQKPGQPPKLLIYWTSTRDSGVPDRFSG
			SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF
			GQGTKVEIKR
			SEQ ID NO: 277
			CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGGGTGATAAGCCCTAACAAT
			GGTGAAACAAACTATGCACAGAAGTTTCAGGAC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGAG
			GCCACGATTTTTGGAATGCTTATTGTACCATTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1848
		AA	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLEWMGWISPNNGETNYAQKFQD
			RVTMTRDTSISTAYMELSRLRSDDTAVYYCAREA
			TIFGMLIVPFDYWGQGTLVTVSS
			SEQ ID NO: 278
		NA	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGGGTGATAAGCCCTAACCAA
			GGTGAAACAAACTATGCACAGAAGTTTCAGGAC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTATATGGAGCTGAGCAGCCTGAGATCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGAG
			GCCACGATTTTTGGAATGCTTATTGTACCATTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1849
		AA	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLEWMGWISPNQGETNYAQKFQD
			RVTMTRDTSISTAYMELSSLRSDDTAVYYCAREA
			TIFGMLIVPFDYWGQGTLVTVSS

IPS:361402	12H11.014	NA	SEQ ID NO: 122
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACTTAGCTTGGTACCAGCAG
			AAACCAGGACAGCCTCCTAAACTGCTCATTTAC
			TGGACTTCTACCCGAGAATCCGGGGTCCCTGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC
			ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT
			GTGGCTGTTTATTACTGTCAGCAATATTATCGTA
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG
			AAATCAAACGA
		AA	SEQ ID NO: 1693
			DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK
			NYLAWYQQKPGQPPKLLIYWTSTRESGVPDRFSG
			SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF
			GQGTKVEIKR
IPS:361406	2C2.005.001	NA	SEQ ID NO: 123
			CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG
			GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT
			CTGGAAGTAGCTCCAACATCGGAAGTCAAACTG
			TAAACTGGTACCAGCACCTCCCAGGAACGGCCC
			CCAAACTCCTCATCTATACTAATAATCAGCGGC
			CCTCAGGGGGTCCCTGACCGATTCTCTGGCTCCAA
			GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG
			CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG
			CAACATTCGATGAAAGCCTGAGTGGTCCGGTAT
			TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT
		AA	SEQ ID NO: 1694
			QSVLTQPPSASGTPGQRVTISCSGSSSNIGSQTVNW
			YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
			ASLAISGLQSEDEADYFCATFDESLSGPVFGGGTK
			LTVLG
		NA	SEQ ID NO: 279
			CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGGGTGGATAAGCCCTAACCAA
			GGTGAAACAAACTATGCACAGAAGTTTCAGGAC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTATATGGAGCTGAGCAGCCTGAGATCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGAG
			GCCACGATTTTTGGAATGCTTATTGTACCATTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
		AA	SEQ ID NO: 1850
			QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLEWMGWISPNQGETNYAQKFQD
			RVTMTRDTSISTAYMELSSLRSDDTAVYYCAREA
			TIFGMLIVPFDYWGQGTLVTVSS
		NA	SEQ ID NO: 280
			CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCCGGATACACCTTCACCGGCTACTAT
			ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGATGGATCAACCCTAACAGT
			GGTGGCACAAACTATGCACAGAAGTTTCAGGGC
			AGGGTCACCATGACCAGGGACACGTCCATCAGT
			ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGGG
			GGGGATTACGTTTGGGGGACTTATCGGCCTCAC
			TACTACTACGGTATGGACGTCTGGGGCCAAGGG
			ACCACGGTCACCGTCTCCTCA
		AA	SEQ ID NO: 1851
			QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY
			MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ
			GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG
			GDYVWGTYRPHYYYGMDVWGQGTTVTVSS

iPS:361412	2C2.005.002	NA	SEQ ID NO: 124
			CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG
			GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT
			CTGGAAGTAGCTCCAACATCGGAAGTCAAACTG
			TAACTGGTACCAGCACCTCCCAGGAACGGCCC
			CCAAACTCCTCATCTATACTAATAATCAGCGGC
			CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA
			GTCTGGCACCTCAGCCTCCCCTTGCCATCAGTGGG
			CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG
			CAACATTCGATGAAAGCCTGCAAGGTCCGGTAT
			TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT
			SEQ ID NO: 1695
		AA	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSQTVNW
			YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
			ASLAISGLQSEDEADYFCATFDESLQGPVFGGGTK
			LTVLG
			SEQ ID NO: 125
iPS:361418	2C2.005.003	NA	CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG
			GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT
			CTGGAAGTAGCTCCAACATCGGAAGTAATTATG
			TAAACTGGTACCAGCACCTCCCAGGAACGGCCC
			CCAAACTCCTCATCTATACTAATAATCAGCGGC
			CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA
			GTCTGGCACCTCAGCCTCCCCTTGCCATCAGTGGG
			CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG
			CAACATTCGATGAAAGCCTGAGTGGTCCGGTAT
			TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT
			SEQ ID NO: 1696
		AA	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNYVNW
			YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
			ASLAISGLQSEDEADYFCATFDESLSGPVFGGGTK
			LTVLG
			SEQ ID NO: 281
			CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCCGGATACACCTTCACCGGCTACTAT
			ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGATGGATCAACCCTAACAGT
			GGTGGCACAAACTATGCACAGAAGTTTCAGGGC
			AGGGTCACCATGACCAGGGACACGTCCATCAGT
			ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGGG
			GGGGATTACGTTTGGGGGACTTATCGGCCTCAC
			TACTACTACGGTATGGACGTCTGGGGCCAAGGG
			ACCACGGTCACCGTCTCCTCA
			SEQ ID NO: 1852
		AA	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY
			MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ
			GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG
			GDYVWGTYRPHYYYGMDVWGQGTTVTVSS
			SEQ ID NO: 282
		NA	CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCCGGATACACCTTCACCGGCTACTAT
			ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGATGGATCAACCCTAACAGT
			GGTGGCACAAACTATGCACAGAAGTTTCAGGGC
			AGGGTCACCATGACCAGGGACACGTCCATCAGT
			ACAGCCTACATGGAGCTGAGGCAGGCTGAGGTCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGGG
			GGGGATTACGTTTGGGGGACTTATCGGCCTCAC
			TACTACTACGGTATGGACGTCTGGGGCCAAGGG
			ACCACGGTCACCGTCTCCTCA
			SEQ ID NO: 1853
		AA	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY
			MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ
			GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG
			GDYVWGTYRPHYYYGMDVWGQGTTVTVSS

iPS:361424	2C2.005.004	NA	SEQ ID NO: 126
			CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG
			GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT
			CTGGAAGTAGCTCCAACATCGGAAGTAATTATG
			TAACTGGTACCAGCACCTCCCAGGAACGGCCC
			CCAAACTCCTCATCTATACTAATAATCAGCGGC
			CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA
			GTCTGGCACCTCAGCCTCCCCTTGCCATCAGTGGG
			CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG
			CAACATTCGATGAAAGCCTGCAAGGTCCGGTAT
			TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT
			SEQ ID NO: 1697
		AA	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNYVNW
			YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
			ASLAISGLQSEDEADYFCATFDESLQGPVFGGGTK
			LTVLG
iPS:361430	2C2.005.005	NA	SEQ ID NO: 127
			CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG
			GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT
			CTGGAAGTAGCTCCAACATCGGAAGTCAAACTG
			TAAACTGGTACCAGCACCTCCCAGGAACGGCCC
			CCAAACTCCTCATCTATACTAATAATCAGCGGC
			CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA
			GTCTGGCACCTCAGCCTCCCCTTGCCATCAGTGGG
			CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG
			CAACATTCGATGACAGCCTGAATGGTCCGGTAT
			TCGGCCGGAGGGACCAAGCTGACCGTCCTAGGT
			SEQ ID NO: 1698
		AA	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSQTVNW
			YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
			ASLAISGLQSEDEADYFCATFDDSLNGPVFGGGTK
			LTVLG

			SEQ ID NO: 283
			CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCCGGATACACCTTCACCGGCTACTAT
			ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGATGGATCAACCCTAACAGT
			GGTGGCACAAACTATGCACAGAAGTTTCAGGGC
			AGGGTCACCATGACCAGGGACACGTCCATCAGT
			ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGGG
			GGGGATTACGTTTGGGGGACTTATCGGCCTCAC
			TACTACTACGGTATGGACGTCTGGGGCCAAGGG
			ACCACGGTCACCGTCTCCTCA
			SEQ ID NO: 1854
		AA	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY
			MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ
			GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG
			GDYVWGTYRPHYYYGMDVWGQGTTVTVSS
			SEQ ID NO: 284
		NA	CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCCGGATACACCTTCACCGGCTACTAT
			ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGATGGATCAACCCTAACAGT
			GGTGGCACAAACTATGCACAGAAGTTTCAGGGC
			AGGGTCACCATGACCAGGGACACGTCCATCAGT
			ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGGG
			GGGGATTACGTTTGGGGGACTTATCGGCCTCAC
			TACTACTACGGTATGGACGTCTGGGGCCAAGGG
			ACCACGGTCACCGTCTCCTCA
			SEQ ID NO: 1855
		AA	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY
			MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ
			GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG
			GDYVWGTYRPHYYYGMDVWGQGTTVTVSS

			SEQ ID NO: 285
		NA	CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCCGGATACACCTTCACCGGCTACTAT
			ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGATGGATCAACCCTAACAGT
			GGTGGCACAAACTATGCACAGAAGTTTCAGGGC
			AGGGTCACCATGACCAGGGACACGTCCATCAGT
			ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGGG
			GGGGATTACGTTTGGGGGACTTATCGGCCTCAC
			TACTACTACGGTATGGACGTCTGGGGCCAAGGG
			ACCACGGTCACCGTCTCCTCA
			SEQ ID NO: 1856
		AA	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY
			MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ
			GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG
			GDYVWGTYRPHYYYGMDVWGQGTTVTVSS
			SEQ ID NO: 286
		NA	CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCCGGATACACCTTCACCGGCTACTAT
			ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGATGGATCAACCCTAACAGT
			GGTGGCACAAACTATGCACAGAAGTTTCAGGGC
			AGGGTCACCATGACCAGGGACACGTCCATCAGT
			ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGGG
			GGGGATTACGTTTGGGGGACTTATCGGCCTCAC
			TACTACTACGGTATGGACGTCTGGGGCCAAGGG
			ACCACGGTCACCGTCTCCTCA
			SEQ ID NO: 1857
		AA	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY
			MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ
			GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG
			GDYVWGTYRPHYYYGMDVWGQGTTVTVSS
			SEQ ID NO: 128
		NA	CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG
			GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT
			CTGGAAGTAGCTCCAACATCGGAAGTAATTATG
			TAACTGGTACCAGCACCTCCCAGGAACGGCCC
			CCAAACTCCTCATCTATACTAATAATCAGCGGC
			CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA
			GTCTGGCACCTCAGCCTCCCCTTGCCATCAGTGGG
			CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG
			CAACATTCGATGACAGCCTGAATGGTCCGGTAT
			TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT
			SEQ ID NO: 1699
		AA	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNYVNW
			YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
			ASLAISGLQSEDEADYFCATFDDSLNGPVFGGGTK
			LTVLG
			SEQ ID NO: 129
		NA	CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG
			GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT
			CTGGAAGTAGCTCCAACATCGGAAGTAATACTG
			TAAACTGGTACCAGCACCTCCCAGGAACGGCCC
			CCAAACTCCTCATCTATACTAATAATCAGCGGC
			CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA
			GTCTGGCACCTCAGCCTCCCCTTGCCATCAGTGGG
			CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG
			CAACATTCGATGAAAGCCTGAATGGTCCGGTAT
			TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT
			SEQ ID NO: 1700
		AA	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNW
			YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
			ASLAISGLQSEDEADYFCATFDESLNGPVFGGGTK
			LTVLG
	iPS:361436	2C2.005.006	
	iPS:361442	2C2.005.007	

IPS:361448	2C2.005.008	NA	SEQ ID NO: 130
			CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG
			GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT
			CTGGAAGTAGCTCCAACATCGGAAGTAATACTG
			TAAACTGGTACCAGCACCTCCCAGGAACGGCCC
			CCAAACTCCTCATCTATACTAATAATCAGCGGC
			CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA
			GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG
			CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG
			CAACATTCGATGACAGCCTGCAAGGTCCGGTAT
			TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT
			SEQ ID NO: 1701
		AA	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNW
			YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
			ASLAISGLQSEDEADYFCATFDDSLQGPVFGGGTK
			LTVLG
			SEQ ID NO: 131
IPS:361454	2C2.005.009	NA	CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG
			GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT
			CTGGAAGTAGCTCCAACATCGGAAGTAATACTG
			TAAACTGGTACCAGCACCTCCCAGGAACGGCCC
			CCAAACTCCTCATCTATACTAATAATCAGCGGC
			CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA
			GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG
			CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG
			CAACATTCGATGACAGCCTGAGTGGTCCGGTAT
			TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT
			SEQ ID NO: 1702
		AA	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNW
			YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
			ASLAISGLQSEDEADYFCATFDDSLSGPVFGGGTK
			LTVLG
			SEQ ID NO: 287
			CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCCGGATACACCTTCACCGGCTACTAT
			ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGATGGATCAACCCTAACAGT
			GGTGGCACAAACTATGCACAGAAGTTTCAGGGC
			AGGGTCACCATGACCAGGGACACGTCCATCAGT
			ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGGG
			GGGGATTACGTTTGGGGGACTTATCGGCCTCAC
			TACTACTACGGTATGGACGTCTGGGGCCAAGGG
			ACCACGGTCACCGTCTCCTCA
			SEQ ID NO: 1858
		AA	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY
			MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ
			GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG
			GDYVWGTYRPHYYYGMDVWGQGTTVTVSS
			SEQ ID NO: 288
		NA	CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCCGGATACACCTTCACCGGCTACTAT
			ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGATGGATCAACCCTAACAGT
			GGTGGCACAAACTATGCACAGAAGTTTCAGGGC
			AGGGTCACCATGACCAGGGACACGTCCATCAGT
			ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGGG
			GGGGATTACGTTTGGGGGACTTATCGGCCTCAC
			TACTACTACGGTATGGACGTCTGGGGCCAAGGG
			ACCACGGTCACCGTCTCCTCA
			SEQ ID NO: 1859
		AA	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY
			MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ
			GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG
			GDYVWGTYRPHYYYGMDVWGQGTTVTVSS

		SEQ ID NO: 132	SEQ ID NO: 289
iPS:361460	2C2.005.010	NA	CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT CTGGAAGTAGCTCCAACATCGGAAGTAATACTG TAACTGGTACCAGCACCTCCCAGGAACGGCCC CCAAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATGACAGCCTGAATGCTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT
		SEQ ID NO: 1703	SEQ ID NO: 1860
		AA	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNW YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDDSLNAPVFGGGTK LTVLG
		SEQ ID NO: 133	SEQ ID NO: 290
		NA	CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT CTGGAAGTAGCTCCAACATCGGAAGTAATACTG TAAACTGGTACCAGCACCTCCCAGGAACGGCCC CCAAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATAGCAGCCTGAATGGTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT
iPS:361466	2C2.005.011		
		SEQ ID NO: 1704	SEQ ID NO: 1861
		AA	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNW YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDSSLNGPVFGGGTK LTVLG
			ACCACGGTCACCGTCTCCTCA GGGGATTACGTTTGGGGGACTTATCGGCCTCAC TACTACTACGGTATGGACGTCTGGGGCCAAGGG GACGACACGGCCGTGTATTACTGTGCGAGAGGG ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT AGGGTCACCATGACCAGGGACACGTCCATCAGT GGTGGCACAAACTATGCACAGAAGTTTCAGGGC CTTGAGTGGATGGGATGGATCAACCCTAACAGT ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG AAGGCTTCCGGATACACCTTCACCGGCTACTAT AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG
		SEQ ID NO: 1862	
		AA	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG GDYVWGTYRPHYYYGMDVWGQGTTVTVSS

IPS:361472	2C2.005.012	NA	SEQ ID NO: 134
			CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG
			GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT
			CTGGAAGTAGCTCCAACATCGGAAGTAATTATG
			TAAACTGGTACCAGCACCTCCCAGGAACGGCCC
			CCAAACTCCTCATCTATACTAATAATCAGCGGC
			CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA
			GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG
			CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG
			CAACATTCGATAGCAGCCTGAATGCTCCGGTAT
			TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT
			SEQ ID NO: 1705
		AA	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNYVNW
			YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
			ASLAISGLQSEDEADYFCATFDSSLNAPVFGGGTK
			LTVLG
			SEQ ID NO: 135
IPS:361478	2C2.005.013	NA	CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG
			GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT
			CTGGAAGTAGCTCCAACATCGGAAGTAATTATG
			TAAACTGGTACCAGCACCTCCCAGGAACGGCCC
			CCAAACTCCTCATCTATACTAATAATCAGCGGC
			CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA
			GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG
			CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG
			CAACATTCGATAGCAGCCTGAATGCTCCGGTAT
			TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT
			SEQ ID NO: 1706
		AA	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNYVNW
			YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
			ASLAISGLQSEDEADYFCATFDSSLNAPVFGGGTK
			LTVLG

			SEQ ID NO: 291
			CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCCGGATACACCTTCACCGGCTACTAT
			ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGATGGATCAACCCTAACAGT
			GGTGGCACAAACTATGCACAGAAGTTTCAGGGC
			AGGGTCACCATGACCAGGGACACGTCCATCAGT
			ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGGG
			GGGGATTACGTTTGGGGGACTTATCGGCCTCAC
			TACTACTACGGTATGGACGTCTGGGGCCAAGGG
			ACCACGGTCACCGTCTCCTCA
			SEQ ID NO: 1862
			QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY
			MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ
			GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG
			GDYVWGTYRPHYYYGMDVWGQGTTVTVSS
			SEQ ID NO: 292
			CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCCGGATACACCTTCACCGGCTACTAT
			ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGATGGATCAACCCTAACAGT
			GGTGGCACAAACTATGCACAGAAGTTTCAGGGC
			AGGGTCACCATGACCAGGGACACGTCCATCAGT
			ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGGG
			GGGGATTACGTTTTCGGGGACTTATCGGCCTCACT
			ACTACTACGGTATGGACGTCTGGGGCCAAGGGA
			CCACGGTCACCGTCTCCTCA
			SEQ ID NO: 1863
			QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY
			MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ
			GRVTMTRDTSISTAYMELSSLRSDDTAVYYCARG
			GDYVFGTYRPHYYYGMDVWGQGTTVTVSS

iPS:361485	2C2.005.014	NA	SEQ ID NO: 293
			CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCCGGATACACCTTCACCGGCTACTAT
			ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGATGGATCAACCCTAACAGT
			GGTGGCACAAACTATGCACAGAAGTTTCAGGGC
			AGGGTCACCATGACCAGGGACACCGTCCATCAGT
			ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGGG
			GGGGATTACGTTTTCGGGACTTATCGGCCTCACT
			ACTACTACGGTATGGACGTCTGGGGCCAAGGGA
			CCACGGTCACCGTCTCCTCA
		AA	SEQ ID NO: 1707
			QSVLTQPPSASGTPGQRVTISCSGSSSNIGSQTVNW
			YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
			ASLAISGLQSEDEADYFCATFDESLSGPVFGGGTK
			LTVLG
	18F2.013	NA	SEQ ID NO: 137
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTATAGGAGACAGAGTCACCATCACTT
			GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG
			GCTGGTATCAACAGAAACCAGGGAAAGCCCCTA
			AGCGCCTGATCTATGGTGCATCCAGTTTGCAAA
			GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT
			CTGGGACAGAATTCACTCTCACAATCAGCAGCC
			TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT
			ACAGCATAATAATTACCCCTTCACTTTCGGCCAA
			GGGACCAAAGTGGATATCAAACGA
		AA	SEQ ID NO: 1708
			DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW
			YQQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTE
			FTLTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDI
			KR

iPS:361851	6H1.009	NA	SEQ ID NO: 138
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTATAGGAGACAGAGTCACCATCACTTT
			GCCGGGCAAGTCAGGACATTAGAGATTATTTTAG
			GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA
			AGCGCCTGATCTATGGTGCATCCAGTTTGCAAA
			GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT
			CTGGGACAGAATTCACTCTCACAATCAGCAGCC
			TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT
			ACAGCATAATAATTACCCCTTCACTTTCGGCCAA
			GGGACCAAAGTGGATATCAAACGA
			SEQ ID NO: 1709
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY
			QQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTEFT
			LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK
			R
			SEQ ID NO: 139
iPS:361855	2C2.005.015	NA	CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG
			GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT
			CTGGAAGTAGCTCCAACATCGGAAGTAATACTG
			TAAACTGGTACCAGCAACTCCCAGGAACGGCCC
			CCAAACTCCTCATCTATACTAATAATCAGCGGC
			CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA
			GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG
			CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG
			CAACATTCGATAGCAGCCTGAGTGGTCCGGTAT
			TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT
			SEQ ID NO: 1710
		AA	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNW
			YQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
			ASLAISGLQSEDEADYFCATFDSSLSGPVFGGGTK
			LTVLG
			SEQ ID NO: 295
			CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
			GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA
			TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC
			TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
			GTAATAAATACTATGCAGACGCCGTGAAGGGCC
			GCTTCACCATCTCCAGAGACAATTCCAAGAACA
			CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
			AGGACACGGCTGTGTATTACTGTGCGCGAGATA
			GGACGATTTTTGGAGTGCTCTTGGGGGACTACT
			GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1866
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM
			HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG
			RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR
			TIFGVLLGDYWGQGTLVTVSS
			SEQ ID NO: 296
		NA	CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCCGGATACACCTTCACCGGCTACTAT
			ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGATGGATCAACCCTAACAGT
			GGTGGCACAAACTATGCACAGAAGTTTCAGGGC
			AGGGTCACCATGACCAGGGACACGTCCATCAGT
			ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGGG
			GGGGATTACGTTTGGGGGACTTATCGGCCTCAC
			TACTACTACGGTATGGACGTCTGGGGCCAAGGG
			ACCACGGTCACCGTCTCCTCA
			SEQ ID NO: 1867
		AA	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY
			MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ
			GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG
			GDYVWGTYRPHYYYGMDVWGQGTTVTVSS

iPS:336067	5G12.006	NA	SEQ ID NO: 140
			GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACTATCACTT GCCGGGCAAGTCAGACCATTAGCAGGTTTTTAA ATTGGTATCAGCAGAAACCTGGGAAAGCCCCTG AGCTCCTGATCTATGTTGCATCCAGTTTGCAAAG TGGGGTCCCATCAAGATTCAGTGGCAGTGGTTC TGGGACAGATTTCACTCTCACCATCAGCAGTCT GCAACCTGAAGATTTTGCAACTTACTACTGTCA ACAGAGTTACAGTACCCTGATCAGTTTTGGCCA GGGGACCAAGCTGGAGATCACACGA
		AA	SEQ ID NO: 1711
			DIQLTQSPSSLSASVGDRVTITCRASQTISRFLNWY QQKPGKAPELLIYVASSLQSGVPSRFSGSGSGTDFT LTISSLQPEDFATYYCQQSYSTLISFGQGTKLEITR
iPS:336169	17B11.002	NA	SEQ ID NO: 141
			CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTG CGGCCCCAGGACAGAAGGTCACCATCTCCTGCT CTGGAAGCAGCTCCAACATTGGAAATAATTATG TATCCTGGTATGAGCAGTTCCCAGGAACACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCCTGACCGATTCTCTGGCTCCAA GTCTGGCACGTCAGCCACCCTGGGCATCACCGG ACTCCAGACTGGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGCTGTGGT ATTCGGCGGAGGGACCAAACTGACCGTCCTAGG T
		AA	SEQ ID NO: 1712
			QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVS WYEQFPGTAPKLLIYDNNKRPSGIPDRFSGSKSGTS ATLGITGLQTGDEADYYCGTWDSSLSAVVFGGGT KLTVLG
			SEQ ID NO: 297
			CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT ACAGCGTCTGGATTCACCTTCAGTAGCTATGGC ATACACTGGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGTTATATGGTGATGGA AGTAATAAGTTCCATGCAGACTCCGTGAAGGGC CGATTCACCATCTCCAGAGACAATTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA AAAGTGGCTGGTATGCCTGAAGCTTTTGAAATC TGGGGCCAAGGGACAAAGGTCACCGTCTCTTCA
		AA	SEQ ID NO: 1868
			QVQLVESGGGVVQPGRSLRLSCTASGFTFSSYGIH WVRQAPGKGLEWVAVIWYDGSNKFHADSVKGRF TISRDNSKNTLYLQMNSLRAEDSAMYFCARGKVA GMPEAFEIWGQGTKVTVSS
		NA	SEQ ID NO: 298
			CAAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCAGTTATGAT ATCAACTGGGTGCGACAGGCCACTGGACAAGGG CTTGAGTGGATGGGATGGAACCCTAACAGT GGTAACACAGGCTATGCACAGAAGTTCCAGGGC AGAGTCACCATGACCAGGGACACCTCCATAAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT CAGGACACGGCCGTGTATTACTGTGCGAGAGGG GGTGATTACGTTTGGGGGAGTTATCGTCCCTACT ACTACTACTACGGTATGGACGTCTGGGGCCAAG GGACCACGGTCACCGTCTCCTCA
		AA	SEQ ID NO: 1869
			QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDI NWVRQATGQGLEWMGWMNPNSGNTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSQDTAVYYCARG GDYVWGSYRPYYYYYGMDVWGQGTTVTVSS

iPS:361127	5G12.006.001	NA	SEQ ID NO: 142
			GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTGTAGGAGACAGAGTCACTATCACTT
			GCCGGGCAAGTCAGACCATTAGCAGGTTTTTAA
			ATTGGTATCAGCAGAAACCTGGGAAAGCCCCTG
			AGCTCCTGATCTATGTTGCATCCAGTTTGCAAAG
			TGGGGTCCCATCAAGATTCAGTGGCAGTGGTTC
			TGGGACAGATTTCACTCTCACCATCAGCAGTCT
			GCAACCTGAAGATTTTGCAACTTACTACTGTCA
			ACAGAGTTACAGTACCCTGATCAGTTTTGGCCA
			GGGGACCAAGCTGGAGATCAAACGA
			SEQ ID NO: 1713
		AA	DIQLTQSPSSLSASVGDRVTITCRASQTISRFLNWY
			QQKPGKAPELLIYVASSLQSGVPSRFSGSGSGTDFT
			LTISSLQPEDFATYYCQQSYSTLISFGQGTKLEIKR
			SEQ ID NO: 143
iPS:361136	5G12.006.002	NA	GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTGTAGGAGACAGAGTCACTATCACTT
			GCCGGGCAAGTCAGACCATTAGCAGGTTTTTAA
			ATTGGTATCAGCAGAAACCTGGGAAAGCCCCTG
			AGCTCCTGATCTATGTTGCATCCAGTTTGCAAAG
			TGGGGTCCCATCAAGATTCAGTGGCAGTGGTTC
			TGGGACAGATTTCACTCTCACCATCAGCAGTCT
			GCAACCTGAAGATTTTGCAACTTACTACTGTCA
			ACAGAGTTACAGTACCCTGATCAGTTTTGGCCA
			GGGGACCAAGCTGGAGATCAAACGA
			SEQ ID NO: 1714
		AA	DIQLTQSPSSLSASVGDRVTITCRASQTISRFLNWY
			QQKPGKAPELLIYVASSLQSGVPSRFSGSGSGTDFT
			LTISSLQPEDFATYYCQQSYSTLISFGQGTKLEIKR

			SEQ ID NO: 299
			CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTG
			GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC
			ATACACTGGGTCCGCCAGGCTCCAGGCAAGGGG
			CTGGAGTGGGTGGCAGTTATATGGTATGATGCA
			AGTAATAAGTTCCATGCAGACGCCGTGAAGGGC
			CGATTCACCATCTCCAGAGACAATTCCAAGAAC
			ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC
			GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA
			AAAGTGGCTGGTATGCCTGAAGCTTTTGAAATC
			TGGGGCCAAGGGACAAAGGTCACCGTCTCTTCA
			SEQ ID NO: 1870
			QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGIH
			WVRQAPGKGLEWVAVIWYDASNKFHADAVKGR
			FTISRDNSKNTLYLQMNSLRAEDSAMYFCARGKV
			AGMPEAFEIWGQGTKVTVSS
			SEQ ID NO: 300
			CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTG
			GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			ACAGCGTCTGGATTCACCTTCAGTAGCTATGGC
			ATACACTGGGTCCGCCAGGCTCCAGGCAAGGGG
			CTGGAGTGGGTGGCAGTTATATGGTATGATGCA
			AGTAATAAGTTCCATGCAGACGCCGTGAAGGGC
			CGATTCACCATCTCCAGAGACAATTCCAAGAAC
			ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC
			GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA
			AAAGTGGCTGGTATGCCTGAAGCTTTTGAAATC
			TGGGGCCAAGGGACAAAGGTCACCGTCTCTTCA
			SEQ ID NO: 1871
			QVQLVESGGGVVQPGRSLRLSCTASGFTFSSYGIH
			WVRQAPGKGLEWVAVIWYDASNKFHADAVKGR
			FTISRDNSKNTLYLQMNSLRAEDSAMYFCARGKV
			AGMPEAFEIWGQGTKVTVSS

		SEQ ID NO: 144	SEQ ID NO: 301
iPS:361140	5G12.006.003	GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACTATCACTT GCCGGGCAAGTCAGACCATTAGCAGGTTTTTAA ATTGGTATCAGCAGAAACCTGGGAAAGCCCCTG AGCTCCTGATCTATGTTGCATCCAGTTTGCAAAG TGGGGTCCCATCAAGATTCAGTGGCAGTGGTTC TGGGACAGATTTCACTCTCACCATCAGCAGTCT GCAACCTGAAGATTTTGCAACTTACTACTGTCA ACAGAGTTACAGTACCCTGATCAGTTTTGGCCA GGGGACCAAGCTGGAGATCACACGA	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC ATACACTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGTTATATGGTATGATGCA AGTAATAAGTTCCATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGAGACAATTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA AAAGTGGCTGGTATGCCTGAAGCTTTTGAAATC TGGGGCCAAGGGACAAAGGTCACCGTCTCTTCA
		SEQ ID NO: 1715	SEQ ID NO: 1872
	AA	DIQLTQSPSSLSASVGDRVTITCRASQTISRFLNWY QQKPGKAPELLIYVASSLQSGVPSRFSGSGSGTDFT LTISSLQPEDFATYYCQQSYSTLISFGQGTKLEITR	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGIH WVRQAPGKGLEWVAVIWYDASNKFHADAVKGR FTISRDNSKNTLYLQMNSLRAEDSAMYFCARGKV AGMPEAFEIWGQGTKVTVSS
		SEQ ID NO: 145	SEQ ID NO: 302
iPS:359919	5G12.006.004	GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACTATCACTT GCCGGGCAAGTCAGACCATTAGCAGGTTTTTAA ATTGGTATCAGCAGAAACCTGGGAAAGCCCCTA AGCTCCTGATCTATGTTGCATCCAGTTTGCAAAG TGGGGTCCCATCAAGATTCAGTGGCAGTGGTTC TGGGACAGATTTCACTCTCACCATCAGCAGTCT GCAACCTGAAGATTTTGCAACTTACTACTGTCA ACAGAGTTACAGTACCCTGATCAGTTTTGGCCA GGGGACCAAGCTGGAGATCAAACGA	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC ATACACTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGTTATATGGTATGATGCA AGTAATAAGTTCCATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGAGACAATTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA AAAGTGGCTGGTATGCCTGAAGCTTTTGAAATC TGGGGCCAAGGGACATTGGTCACCGTCTCTTCA
		SEQ ID NO: 1716	SEQ ID NO: 1873
	AA	DIQLTQSPSSLSASVGDRVTITCRASQTISRFLNWY QQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDF TLTISSLQPEDFATYYCQQSYSTLISFGQGTKLEIKR	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGIH WVRQAPGKGLEWVAVIWYDASNKFHADAVKGR FTISRDNSKNTLYLQMNSLRAEDSAMYFCARGKV AGMPEAFEIWGQGTLVTVSS

		SEQ ID NO: 146	SEQ ID NO: 303
iPS:361144	5G12.006.005	NA	GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACTATCACTT GCCGGGCAAGTCAGACCATTAGCAGGTTTTTAA ATTGGTATCAGCAGAAACCTGGGAAAGCCCCTG AGCTCCTGATCTATGTTGCATCCAGTTTGCAAAG TGGGGTCCCATCAAGATTCAGTGGCAGTGGTTC TGGGACAGATTTCACTCTCACCATCAGCAGTCT GCAACCTGAAGATTTTGCAACTTACTACTGTCA ACAGAGTTACAGTACCCTGATCAGTTTTGGCCA GGGGACCAAGCTGGAGATCAAACGA
			SEQ ID NO: 1717
		AA	DIQLTQSPSSLSASVGDRVTITCRASQTISRFLNWY QQKPGKAPELLIYVASSLQSGVPSRFSGSGSGTDFT LTISSLQPEDFATYYCQQSYSTLISFGQGTKLEIKR
			SEQ ID NO: 147
iPS:361151	5G12.006.006	NA	GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACTATCACTT GCCGGGCAAGTCAGACCATTAGCAGGTTTTTAA ATTGGTATCAGCAGAAACCTGGGAAAGCCCCTG AGCTCCTGATCTATGTTGCATCCAGTTTGCAAAG TGGGGTCCCATCAAGATTCAGTGGCAGTGGTTC TGGGACAGATTTCACTCTCACCATCAGCAGTCT GCAACCTGAAGATTTTGCAACTTACTACTGTCA ACAGAGTTACAGTACCCTGATCAGTTTTGGCCA GGGGACCAAGCTGGAGATCAAACGA
			SEQ ID NO: 1718
		AA	DIQLTQSPSSLSASVGDRVTITCRASQTISRFLNWY QQKPGKAPELLIYVASSLQSGVPSRFSGSGSGTDFT LTISSLQPEDFATYYCQQSYSTLISFGQGTKLEIKR
			SEQ ID NO: 1875
			QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGIH WVRQAPGKGLEWVAVIWYDGSNKFHADAVKGR FTISRDNSKNTLYLQMNSLRAEDSAMYFCARGKV AGMPEAFEIWGQGTKVTVSS
			SEQ ID NO: 304
			CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC ATACACTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGTTATATGGTATGATGCA AGTAATAAGTTCCATGCAGACTCCGTGAAGGGC CGATTCACCATCTCCAGAGACAATTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA AAAGTGGCTGGTATGCCTGAAGCTTTTGAAATC TGGGGCCAAGGGACAAAGGTCACCGTCTCTTCA

iPS:361491	17B11.002.001	NA	SEQ ID NO: 148
			CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTG CGGCCCCAGGACAGAAGGTCACCATCTCCTGCT CTGGAAGCAGCTCCAACATTGGAAATAATTATG TATCCTGGTATCAGCAGCTCCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCCTGACCGATTCTCTGGCTCCAA GTCTGGCACGTCAGCCACCCTGGGCATCACCGG ACTCCAGACTGGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGCTGTGGT ATTCGGCGGAGGGACCAAACTGACCGTCCTAGG T
		AA	SEQ ID NO: 1719 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLGITGLQTGDEADYYCGTWDSSLSAVVFGGG TKLTVLG
iPS:361499	17B11.002.002	NA	SEQ ID NO: 149 CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTG CGGCCCCAGGACAGAAGGTCACCATCTCCTGCT CTGGAAGCAGCTCCAACATTGGAAATAATTATG TATCCTGGTATCAGCAGCTCCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCCTGACCGATTCTCTGGCTCCAA GTCTGGCACGTCAGCCACCCTGGGCATCACCGG ACTCCAGACTGGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGCTGTGGT ATTCGGCGGAGGGACCAAACTGACCGTCCTAGG T
		AA	SEQ ID NO: 1720 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLGITGLQTGDEADYYCGTWDSSLSAVVFGGG TKLTVLG

iPS:361491	17B11.002.001	NA	SEQ ID NO: 305 CAAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCAGTTATGAT ATCAACTGGGTGCGACAGGCCACTGGACAAGGG CTTGAGTGGATGGGATGGAACCCTAACAGT GGTGGCACAGGCTATGCACAGAAGTTCCAGGGC AGAGTCACCATGACCAGGGACACCTCCATAAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT CAGGACACGGCCGTGTATTACTGTGCGAGAGGG GGTGATTACGTTTGGGGGAGTTATCGTCCCTACT ACTACTACGGTATGGACGTCTGGGGCCAAG GGACCACGGTCACCGTCTCCTCA
		AA	SEQ ID NO: 1876 QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDI NWVRQATGQGLEWMGWMNPNSGGTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSQDTAVYYCARG GDYVWGSYRPYYYYYGMDVWGQGTTVTVSS
iPS:361499	17B11.002.002	NA	SEQ ID NO: 306 CAAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCAGTTATGAT ATCAACTGGGTGCGACAGGCCACTGGACAAGGG CTTGAGTGGATGGGATGGAACCCTAACAGT GGTAACACAGGCTATGCACAGAAGTTCCAGGGC AGAGTCACCATGACCAGGGACACCTCCATAAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT CAGGACACGGCCGTGTATTACTGTGCGAGAGGG GGTGATTACGTTTGGGGGAGTTATCGTCCCTACT ACTACTACGGTATGGACGTCTGGGGCCAAG GGACCACGGTCACCGTCTCCTCA
		AA	SEQ ID NO: 1877 QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDI NWVRQATGQGLEWMGWMNPNSGNTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSQDTAVYYCARG GDYVWGSYRPYYYYYGMDVWGQGTTVTVSS

iPS:361503	17B11.002.003	NA	SEQ ID NO: 150
			CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTG CGGCCCCAGGACAGAAGGTCACCATCTCCTGCT CTGGAAGCAGCTCCAACATTGGAAATAATTATG TATCCTGGTATGAGCAGTTCCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCCTGACCGATTCTCTGGCTCCAA GTCTGGCACGTCAGCCACCCTGGGCATCACCGG ACTCCAGACTGGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGCTGTGGT ATTCGGCGGAGGGACCAAACTGACCGTCCTAGG T
			SEQ ID NO: 1721
		AA	QSVLTQPPSVSAAPGQKVTISCSGSSNIGNNYVS WYEQFPGTAPKLLIYDNNKRPSGIPDRFSGSKSGTS ATLGITGLQTGDEADYYCGTWDSSLSAVVFGGGT KLTVLG
			SEQ ID NO: 151
iPS:361507	17B11.002.004	NA	CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTG CGGCCCCAGGACAGAAGGTCACCATCTCCTGCT CTGGAAGCAGCTCCAACATTGGAAATAATTATG TATCCTGGTATCAGCAGCTCCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCCTGACCGATTCTCTGGCTCCAA GTCTGGCACGTCAGCCACCCTGGCCATCACCGG ACTCCAGACTGGGGACGAGGCCGATTATTACTG CGGAACATTCGAAAGCAGCCTGAGTGCTGTGGT ATTCGGCGGAGGGACCAAACTGACCGTCCTAGG T
			SEQ ID NO: 1722
		AA	QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLAITGLQTGDEADYYCGTFESSLSAVVFGGGT KLTVLG
			SEQ ID NO: 307
			CAAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCAGTTATGAT ATCAACTGGGTGCGACAGGCCACTGGACAAGGG CTTGAGTGGATGGGATGGAACCCTAACAGT GGTGGCACAGGCTATGCACAGAAGTTCCAGGGC AGAGTCACCATGACCAGGGACACCTCCATAAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT CAGGACACGGCCGTGTATTACTGTGCGAGAGGG GGTGATTACGTTTGGGGGAGTTATCGTCCCTACT ACTACTACTACGGTATGGACGTCTGGGGCCAAG GGACCACGGTCACCGTCTCCTCA
			SEQ ID NO: 1878
		AA	QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDI NWVRQATGQGLEWMGWMNPNSGGTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSQDTAVYYCARG GDYVWGSYRPYYYYYGMDVWGQGTTVTVSS
			SEQ ID NO: 308
		NA	CAAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCAGTTATGAT ATCAACTGGGTGCGACAGGCCCCTGGACAAGGG CTTGAGTGGATGGGATGGAACCCTAACAGT GGTGGCACAGGCTATGCACAGAAGTTCCAGGGC AGAGTCACCATGACCAGGGACACCTCCATAAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGGG GGTGATTACGTTTGGGGGAGTTATCGTCCCTACT ACTACTACTACGGTATGGACGTCTGGGGCCAAG GGACCACGGTCACCGTCTCCTCA
			SEQ ID NO: 1879
		AA	QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDI NWVRQAPGQGLEWMGWMNPNSGGTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSDDTAVYYCARG GDYVWGSYRPYYYYYGMDVWGQGTTVTVSS

iPS:361514	17B11.002.005	NA	SEQ ID NO: 152
			CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTG CGGCCCCAGGACAGAAGGTCACCATCTCCTGCT CTGGAAGCAGCTCCAACATTGGAAATAATTATG TATCCTGGTATCAGCAGCTCCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCCTGACCGATTCTCTGGCTCCAA GTCTGGCACGTCAGCCACCCTGGCCATCACCGG ACTCCAGACTGGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGCTGTGGT ATTCGGCGGAGGGACCAAACTGACCGTCCTAGG T
		AA	SEQ ID NO: 1723
			QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLAITGLQTGDEADYYCGTWDSSLSAVVFGGG TKLTVLG
	17B11.002.006	NA	SEQ ID NO: 153
			CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTG CGGCCCCAGGACAGAAGGTCACCATCTCCTGCT CTGGAAGCAGCTCCAACATTGGAAATAATTATG TATCCTGGTATCAGCAGCTCCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCCTGACCGATTCTCTGGCTCCAA GTCTGGCACGTCAGCCACCCTGGCCATCACCGG ACTCCAGACTGGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGCTGTGGT ATTCGGCGGAGGGACCAAACTGACCGTCCTAGG T
		AA	SEQ ID NO: 1724
			QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLAITGLQTGDEADYYCGTWDSSLSAVVFGGG TKLTVLG

			SEQ ID NO: 309
			CAAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCAGTTATGAT ATCAACTGGGTGCGACAGGCCACTGGACAAGGG CTTGAGTGGATGGGATGGAACCCTAACAGT GGTGGCACAGGCTATGCACAGAAGTTCCAGGGC AGAGTCACCATGACCAGGGACACCTCCATAAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT CAGGACACGGCCGTGTATTACTGTGCGAGAGGG GGTGATTACGTTTGGGGGAGTTATCGTCCCTACT ACTACTACTACGGTATGGACGTCTGGGGCCAAG GGACCACGGTCACCGTCTCCTCA
			SEQ ID NO: 1880
			QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDI NWVRQATGQGLEWMGWMNPNSGGTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSQDTAVYYCARG GDYVWGSYRPYYYYYGMDVWGQGTTVTVSS
			SEQ ID NO: 310
			CAAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCAGTTATGAT ATCAACTGGGTGCGACAGGCCCCTGGACAAGGG CTTGAGTGGATGGGATGGAACCCTAACAGT GGTAACACAGGCTATGCACAGAAGTTCCAGGGC AGAGTCACCATGACCAGGGACACCTCCATAAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGGG GGTGATTACGTTTGGGGGAGTTATCGTCCCTACT ACTACTACTACGGTATGGACGTCTGGGGCCAAG GGACCACGGTCACCGTCTCCTCA
			SEQ ID NO: 1881
			QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDI NWVRQAPGQGLEWMGWMNPNSGNTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSDDTAVYYCARG GDYVWGSYRPYYYYYGMDVWGQGTTVTVSS

iPS:361518	17B11.002.007	NA	SEQ ID NO: 154
			CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTG CGGCCCCAGGACAGAAGGTCACCATCTCCTGCT CTGGAAGCAGCTCCAACATTGGAAATAATTATG TATCCTGGTATCAGCAGCTCCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCCTGACCGATTCTCTGGCTCCAA GTCTGGCACGTCAGCCACCCTGGGCATCACCGG ACTCCAGACTGGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGCTGTGGT ATTCGGCGGAGGGACCAAACTGACCGTCCTAGG T
		AA	SEQ ID NO: 1725
			QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLGITGLQTGDEADYYCGTWDSSLSAVVFGGG TKLTVLG
iPS:360570	17B11.002.008	NA	SEQ ID NO: 155
			CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTG CGGCCCCAGGACAGAAGGTCACCATCTCCTGCT CTGGAAGCAGCTCCAACATTGGAAATAATTATG TATCCTGGTATCAGCAGCTCCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCCTGACCGATTCTCTGGCTCCAA GTCTGGCACGTCAGCCACCCTGGCCATCACCGG ACTCCAGACTGGGGACGAGGCCGATTATTACTG CGGAACATTCGAAAGCAGCCTGAGTGCTGTGGT ATTCGGCGGAGGGACCAAACTGACCGTCCTAGG T
		AA	SEQ ID NO: 1726
			QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLAITGLQTGDEADYYCGTFESSLSAVVFGGGT KLTVLG

	SEQ ID NO: 311
	CAAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCAGTTATGAT ATCAACTGGGTGCGACAGGCCACTGGACAAGGG CTTGAGTGGATGGGATGGAACCCTAACAGT GGTGGCACAGGCTATGCACAGAAGTTCCAGGGC AGAGTCACCATGACCAGGGACACCTCCATAAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT CAGGACACGGCCGTGTATTACTGTGCGAGAGGG GGTGATTACGTTTTCGGGAGTTATCGTCCCTACT ACTACTACTACGGTATGGACGTCTGGGGCCAAG GGACCACGGTCACCGTCTCCTCA
	SEQ ID NO: 1882
	QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDI NWVRQATGQGLEWMGWMNPNSGGTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSQDTAVYYCARG GDYVFGSYRPYYYYYGMDVWGQGTTVTVSS
	SEQ ID NO: 312
	CAAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCAGTTATGAT ATCAACTGGGTGCGACAGGCCCCTGGACAAGGG CTTGAGTGGATGGGATGGAACCCTAACAGT GGTGGCACAGGCTATGCACAGAAGTTCCAGGGC AGAGTCACCATGACCAGGGACACCTCCATAAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGGG GGTGATTACGTTTTCGGGAGTTATCGTCCCTACT ACTACTACTACGGTATGGACGTCTGGGGCCAAG GGACCACGGTCACCGTCTCCTCA
	SEQ ID NO: 1883
	QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDI NWVRQAPGQGLEWMGWMNPNSGGTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSDDTAVYYCARG GDYVFGSYRPYYYYYGMDVWGQGTTVTVSS

iPS:362051			
5G12.005.001			
	NA	SEQ ID NO: 156	GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACTATCACTT GCCGGGCAAGTCAGACCATTAGCAGGTTTTTAA ATTGGTATCAGCAGAAACCTGGGAAAGCCCCTA AGCTCCTGATCTATGTTGCATCCAGTTTGCAAAG TGGGGTCCCATCAAGATTCAGTGGCAGTGGTTC TGGGACAGATTTCACTCTCACCATCAGCAGTCT GCAACCTGAAGATTTTGCAACTTACTACTGTCA ACAGAGTTACAGTACCCTGCTCAGTTTTGGCCA GGGGACCAAGCTGGAGATCAAACGA
		SEQ ID NO: 1727	SEQ ID NO: 1884
	AA	DIQLTQSPSSLSASVGDRVTITCRASQTISRFLNWY QQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDF TLTISSLQPEDFATYYCQQSYSTLLSFGQGTKLEIK R	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGIH WVRQAPGKGLEWVAVIWYDASNKFHADAVKGR FTISRDNSKNTLYLQMNSLRAEDSAMYFCARGKV AGMPEAFEIWGQGTLVTVSS
		SEQ ID NO: 157	SEQ ID NO: 314

Table 4. Exemplary CDRL1, CDRL2, CDRL3, CDRH1, CDRH2, and CDRH3 Nucleic Acid ("NA") and Amino Acid ("AA") Sequences

Table 4A. Exemplary CDRL1, CDRL2, and CDRL3 Nucleic Acid ("NA") and Amino Acid ("AA") Sequences

iPS#	Ab	Type	CDRL1	CDRL2	CDRL3
iPS:336175	2C2.005	NA	TCTGGAAGTAGCTCCAACATCG GAAGTAATACTGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATTCGATGACAGCCTG AATGGTCCGGTA
			SEQ ID NO: 2199	SEQ ID NO: 2356	SEQ ID NO: 2513
		AA	SGSSSNIGSNTVN	TNNQRPS	ATFDDSLNGPV
			SEQ ID NO: 629	SEQ ID NO: 786	SEQ ID NO: 943
iPS:335914	4B1	NA	CGGGCAAGTCAGGACATTAGAG ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
			SEQ ID NO: 2200	SEQ ID NO: 2357	SEQ ID NO: 2514
		AA	RASQDIRDYLG	GASSLQS	LQHNNYPFT
			SEQ ID NO: 630	SEQ ID NO: 787	SEQ ID NO: 944

iPS:335938	6H1	NA	CGGGCAAGTCAGGACATTAGAG ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
			SEQ ID NO: 2201	SEQ ID NO: 2358	SEQ ID NO: 2515
		AA	RASQDIRDYLG	GASSLQS	LQHNNYPFT
			SEQ ID NO: 631	SEQ ID NO: 788	SEQ ID NO: 945
iPS:335941	2F11	NA	CAGGCGAGTCAGGACATTAGCA ACTATTTAAAT	GATGCATCCAATTTGGAAACA	CAACAGTATGATATTCTCCTCA CT
			SEQ ID NO: 2202	SEQ ID NO: 2359	SEQ ID NO: 2516
		AA	QASQDISNYLN	DASNLET	QQYDILLT
			SEQ ID NO: 632	SEQ ID NO: 789	SEQ ID NO: 946
iPS:335970	5C2	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
			SEQ ID NO: 2203	SEQ ID NO: 2360	SEQ ID NO: 2517
		AA	KSSQSVLSSSNNKNYIA	WASTRES	QQYYSTPWT
			SEQ ID NO: 633	SEQ ID NO: 790	SEQ ID NO: 947
iPS:335978	13H12	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
			SEQ ID NO: 2204	SEQ ID NO: 2361	SEQ ID NO: 2518
		AA	KSSQSVLSSSNNKNYIA	WASTRES	QQYYSTPWT
			SEQ ID NO: 634	SEQ ID NO: 791	SEQ ID NO: 948
iPS:335986	11C1	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGATTCC	CAGCAATATTATCGTACTCCGT GGACG
			SEQ ID NO: 2205	SEQ ID NO: 2362	SEQ ID NO: 2519
		AA	KSSQSVLSSSNNKNYLA	WTSTRDS	QQYYRTPWT
			SEQ ID NO: 635	SEQ ID NO: 792	SEQ ID NO: 949
iPS:3359 94	12H11	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGATTCC	CAGCAATATTATCGTACTCCGT GGACG
			SEQ ID NO: 2206	SEQ ID NO: 2363	SEQ ID NO: 2520

		KSSQSVLSSSNNKNYLA	WTSTRDS	QQYYRTPWT
iPS:336099	17H11.004	AA	SEQ ID NO: 641	SEQ ID NO: 798	SEQ ID NO: 955
		NA	CGGGCGAGTCAGGGTCTTATCA TCTGGTTAGCC	GCTGCATCCAGTTTGCAAAGT	CAACAGACTAACAGTTTCCCTC CGACG
		AA	RASQGLIIWLA	AASSLQS	QQTNSFPPT
		NA	SEQ ID NO: 2211	SEQ ID NO: 2368	SEQ ID NO: 2525
iPS:336088	6A5.004	AA	QASQDITNYLN	DASNLEP	QQYDDLFT
		NA	SEQ ID NO: 640	SEQ ID NO: 797	SEQ ID NO: 954
		AA	SEQ ID NO: 2210	SEQ ID NO: 2367	SEQ ID NO: 2524
iPS:336077	4H9.004	NA	CAGGCGAGTCAGGACATTACCA ACTATTTAAAT	GATGCTTCCAATTTGGAGCCA	CAACAGTATGATCTATTCA CT
		AA	RASQGIRNELG	GASSLQS	LQHNSYPFT
		NA	SEQ ID NO: 639	SEQ ID NO: 796	SEQ ID NO: 953
iPS:336041	2G10_LC1	AA	SEQ ID NO: 2209	SEQ ID NO: 2366	SEQ ID NO: 2523
		NA	CGGGCAAGTCAGGGCATTAGAA ATGAGTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAGTTACCCAT TCACT
		AA	SEQ ID NO: 2208	SEQ ID NO: 2365	SEQ ID NO: 2522
		NA	AGGGCCAGTCAGAGTGTTAGCA GCAACTTAGCC	GGTGCAGCCACCAGGGCCACT	CAGCAGTATAATAACTGGCCTC TCACT
iPS:336024	18E3	AA	RASQSISYSYLA	GASSRAT	QQYGSSPLT
		NA	SEQ ID NO: 637	SEQ ID NO: 794	SEQ ID NO: 951
		AA	AGGGCCAGTCAGAGTATTAGTT ACAGTTACTTAGCC	GGTGCATCCAGCAGGGCCACT	CAGCAGTATGGTAGTTCACCGC TCACT
		NA	SEQ ID NO: 2207	SEQ ID NO: 2364	SEQ ID NO: 2521
		AA	SEQ ID NO: 636	SEQ ID NO: 793	SEQ ID NO: 950

rs35962121	17H11.004.001	NA	CGGGCGAGTCAGGGTCTTATCA TCTGGTTAGCC	GCTGCATCCAGTTTGCAAAGT
			SEQ ID NO: 2212	SEQ ID NO: 2369
		AA	RASQGLIIWLA	AASSLQS
			SEQ ID NO: 642	SEQ ID NO: 799
rs35978181	4H9.004.001	NA	CGGGCAAGTCAGGGCATTAGAA ATGAGTTAGGC	GGTGCATCCAGTTTGCAAAGT
			SEQ ID NO: 2213	SEQ ID NO: 2370
		AA	RASQGIRNELG	GASSLQS
			SEQ ID NO: 643	SEQ ID NO: 800
rs36092929	4H9.004.002	NA	CGGGCAAGTCAGGGCATTAGAA ATGAGTTAGGC	GGTGCATCCAGTTTGCAAAGT
			SEQ ID NO: 2214	SEQ ID NO: 2371
		AA	RASQGIRNELG	GASSLQS
			SEQ ID NO: 644	SEQ ID NO: 801
rs36093636	4H9.004.003	NA	CGGGCAAGTCAGGGCATTAGAA ATGAGTTAGGC	GGTGCATCCAGTTTGCAAAGT
			SEQ ID NO: 2215	SEQ ID NO: 2372
		AA	RASQGIRNELG	GASSLQS
			SEQ ID NO: 645	SEQ ID NO: 802
rs36094343	4H9.004.004	NA	CGGGCAAGTCAGGGCATTAGAA ATGAGTTAGGC	GGTGCATCCAGTTTGCAAAGT
			SEQ ID NO: 2216	SEQ ID NO: 2373
		AA	RASQGIRNELG	GASSLQS
			SEQ ID NO: 646	SEQ ID NO: 803
rs36094949	4H9.004.005	NA	CGGGCAAGTCAGGGCATTAGAA ATGAGTTAGGC	GGTGCATCCAGTTTGCAAAGT
			SEQ ID NO: 2217	SEQ ID NO: 2374
		AA	RASQGIRNELG	GASSLQS
			SEQ ID NO: 647	SEQ ID NO: 804

CAACAGACTAACAGTTTCCCTC CGACG
SEQ ID NO: 2526
QQTNSFPPT
SEQ ID NO: 956
CTACAGCATAATAGTTACCCAT TCACT
SEQ ID NO: 2527
LQHNSYPFT
SEQ ID NO: 957
CTACAGCATAATAGTTACCCAT TCACT
SEQ ID NO: 2528
LQHNSYPFT
SEQ ID NO: 958
CTACAGCATAATAGTTACCCAT TCACT
SEQ ID NO: 2529
LQHNSYPFT
SEQ ID NO: 959
CTACAGCATAATAGTTACCCAT TCACT
SEQ ID NO: 2530
LQHNSYPFT
SEQ ID NO: 960
CTACAGCATAATAGTTACCCAT TCACT
SEQ ID NO: 2531
LQHNSYPFT
SEQ ID NO: 961

rs35976161	4H9.004.006	NA	CGGGCAAGTCAGGGCATTAGAA ATGAGTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAGTTACCCAT TCACT
			SEQ ID NO: 2218	SEQ ID NO: 2375	SEQ ID NO: 2532
		AA	RASQGIRNELG	GASSLQS	LQHNSYPFT
			SEQ ID NO: 648	SEQ ID NO: 805	SEQ ID NO: 962
rs3609655	4B1.010	NA	CGGGCAAGTCAGGACATTAGAG ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
			SEQ ID NO: 2219	SEQ ID NO: 2376	SEQ ID NO: 2533
		AA	RASQDIRDYLG	GASSLQS	LQHNNYPFT
			SEQ ID NO: 649	SEQ ID NO: 806	SEQ ID NO: 963
rs3609662	4B1.011	NA	CGGGCAAGTCAGGACATTAGAG ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
			SEQ ID NO: 2220	SEQ ID NO: 2377	SEQ ID NO: 2534
		AA	RASQDIRDYLG	GASSLQS	LQHNNYPFT
			SEQ ID NO: 650	SEQ ID NO: 807	SEQ ID NO: 964
rs3609668	4B1.012	NA	CGGGCAAGTCAGGACATTAGAG ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
			SEQ ID NO: 2221	SEQ ID NO: 2378	SEQ ID NO: 2535
		AA	RASQDIRDYLG	GASSLQS	LQHNNYPFT
			SEQ ID NO: 651	SEQ ID NO: 808	SEQ ID NO: 965
rs3609674	4B1.013	NA	CGGGCAAGTCAGGACATTAGAG ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
			SEQ ID NO: 2222	SEQ ID NO: 2379	SEQ ID NO: 2536
		AA	RASQDIRDYLG	GASSLQS	LQHNNYPFT
			SEQ ID NO: 652	SEQ ID NO: 809	SEQ ID NO: 966
rs3609678	4B1.014	NA	CGGGCAAGTCAGGACATTAGAG ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
			SEQ ID NO: 2223	SEQ ID NO: 2380	SEQ ID NO: 2537
		AA	RASQDIRDYLG	GASSLQS	LQHNNYPFT
			SEQ ID NO: 653	SEQ ID NO: 810	SEQ ID NO: 967

iPS:359785	4B1.015	NA	CGGGCAAGTCAGGACATTAGAG ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
			SEQ ID NO: 2224	SEQ ID NO: 2381	SEQ ID NO: 2538
		AA	RASQDIRDYLG	GASSLQS	LQHNNYPFT
			SEQ ID NO: 654	SEQ ID NO: 811	SEQ ID NO: 968
iPS:360982	4B1.016	NA	CGGGCAAGTCAGGACATTAGAG ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
			SEQ ID NO: 2225	SEQ ID NO: 2382	SEQ ID NO: 2539
		AA	RASQDIRDYLG	GASSLQS	LQHNNYPFT
			SEQ ID NO: 655	SEQ ID NO: 812	SEQ ID NO: 969
iPS:335922	18F2	NA	CGGGCAAGTCAGGACCTTAGAA ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
			SEQ ID NO: 2226	SEQ ID NO: 2383	SEQ ID NO: 2540
		AA	RASQDLRNYLG	GASSLQS	LQHNNYPFT
			SEQ ID NO: 656	SEQ ID NO: 813	SEQ ID NO: 970
iPS:360986	18F2.002	NA	CGGGCAAGTCAGGACCTTAGAA ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
			SEQ ID NO: 2227	SEQ ID NO: 2384	SEQ ID NO: 2541
		AA	RASQDLRNYLG	GASSLQS	LQHNNYPFT
			SEQ ID NO: 657	SEQ ID NO: 814	SEQ ID NO: 971
iPS:360995	18F2.003	NA	CGGGCAAGTCAGGACCTTAGAA ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
			SEQ ID NO: 2228	SEQ ID NO: 2385	SEQ ID NO: 2542
		AA	RASQDLRNYLG	GASSLQS	LQHNNYPFT
			SEQ ID NO: 658	SEQ ID NO: 815	SEQ ID NO: 972
iPS:360999	18F2.004	NA	CGGGCAAGTCAGGACCTTAGAA ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
			SEQ ID NO: 2229	SEQ ID NO: 2386	SEQ ID NO: 2543
		AA	RASQDLRNYLG	GASSLQS	LQHNNYPFT
			SEQ ID NO: 659	SEQ ID NO: 816	SEQ ID NO: 973

iPS:361005	18F2.005	NA	CGGGCAAGTCAGGACCTTAGAA ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT
			SEQ ID NO: 2230	SEQ ID NO: 2387
		AA	RASQDLRNYLG	GASSLQS
			SEQ ID NO: 660	SEQ ID NO: 817
iPS:361009	18F2.006	NA	CGGGCAAGTCAGGACCTTAGAA ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT
			SEQ ID NO: 2231	SEQ ID NO: 2388
		AA	RASQDLRNYLG	GASSLQS
			SEQ ID NO: 661	SEQ ID NO: 818
iPS:361013	18F2.007	NA	CGGGCAAGTCAGGACCTTAGAA ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT
			SEQ ID NO: 2232	SEQ ID NO: 2389
		AA	RASQDLRNYLG	GASSLQS
			SEQ ID NO: 662	SEQ ID NO: 819
iPS:361017	18F2.008	NA	CGGGCAAGTCAGGACCTTAGAA ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT
			SEQ ID NO: 2233	SEQ ID NO: 2390
		AA	RASQDLRNYLG	GASSLQS
			SEQ ID NO: 663	SEQ ID NO: 820
iPS:361021	18F2.009	NA	CGGGCAAGTCAGGACCTTAGAA ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT
			SEQ ID NO: 2234	SEQ ID NO: 2391
		AA	RASQDLRNYLG	GASSLQS
			SEQ ID NO: 664	SEQ ID NO: 821
iPS:361028	18F2.010	NA	CGGGCAAGTCAGGACCTTAGAA ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT
			SEQ ID NO: 2235	SEQ ID NO: 2392
		AA	RASQDLRNYLG	GASSLQS
			SEQ ID NO: 665	SEQ ID NO: 822

CTACAGCATAATAATTACCCCT TCACT	
SEQ ID NO: 2544	
LQHNNYPFT	
SEQ ID NO: 974	
CTACAGCATAATAATTACCCCT TCACT	
SEQ ID NO: 2545	
LQHNNYPFT	
SEQ ID NO: 975	
CTACAGCATAATAATTACCCCT TCACT	
SEQ ID NO: 2546	
LQHNNYPFT	
SEQ ID NO: 976	
CTACAGCATAATAATTACCCCT TCACT	
SEQ ID NO: 2547	
LQHNNYPFT	
SEQ ID NO: 977	
CTACAGCATAATAATTACCCCT TCACT	
SEQ ID NO: 2548	
LQHNNYPFT	
SEQ ID NO: 978	
CTACAGCATAATAATTACCCCT TCACT	
SEQ ID NO: 2549	
LQHNNYPFT	
SEQ ID NO: 979	

rs360535	18F2.011	NA	CGGGCAAGTCAGGACCTTAGAAATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCTTCACT
			SEQ ID NO: 2236	SEQ ID NO: 2393	SEQ ID NO: 2550
		AA	RASQDLRNYLG	GASSLQS	LQHNNYPFT
			SEQ ID NO: 666	SEQ ID NO: 823	SEQ ID NO: 980
rs361035	18F2.012	NA	CGGGCAAGTCAGGACCTTAGAAATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCTTCACT
			SEQ ID NO: 2237	SEQ ID NO: 2394	SEQ ID NO: 2551
		AA	RASQDLRNYLG	GASSLQS	LQHNNYPFT
			SEQ ID NO: 667	SEQ ID NO: 824	SEQ ID NO: 981
rs359940	2F11.002	NA	CAGGCGAGTCAGGACATTAGCAACTATTTAAAT	GATGCATCCAATTTGGAAACA	CAACAGTATGATATTCTCCTCACT
			SEQ ID NO: 2238	SEQ ID NO: 2395	SEQ ID NO: 2552
		AA	QASQDISNYLN	DASNLET	QQYDILLT
			SEQ ID NO: 668	SEQ ID NO: 825	SEQ ID NO: 982
rs361039	2F11.003	NA	CAGGCGAGTCAGGACATTAGCAACTATTTAAAT	GATGCATCCAATTTGGAAACA	CAACAGTATGATATTCTCCTCACT
			SEQ ID NO: 2239	SEQ ID NO: 2396	SEQ ID NO: 2553
		AA	QASQDISNYLN	DASNLET	QQYDILLT
			SEQ ID NO: 669	SEQ ID NO: 826	SEQ ID NO: 983
rs361043	2F11.004	NA	CAGGCGAGTCAGGACATTAGCAACTATTTAAAT	GATGCATCCAATTTGGAAACA	CAACAGTATGATATTCTCCTCACT
			SEQ ID NO: 2240	SEQ ID NO: 2397	SEQ ID NO: 2554
		AA	QASQDISNYLN	DASNLET	QQYDILLT
			SEQ ID NO: 670	SEQ ID NO: 827	SEQ ID NO: 984
rs361049	2F11.005	NA	CAGGCGAGTCAGGACATTAGCAACTATTTAAAT	GATGCATCCAATTTGGAAACA	CAACAGTATGATATTCTCCTCACT
			SEQ ID NO: 2241	SEQ ID NO: 2398	SEQ ID NO: 2555
		AA	QASQDISNYLN	DASNLET	QQYDILLT
			SEQ ID NO: 671	SEQ ID NO: 828	SEQ ID NO: 985

rs361055	2F11.006	NA	CAGGCGAGTCAGGACATTAGCA ACTATTTAAAT	GATGCATCCAATTTGGAAACA	CAACAGTATGATATTCTCCTCA CT
			SEQ ID NO: 2242	SEQ ID NO: 2399	SEQ ID NO: 2556
		AA	QASQDISNYLN	DASNLET	QQYDILLT
			SEQ ID NO: 672	SEQ ID NO: 829	SEQ ID NO: 986
rs361059	2F11.007	NA	CAGGCGAGTCAGGACATTAGCA ACTATTTAAAT	GATGCATCCAATTTGGAAACA	CAACAGTATGATATTCTCCTCA CT
			SEQ ID NO: 2243	SEQ ID NO: 2400	SEQ ID NO: 2557
		AA	QASQDISNYLN	DASNLET	QQYDILLT
			SEQ ID NO: 673	SEQ ID NO: 830	SEQ ID NO: 987
rs361063	2F11.008	NA	CAGGCGAGTCAGGACATTAGCA ACTATTTAAAT	GATGCATCCAATTTGGAAACA	CAACAGTATGATATTCTCCTCA CT
			SEQ ID NO: 2244	SEQ ID NO: 2401	SEQ ID NO: 2558
		AA	QASQDISNYLN	DASNLET	QQYDILLT
			SEQ ID NO: 674	SEQ ID NO: 831	SEQ ID NO: 988
rs359949	2F11.009	NA	CAGGCGAGTCAGGACATTAGCA ACTATTTAAAT	GATGCATCCAATTTGGAAACA	CAACAGTATGATATTCTCCTCA CT
			SEQ ID NO: 2245	SEQ ID NO: 2402	SEQ ID NO: 2559
		AA	QASQDISNYLN	DASNLET	QQYDILLT
			SEQ ID NO: 675	SEQ ID NO: 832	SEQ ID NO: 989
rs359956	2F11.010	NA	CAGGCGAGTCAGGACATTAGCA ACTATTTAAAT	GATGCATCCAATTTGGAAACA	CAACAGTATGATATTCTCCTCA CT
			SEQ ID NO: 2246	SEQ ID NO: 2403	SEQ ID NO: 2560
		AA	QASQDISNYLN	DASNLET	QQYDILLT
			SEQ ID NO: 676	SEQ ID NO: 833	SEQ ID NO: 990
rs359865	6H1.002	NA	CGGGCAAGTCAGGACATTAGAG ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
			SEQ ID NO: 2247	SEQ ID NO: 2404	SEQ ID NO: 2561
		AA	RASQDIRDYLG	GASSLQS	LQHNNYPFT
			SEQ ID NO: 677	SEQ ID NO: 834	SEQ ID NO: 991

rs359869	6H1.003	NA	CGGGCAAGTCAGGACATTAGAG ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
			SEQ ID NO: 2248	SEQ ID NO: 2405	SEQ ID NO: 2562
		AA	RASQDIRDYLG	GASSLQS	LQHNNYPFT
			SEQ ID NO: 678	SEQ ID NO: 835	SEQ ID NO: 992
rs359873	6H1.004	NA	CGGGCAAGTCAGGACATTAGAG ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
			SEQ ID NO: 2249	SEQ ID NO: 2406	SEQ ID NO: 2563
		AA	RASQDIRDYLG	GASSLQS	LQHNNYPFT
			SEQ ID NO: 679	SEQ ID NO: 836	SEQ ID NO: 993
rs359877	6H1.005	NA	CGGGCAAGTCAGGACATTAGAG ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
			SEQ ID NO: 2250	SEQ ID NO: 2407	SEQ ID NO: 2564
		AA	RASQDIRDYLG	GASSLQS	LQHNNYPFT
			SEQ ID NO: 680	SEQ ID NO: 837	SEQ ID NO: 994
rs361067	6H1.006	NA	CGGGCAAGTCAGGACATTAGAG ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
			SEQ ID NO: 2251	SEQ ID NO: 2408	SEQ ID NO: 2565
		AA	RASQDIRDYLG	GASSLQS	LQHNNYPFT
			SEQ ID NO: 681	SEQ ID NO: 838	SEQ ID NO: 995
rs361071	6H1.007	NA	CGGGCAAGTCAGGACATTAGAG ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
			SEQ ID NO: 2252	SEQ ID NO: 2409	SEQ ID NO: 2566
		AA	RASQDIRDYLG	GASSLQS	LQHNNYPFT
			SEQ ID NO: 682	SEQ ID NO: 839	SEQ ID NO: 996
rs361075	6H1.008	NA	CGGGCAAGTCAGGACATTAGAG ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
			SEQ ID NO: 2253	SEQ ID NO: 2410	SEQ ID NO: 2567
		AA	RASQDIRDYLG	GASSLQS	LQHNNYPFT
			SEQ ID NO: 683	SEQ ID NO: 840	SEQ ID NO: 997

iPS:361079	6A5.004.001	NA	CAGGCGAGTCAGGACATTACCA ACTATTTAAAT	GATGCTTCCAATTTGGAGCCA	CAACAGTATGATGATCTATTCA CT
			SEQ ID NO: 2254	SEQ ID NO: 2411	SEQ ID NO: 2568
		AA	QASQDITNYLN	DASNLEP	QQYDDLFT
			SEQ ID NO: 684	SEQ ID NO: 841	SEQ ID NO: 998
iPS:361085	6A5.004.002	NA	CAGGCGAGTCAGGACATTACCA ACTATTTAAAT	GATGCTTCCAATTTGGAGCCA	CAACAGTATGATGATCTATTCA CT
			SEQ ID NO: 2255	SEQ ID NO: 2412	SEQ ID NO: 2569
		AA	QASQDITNYLN	DASNLEP	QQYDDLFT
			SEQ ID NO: 685	SEQ ID NO: 842	SEQ ID NO: 999
iPS:361091	6A5.004.003	NA	CAGGCGAGTCAGGACATTACCA ACTATTTAAAT	GATGCTTCCAATTTGGAGCCA	CAACAGTATGATGATCTATTCA CT
			SEQ ID NO: 2256	SEQ ID NO: 2413	SEQ ID NO: 2570
		AA	QASQDITNYLN	DASNLEP	QQYDDLFT
			SEQ ID NO: 686	SEQ ID NO: 843	SEQ ID NO: 1000
iPS:361095	6A5.004.004	NA	CAGGCGAGTCAGGACATTACCA ACTATTTAAAT	GATGCTTCCAATTTGGAGCCA	CAACAGTATGATGATCTATTCA CT
			SEQ ID NO: 2257	SEQ ID NO: 2414	SEQ ID NO: 2571
		AA	QASQDITNYLN	DASNLEP	QQYDDLFT
			SEQ ID NO: 687	SEQ ID NO: 844	SEQ ID NO: 1001
iPS:361101	6A5.004.005	NA	CAGGCGAGTCAGGACATTACCA ACTATTTAAAT	GATGCTTCCAATTTGGAGCCA	CAACAGTATGATGATCTATTCA CT
			SEQ ID NO: 2258	SEQ ID NO: 2415	SEQ ID NO: 2572
		AA	QASQDITNYLN	DASNLEP	QQYDDLFT
			SEQ ID NO: 688	SEQ ID NO: 845	SEQ ID NO: 1002
iPS:361105	6A5.004.006	NA	CAGGCGAGTCAGGACATTACCA ACTATTTAAAT	GATGCTTCCAATTTGGAGCCA	CAACAGTATGATGATCTATTCA CT
			SEQ ID NO: 2259	SEQ ID NO: 2416	SEQ ID NO: 2573
		AA	QASQDITNYLN	DASNLEP	QQYDDLFT
			SEQ ID NO: 689	SEQ ID NO: 846	SEQ ID NO: 1003

rs3611109	6A5.004.007	NA	CAGGCGAGTCAGGACATTACCA ACTATTTAAAT	GATGCTTCCAATTTGGAGCCA	CAACAGTATGATGATCTATTCA CT
			SEQ ID NO: 2260	SEQ ID NO: 2417	SEQ ID NO: 2574
		AA	QASQDITNYLN	DASNLEP	QQYDDLFT
			SEQ ID NO: 690	SEQ ID NO: 847	SEQ ID NO: 1004
rs3611113	6A5.004.008	NA	CAGGCGAGTCAGGACATTACCA ACTATTTAAAT	GATGCTTCCAATTTGGAGCCA	CAACAGTATGATGATCTATTCA CT
			SEQ ID NO: 2261	SEQ ID NO: 2418	SEQ ID NO: 2575
		AA	QASQDITNYLN	DASNLEP	QQYDDLFT
			SEQ ID NO: 691	SEQ ID NO: 848	SEQ ID NO: 1005
rs3611120	6A5.004.009	NA	CAGGCGAGTCAGGACATTACCA ACTATTTAAAT	GATGCTTCCAATTTGGAGCCA	CAACAGTATGATGATCTATTCA CT
			SEQ ID NO: 2262	SEQ ID NO: 2419	SEQ ID NO: 2576
		AA	QASQDITNYLN	DASNLEP	QQYDDLFT
			SEQ ID NO: 692	SEQ ID NO: 849	SEQ ID NO: 1006
rs359896	6A5.004.010	NA	CAGGCGAGTCAGGACATTACCA ACTATTTAAAT	GATGCTTCCAATTTGGAGCCA	CAACAGTATGATGATCTATTCA CT
			SEQ ID NO: 2263	SEQ ID NO: 2420	SEQ ID NO: 2577
		AA	QASQDITNYLN	DASNLEP	QQYDDLFT
			SEQ ID NO: 693	SEQ ID NO: 850	SEQ ID NO: 1007
rs359890	6A5.004.011	NA	CAGGCGAGTCAGGACATTACCA ACTATTTAAAT	GATGCTTCCAATTTGGAGCCA	CAACAGTATGATGATCTATTCA CT
			SEQ ID NO: 2264	SEQ ID NO: 2421	SEQ ID NO: 2578
		AA	QASQDITNYLN	DASNLEP	QQYDDLFT
			SEQ ID NO: 694	SEQ ID NO: 851	SEQ ID NO: 1008
rs359567	2A11.002	NA	AGGGCCAGTCAGATTTTTACCA GCACCTACTTAGCC	GGTGCATCCAGCAGGGCCACT	CAGCAGTATGGTAGCTCACCTC GC
			SEQ ID NO: 2265	SEQ ID NO: 2422	SEQ ID NO: 2579
		AA	RASQIFTSTYLA	GASSRAT	QQYGSSPR
			SEQ ID NO: 695	SEQ ID NO: 852	SEQ ID NO: 1009

rs3359653	2A11.003	NA	AGGGCCAGTCAGATTTTTACCA GCACCTACTTAGCC	GGTGCATCCAGCAGGGCCACT	CAGCAGTATGGTAGCTCACCTC GC
			SEQ ID NO: 2266	SEQ ID NO: 2423	SEQ ID NO: 2580
		AA	RASQIFTSTYLA	GASSRAT	QQYGSSPR
			SEQ ID NO: 696	SEQ ID NO: 853	SEQ ID NO: 1010
rs3611158	2A11.004	NA	AGGGCCAGTCAGATTTTTACCA GCACCTACTTAGCC	GGTGCATCCAGCAGGGCCACT	CAGCAGTATGGTAGCTCACCTC GC
			SEQ ID NO: 2267	SEQ ID NO: 2424	SEQ ID NO: 2581
		AA	RASQIFTSTYLA	GASSRAT	QQYGSSPR
			SEQ ID NO: 697	SEQ ID NO: 854	SEQ ID NO: 1011
rs3611165	2A11.005	NA	AGGGCCAGTCAGATTTTTACCA GCACCTACTTAGCC	GGTGCATCCAGCAGGGCCACT	CAGCAGTATGGTAGCTCACCTC GC
			SEQ ID NO: 2268	SEQ ID NO: 2425	SEQ ID NO: 2582
		AA	RASQIFTSTYLA	GASSRAT	QQYGSSPR
			SEQ ID NO: 698	SEQ ID NO: 855	SEQ ID NO: 1012
rs3611172	2G10_LC1.00 3	NA	AGGGCCAGTCAGAGTGTTAGCA GCAACTTAGCC	GGTGCAGCCACCAGGGCCACT	CAGCAGTATAATAACTGGCCTC TCACT
			SEQ ID NO: 2269	SEQ ID NO: 2426	SEQ ID NO: 2583
		AA	RASQSVSSNLA	GAATRAT	QQYNNWPLT
			SEQ ID NO: 699	SEQ ID NO: 856	SEQ ID NO: 1013
rs3611178	2G10_LC1.00 4	NA	AGGGCCAGTCAGAGTGTTAGCA GCAACTTAGCC	GGTGCAGCCACCAGGGCCACT	CAGCAGTATAATAACTGGCCTC TCACT
			SEQ ID NO: 2270	SEQ ID NO: 2427	SEQ ID NO: 2584
		AA	RASQSVSSNLA	GAATRAT	QQYNNWPLT
			SEQ ID NO: 700	SEQ ID NO: 857	SEQ ID NO: 1014
rs3611185	2G10_LC1.00 5	NA	AGGGCCAGTCAGAGTGTTAGCA GCAACTTAGCC	GGTGCAGCCACCAGGGCCACT	CAGCAGTATAATAACTGGCCTC TCACT
			SEQ ID NO: 2271	SEQ ID NO: 2428	SEQ ID NO: 2585
		AA	RASQSVSSNLA	GAATRAT	QQYNNWPLT
			SEQ ID NO: 701	SEQ ID NO: 858	SEQ ID NO: 1015

2G10_LC1.00 6	NA	AGGGCCAGTCAGAGTGTTAGCA GCAACTTAGCC	GGTGCAGCCACCAGGGCCACT	CAGCAGTATAATAACTGGCCTC TCACT
		SEQ ID NO: 2272	SEQ ID NO: 2429	SEQ ID NO: 2586
	AA	RASQSVSSNLA	GAATRAT	QQYNNWPLT
		SEQ ID NO: 702	SEQ ID NO: 859	SEQ ID NO: 1016
2G10_LC1.00 7	NA	AGGGCCAGTCAGAGTGTTAGCA GCAACTTAGCC	GGTGCAGCCACCAGGGCCACT	CAGCAGTATAATAACTTCCCTC TCACT
		SEQ ID NO: 2273	SEQ ID NO: 2430	SEQ ID NO: 2587
	AA	RASQSVSSNLA	GAATRAT	QQYNNFPLT
		SEQ ID NO: 703	SEQ ID NO: 860	SEQ ID NO: 1017
2G10_LC1.00 8	NA	AGGGCCAGTCAGAGTGTTAGCA GCAACTTAGCC	GGTGCAGCCACCAGGGCCACT	CAGCAGTATAATAACTATCCTC TCACT
		SEQ ID NO: 2274	SEQ ID NO: 2431	SEQ ID NO: 2588
	AA	RASQSVSSNLA	GAATRAT	QQYNNYPLT
		SEQ ID NO: 704	SEQ ID NO: 861	SEQ ID NO: 1018
2G10_LC1.00 9	NA	AGGGCCAGTCAGAGTGTTAGCA GCAACTTAGCC	GGTGCAGCCACCAGGGCCACT	CAGCAGTATAATAACTGGCCTC TCACT
		SEQ ID NO: 2275	SEQ ID NO: 2432	SEQ ID NO: 2589
	AA	RASQSVSSNLA	GAATRAT	QQYNNWPLT
		SEQ ID NO: 705	SEQ ID NO: 862	SEQ ID NO: 1019
2G10_LC1.01 0	NA	AGGGCCAGTCAGAGTGTTAGCA GCAACTTAGCC	GGTGCAGCCACCAGGGCCACT	CAGCAGTATAATAACTGGCCTC TCACT
		SEQ ID NO: 2276	SEQ ID NO: 2433	SEQ ID NO: 2590
	AA	RASQSVSSNLA	GAATRAT	QQYNNWPLT
		SEQ ID NO: 706	SEQ ID NO: 863	SEQ ID NO: 1020
18E3.002	NA	AGGGCCAGTCAGAGTATTAGTT ACAGTTACTTAGCC	GGTGCATCCAGCAGGGCCACT	CAGCAGTATGGTAGTTCACCGC TCACT
		SEQ ID NO: 2277	SEQ ID NO: 2434	SEQ ID NO: 2591
	AA	RASQSISYSYLA	GASSRAT	QQYGSSPLT
		SEQ ID NO: 707	SEQ ID NO: 864	SEQ ID NO: 1021

2G10_LC1.00 6	rs3611192
2G10_LC1.00 7	rs3596091
2G10_LC1.00 8	rs3596153
2G10_LC1.00 9	rs3611196
2G10_LC1.01 0	rs3612022
18E3.002	rs3596442

rs361206	18E3.003	NA	AGGGCCAGTCAGAGTATTAGTT ACAGTTACTTAGCC	GGTGCATCCAGCAGGGCCACT	CAGCAGTATGGTAGTTCACCGC TCACT
			SEQ ID NO: 2278	SEQ ID NO: 2435	SEQ ID NO: 2592
		AA	RASQSISYSYLA	GASSRAT	QQYGSSPLT
			SEQ ID NO: 708	SEQ ID NO: 865	SEQ ID NO: 1022
rs359628	18E3.004	NA	AGGGCCAGTCAGAGTATTAGTT ACAGTTACTTAGCC	GGTGCATCCAGCAGGGCCACT	CAGCAGTATGGTAGTTCACCGC TCACT
			SEQ ID NO: 2279	SEQ ID NO: 2436	SEQ ID NO: 2593
		AA	RASQSISYSYLA	GASSRAT	QQYGSSPLT
			SEQ ID NO: 709	SEQ ID NO: 866	SEQ ID NO: 1023
rs359637	18E3.005	NA	AGGGCCAGTCAGAGTATTAGTT ACAGTTACTTAGCC	GGTGCATCCAGCAGGGCCACT	CAGCAGTATGGTAGTTCACCGC TCACT
			SEQ ID NO: 2280	SEQ ID NO: 2437	SEQ ID NO: 2594
		AA	RASQSISYSYLA	GASSRAT	QQYGSSPLT
			SEQ ID NO: 710	SEQ ID NO: 867	SEQ ID NO: 1024
rs361210	18E3.006	NA	AGGGCCAGTCAGAGTATTAGTT ACAGTTACTTAGCC	GGTGCATCCAGCAGGGCCACT	CAGCAGTATGGTAGTTCACCGC TCACT
			SEQ ID NO: 2281	SEQ ID NO: 2438	SEQ ID NO: 2595
		AA	RASQSISYSYLA	GASSRAT	QQYGSSPLT
			SEQ ID NO: 711	SEQ ID NO: 868	SEQ ID NO: 1025
rs361214	18E3.007	NA	AGGGCCAGTCAGAGTATTAGTT ACAGTTACTTAGCC	GGTGCATCCAGCAGGGCCACT	CAGCAGTATGGTAGTTCACCGC TCACT
			SEQ ID NO: 2282	SEQ ID NO: 2439	SEQ ID NO: 2596
		AA	RASQSISYSYLA	GASSRAT	QQYGSSPLT
			SEQ ID NO: 712	SEQ ID NO: 869	SEQ ID NO: 1026
rs361218	18E3.008	NA	AGGGCCAGTCAGAGTATTAGTT ACAGTTACTTAGCC	GGTGCATCCAGCAGGGCCACT	CAGCAGTATGGTAGTTCACCGC TCACT
			SEQ ID NO: 2283	SEQ ID NO: 2440	SEQ ID NO: 2597
		AA	RASQSISYSYLA	GASSRAT	QQYGSSPLT
			SEQ ID NO: 713	SEQ ID NO: 870	SEQ ID NO: 1027

rs361222	5C2.006	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
			SEQ ID NO: 2284	SEQ ID NO: 2441	SEQ ID NO: 2598
		AA	KSSQSVLSSSNNKNYIA	WASTRES	QQYYSTPWT
			SEQ ID NO: 714	SEQ ID NO: 871	SEQ ID NO: 1028
rs361229	5C2.007	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
			SEQ ID NO: 2285	SEQ ID NO: 2442	SEQ ID NO: 2599
		AA	KSSQSVLSSSNNKNYIA	WASTRES	QQYYSTPWT
			SEQ ID NO: 715	SEQ ID NO: 872	SEQ ID NO: 1029
rs361236	5C2.008	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
			SEQ ID NO: 2286	SEQ ID NO: 2443	SEQ ID NO: 2600
		AA	KSSQSVLSSSNNKNYIA	WASTRES	QQYYSTPWT
			SEQ ID NO: 716	SEQ ID NO: 873	SEQ ID NO: 1030
rs359685	5C2.009	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
			SEQ ID NO: 2287	SEQ ID NO: 2444	SEQ ID NO: 2601
		AA	KSSQSVLSSSNNKNYIA	WASTRES	QQYYSTPWT
			SEQ ID NO: 717	SEQ ID NO: 874	SEQ ID NO: 1031
rs361240	5C2.010	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
			SEQ ID NO: 2288	SEQ ID NO: 2445	SEQ ID NO: 2602
		AA	KSSQSVLSSSNNKNYIA	WASTRES	QQYYSTPWT
			SEQ ID NO: 718	SEQ ID NO: 875	SEQ ID NO: 1032

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

rs359678	5C2.016	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
			SEQ ID NO: 2294		SEQ ID NO: 2608
		AA	KSSQSVLSSSNNKNYIA		WASTRES		QQYYSTPWT
			SEQ ID NO: 724		SEQ ID NO: 881		SEQ ID NO: 1038
rs361275	11C1.002	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGAATCC	CAGCAATATTATCGTACTCCGT GGACG
			SEQ ID NO: 2295		SEQ ID NO: 2452		SEQ ID NO: 2609
		AA	KSSQSVLSSSNNKNYLA		WTSTRES		QQYYRTPWT
			SEQ ID NO: 725		SEQ ID NO: 882		SEQ ID NO: 1039
rs361282	11C1.003	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGAATCC	CAGCAATATTATCGTACTCCGT GGACG
			SEQ ID NO: 2296		SEQ ID NO: 2453		SEQ ID NO: 2610
		AA	KSSQSVLSSSNNKNYLA		WTSTRES		QQYYRTPWT
			SEQ ID NO: 726		SEQ ID NO: 883		SEQ ID NO: 1040
rs361289	11C1.004	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGATTCC	CAGCAATATTATCGTACTCCGT GGACG
			SEQ ID NO: 2297		SEQ ID NO: 2454		SEQ ID NO: 2611
		AA	KSSQSVLSSSNNKNYLA		WTSTRDS		QQYYRTPWT
			SEQ ID NO: 727		SEQ ID NO: 884		SEQ ID NO: 1041
rs359712	11C1.005	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGAATCC	CAGCAATATTATCGTACTCCGT GGACG
			SEQ ID NO: 2298		SEQ ID NO: 2455		SEQ ID NO: 2612
		AA	KSSQSVLSSSNNKNYLA		WTSTRES		QQYYRTPWT
			SEQ ID NO: 728		SEQ ID NO: 885		SEQ ID NO: 1042

rs361293	11C1.006	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGAATCC	CAGCAATATTATCGTACTCCGT GGACG
			SEQ ID NO: 2299	SEQ ID NO: 2456	SEQ ID NO: 2613
		AA	KSSQSVLSSSNNKNYLA	WTSTRES	QQYYRTPWT
			SEQ ID NO: 729	SEQ ID NO: 886	SEQ ID NO: 1043
rs361297	11C1.007	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGATTCC	CAGCAATATTATCGTACTCCGT GGACG
			SEQ ID NO: 2300	SEQ ID NO: 2457	SEQ ID NO: 2614
		AA	KSSQSVLSSSNNKNYLA	WTSTRDS	QQYYRTPWT
			SEQ ID NO: 730	SEQ ID NO: 887	SEQ ID NO: 1044
rs361301	11C1.008	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGATTCC	CAGCAATATTATCGTACTCCGT GGACG
			SEQ ID NO: 2301	SEQ ID NO: 2458	SEQ ID NO: 2615
		AA	KSSQSVLSSSNNKNYLA	WTSTRDS	QQYYRTPWT
			SEQ ID NO: 731	SEQ ID NO: 888	SEQ ID NO: 1045
rs359703	11C1.009	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGAATCC	CAGCAATATTATCGTACTCCGT GGACG
			SEQ ID NO: 2302	SEQ ID NO: 2459	SEQ ID NO: 2616
		AA	KSSQSVLSSSNNKNYLA	WTSTRES	QQYYRTPWT
			SEQ ID NO: 732	SEQ ID NO: 889	SEQ ID NO: 1046
rs361305	11C1.010	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGAATCC	CAGCAATATTATCGTACTCCGT GGACG
			SEQ ID NO: 2303	SEQ ID NO: 2460	SEQ ID NO: 2617
		AA	KSSQSVLSSSNNKNYLA	WTSTRES	QQYYRTPWT
			SEQ ID NO: 733	SEQ ID NO: 890	SEQ ID NO: 1047

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

rs:36133O	12H11.002	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGATTCC	CAGCAATATTATCGTACTCCGT GGACG
			SEQ ID NO: 2309	SEQ ID NO: 2466	SEQ ID NO: 2623
		AA	KSSQSVLSSSNNKNYLA	WTSTRDS	QQYYRTPWT
			SEQ ID NO: 739	SEQ ID NO: 896	SEQ ID NO: 1053
rs:36133Z	12H11.003	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGATTCC	CAGCAATATTATCGTACTCCGT GGACG
			SEQ ID NO: 2310	SEQ ID NO: 2467	SEQ ID NO: 2624
		AA	KSSQSVLSSSNNKNYLA	WTSTRDS	QQYYRTPWT
			SEQ ID NO: 740	SEQ ID NO: 897	SEQ ID NO: 1054
rs:36134Y	12H11.004	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGATTCC	CAGCAATATTATCGTACTCCGT GGACG
			SEQ ID NO: 2311	SEQ ID NO: 2468	SEQ ID NO: 2625
		AA	KSSQSVLSSSNNKNYLA	WTSTRDS	QQYYRTPWT
			SEQ ID NO: 741	SEQ ID NO: 898	SEQ ID NO: 1055
rs:36135I	12H11.005	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGATTCC	CAGCAATATTATCGTACTCCGT GGACG
			SEQ ID NO: 2312	SEQ ID NO: 2469	SEQ ID NO: 2626
		AA	KSSQSVLSSSNNKNYLA	WTSTRDS	QQYYRTPWT
			SEQ ID NO: 742	SEQ ID NO: 899	SEQ ID NO: 1056
rs:36135X	12H11.006	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGATTCC	CAGCAATATTATCGTACTCCGT GGACG
			SEQ ID NO: 2313	SEQ ID NO: 2470	SEQ ID NO: 2627
		AA	KSSQSVLSSSNNKNYLA	WTSTRDS	QQYYRTPWT
			SEQ ID NO: 743	SEQ ID NO: 900	SEQ ID NO: 1057

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

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

rs:36141	2C2.005.003	NA	TCTGGAAGTAGCTCCAACATCG GAAGTAATTATGTAAAC	ACTAATAATCAGCGGCCCTCA
			SEQ ID NO: 2324	SEQ ID NO: 2481
		AA	SGSSSNIGSNYVN	TNNQRPS
			SEQ ID NO: 754	SEQ ID NO: 911
rs:36142	2C2.005.004	NA	TCTGGAAGTAGCTCCAACATCG GAAGTAATTATGTAAAC	ACTAATAATCAGCGGCCCTCA
			SEQ ID NO: 2325	SEQ ID NO: 2482
		AA	SGSSSNIGSNYVN	TNNQRPS
			SEQ ID NO: 755	SEQ ID NO: 912
rs:36143	2C2.005.005	NA	TCTGGAAGTAGCTCCAACATCG GAAGTCAAACTGTAAAC	ACTAATAATCAGCGGCCCTCA
			SEQ ID NO: 2326	SEQ ID NO: 2483
		AA	SGSSSNIGSQTVN	TNNQRPS
			SEQ ID NO: 756	SEQ ID NO: 913
rs:36143	2C2.005.006	NA	TCTGGAAGTAGCTCCAACATCG GAAGTAATTATGTAAAC	ACTAATAATCAGCGGCCCTCA
			SEQ ID NO: 2327	SEQ ID NO: 2484
		AA	SGSSSNIGSNYVN	TNNQRPS
			SEQ ID NO: 757	SEQ ID NO: 914
rs:36144	2C2.005.007	NA	TCTGGAAGTAGCTCCAACATCG GAAGTAATACTGTAAAC	ACTAATAATCAGCGGCCCTCA
			SEQ ID NO: 2328	SEQ ID NO: 2485
		AA	SGSSSNIGSNTVN	TNNQRPS
			SEQ ID NO: 758	SEQ ID NO: 915
rs:36144	2C2.005.008	NA	TCTGGAAGTAGCTCCAACATCG GAAGTAATACTGTAAAC	ACTAATAATCAGCGGCCCTCA
			SEQ ID NO: 2329	SEQ ID NO: 2486
		AA	SGSSSNIGSNTVN	TNNQRPS
			SEQ ID NO: 759	SEQ ID NO: 916

GCAACATTCGATGAAAGCCTG AGTGGTCCGGTA			
SEQ ID NO: 2638			
ATFDESLSGPV			
SEQ ID NO: 1068			
GCAACATTCGATGAAAGCCTG CAAGGTCCGGTA			
SEQ ID NO: 2639			
ATFDESLQGPV			
SEQ ID NO: 1069			
GCAACATTCGATGACAGCCTG AATGGTCCGGTA			
SEQ ID NO: 2640			
ATFDDSLNGPV			
SEQ ID NO: 1070			
GCAACATTCGATGACAGCCTG AATGGTCCGGTA			
SEQ ID NO: 2641			
ATFDDSLNGPV			
SEQ ID NO: 1071			
GCAACATTCGATGAAAGCCTG AATGGTCCGGTA			
SEQ ID NO: 2642			
ATFDESLNGPV			
SEQ ID NO: 1072			
GCAACATTCGATGACAGCCTGC AAGGTCCGGTA			
SEQ ID NO: 2643			
ATFDDSLQGPV			
SEQ ID NO: 1073			

rs:36145	2C2.005.009	NA	TCTGGAAGTAGCTCCAACATCG GAAGTAATACTGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATTCGATGACAGCCTG AGTGGTCCGGTA
			SEQ ID NO: 2330	SEQ ID NO: 2487	SEQ ID NO: 2644
		AA	SGSSSNIGSNTVN	TNNQRPS	ATFDDSLSGPV
			SEQ ID NO: 760	SEQ ID NO: 917	SEQ ID NO: 1074
rs:36146	2C2.005.010	NA	TCTGGAAGTAGCTCCAACATCG GAAGTAATACTGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATTCGATGACAGCCTG AATGCTCCGGTA
			SEQ ID NO: 2331	SEQ ID NO: 2488	SEQ ID NO: 2645
		AA	SGSSSNIGSNTVN	TNNQRPS	ATFDDSLNAPV
			SEQ ID NO: 761	SEQ ID NO: 918	SEQ ID NO: 1075
rs:36146	2C2.005.011	NA	TCTGGAAGTAGCTCCAACATCG GAAGTAATACTGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATTCGATAGCAGCCTG AATGGTCCGGTA
			SEQ ID NO: 2332	SEQ ID NO: 2489	SEQ ID NO: 2646
		AA	SGSSSNIGSNTVN	TNNQRPS	ATFDSSLNGPV
			SEQ ID NO: 762	SEQ ID NO: 919	SEQ ID NO: 1076
rs:36147	2C2.005.012	NA	TCTGGAAGTAGCTCCAACATCG GAAGTAATTATGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATTCGATAGCAGCCTG AATGCTCCGGTA
			SEQ ID NO: 2333	SEQ ID NO: 2490	SEQ ID NO: 2647
		AA	SGSSSNIGSNYVN	TNNQRPS	ATFDSSLNAPV
			SEQ ID NO: 763	SEQ ID NO: 920	SEQ ID NO: 1077
rs:36147	2C2.005.013	NA	TCTGGAAGTAGCTCCAACATCG GAAGTAATTATGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATTCGATAGCAGCCTG AATGCTCCGGTA
			SEQ ID NO: 2334	SEQ ID NO: 2491	SEQ ID NO: 2648
		AA	SGSSSNIGSNYVN	TNNQRPS	ATFDSSLNAPV
			SEQ ID NO: 764	SEQ ID NO: 921	SEQ ID NO: 1078
rs:36148	2C2.005.014	NA	TCTGGAAGTAGCTCCAACATCG GAAGTCAAACTGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATTCGATGAAAGCCTG AGTGGTCCGGTA
			SEQ ID NO: 2335	SEQ ID NO: 2492	SEQ ID NO: 2649
		AA	SGSSSNIGSQTVN	TNNQRPS	ATFDESLSGPV
			SEQ ID NO: 765	SEQ ID NO: 922	SEQ ID NO: 1079

rs361845	18F2.013	NA	CGGGCAAGTCAGGACCTTAGAA ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT
			SEQ ID NO: 2336	SEQ ID NO: 2493
		AA	RASQDLRNYLG	GASSLQS
			SEQ ID NO: 766	SEQ ID NO: 923
rs361851	6H1.009	NA	CGGGCAAGTCAGGACATTAGAG ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT
			SEQ ID NO: 2337	SEQ ID NO: 2494
		AA	RASQDIRDYLG	GASSLQS
			SEQ ID NO: 767	SEQ ID NO: 924
rs361855	2C2.005.015	NA	TCTGGAAGTAGCTCCAACATCG GAAGTAATACTGTAAAC	ACTAATAATCAGCGGCCCTCA
			SEQ ID NO: 2338	SEQ ID NO: 2495
		AA	SGSSSNIGSNTVN	TNNQRPS
			SEQ ID NO: 768	SEQ ID NO: 925
rs336067	5G12.006	NA	CGGGCAAGTCAGACCATTAGCA GGTTTTTAAAT	GTTGCATCCAGTTTGCAAAGT
			SEQ ID NO: 2339	SEQ ID NO: 2496
		AA	RASQTISRFLN	VASSLQS
			SEQ ID NO: 769	SEQ ID NO: 926
rs336169	17B11.002	NA	TCTGGAAGCAGCTCCAACATTG GAAATAATTATGTATCC	GACAATAATAAGCGACCCTCA
			SEQ ID NO: 2340	SEQ ID NO: 2497
		AA	SGSSSNIGNNYVS	DNNKRPS
			SEQ ID NO: 770	SEQ ID NO: 927
rs361127	5G12.006.001	NA	CGGGCAAGTCAGACCATTAGCA GGTTTTTAAAT	GTTGCATCCAGTTTGCAAAGT
			SEQ ID NO: 2341	SEQ ID NO: 2498
		AA	RASQTISRFLN	VASSLQS
			SEQ ID NO: 771	SEQ ID NO: 928

rs361845	18F2.013	NA	CTACAGCATAATAATTACCCCT TCACT
			SEQ ID NO: 2650
		AA	LQHNNYPFT
			SEQ ID NO: 1080
rs361851	6H1.009	NA	CTACAGCATAATAATTACCCCT TCACT
			SEQ ID NO: 2651
		AA	LQHNNYPFT
			SEQ ID NO: 1081
rs361855	2C2.005.015	NA	GCAACATTCGATAGCAGCCTG AGTGGTCCGGTA
			SEQ ID NO: 2652
		AA	ATFDSSLSGPV
			SEQ ID NO: 1082
rs336067	5G12.006	NA	CAACAGAGTTACAGTACCCTG ATCAGT
			SEQ ID NO: 2653
		AA	QQSYSTLIS
			SEQ ID NO: 1083
rs336169	17B11.002	NA	GGAACATGGGATAGCAGCCTG AGTGCTGTGGTA
			SEQ ID NO: 2654
		AA	GTWDSSLSAVV
			SEQ ID NO: 1084
rs361127	5G12.006.001	NA	CAACAGAGTTACAGTACCCTG ATCAGT
			SEQ ID NO: 2655
		AA	QQSYSTLIS
			SEQ ID NO: 1085

rs361136	5G12.006.002	NA	CGGGCAAGTCAGACCATTAGCA GGTTTTTAAAT	GTTGCATCCAGTTTGCAAAGT	CAACAGAGTTACAGTACCCTG ATCAGT
			SEQ ID NO: 2342	SEQ ID NO: 2499	SEQ ID NO: 2656
		AA	RASQTISRFLN	VASSLQS	QQSYSTLIS
			SEQ ID NO: 772	SEQ ID NO: 929	SEQ ID NO: 1086
rs361140	5G12.006.003	NA	CGGGCAAGTCAGACCATTAGCA GGTTTTTAAAT	GTTGCATCCAGTTTGCAAAGT	CAACAGAGTTACAGTACCCTG ATCAGT
			SEQ ID NO: 2343	SEQ ID NO: 2500	SEQ ID NO: 2657
		AA	RASQTISRFLN	VASSLQS	QQSYSTLIS
			SEQ ID NO: 773	SEQ ID NO: 930	SEQ ID NO: 1087
rs359919	5G12.006.004	NA	CGGGCAAGTCAGACCATTAGCA GGTTTTTAAAT	GTTGCATCCAGTTTGCAAAGT	CAACAGAGTTACAGTACCCTG ATCAGT
			SEQ ID NO: 2344	SEQ ID NO: 2501	SEQ ID NO: 2658
		AA	RASQTISRFLN	VASSLQS	QQSYSTLIS
			SEQ ID NO: 774	SEQ ID NO: 931	SEQ ID NO: 1088
rs361144	5G12.006.005	NA	CGGGCAAGTCAGACCATTAGCA GGTTTTTAAAT	GTTGCATCCAGTTTGCAAAGT	CAACAGAGTTACAGTACCCTG ATCAGT
			SEQ ID NO: 2345	SEQ ID NO: 2502	SEQ ID NO: 2659
		AA	RASQTISRFLN	VASSLQS	QQSYSTLIS
			SEQ ID NO: 775	SEQ ID NO: 932	SEQ ID NO: 1089
rs361151	5G12.006.006	NA	CGGGCAAGTCAGACCATTAGCA GGTTTTTAAAT	GTTGCATCCAGTTTGCAAAGT	CAACAGAGTTACAGTACCCTG ATCAGT
			SEQ ID NO: 2346	SEQ ID NO: 2503	SEQ ID NO: 2660
		AA	RASQTISRFLN	VASSLQS	QQSYSTLIS
			SEQ ID NO: 776	SEQ ID NO: 933	SEQ ID NO: 1090
rs361491	17B11.002.00 1	NA	TCTGGAAGCAGCTCCAACATTG GAAATAATTATGTATCC	GACAATAATAAGCGACCCTCA	GGAACATGGGATAGCAGCCTG AGTGCTGTGGTA
			SEQ ID NO: 2347	SEQ ID NO: 2504	SEQ ID NO: 2661
		AA	SGSSSNIGNNYVS	DNNKRPS	GTWDSSLSAVV
			SEQ ID NO: 777	SEQ ID NO: 934	SEQ ID NO: 1091

rs3614499	17B11.002.00 2	NA	TCTGGAAGCAGCTCCAACATTG GAAATAATTATGTATCC
			SEQ ID NO: 2348
		AA	SGSSSNIGNNYVS
			SEQ ID NO: 778
rs361503	17B11.002.00 3	NA	TCTGGAAGCAGCTCCAACATTG GAAATAATTATGTATCC
			SEQ ID NO: 2349
		AA	SGSSSNIGNNYVS
			SEQ ID NO: 779
rs361507	17B11.002.00 4	NA	TCTGGAAGCAGCTCCAACATTG GAAATAATTATGTATCC
			SEQ ID NO: 2350
		AA	SGSSSNIGNNYVS
			SEQ ID NO: 780
rs3615514	17B11.002.00 5	NA	TCTGGAAGCAGCTCCAACATTG GAAATAATTATGTATCC
			SEQ ID NO: 2351
		AA	SGSSSNIGNNYVS
			SEQ ID NO: 781
rs360582	17B11.002.00 6	NA	TCTGGAAGCAGCTCCAACATTG GAAATAATTATGTATCC
			SEQ ID NO: 2352
		AA	SGSSSNIGNNYVS
			SEQ ID NO: 782
rs3615518	17B11.002.00 7	NA	TCTGGAAGCAGCTCCAACATTG GAAATAATTATGTATCC
			SEQ ID NO: 2353
		AA	SGSSSNIGNNYVS
			SEQ ID NO: 783

GACAATAATAAGCGACCCTCA	GGAACATGGGATAGCAGCCTG AGTGCTGTGGTA
SEQ ID NO: 2505	SEQ ID NO: 2662
DNNKRPS	GTWDSSLSAVV
SEQ ID NO: 935	SEQ ID NO: 1092
GACAATAATAAGCGACCCTCA	GGAACATGGGATAGCAGCCTG AGTGCTGTGGTA
SEQ ID NO: 2506	SEQ ID NO: 2663
DNNKRPS	GTWDSSLSAVV
SEQ ID NO: 936	SEQ ID NO: 1093
GACAATAATAAGCGACCCTCA	GGAACATTCGAAAGCAGCCTG AGTGCTGTGGTA
SEQ ID NO: 2507	SEQ ID NO: 2664
DNNKRPS	GTFESSLSAVV
SEQ ID NO: 937	SEQ ID NO: 1094
GACAATAATAAGCGACCCTCA	GGAACATGGGATAGCAGCCTG AGTGCTGTGGTA
SEQ ID NO: 2508	SEQ ID NO: 2665
DNNKRPS	GTWDSSLSAVV
SEQ ID NO: 938	SEQ ID NO: 1095
GACAATAATAAGCGACCCTCA	GGAACATGGGATAGCAGCCTG AGTGCTGTGGTA
SEQ ID NO: 2509	SEQ ID NO: 2666
DNNKRPS	GTWDSSLSAVV
SEQ ID NO: 939	SEQ ID NO: 1096
GACAATAATAAGCGACCCTCA	GGAACATGGGATAGCAGCCTG AGTGCTGTGGTA
SEQ ID NO: 2510	SEQ ID NO: 2667
DNNKRPS	GTWDSSLSAVV
SEQ ID NO: 940	SEQ ID NO: 1097

IPS:360570	17B11.002.008	NA	TCTGGAAGCAGCTCCAACATTG GAAATAATTATGTATCC	GACAATAATAAGCGACCCTCA	GGAACATTCGAAAGCAGCCTG AGTGCTGTGGTA
			SEQ ID NO: 2354	SEQ ID NO: 2511	SEQ ID NO: 2668
		AA	SGSSSNIGNNYVS	DNNKRPS	GTFESSLSAVV
			SEQ ID NO: 784	SEQ ID NO: 941	SEQ ID NO: 1098
IPS:362051	5G12.005.001	NA	CGGGCAAGTCAGACCATTAGCA GGTTTTTAAAT	GTTGCATCCAGTTTGCAAAGT	CAACAGAGTTACAGTACCCTGC TCAGT
			SEQ ID NO: 2355	SEQ ID NO: 2512	SEQ ID NO: 2669
		AA	RASQTISRFLN	VASSLQS	QQSYSTLLS
			SEQ ID NO: 785	SEQ ID NO: 942	SEQ ID NO: 1099

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

iPS#	Ab	Type	CDRH1	CDRH2	CDRH3
iPS:336175	2C2.005	NA	GGCTACTATATGCAT	TGGATCAACCCTAACAGTGGTG GCACAAACTATGCACAGAAGT TTCAGGGC	GGGGGGGATTACGTTTGGGGG ACTTATCGGCCTCACTACTAC ACGGTATGGACGTC
			SEQ ID NO: 2670	SEQ ID NO: 2827	SEQ ID NO: 2984
		AA	GYYMH	WINPNSGGTNYAQKFQG	GGDYVWGTYRPHYYYGMDV
			SEQ ID NO: 1100	SEQ ID NO: 1257	SEQ ID NO: 1414
iPS:335914	4B1	NA	AACTTTGGCATGCAC	GTTATATGGTATGATGGAAGTA ATGAAAACTATGCAGACTCCGT GAAGGGC	GATGGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
			SEQ ID NO: 2671	SEQ ID NO: 2828	SEQ ID NO: 2985
		AA	NFGMH	VIWYDGSNENYADSVKG	DGTIFGVVLGDY
			SEQ ID NO: 1101	SEQ ID NO: 1258	SEQ ID NO: 1415

rs:33593938	6H1	NA	TACTTTGGCATGCAC	GTTATATGGTATGATGGAAGTA ATAAATACTATGCAGACTCCGT GAAGGGC	GATGGGACGATTTTTGGAGTGC TCTTGGGGGACTAC
			SEQ ID NO: 2672	SEQ ID NO: 2829	SEQ ID NO: 2986
		AA	YFGMH	VIWYDGSNKYYADSVKG	DGTIFGVLLGDY
			SEQ ID NO: 1102	SEQ ID NO: 1259	SEQ ID NO: 1416
rs:33593941	2F11	NA	AGCTATGGCATGCAC	GTTATATGGTATGATGGAAGTA ATAAATACTATGCAGACTCCGT GAAGGGC	GATAGGACGATTTTTGGAGTGG TTCTTGACTAC
			SEQ ID NO: 2673	SEQ ID NO: 2830	SEQ ID NO: 2987
		AA	SYGMH	VIWYDGSNKYYADSVKG	DRTIFGVVLDY
			SEQ ID NO: 1103	SEQ ID NO: 1260	SEQ ID NO: 1417
rs:33593970	5C2	NA	GGCTACTATATCCAC	TGGATCAACCCTGACAGTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC	GAGGCCACGATTTTTGGAATGG TTATTGTACCGTTTGACTAC
			SEQ ID NO: 2674	SEQ ID NO: 2831	SEQ ID NO: 2988
		AA	GYYIH	WINPDSGGTDYSQRFQG	EATIFGMVIVPFDY
			SEQ ID NO: 1104	SEQ ID NO: 1261	SEQ ID NO: 1418
rs:33593978	13H12	NA	GGCTACTATATCCAC	TGGATCAACCCTGACAGTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC	GAGGCCACGATTTTTGGAATGG TTATTGTACCGTTTGACTAC
			SEQ ID NO: 2675	SEQ ID NO: 2832	SEQ ID NO: 2989
		AA	GYYIH	WINPDSGGTDYSQRFQG	EATIFGMVIVPFDY
			SEQ ID NO: 1105	SEQ ID NO: 1262	SEQ ID NO: 1419
rs:33593986	11C1	NA	GGCTACTATATACAC	TGGATCAGCCCTAACAGTGGTG ACACAAGCTATGCACAGAAGT TTCAGGAC	GAGGCCACGATTTTTGGAATGC TTATTGTACCATTTGACTAC
			SEQ ID NO: 2676	SEQ ID NO: 2833	SEQ ID NO: 2990
		AA	GYYIH	WISPNSGDTSYAQKFQD	EATIFGMLIVPFDY
			SEQ ID NO: 1106	SEQ ID NO: 1263	SEQ ID NO: 1420

rs335994	12H11	NA	GGCTACTATATACAC	SEQ ID NO: 2677
		AA	GYYIH	SEQ ID NO: 2834
			WISPNNGDTNYAQKFQD	SEQ ID NO: 1107
			EATIFGMLIVPFDY	SEQ ID NO: 1264
rs336024	18E3	NA	AGTGGTGGTTACTACTGGAGC	SEQ ID NO: 2678
		AA	SGGYYWS	SEQ ID NO: 2835
			YIYYSGSTYYNPSLKS	SEQ ID NO: 1108
			DRITIFGVVMGGGMDV	SEQ ID NO: 1265
rs336041	2G10_LC1	NA	AACTATGGCATGCAC	SEQ ID NO: 2679
		AA	NYGMH	SEQ ID NO: 2836
			AIWFDGSDKYYADSVKG	SEQ ID NO: 1109
			DQAIFGVVPDY	SEQ ID NO: 1266
rs336077	4H9.004	NA	TACTTTGGCATGCAC	SEQ ID NO: 2680
		AA	YFGMH	SEQ ID NO: 2837
			VIWYDGSNKYYADSVKG	SEQ ID NO: 1110
			DGTIFGVLLGDY	SEQ ID NO: 1267
rs336088	6A5.004	NA	AGCTATGGCATGCAC	SEQ ID NO: 2681
		AA	SYGMH	SEQ ID NO: 2838
			AIWYDGNNKYYADSVKG	SEQ ID NO: 1111
			DRTIFGVVLEY	SEQ ID NO: 1268

rs335994	12H11	NA	TGGATAAGCCCTAACAATGGTG ACACAAACTATGCACAGAAGT TTCAGGAC	SEQ ID NO: 2991
		AA	GYYIH	SEQ ID NO: 3164
			WISPNNGDTNYAQKFQD	SEQ ID NO: 1421
			EATIFGMLIVPFDY	SEQ ID NO: 1578
rs336024	18E3	NA	TACATCTATTACAGTGGGAGCA CCTACTACAACCCGTCCCTCAA GAGT	SEQ ID NO: 3165
		AA	YIYYSGSTYYNPSLKS	SEQ ID NO: 3166
			DRITIFGVVMGGGMDV	SEQ ID NO: 1579
rs336041	2G10_LC1	NA	GCTATATGGTTTGATGGAAGTG ATAAATACTATGCAGACTCCGT GAAGGGC	SEQ ID NO: 3167
		AA	AIWFDGSDKYYADSVKG	SEQ ID NO: 3168
			DQAIFGVVPDY	SEQ ID NO: 1580
rs336077	4H9.004	NA	GTTATATGGTATGATGGAAGTA ATAAATACTATGCAGACTCCGT GAAGGGC	SEQ ID NO: 3169
		AA	VIWYDGSNKYYADSVKG	SEQ ID NO: 3170
			DGTIFGVLLGDY	SEQ ID NO: 1581
rs336088	6A5.004	NA	GCTATATGGTATGATGGAAATA ATAAATACTATGCAGACTCCGT GAAGGGC	SEQ ID NO: 3171
		AA	AIWYDGNNKYYADSVKG	SEQ ID NO: 3172
			DRTIFGVVLEY	SEQ ID NO: 1582

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

rs360962	4B1.011	NA	TACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGGC	GATGGGACGATTTTTGGAGTGC TCTTGGGGGACTAC
			SEQ ID NO: 2691	SEQ ID NO: 2692	SEQ ID NO: 3005
		AA	NFGMH	VIWYDASNENYADAVKG	DGTIFGVVLGDY
			SEQ ID NO: 1121	SEQ ID NO: 1278	SEQ ID NO: 1435
rs360955	4B1.010	NA	AACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACGCCG TGAAGGGC	GATGGGACGATCTTTTGGAGTGG TCTTGGGGGACTAC
			SEQ ID NO: 2690	SEQ ID NO: 2847	SEQ ID NO: 3004
		AA	NFGMH	VIWYDASNENYADAVKG	DGTIFGVVLGDY
			SEQ ID NO: 1120	SEQ ID NO: 1277	SEQ ID NO: 1434
rs359761	4H9.004.006	NA	TACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGGC	GATAGGACGATTTTTGGAGTGC TCTTGGGGGACTAC
			SEQ ID NO: 2689	SEQ ID NO: 2846	SEQ ID NO: 3003
		AA	YFGMH	VIWYDASNKYYADAVKG	DRTIFGVLLGDY
			SEQ ID NO: 1118	SEQ ID NO: 1275	SEQ ID NO: 1432
rs360949	4H9.004.005	NA	TACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGGC	GATGGGACGATTTTTGGAGTGC TCTTGGGGGACTAC
			SEQ ID NO: 2688	SEQ ID NO: 2845	SEQ ID NO: 3002
		AA	YFGMH	VIWYDASNKYYADAVKG	DGTIFGVLLGDY
			SEQ ID NO: 1117	SEQ ID NO: 1274	SEQ ID NO: 1431
rs360943	4H9.004.004	NA	TACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGGC	GATGGGACGATTTTTGGAGTGC TCTTGGGGGACTAC
			SEQ ID NO: 2687	SEQ ID NO: 2844	SEQ ID NO: 3001
		AA	YFGMH	VIWYDASNKYYADAVKG	DGTIFGVLLGDY
			SEQ ID NO: 1117	SEQ ID NO: 1274	SEQ ID NO: 1431

rs360968	4BI.012	NA	AACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACGCCG TGAAGGGC	GATGGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
			SEQ ID NO: 2692	SEQ ID NO: 2849	SEQ ID NO: 3006
		AA	NFGMH	VIWYDASNENYADAVKG	DGTIFGVVLGDY
			SEQ ID NO: 1122	SEQ ID NO: 1279	SEQ ID NO: 1436
rs360974	4BI.013	NA	AACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACTCCGT GAAGGGC	GATGGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
			SEQ ID NO: 2693	SEQ ID NO: 2850	SEQ ID NO: 3007
		AA	NFGMH	VIWYDASNENYADSVKG	DGTIFGVVLGDY
			SEQ ID NO: 1123	SEQ ID NO: 1280	SEQ ID NO: 1437
rs360978	4BI.014	NA	AACTTTGGCATGCAC	GTTATATGGTATGATGGAAGTA ATGAAAACTATGCAGACGCCG TGAAGGGC	GATGGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
			SEQ ID NO: 2694	SEQ ID NO: 2851	SEQ ID NO: 3008
		AA	NFGMH	VIWYDGSNENYADAVKG	DGTIFGVVLGDY
			SEQ ID NO: 1124	SEQ ID NO: 1281	SEQ ID NO: 1438
rs359785	4BI.015	NA	AACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACGCCG TGAAGGGC	GATAGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
			SEQ ID NO: 2695	SEQ ID NO: 2852	SEQ ID NO: 3009
		AA	NFGMH	VIWYDASNENYADAVKG	DRTIFGVVLGDY
			SEQ ID NO: 1125	SEQ ID NO: 1282	SEQ ID NO: 1439
rs360982	4BI.016	NA	AACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACGCCG TGAAGGGC	GATGGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
			SEQ ID NO: 2696	SEQ ID NO: 2853	SEQ ID NO: 3010
		AA	NFGMH	VIWYDASNENYADAVKG	DGTIFGVVLGDY
			SEQ ID NO: 1126	SEQ ID NO: 1283	SEQ ID NO: 1440

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

iPS:361009	18F2.006	NA	AACTTTGGCATGCAC	SEQ ID NO: 2702
		AA	NFGMH	SEQ ID NO: 1132
iPS:361013	18F2.007	NA	AACTTTGGCATGCAC	SEQ ID NO: 2703
		AA	NFGMH	SEQ ID NO: 1133
iPS:361017	18F2.008	NA	AACTTTGGCATGCAC	SEQ ID NO: 2704
		AA	NFGMH	SEQ ID NO: 1134
iPS:361021	18F2.009	NA	AACTTTGGCATGCAC	SEQ ID NO: 2705
		AA	NFGMH	SEQ ID NO: 1135
iPS:361028	18F2.010	NA	AACTTTGGCATGCAC	SEQ ID NO: 2706
		AA	NFGMH	SEQ ID NO: 1136

iPS:361009	18F2.006	NA	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACGCCG TGAAGGGC	SEQ ID NO: 2859
		AA	VIWYDASNENYADAVKG	SEQ ID NO: 1289
iPS:361013	18F2.007	NA	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACGCCG TGAAGGGC	SEQ ID NO: 2860
		AA	VIWYDASNENYADAVKG	SEQ ID NO: 1290
iPS:361017	18F2.008	NA	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACGCCG TGAAGGGC	SEQ ID NO: 2861
		AA	VIWYDASNENYADAVKG	SEQ ID NO: 1291
iPS:361021	18F2.009	NA	GTTATATGGTATGATGGAAGTA ATGAAAACTATGCAGACGCCG TGAAGGGC	SEQ ID NO: 2862
		AA	VIWYDGSNENYADAVKG	SEQ ID NO: 1292
iPS:361028	18F2.010	NA	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACTCCGT GAAGGGC	SEQ ID NO: 2863
		AA	VIWYDASNENYADSVKG	SEQ ID NO: 1293

iPS:361009	18F2.006	NA	GATGGGACGATCTTTGGAGTGG TCTTGGGGGACTAC	SEQ ID NO: 3016
		AA	DGTIFGVVLGDY	SEQ ID NO: 1446
iPS:361013	18F2.007	NA	GATGGGACGATCTTTGGAGTGG TCTTGGGGGACTAC	SEQ ID NO: 3017
		AA	DGTIFGVVLGDY	SEQ ID NO: 1447
iPS:361017	18F2.008	NA	GATGGGACGATCTTTGGAGTGG TCTTGGGGGACTAC	SEQ ID NO: 3018
		AA	DGTIFGVVLGDY	SEQ ID NO: 1448
iPS:361021	18F2.009	NA	GATGGGACGATCTTTGGAGTGG TCTTGGGGGACTAC	SEQ ID NO: 3019
		AA	DGTIFGVVLGDY	SEQ ID NO: 1449
iPS:361028	18F2.010	NA	GATGGGACGATCTTTGGAGTGG TCTTGGGGGACTAC	SEQ ID NO: 3020
		AA	DGTIFGVVLGDY	SEQ ID NO: 1450

iPS:360535	18F2.011	NA	AACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACGCCG TGAAGGGC	GATAGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
			SEQ ID NO: 2707	SEQ ID NO: 2864	SEQ ID NO: 3021
		AA	NFGMH	VIWYDASNENYADAVKG	DRTIFGVVLGDY
			SEQ ID NO: 1137	SEQ ID NO: 1294	SEQ ID NO: 1451
iPS:361035	18F2.012	NA	AACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACGCCG TGAAGGGC	GATGGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
			SEQ ID NO: 2708	SEQ ID NO: 2865	SEQ ID NO: 3022
		AA	NFGMH	VIWYDASNENYADAVKG	DGTIFGVVLGDY
			SEQ ID NO: 1138	SEQ ID NO: 1295	SEQ ID NO: 1452
iPS:359940	2F11.002	NA	AGCTATGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGGC	GATAGGACGATTTTTGGAGTGG TTCTTGACTAC
			SEQ ID NO: 2709	SEQ ID NO: 2866	SEQ ID NO: 3023
		AA	SYGMH	VIWYDASNKYYADAVKG	DRTIFGVVLDY
			SEQ ID NO: 1139	SEQ ID NO: 1296	SEQ ID NO: 1453
iPS:361039	2F11.003	NA	AGCTATGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGGC	GATAGGACGATTTTTGGAGTGG TTCTTGACTAC
			SEQ ID NO: 2710	SEQ ID NO: 2867	SEQ ID NO: 3024
		AA	SYGMH	VIWYDASNKYYADAVKG	DRTIFGVVLDY
			SEQ ID NO: 1140	SEQ ID NO: 1297	SEQ ID NO: 1454
iPS:361043	2F11.004	NA	AGCTATGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGGC	GATAGGACGATTTTTGGAGTGG TTCTTGACTAC
			SEQ ID NO: 2711	SEQ ID NO: 2868	SEQ ID NO: 3025
		AA	SYGMH	VIWYDASNKYYADAVKG	DRTIFGVVLDY
			SEQ ID NO: 1141	SEQ ID NO: 1298	SEQ ID NO: 1455

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

iPS:359956	2F11.010	NA	AGCTATGGCATGCAC	SEQ ID NO: 2717
				SEQ ID NO: 2874
		AA	SYGMH	VIWYDGSNKYYADAVKG
				SEQ ID NO: 1147
				SEQ ID NO: 1304
iPS:359865	6H1.002	NA	TACTTTGGCATGCAC	GTTATATGGTATGATGGAAGTA ATAAATACTATGCAGACGCCGT GAAGGGC
				SEQ ID NO: 2718
				SEQ ID NO: 2875
		AA	YFGMH	VIWYDASNKYYADAVKG
				SEQ ID NO: 1148
				SEQ ID NO: 1305
iPS:359869	6H1.003	NA	TACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGGC
				SEQ ID NO: 2719
				SEQ ID NO: 2876
		AA	YFGMH	VIWYDASNKYYADAVKG
				SEQ ID NO: 1149
				SEQ ID NO: 1306
iPS:359873	6H1.004	NA	TACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGGC
				SEQ ID NO: 2720
				SEQ ID NO: 2877
		AA	YFGMH	VIWYDASNKYYADAVKG
				SEQ ID NO: 1150
				SEQ ID NO: 1307
iPS:359877	6H1.005	NA	TACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGGC
				SEQ ID NO: 2721
				SEQ ID NO: 2878
		AA	YFGMH	VIWYDASNKYYADAVKG
				SEQ ID NO: 1151
				SEQ ID NO: 1308

iPS:359956	2F11.010	NA	GATAGGACGATTTTTGGAGTGG TTCTTGACTAC	SEQ ID NO: 3031
		AA	DRTIFGVVLDY	SEQ ID NO: 1461
iPS:359865	6H1.002	NA	GATGGGACGATTTTTGGAGTGC TCTTGGGGGACTAC	SEQ ID NO: 3032
		AA	DGTIFGVLLGDY	SEQ ID NO: 1462
iPS:359869	6H1.003	NA	GATAGGACGATTTTTGGAGTGC TCTTGGGGGACTAC	SEQ ID NO: 3033
		AA	DRTIFGVLLGDY	SEQ ID NO: 1463
iPS:359873	6H1.004	NA	GATGGGACGATTTTTGGAGTGC TCTTGGGGGACTAC	SEQ ID NO: 3034
		AA	DGTIFGVLLGDY	SEQ ID NO: 1464
iPS:359877	6H1.005	NA	GATAGGACGATTTTTGGAGTGC TCTTGGGGGACTAC	SEQ ID NO: 3035
		AA	DRTIFGVLLGDY	SEQ ID NO: 1465

!PS:3610867	6H1.006	NA	TACTTTGGCATGCAC	GTTATATGGTATGATGGAAGTA ATAAATACTATGCAGACTCCGT GAAGGGC	GATGGGACGATTTTTGGAGTGC TCTTGGGGGACTAC
			SEQ ID NO: 2722	SEQ ID NO: 2879	SEQ ID NO: 3036
		AA	YFGMH	VIWYDGSNKYYADSVKG	DGTIFGVLLGDY
			SEQ ID NO: 1152	SEQ ID NO: 1309	SEQ ID NO: 1466
!PS:3610871	6H1.007	NA	TACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACTCCGT GAAGGGC	GATGGGACGATTTTTGGAGTGC TCTTGGGGGACTAC
			SEQ ID NO: 2723	SEQ ID NO: 2880	SEQ ID NO: 3037
		AA	YFGMH	VIWYDASNKYYADSVKG	DGTIFGVLLGDY
			SEQ ID NO: 1153	SEQ ID NO: 1310	SEQ ID NO: 1467
!PS:3610875	6H1.008	NA	TACTTTGGCATGCAC	GTTATATGGTATGATGGAAGTA ATAAATACTATGCAGACCGCCGT GAAGGGC	GATGGGACGATTTTTGGAGTGC TCTTGGGGGACTAC
			SEQ ID NO: 2724	SEQ ID NO: 2881	SEQ ID NO: 3038
		AA	YFGMH	VIWYDGSNKYYADAVKG	DGTIFGVLLGDY
			SEQ ID NO: 1154	SEQ ID NO: 1311	SEQ ID NO: 1468
!PS:3610879	6AS.004.001	NA	AGCTATGGCATGCAC	GCTATATGGTATGATGCAAATA ATAAATACTATGCAGACGCCGT GAAGGGC	GATCGGACGATTTTTGGAGTGG TCCTTGAGTAC
			SEQ ID NO: 2725	SEQ ID NO: 2882	SEQ ID NO: 3039
		AA	SYGMH	AIWYDANNKYYADAVKG	DRTIFGVVLEY
			SEQ ID NO: 1155	SEQ ID NO: 1312	SEQ ID NO: 1469
!PS:3610885	6AS.004.002	NA	AGCTATGGCATGCAC	GCTATATGGTATGATGCAAATA ATAAATACTATGCAGACGCCGT GAAGGGC	GATCGGACGATTTTTGGAGTGG TCCTTGAGTAC
			SEQ ID NO: 2726	SEQ ID NO: 2883	SEQ ID NO: 3040
		AA	SYGMH	AIWYDANNKYYADAVKG	DRTIFGVVLEY
			SEQ ID NO: 1156	SEQ ID NO: 1313	SEQ ID NO: 1470

iPS:361091	6A5.004.003	NA	AGCTATGGCATGCAC	GCTATATGGTATGATGCAAATA ATAAATACTATGCAGACGCCGT GAAGGGC
			SEQ ID NO: 2727	SEQ ID NO: 2884
		AA	SYGMH	AIWYDANNKYYADAVKG
			SEQ ID NO: 1157	SEQ ID NO: 1314
iPS:361095	6A5.004.004	NA	AGCTATGGCATGCAC	GCTATATGGTATGATGCAAATA ATAAATACTATGCAGACGCCGT GAAGGGC
			SEQ ID NO: 2728	SEQ ID NO: 2885
		AA	SYGMH	AIWYDANNKYYADAVKG
			SEQ ID NO: 1158	SEQ ID NO: 1315
iPS:361101	6A5.004.005	NA	AGCTATGGCATGCAC	GCTATATGGTATGATGCAAATA ATAAATACTATGCAGACGCCGT GAAGGGC
			SEQ ID NO: 2729	SEQ ID NO: 2886
		AA	SYGMH	AIWYDANNKYYADAVKG
			SEQ ID NO: 1159	SEQ ID NO: 1316
iPS:361105	6A5.004.006	NA	AGCTATGGCATGCAC	GCTATATGGTATGATGCAAATA ATAAATACTATGCAGACGCCGT GAAGGGC
			SEQ ID NO: 2730	SEQ ID NO: 2887
		AA	SYGMH	AIWYDANNKYYADAVKG
			SEQ ID NO: 1160	SEQ ID NO: 1317
iPS:361109	6A5.004.007	NA	AGCTATGGCATGCAC	GCTATATGGTATGATGCAAATA ATAAATACTATGCAGACGCCGT GAAGGGC
			SEQ ID NO: 2731	SEQ ID NO: 2888
		AA	SYGMH	AIWYDANNKYYADAVKG
			SEQ ID NO: 1161	SEQ ID NO: 1318

GATCGGACGATTTTTGGAGTGG TCCTTGAGTAC
SEQ ID NO: 3041
DRTIFGVVLEY
SEQ ID NO: 1471
GATCGGACGATTTTTGGAGTGG TCCTTGAGTAC
SEQ ID NO: 3042
DRTIFGVVLEY
SEQ ID NO: 1472
GATCGGACGATTTTTGGAGTGG TCCTTGAGTAC
SEQ ID NO: 3043
DRTIFGVVLEY
SEQ ID NO: 1473
GATCGGACGATTTTTGGAGTGG TCCTTGAGTAC
SEQ ID NO: 3044
DRTIFGVVLEY
SEQ ID NO: 1474
GATCGGACGATTTTTGGAGTGG TCCTTGAGTAC
SEQ ID NO: 3045
DRTIFGVVLEY
SEQ ID NO: 1475

iPS:361113	6A5.004.008	NA	AGCTATGGCATGCAC	GCTATATGGTATGATGGAAATA ATAAATACTATGCAGACGCCGT GAAGGGC
			SEQ ID NO: 2732	SEQ ID NO: 2889
		AA	SYGMH	AIWYDGNNKYYADAVKG
			SEQ ID NO: 1162	SEQ ID NO: 1319
iPS:361120	6A5.004.009	NA	AGCTATGGCATGCAC	GCTATATGGTATGATGCAAATA ATAAATACTATGCAGACTCCGT GAAGGGC
			SEQ ID NO: 2733	SEQ ID NO: 2890
		AA	SYGMH	AIWYDANNKYYADSVKG
			SEQ ID NO: 1163	SEQ ID NO: 1320
iPS:359896	6A5.004.010	NA	AGCTATGGCATGCAC	GCTATATGGTATGATGCAAATA ATAAATACTATGCAGACGCCGT GAAGGGC
			SEQ ID NO: 2734	SEQ ID NO: 2891
		AA	SYGMH	AIWYDANNKYYADAVKG
			SEQ ID NO: 1164	SEQ ID NO: 1321
iPS:359890	6A5.004.011	NA	AGCTATGGCATGCAC	GCTATATGGTATGATGCAAATA ATAAATACTATGCAGACGCCGT GAAGGGC
			SEQ ID NO: 2735	SEQ ID NO: 2892
		AA	SYGMH	AIWYDANNKYYADAVKG
			SEQ ID NO: 1165	SEQ ID NO: 1322
iPS:359567	2A11.002	NA	AGCTATGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGAAGACGCCGT GAAGGGC
			SEQ ID NO: 2736	SEQ ID NO: 2893
		AA	SYGMH	VIWYDASNKYYEDAVKG
			SEQ ID NO: 1166	SEQ ID NO: 1323

GATCGGACGATTTTTGGAGTGG TCCTTGAGTAC	
SEQ ID NO: 3046	
DRTIFGVVLEY	
SEQ ID NO: 1476	
GATCGGACGATTTTTGGAGTGG TCCTTGAGTAC	
SEQ ID NO: 3047	
DRTIFGVVLEY	
SEQ ID NO: 1477	
GATCGGACGATTTTTGGAGTGG TCCTTGAGTAC	
SEQ ID NO: 3048	
DRTIFGVVLEY	
SEQ ID NO: 1478	
GATCGGACGATTTTTGGAGTGG TCCTTGAGTAC	
SEQ ID NO: 3049	
DRTIFGVVLEY	
SEQ ID NO: 1479	
GGGATTACGATTTTTGGTCATG GGTTTGAATAT	
SEQ ID NO: 3050	
GITIFGHGFEY	
SEQ ID NO: 1480	

rs:335965	2A11.003	NA	AGCTATGGCATGCAC	GTTATATGGTATGATGGAAGTA ATAAATACTATGAAGACTCCGT GAAGGGC
			SEQ ID NO: 2737	SEQ ID NO: 2894
		AA	SYGMH	VIWYDGSNKYYEDSVKG
			SEQ ID NO: 1167	SEQ ID NO: 1324
rs:361158	2A11.004	NA	AGCTATGGCATGCAC	GTTATATGGTATGATGGAAGTA ATAAATACTATGAAGACGCCGT GAAGGGC
			SEQ ID NO: 2738	SEQ ID NO: 2895
		AA	SYGMH	VIWYDGSNKYYEDAVKG
			SEQ ID NO: 1168	SEQ ID NO: 1325
rs:361165	2A11.005	NA	AGCTATGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGAAGACTCCGT GAAGGGC
			SEQ ID NO: 2739	SEQ ID NO: 2896
		AA	SYGMH	VIWYDASNKYYEDSVKG
			SEQ ID NO: 1169	SEQ ID NO: 1326
rs:361172	2G10_LC1.003	NA	AACTATGGCATGCAC	GCTATATGGTTTGATGCAAGTG ATAAATACTATGCAGACGCCGT GAAGGGC
			SEQ ID NO: 2740	SEQ ID NO: 2897
		AA	NYGMH	AIWFDASDKYYADAVKG
			SEQ ID NO: 1170	SEQ ID NO: 1327
rs:361178	2G10_LC1.004	NA	AACTATGGCATGCAC	GCTATATGGTTTGATGCAAGTG ATAAATACTATGCAGACTCCGT GAAGGGC
			SEQ ID NO: 2741	SEQ ID NO: 2898
		AA	NYGMH	AIWFDASDKYYADSVKG
			SEQ ID NO: 1171	SEQ ID NO: 1328

rs:335965	2A11.003	NA	GGGATTACGATTTTTGGTCATG GGTTTGAATAT	
			SEQ ID NO: 3051	
		AA	GITIFGHGFEY	
			SEQ ID NO: 1481	
rs:361158	2A11.004	NA	GGGATTACGATTTTTGGTCATG GGTTTGAATAT	
			SEQ ID NO: 3052	
		AA	GITIFGHGFEY	
			SEQ ID NO: 1482	
rs:361165	2A11.005	NA	GGGATTACGATTTTTGGTCATG GGTTTGAATAT	
			SEQ ID NO: 3053	
		AA	GITIFGHGFEY	
			SEQ ID NO: 1483	
rs:361172	2G10_LC1.003	NA	GATCAGGCGATTTTTGGAGTGG TCCCCGACTAC	
			SEQ ID NO: 3054	
		AA	DQAIFGVVPDY	
			SEQ ID NO: 1484	
rs:361178	2G10_LC1.004	NA	GATCAGGCGATTTTTGGAGTGG TCCCCGACTAC	
			SEQ ID NO: 3055	
		AA	DQAIFGVVPDY	
			SEQ ID NO: 1485	

rs:3611185	2G10_LC1.005	NA	AACTATGGCATGCAC	GCTATATGGTTTGATGGAAGTG ATAAATACTATGCAGACGCCGT GAAGGGC	GATCAGGCGATTTTTGGAGTGG TCCCCGACTAC
			SEQ ID NO: 2742	SEQ ID NO: 2899	SEQ ID NO: 3056
		AA	NYGMH	AIWFDGSDKYYADAVKG	DQAIFGVVPDY
			SEQ ID NO: 1172	SEQ ID NO: 1329	SEQ ID NO: 1486
rs:3611192	2G10_LC1.006	NA	AACTATGGCATGCAC	GCTATATGGTTTGATGCAAGTG ATAAATACTATGCAGACGCCGT GAAGGGC	GATCAGGCGATTTTTGGAGTGG TCCCCGACTAC
			SEQ ID NO: 2743	SEQ ID NO: 2900	SEQ ID NO: 3057
		AA	NYGMH	AIWFDASDKYYADAVKG	DQAIFGVVPDY
			SEQ ID NO: 1173	SEQ ID NO: 1330	SEQ ID NO: 1487
rs:3596091	2G10_LC1.007	NA	AACTATGGCATGCAC	GCTATATGGTTTGATGCAAGTG ATAAATACTATGCAGACGCCGT GAAGGGC	GATCAGGCGATTTTTGGAGTGG TCCCCGACTAC
			SEQ ID NO: 2744	SEQ ID NO: 2901	SEQ ID NO: 3058
		AA	NYGMH	AIWFDASDKYYADAVKG	DQAIFGVVPDY
			SEQ ID NO: 1174	SEQ ID NO: 1331	SEQ ID NO: 1488
rs:3596015	2G10_LC1.008	NA	AACTATGGCATGCAC	GCTATATGGTTTGATGCAAGTG ATAAATACTATGCAGACGCCGT GAAGGGC	GATCAGGCGATTTTTGGAGTGG TCCCCGACTAC
			SEQ ID NO: 2745	SEQ ID NO: 2902	SEQ ID NO: 3059
		AA	NYGMH	AIWFDASDKYYADAVKG	DQAIFGVVPDY
			SEQ ID NO: 1175	SEQ ID NO: 1332	SEQ ID NO: 1489
rs:3611196	2G10_LC1.009	NA	AACTATGGCATGCAC	GCTATATGGTTTGATGCAAGTG ATAAATACTATGCAGACGCCGT GAAGGGC	GATCAGGCGATTTTTGGAGTGG TCCCCGACTAC
			SEQ ID NO: 2746	SEQ ID NO: 2903	SEQ ID NO: 3060
		AA	NYGMH	AIWFDASDKYYADAVKG	DQAIFGVVPDY
			SEQ ID NO: 1176	SEQ ID NO: 1333	SEQ ID NO: 1490

iPS:361202	2G10_LC1.010	NA	AACTATGGCATGCAC	GCTATATGGTTTGATGCAAGTG ATAAATACTATGCAGACGCCGT GAAGGGC	GATCAGGCGATTTTTGGAGTGG TCCCCGACTAC
			SEQ ID NO: 2747	SEQ ID NO: 2904	SEQ ID NO: 3061
		AA	NYGMH	AIWFDASDKYYADAVKG	DQAIFGVVPDY
			SEQ ID NO: 1177	SEQ ID NO: 1334	SEQ ID NO: 1491
iPS:359644	18E3.002	NA	AGTGGTGGTTACTACTGGAGC	TACATCTATTACAGTGGGAGCA CCTACTACAACCCGTCCCTCAA GAGT	GATCGTATTACGATTTTTGGAG TGGTTATGGGGGGCGGTATGG ACGTC
			SEQ ID NO: 2748	SEQ ID NO: 2905	SEQ ID NO: 3062
		AA	SGGYYWS	YIYYSGSTYYNPSLKS	DRITIFGVVMGGGMDV
			SEQ ID NO: 1178	SEQ ID NO: 1335	SEQ ID NO: 1492
iPS:361206	18E3.003	NA	AGTGGTGGTTACTACTGGAGC	TACATCTATTACAGTGGGAGCA CCTACTACAACCCGTCCCTCAA GAGT	GATCGTATTACGATTTTTGGAG TGGTTATGGGGGGCGGTATGG ACGTC
			SEQ ID NO: 2749	SEQ ID NO: 2906	SEQ ID NO: 3063
		AA	SGGYYWS	YIYYSGSTYYNPSLKS	DRITIFGVVMGGGMDV
			SEQ ID NO: 1179	SEQ ID NO: 1336	SEQ ID NO: 1493
iPS:359628	18E3.004	NA	AGTGGTGGTTACTACTGGAGC	TACATCTATTACAGTGGGAGCA CCTACTACAACCCGTCCCTCAA GAGT	GATCGTATTACGATTTTTGGAG TGGTTATGGGGGGCGGTATGG ACGTC
			SEQ ID NO: 2750	SEQ ID NO: 2907	SEQ ID NO: 3064
		AA	SGGYYWS	YIYYSGSTYYNPSLKS	DRITIFGVVMGGGMDV
			SEQ ID NO: 1180	SEQ ID NO: 1337	SEQ ID NO: 1494
iPS:359637	18E3.005	NA	AGTGGTGGTTACTACTGGAGC	TACATCTATTACAGTGGGAGCA CCTACTACAACCCGTCCCTCAA GAGT	GATCGTATTACGATTTTTGGAG TGGTTATGGGGGGCGGTATGG ACGTC
			SEQ ID NO: 2751	SEQ ID NO: 2908	SEQ ID NO: 3065
		AA	SGGYYWS	YIYYSGSTYYNPSLKS	DRITIFGVVMGGGMDV
			SEQ ID NO: 1181	SEQ ID NO: 1338	SEQ ID NO: 1495

rs361210		AGTGGTGGTTACTACTGGAGC	TACATCTATTACAGTGGGAGCA CCTACTACAACCCGTCCCTCAA GAGT	GATCGTATTACGATTTTTGGAG TGGTTATGGGGGGCGGTATGG ACGTC
18E3.006	NA	SEQ ID NO: 2752	SEQ ID NO: 2909	SEQ ID NO: 3066
	AA	SGGYYWS	YIYYSGSTYYNPSLKS	DRITIFGVVMGGGMDV
		SEQ ID NO: 1182	SEQ ID NO: 1339	SEQ ID NO: 1496
rs361214		AGTGGTGGTTACTACTGGAGC	TACATCTATTACAGTGGGAGCA CCTACTACAACCCGTCCCTCAA GAGT	GATCGTATTACGATTTTTGGAG TGGTTATGGGGGGCGGTATGG ACGTC
18E3.007	NA	SEQ ID NO: 2753	SEQ ID NO: 2910	SEQ ID NO: 3067
	AA	SGGYYWS	YIYYSGSTYYNPSLKS	DRITIFGVVMGGGMDV
		SEQ ID NO: 1183	SEQ ID NO: 1340	SEQ ID NO: 1497
rs361218		AGTGGTGGTTACTACTGGAGC	TACATCTATTACAGTGGGAGCA CCTACTACAACCCGTCCCTCAA GAGT	GATCGTATTACGATTTTTGGAG TGGTTATGGGGGGCGGTATGG ACGTC
18E3.008	NA	SEQ ID NO: 2754	SEQ ID NO: 2911	SEQ ID NO: 3068
	AA	SGGYYWS	YIYYSGSTYYNPSLKS	DRITIFGVVMGGGMDV
		SEQ ID NO: 1184	SEQ ID NO: 1341	SEQ ID NO: 1498
rs361222		GGCTACTATATCCAC	TGGATCAACCCTGAAAGTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC	GAGGCCACGATTTTTGGAATGG TTATTGTACCGTTTGACTAC
5C2.006	NA	SEQ ID NO: 2755	SEQ ID NO: 2912	SEQ ID NO: 3069
	AA	GYYIH	WINPESGGTDYSQRFQG	EATIFGMVIVPFDY
		SEQ ID NO: 1185	SEQ ID NO: 1342	SEQ ID NO: 1499
rs361229		GGCTACTATATCCAC	TGGATCAACCCTGAAAGTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC	GAGGCCACGATTTTTGGAATGG TTATTGTACCGTTTGACTAC
5C2.007	NA	SEQ ID NO: 2756	SEQ ID NO: 2913	SEQ ID NO: 3070
	AA	GYYIH	WINPESGGTDYSQRFQG	EATIFGMVIVPFDY
		SEQ ID NO: 1186	SEQ ID NO: 1343	SEQ ID NO: 1500

rs361236	SC2.008	NA	GGCTACTATATCCAC	TGGATCAACCCTGACGCTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC
			SEQ ID NO: 2757	SEQ ID NO: 2914
		AA	GYYIH	WINPDAGGTDYSQRFQG
			SEQ ID NO: 1187	SEQ ID NO: 1344
rs359685	SC2.009	NA	GGCTACTATATCCAC	TGGATCAACCCTGACGCTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC
			SEQ ID NO: 2758	SEQ ID NO: 2915
		AA	GYYIH	WINPDAGGTDYSQRFQG
			SEQ ID NO: 1188	SEQ ID NO: 1345
rs361240	SC2.010	NA	GGCTACTATATCCAC	TGGATCAACCCTGACAGTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC
			SEQ ID NO: 2759	SEQ ID NO: 2916
		AA	GYYIH	WINPDSGGTDYSQRFQG
			SEQ ID NO: 1189	SEQ ID NO: 1346
rs361247	SC2.011	NA	GGCTACTATATCCAC	TGGATCAACCCTGACAGTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC
			SEQ ID NO: 2760	SEQ ID NO: 2917
		AA	GYYIH	WINPDSGGTDYSQRFQG
			SEQ ID NO: 1190	SEQ ID NO: 1347
rs361254	SC2.012	NA	GGCTACTATATCCAC	TGGATCAACCCTGACAGTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC
			SEQ ID NO: 2761	SEQ ID NO: 2918
		AA	GYYIH	WINPDSGGTDYSQRFQG
			SEQ ID NO: 1191	SEQ ID NO: 1348

GAGGCCACCGATTTTTTGGAATGG TTATTGTACCGTTTGACTAC	
SEQ ID NO: 3071	
EATIFGMVIVPFDY	
SEQ ID NO: 1501	
GAGGCCACCGATTTTTTGGAATGG TTATTGTACCGTTTGACTAC	
SEQ ID NO: 3072	
EATIFGMVIVPFDY	
SEQ ID NO: 1502	
GAGGCCACCGATTTTTTGGAATGG TTATTGTACCGTTTGACTAC	
SEQ ID NO: 3073	
EATIFGMVIVPFDY	
SEQ ID NO: 1503	
GAGGCCACCGATTTTTTGGAATGG TTATTGTACCGTTTGACTAC	
SEQ ID NO: 3074	
EATIFGMVIVPFDY	
SEQ ID NO: 1504	
GAGGCCACCGATTTTTTGGAATGG TTATTGTACCGTTTGACTAC	
SEQ ID NO: 3075	
EATIFGMVIVPFDY	
SEQ ID NO: 1505	

rs361261	5C2.013	NA	GGCTACTATATCCAC	TGGATCAACCCTGACGCTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC	GAGGCCACGATTTTTGGAATGG TTATTGTACCGTTTGACTAC
			SEQ ID NO: 2762	SEQ ID NO: 2919	SEQ ID NO: 3076
		AA	GYYIH	WINPDAGGTDYSQRFQG	EATIFGMVIVPFDY
			SEQ ID NO: 1192	SEQ ID NO: 1349	SEQ ID NO: 1506
rs361268	5C2.014	NA	GGCTACTATATCCAC	TGGATCAACCCTGACGCTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC	GAGGCCACGATTTTTGGAATGG TTATTGTACCGTTTGACTAC
			SEQ ID NO: 2763	SEQ ID NO: 2920	SEQ ID NO: 3077
		AA	GYYIH	WINPDAGGTDYSQRFQG	EATIFGMVIVPFDY
			SEQ ID NO: 1193	SEQ ID NO: 1350	SEQ ID NO: 1507
rs359669	5C2.015	NA	GGCTACTATATCCAC	TGGATCAACCCTGACGCTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC	GAGGCCACGATTTTTGGAATGG TTATTGTACCGTTTGACTAC
			SEQ ID NO: 2764	SEQ ID NO: 2921	SEQ ID NO: 3078
		AA	GYYIH	WINPDAGGTDYSQRFQG	EATIFGMVIVPFDY
			SEQ ID NO: 1194	SEQ ID NO: 1351	SEQ ID NO: 1508
rs359678	5C2.016	NA	GGCTACTATATCCAC	TGGATCAACCCTGAAAGTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC	GAGGCCACGATTTTTGGAATGG TTATTGTACCGTTTGACTAC
			SEQ ID NO: 2765	SEQ ID NO: 2922	SEQ ID NO: 3079
		AA	GYYIH	WINPESGGTDYSQRFQG	EATIFGMVIVPFDY
			SEQ ID NO: 1195	SEQ ID NO: 1352	SEQ ID NO: 1509
rs361275	11C1.002	NA	GGCTACTATATACAC	TGGATCAGCCCTAACAGTGGTG AAACAAGCTATGCACAGAAGT TTCAGGAC	GAGGCCACGATTTTTGGAATGC TTATTGTACCATTTGACTAC
			SEQ ID NO: 2766	SEQ ID NO: 2923	SEQ ID NO: 3080
		AA	GYYIH	WISPNSGETSYAQKFQD	EATIFGMLIVPFDY
			SEQ ID NO: 1196	SEQ ID NO: 1353	SEQ ID NO: 1510

rs361282	11C1.003	NA	GGCTACTATATACAC	TGGATCAGCCCTAACAGTGGTG ACACAAGCTATGCACAGAAGT TTCAGGAC	GAGGCCACGATTTTTGGAATGC TTATTGTACCATTTGACTAC
			SEQ ID NO: 2767	SEQ ID NO: 2924	SEQ ID NO: 3081
		AA	GYYIH	WISPNSGDTSYAQKFQD	EATIFGMLIVPFDY
			SEQ ID NO: 1197	SEQ ID NO: 1354	SEQ ID NO: 1511
rs361289	11C1.004	NA	GGCTACTATATACAC	TGGATCAGCCCTAACAGTGGTG AAACAAGCTATGCACAGAAGT TTCAGGAC	GAGGCCACGATTTTTGGAATGC TTATTGTACCATTTGACTAC
			SEQ ID NO: 2768	SEQ ID NO: 2925	SEQ ID NO: 3082
		AA	GYYIH	WISPNSGETSYAQKFQD	EATIFGMLIVPFDY
			SEQ ID NO: 1198	SEQ ID NO: 1355	SEQ ID NO: 1512
rs359712	11C1.005	NA	GGCTACTATATACAC	TGGATCAGCCCTAACAGTGGTG AAACAAGCTATGCACAGAAGT TTCAGGAC	GAGGCCACGATTTTTGGAATGC TTATTGTACCATTTGACTAC
			SEQ ID NO: 2769	SEQ ID NO: 2926	SEQ ID NO: 3083
		AA	GYYIH	WISPNSGETSYAQKFQD	EATIFGMLIVPFDY
			SEQ ID NO: 1199	SEQ ID NO: 1356	SEQ ID NO: 1513
rs361293	11C1.006	NA	GGCTACTATATACAC	TGGATCAGCCCTAACAGTGGTG ACACAAGCTATGCACAGAAGT TTCAGGAC	GAGGCCACGATTTTTGGAATGC TTATTGTACCATTTGACTAC
			SEQ ID NO: 2770	SEQ ID NO: 2927	SEQ ID NO: 3084
		AA	GYYIH	WISPNSGDTSYAQKFQD	EATIFGMLIVPFDY
			SEQ ID NO: 1200	SEQ ID NO: 1357	SEQ ID NO: 1514
rs361297	11C1.007	NA	GGCTACTATATACAC	TGGATCAGCCCTAACAGTGGTG AAACAAGCTATGCACAGAAGT TTCAGGAC	GAGGCCACGATTTTTGGAATGC TTATTGTACCATTTGACTAC
			SEQ ID NO: 2771	SEQ ID NO: 2928	SEQ ID NO: 3085
		AA	GYYIH	WISPNSGETSYAQKFQD	EATIFGMLIVPFDY
			SEQ ID NO: 1201	SEQ ID NO: 1358	SEQ ID NO: 1515

iPS:361301	11C1.008	NA	GGCTACTATATACAC	TGGATCAGCCCTAACAGTGGTG ACACAAGCTATGCACAGAAGT TTCAGGAC	GAGGCCACGATTTTTGGAATGC TTATTGTACCATTTGACTAC
			SEQ ID NO: 2772	SEQ ID NO: 2929	SEQ ID NO: 3086
		AA	GYYIH	WISPNSGDTSYAQKFQD	EATIFGMLIVPFDY
			SEQ ID NO: 1202	SEQ ID NO: 1359	SEQ ID NO: 1516
iPS:359703	11C1.009	NA	GGCTACTATATACAC	TGGATCAGCCCTAACAGTGGTG AAACAAGCTATGCACAGAAGT TTCAGGAC	GAGGCCACGATTTTTGGAATGC TTATTGTACCATTTGACTAC
			SEQ ID NO: 2773	SEQ ID NO: 2930	SEQ ID NO: 3087
		AA	GYYIH	WISPNSGETSYAQKFQD	EATIFGMLIVPFDY
			SEQ ID NO: 1203	SEQ ID NO: 1360	SEQ ID NO: 1517
iPS:361305	11C1.010	NA	GGCTACTATATACAC	TGGATCAGCCCTAACAGTGGTG AAACAAGCTATGCACAGAAGT TTCAGGAC	GAGGCCACGATTTTTGGAATGC TTATTGTACCATTTGACTAC
			SEQ ID NO: 2774	SEQ ID NO: 2931	SEQ ID NO: 3088
		AA	GYYIH	WISPNSGETSYAQKFQD	EATIFGMLIVPFDY
			SEQ ID NO: 1204	SEQ ID NO: 1361	SEQ ID NO: 1518
iPS:361312	13H12.002	NA	GGCTACTATATCCAC	TGGATCAACCCTGAAAGTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC	GAGGCCACGATTTTTGGAATGG TTATTGTACCGTTTGACTAC
			SEQ ID NO: 2775	SEQ ID NO: 2932	SEQ ID NO: 3089
		AA	GYYIH	WINPESGGTDYSQRFQG	EATIFGMVIVPFDY
			SEQ ID NO: 1205	SEQ ID NO: 1362	SEQ ID NO: 1519
iPS:359744	13H12.003	NA	GGCTACTATATCCAC	TGGATCAACCCTGAAAGTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC	GAGGCCACGATTTTTGGAATGG TTATTGTACCGTTTGACTAC
			SEQ ID NO: 2776	SEQ ID NO: 2933	SEQ ID NO: 3090
		AA	GYYIH	WINPESGGTDYSQRFQG	EATIFGMVIVPFDY
			SEQ ID NO: 1206	SEQ ID NO: 1363	SEQ ID NO: 1520

rs361337	12H11.003	NA	GGCTACTATATACAC	TGGATAAGCCCTAACCAAGGT GACACAAACTATGCACAGAAG TTTCAGGAC	GAGGCCACCGATTTTTGGAATGC TTATTGTACCATTTGACTAC
			SEQ ID NO: 2781	SEQ ID NO: 2938	SEQ ID NO: 3095
		AA	GYYIH	WISPNQGDTNYAQKFQD	EATIFGMLIVPFDY
			SEQ ID NO: 1211	SEQ ID NO: 1368	SEQ ID NO: 1525
rs361330	12H11.002	NA	GGCTACTATATACAC	TGGATAAGCCCTAACCAAGGT GAAACAAACTATGCACAGAAG TTTCAGGAC	GAGGCCACCGATTTTTGGAATGC TTATTGTACCATTTGACTAC
			SEQ ID NO: 2780	SEQ ID NO: 2937	SEQ ID NO: 3094
		AA	GYYIH	WISPNQGETNYAQKFQD	EATIFGMLIVPFDY
			SEQ ID NO: 1210	SEQ ID NO: 1367	SEQ ID NO: 1524
rs361326	13H12.006	NA	GGCTACTATATCCAC	TGGATCAACCCTGAAAGTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC	GAGGCCACGATTTTTGGAATGG TTATTGTACCGTTTGACTAC
			SEQ ID NO: 2779	SEQ ID NO: 2936	SEQ ID NO: 3093
		AA	GYYIH	WINPESGGTDYSQRFQG	EATIFGMVIVPFDY
			SEQ ID NO: 1209	SEQ ID NO: 1366	SEQ ID NO: 1523
rs359737	13H12.005	NA	GGCTACTATATCCAC	TGGATCAACCCTGAAAGTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC	GAGGCCACGATTTTTGGAATGG TTATTGTACCGTTTGACTAC
			SEQ ID NO: 2778	SEQ ID NO: 2935	SEQ ID NO: 3092
		AA	GYYIH	WINPESGGTDYSQRFQG	EATIFGMVIVPFDY
			SEQ ID NO: 1208	SEQ ID NO: 1365	SEQ ID NO: 1522
rs361319	13H12.004	NA	GGCTACTATATCCAC	TGGATCAACCCTGACAGTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC	GAGGCCACCGATTTTTGGAATGG TTATTGTACCGTTTGACTAC
			SEQ ID NO: 2777	SEQ ID NO: 2934	SEQ ID NO: 3091
		AA	GYYIH	WINPDSGGTDYSQRFQG	EATIFGMVIVPFDY
			SEQ ID NO: 1207	SEQ ID NO: 1364	SEQ ID NO: 1521

iPS:361344	12H11.004	NA	GGCTACTATATACAC	TGGATAAGCCCTAACCAAGGT GAAACAAACTATGCACAGAAG TTTCAGGAC	GAGGCCACCGATTTTTTGGAATGC TTATTGTACCATTTGACTAC
			SEQ ID NO: 2782	SEQ ID NO: 2939	SEQ ID NO: 3096
		AA	GYYIH	WISPNQGETNYAQKFQD	EATIFGMLIVPFDY
			SEQ ID NO: 1212	SEQ ID NO: 1369	SEQ ID NO: 1526
iPS:361351	12H11.005	NA	GGCTACTATATACAC	TGGATAAGCCCTAACAATGGTG AAACAAACTATGCACACAGAAGT TTCAGGAC	GAGGCCACCGATTTTTTGGAATGC TTATTGTACCATTTGACTAC
			SEQ ID NO: 2783	SEQ ID NO: 2940	SEQ ID NO: 3097
		AA	GYYIH	WISPNNGETNYAQKFQD	EATIFGMLIVPFDY
			SEQ ID NO: 1213	SEQ ID NO: 1370	SEQ ID NO: 1527
iPS:361358	12H11.006	NA	GGCTACTATATACAC	TGGATAAGCCCTAACAATGGTG ACACAAACTATGCACACAGAAGT TTCAGGAC	GAGGCCACCGATTTTTTGGAATGC TTATTGTACCATTTGACTAC
			SEQ ID NO: 2784	SEQ ID NO: 2941	SEQ ID NO: 3098
		AA	GYYIH	WISPNNGDTNYAQKFQD	EATIFGMLIVPFDY
			SEQ ID NO: 1214	SEQ ID NO: 1371	SEQ ID NO: 1528
iPS:361365	12H11.007	NA	GGCTACTATATACAC	TGGATAAGCCCTAACCAAGGT GACACAAACTATGCACACAGAAG TTTCAGGAC	GAGGCCACCGATTTTTTGGAATGC TTATTGTACCATTTGACTAC
			SEQ ID NO: 2785	SEQ ID NO: 2942	SEQ ID NO: 3099
		AA	GYYIH	WISPNQGDTNYAQKFQD	EATIFGMLIVPFDY
			SEQ ID NO: 1215	SEQ ID NO: 1372	SEQ ID NO: 1529
iPS:361372	12H11.008	NA	GGCTACTATATACAC	TGGATAAGCCCTAACAATGGTG AAACAAACTATGCACACAGAAGT TTCAGGAC	GAGGCCACCGATTTTTTGGAATGC TTATTGTACCATTTGACTAC
			SEQ ID NO: 2786	SEQ ID NO: 2943	SEQ ID NO: 3100
		AA	GYYIH	WISPNNGETNYAQKFQD	EATIFGMLIVPFDY
			SEQ ID NO: 1216	SEQ ID NO: 1373	SEQ ID NO: 1530

rs361379	12H11.009	NA	GGCTACTATATACAC	SEQ ID NO: 2787
				TGGATAAGCCCTAACCAAGGT GAAACAAACTATGCACAGAAG TTTCAGGAC
				SEQ ID NO: 2944
		AA	GYYIH	WISPNQGETNYAQKFQD
				SEQ ID NO: 1374
				GAGGCCACGATTTTTGGAATGC TTATTGTACCATTTGACTAC
				SEQ ID NO: 3101
				EATIFGMLIVPFDY
				SEQ ID NO: 1531
rs361383	12H11.010	NA	GGCTACTATATACAC	SEQ ID NO: 2788
				TGGATAAGCCCTAACAATGGTG ACACAAACTATGCACAGAAGT TTCAGGAC
				SEQ ID NO: 2945
		AA	GYYIH	WISPNNGDTNYAQKFQD
				SEQ ID NO: 1375
				GAGGCCACGATTTTTGGAATGC TTATTGTACCATTTGACTAC
				SEQ ID NO: 3102
				EATIFGMLIVPFDY
				SEQ ID NO: 1532
rs361387	12H11.011	NA	GGCTACTATATACAC	SEQ ID NO: 2789
				TGGATAAGCCCTAACCAAGGT GACACAAACTATGCACAGAAG TTTCAGGAC
				SEQ ID NO: 2946
		AA	GYYIH	WISPNQGDTNYAQKFQD
				SEQ ID NO: 1376
				GAGGCCACGATTTTTGGAATGC TTATTGTACCATTTGACTAC
				SEQ ID NO: 3103
				EATIFGMLIVPFDY
				SEQ ID NO: 1533
rs361391	12H11.012	NA	GGCTACTATATACAC	SEQ ID NO: 2790
				TGGATAAGCCCTAACAATGGTG AAACAAACTATGCACAGAAGT TTCAGGAC
				SEQ ID NO: 2947
		AA	GYYIH	WISPNNGETNYAQKFQD
				SEQ ID NO: 1377
				GAGGCCACGATTTTTGGAATGC TTATTGTACCATTTGACTAC
				SEQ ID NO: 3104
				EATIFGMLIVPFDY
				SEQ ID NO: 1534
rs361395	12H11.013	NA	GGCTACTATATACAC	SEQ ID NO: 2791
				TGGATAAGCCCTAACCAAGGT GAAACAAACTATGCACAGAAG TTTCAGGAC
				SEQ ID NO: 2948
		AA	GYYIH	WISPNQGETNYAQKFQD
				SEQ ID NO: 1378
				GAGGCCACGATTTTTGGAATGC TTATTGTACCATTTGACTAC
				SEQ ID NO: 3105
				EATIFGMLIVPFDY
				SEQ ID NO: 1535

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

rs:36143054	2C2.005.009	NA	GGCTACTATATGCAT	TGGATCAACCCTAACAGTGGTG GCACAAACTATGCACAGAAGT TTCAGGGC	GGGGGGGATTACGTTTGGGGG ACTTATCGGCCTCACTACT ACGGTATGGACGTC
			SEQ ID NO: 2801	SEQ ID NO: 2958	SEQ ID NO: 3115
		AA	GYYMH	WINPNSGGTNYAQKFQG	GGDYVWGTYRPHYYYGMDV
			SEQ ID NO: 1231	SEQ ID NO: 1388	SEQ ID NO: 1545
rs:36144842	2C2.005.007	NA	GGCTACTATATGCAT	TGGATCAACCCTAACAGTGGTG GCACAAACTATGCACAGAAGT TTCAGGGC	GGGGGGGATTACGTTTGGGGG ACTTATCGGCCTCACTACT ACGGTATGGACGTC
			SEQ ID NO: 2799	SEQ ID NO: 2956	SEQ ID NO: 3113
		AA	GYYMH	WINPNSGGTNYAQKFQG	GGDYVWGTYRPHYYYGMDV
			SEQ ID NO: 1229	SEQ ID NO: 1386	SEQ ID NO: 1543
rs:36143654	2C2.005.008	NA	GGCTACTATATGCAT	TGGATCAACCCTAACAGTGGTG GCACAAACTATGCACAGAAGT TTCAGGGC	GGGGGGGATTACGTTTGGGGG ACTTATCGGCCTCACTACT ACGGTATGGACGTC
			SEQ ID NO: 2800	SEQ ID NO: 2957	SEQ ID NO: 3114
		AA	GYYMH	WINPNSGGTNYAQKFQG	GGDYVWGTYRPHYYYGMDV
			SEQ ID NO: 1230	SEQ ID NO: 1387	SEQ ID NO: 1544
rs:36143436	2C2.005.006	NA	GGCTACTATATGCAT	TGGATCAACCCTAACAGTGGTG GCACAAACTATGCACAGAAGT TTCAGGGC	GGGGGGGATTACGTTTGGGGG ACTTATCGGCCTCACTACT ACGGTATGGACGTC
			SEQ ID NO: 2798	SEQ ID NO: 2955	SEQ ID NO: 3112
		AA	GYYMH	WINPNSGGTNYAQKFQG	GGDYVWGTYRPHYYYGMDV
			SEQ ID NO: 1228	SEQ ID NO: 1385	SEQ ID NO: 1542
rs:36143054	2C2.005.005	NA	GGCTACTATATGCAT	TGGATCAACCCTAACAGTGGTG GCACAAACTATGCACAGAAGT TTCAGGGC	GGGGGGGATTACGTTTGGGGG ACTTATCGGCCTCACTACT ACGGTATGGACGTC
			SEQ ID NO: 2797	SEQ ID NO: 2954	SEQ ID NO: 3111
		AA	GYYMH	WINPNSGGTNYAQKFQG	GGDYVWGTYRPHYYYGMDV
			SEQ ID NO: 1227	SEQ ID NO: 1384	SEQ ID NO: 1541

iPS:361460	2C2.005.010	NA	GGCTACTATATGCAT	TGGATCAACCCTAACAGTGGTG GCACAAACTATGCACACAGAAGT TTCAGGGC	GGGGGGGATTACGTTTGGGGG ACTTATCGGCCTCACTACTACT ACGGTATGGACGTC
			SEQ ID NO: 2802	SEQ ID NO: 2959	SEQ ID NO: 3116
		AA	GYYMH	WINPNSGGTNYAQKFQG	GGDYVWGTYRPHYYYGMDV
			SEQ ID NO: 1232	SEQ ID NO: 1389	SEQ ID NO: 1546
iPS:361466	2C2.005.011	NA	GGCTACTATATGCAT	TGGATCAACCCTAACAGTGGTG GCACAAACTATGCACACAGAAGT TTCAGGGC	GGGGGGGATTACGTTTGGGGG ACTTATCGGCCTCACTACTACT ACGGTATGGACGTC
			SEQ ID NO: 2803	SEQ ID NO: 2960	SEQ ID NO: 3117
		AA	GYYMH	WINPNSGGTNYAQKFQG	GGDYVWGTYRPHYYYGMDV
			SEQ ID NO: 1233	SEQ ID NO: 1390	SEQ ID NO: 1547
iPS:361472	2C2.005.012	NA	GGCTACTATATGCAT	TGGATCAACCCTAACAGTGGTG GCACAAACTATGCACACAGAAGT TTCAGGGC	GGGGGGGATTACGTTTGGGGG ACTTATCGGCCTCACTACTACT ACGGTATGGACGTC
			SEQ ID NO: 2804	SEQ ID NO: 2961	SEQ ID NO: 3118
		AA	GYYMH	WINPNSGGTNYAQKFQG	GGDYVWGTYRPHYYYGMDV
			SEQ ID NO: 1234	SEQ ID NO: 1391	SEQ ID NO: 1548
iPS:361478	2C2.005.013	NA	GGCTACTATATGCAT	TGGATCAACCCTAACAGTGGTG GCACAAACTATGCACACAGAAGT TTCAGGGC	GGGGGGGATTACGTTTTTCGGGA CTTATCGGCCTCACTACTACTA CGGTATGGACGTC
			SEQ ID NO: 2805	SEQ ID NO: 2962	SEQ ID NO: 3119
		AA	GYYMH	WINPNSGGTNYAQKFQG	GGDYVFGTYRPHYYYGMDV
			SEQ ID NO: 1235	SEQ ID NO: 1392	SEQ ID NO: 1549
iPS:361485	2C2.005.014	NA	GGCTACTATATGCAT	TGGATCAACCCTAACAGTGGTG GCACAAACTATGCACACAGAAGT TTCAGGGC	GGGGGGGATTACGTTTTTCGGGA CTTATCGGCCTCACTACTACTA CGGTATGGACGTC
			SEQ ID NO: 2806	SEQ ID NO: 2963	SEQ ID NO: 3120
		AA	GYYMH	WINPNSGGTNYAQKFQG	GGDYVFGTYRPHYYYGMDV
			SEQ ID NO: 1236	SEQ ID NO: 1393	SEQ ID NO: 1550

iPS:361845	18F2.013	NA	AACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACGCCG TGAAGGGC
			SEQ ID NO: 2807	SEQ ID NO: 2964
		AA	NFGMH	VIWYDASNENYADAVKG
			SEQ ID NO: 1237	SEQ ID NO: 1394
iPS:361851	6H1.009	NA	TACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGGC
			SEQ ID NO: 2808	SEQ ID NO: 2965
		AA	YFGMH	VIWYDASNKYYADAVKG
			SEQ ID NO: 1238	SEQ ID NO: 1395
iPS:361855	2C2.005.015	NA	GGCTACTATATGCAT	TGGATCAACCCTAACAGTGGTG GCACAAACTATGCACAGAAGT TTCAGGGC
			SEQ ID NO: 2809	SEQ ID NO: 2966
		AA	GYYMH	WINPNSGGTNYAQKFQG
			SEQ ID NO: 1239	SEQ ID NO: 1396
iPS:336067	5G12.006	NA	AGCTATGGCATACAC	GTTATATGGTATGATGGAAGTA ATAAGTTCCATGCAGACTCCGT GAAGGGC
			SEQ ID NO: 2810	SEQ ID NO: 2967
		AA	SYGIH	VIWYDGSNKFHADSVKG
			SEQ ID NO: 1240	SEQ ID NO: 1397
iPS:336169	17B11.002	NA	AGTTATGATATCAAC	TGGATGAACCCTAACAGTGGTA ACACAGGCTATGCACAGAAGT TCCAGGGC
			SEQ ID NO: 2811	SEQ ID NO: 2968
		AA	SYDIN	WMNPNSGNTGYAQKFQG
			SEQ ID NO: 1241	SEQ ID NO: 1398

GATAGGACGATCTTTGGAGTGG TCTTGGGGGACTAC			
SEQ ID NO: 3121			
DRTIFGVVLGDY			
SEQ ID NO: 1551			
GATAGGACGATTTTTGGAGTGC TCTTGGGGGACTAC			
SEQ ID NO: 3122			
DRTIFGVLLGDY			
SEQ ID NO: 1552			
GGGGGGGATTACGTTTGGGGG ACTTATCGGCCTCACTACTACT ACGGTATGGACGTC			
SEQ ID NO: 3123			
GGDYVWGTYRPHYYYGMDV			
SEQ ID NO: 1553			
GGAAAAGTGGCTGGTATGCCT GAAGCTTTTGAAATC			
SEQ ID NO: 3124			
GKVAGMPEAFEI			
SEQ ID NO: 1554			
GGGGGTGATTACGTTTGGGGG AGTTATCGTCCCTACTACTACT ACTACGGTATGGACGTC			
SEQ ID NO: 3125			
GGDYVWGSYRPYYYYGMDV			
SEQ ID NO: 1555			

rs361127	5G12.006.001	NA	AGCTATGGCATACAC	GTTATATGGTATGATGCAAGTA ATAAGTTCCATGCAGACGCCGT GAAGGGC	GGAAAAGTGGCTGGTATGCCT GAAGCTTTTGAAATC
			SEQ ID NO: 2812	SEQ ID NO: 2969	SEQ ID NO: 3126
		AA	SYGIH	VIWYDASNKFHADAVKG	GKVAGMPEAFEI
			SEQ ID NO: 1242	SEQ ID NO: 1399	SEQ ID NO: 1556
rs361136	5G12.006.002	NA	AGCTATGGCATACAC	GTTATATGGTATGATGCAAGTA ATAAGTTCCATGCAGACGCCGT GAAGGGC	GGAAAAGTGGCTGGTATGCCT GAAGCTTTTGAAATC
			SEQ ID NO: 2813	SEQ ID NO: 2970	SEQ ID NO: 3127
		AA	SYGIH	VIWYDASNKFHADAVKG	GKVAGMPEAFEI
			SEQ ID NO: 1243	SEQ ID NO: 1400	SEQ ID NO: 1557
rs361140	5G12.006.003	NA	AGCTATGGCATACAC	GTTATATGGTATGATGCAAGTA ATAAGTTCCATGCAGACGCCGT GAAGGGC	GGAAAAGTGGCTGGTATGCCT GAAGCTTTTGAAATC
			SEQ ID NO: 2814	SEQ ID NO: 2971	SEQ ID NO: 3128
		AA	SYGIH	VIWYDASNKFHADAVKG	GKVAGMPEAFEI
			SEQ ID NO: 1244	SEQ ID NO: 1401	SEQ ID NO: 1558
rs359919	5G12.006.004	NA	AGCTATGGCATACAC	GTTATATGGTATGATGCAAGTA ATAAGTTCCATGCAGACGCCGT GAAGGGC	GGAAAAGTGGCTGGTATGCCT GAAGCTTTTGAAATC
			SEQ ID NO: 2815	SEQ ID NO: 2972	SEQ ID NO: 3129
		AA	SYGIH	VIWYDASNKFHADAVKG	GKVAGMPEAFEI
			SEQ ID NO: 1245	SEQ ID NO: 1402	SEQ ID NO: 1559
rs361144	5G12.006.005	NA	AGCTATGGCATACAC	GTTATATGGTATGATGCAAGTA ATAAGTTCCATGCAGACTCCGT GAAGGGC	GGAAAAGTGGCTGGTATGCCT GAAGCTTTTGAAATC
			SEQ ID NO: 2816	SEQ ID NO: 2973	SEQ ID NO: 3130
		AA	SYGIH	VIWYDASNKFHADSVKG	GKVAGMPEAFEI
			SEQ ID NO: 1246	SEQ ID NO: 1403	SEQ ID NO: 1560

iPS:361151	5G12.006.006	NA	AGCTATGGCATACAC	SEQ ID NO: 2817
		AA		SYGIH
				SEQ ID NO: 1247
iPS:361491	17B11.002.001	NA	AGTTATGATATCAAC	SEQ ID NO: 2818
		AA		SYDIN
				SEQ ID NO: 1248
iPS:361499	17B11.002.002	NA	AGTTATGATATCAAC	SEQ ID NO: 2819
		AA		SYDIN
				SEQ ID NO: 1249
iPS:361503	17B11.002.003	NA	AGTTATGATATCAAC	SEQ ID NO: 2820
		AA		SYDIN
				SEQ ID NO: 1250
iPS:361507	17B11.002.004	NA	AGTTATGATATCAAC	SEQ ID NO: 2821
		AA		SYDIN
				SEQ ID NO: 1251

iPS:361151	5G12.006.006	NA	GTTATATGGTATGATGGAAGTA ATAAGTTCCATGCAGACGCCGT GAAGGGC	GGAAAAGTGGCTGGTATGCCT GAAGCTTTTGAAATC
				SEQ ID NO: 3131
		AA	VIWYDGSNKFHADAVKG	GKVAGMPEAFEI
			SEQ ID NO: 1404	SEQ ID NO: 1561
iPS:361491	17B11.002.001	NA	TGGATGAACCCTAACAGTGGTG GCACAGGCTATGCACAGAAGT TCCAGGGC	GGGGGTGATTACGTTTGGGGG AGTTATCGTCCCTACTACTACT ACTACGGTATGGACGTC
				SEQ ID NO: 3132
		AA	WMNPNSGGTGYAQKFQG	GGDYVWGSYRPYYYYYGMDV
			SEQ ID NO: 1405	SEQ ID NO: 1562
iPS:361499	17B11.002.002	NA	TGGATGAACCCTAACAGTGGTA ACACAGGCTATGCACAGAAGT TCCAGGGC	GGGGGTGATTACGTTTGGGGG AGTTATCGTCCCTACTACTACT ACTACGGTATGGACGTC
				SEQ ID NO: 3133
		AA	WMNPNSGNTGYAQKFQG	GGDYVWGSYRPYYYYYGMDV
			SEQ ID NO: 1406	SEQ ID NO: 1563
iPS:361503	17B11.002.003	NA	TGGATGAACCCTAACAGTGGTG GCACAGGCTATGCACAGAAGT TCCAGGGC	GGGGGTGATTACGTTTGGGGG AGTTATCGTCCCTACTACTACT ACTACGGTATGGACGTC
				SEQ ID NO: 3134
		AA	WMNPNSGGTGYAQKFQG	GGDYVWGSYRPYYYYYGMDV
			SEQ ID NO: 1407	SEQ ID NO: 1564
iPS:361507	17B11.002.004	NA	TGGATGAACCCTAACAGTGGTG GCACAGGCTATGCACAGAAGT TCCAGGGC	GGGGGTGATTACGTTTGGGGG AGTTATCGTCCCTACTACTACT ACTACGGTATGGACGTC
				SEQ ID NO: 3135
		AA	WMNPNSGGTGYAQKFQG	GGDYVWGSYRPYYYYYGMDV
			SEQ ID NO: 1408	SEQ ID NO: 1565

iPS:361514	17B11.002.005	NA	AGTTATGATATCAAC	TGGATGAACCCTAACAGTGGTG GCACAGGCTATGCACAGAAGT TCCAGGGC
			SEQ ID NO: 2822	SEQ ID NO: 2979
		AA	SYDIN	WMNPNSGGTGYAQKFQG
			SEQ ID NO: 1252	SEQ ID NO: 1409
iPS:360582	17B11.002.006	NA	AGTTATGATATCAAC	TGGATGAACCCTAACAGTGGTA ACACAGGCTATGCACAGAAGT TCCAGGGC
			SEQ ID NO: 2823	SEQ ID NO: 2980
		AA	SYDIN	WMNPNSGNTGYAQKFQG
			SEQ ID NO: 1253	SEQ ID NO: 1410
iPS:361518	17B11.002.007	NA	AGTTATGATATCAAC	TGGATGAACCCTAACAGTGGTG GCACAGGCTATGCACAGAAGT TCCAGGGC
			SEQ ID NO: 2824	SEQ ID NO: 2981
		AA	SYDIN	WMNPNSGGTGYAQKFQG
			SEQ ID NO: 1254	SEQ ID NO: 1411
iPS:360570	17B11.002.008	NA	AGTTATGATATCAAC	TGGATGAACCCTAACAGTGGTG GCACAGGCTATGCACAGAAGT TCCAGGGC
			SEQ ID NO: 2825	SEQ ID NO: 2982
		AA	SYDIN	WMNPNSGGTGYAQKFQG
			SEQ ID NO: 1255	SEQ ID NO: 1412
iPS:362051	5G12.005.001	NA	AGCTATGGCATACAC	GTTATATGGTATGATGCAAGTA ATAAGTTCCATGCAGACGCCGT GAAGGGC
			SEQ ID NO: 2826	SEQ ID NO: 2983
		AA	SYGIH	VIWYDASNKFHADAVKG
			SEQ ID NO: 1256	SEQ ID NO: 1413

GGGGGTGATTACGTTTGGGGG AGTTATCGTCCCTACTACTACT ACTACGGTATGGACGTC
SEQ ID NO: 3136
GGDYVWGSYRPYYYYYGMDV
SEQ ID NO: 1566
GGGGGTGATTACGTTTGGGGG AGTTATCGTCCCTACTACTACT ACTACGGTATGGACGTC
SEQ ID NO: 3137
GGDYVWGSYRPYYYYYGMDV
SEQ ID NO: 1567
GGGGGTGATTACGTTTTCGGGA GTTATCGTCCCTACTACTACTA CTACGGTATGGACGTC
SEQ ID NO: 3138
GGDYVFGSYRPYYYYYGMDV
SEQ ID NO: 1568
GGGGGTGATTACGTTTTCGGGA GTTATCGTCCCTACTACTACTA CTACGGTATGGACGTC
SEQ ID NO: 3139
GGDYVFGSYRPYYYYYGMDV
SEQ ID NO: 1569
GGAAAAGTGGCTGGTATGCCT GAAGCTTTTGAAATC
SEQ ID NO: 3140
GKVAGMPEAFEI
SEQ ID NO: 1570

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	CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG	CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG
			GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT	AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			CTGGAAGTAGCTCCAACATCGGAAGTAATACTG	AAGGCTTCCGGATACACCTTCACCGGCTACTAT
			TAAACTGGTACCAGCACCTCCCAGGAACGGCCC	ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG
			CCAAACTCCTCATCTATACTAATAATCAGCGGC	CTTGAGTGGATGGGATGGATCAACCCTAACAGT
			CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA	GGTGGCACAAACTATGCACAGAAGTTTCAGGGC
			GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG	AGGGTCACCATGACCAGGGACACCGTCCATCAGT
			CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG	ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT
			CAACATTCGATGACAGCCTGAATGGTCCGGTAT	GACGACACGGCCGTGTATTACTGTGCGAGAGGG
			TCGGCGGAGGGACCAAGCTGACCGTCCTAGGTC	GGGGATTACGTTTGGGGGACTTATCGGCCTCAC
			AGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCC	TACTACTACGGTATGGACGTCTGGGGCCAAGGG
			GCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGC	ACCACGGTCACCGTCTCCTCAGCCTCCACCAAG
			CACACTGGTGTGTCTCATAAGTGACTTCTACCCG	GGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCA
			GGAGCCGTGACAGTGGCCTGGAAGGCAGATAG	AGAGCACCTCTCTGGGGGCACAGCGGCCCTGGGCT
			CAGCCCCGTCAAGGCGGGAGTGGAGACCACCAC	GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA
			ACCCTCCAAACAAAGCAACAACAAGTACGCGGGC	CGGTGTCGTGGAACTCAGGCGCCCTGACCAGCG
			CAGCAGCTATCTGAGCCTGACGCCTGAGCAGTG	GCGTGCACACCTTCCCGGCTGTCCTACAGTCCTC
			GAAGTCCCACAGAAGCTACAGCTGCCAGGTCAC	AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT
			GCATGAAGGGAGCACCGTGGAGAAGACAGTGG	GCCCTCCAGCAGCTTGGGCACCCAGACCTACAT
			CCCCTACAGAATGTTCA	CTGCAACGTGAATCACAAGCCCAGCAACACCAA
				GGTGGACAAGAAAGTTGAGCCCAAATCTTGTGA
				CAAAACTCACACATGCCCACCGTGCCCAGCACC
				TGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTC
				CCCCCAAAACCCAAGGACACCCTCATGATCTCC
				CGGACCCCCTGAGGTCACATGCGTGGTGGTGGAC
				GTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC
				TGGTACGTGGACGGCGTGGAGGTGCATAATGCC
				AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG
				CACGTACCGTTGTGTCAGCGTCCTCACCGTCCTG
				CACCAGGACTGGCTGAATGGCAAGGAGTACAA
				GTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCC
				CATCGAGAAAACCATCTCCAAAGCCAAAGGGCA

		GCCCCGAGAACCACAGGTGTACACCCTGCCCCC ATCCCGGGAGGAGATGACCAAGAACCAGGTCA GCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA GCGACATCGCCGTGGAGTGGGAGAGCAATGGG CAGCCGGAGAACAACTACAAGACCACGCCTCCC GTGCTGGACTCCGACGGCTCCTTCTTCCTCTATA GCAAGCTCACCGTGGACAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAACCACTACACGCAGAAGAGC CTCTCCCTGTCTCCGGGTAAA
AA	SEQ ID NO: 1885	SEQ ID NO: 2042
	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNW YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDDSLNGPVFGGGTK LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD FYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKY AASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV APTECS	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG GDYVWGTYRPHYYYGMDVWGQGTTVTVSSAST KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK
	SEQ ID NO: 315	SEQ ID NO: 472
NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCGCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGAACGGTGGCT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGGAA GTAATGAAAACTATGCAGACTCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAATA CGCTGTATCTGCACATGAACAGCCTGAGAGTCG CGGACACGGCTGTGTATTATTGTGCGCGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT
4B1		
iPS:3359144		

GCACCATCTGTCTTCATCTTCCCGCCATCTGATG		GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT		CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC
GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA		ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC
AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT		GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC
CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG		CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC
ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA		CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT
CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC		CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC
ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG		GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA		CAGACCTACATCTGCAACGTGAATCACAAGCCC
GGGGAGAGTGT		AGCAACACCAAGGTGGACAAGAAAGTTGAGCC
		CAAATCTTGTGACAAAACTCACACATGCCCACC
		GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC
		AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC
		CCTCATGATCTCCCGGACCCCTGAGGTCACATG
		CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA
		GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
		GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA
		GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT
		CCTCACCGTCCTGCACCAGGACTGGCTGAATGG
		CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
		CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
		AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
		ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
		AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
		GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
		AGAGCAATGGGCAGCCGGAGAACAACTACAAG
		ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
		TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
		AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
		TCCGTGATGCATGAGGCTCTGCACAACCACTAC
		ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
SEQ ID NO: 1886		SEQ ID NO: 2043
AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM
	QQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTEFT	HWVRQAPGKGLEWVAVIWYDGSNENYADSVKG
	LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	RFTISRDNSKNTLYLHMNSLRVADTAVYYCARDG
	TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA	TIFGVVLGDYWGQGTLVTVSSASTKGPSVFPLAPS

KVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC	SEQ ID NO: 316	SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
NA	SEQ ID NO: 473	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGGAA GTAATAAATACTATGCAGACTCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTTGGAGTGCTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCCACC GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC AGTCTTCCTCTTCCCCCCAAAACCCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATG CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA

			GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
			GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA
			GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT
			CCTCACCGTCCTGCACCAGGACTGGCTGAATGG
			CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
			CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
			AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
			ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
			AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
			GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
			AGAGCAATGGGCAGCCGGAGAACAACTACAAG
			ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
			TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
			AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
			TCCGTGATGCATGAGGCTCTGCACAACCACTAC
			ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
		SEQ ID NO: 1887	SEQ ID NO: 2044
	AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAVIWYDGSNKYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
		SEQ ID NO: 317	SEQ ID NO: 474
	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCAGGGCGAGTCAGGACATTAGCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG
	2F11		
	iPS:335 941		

CTGGAGTGGGTGGCAGTTATATGGTATGATGGA	AGCTCCTGATCTACGATGCATCCAATTTGGAAA	
AGTAATAAATACTATGCAGACTCCGTGAAGGGC	CAGGGGTCCCATCAAGGTTCAGTGGAAGTGGAT	
CGATTCACCATCTCCAGCGACAATTCCAAGAAC	CTGGGACAGATTTTAGTTTCACCATCAGCAGCCT	
ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC	GCAGCCTGAAGATATTGCAACATATTACTGTCA	
GAGGACACGGCTGTGTATTACTGTGCGAGAGAT	ACAGTATGATATTCTCCTCACTTTCGGCGGAGG	
AGGACGATTTTTGGAGTGGTTCTTGACTACTGG	GACCAAGGTGGAGATCAAGCGAACGGTGGCTG	
GGCCAGGGAACCCTGGTCACCGTCTCCTCAGCC	CACCATCTGTCTTCATCTTCCCGCCATCTGATGA	
TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA	GCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGC	
CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG	CTGCTGAATAACTTCTATCCCAGAGAGGCCAAA	
GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC	GTACAGTGGAAGGTGGATAACGCCCTCCAATCG	
GAACCGGTGACGGTGTCGTGGAACTCAGGCGCC	GGTAACTCCCAGGAGAGTGTCACAGAGCAGGAC	
CTGACCAGCGGCGTGCACACCTTCCCGGCTGTC	AGCAAGGACAGCACCTACAGCCTCAGCAGCACC	
CTACAGTCCTCAGGACTCTACTCCCTCAGCAGC	CTGACGCTGAGCAAAGCAGACTACGAGAAACA	
GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC	CAAAGTCTACGCCTGCGAAGTCACCCATCAGGG	
CAGACCTACATCTGCAACGTGAATCACAAGCCC	CCTGAGCTCGCCCGTCACAAAGAGCTTCAACAG	
AGCAACACCAAGGTGGACAAGAAAGTTGAGCC	GGGAGAGTGT	
CAAATCTTGTGACAAAACTCACACATGCCCACC		
GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC		
AGTCTTCCTCTTCCCCCCAAAACCCAAGGACAC		
CCTCATGATCTCCCGGACCCCTGAGGTCACATG		
CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA		
GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA		
GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA		
GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT		
CCTCACCGTCCTGCACCAGGACTGGCTGAATGG		
CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC		
CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA		
AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT		
ACACCCTGCCCCCATCCCGGGAGGAGATGACCA		
AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG		
GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG		
AGAGCAATGGGCAGCCGGAGAACAACTACAAG		
ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC		
TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG		
AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC		

		TCCGTGATGCATGAGGCTCTGCACAACCACTAC
		ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1888	SEQ ID NO: 2045
AA	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGM
	YQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTD	HWVRQAPGKGLEWVAVIWYDGSNKYYADSVKG
	FSFTISSLQPEDIATYYCQQYDILLTFGGGTKVEIKR	RFTISSDNSKNTLYLQMNSLRAEDTAVYYCARDR
	TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA	TIFGVVLDYWGQGTLVTVSSASTKGPSVFPLAPSS
	KVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST	KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG
	LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG	VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV
	EC	NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG
		GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
		VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV
		LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
		KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP
		SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
		LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS
		LSPGK
	SEQ ID NO: 318	SEQ ID NO: 475
NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG	CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG
	GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC	AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
	TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC	AAGGCTTCTGGATACACCTTCACCGGCTACTAT
	AACAATAAGAACTACATAGCTTGGTACCAGCAG	ATCCACTGGGTGCGACAGGCCCCTGGACAAGGG
	CAACCAGGACATCCTCCTAAGCTGCTCATTTACT	CTTGAGTGGATGGGGGTGGATCAACCCTGACAGT
	GGGCATCTACCCGGGAATCCGGGGTCCCTGACC	GGTGGCACAGACTATTCACAGAGGTTTCAGGGC
	GATTCAGTGGCAGCGGGTCTGGGACAGATTTCA	AGGTTCACCATGACCAGGGACACGTCCATCAGC
	CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG	ACAGCCTACATGGAACTGAACAGGCTGAGATCT
	TGGCAGTTTTTTACTGTCAACAATATTATAGTAC	GACGACACGGCCGTGTATTACTGTGCGAGAGAG
	TCCGTGGACGTTCGGCCAAGGGACCAAGGTGGA	GCCACGATTTTTGGAATGGTTATTGTACCGTTTG
	AATCAAACGAACGGTGGCTGCACCATCTGTCTT	ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
	CATCTTCCCGCCATCTGATGAGCAGTTGAAATCT	CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC
	GGAACTGCCTCTGTTGTGTGCCTGCTGAATAACT	CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGG
	TCTATCCCAGAGAGGCCAAAGTACAGTGGAAGG	CACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA
	TGGATAACGCCCTCCAATCGGGTAACTCCCAGG	CTTCCCCGAACCGGTGACGGTGTCGTGGAACTC
	AGAGTGTCACAGAGCAGGACAGCAAGGACAGC	AGGCGCCCTGACCAGCGGCGTGCACACCTTCCC
	ACCTACAGCCTCAGCAGCACCCTGACGCTGAGC	GGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC
	AAAGCAGACTACGAGAAACACAAAGTCTACGC	AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG

CTGCGAAGTCACCCATCAGGGCCTGAGCTCGCC CGTCACAAAGAGCTTCAACAGGGGAGAGTGT		GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCCAGCAACACCAAGGTGGACAAGAAAGT TGAGCCCAAATCTTGTGACAAAACTCACACATG CCCACCGTGCCCAGCACCTGAACTCCTGGGGGG ACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAG GACACCCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT GAGGAGCAGTACGGCAGCACCGTACCGTTGTGTC AGCGTCCTCACCGTCCTGCACCAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCCAGCCCCCATCGAGAAAACCATC TCCAAAGCCAAAGGGCAGCCCCGAGAACCACA GGTGTACACCCTGCCCCCATCCCGGGAGGAGAT GACCAAGAACCAGGTCAGCCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGCAGCCGGAGAACAACT ACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG TAAA
	SEQ ID NO: 1889	SEQ ID NO: 2046
	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK NYIAWYQQQPGHPPKLLIYWASTRESGVPDRFSGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWINPDSGGTDYSQRFQGR FTMTRDTSISTAYMELNRLRSDDTAVYYCAREATI FGMVIVPFDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF
AA		

		YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
	SEQ ID NO: 319	SEQ ID NO: 476
	NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAGCAG AAACCAGGACATCCTCCTAAGCTGCTCATTTACT GGGCATCTACCCGGGAATCCGGGGTCCCTGACC GATTCAGTGGCAGCGGGTCTGGGACAGATTTCA CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCGGCCAAGGGACCAAGGTGGA AATCAAACGAACGGTGGCTGCACCATCTGTCTT CATCTTCCCGCCATCTGATGAGCAGTTGAAATCT GGAACTGCCTCTGTTGTGTGCCTGCTGAATAACT TCTATCCCAGAGAGGCCAAAGTACAGTGGAAGG TGGATAACGCCCTCCAATCGGGTAACTCCCAGG AGAGTGTCACAGAGCAGGACAGCAAGGACAGC ACCTACAGCCTCAGCAGCACCCTGACGCTGAGC AAAGCAGACTACGAGAAAACACAAAGTCTACGC CTGCGAAGTCACCCATCAGGGCCTGAGCTCGCC CGTCACAAAGAGCTTCAACAGGGGAGAGTGT
	iPS:335978	
	13H12	

		GGTGTACACCCTGCCCCCATCCCGGGAGGAGAT GACCAAGAACCAGGTCAGCCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGCAGCCGGAGAACAACT ACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG TAAA
	SEQ ID NO: 1890	SEQ ID NO: 2047
	AA	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWINPDSGGTDYSQRFQGR FTMTRDTSISTAYMELSRLRSDDTAVYYCAREATI FGMVIVPFDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
	SEQ ID NO: 320	SEQ ID NO: 477
iPS:33598	NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC AACAATAAGAACTACTTAGCTTGGTACCAACAG AAACCAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTCAGCAATATTATCGTA
	11C1	CAGGTGCCGCTGGTACAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCGGCTACTAT ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG CTTGTGTGGATGGGGTGGATCAGCCCTAACAGT GGTGACACAAGCTATGCACAGAAGTTTCAGGAC AGGGTCACCATGACCAGGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGACTGAGATCT GACGACACGGCCGTGTATTTCTGTACGAGAGAG

CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG	GCCACGATTTTTGGAATGCTTATTGTACCATTTG	
AAATCAAACGAACGGTGGCTGCACCATCTGTCT	ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT	
TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC	CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC	
TGGAACTGCCTCTGTTGTGCCTGCTGAATAAC	CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGG	
TTCTATCCCAGAGAGGCCAAAGTACAGTGGAAG	CACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA	
GTGGATAACGCCCTCCAATCGGGTAACTCCCAG	CTTCCCCGAACCGGTGACGGTGTCGTGGAACTC	
GAGAGTGTCACAGAGCAGGACAGCAAGGACAG	AGGCGCCCTGACCAGCGGCGTGCACACCTTCCC	
CACCTACAGCCTCAGCAGCACCCTGACGCTGAG	GGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC	
CAAAGCAGACTACGAGAAACACAAAGTCTACG	AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG	
CCTGCGAAGTCACCCATCAGGGCCTGAGCTCGC	GGCACCCAGACCTACATCTGCAACGTGAATCAC	
CCGTCACAAAGAGCTTCAACAGGGGAGAGTGT	AAGCCCAGCAACACCAAGGTGGACAAGAAAGT	
	TGAGCCCAAATCTTGTGACAAAACTCACACATG	
	CCCACCGTGCCCAGCACCTGAACTCCTGGGGGG	
	ACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAG	
	GACACCCTCATGATCTCCCGGACCCCTGAGGTC	
	ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC	
	CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC	
	GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT	
	GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC	
	AGCGTCCTCACCGTCCTGCACCAGGACTGGCTG	
	AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC	
	AAAGCCCTCCCAGCCCCCATCGAGAAAACCATC	
	TCCAAAGCCAAAGGGCAGCCCCGAGAACCACA	
	GGTGTACACCCTGCCCCCATCCCGGGAGGAGAT	
	GACCAAGAACCAGGTCAGCCTGACCTGCCTGGT	
	CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA	
	GTGGGAGAGCAATGGGCAGCCGGAGAACAACT	
	ACAAGACCACGCCTCCCGTGCTGGACTCCGACG	
	GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA	
	CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC	
	ATGCTCCGTGATGCATGAGGCTCTGCACAACCA	
	CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG	
	TAAA	
SEQ ID NO: 1891	SEQ ID NO: 2048	
AA	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
	NYLAWYQQKPGQPPNLLIYWTSTRDSGVPDRFSG	HWVRQAPGQGLVWMGWISPNSGDTSYAQKFQDR

iPS:335994		
12H11		
NA		
SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC	SEQ ID NO: 321	VTMTRDTSISTAYMELSRLRSDDTAVYFCTREATI FGMLIVPFDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
		SEQ ID NO: 478
	GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC AACAATAAGAACTACTTAGCTTGGTACCAGCAG AAACCAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTCAGCAATATTATCGTA CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG AAATCAAACGAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAAC TTCTATCCCAGAGAGGCCAAAGTACAGTGGAAG GTGGATAACGCCCTCCAATCGGGTAACTCCCAG GAGAGTGTCACAGAGGACAGGACCAAGGACAG CACCTACAGCCTCAGCAGCACCCTGACGCTGAG CAAAGCAGACTACGAGAAACACAAAGTCTACG CCTGCGAAGTCACCCATCAGGGCCTGAGCTCGC CCGTCACAAAGAGCTTCAACAGGGGAGAGTGT	CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCGGCTACTAT ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG CTTGAGTGGATGGGGGTGGATAAGCCCTAACAAT GGTGACACAAACTATGCACAGAAGTTTCAGGAC AGGGTCACCATGACCAGGGACACCGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT GACGACACGGCCGTGTATTACTGTACGAGAGAG GCCACGATTTTTGGAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGG CACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTCGTGGAACTC AGGCGCCCTGACCAGCGGCGTGCACACCTTCCC GGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCCAGCAACACCAAGGTGGACAAGAAAGT TGAGCCCAAATCTTGTGACAAAACTCACACATG CCCACCGTGCCCAGCACCTGAACTCCTGGGGGG ACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAG

GACACCCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC AGCGTCCTCACCGTCCTGCACCAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCCAGCCCCCATCGAGAAAACCATC TCCAAAGCCAAAGGGCAGCCCCGAGAACCACA GGTGTACACCCTGCCCCCATCCCGGGAGGAGAT GACCAAGAACCAGGTCAGCCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGCAGCCGGAGAACAACT ACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCTCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG TAAA	SEQ ID NO: 2049	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWISPNNGDTNYAQKFQD RVTMTRDTSISTAYMELSRLRSDDTAVYYCTREA TIFGMLIVPFDYWGQGTLVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK SLSLSPGK
		AA

iPS:336024		
18E3		
NA	SEQ ID NO: 322	SEQ ID NO: 479
	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTG	CAGGTGCAGTTGCAGGAGTCGGGCCCAGGACTG
	TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT	GTGAAGCCTTCACAGACCCTGTCCCTCACCTGC
	GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT	ACTGTCTCTGGTGACTCCATCAGCAGTGGTGGTT
	TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC	ACTACTGGAGCTGGATCCGCCAGCACCCAGGGA
	CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG	AGGGCCTGGAGTGGATTGGGTACATCTATTACA
	CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG	GTGGGAGCACCTACTACAACCCGTCCCTCAAGA
	GGTCTGGGACAGACTTCACTCTCACCATCAGCA	GTCGAGTTACCATATCAGTAGACACGTCTAAGA
	GACAGGAGCCTGATGATTTTGCAGTGTATTACT	ACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC
	GTCAGCAGTATGGTAGTTCACCGCTCACTTTCGG	CGCGGACACGGCCGTGTATTACTGTGCGAGAGA
	CGGAGGGACCAAGGTGGAGATCAAACGAACGG	TCGTATTACGATTTTTGGAGTGGTTATGGGGGGC
	TGGCTGCACCATCTGTCTTCATCTTCCCGCCATC	GGTATGGACGTCTGGGGCCAAGGGACCACGGTC
	TGATGAGCAGTTGAAATCTGGAACTGCCTCTGT	ACCGTCTCCTCAGCCTCCACCAAGGGCCCATCG
	TGTGTGCCTGCTGAATAACTTCTATCCCAGAGA	GTCTTCCCCCCTGGCACCCTCCTCCAAGAGCACCT
	GGCCAAAGTACAGTGGAAGGTGGATAACGCCCT	CTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCA
	CCAATCGGGTAACTCCCAGGAGAGTGTGTCACAGA	AGGACTACTTCCCCGAACCGGTGACGGTGTCGT
	GCAGGACAGCAAGGACAGCACCTACAGCCTCA	GGAACTCAGGCGCCCTGACCAGCGGCGTGCACA
	GCAGCACCCTGACGCTGAGCAAAGCAGACTACG	CCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTA
	AGAAACACACAAAGTCTACGCCTGCGAAGTCACCC	CTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAG
	ATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCT	CAGCTTGGGCACCCAGACCTACATCTGCAACGT
	TCAACAGGGGAGAGTGT	GAATCACAAGCCCAGCAACACCAAGGTGGACA
		AGAAAGTTGAGCCCAAATCTTGTGACAAAACTC
		ACACATGCCCACCGTGCCCAGCACCTGAACTCC
		TGGGGGGACCGTCAGTCTTCCTCTTCCCCCAAA
		ACCCAAGGACACCCTCATGATCTCCCGGACCCC
		TGAGGTCACATGCGTGGTGGTGGACGTGAGCCA
		CGAAGACCCTGAGGTCAAGTTCAACTGGTACGT
		GGACGGCGTGGAGGTGCATAATGCCAAGACAA
		AGCCGTGTGAGGAGCAGTACGGCAGCACGTACC
		GTTGTGTCAGCGTCCTCACCGTCCTGCACCAGG
		ACTGGCTGAATGGCAAGGAGTACAAGTGCAAG
		GTCTCCAACAAAGCCCTCCCAGCCCCCATCGAG
		AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGA
		GAACCACAGGTGTACACCCTGCCCCCATCCCGG
		GAGGAGATGACCAAGAACCAGGTCAGCCTGAC
		CTGCCTGGTCAAAGGCTTCTATCCCAGCGACAT

		CGCCGTGGAGTGGGAGAGCAATGGGCAGCCGG
		AGAACAACTACAAGACCACGCCTCCCGTGCTGG
		ACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCT
		CACCGTGGACAAGAGCAGGTGGCAGCAGGGGA
		ACGTCTTCTCATGCTCCGTGATGCATGAGGCTCT
		GCACAACCACTACACGCAGAAGAGCCTCTCCCT
		GTCTCCGGGTAAA
	SEQ ID NO: 1893	SEQ ID NO: 2050
AA	EIVLTQSPGTLSLSPGERATLSCRASQSISYSYLAW YQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF TLTISRQEPDDFAVYYCQQYGSSPLTFGGGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC	QVQLQESGPGLVKPSQTLSLTCTVSGDSISSGGYY WSWIRQHPGKGLEWIGYIYYSGSTYYNPSLKSRVT ISVDTSKNQFSLKLSSVTAADTAVYYCARDRITIFG VVMGGGMDVWGQGTTVTVSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
	SEQ ID NO: 323	SEQ ID NO: 480
NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTG TCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCC TGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGCAGCCACCAGGGCC ACTGGTATCCCAGCCAGGGTCAGTGGCAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGCAGTCTGAAGATTTTGCAGTTTATTACTGTC AGCAGTATAATAACTGGCCTCTCACTTTCGGCG GAGGGACCAAGGTGGAGATCAAACGAACGGTG GCTGCACCATCTGTCTTCATCTTCCCGCCATCTG ATGAGCAGTTGAAATCTGGAACTGCCTCTGTTG TGTGCCTGCTGAATAACTTCTATCCCAGAGAGG	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACCTTCAGTAACTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCGAGGGG CTGGAGTGGGTGGCAGCTATATGGTTTGATGGA AGTGATAAATACTATGCAGACTCCGTGAAGGGC CGATTCACCATCTCCAGAGACAACTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGGCGATTTTTGGAGTGGTCCCCGACTACTGG GGCCAGGGAACCCTGGTCACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG
		iPS:336041
		2G10_LC1

CCAAAGTACAGTGGAAGGTGGATAACGCCCTCC AATCGGGTAACTCCCAGGAGAGTGTCACAGAGC AGGACAGCAAGGACAGCACCTACAGCCTCAGC AGCACCCTGACGCTGAGCAAAGCAGACTACGAG AAACACAAAGTCTACGCCTGCGAAGTCACCCAT CAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTC AACAGGGGAGAGTGT	GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC GAACCGGTGACGGTGTCGTGGAACTCAGGCGCC CTGACCAGCGGCGTGCACACCTTCCCGGCTGTC CTACAGTCCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCCACC GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATG CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT CCTCACCGTCCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT ACACCCTGCCCCCATCCCGGGAGGAGATGACCA AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGAACAACTACAAG ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
SEQ ID NO: 1894	SEQ ID NO: 2051
AA	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGAATRATGIPARVSGSGSGTE FTLTISSLQSEDFAVYYCQQYNNWPLTFGGGTKVE IKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGM HWVRQAPGEGLEWVAAIWFDGSDKYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGTLVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG

			GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
			VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV
			LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
			KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP
			SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
			LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS
			LSPGK
		SEQ ID NO: 324	SEQ ID NO: 481
		GACATTCAGATGACCCAGTCTCCATCCTCCCTGT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
		CTGCATCTGTAGGAGACAGAGTCACCATCACTT	GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
		GCCGGGCAAGTCAGGGCATTAGAAATGAGTTAG	GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA
		GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA	TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC
		AACGCCTGATCTATGGTGCATCCAGTTTGCAAA	TGGAGTGGGTGGCAGTTATATGGTATGATGGAA
		GTGGGGTCCCATCAAGGTTCAGCGGCAGTGGAT	GTAATAAATACTATGCAGACTCCGTGAAGGGCC
		CTGGGACAGAGTTCACTCTCACAATCAGCAGCC	GCTTCACCATCTCCAGAGACAATTCCAAGAACA
		TGCAGCCTGAAGATTTTGTAACTTATTACTGTCT	CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
		ACAGCATAATAGTTACCCATTCACTTTCGGCCCT	AGGACACGGCTGTGTATTACTGTGCGCGAGATG
		GGGACCAAAGTGGATGTCAAACGAACGGTGGCT	GGACGATTTTTGGAGTGCTCTTGGGGGACTACT
		GCACCATCTGTCTTCATCTTCCCGCCATCTGATG	GGGGCCAGGGAACCCCTGGTCACCGTCTCCTCAG
		AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT	CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC
		GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA	ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC
		AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT	GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC
		CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG	CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC
		ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA	CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT
		CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC	CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC
		ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG	GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
		GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA	CAGACCTACATCTGCAACGTGAATCACAAGCCC
		GGGGAGAGTGT	AGCAACACCAAGGTGGACAAGAAAGTTGAGCC
			CAAATCTTGTGACAAAACTCACACATGCCCACC
			GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC
			AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC
			CCTCATGATCTCCCGGACCCCTGAGGTCACATG
			CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA
			GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
			GGTGCATAATGCCAAGACAAAGCCGCGTGTGAGGA
			GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT
	NA		
	4H9.004		
	iPS:336077		

			CCTCACCGTCCTGCACCAGGACTGGCTGAATGG
			CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
			CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
			AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
			ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
			AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
			GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
			AGAGCAATGGGCAGCCGGAGAACAACTACAAG
			ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
			TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
			AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
			TCCGTGATGCATGAGGCTCTGCACAACCACTAC
			ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
		SEQ ID NO: 1895	SEQ ID NO: 2052
	AA	DIQMTQSPSSLSASVGDRVTITCRASQGIRNELGW YQQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFVTYYCLQHNSYPFTFGPGTKVDV KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAVIWYDGSNKYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
	NA	SEQ ID NO: 325	SEQ ID NO: 482
		GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTACGATGCTTCCAATTTGGAGCC AGGGGTCCCATCAAGGTTCAGTGGAAGTGGATC TGGGACAGATTTTACTTTCACCATCAGCAGCCTG	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCTCCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGCTATATGGTATGATGGAA ATAATAAATACTATGCAGACTCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCAAGAACA
		iPS:33608	6A5.004

		CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
		AGGACACGGCTGTGTATTACTGTGCGAGAGATC
		GGACGATTTTTGGAGTGGTCCTTGAGTACCTCG
		GCCAGGGAACCCTGGTCACCGTCTCCTCAGCCT
		CCACCAAGGGCCCATCGGTCTTCCCCCTGGCAC
		CCTCCTCCAAGAGCACCTCTGGGGGCACAGCGG
		CCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG
		AACCGGTGACGGTGTCGTGGAACTCAGGCGCCC
		TGACCAGCGGCGTGCACACCTTCCCGGCTGTCC
		TACAGTCCTCAGGACTCTACTCCCTCAGCAGCGT
		GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCA
		GACCTACATCTGCAACGTGAATCACAAGCCCAG
		CAACACCAAGGTGGACAAGAAAGTTGAGCCCA
		AATCTTGTGACAAAACTCACACATGCCCACCGT
		GCCCAGCACCTGAACTCCTGGGGGGACCGTCAG
		TCTTCCTCTTCCCCCCAAAACCCAAGGACACCCT
		CATGATCTCCCGGACCCCTGAGGTCACATGCGT
		GGTGGTGGACGTGAGCCACGAAGACCCTGAGGT
		CAAGTTCAACTGGTACGTGGACGGCGTGGAGGT
		GCATAATGCCAAGACAAAGCCGTGTGAGGAGC
		AGTACGGCAGCACGTACCGTTGTGTCAGCGTCC
		TCACCGTCCTGCACCAGGACTGGCTGAATGGCA
		AGGAGTACAAGTGCAAGGTCTCCAACAAAGCCC
		TCCCAGCCCCCATCGAGAAAACCATCTCCAAAG
		CCAAAGGGCAGCCCCGAGAACCACAGGTGTAC
		ACCCTGCCCCCATCCCGGGAGGAGATGACCAAG
		AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC
		TTCTATCCCAGCGACATCGCCGTGGAGTGGGAG
		AGCAATGGGCAGCCGGAGAACAACTACAAGAC
		CACGCCTCCCCGTGCTGGACTCCGACGGCTCCTTC
		TTCCTCTATAGCAAGCTCACCGTGGACAAGAGC
		AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC
		GTGATGCATGAGGCTCTGCACAACCACTACACG
		CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
CAGCCTGAAGATATTGCAACATATTACTGTCAA		SEQ ID NO: 2053
CAGTATGATGATCTATTCACTTTCGGCCCTGGGA		
CCAAAGTGGATATCAACGAACGGTGGCTGCAC		
CATCTGTCTTCATCTTCCCGCCATCTGATGAGCA		
GTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTG		
CTGAATAACTTCTATCCCAGAGAGGCCAAAGTA		
CAGTGGAAGGTGGATAACGCCCTCCAATCGGGT		
AACTCCCAGGAGAGTGTCACAGAGCAGGACAG		
CAAGGACAGCACCTACAGCCTCAGCAGCACCCT		
GACGCTGAGCAAAGCAGACTACGAGAAACACA		
AAGTCTACGCCTGCGAAGTCACCCATCAGGGCC		
TGAGCTCGCCCGTCACAAAGAGCTTCAACAGGG		
GAGAGTGT		
		SEQ ID NO: 1896

	IPS:33099	
	17H11.004	
AA	NA	
DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGSGTD FTFTISSLQPEDIATYYCQQYDDLFTFGPGTKVDIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR GEC	SEQ ID NO: 326	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAAIWYDGNNKYYADSVKG RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYLGQGTLVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVL TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL SPGK
	SEQ ID NO: 483	
	CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTG GTGAAGCCTTCGGAGACCCTGTCCCTCACCTGC ACTGTCTCTCAGGGCTCCATCAGTAGTTACTACT GGAGCTGGATCCGGCAGCCCGCCGGGAAGGGA CTAGAGTGGATTGGCCGTATCTATACCAGTGGG AGCACCAACTACAACCCCTCCCTCAAGAGTCGA GTCACCATGTCAATAGACACGTCCAAGAACCAG TTCTCCCTGAAACTGAACTCTGTGACCGCCGCG GACACGGCCGTGTATTACTGTGCGAGAGATGTA GCAGTGGCTGGCTTTGACTACTGGGGCCAGGGA ACCCTGGTCACCGTCTCCTCAGCCTCCACCAAG GGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCA AGAGCACCTCTGGGGGCACAGCGGCCCTGGGCT GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA CGGTGTCGTGGAACTCAGGCGCCCTGACCAGCG GCGTGCACACCTTCCCGGCTGTCCTACAGTCCTC AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT GCCCTCCAGCAGCTTGGGCACCCAGACCTACAT CTGCAACGTGAATCACAAGCCCAGCAACCACAA GGTGGACAAGAAAGTTGAGCCCAAATCTTGTGA CAAAACTCACACATGCCCACCGTGCCCAGCACC

TGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTC CCCCCAAAACCCAAGGACACCCTCATGATCTCC CGGACCCCTGAGGTCACATGCGTGGTGGTGGAC GTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC TGGTACGTGGACGGCGTGGAGGTGCATAATGCC AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG CACGTACCGTTGTGTCAGCGTCCTCACCGTCCTG CACCAGGACTGGCTGAATGGCAAGGAGTACAA GTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCC CATCGAGAAAACCATCTCCAAAGCCAAAGGGCA GCCCCGAGAACCACAGGTGTACACCCTGCCCCC ATCCCGGGAGGAGATGACCAAGAACCAGGTCA GCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA GCGACATCGCCGTGGAGTGGGAGAGCAATGGG CAGCCGGAGAACAACTACAAGACCACGCCTCCC GTGCTGGACTCCGACGGCTCCTTCTTCCTCTATA GCAAGCTCACCGTGGACAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAACCACTACACGCAGAAGAGC CTCTCCCTGTCTCCGGGTAAA	SEQ ID NO: 1897	SEQ ID NO: 2054
	AA	DIQMTQSPSSVSASVGDRVTITCRASQGLIIWLAW YQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTD FTLTISSLQPEDFATYYCQQTNSFPPTFGQGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC	QVQLQESGPGLVKPSETLSLTCTVSQGSISSYYWS WIRQPAGKGLEWIGRIYTSGSTNYNPSLKSRVTMS IDTSKNQFSLKLNSVTAADTAVYYCARDVAVAGF DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFP PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQ DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

iPS:359621		SEQ ID NO: 327	SEQ ID NO: 484
17H11.004.001			
NA		GACATCCAGATGACCCAGTCTCCATCTTCCGTGT	CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTG
		CTGCATCTGTAGGAGACAGAGTCACCATCACTT	GTGAAGCCTTCGGAGACCCTGTCCCTCACCTGC
		GTCGGGCGAGTCAGGGTCTTATCATCTGGTTAG	ACTGTCTCTGGGGGCTCCATCAGTAGTTACTACT
		CCTGGTATCAGCAGAAACCGGGGAAAGCCCCTA	GGAGCTGGATCCGGCAGCCCGCCGGGAAGGGA
		AACTCCTGATCTATGCTGCATCCAGTTTGCAAAG	CTAGAGTGGATTGGCCGTATCTATACCAGTGGG
		TGGGGTCCCATCAAGGTTCAGCGGCAGTGGCTC	AGCACCAACTACAACCCCTCCCTCAAGAGTCGA
		TGGGACAGATTTCACTCTCACCATCAGCAGCCT	GTCACCATGTCAATAGACACGTCCAAGAACCAG
		ACAGCCTGAAGATTTTGCAACTTACTATTGTCAA	TTCTCCCTGAAACTGAACTCTGTGACCGCCGCG
		CAGACTAACAGTTTCCCTCCGACGTTCGGCCAA	GACACGGCCGTGTATTACTGTGCGAGAGATGTA
		GGGACCAAGGTGGAAATCAAACGAACGGTGGC	GCAGTGGCTGGCTTTTGACTACTGGGGCCAGGGA
		TGCACCATCTGTCTTCATCTTCCCGCCATCTGAT	ACCCTGGTCACCGTCTCCTCAGCCTCCACCAAG
		GAGCAGTTGAAATCTGGAACTGCCTCTGTTGTG	GGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCA
		TGCCTGCTGAATAACTTCTATCCCAGAGAGGCC	AGAGCACCTCTGGGGGCACAGCGGCCCTGGGCT
		AAAGTACAGTGGAAGGTGGATAACGCCCTCCAA	GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA
		TCGGGTAACTCCCAGGAGAGTGTCACAGAGCAG	CGGTGTCGTGGAACTCAGGCGCCCTGACCAGCG
		GACAGCAAGGACAGCACCTACAGCCTCAGCAGC	GCGTGCACACCTTCCCGGCTGTCCTACAGTCCTC
		ACCCTGACGCTGAGCAAAGCAGACTACGAGAA	AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT
		ACACAAAGTCTACGCCTGCGAAGTCACCCATCA	GCCCTCCAGCAGCTTGGGCACCCAGACCTACAT
		GGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAA	CTGCAACGTGAATCACAAGCCCAGCAACACCAA
		CAGGGGAGAGTGT	GGTGGACAAGAAAGTTGAGCCCAAATCTTGTGA
			CAAAACTCACACATGCCCACCGTGCCCAGCACC
			TGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTC
			CCCCCAAAACCCAAGGACACCCTCATGATCTCC
			CGGACCCCTGAGGTCACATGCGTGGTGGTGGAC
			GTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC
			TGGTACGTGGACGGCGTGGAGGTGCATAATGCC
			AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG
			CACGTACCGTTGTGTCAGCGTCCTCACCGTCCTG
			CACCAGGACTGGCTGAATGGCAAGGAGTACAA
			GTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCC
			CATCGAGAAAACCATCTCCAAAGCCAAAGGGCA
			GCCCCGAGAACCACAGGTGTACACCCTGCCCCC
			ATCCCGGGAGGAGATGACCAAGAACCAGGTCA
			GCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA
			GCGACATCGCCGTGGAGTGGGAGAGCAATGGG

		CAGCCGGAGAACAACTACAAGACCACGCCTCCC
		GTGCTGGACTCCGACGGCTCCTTCTTCCTCTATA
		GCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
		CAGGGGAACGTCTTCTCATGCTCCGTGATGCAT
		GAGGCTCTGCACAACCACTACACGCAGAAGAGC
		CTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1898	SEQ ID NO: 2055
AA	DIQMTQSPSSVSASVGDRVTITCRASQGLIIWLAW YQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTD FTLTISSLQPEDFATYYCQQTNSFPPTFGQGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWS WIRQPAGKGLEWIGRIYTSGSTNYNPSLKSRVTMS IDTSKNQFSLKLNSVTAADTAVYYCARDVAVAGF DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFP PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQ DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
	SEQ ID NO: 328	SEQ ID NO: 485
NA	GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGGCATTAGAAATGAGTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCATCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAGTTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTTGTAACTTATTACTGTCT ACAGCATAATAGTTACCCATTCACTTTCGGCCA AGGGACCAAAGTGGATGTTCAAACGAACGGTGG CTGCACCATCTGTCTTCATCTTCCCGCCATCTGA TGAGCAGTTGAAATCTGGAACTGCCTCTGTTGT GTGCCTGCTGAATAACTTCTATCCCAGAGAGGC CAAAGTACAGTGGAAGGTGGATAACGCCCTCCA ATCGGGTAACTCCCAGGAGAGTGTCACAGAGCA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTTGGAGTGCTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC

GGACAGCAAGGACAGCACCTACAGCCTCAGCA GCACCCTGACGCTGAGCAAAGCAGACTACGAGA AACACAAAGTCTACGCCTGCGAAGTCACCCATC AGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCA ACAGGGGAGAGTGT	CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCCACC GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATG CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA GCAGTACGGCAGCACCGTACCGTTGTGTCAGCGT CCTCACCGTCCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT ACACCCTGCCCCCATCCCGGGAGGAGATGACCA AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGAACAACTACAAG ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA	SEQ ID NO: 2056
	DIQMTQSPSSLSASVGDRVTITCRASQGIRNELGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFVTYYCLQHNSYPFTFGQGTKVD VKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF NRGEC	SEQ ID NO: 1899
AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV	

		SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
		SEQ ID NO: 329
		GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGGCATTAGAAATGAGTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCATCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAGTTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTTGTAACTTATTACTGTCT ACAGCATAATAGTTACCCATTCACTTTCGGCCA AGGGACCAAAGTGGATGTCAAACGAACGGTGG CTGCACCATCTGTCTTCATCTTCCCGCCATCTGA TGAGCAGTTGAAATCTGGAACTGCCTCTGTTGT GTGCCTGCTGAATAACTTCTATCCCAGAGAGGC CAAAGTACAGTGGAAGGTGGATAACGCCCTCCA ATCGGGTAACTCCCAGGAGAGTGTCACAGAGCA GGACAGCAAGGACAGCACCTACAGCCTCAGCA GCACCCTGACGCTGAGCAAAGCAGACTACGAGA AACACAAAGTCTACGCCTGCGAAGTCACCCATC AGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCA ACAGGGGAGAGTGT
		CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATAAATACTATGCAGACTCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTTGGAGTGCTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCCACC GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATG CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA GGTGCATAATGCCAAGACAAAGCCGCGTGTGAGGA GCAGTACGGCAGCACGTACCGTGTGGTCAGCGT CCTCACCGTCCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
	NA	
	4H9.004.002	
	iPS:360929	

			CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
			AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
			ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
			AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
			GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
			AGAGCAATGGGCAGCCGGAGAACAACTACAAG
			ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
			TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
			AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
			TCCGTGATGCATGAGGCTCTGCACAACCACTAC
			ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
		SEQ ID NO: 1900	SEQ ID NO: 2057
	AA	DIQMTQSPSSLSASVGDRVTITCRASQGIRNELGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFVTYYCLQHNSYPFTFGQGTKVD VKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF NRGEC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAVIWYDASNKYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
	NA	SEQ ID NO: 330	SEQ ID NO: 487
		GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGGCATTAGAAATGAGTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCATCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAGTTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTTGTAACTTATTACTGTCT ACAGCATAATAGTTACCCATTCACTTTCGGCCA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTGATGGAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG

AGGGACCAAAGTGGATGTCAAACGAACGGTGG	GGACGATTTTTGGAGTGCTCTTGGGGGACTACT
CTGCACCATCTGTCTTCATCTTCCCGCCATCTGA	GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
TGAGCAGTTGAAATCTGGAACTGCCTCTGTTGT	CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC
GTGCCTGCTGAATAACTTCTATCCCAGAGAGGC	ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC
CAAAGTACAGTGGAAGGTGGATAACGCCCTCCA	GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC
ATCGGGTAACTCCCAGGAGAGTGTCACAGAGCA	CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC
GGACAGCAAGGACAGCACCTACAGCCTCAGCA	CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT
GCACCCTGACGCTGAGCAAAGCAGACTACGAGA	CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC
AACACAAAGTCTACGCCTGCGAAGTCACCCATC	GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
AGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCA	CAGACCTACATCTGCAACGTGAATCACAAGCCC
ACAGGGGAGAGTGT	AGCAACACCAAGGTGGACAAGAAAGTTGAGCC
	CAAATCTTGTGACAAAACTCACACATGCCCACC
	GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC
	AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC
	CCTCATGATCTCCCGGACCCCTGAGGTCACATG
	CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA
	GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
	GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA
	GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT
	CCTCACCGTCCTGCACCAGGACTGGCTGAATGG
	CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
	CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
	AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
	ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
	AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
	GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
	AGAGCAATGGGCAGCCGGAGAACAACTACAAG
	ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
	TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
	AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
	TCCGTGATGCATGAGGCTCTGCACAACCACTAC
	ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
SEQ ID NO: 1901	SEQ ID NO: 2058
AA	DIQMTQSPSSLSASVGDRVTITCRASQGIRNELGW
	YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE
	FTLTISSLQPEDFVTYYCLQHNSYPFTFGQGTKVD
	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM
	HWVRQAPGKGLEWVAVIWYDGSNKYYADAVKG
	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG

VKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF NRGEC	SEQ ID NO: 331	TIFGVLLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
NA	SEQ ID NO: 488	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTTGGAGTGCTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCCACC GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATG

CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT CCTCACCGTCCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT ACACCCTGCCCCCATCCCGGGAGGAGATGACCA AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGAACAACTACAAG ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA	SEQ ID NO: 2059	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
	SEQ ID NO: 1902	DIQMTQSPSSLSASVGDRVTITCRASQGIRNELGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFVTYYCLQHNSYPFTFGPGTKVDV KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC
		AA

iPS:360949	4H9.004.005	NA	SEQ ID NO: 332
			GACATTCAGATGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTGTAGGAGACAGAGTCACCATCACTT
			GCCGGGCAAGTCAGGGCATTAGAAATGAGTTAG
			GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA
			AACGCCTGATCTATGGTGCATCCAGTTTGCAAA
			GTGGGGTCCCATCAAGGTTCAGCGGCAGTGGAT
			CTGGGACAGAGTTCACTCTCACAATCAGCAGCC
			TGCAGCCTGAAGATTTTGTAACTTATTACTGTCT
			ACAGCATAATAGTTACCCATTCACTTTCGGCCA
			AGGGACCAAAGTGGATGTCAAACGAACGGTGG
			CTGCACCATCTGTCTTCATCTTCCCGCCATCTGA
			TGAGCAGTTGAAATCTGGAACTGCCTCTGTTGT
			GTGCCTGCTGAATAACTTCTATCCCAGAGAGGC
			CAAAGTACAGTGGAAGGTGGATAACGCCCTCCA
			ATCGGGTAACTCCCAGGAGAGTGTCACAGAGCA
			GGACAGCAAGGACAGCACCTACAGCCTCAGCA
			GCACCCTGACGCTGAGCAAAGCAGACTACGAGA
			AACACAAAGTCTACGCCTGCGAAGTCACCCATC
			AGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCA
			ACAGGGGAGAGTGT

SEQ ID NO: 489	
CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG	
GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT	
GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA	
TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC	
TGGAGTGGGTGGCAGTTATATGGTATGATGCAA	
GTAATAAATACTATGCAGACGCCGTGAAGGGCC	
GCTTCACCATCTCCAGAGACAATTCCAAGAACA	
CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG	
AGGACACGGCTGTGTATTACTGTGCGCGAGATG	
GGACGATTTTTGGAGTGCTCTTGGGGGACTACT	
GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG	
CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC	
ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC	
GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC	
CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC	
CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT	
CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC	
GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC	
CAGACCTACATCTGCAACGTGAATCACAAGCCC	
AGCAACACCAAGGTGGACAAGAAAGTTGAGCC	
CAAATCTTGTGACAAAACTCACACATGCCCACC	
GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC	
AGTCTTCCTCTTCCCCCCAAAACCCAAGGACAC	
CCTCATGATCTCCCGGACCCCTGAGGTCACATG	
CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA	
GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA	
GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA	
GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT	
CCTCACCGTCCTGCACCAGGACTGGCTGAATGG	
CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC	
CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA	
AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT	
ACACCCTGCCCCCATCCCGGGAGGAGATGACCA	
AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG	
GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG	

		AGAGCAATGGGCAGCCGGAGAACAACTACAAG
		ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
		TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
		AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
		TCCGTGATGCATGAGGCTCTGCACAACCACTAC
		ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1903	SEQ ID NO: 2060
AA	DIQMTQSPSSLSASVGDRVTITCRASQGIRNELGW YQQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFVTYYCLQHNSYPFTFGQGTKVD VKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF NRGEC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
	SEQ ID NO: 333	SEQ ID NO: 490
NA	GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGGCATTAGAAATGAGTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCATCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAGTTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTTGTAACTTATTACTGTCT ACAGCATAATAGTTACCCATTCACTTTCGGCCA AGGGACCAAAGTGGATGTCAAACGAACGGTGG CTGCACCATCTGTCTTCATCTTCCCGCCATCTGA TGAGCAGTTGAAATCTGGAACTGCCTCTGTTGT GTGCCTGCTGAATAACTTCTATCCCAGAGAGGC CAAAGTACAGTGGAAGGTGGATAACGCCCTCCA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATA GGACGATTTTTGGAGTGCTCTTGGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC

ATCGGGTAACTCCCAGGAGAGTGTCACAGAGCA GGACAGCAAGGACAGCACCTACAGCCTCAGCA GCACCCTGACGCTGAGCAAAGCAGACTACGAGA AACACAAAGTCTACGCCTGCGAAGTCACCCATC AGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCA ACAGGGGAGAGTGT	SEQ ID NO: 1904	CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCCACC GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATG CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT CCTCACCGTCCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT ACACCCTGCCCCCATCCCGGGAGGAGATGACCA AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGAACAACTACAAG ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
AA	DIQMTQSPSSLSASVGDRVTITCRASQGIRNELGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFVTYYCLQHNSYPFTFGQGTKVD VKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF NRGEC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVLLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED

		PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV
		SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK
		AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF
		YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
		SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS
		LSLSPGK
	SEQ ID NO: 334	SEQ ID NO: 491
	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
	CTGCATCTATAGGAGACAGAGTCACCATCACTT	GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
	GCCGGGCAAGTCAGGACATTAGAGATTATTTAG	GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA
	GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA	TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC
	AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA	TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
	GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT	GTAATGAAAACTATGCAGACGCCGTGAAGGGCC
	CTGGGACAGAATTCACTCTCACAATCAGCAGCC	GATTCACCATCTCCAGAGACAATTCCAAGAATA
	TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT	CGCTGTATCTGCAAATGAACAGCCTGAGAGTCG
	ACAGCATAATAATTACCCCTTCACTTTCGGCCAA	CGGACACGGCTGTGTATTATTGTGCGCGAGATG
	GGGACCAAAGTGGATATCAAACGAACGGTGGCT	GGACGATCTTTGGAGTGGTCTTGGGGGACTACT
	GCACCATCTGTCTTCATCTTCCCGCCATCTGATG	GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
	AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT	CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC
	GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA	ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC
	AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT	GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC
	CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG	CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC
	ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA	CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT
	CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC	CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC
	ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG	GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
	GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA	CAGACCTACATCTGCAACGTGAATCACAAGCCC
	GGGGAGAGTGT	AGCAACACCAAGGTGGACAAGAAAGTTGAGCC
		CAAATCTTGTGACAAAACTCACACATGCCCACC
		GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC
		AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC
		CCTCATGATCTCCCGGACCCCTGAGGTCACATG
		CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA
		GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
		GGTGCATAATGCCAAGACAAAGCCGCGTGTGAGGA
		GCAGTACGGCAGCACGTACCGTGTGGTCAGCGT
		CCTCACCGTCCTGCACCAGGACTGGCTGAATGG

		iPS:360955
		4B1.010
		NA

			CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
			CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
			AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
			ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
			AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
			GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
			AGAGCAATGGGCAGCCGGAGAACAACTACAAG
			ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
			TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
			AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
			TCCGTGATGCATGAGGCTCTGCACAACCACTAC
			ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
		SEQ ID NO: 1905	SEQ ID NO: 2062
	AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR GEC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDASNENYADAVKG RFTISRDNSKNTLYLQMNSLRVADTAVYYCARDG TIFGVVLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
	NA	SEQ ID NO: 335	SEQ ID NO: 492
		GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCGCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAATA CGCTGTATCTGCAAATGAACAGCCTGAGAGTCG
	4B1.011		
	iPS:360962		

ACAGCATAATAATTACCCCTTCACTTTCGGCCAA	CGGACACGGCTGTGTATTATTGTGCGCGAGATG
GGGACCAAAGTGGATATCAAACGAACGGTGGCT	GGACGATCTTTGGAGTGGTCTTGGGGGACTACT
GCACCATCTGTCTTCATCTTCCCGCCATCTGATG	GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT	CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC
GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA	ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC
AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT	GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC
CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG	CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC
ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA	CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT
CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC	CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC
ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG	GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA	CAGACCTACATCTGCAACGTGAATCACAAGCCC
GGGGAGAGTGT	AGCAACACCAAGGTGGACAAGAAAGTTGAGCC
	CAAATCTTGTGACAAAACTCACACATGCCCACC
	GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC
	AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC
	CCTCATGATCTCCCGGACCCCTGAGGTCACATG
	CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA
	GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
	GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA
	GCAGTACGGCAGCACGTACCGTGTGTCAGCGT
	CCTCACCGTCCTGCACCAGGACTGGCTGAATGG
	CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
	CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
	AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
	ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
	AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
	GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
	AGAGCAATGGGCAGCCGGAGAACAACTACAAG
	ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
	TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
	AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
	TCCGTGATGCATGAGGCTCTGCACAACCACTAC
	ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
SEQ ID NO: 1906	SEQ ID NO: 2063
AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY
	QQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTEFT
	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM
	HWVRQAPGKGLEWVAVIWYDASNENYADAVKG

iPS:309698				
4B1.012				
NA				
SEQ ID NO: 336			SEQ ID NO: 493	
GACATCCAGATGACCCAGTCTCCATCCTCCCTGT	LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK		CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG	RFTISRDNSKNTLYLQMNSLRVADTAVYYCARDG
CTGCATCTATAGGAGACAGAGTCACCATCACTT	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE		GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT	TIFGVVLGDYWGQGTLVTVSSASTKGPSVFPLAPS
GCCGGGCAAGTCAGGACATTAGAGATTATTTAG	AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS		GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA	SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS
GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA	TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR		TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC	GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN
AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA	GEC		TGGAGTGGGTGGCAGTTATATGGTATGATGCAA	VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL
GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT			GTAATGAAAACTATGCAGACGCCGTGAAGGGCC	GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED
CTGGGACAGAATTCACTCTCACAATCAGCAGCC			GATTCACCATCTCCAGAGACAATTCCAAGAATA	PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV
TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT			CGCTGTATCTGCAAATGAACAGCCTGAGAGTCG	SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK
ACAGCATAAATTAACCCCTTCACTTTCGGCCCT			CGGACACGGCTGTGTATTATTGTGCGCGAGATG	AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF
GGGACCAAAGTGGATATCAAACGAACGGTGGCT			GGACGATCTTTGGAGTGGTCTTGGGGGACTACT	YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
GCACCATCTGTCTTCATCTTCCCGCCATCTGATG			GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG	SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS
AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT			CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC	LSLSPGK
GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA			ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC	
AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT			GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC	
CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG			CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC	
ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA			CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT	
CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC			CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC	
ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG			GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC	
GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA			CAGACCTACATCTGCAACGTGAATCACAAGCCC	
GGGGAGAGTGT			AGCAACACCAAGGTGGACAAGAAAGTTGAGCC	
			CAAATCTTGTGACAAAACTCACACATGCCCACC	
			GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC	
			AGTCTTCCTCTTCCCCCCAAAACCCAAGGACAC	

CCTCATGATCTCCCGGACCCCCTGAGGTCACATG	
CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA	
GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA	
GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA	
GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT	
CCTCACCGTCCTGCACCAGGACTGGCTGAATGG	
CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC	
CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA	
AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT	
ACACCCTGCCCCCATCCCGGGAGGAGATGACCA	
AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG	
GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG	
AGAGCAATGGGCAGCCGGAGAACAACTACAAG	
ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC	
TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG	
AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC	
TCCGTGATGCATGAGGCTCTGCACAACCACTAC	
ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA	
SEQ ID NO: 2064	SEQ ID NO: 1907
QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY
HWVRQAPGKGLEWVAVIWYDASNENYADAVKG	QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFT
RFTISRDNSKNTLYLQMNSLRVADTAVYYCARDG	LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR
TIFGVVLGDYWGQGTLVTVSSASTKGPSVFPLAPS	TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA
SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS	KVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST
GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN	LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG
VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL	EC
GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED	AA
PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV	
SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK	
AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF	
YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY	
SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS	
LSLSPGK	

iPS:360974	4B1.013	NA	SEQ ID NO: 337
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTATAGGAGACAGAGTCACCATCACTT
			GCCGGGCAAGTCAGGACATTAGAGATTATTTAG
			GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA
			AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA
			GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT
			CTGGGACAGAATTCACTCTCACAATCAGCAGCC
			TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT
			ACAGCATAATAATTACCCCTTCACTTTCGGCCAA
			GGGACCAAAGTGGATATCAAACGAACGGTGGCT
			GCACCATCTGTCTTCATCTTCCCGCCATCTGATG
			AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT
			GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA
			AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT
			CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG
			ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA
			CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC
			ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG
			GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA
			GGGGAGAGTGT

SEQ ID NO: 494	
CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG	
GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT	
GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA	
TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC	
TGGAGTGGGTGGCAGTTATATGGTATGATGCAA	
GTAATGAAAACTATGCAGACTCCGTGAAGGGCC	
GATTCACCATCTCCAGAGACAATTCCAAGAATA	
CGCTGTATCTGCACATGAACAGCCTGAGAGTCG	
CGGACACGGCTGTGTATTATTGTGCGCGAGATG	
GGACGATCTTTGGAGTGGTCTTGGGGGACTACT	
GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG	
CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC	
ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC	
GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC	
CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC	
CCTGACCAGCGGCGTGCACACCTTCCGGCTGT	
CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC	
GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC	
CAGACCTACATCTGCAACGTGAATCACAAGCCC	
AGCAACACCAAGGTGGACAAGAAAGTTGAGCC	
CAAATCTTGTGACAAAACTCACACATGCCCACC	
GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC	
AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC	
CCTCATGATCTCCCGGACCCCTGAGGTCACATG	
CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA	
GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA	
GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA	
GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT	
CCTCACCGTCCTGCACCAGGACTGGCTGAATGG	
CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC	
CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA	
AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT	
ACACCCTGCCCCCATCCCGGGAGGAGATGACCA	
AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG	
GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG	

		AGAGCAATGGGCAGCCGGAGAACAACTACAAG
		ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
		TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
		AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
		TCCGTGATGCATGAGGCTCTGCACAACCACTAC
		ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1908	SEQ ID NO: 2065
AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR GEC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDASNENYADSVKG RFTISRDNSKNTLYLHMNSLRVADTAVYYCARDG TIFGVVLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
	SEQ ID NO: 338	SEQ ID NO: 495
NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATTACCCCTTCACTTTCGGCCAA GGGACCAAAGTGGATATCAAACGAACGGTGGCT GCACCATCTGTCTTCATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGGAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAATA CGCTGTATCTGCACATGAACAGCCTGAGAGTCG CGGACACGGCTGTGTATTATTGTGCGCGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC
	iPS:360978	
	4B1.014	

CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT	SEQ ID NO: 1909	CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCCACC GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATG CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT CCTCACCGTCCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT ACACCCTGCCCCCATCCCGGGAGGAGATGACCA AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGAACAACTACAAG ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
AA	SEQ ID NO: 2066	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDGSNENYADAVKG RFTISRDNSKNTLYLHMNSLRVADTAVYYCARDG TIFGVVLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED

		PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
	SEQ ID NO: 339	SEQ ID NO: 496
iPS:359785	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCAA GGGACCAAAGTGGATATCAAACGAACGGTGGCT GCACCATCTGTCTTCATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAATA CGCTGTATCTGCAAATGAACAGCCTGAGAGTCG AGGACACGGCTGTGTATTATTGTGCGCGAGATA GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCCACC GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATG CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA GGTGCATAATGCCAAGACAAAGCCGCGTGTGAGGA GCAGTACGGCAGCACGTACCGTGTGGTCAGCGT CCTCACCGTCCTGCACCAGGACTGGCTGAATGG
NA		
4B1.015		

			CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
			CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
			AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
			ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
			AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
			GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
			AGAGCAATGGGCAGCCGGAGAACAACTACAAG
			ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
			TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
			AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
			TCCGTGATGCATGAGGCTCTGCACAACCACTAC
			ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
		SEQ ID NO: 1910	SEQ ID NO: 2067
	AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR GEC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDASNENYADAVKG RFTISRDNSKNTLYLQMNSLRVEDTAVYYCARDR TIFGVVLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
		SEQ ID NO: 340	SEQ ID NO: 497
	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAATA CGCTGTATCTGCAAATGAACAGCCTGAGAGTCG
	4B1.016		
	iPS:360982		

ACAGCATAATAATTACCCCTTCACTTTCGGCCAA	AGGACACGGCTGTGTATTATTGTGCGCGAGATG	
GGGACCAAAGTGGATATCAAACGAACGGTGGCT	GGACGATCTTTGGAGTGGTCTTGGGGGACTACT	
GCACCATCTGTCTTCATCTTCCGCCATCTGATG	GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG	
AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT	CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC	
GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA	ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC	
AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT	GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC	
CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG	CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC	
ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA	CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT	
CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC	CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC	
ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG	GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC	
GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA	CAGACCTACATCTGCAACGTGAATCACAAGCCC	
GGGGAGAGTGT	AGCAACACCAAGGTGGACAAGAAAGTTGAGCC	
	CAAATCTTGTGACAAAACTCACACATGCCCACC	
	GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC	
	AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC	
	CCTCATGATCTCCCGGACCCCTGAGGTCACATG	
	CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA	
	GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA	
	GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA	
	GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT	
	CCTCACCGTCCTGCACCAGGACTGGCTGAATGG	
	CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC	
	CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA	
	AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT	
	ACACCCTGCCCCCATCCCGGGAGGAGATGACCA	
	AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG	
	GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG	
	AGAGCAATGGGCAGCCGGAGAACAACTACAAG	
	ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC	
	TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG	
	AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC	
	TCCGTGATGCATGAGGCTCTGCACAACCACTAC	
	ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA	
SEQ ID NO: 1911	SEQ ID NO: 2068	
AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM
	QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFT	HWVRQAPGKGLEWVAVIWYDASNENYADAVKG

iPS:335922	18F2	NA	LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR GEC	RFTISRDNSKNTLYLQMNSLRVEDTAVYYCARDG TIFGVVLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
		SEQ ID NO: 341	SEQ ID NO: 498	
		GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCACCAGAAACCAGGGAAAGCCCCTA AGCGCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGAACGGTGGCT GCACCATCTGTCTTCATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTGATGGAA GTAATGAAAACTATGCAGACTCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCACATGAACAGCCTGAGAGCCG CGGACACGGCTGTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCCACC GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC AGTCTTCCTCTTCCCCCCAAAACCCAAGGACAC

CCTCATGATCTCCCGGACCCCCTGAGGTCACATG CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT CCTCACCGTCCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT ACACCCTGCCCCCATCCCGGGAGGAGATGACCA AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGAACAACTACAAG ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA	SEQ ID NO: 2069
	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDGSNENYADSVKG RFTISRDNSKNTLYLHMNSLRAADTAVYYCARDG TIFGVVLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
	SEQ ID NO: 1912
	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YHQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC
	AA

iPS:360986		SEQ ID NO: 342	SEQ ID NO: 499
18F2.002			
NA		GACATCCAGATGACCCAGTCTCCATCCTCCCTGT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
		CTGCATCTATAGGAGACAGAGTCACCATCACTT	GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
		GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG	GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA
		GCTGGTATCAACAGAAACCAGGGAAAGCCCCTA	TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC
		AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA	TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
		GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT	GTAATGAAAACTATGCAGACGCCGTGAAGGGCC
		CTGGGACAGAATTCACTCTCACAATCAGCAGCC	GATTCACCATCTCCAGAGACAATTCCAAGAACA
		TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT	CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
		ACAGCATAATAATTACCCCTTCACTTTCGGCCCT	CGGACACGGCTGTGTATTACTGTGCGAGAGATG
		GGGACCAAAGTGGATATCAAACGAACGGTGGCT	GGACGATCTTTGGAGTGGTCTTGGGGGACTACT
		GCACCATCTGTCTTCATCTTCCCGCCATCTGATG	GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
		AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT	CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC
		GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA	ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC
		AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT	GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC
		CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG	CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC
		ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA	CCTGACCAGCGGCGTGCACACCTTCCGGCTGT
		CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC	CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC
		ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG	GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
		GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA	CAGACCTACATCTGCAACGTGAATCACAAGCCC
		GGGGAGAGTGT	AGCAACACCAAGGTGGACAAGAAAGTTGAGCC
			CAAATCTTGTGACAAAACTCACACATGCCCACC
			GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC
			AGTCTTCCTCTTCCCCCCAAAACCCAAGGACAC
			CCTCATGATCTCCCGGACCCCTGAGGTCACATG
			CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA
			GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
			GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA
			GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT
			CCTCACCGTCCTGCACCAGGACTGGCTGAATGG
			CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
			CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
			AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
			ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
			AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
			GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG

		AGAGCAATGGGCAGCCGGAGAACAACTACAAG
		ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
		TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
		AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
		TCCGTGATGCATGAGGCTCTGCACAACCACTAC
		ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1913	SEQ ID NO: 2070
AA	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDASNENYADAVKG RFTISRDNSKNTLYLQMNSLRAADTAVYYCARDG TIFGVVLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
	SEQ ID NO: 343	SEQ ID NO: 500
NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCAACAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGAACGGTGGCT GCACCATCTGTCTTCATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCACATGAACAGCCTGAGAGCCG CGGACACGGCTGTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC
	18F2.003	
	iPS:360995	

CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT	CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCCACC GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATG CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT CCTCACCGTCCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT ACACCCTGCCCCCATCCCGGGAGGAGATGACCA AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGAACAACTACAAG ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
SEQ ID NO: 1914	SEQ ID NO: 2071
AA	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDASNENYADAVKG RFTISRDNSKNTLYLHMNSLRAADTAVYYCARDG TIFGVVLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED

		PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
		SEQ ID NO: 344
iPS:36099	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCACCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGAACGGTGGCT GCACCATCTGTCTTCATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT
18F2.004		
		SEQ ID NO: 501
		CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG CGGACACGGCTGTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCCACC GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATG CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA GGTGCATAATGCCAAGACAAAGCCGCGTGTGAGGA GCAGTACGGCAGCACGTACCGTGTGGTCAGCGT CCTCACCGTCCTGCACCAGGACTGGCTGAATGG

iPS:361005	18F2.005		
	NA	AA	
	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT	SEQ ID NO: 345	SEQ ID NO: 1915
	CTGCATCTATAGGAGACAGAGTCACCATCACTT	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW	
	GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG	YHQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE	
	GCTGGTATCAACAGAAACCAGGGAAAGCCCCTA	FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI	
	AGCGCCTGATCTATGGTGCATCCAGTTTGCAAA	KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR	
	GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT	EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS	
	CTGGGACAGAATTCACTCTCACAATCAGCAGCC	STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN	
	TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT	RGEC	
	CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC	SEQ ID NO: 2072	SEQ ID NO: 502
	CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM	
	AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT	HWVRQAPGKGLEWVAVIWYDASNENYADAVKG	
	ACACCCTGCCCCCATCCCGGGAGGAGATGACCA	RFTISRDNSKNTLYLQMNSLRAADTAVYYCARDG	
	AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG	TIFGVVLGDYWGQGTLVTVSSASTKGPSVFPLAPS	
	GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG	SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS	
	AGAGCAATGGGCAGCCGGAGAACAACTACAAG	GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN	
	ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC	VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL	
	TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG	GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED	
	AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC	PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV	
	TCCGTGATGCATGAGGCTCTGCACAACCACTAC	SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK	
	ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA	AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF	
		YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY	
		SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS	
		LSLSPGK	

ACAGCATAATAATTACCCCTTCACTTTCGGCCCT	CGGACACGGCTGTGTATTACTGTGCGAGAGATG	
GGGACCAAAGTGGATATCAAACGAACGGTGGCT	GGACGATCTTTGGAGTGGTCTTGGGGGACTACT	
GCACCATCTGTCTTCATCTTCCCGCCATCTGATG	GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG	
AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT	CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC	
GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA	ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC	
AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT	GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC	
CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG	CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC	
ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA	CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT	
CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC	CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC	
ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG	GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC	
GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA	CAGACCTACATCTGCAACGTGAATCACAAGCCC	
GGGGAGAGTGT	AGCAACACCAAGGTGGACAAGAAAGTTGAGCC	
	CAAATCTTGTGACAAAACTCACACATGCCCACC	
	GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC	
	AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC	
	CCTCATGATCTCCCGGACCCCTGAGGTCACATG	
	CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA	
	GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA	
	GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA	
	GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT	
	CCTCACCGTCCTGCACCAGGACTGGCTGAATGG	
	CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC	
	CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA	
	AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT	
	ACACCCTGCCCCCATCCCGGGAGGAGATGACCA	
	AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG	
	GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG	
	AGAGCAATGGGCAGCCGGAGAACAACTACAAG	
	ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC	
	TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG	
	AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC	
	TCCGTGATGCATGAGGCTCTGCACAACCACTAC	
	ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA	
SEQ ID NO: 1916	SEQ ID NO: 2073	
AA	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM
	YQQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTE	HWVRQAPGKGLEWVAVIWYDASNENYADAVKG

FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC	SEQ ID NO: 346	RFTISRDNSKNTLYLQMNSLRAADTAVYYCARDG TIFGVVLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
	NA	SEQ ID NO: 503 CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTGATGCAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCACATGAACAGCCTGAGAGCCG CGGACACGGCTGTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCCACC GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC AGTCTTCCTCTTCCCCCCAAAACCCAAGGACAC
	18F2.006	
	iPS:361009	

CCTCATGATCTCCCGGACCCCCTGAGGTCACATG CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT CCTCACCGTCCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT ACACCCTGCCCCCATCCCGGGAGGAGATGACCA AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGAACAACTACAAG ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA	SEQ ID NO: 2074	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDASNENYADAVKG RFTISRDNSKNTLYLHMNSLRAADTAVYYCARDG TIFGVVLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
	SEQ ID NO: 1917	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YQQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC
		AA

iPS:361013		SEQ ID NO: 504
18F2.007		CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
		GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
		GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA
		TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC
		TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
		GTAATGAAAACTATGCAGACGCCGTGAAGGGCC
		GATTCACCATCTCCAGAGACAATTCCAAGAACA
		CGCTGTATCTGCACATGAACAGCCTGAGAGCCG
		CGGACACGGCTGTGTATTACTGTGCGAGAGATG
		GGACGATCTTTGGAGTGGTCTTGGGGGACTACT
		GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
		CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC
		ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC
		GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC
		CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC
		CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT
		CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC
		GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
		CAGACCTACATCTGCAACGTGAATCACAAGCCC
		AGCAACACCAAGGTGGACAAGAAAGTTGAGCC
		CAAATCTTGTGACAAAACTCACACATGCCCACC
		GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC
		AGTCTTCCTCTTCCCCCCAAAACCCAAGGACAC
		CCTCATGATCTCCCGGACCCCTGAGGTCACATG
		CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA
		GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
		GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA
		GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT
		CCTCACCGTCCTGCACCAGGACTGGCTGAATGG
		CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
		CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
		AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
		ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
		AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
		GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
NA		
		SEQ ID NO: 347
		GACATCCAGATGACCCAGTCTCCATCCTCCCTGT
		CTGCATCTATAGGAGACAGAGTCACCATCACTT
		GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG
		GCTGGTATCACCAGAAACCAGGGAAAGCCCCTA
		AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA
		GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT
		CTGGGACAGAATTCACTCTCACAATCAGCAGCC
		TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT
		ACAGCATAATAATTACCCCTTCACTTTCGGCCCT
		GGGACCAAAGTGGATATCAAACGAACGGTGGCT
		GCACCATCTGTCTTCATCTTCCCGCCATCTGATG
		AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT
		GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA
		AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT
		CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG
		ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA
		CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC
		ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG
		GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA
		GGGGAGAGTGT

		AGAGCAATGGGCAGCCGGAGAACAACTACAAG
		ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
		TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
		AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
		TCCGTGATGCATGAGGCTCTGCACAACCACTAC
		ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1918	SEQ ID NO: 2075
AA	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YHQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDASNENYADAVKG RFTISRDNSKNTLYLHMNSLRAADTAVYYCARDG TIFGVVLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
	SEQ ID NO: 348	SEQ ID NO: 505
NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCACCAGAAACCAGGGAAAGCCCCTA AGCGCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGAACGGTGGCT GCACCATCTGTCTTCATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG CGGACACGGCTGTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC
	18F2.008	
	iPS:361017	

CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT	CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCCACC GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATG CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT CCTCACCGTCCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT ACACCCTGCCCCCATCCCGGGAGGAGATGACCA AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGAACAACTACAAG ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
SEQ ID NO: 1919	SEQ ID NO: 2076
AA	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YHQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDASNENYADAVKG RFTISRDNSKNTLYLQMNSLRAADTAVYYCARDG TIFGVVLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED

		PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
	SEQ ID NO: 349	SEQ ID NO: 506
	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCAACAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGAACGGTGGCT GCACCATCTGTCTTCATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGGAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG CGGACACGGCTGTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCCACC GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATG CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA GGTGCATAATGCCAAGACAAAGCCGCGTGTGAGGA GCAGTACGGCAGCACGTACCGTGTGGTCAGCGT CCTCACCGTCCTGCACCAGGACTGGCTGAATGG
	NA	
	18F2.009	
	iPS:361021	

			CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
			CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
			AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
			ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
			AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
			GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
			AGAGCAATGGGCAGCCGGAGAACAACTACAAG
			ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
			TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
			AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
			TCCGTGATGCATGAGGCTCTGCACAACCACTAC
			ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
		SEQ ID NO: 1920	SEQ ID NO: 2077
	AA	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDGSNENYADAVKG RFTISRDNSKNTLYLQMNSLRAADTAVYYCARDG TIFGVVLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
		SEQ ID NO: 350	SEQ ID NO: 507
	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCAACAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCCCCAGGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACTATGCAGACTCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
	18F2.010		
	iPS:361028		

ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGAACGGTGGCT GCACCATCTGTCTTCATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT	SEQ ID NO: 1921	CGGACACGGCTGTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCCACC GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATG CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA GGTGCATAATGCCAAGACAAAGCCGCGTGTGAGGA GCAGTACGGCAGCACGTACCGTGTGGTCAGCGT CCTCACCGTCCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT ACACCCTGCCCCCATCCCGGGAGGAGATGACCA AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGAACAACTACAAG ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
AA	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDASNENYADSVKG

FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC	SEQ ID NO: 351	RFTISRDNSKNTLYLQMNSLRAADTAVYYCARDG TIFGVVLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
NA		
18F2.011		
iPS:360535		

CCTCATGATCTCCCGGACCCCCTGAGGTCACATG	
CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA	
GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA	
GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA	
GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT	
CCTCACCGTCCTGCACCAGGACTGGCTGAATGG	
CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC	
CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA	
AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT	
ACACCCTGCCCCCATCCCGGGAGGAGATGACCA	
AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG	
GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG	
AGAGCAATGGGCAGCCGGAGAACAACTACAAG	
ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC	
TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG	
AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC	
TCCGTGATGCATGAGGCTCTGCACAACCACTAC	
ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA	
SEQ ID NO: 2079	SEQ ID NO: 1922
QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW
HWVRQAPGKGLEWVAVIWYDASNENYADAVKG	YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE
RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR	FTLTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDI
TIFGVVLGDYWGQGTLVTVSSASTKGPSVFPLAPS	KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR
SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS	EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS
GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN	STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN
VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL	RGEC
GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED	AA
PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV	
SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK	
AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF	
YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY	
SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS	
LSLSPGK	

iPS:361035		SEQ ID NO: 352	SEQ ID NO: 509
18F2.012		GACATCCAGATGACCCAGTCTCCATCCTCCCTGT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
		CTGCATCTATAGGAGACAGAGTCACCATCACTT	GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
		GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG	GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA
		GCTGGTATCAACAGAAACCAGGGAAAGCCCCTA	TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC
		AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA	TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
		GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT	GTAATGAAAACTATGCAGACGCCGTGAAGGGCC
		CTGGGACAGAATTCACTCTCACAATCAGCAGCC	GATTCACCATCTCCAGAGACAATTCCAAGAACA
		TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT	CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
		ACAGCATAATAATTACCCCTTCACTTTCGGCCCT	AGGACACGGCTGTGTATTACTGTGCGAGAGATG
		GGGACCAAAGTGGATATCAAACGAACGGTGGCT	GGACGATCTTTGGAGTGGTCTTGGGGGACTACT
		GCACCATCTGTCTTCATCTTCCCGCCATCTGATG	GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
		AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT	CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC
		GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA	ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC
		AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT	GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC
		CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG	CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC
		ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA	CCTGACCAGCGGCGTGCACACCTTCCGGCTGT
		CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC	CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC
		ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG	GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
		GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA	CAGACCTACATCTGCAACGTGAATCACAAGCCC
		GGGGAGAGTGT	AGCAACACCAAGGTGGACAAGAAAGTTGAGCC
			CAAATCTTGTGACAAAACTCACACATGCCCACC
			GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC
			AGTCTTCCTCTTCCCCCCAAAACCCAAGGACAC
			CCTCATGATCTCCCGGACCCCTGAGGTCACATG
			CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA
			GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
			GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA
			GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT
			CCTCACCGTCCTGCACCAGGACTGGCTGAATGG
			CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
			CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
			AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
			ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
			AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
			GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG

		AGAGCAATGGGCAGCCGGAGAACAACTACAAG
		ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
		TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
		AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
		TCCGTGATGCATGAGGCTCTGCACAACCACTAC
		ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1923	SEQ ID NO: 2080
AA	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDASNENYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVVLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
	SEQ ID NO: 353	SEQ ID NO: 510
NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTAGCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTACGATGCATCCAATTTGGAAA CAGGGGTCCCATCAAGGTTCAGTGGAAGTGGAT CTGGGACAGATTTTAGTCTCACCATCAGCAGCC TGCAGCCTGAAGATTTTGCAACATATTACTGTCA ACAGTATGATATTCTCCTCACTTTCGGCGGAGG GACCAAGGTGGAGATCAAGCGAACGGTGGCTG CACCATCTGTCTTCATCTTCCCGCCATCTGATGA GCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGC CTGCTGAATAACTTCTATCCCAGAGAGGCCAAA GTACAGTGGAAGGTGGATAACGCCCTCCAATCG	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGTTATATGGTATGATGCA AGTAATAAATACTATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGGGACAATTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT AGGACGATTTTTGGAGTGGTTCTTGACTACTGG GGCCAGGGAACCCTGGTCACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC

GGTAACTCCCAGGAGAGTGTCACAGAGCAGGAC AGCAAGGACAGCACCTACAGCCTCAGCAGCACC CTGACGCTGAGCAAAGCAGACTACGAGAAACA CAAAGTCTACGCCTGCGAAGTCACCCATCAGGG CCTGAGCTCGCCCGTCACAAAGAGCTTCAACAG GGGAGAGTGT	GAACCGGTGACGGTGTCGTGGAACTCAGGCGCC CTGACCAGCGGCGTGCACACCTTCCCGGCTGTC CTACAGTCCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCCACC GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATG CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT CCTCACCGTCCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT ACACCCTGCCCCCATCCCGGGAGGAGATGACCA AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGAACAACTACAAG ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA	SEQ ID NO: 1924
		SEQ ID NO: 2081
AA	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW YQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTD FSLTISSLQPEDFATYYCQQYDILLTFGGGTKVEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR GEC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGM HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLDYWGQGTLVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE

		VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
		SEQ ID NO: 354
iPS:361039	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTAGCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTACGATGCATCCAATTTGGAAA CAGGGGTCCCATCAAGGTTCAGTGGAAGTGGAT CTGGGACAGATTTTAGTCTCACCATCAGCAGCC TGCAGCCTGAAGATTTTGCAACATATTACTGTCA ACAGTATGATATTCTCCTCACTTTCGGCGGAGG GACCAAGGTGGAGATCAAGCGAACGGTGGCTG CACCATCTGTCTTCATCTTCCCGCCATCTGATGA GCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGC CTGCTGAATAACTTCTATCCCAGAGAGGCCAAA GTACAGTGGAAGGTGGATAACGCCCTCCAATCG GGTAACTCCCAGGAGAGTGTCACAGAGCAGGAC AGCAAGGACAGCACCTACAGCCTCAGCAGCACC CTGACGCTGAGCAAAGCAGACTACGAGAAACA CAAAGTCTACGCCTGCGAAGTCACCCATCAGGG CCTGAGCTCGCCCGTCACAAAGAGCTTCAACAG GGGAGAGTGT
2F11.003		
		SEQ ID NO: 511
		CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGTTATATGGTATGATGCA AGTAATAAATACTATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGCGACAATTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT AGGACGATTTTTGGAGTGGTTCTTGACTACTGG GGCCAGGGAACCCTGGTCACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC GAACCGGTGACGGTGTCGTGGAACTCAGGCGCC CTGACCAGCGGCGTGCACACCTTCCCGGCTGTC CTACAGTCCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCCACC GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATG CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA GGTGCATAATGCCAAGACAAAGCCGCGTGTGAGGA GCAGTACGGCAGCACGTACCGTGTGGTCAGCGT CCTCACCGTCCTGCACCAGGACTGGCTGAATGG

			CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
			CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
			AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
			ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
			AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
			GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
			AGAGCAATGGGCAGCCGGAGAACAACTACAAG
			ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
			TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
			AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
			TCCGTGATGCATGAGGCTCTGCACAACCACTAC
			ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
		SEQ ID NO: 1925	SEQ ID NO: 2082
	AA	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW YQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTD FSLTISSLQPEDFATYYCQQYDILLTFGGGTKVEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR GEC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGM HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG RFTISSDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLDYWGQGTLVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
	NA	SEQ ID NO: 355	SEQ ID NO: 512
		GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCAGGGCGAGTCAGGACATTAGCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTACGATGCATCCAATTTGGAAA CAGGGGTCCCATCAAGGTTCAGTGGAAGTGGAT CTGGGACAGATTTTAGTCTCACCATCAGCAGCC TGCAGCCTGAAGATATTGCAACATATTACTGTC	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGTTATATGGTATGATGCA AGTAATAAATACTATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGGGACAATTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC
	2F11.004		
	iPS:361043		

AACAGTATGATATTCTCCTCACTTTCGGCGGAG	GAGGACACGGCTGTGTATTACTGTGCGAGAGAT
GGACCAAGGTGGAGATCAAGCGAACGGTGGCT	AGGACGATTTTTGGAGTGGTTCTTGACTACTGG
GCACCATCTGTCTTCATCTTCCCGCCATCTGATG	GGCCAGGGAACCCTGGTCACCGTCTCCTCAGCC
AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT	TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA
GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA	CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG
AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT	GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC
CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG	GAACCGGTGACGGTGTCGTGGAACTCAGGCGCC
ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA	CTGACCAGCGGCGTGCACACCTTCCCGGCTGTC
CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC	CTACAGTCCTCAGGACTCTACTCCCTCAGCAGC
ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG	GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA	CAGACCTACATCTGCAACGTGAATCACAAGCCC
GGGGAGAGTGT	AGCAACACCAAGGTGGACAAGAAAGTTGAGCC
	CAAATCTTGTGACAAAACTCACACATGCCCACC
	GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC
	AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC
	CCTCATGATCTCCCGGACCCCTGAGGTCACATG
	CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA
	GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
	GGTGCATAATGCCAAGACAAAGCCGCGTGTGAGGA
	GCAGTACGGCAGCACCGTACCGTCCTGTCGTC
	CCTCACCGTCCTGCACCAGGACTGGCTGAATGG
	CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
	CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
	AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
	ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
	AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
	GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
	AGAGCAATGGGCAGCCGGAGAACAACTACAAG
	ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
	TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
	AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
	TCCGTGATGCATGAGGCTCTGCACAACCACTAC
	ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
SEQ ID NO: 1926	SEQ ID NO: 2083
AA	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW YQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTD
	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGM HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG

FSLTISSLQPEDIATYYCQQYDILLTFGGGTKVEIKR	SEQ ID NO: 356	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR
TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT	TIFGVVLDYWGQGTLVTVSSASTKGPSVFPLAPSS
KVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST	CTGCATCTGTAGGAGACAGAGTCACCATCACTT	KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG
LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG	GCCAGGCGAGTCAGGACATTAGCAACTATTTAA	VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV
EC	ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA	NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG
	AGCTCCTGATCTACGATGCATCCAATTTGGAAA	GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
	CAGGGGTCCCATCAAGGTTCAGTGGAAGTGGAT	VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV
	CTGGGACAGATTTTAGTTTCACCATCAGCAGCCT	LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
	GCAGCCTGAAGATTTTGCAACATATTACTGTCA	KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP
	ACAGTATGATATTCTCCTCACTTTCGGCGGAGG	SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
	GACCAAGGTGGAGATCAAGCGAACGGTGGCTG	LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS
	CACCATCTGTCTTCATCTTCCCGCCATCTGATGA	LSPGK
	GCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGC	SEQ ID NO: 513
	CTGCTGAATAACTTCTATCCCAGAGAGGCCAAA	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG
	GTACAGTGGAAGGTGGATAACGCCCTCCAATCG	GTCCAGCCTGGGAGGGTCCCTGAGACTCTCCTGT
	GGTAACTCCCAGGAGAGTGTCACAGAGCAGGAC	GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC
	AGCAAGGACAGCACCTACAGCCTCAGCAGCACC	ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG
	CTGACGCTGAGCAAAGCAGACTACGAAAACA	CTGGAGTGGGTGGCAGTTATATGGTATGATGCA
	CAAAGTCTACGCCTGCGAAGTCACCCATCAGGG	AGTAATAAATACTATGCAGACGCCGTGAAGGGC
	CCTGAGCTCGCCCGTCACAAAGAGCTTCAACAG	CGATTCACCATCTCCAGGGACAATTCCAAGAAC
	GGGAGAGTGT	ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC
		GAGGACACGGCTGTGTATTACTGTGCGAGAGAT
		AGGACGATTTTTGGAGTGGTTCTTGACTACTGG
		GGCCAGGGAACCCTGGTCACCGTCTCCTCAGCC
		TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA
		CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG
		GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC
		GAACCGGTGACGGTGTCGTGGAACTCAGGCGCC
		CTGACCAGCGGCGTGCACACCTTCCCGGCTGTC
		CTACAGTCCTCAGGACTCTACTCCCTCAGCAGC
		GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
		CAGACCTACATCTGCAACGTGAATCACAAGCCC
		AGCAACACCAAGGTGGACAAGAAAGTTGAGCC
		CAAATCTTGTGACAAAACTCACACATGCCCACC
		GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC
		AGTCTTCCTCTTCCCCCCAAAACCCAAGGACAC

		iPS:361049
		2F11.005
		NA

	CCTCATGATCTCCCGGACCCCCTGAGGTCACATG
	CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA
	GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
	GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA
	GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT
	CCTCACCGTCCTGCACCAGGACTGGCTGAATGG
	CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
	CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
	AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
	ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
	AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
	GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
	AGAGCAATGGGCAGCCGGAGAACAACTACAAG
	ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
	TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
	AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
	TCCGTGATGCATGAGGCTCTGCACAACCACTAC
	ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 2084
SEQ ID NO: 1927	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGM
DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW	HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG
YQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTD	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR
FSFTISSLQPEDFATYYCQQYDILLTFGGGTKVEIK	TIFGVVLDYWGQGTLVTVSSASTKGPSVFPLAPSS
RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE	KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG
AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS	VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV
TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR	NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG
GEC	GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
	VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV
	LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
	KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP
	SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
	LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS
	LSPGK
AA	

iPS:361055	2F11.006	NA	SEQ ID NO: 357
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTGTAGGAGACAGAGTCACCATCACTT
			GCCAGGCGAGTCAGGACATTAGCAACTATTTAA
			ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA
			AGCTCCTGATCTACGATGCATCCAATTTGGAAA
			CAGGGGTCCCATCAAGGTTCAGTGGAAGTGGAT
			CTGGGACAGATTTTAGTCTCACCATCAGCAGCC
			TGCAGCCTGAAGATATTGCAACATATTACTGTC
			AACAGTATGATATTCTCCTCACTTTCGGCGGAG
			GGACCAAGGTGGAGATCAAGCGAACGGTGGCT
			GCACCATCTGTCTTCATCTTCCCGCCATCTGATG
			AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT
			GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA
			AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT
			CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG
			ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA
			CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC
			ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG
			GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA
			GGGGAGAGTGT

		SEQ ID NO: 514
		CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG
		GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
		GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC
		ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG
		CTGGAGTGGGTGGCAGTTATATGGTATGATGCA
		AGTAATAAATACTATGCAGACGCCGTGAAGGGC
		CGATTCACCATCTCCAGCGACAATTCCAAGAAC
		ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC
		GAGGACACGGCTGTGTATTACTGTGCGAGAGAT
		AGGACGATTTTTGGAGTGGTTCTTGACTACTGG
		GGCCAGGGAACCCTGGTCACCGTCTCCTCAGCC
		TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA
		CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG
		GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC
		GAACCGGTGACGGTGTCGTGGAACTCAGGCGCC
		CTGACCAGCGGCGTGCACACCTTCCCGGCTGTC
		CTACAGTCCTCAGGACTCTACTCCCTCAGCAGC
		GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
		CAGACCTACATCTGCAACGTGAATCACAAGCCC
		AGCAACACCAAGGTGGACAAGAAAGTTGAGCC
		CAAATCTTGTGACAAAACTCACACATGCCCACC
		GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC
		AGTCTTCCTCTTCCCCCCAAAACCCAAGGACAC
		CCTCATGATCTCCCGGACCCCTGAGGTCACATG
		CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA
		GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
		GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA
		GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT
		CCTCACCGTCCTGCACCAGGACTGGCTGAATGG
		CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
		CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
		AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
		ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
		AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
		GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG

		AGAGCAATGGGCAGCCGGAGAACAACTACAAG
		ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
		TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
		AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
		TCCGTGATGCATGAGGCTCTGCACAACCACTAC
		ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1928	SEQ ID NO: 2085
AA	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW YQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTD FSLTISSLQPEDIATYYCQQYDILLTFGGGTKVEIKR TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGM HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG RFTISSDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLDYWGQGTLVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
	SEQ ID NO: 358	SEQ ID NO: 515
NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTAGCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTACGATGCATCCAATTTGGAAA CAGGGGTCCCATCAAGGTTCAGTGGAAGTGGAT CTGGGACAGATTTTAGTTTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACATATTACTGTCA ACAGTATGATATTCTCCTCACTTTCGGCGGAGG GACCAAGGTGGAGATCAAGCGAACGGTGGCTG CACCATCTGTCTTCATCTTCCCGCCATCTGATGA GCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGC CTGCTGAATAACTTCTATCCCAGAGAGGCCAAA GTACAGTGGAAGGTGGATAACGCCCTCCAATCG	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGTTATATGGTATGATGCA AGTAATAAATACTATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGCGACAATTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT AGGACGATTTTTGGAGTGGTTCTTGACTACTGG GGCCAGGGAACCCTGGTCACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC
2F11.007		
iPS:361059		

GGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT		GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACGCCAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA	
	SEQ ID NO: 1929	SEQ ID NO: 2086
	AA	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFSFTISSLQPEDFATYYCQQYDILLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDASNKYYADAVKGRFTISSDNSKNTLYLQMNSLRAEDTAVYYCARDRTIFGVVLDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE

		VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
		SEQ ID NO: 516
		CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGTTATATGGTATGATGCA AGTAATAAATACTATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGGGACAATTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT AGGACGATTTTTGGAGTGGTTCTTGACTACTGG GGCCAGGGAACCCTGGTCACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC GAACCGGTGACGGTGTCGTGGAACTCAGGCGCC CTGACCAGCGGCGTGCACACCTTCCCGGCTGTC CTACAGTCCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCCACC GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATG CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA GGTGCATAATGCCAAGACAAAGCCGCGTGTGAGGA GCAGTACGGCAGCACGTACCGTGTGGTCAGCGT CCTCACCGTCCTGCACCAGGACTGGCTGAATGG
		SEQ ID NO: 359
		GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTAGCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTACGATGCATCCAATTTGGAAA CAGGGGTCCCATCAAGGTTCAGTGGAAGTGGAT CTGGGACAGATTTTAGTTTCACCATCAGCAGCCT GCAGCCTGAAGATATTGCAACATATTACTGTCA ACAGTATGATATTCTCCTCACTTTCGGCGGAGG GACCAAGGTGGAGATCAAGCGAACGGTGGCTG CACCATCTGTCTTCATCTTCCCGCCATCTGATGA GCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGC CTGCTGAATAACTTCTATCCCAGAGAGGCCAAA GTACAGTGGAAGGTGGATAACGCCCTCCAATCG GGTAACTCCCAGGAGAGTGTCACAGAGCAGGAC AGCAAGGACAGCACCTACAGCCTCAGCAGCACC CTGACGCTGAGCAAAGCAGACTACGAGAAACA CAAAGTCTACGCCTGCGAAGTCACCCATCAGGG CCTGAGCTCGCCCGTCACAAAGAGCTTCAACAG GGGAGAGTGT
	NA	
	2F11.008	
	iPS:361063	

			CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
			CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
			AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
			ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
			AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
			GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
			AGAGCAATGGGCAGCCGGAGAACAACTACAAG
			ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
			TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
			AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
			TCCGTGATGCATGAGGCTCTGCACAACCACTAC
			ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
		SEQ ID NO: 1930	SEQ ID NO: 2087
	AA	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW YQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTD FSFTISSLQPEDIATYYCQQYDILLTFGGGTKVEIKR TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGM HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLDYWGQGTLVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
	NA	SEQ ID NO: 360	SEQ ID NO: 517
		GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCAGGGCGAGTCAGGACATTAGCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTACGATGCATCCAATTTGGAAA CAGGGGTCCCATCAAGGTTCAGTGGAAGTGGAT CTGGGACAGATTTTAGTCTCACCATCAGCAGCC TGCAGCCTGAAGATTTTGCAACATATTACTGTCA	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGTTATATGGTATGATGCA AGTAATAAATACTATGCAGACTCCGTGAAGGGC CGATTCACCATCTCCAGGGACAATTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC
	2F11.009		
	iPS:359949		

ACAGTATGATATTCTCCTCACTTTCGGCGGAGG	GAGGACACGGCTGTGTATTACTGTGCGAGAGAT
GACCAAGGTGGAGATCAAGCGAACGGTGGCTG	AGGACGATTTTTGGAGTGGTTCTTGACTACTGG
CACCATCTGTCTTCATCTTCCCGCCATCTGATGA	GGCCAGGGAACCCTGGTCACCGTCTCCTCAGCC
GCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGC	TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA
CTGCTGAATAACTTCTATCCCAGAGAGGCCAAA	CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG
GTACAGTGGAAGGTGGATAACGCCCTCCAATCG	GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC
GGTAACTCCCAGGAGAGTGTCACAGAGCAGGAC	GAACCGGTGACGGTGTCGTGGAACTCAGGCGCC
AGCAAGGACAGCACCTACAGCCTCAGCAGCACC	CTGACCAGCGGCGTGCACACCTTCCCGGCTGTC
CTGACGCTGAGCAAAGCAGACTACGAGAAACA	CTACAGTCCTCAGGACTCTACTCCCTCAGCAGC
CAAAGTCTACGCCTGCGAAGTCACCCATCAGGG	GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
CCTGAGCTCGCCCGTCACAAAGAGCTTCAACAG	CAGACCTACATCTGCAACGTGAATCACAAGCCC
GGGAGAGTGT	AGCAACACCAAGGTGGACAAGAAAGTTGAGCC
	CAAATCTTGTGACAAAACTCACACATGCCCACC
	GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC
	AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC
	CCTCATGATCTCCCGGACCCCTGAGGTCACATG
	CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA
	GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
	GGTGCATAATGCCAAGACAAAGCCGCGTGTGAGGA
	GCAGTACGGCAGCACCGTACCGTCAGCGT
	CCTCACCGTCCTGCACCAGGACTGGCTGAATGG
	CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
	CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
	AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
	ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
	AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
	GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
	AGAGCAATGGGCAGCCGGAGAACAACTACAAG
	ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
	TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
	AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
	TCCGTGATGCATGAGGCTCTGCACAACCACTAC
	ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
SEQ ID NO: 1931	SEQ ID NO: 2088
AA	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW YQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTD
	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGM HWVRQAPGKGLEWVAVIWYDASNKYYADSVKG

		RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR
		TIFGVVLDYWGQGTLVTVSSASTKGPSVFPLAPSS
		KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG
		VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV
		NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG
		GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
		VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV
		LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
		KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP
		SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
		LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS
		LSPGK
	SEQ ID NO: 361	SEQ ID NO: 518
	NA	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG
		GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
		GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC
		ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG
		CTGGAGTGGGTGGCAGTTATATGGTATGATGGA
		AGTAATAAATACTATGCAGACGCCGTGAAGGGC
		CGATTCACCATCTCCAGGGACAATTCCAAGAAC
		ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC
		GAGGACACGGCTGTGTATTACTGTGCGAGAGAT
		AGGACGATTTTTGGAGTGGTTCTTGACTACTGG
		GGCCAGGGAACCCTGGTCACCGTCTCCTCAGCC
		TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA
		CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG
		GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC
		GAACCGGTGACGGTGTCGTGGAACTCAGGCGCC
		CTGACCAGCGGCGTGCACACCTTCCCGGCTGTC
		CTACAGTCCTCAGGACTCTACTCCCTCAGCAGC
		GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
		CAGACCTACATCTGCAACGTGAATCACAAGCCC
		AGCAACACCAAGGTGGACAAGAAAGTTGAGCC
		CAAATCTTGTGACAAAACTCACACATGCCCACC
		GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC
		AGTCTTCCTCTTCCCCCCAAAACCCAAGGACAC

	CCTCATGATCTCCCGGACCCCCTGAGGTCACATG
	CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA
	GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
	GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA
	GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT
	CCTCACCGTCCTGCACCAGGACTGGCTGAATGG
	CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
	CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
	AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
	ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
	AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
	GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
	AGAGCAATGGGCAGCCGGAGAACAACTACAAG
	ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
	TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
	AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
	TCCGTGATGCATGAGGCTCTGCACAACCACTAC
	ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 2089
SEQ ID NO: 1932	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGM
DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW	HWVRQAPGKGLEWVAVIWYDGSNKYYADAVKG
YQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTD	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR
FSLTISSLQPEDFATYYCQQYDILLTFGGGTKVEIK	TIFGVVLDYWGQGTLVTVSSASTKGPSVFPLAPSS
RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE	KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG
AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS	VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV
TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR	NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG
GEC	GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
	VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV
	LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
	KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP
	SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
	LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS
	LSPGK
AA	

jPS:359865		SEQ ID NO: 362	SEQ ID NO: 519
6H1.002		GACATCCAGATGACCCAGTCTCCATCCTCCCTGT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
		CTGCATCTATAGGAGACAGAGTCACCATCACTT	GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
		GCCGGGCAAGTCAGGACATTAGAGATTATTTAG	GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA
		GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA	TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC
		AGCGCCTGATCTATGGTGCATCCAGTTTGCAAA	TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
		GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT	GTAATAAATACTATGCAGACGCCGTGAAGGGCC
		CTGGGACAGAATTCACTCTCACAATCAGCAGCC	GCTTCACCATCTCCAGAGGACAATTCCAAGAACA
		TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT	CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
		ACAGCATAATAATTACCCCTTCACTTTCGGCCCT	AGGACACGGCTGTGTATTACTGTGCGCGAGATG
		GGGACCAAAGTGGATATCAAACGAACGGTGGCT	GGACGATTTTTGGAGTGCTCTTGGGGGACTACT
		GCACCATCTGTCTTCATCTTCCCGCCATCTGATG	GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
		AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT	CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC
		GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA	ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC
		AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT	GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC
		CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG	CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC
		ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA	CCTGACCAGCGGCGTGCACACCTTCCGGCTGT
		CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC	CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC
		ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG	GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
		GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA	CAGACCTACATCTGCAACGTGAATCACAAGCCC
		GGGGAGAGTGT	AGCAACACCAAGGTGGACAAGAAAGTTGAGCC
			CAAATCTTGTGACAAAACTCACACATGCCCACC
			GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC
			AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC
			CCTCATGATCTCCCGGACCCCTGAGGTCACATG
			CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA
			GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
			GGTGCATAATGCCAAGACAAAGCCGCGTGTGAGGA
			GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT
			CCTCACCGTCCTGCACCAGGACTGGCTGAATGG
			CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
			CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
			AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
			ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
			AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
			GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG

		AGAGCAATGGGCAGCCGGAGAACAACTACAAG
		ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
		TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
		AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
		TCCGTGATGCATGAGGCTCTGCACAACCACTAC
		ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1933	SEQ ID NO: 2090
AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
	SEQ ID NO: 363	SEQ ID NO: 520
NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCGCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGAACGGTGGCT GCACCATCTGTCTTCATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATA GGACGATTTTTGGAGTGCTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC

CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG	CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC
ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA	CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT
CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC	CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC
ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG	GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA	CAGACCTACATCTGCAACGTGAATCACAAGCCC
GGGGAGAGTGT	AGCAACACCAAGGTGGACAAGAAAGTTGAGCC
	CAAATCTTGTGACAAAACTCACACATGCCCACC
	GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC
	AGTCTTCCTCTTCCCCCCAAAACCCAAGGACAC
	CCTCATGATCTCCCGGACCCCTGAGGTCACATG
	CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA
	GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
	GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA
	GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT
	CCTCACCGTCCTGCACCAGGACTGGCTGAATGG
	CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
	CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
	AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
	ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
	AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
	GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
	AGAGCAATGGGCAGCCGGAGAACAACTACAAG
	ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
	TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
	AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
	TCCGTGATGCATGAGGCTCTGCACAACCACTAC
	ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
SEQ ID NO: 1934	SEQ ID NO: 2091
AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC
	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVLLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED

			PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
		SEQ ID NO: 364	SEQ ID NO: 521
iPS:359873	6H1.004	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCAA GGGACCAAAGTGGATATCAAACGAACGGTGGCT GCACCATCTGTCTTCATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTTGGAGTGCTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCCACC GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATG CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA GGTGCATAATGCCAAGACAAAGCCGCGTGTGAGGA GCAGTACGGCAGCACGTACCGTGTGGTCAGCGT CCTCACCGTCCTGCACCAGGACTGGCTGAATGG

			CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
			CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
			AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
			ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
			AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
			GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
			AGAGCAATGGGCAGCCGGAGAACAACTACAAG
			ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
			TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
			AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
			TCCGTGATGCATGAGGCTCTGCACAACCACTAC
			ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
		SEQ ID NO: 1935	SEQ ID NO: 2092
	AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM
		QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFT	HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG
		LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG
		RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE	TIFGVLLGDYWGQGTLVTVSSASTKGPSVFPLAPS
		AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS	SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS
		TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR	GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN
		GEC	VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL
			GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED
			PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV
			SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK
			AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF
			YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
			SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS
			LSLSPGK
		SEQ ID NO: 365	SEQ ID NO: 522
	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
		CTGCATCTATAGGAGACAGAGTCACCATCACTT	GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
		GCCGGGCAAGTCAGGACATTAGAGATTATTTAG	GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA
		GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA	TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC
		AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA	TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
		GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT	GTAATAAATACTATGCAGACGCCGTGAAGGGCC
		CTGGGACAGAATTCACTCTCACAATCAGCAGCC	GCTTCACCATCTCCAGAGACAATTCCAAGAACA
		TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT	CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG

ACAGCATAATAATTACCCCTTCACTTTCGGCCAA	AGGACACGGCTGTGTATTACTGTGCGCGAGATA	
GGGACCAAAGTGGATATCAAACGAACGGTGGCT	GGACGATTTTTGGAGTGCTCTTGGGGGACTACT	
GCACCATCTGTCTTCATCTTCCCGCCATCTGATG	GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG	
AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT	CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC	
GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA	ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC	
AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT	GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC	
CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG	CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC	
ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA	CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT	
CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC	CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC	
ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG	GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC	
GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA	CAGACCTACATCTGCAACGTGAATCACAAGCCC	
GGGGAGAGTGT	AGCAACACCAAGGTGGACAAGAAAGTTGAGCC	
	CAAATCTTGTGACAAAACTCACACATGCCCACC	
	GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC	
	AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC	
	CCTCATGATCTCCCGGACCCCTGAGGTCACATG	
	CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA	
	GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA	
	GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA	
	GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT	
	CCTCACCGTCCTGCACCAGGACTGGCTGAATGG	
	CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC	
	CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA	
	AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT	
	ACACCCTGCCCCCATCCCGGGAGGAGATGACCA	
	AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG	
	GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG	
	AGAGCAATGGGCAGCCGGAGAACAACTACAAG	
	ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC	
	TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG	
	AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC	
	TCCGTGATGCATGAGGCTCTGCACAACCACTAC	
	ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA	
SEQ ID NO: 1936	SEQ ID NO: 2093	
AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM
	QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFT	HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG

LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR GEC	SEQ ID NO: 366	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVLLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
	NA	SEQ ID NO: 523
	6H1.006	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGAACGGTGGCT GCACCATCTGTCTTCATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTGATGGAA GTAATAAATACTATGCAGACTCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTTGGAGTGCTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCCACC GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC AGTCTTCCTCTTCCCCCCAAAACCCAAGGACAC

CCTCATGATCTCCCGGACCCCCTGAGGTCACATG	
CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA	
GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA	
GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA	
GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT	
CCTCACCGTCCTGCACCAGGACTGGCTGAATGG	
CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC	
CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA	
AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT	
ACACCCTGCCCCCATCCCGGGAGGAGATGACCA	
AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG	
GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG	
AGAGCAATGGGCAGCCGGAGAACAACTACAAG	
ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC	
TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG	
AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC	
TCCGTGATGCATGAGGCTCTGCACAACCACTAC	
ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA	
SEQ ID NO: 2094	SEQ ID NO: 1937
QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY
HWVRQAPGKGLEWVAVIWYDGSNKYYADSVKG	QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFT
RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG	LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR
TIFGVLLGDYWGQGTLVTVSSASTKGPSVFPLAPS	TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA
SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS	KVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST
GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN	LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG
VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL	EC
GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED	AA
PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV	
SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK	
AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF	
YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY	
SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS	
LSLSPGK	

SEQ ID NO: 367			SEQ ID NO: 524
GACATCCAGATGACCCAGTCTCCATCCTCCCTGT			CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
CTGCATCTATAGGAGACAGAGTCACCATCACTT			GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
GCCGGGCAAGTCAGGACATTAGAGATTATTTAG			GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA
GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA			TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC
AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA			TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT			GTAATAAATACTATGCAGACTCCGTGAAGGGCC
CTGGGACAGAATTCACTCTCACAATCAGCAGCC			GCTTCACCATCTCCAGAGACAATTCCAAGAACA
TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT			CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
ACAGCATAATAATTACCCCTTCACTTTCGGCCCT			AGGACACGGCTGTGTATTACTGTGCGCGAGATG
GGGACCAAAGTGGATATCAAACGAACGGTGGCT			GGACGATTTTTGGAGTGCTCTTGGGGGACTACT
GCACCATCTGTCTTCATCTTCCCGCCATCTGATG			GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT			CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC
GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA			ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC
AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT			GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC
CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG			CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC
ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA			CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT
CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC			CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC
ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG			GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA			CAGACCTACATCTGCAACGTGAATCACAAGCCC
GGGGAGAGTGT			AGCAACACCAAGGTGGACAAGAAAGTTGAGCC
			CAAATCTTGTGACAAAACTCACACATGCCCACC
			GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC
			AGTCTTCCTCTTCCCCCCAAAACCCAAGGACAC
			CCTCATGATCTCCCGGACCCCTGAGGTCACATG
			CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA
			GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
			GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA
			GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT
			CCTCACCGTCCTGCACCAGGACTGGCTGAATGG
			CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
			CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
			AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
			ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
			AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
			GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG

		AGAGCAATGGGCAGCCGGAGAACAACTACAAG
		ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
		TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
		AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
		TCCGTGATGCATGAGGCTCTGCACAACCACTAC
		ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1938	SEQ ID NO: 2095
AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAVIWYDASNKYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
	SEQ ID NO: 368	SEQ ID NO: 525
NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGAACGGTGGCT GCACCATCTGTCTTCATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTGATGGAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTTGGAGTGCTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC

CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT	SEQ ID NO: 1939	CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCCACC GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC AGTCTTCCTCTTCCCCCCAAAACCCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATG CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT CCTCACCGTCCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT ACACCCTGCCCCCATCCCGGGAGGAGATGACCA AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGAACAACTACAAG ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
AA	SEQ ID NO: 2096	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAVIWYDGSNKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED

		PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
		SEQ ID NO: 369
iPS:361079	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTACGATGCTTCCAATTTGGAGCC AGGGGTCCCATCAAGGTTCAGTGGAAGTGGATC TGGGACAGATTTTACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACATATTACTGTCA ACAGTATGATGATCTATTCACTTTCGGCCCTGGG ACCAAAGTGGATATCAAACGAACGGTGGCTGCA CCATCTGTCTTCATCTTCCCGCCATCTGATGAGC AGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCT GCTGAATAACTTCTATCCCAGAGAGGCCAAAGT ACAGTGGAAGGTGGATAACGCCCTCCAATCGGG TAACTCCCAGGAGAGTGTCACAGAGCAGGACAG CAAGGACAGCACCTACAGCCTCAGCAGCACCCT GACGCTGAGCAAAGCAGACTACGAGAAACACA AAGTCTACGCCTGCGAAGTCACCCATCAGGGCC TGAGCTCGCCCGTCACAAAGAGCTTCAACAGGG GAGAGTGT
6AS.004.001		
		SEQ ID NO: 526
		CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCTCCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGCTATATGGTATGATGCAA ATAATAAATACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATC GGACGATTTTTGGAGTGGTCCTTGAGTACTGGG GCCAGGGAACCCTGGTCACCGTCTCCTCAGCCT CCACCAAGGGCCCATCGGTCTTCCCCCTGGCAC CCTCCTCCAAGAGCACCTCTGGGGGCACAGCGG CCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG AACCGGTGACGGTGTCGTGGAACTCAGGCGCCC TGACCAGCGGCGTGCACACCTTCCCGGCTGTCC TACAGTCCTCAGGACTCTACTCCCTCAGCAGCGT GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCACAAGCCCAG CAACACCAAGGTGGACAAGAAAGTTGAGCCCA AATCTTGTGACAAAACTCACACATGCCCACCGT GCCCAGCACCTGAACTCCTGGGGGGACCGTCAG TCTTCCTCTTCCCCCCAAAACCCAAGGACACCCT CATGATCTCCCGGACCCCTGAGGTCACATGCGT GGTGGTGGACGTGAGCCACGAAGACCCTGAGGT CAAGTTCAACTGGTACGTGGACGGCGTGGAGGT GCATAATGCCAAGACAAAGCCGTGTGAGGAGC AGTACGGCAGCACGTACCGTTGTGTCAGCGTCC TCACCGTCCTGCACCAGGACTGGCTGAATGGCA

		AGGAGTACAAGTGCAAGGTCTCCAACAAAGCCC
		TCCCAGCCCCCATCGAGAAAACCATCTCCAAAG
		CCAAAGGGCAGCCCCCGAGAACCACAGGTGTAC
		ACCCTGCCCCCATCCCGGGAGGAGATGACCAAG
		AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC
		TTCTATCCCAGCGACATCGCCGTGGAGTGGGAG
		AGCAATGGGCAGCCGGAGAACAACTACAAGAC
		CACGCCTCCCGTGCTGGACTCCGACGGCTCCTTC
		TTCCTCTATAGCAAGCTCACCGTGGACAAGAGC
		AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC
		GTGATGCATGAGGCTCTGCACAACCACTACACG
		CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1940	SEQ ID NO: 2097
	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM
	YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGSGTD	HWVRQPPGKGLEWVAAIWYDANNKYYADAVKG
	FTLTISSLQPEDFATYYCQQYDDLFTFGPGTKVDIK	RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR
	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE	TIFGVVLEYWGQGTLVTVSSASTKGPSVFPLAPSS
	AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS	KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG
	TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR	VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV
	GEC	NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG
		GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
		VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV
		LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
		KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP
		SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
		LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS
		LSPGK
AA	SEQ ID NO: 370	SEQ ID NO: 527
NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
	CTGCATCTGTGGGGGACAGAGTCACCATCACTT	GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
	GCCAGGCGAGTCAGGACATTACCAACTATTTAA	GCAGCGTCTGGATTCTCCTTCAGTAGCTATGGCA
	ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA	TGCACTGGGTCCGCCAGCCTCCAGGCAAGGGGC
	AACTCCTGATCTACGATGCTTCCAATTTGGAGCC	TGGAGTGGGTGGCAGCTATATGGTATGATGCAA
	AGGGGTCCCATCAAGGTTCAGTGGAAGTGGATC	ATAATAAATACTATGCAGACGCCGTGAAGGGCC
	TGGGACAGATTTTACTCTCACCATCAGCAGCCT	GATTCACCATCTCCAGAGACAGTTCCAAGAACA
	GCAGCCTGAAGATATTGCAACATATTACTGTCA	CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG

ACAGTATGATGATCTATTCACTTTCGGCCCTGGG	AGGACACGGCTGTGTATTACTGTGCGAGAGATC
ACCAAAGTGGATATCAAACGAACGGTGGCTGCA	GGACGATTTTTGGAGTGGTCCTTGAGTACTGGG
CCATCTGTCTTCATCTTCCCGCCATCTGATGAGC	GCCAGGGAACCCTGGTCACCGTCTCCTCAGCCT
AGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCT	CCACCAAGGGCCCATCGGTCTTCCCCCTGGCAC
GCTGAATAACTTCTATCCCAGAGAGGCCAAAGT	CCTCCTCCAAGAGCACCTCTGGGGGCACAGCGG
ACAGTGGAAGGTGGATAACGCCCTCCAATCGGG	CCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG
TAACTCCCAGGAGAGTGTCACAGAGCAGGACAG	AACCGGTGACGGTGTCGTGGAACTCAGGCGCCC
CAAGGACAGCACCTACAGCCTCAGCAGCACCCT	TGACCAGCGGCGTGCACACCTTCCCGGCTGTCC
GACGCTGAGCAAAGCAGACTACGAGAAACACA	TACAGTCCTCAGGACTCTACTCCCTCAGCAGCGT
AAGTCTACGCCTGCGAAGTCACCCATCAGGGCC	GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCA
TGAGCTCGCCCGTCACAAAGAGCTTCAACAGGG	GACCTACATCTGCAACGTGAATCACAAGCCCAG
GAGAGTGT	CAACACCAAGGTGGACAAGAAAGTTGAGCCCA
	AATCTTGTGACAAAACTCACACATGCCCACCGT
	GCCCAGCACCTGAACTCCTGGGGGGACCGTCAG
	TCTTCCTCTTCCCCCAAAACCCAAGGACACCCT
	CATGATCTCCCGGACCCCTGAGGTCACATGCGT
	GGTGGTGGACGTGAGCCACGAAGACCCTGAGGT
	CAAGTTCAACTGGTACGTGGACGGCGTGGAGGT
	GCATAATGCCAAGACAAAGCCGTGTGAGGAGC
	AGTACGGCAGCACGTACCGTTGTGTCAGCGTCC
	TCACCGTCCTGCACCAGGACTGGCTGAATGGCA
	AGGAGTACAAGTGCAAGGTCTCCAACAAAGCCC
	TCCCAGCCCCCATCGAGAAAACCATCTCCAAAG
	CCAAAGGGCAGCCCCGAGAACCACAGGTGTAC
	ACCCTGCCCCCATCCCGGGAGGAGATGACCAAG
	AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC
	TTCTATCCCAGCGACATCGCCGTGGAGTGGGAG
	AGCAATGGGCAGCCGGAGAACAACTACAAGAC
	CACGCCTCCCCGTGCTGGACTCCGACGGCTCCTTC
	TTCCTCTATAGCAAGCTCACCGTGGACAAGAGC
	AGGTGGCAGCAGGGGAACCGTCTTCTCATGCTCC
	GTGATGCATGAGGCTCTGCACAACCACTACACG
	CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
SEQ ID NO: 1941	SEQ ID NO: 2098
AA	
DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM
YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGSGTD	HWVRQPPGKGLEWVAAIWYDANNKYYADAVKG

FTLTISSLQPEDIATYYCQQYDDLFTFGPGTKVDIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR GEC	SEQ ID NO: 371	RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYWGQGTLVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
	NA	SEQ ID NO: 528
		CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCTCCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGCCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGCTATATGGTATGATGCAA ATAATAAATACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATC GGACGATTTTTGGAGTGGTCCTTGAGTACCTCG GCCAGGGAACCCTGGTCACCGTCTCCTCAGCCT CCACCAAGGGCCCATCGGTCTTCCCCCTGGCAC CCTCCTCCAAGAGCACCTCTGGGGGCACAGCGG CCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG AACCGGTGACGGTGTCGTGGAACTCAGGCGCCC TGACCAGCGGCGTGCACACCTTCCCGGCTGTCC TACAGTCCTCAGGACTCTACTCCCTCAGCAGCGT GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCACAAGCCCAG CAACACCAAGGTGGACAAGAAAGTTGAGCCCA AATCTTGTGACAAAACTCACACATGCCCACCGT GCCCAGCACCTGAACTCCTGGGGGGACCGTCAG TCTTCCTCTTCCCCCCAAAACCCAAGGACACCCT
	6A5.004.003	
	iPS:361091	

	CATGATCTCCCGGACCCCCTGAGGTCACATGCGT
	GGTGGTGGACGTGAGCCACGAAGACCCTGAGGT
	CAAGTTCAACTGGTACGTGGACGGCGTGGAGGT
	GCATAATGCCAAGACAAAGCCGTGTGAGGAGC
	AGTACGGCAGCACGTACCGTTGTGTCAGCGTCC
	TCACCGTCCTGCACCAGGACTGGCTGAATGGCA
	AGGAGTACAAGTGCAAGGTCTCCAACAAAGCCC
	TCCCAGCCCCCATCGAGAAAACCATCTCCAAAG
	CCAAAGGGCAGCCCCGAGAACCACAGGTGTAC
	ACCCTGCCCCCATCCCGGGAGGAGATGACCAAG
	AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC
	TTCTATCCCAGCGACATCGCCGTGGAGTGGGAG
	AGCAATGGGCAGCCGGAGAACAACTACAAGAC
	CACGCCTCCCCGTGCTGGACTCCGACGGCTCCTTC
	TTCCTCTATAGCAAGCTCACCGTGGACAAGAGC
	AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC
	GTGATGCATGAGGCTCTGCACAACCACTACACG
	CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 2099
SEQ ID NO: 1942	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM
DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW	HWVRQPPGKGLEWVAAIWYDANNKYYADAVKG
YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGSGTD	RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR
FTLTISSLQPEDFATYYCQQYDDLFTFGPGTKVDIK	TIFGVVLEYLGQGTLVTVSSASTKGPSVFPLAPSSK
RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE	STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV
AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS	HTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR	HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP
GEC	SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
AA	KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVL
	TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
	GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS
	DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL
	TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL
	SPGK

		SEQ ID NO: 372	SEQ ID NO: 529
iPS:361095	6A5.004.004	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
		CTGCATCTGTGGGGGACAGAGTCACCATCACTT	GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
		GCCAGGCGAGTCAGGACATTACCAACTATTTAA	GCAGCGTCTGGATTCTCCTTCAGTAGCTATGGCA
		ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA	TGCACTGGGTCCGCCAGCCTCCAGGCAAGGGGC
		AACTCCTGATCTACGATGCTTCCAATTTGGAGCC	TGGAGTGGGTGGCAGCTATATGGTATGATGCAA
		AGGGGTCCCATCAAGGTTCAGTGGAAGTGGATC	ATAATAAATACTATGCAGACGCCGTGAAGGGCC
		TGGGACAGATTTTACTTTCACCATCAGCAGCCTG	GATTCACCATCTCCAGAGACAGTTCCAAGAACA
		CAGCCTGAAGATTTTTGCAACATATTACTGTCAA	CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
		CAGTATGATGATCTATTCACTTTCGGCCCTGGGA	AGGACACGGCTGTGTATTACTGTGCGAGAGATC
		CCAAAGTGGATATCAACGAACGGTGGCTGCAC	GGACGATTTTTGGAGTGGTCCTTGAGTACTGGG
		CATCTGTCTTCATCTTCCCGCCATCTGATGAGCA	GCCAGGGAACCCTGGTCACCGTCTCCTCAGCCT
		GTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTG	CCACCAAGGGCCCATCGGTCTTCCCCCTGGCAC
		CTGAATAACTTCTATCCCAGAGAGGCCAAAGTA	CCTCCTCCAAGAGCACCTCTGGGGGCACAGCGG
		CAGTGGAAGGTGGATAACGCCCTCCAATCGGGT	CCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG
		AACTCCCAGGAGAGTGTGTCACAGAGCAGGACAG	AACCGGTGACGGTGTCGTGGAACTCAGGCGCCC
		CAAGGACAGCACCTACAGCCTCAGCAGCACCCT	TGACCAGCGGCGTGCACACCTTCCCGGCTGTCC
		GACGCTGAGCAAAGCAGACTACGAGAAACACA	TACAGTCCTCAGGACTCTACTCCCTCAGCAGCGT
		AAGTCTACGCCTGCGAAGTCACCCATCAGGGCC	GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCA
		TGAGCTCGCCCGTCACAAAGAGCTTCAACAGGG	GACCTACATCTGCAACGTGAATCACAAGCCCAG
		GAGAGTGT	CAACACCAAGGTGGACAAGAAAGTTGAGCCCA
			AATCTTGTGACAAAACTCACACATGCCCACCGT
			GCCCAGCACCTGAACTCCTGGGGGGACCGTCAG
			TCTTCCTCTTCCCCCCAAAACCCAAGGACACCCT
			CATGATCTCCCGGACCCCTGAGGTCACATGCGT
			GGTGGTGGACGTGAGCCACGAAGACCCTGAGGT
			CAAGTTCAACTGGTACGTGGACGGCGTGGAGGT
			GCATAATGCCAAGACAAAGCCGTGTGAGGAGC
			AGTACGGCAGCACGTACCGTTGTGTCAGCGTCC
			TCACCGTCCTGCACCAGGACTGGCTGAATGGCA
			AGGAGTACAAGTGCAAGGTCTCCAACAAAGCCC
			TCCCAGCCCCCATCGAGAAAACCATCTCCAAAG
			CCAAAGGGCAGCCCCGAGAACCACAGGTGTAC
			ACCCTGCCCCCATCCCGGGAGGAGATGACCAAG
			AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC
			TTCTATCCCAGCGACATCGCCGTGGAGTGGGAG

		AGCAATGGGCAGCCGGAGAACAACTACAAGAC CACGCCTCCCGTGCTGGACTCCGACGGCTCCTTC TTCCTCTATAGCAAGCTCACCGTGGACAAGAGC AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC GTGATGCATGAGGCTCTGCACAACCACTACACG CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1943	SEQ ID NO: 2100
AA	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGSGTD FTFTISSLQPEDFATYYCQQYDDLFTFGPGTKVDIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR GEC	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAAIWYDANNKYYADAVKG RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYWGQGTLVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
	SEQ ID NO: 373	SEQ ID NO: 530
NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTACGATGCTTCCAATTTGGAGCC AGGGGTCCCATCAAGGTTCAGTGGAAGTGGATC TGGGACAGATTTTACTCTCACCATCAGCAGCCT GCAGCCTGAAGATATTGCAACATATTACTGTCA ACAGTATGATGATCTATTCACTTTCGGCCCTGGG ACCAAAGTGGATATCAAACGAACGGTGGCTGCA CCATCTGTCTTCATCTTCCCGCCATCTGATGAGC	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCTCCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGCTATATGGTATGATGCAA ATAATAAATACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATC GGACGATTTTTGGAGTGGTCCTTGAGTACCTCG GCCAGGGAACCCTGGTCACCGTCTCCTCAGCCT
6A5.004.005		
iPS:361101		

AGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCT		CCACCAAGGGCCCATCGGTCTTCCCCCTGGCAC
GCTGAATAACTTCTATCCCAGAGAGGCCAAAGT		CCTCCTCCAAGAGCACCTCTGGGGGCACAGCGG
ACAGTGGAAGGTGGATAACGCCCTCCAATCGGG		CCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG
TAACTCCCAGGAGAGTGTCACAGAGCAGGACAG		AACCGGTGACGGTGTCGTGGAACTCAGGCGCCC
CAAGGACAGCACCTACAGCCTCAGCAGCACCCT		TGACCAGCGGCGTGCACACCTTCCCGGCTGTCC
GACGCTGAGCAAAGCAGACTACGAGAAACACA		TACAGTCCTCAGGACTCTACTCCCTCAGCAGCGT
AAGTCTACGCCTGCGAAGTCACCCATCAGGGCC		GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCA
TGAGCTCGCCCGTCACAAAGAGCTTCAACAGGG		GACCTACATCTGCAACGTGAATCACAAGCCCAG
GAGAGTGT		CAACACCAAGGTGGACAAGAAAGTTGAGCCCA
		AATCTTGTGACAAAACTCACACATGCCCACCGT
		GCCCAGCACCTGAACTCCTGGGGGGACCGTCAG
		TCTTCCTCTTCCCCCAAAACCCAAGGACACCCT
		CATGATCTCCCGGACCCCTGAGGTCACATGCGT
		GGTGGTGGACGTGAGCCACGAAGACCCTGAGGT
		CAAGTTCAACTGGTACGTGGACGGCGTGGAGGT
		GCATAATGCCAAGACAAAGCCGTGTGAGGAGC
		AGTACGGCAGCACGTACCGTTGTGTCAGCGTCC
		TCACCGTCCTGCACCAGGACTGGCTGAATGGCA
		AGGAGTACAAGTGCAAGGTCTCCAACAAAGCCC
		TCCCAGCCCCCATCGAGAAAACCATCTCCAAAG
		CCAAAGGGCAGCCCCGAGAACCACAGGTGTAC
		ACCCTGCCCCCATCCCGGGAGGAGATGACCAAG
		AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC
		TTCTATCCCAGCGACATCGCCGTGGAGTGGGAG
		AGCAATGGGCAGCCGGAGAACAACTACAAGAC
		CACGCCTCCCGTGCTGGACTCCGACGGCTCCTTC
		TTCCTCTATAGCAAGCTCACCGTGGACAAGAGC
		AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC
		GTGATGCATGAGGCTCTGCACAACCACTACACG
		CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
SEQ ID NO: 1944		SEQ ID NO: 2101
AA	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM
	YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGSGTD	HWVRQPPGKGLEWVAAIWYDANNKYYADAVKG
	FTLTISSLQPEDIATYYCQQYDDLFTFGPGTKVDIK	RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR
	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE	TIFGVVLEYLGQGTLVTVSSASTKGPSVFPLAPSSK
	AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS	STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV

TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR GEC	SEQ ID NO: 374	HTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVL TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL SPGK
	NA	SEQ ID NO: 531
		GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTACGATGCTTCCAATTTGGAGCC AGGGGTCCCATCAAGGTTCAGTGGAAGTGGATC TGGGACAGATTTTACTTTCACCATCAGCAGCCTG CAGCCTGAAGATTTTGCAACATATTACTGTCAA CAGTATGATGATCTATTCACTTTCGGCCCTGGGA CCAAAGTGGATATCAAACGAACGGTGGCTGCAC CATCTGTCTTCATCTTCCCGCCATCTGATGAGCA GTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTG CTGAATAACTTCTATCCCAGAGAGGCCAAAGTA CAGTGGAAGGTGGATAACGCCCTCCAATCGGGT AACTCCCAGGAGAGTGTCACAGAGCAGGACAG CAAGGACAGCACCTACAGCCTCAGCAGCACCCT GACGCTGAGCAAAGCAGACTACGAGAAACACA AAGTCTACGCCTGCGAAGTCACCCATCAGGGCC TGAGCTCGCCCGTCACAAAGAGCTTCAACAGGG GAGAGTGT	

		GCATAATGCCAAGACAAAGCCGTGTGAGGAGC
		AGTACGGCAGCACGTACCGTTGTGTCAGCGTCC
		TCACCGTCCTGCACCAGGACTGGCTGAATGGCA
		AGGAGTACAAGTGCAAGGTCTCCAACAAAGCCC
		TCCCAGCCCCCATCGAGAAAACCATCTCCAAAG
		CCAAAGGGCAGCCCCGAGAACCACAGGTGTAC
		ACCCTGCCCCCATCCCGGGAGGAGATGACCAAG
		AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC
		TTCTATCCCAGCGACATCGCCGTGGAGTGGGAG
		AGCAATGGGCAGCCGGAGAACAACTACAAGAC
		CACGCCTCCCGTGCTGGACTCCGACGGCTCCTTC
		TTCCTCTATAGCAAGCTCACCGTGGACAAGAGC
		AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC
		GTGATGCATGAGGCTCTGCACAACCACTACACG
		CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1945	SEQ ID NO: 2102
	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM
	YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGSGTD	HWVRQPPGKGLEWVAAIWYDANNKYYADAVKG
	FTFTISSLQPEDFATYYCQQYDDLFTFGPGTKVDIK	RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR
	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE	TIFGVVLEYLGQGTLVTVSSASTKGPSVFPLAPSSK
	AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS	STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV
	TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR	HTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
	GEC	HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP
AA		SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
		KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVL
		TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
		GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS
		DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL
		TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL
		SPGK
	SEQ ID NO: 375	SEQ ID NO: 532
NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
	CTGCATCTGTGGGGGACAGAGTCACCATCACTT	GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
	GCCAGGCGAGTCAGGACATTACCAACTATTTAA	GCAGCGTCTGGATTCTCCTTCAGTAGCTATGGCA
	ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA	TGCACTGGGTCCGCCAGCCTCCAGGCAAGGGGC
	AACTCCTGATCTACGATGCTTCCAATTTGGAGCC	TGGAGTGGGTGGCAGCTATATGGTATGATGCAA

ATAATAAATACTATGCAGACGCCGTGAAGGGCC	AGGGGTCCCATCAAGGTTCAGTGGAAGTGGATC		
GATTCACCATCTCCAGAGACAGTTCCAAGAACA	TGGGACAGATTTTACTTTCACCATCAGCAGCCTG		
CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG	CAGCCTGAAGATATTGCAACATATTACTGTCAA		
AGGACACGGCTGTGTATTACTGTGCGAGAGATC	CAGTATGATGATCTATTCACTTTCGGCCCTGGGA		
GGACGATTTTTTGGAGTGGTCCTTGAGTACTGGG	CCAAAGTGGATATCAAACGAACGGTGGCTGCAC		
GCCAGGGAACCCTGGTCACCGTCTCCTCAGCCT	CATCTGTCTTCATCTTCCCGCCATCTGATGAGCA		
CCACCAAGGGCCCATCGGTCTTCCCCCTGGCAC	GTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTG		
CCTCCTCCAAGAGCACCTCTGGGGGCACAGCGG	CTGAATAACTTCTATCCCAGAGAGGCCAAAGTA		
CCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG	CAGTGGAAGGTGGATAACGCCCTCCAATCGGGT		
AACCGGTGACGGTGTCGTGGAACTCAGGCGCCC	AACTCCCAGGAGAGTGTCACAGAGCAGGACAG		
TGACCAGCGGCGTGCACACCTTCCCGGCTGTCC	CAAGGACAGCACCTACAGCCTCAGCACCCCT		
TACAGTCCTCAGGACTCTACTCCCTCAGCAGCGT	GACGCTGAGCAAAGCAGACTACGAGAAACACA		
GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCA	AAGTCTACGCCTGCGAAGTCACCCATCAGGGCC		
GACCTACATCTGCAACGTGAATCACAAGCCCAG	TGAGCTCGCCCGTCACAAAGAGCTTCAACAGGG		
CAACACCAAGGTGGACAAGAAAGTTGAGCCCA	GAGAGTGT		
AATCTTGTGACAAAACTCACACATGCCCACCGT			
GCCCAGCACCTGAACTCCTGGGGGGACCGTCAG			
TCTTCCTCTTCCCCCAAAACCCAAGGACACCCT			
CATGATCTCCCGGACCCCTGAGGTCACATGCGT			
GGTGGTGGACGTGAGCCACGAAGACCCTGAGGT			
CAAGTTCAACTGGTACGTGGACGGCGTGGAGGT			
GCATAATGCCAAGACAAAGCCGTGTGAGGAGC			
AGTACGGCAGCACGTACCGTTGTGTCAGCGTCC			
TCACCGTCCTGCACCAGGACTGGCTGAATGGCA			
AGGAGTACAAGTGCAAGGTCTCCAACAAAGCCC			
TCCCAGCCCCCATCGAGAAAACCATCTCCAAAG			
CCAAAGGGCAGCCCCGAGAACCACAGGTGTAC			
ACCCTGCCCCCATCCCGGGAGGAGATGACCAAG			
AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC			
TTCTATCCCAGCGACATCGCCGTGGAGTGGGAG			
AGCAATGGGCAGCCGGAGAACAACTACAAGAC			
CACGCCTCCCGTGCTGGACTCCGACGGCTCCTTC			
TTCCTCTATAGCAAGCTCACCGTGGACAAGAGC			
AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC			
GTGATGCATGAGGCTCTGCACAACCACTACACG			
CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA			

		iPS;361113
		6A5.004.008
AA	SEQ ID NO: 1946	SEQ ID NO: 2103
	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGSGTD FTFTISSLQPEDIATYYCQQYDDLFTFGPGTKVDIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR GEC	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAAIWYDANNKYYADAVKG RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYWGQGTLVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
NA	SEQ ID NO: 376	SEQ ID NO: 533
	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTACGATGCTTCCAATTTGGAGCC AGGGGTCCCATCAAGGTTCAGTGGAAGTGGATC TGGGACAGATTTTACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACATATTACTGTCA ACAGTATGATGATCTATTCACTTTCGGCCCTGGG ACCAAAGTGGATATCAAACGAACGGTGGCTGCA CCATCTGTCTTCATCTTCCCGCCATCTGATGAGC AGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCT GCTGAATAACTTCTATCCCAGAGAGGCCAAAGT ACAGTGGAAGGTGGATAACGCCCTCCAATCGGG TAACTCCCAGGAGAGTGTCACAGAGCAGGACAG CAAGGACAGCACCTACAGCCTCAGCAGCACCCT GACGCTGAGCAAAGCAGACTACGAGAAACACA AAGTCTACGCCTGCGAAGTCACCCATCAGGGCC TGAGCTCGCCCGTCACAAAGAGCTTCAACAGGG GAGAGTGT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCTCCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGCTATATGGTATGATGGAA ATAATAAATACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATC GGACGATTTTTGGAGTGGTCCTTGAGTACTGGG GCCAGGGAACCCTGGTCACCGTCTCCTCAGCCT CCACCAAGGGCCCATCGGTCTTCCCCCTGGCAC CCTCCTCCAAGAGCACCTCTGGGGGCACAGCGG CCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG AACCGGTGACGGTGTCGTGGAACTCAGGCGCCC TGACCAGCGGCGTGCACACCTTCCCGGCTGTCC TACAGTCCTCAGGACTCTACTCCCTCAGCAGCGT GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCACAAGCCCAG CAACACCAAGGTGGACAAGAAAGTTGAGCCCA

AATCTTGTGACAAAACTCACACATGCCCACCGT GCCCAGCACCTGAACTCCTGGGGGGACCGTCAG TCTTCCTCTTCCCCCAAAACCCAAGGACACCCT CATGATCTCCCGGACCCCTGAGGTCACATGCGT GGTGGTGGACGTGAGCCACGAAGACCCTGAGGT CAAGTTCAACTGGTACGTGGACGGCGTGGAGGT GCATAATGCCAAGACAAAGCCGTGTGAGGAGC AGTACGGCAGCACGTACCGTTGTGTCAGCGTCC TCACCGTCCTGCACCAGGACTGGCTGAATGGCA AGGAGTACAAGTGCAAGGTCTCCAACAAAGCCC TCCCAGCCCCCATCGAGAAAACCATCTCCAAAG CCAAAGGGCAGCCCCGAGAACCACAGGTGTAC ACCCTGCCCCCATCCCGGGAGGAGATGACCAAG AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC TTCTATCCCAGCGACATCGCCGTGGAGTGGGAG AGCAATGGGCAGCCGGAGAACAACTACAAGAC CACGCCTCCCCGTGCTGGACTCCGACGGCTCCTTC TTCCTCTATAGCAAGCTCACCGTGGACAAGAGC AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC GTGATGCATGAGGCTCTGCACAACCACTACACG CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA	SEQ ID NO: 2104 QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAAIWYDGNNKYYADAVKG RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYWGQGTLVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
	AA

		SEQ ID NO: 377	SEQ ID NO: 534
iPS:361120		GACATCCAGATGACCCAGTCTCCATCCTCCCTGT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
		CTGCATCTGTGGGGGACAGAGTCACCATCACTT	GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
		GCCAGGCGAGTCAGGACATTACCAACTATTTAA	GCAGCGTCTGGATTCTCCTTCAGTAGCTATGGCA
		ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA	TGCACTGGGTCCGCCAGCCTCCAGGCAAGGGGC
		AACTCCTGATCTACGATGCTTCCAATTTGGAGCC	TGGAGTGGGTGGCAGCTATATGGTATGATGCAA
		AGGGGTCCCATCAAGGTTCAGTGGAAGTGGATC	ATAATAAATACTATGCAGACTCCGTGAAGGGCC
		TGGGACAGATTTTACTCTCACCATCAGCAGCCT	GATTCACCATCTCCAGAGACAGTTCCAAGAACA
		GCAGCCTGAAGATTTTTGCAACATATTACTGTCA	CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
		ACAGTATGATGATCTATTCACTTTCGGCCCTGGG	AGGACACGGCTGTGTATTACTGTGCGAGAGATC
		ACCAAAGTGGATATCAAACGAACGGTGGCTGCA	GGACGATTTTTGGAGTGGTCCTTGAGTACTGGG
		CCATCTGTCTTCATCTTCCCGCCATCTGATGAGC	GCCAGGGAACCCTGGTCACCGTCTCCTCAGCCT
		AGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCT	CCACCAAGGGCCCATCGGTCTTCCCCCTGGCAC
		GCTGAATAACTTCTATCCCAGAGAGGCCAAAGT	CCTCCTCCAAGAGCACCTCTGGGGGCACAGCGG
		ACAGTGGAAGGTGGATAACGCCCTCCAATCGGG	CCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG
		TAACTCCCAGGAGAGTGTCACAGAGCAGGACAG	AACCGGTGACGGTGTCGTGGAACTCAGGCGCCC
		CAAGGACAGCACCTACAGCCTCAGCAGCACCCT	TGACCAGCGGCGTGCACACCTTCCCGGCTGTCC
		GACGCTGAGCAAAGCAGACTACGAGAAACACA	TACAGTCCTCAGGACTCTACTCCCTCAGCAGCGT
		AAGTCTACGCCTGCGAAGTCACCCATCAGGGCC	GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCA
		TGAGCTCGCCCGTCACAAAGAGCTTCAACAGGG	GACCTACATCTGCAACGTGAATCACAAGCCCAG
		GAGAGTGT	CAACACCAAGGTGGACAAGAAAGTTGAGCCCA
			AATCTTGTGACAAAACTCACACATGCCCACCGT
			GCCCAGCACCTGAACTCCTGGGGGGACCGTCAG
			TCTTCCTCTTCCCCCCAAAACCCAAGGACACCCT
			CATGATCTCCCGGACCCCTGAGGTCACATGCGT
			GGTGGTGGACGTGAGCCACGAAGACCCTGAGGT
			CAAGTTCAACTGGTACGTGGACGGCGTGGAGGT
			GCATAATGCCAAGACAAAGCCGTGTGAGGAGC
			AGTACGGCAGCACGTACCGTTGTGTCAGCGTCC
			TCACCGTCCTGCACCAGGACTGGCTGAATGGCA
			AGGAGTACAAGTGCAAGGTCTCCAACAAAGCCC
			TCCCAGCCCCCATCGAGAAAACCATCTCCAAAG
			CCAAAGGGCAGCCCCGAGAACCACAGGTGTAC
			ACCCTGCCCCCATCCCGGGAGGAGATGACCAAG
			AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC
			TTCTATCCCAGCGACATCGCCGTGGAGTGGGAG

		AGCAATGGGCAGCCGGAGAACAACTACAAGAC
		CACGCCTCCCGTGCTGGACTCCGACGGCTCCTTC
		TTCCTCTATAGCAAGCTCACCGTGGACAAGAGC
		AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC
		GTGATGCATGAGGCTCTGCACAACCACTACACG
		CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1948	SEQ ID NO: 2105
AA	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGSGTD FTLTISSLQPEDFATYYCQQYDDLFTFGPGTKVDIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR GEC	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAAIWYDANNKYYADSVKG RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYWGQGTLVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
	SEQ ID NO: 378	SEQ ID NO: 535
NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTACGATGCTTCCAATTTGGAGCC AGGGGTCCCATCAAGGTTCAGTGGAAGTGGATC TGGGACAGATTTTACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACATATTACTGTCA ACAGTATGATGATCTATTCACTTTCGGCCAAGG GACCAAAGTGGATATCAAACGAACGGTGGCTGC ACCATCTGTCTTCATCTTCCCGCCATCTGATGAG CAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCC TGCTGAATAACTTCTATCCCAGAGAGGCCAAAG TACAGTGGAAGGTGGATAACGCCCTCCAATCGG	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCTCCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGCTATATGGTATGATGCAA ATAATAAATACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATC GGACGATTTTTGGAGTGGTCCTTGAGTACTGGG GCCAGGGAACCCTGGTCACCGTCTCCTCAGCCT CCACCAAGGGCCCATCGGTCTTCCCCCTGGCAC CCTCCTCCAAGAGCACCTCTGGGGGCACAGCGG CCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG
		6A5.004.010
		iPS:359896

GTAACTCCCAGGAGAGTGTCACAGAGCAGGACA GCAAGGACAGCACCTACAGCCTCAGCAGCACCC TGACGCTGAGCAAAGCAGACTACGAGAAACAC AAAGTCTACGCCTGCGAAGTCACCCATCAGGGC CTGAGCTCGCCCGTCACAAAGAGCTTCAACAGG GGAGAGTGT	SEQ ID NO: 1949	AACCGGTGACGGTGTCGTGGAACTCAGGCGCCC TGACCAGCCGGCGTGCACACCTTCCCGGCTGTCC TACAGTCCTCAGGACTCTACTCCCTCAGCAGCGT GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCACAAGCCCAG CAACACCAAGGTGGACAAGAAAGTTGAGCCCA AATCTTGTGACAAAACTCACACATGCCCACCGT GCCCAGCACCTGAACTCCTGGGGGGACCGTCAG TCTTCCTCTTCCCCCAAAACCCAAGGACACCCT CATGATCTCCCGGACCCCTGAGGTCACATGCGT GGTGGTGGACGTGAGCCACGAAGACCCTGAGGT CAAGTTCAACTGGTACGTGGACGGCGTGGAGGT GCATAATGCCAAGACAAAGCCGTGTGAGGAGC AGTACGGCAGCACGTACCGTTGTGTCAGCGTCC TCACCGTCCTGCACCAGGACTGGCTGAATGGCA AGGAGTACAAGTGCAAGGTCTCCAACAAAGCCC TCCCAGCCCCCATCGAGAAAACCATCTCCAAAG CCAAAGGGCAGCCCCGAGAACCACAGGTGTAC ACCCTGCCCCCATCCCGGGAGGAGATGACCAAG AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC TTCTATCCCAGCGACATCGCCGTGGAGTGGGAG AGCAATGGGCAGCCGGAGAACAACTACAAGAC CACGCCTCCCGTGCTGGACTCCGACGGCTCCTTC TTCCTCTATAGCAAGCTCACCGTGGACAAGAGC AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC GTGATGCATGAGGCTCTGCACAACCACTACACG CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
AA	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGSGTD FTLTISSLQPEDFATYYCQQYDDLFTFGQGTKVDI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAAIWYDANNKYYADAVKG RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYWGQGTLVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE

		VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
		SEQ ID NO: 536
	SEQ ID NO: 379	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCTCCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGCTATATGGTATGATGCAA ATAATAAATACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATC GGACGATTTTTGGAGTGGTCCTTGAGTACCTCG GCCAGGGAACCCTGGTCACCGTCTCCTCAGCCT CCACCAAGGGCCCATCGGTCTTCCCCCTGGCAC CCTCCTCCAAGAGCACCTCTGGGGGCACAGCGG CCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG AACCGGTGACGGTGTCGTGGAACTCAGGCGCCC TGACCAGCGGCGTGCACACCTTCCCGGCTGTCC TACAGTCCTCAGGACTCTACTCCCTCAGCAGCGT GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCACAAGCCCAG CAACACCAAGGTGGACAAGAAAGTTGAGCCCA AATCTTGTGACAAAACTCACACATGCCCACCGT GCCCAGCACCTGAACTCCTGGGGGGACCGTCAG TCTTCCTCTTCCCCCCAAAACCCAAGGACACCCT CATGATCTCCCGGACCCCTGAGGTCACATGCGT GGTGGTGGACGTGAGCCACGAAGACCCTGAGGT CAAGTTCAACTGGTACGTGGACGGCGTGGAGGT GCATAATGCCAAGACAAAGCCGCGTGTGAGGAGC AGTACGGCAGCACGTACCGTGTGGTCAGCGTCC TCACCGTCCTGCACCAGGACTGGCTGAATGGCA
	NA	
	6AS.004.011	
	iPS:359890	

			AGGAGTACAAGTGCAAGGTCTCCAACAAAGCCC
			TCCCAGCCCCCATCGAGAAAACCATCTCCAAAG
			CCAAAGGGCAGCCCCGAGAACCACAGGTGTAC
			ACCCTGCCCCCATCCCGGGAGGAGATGACCAAG
			AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC
			TTCTATCCCAGCGACATCGCCGTGGAGTGGGAG
			AGCAATGGGCAGCCGGAGAACAACTACAAGAC
			CACGCCTCCCGTGCTGGACTCCGACGGCTCCTTC
			TTCCTCTATAGCAAGCTCACCGTGGACAAGAGC
			AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC
			GTGATGCATGAGGCTCTGCACAACCACTACACG
			CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
		SEQ ID NO: 1950	SEQ ID NO: 2107
	AA	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGSGTD FTLTISSLQPEDFATYYCQQYDDLFTFGQGTKVDI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAAIWYDANNKYYADAVKG RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYLGQGTLVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVL TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL SPGK
		SEQ ID NO: 380	SEQ ID NO: 537
	NA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT GCAGGGCCAGTCAGATTTTTACCAGCACCTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCAGGCTCCTCATCTATGGTGCATCCAGCAGGG CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG GGTCTGGGACAGACTTCACTCTCACCATCAGCA GATTGGAGCCTGAAGATTTTGCAGTGTATTACT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCAGTTTCAGTAGCTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGA CTGGAGTGGGTGGCAGTTATATGGTATGATGCA AGTAATAAATACTATGCAGACTCCGTGAAGGGC CGATTCACCATCTCCAGAGACAATTCCAAGAAC ACGCTGTTTCTGCAAGTGAACAGCCTGAGAGCC

GTCAGCAGTATGGTAGCTCACCTCGCTTCGGCC	GAGGACACGGCTGTGTATTACTGTGCGAGAGGG
AAGGGACACGACTGGAGATTAAACGAACGGTG	ATTACGATTTTTGGTCATGGGTTTGAATATTGGG
GCTGCACCATCTGTCTTCATCTTCCCGCCATCTG	GCCAGGGAACCCTGGTCACCGTCTCCTCAGCCT
ATGAGCAGTTGAAATCTGGAACTGCCTCTGTTG	CCACCAAGGGCCCATCGGTCTTCCCCCTGGCAC
TGTGCCTGCTGAATAACTTCTATCCCAGAGAGG	CCTCCTCCAAGAGCACCTCTGGGGGCACAGCGG
CCAAAGTACAGTGGAAGGTGGATAACGCCCTCC	CCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG
AATCGGGTAACTCCCAGGAGAGTGTCACAGAGC	AACCGGTGACGGTGTCGTGGAACTCAGGCGCCC
AGGACAGCAAGGACAGCACCTACAGCCTCAGC	TGACCAGCGGCGTGCACACCTTCCCGGCTGTCC
AGCACCCTGACGCTGAGCAAAGCAGACTACGAG	TACAGTCCTCAGGACTCTACTCCCTCAGCAGCGT
AAACACAAAGTCTACGCCTGCGAAGTCACCCAT	GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCA
CAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTC	GACCTACATCTGCAACGTGAATCACAAGCCCAG
AACAGGGGAGAGTGT	CAACACCAAGGTGGACAAGAAAGTTGAGCCCA
	AATCTTGTGACAAAACTCACACATGCCCACCGT
	GCCCAGCACCTGAACTCCTGGGGGGACCGTCAG
	TCTTCCTCTTCCCCCAAAACCCAAGGACACCCT
	CATGATCTCCCGGACCCCTGAGGTCACATGCGT
	GGTGGTGGACGTGAGCCACGAAGACCCTGAGGT
	CAAGTTCAACTGGTACGTGGACGGCGTGGAGGT
	GCATAATGCCAAGACAAAGCCGTGTGAGGAGC
	AGTACGGCAGCACGTACCGTTGTGTCAGCGTCC
	TCACCGTCCTGCACCAGGACTGGCTGAATGGCA
	AGGAGTACAAGTGCAAGGTCTCCAACAAAGCCC
	TCCCAGCCCCCATCGAGAAAACCATCTCCAAAG
	CCAAAGGGCAGCCCCGAGAACCACAGGTGTAC
	ACCCTGCCCCCATCCCGGGAGGAGATGACCAAG
	AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC
	TTCTATCCCAGCGACATCGCCGTGGAGTGGGAG
	AGCAATGGGCAGCCGGAGAACAACTACAAGAC
	CACGCCTCCCCGTGCTGGACTCCGACGGCTCCTTC
	TTCCTCTATAGCAAGCTCACCGTGGACAAGAGC
	AGGTGGCAGCAGGGGAACCGTCTTCTCATGCTCC
	GTGATGCATGAGGCTCTGCACAACCACTACACG
	CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
SEQ ID NO: 1951	SEQ ID NO: 2108
AA	EIVLTQSPGTLSLSPGERATLSCRASQIFTSTYLAW
	YQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF
	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM
	HWVRQAPGKGLEWVAVIWYDASNKYYEDAVKG

TLTISRLEPEDFAVYYCQQYGSSPRFGQGTRLEIKR TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC	SEQ ID NO: 381	RFTISRDNSKNTLFLQVNSLRAEDTAVYYCARGITI FGHGFEYWGQGTLVTVSSASTKGPSVFPLAPSSKS TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP GK
NA	SEQ ID NO: 538	
GAAATTGTGTTGACGCAGTCTCCAGGCACCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT GCAGGGCCAGTCAGATTTTTACCAGCACCTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCAGGCTCCTCATCTATGGTGCATCCAGCAGGG CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG GGTCTGGGACAGACTTCACTCTCACCATCAGCA GATTGGAGCCTGAAGATTTTGCAGTGTATTACT GTCAGCAGTATGGTAGCTCACCTCGCTTCGGCC AAGGGACACGACTGGAGATTAAACGAACGGTG GCTGCACCATCTGTCTTCATCTTCCCGCCATCTG ATGAGCAGTTGAAATCTGGAACTGCCTCTGTTG TGTGCCTGCTGAATAACTTCTATCCCAGAGAGG CCAAAGTACAGTGGAAGGTGGATAACGCCCTCC AATCGGGTAACTCCCAGGAGAGTGTCACAGAGC AGGACAGCAAGGACAGCACCTACAGCCTCAGC AGCACCCTGACGCTGAGCAAAGCAGACTACGAG AAACACAAAGTCTACGCCTGCGAAGTCACCCAT CAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTC AACAGGGGAGAGTGT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCAGTTTCAGTAGCTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGA CTGGAGTGGGTGGCAGTTATATGGTATGATGGA AGTAATAAATACTATGCAGACTCCGTGAAGGGC CGATTCACCATCTCCAGAGACAATTCCAAGAAC ACGCTGTTTCTGCAAGTGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGGG ATTACGATTTTTGGTCATGGGTTTGAATATTGGG GCCAGGGAACCCTGGTCACCGTCTCCTCAGCCT CCACCAAGGGCCCATCGGTCTTCCCCCTGGCAC CCTCCTCCAAGAGCACCTCTGGGGGCACAGCGG CCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG AACCGGTGACGGTGTCGTGGAACTCAGGCGCCC TGACCAGCGGCGTGCACACCTTCCCGGCTGTCC TACAGTCCTCAGGACTCTACTCCCTCAGCAGCGT GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCACAAGCCCAG CAACACCAAGGTGGACAAGAAAGTTGAGCCCA AATCTTGTGACAAAACTCACACATGCCCACCGT GCCCAGCACCTGAACTCCTGGGGGGACCGTCAG TCTTCCTCTTCCCCCCAAAACCCAAGGACACCCT

CATGATCTCCCGGACCCCCTGAGGTCACATGCGT GGTGGTGGACGTGAGCCACGAAGACCCTGAGGT CAAGTTCAACTGGTACGTGGACGGCGTGGAGGT GCATAATGCCAAGACAAAGCCGTGTGAGGAGC AGTACGGCAGCACGTACCGTTGTGTCAGCGTCC TCACCGTCCTGCACCAGGACTGGCTGAATGGCA AGGAGTACAAGTGCAAGGTCTCCAACAAAGCCC TCCCAGCCCCCATCGAGAAAACCATCTCCAAAG CCAAAGGGCAGCCCCGAGAACCACAGGTGTAC ACCCTGCCCCCATCCCGGGAGGAGATGACCAAG AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC TTCTATCCCAGCGACATCGCCGTGGAGTGGGAG AGCAATGGGCAGCCGGAGAACAACTACAAGAC CACGCCTCCCCGTGCTGGACTCCGACGGCTCCTTC TTCCTCTATAGCAAGCTCACCGTGGACAAGAGC AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC GTGATGCATGAGGCTCTGCACAACCACTACACG CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA	SEQ ID NO: 2109
	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQAPGKGLEWVAVIWYDGSNKYYEDSVKG RFTISRDNSKNTLFLQVNSLRAEDTAVYYCARGITI FGHGFEYWGQGTLVTVSSASTKGPSVFPLAPSSKS TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP GK
	EIVLTQSPGTLSLSPGERATLSCRASQIFTSTYLAW YQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF TLTISRLEPEDFAVYYCQQYGSSPRFGQGTRLEIKR TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC
	AA

iPS:361158	2A11.004	NA	SEQ ID NO: 382
			GAAATTGTGTTGACGCAGTCTCCAGGCACCCTG
			TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT
			GCAGGGCCAGTCAGATTTTTACCAGCACCTACT
			TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC
			CCAGGCTCCTCATCTATGGTGCATCCAGCAGGG
			CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG
			GGTCTGGGACAGACTTCACTCTCACCATCAGCA
			GATTGGAGCCTGAAGATTTTGCAGTGTATTACT
			GTCAGCAGTATGGTAGCTCACCTCGCTTCGGCC
			AAGGGACACGACTGGAGATTAAACGAACGGTG
			GCTGCACCATCTGTCTTCATCTTCCCGCCATCTG
			ATGAGCAGTTGAAATCTGGAACTGCCTCTGTTG
			TGTGCCTGCTGAATAACTTCTATCCCAGAGAGG
			CCAAAGTACAGTGGAAGGTGGATAACGCCCTCC
			AATCGGGTAACTCCCAGGAGAGTGTCACAGAGC
			AGGACAGCAAGGACAGCACCTACAGCCTCAGC
			AGCACCCTGACGCTGAGCAAAGCAGACTACGAG
			AAACACAAAGTCTACGCCTGCGAAGTCACCCAT
			CAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTC
			AACAGGGGAGAGTGT

		AGCAATGGGCAGCCGGAGAACAACTACAAGAC
		CACGCCTCCCGTGCTGGACTCCGACGGCTCCTTC
		TTCCTCTATAGCAAGCTCACCGTGGACAAGAGC
		AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC
		GTGATGCATGAGGCTCTGCACAACCACTACACG
		CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1953	SEQ ID NO: 2110
AA	EIVLTQSPGTLSLSPGERATLSCRASQIFTSTYLAW YQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF TLTISRLEPEDFAVYYCQQYGSSPRFGQGTRLEIKR TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQAPGKGLEWVAVIWYDGSNKYYEDAVKG RFTISRDNSKNTLFLQVNSLRAEDTAVYYCARGITI FGHGFEYWGQGTLVTVSSASTKGPSVFPLAPSSKS TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP GK
	SEQ ID NO: 383	SEQ ID NO: 540
NA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT GCAGGGCCAGTCAGATTTTTACCAGCACCTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCAGGCTCCTCATCTATGGTGCATCCAGCAGGG CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG GGTCTGGGACAGACTTCACTCTCACCATCAGCA GATTGGAGCCTGAAGATTTTGCAGTGTATTACT GTCAGCAGTATGGTAGCTCACCTCGCTTCGGCC AAGGGACACGACTGGAGATTAAACGAACGGTG GCTGCACCATCTGTCTTCATCTTCCCGCCATCTG ATGAGCAGTTGAAATCTGGAACTGCCTCTGTTG TGTGCCTGCTGAATAACTTCTATCCCAGAGAGG CCAAAGTACAGTGGAAGGTGGATAACGCCCTCC	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCAGTTTCAGTAGCTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGA CTGGAGTGGGTGGCAGTTATATGGTATGATGCA AGTAATAAATACTATGAAGACTCCGTGAAGGGC CGATTCACCATCTCCAGAGACAATTCCAAGAAC ACGCTGTTTCTGCAAGTGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGGG ATTACGATTTTTGGTCATGGGTTTGAATATTGGG GCCAGGGAACCCTGGTCACCGTCTCCTCAGCCT CCACCAAGGGCCCATCGGTCTTCCCCCTGGCAC CCTCCTCCAAGAGCACCTCTGGGGGCACAGCGG CCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG
		2A11.005
		iPS:361165

AATCGGGTAACTCCCAGGAGAGTGTCACAGAGC AGGACAGCAAGGACAGCACCTACAGCCTCAGC AGCACCCTGACGCTGAGCAAAGCAGACTACGAG AAACACAAAGTCTACGCCTGCGAAGTCACCCAT CAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTC AACAGGGGAGAGTGT	SEQ ID NO: 1954	AA
	EIVLTQSPGTLSLSPGERATLSCRASQIFTSTYLAW YQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF TLTISRLEPEDFAVYYCQQYGSSPRFGQGTRLEIKR TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC	
AACCGGTGACGGTGTCGTGGAACTCAGGCGCCC TGACCAGCGGCGTGCACACCTTCCCGGCTGTCC TACAGTCCTCAGGACTCTACTCCCTCAGCAGCGT GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCACAAGCCCAG CAACACCAAGGTGGACAAGAAAGTTGAGCCCA AATCTTGTGACAAAACTCACACATGCCCACCGT GCCCAGCACCTGAACTCCTGGGGGGACCGTCAG TCTTCCTCTTCCCCCAAAACCCAAGGACACCCT CATGATCTCCCGGACCCCTGAGGTCACATGCGT GGTGGTGGACGTGAGCCACGAAGACCCTGAGGT CAAGTTCAACTGGTACGTGGACGGCGTGGAGGT GCATAATGCCAAGACAAAGCCGTGTGAGGAGC AGTACGGCAGCACGTACCGTTGTGTCAGCGTCC TCACCGTCCTGCACCAGGACTGGCTGAATGGCA AGGAGTACAAGTGCAAGGTCTCCAACAAAGCCC TCCCAGCCCCCATCGAGAAAACCATCTCCAAAG CCAAAGGGCAGCCCCGAGAACCACAGGTGTAC ACCCTGCCCCCATCCCGGGAGGAGATGACCAAG AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC TTCTATCCCAGCGACATCGCCGTGGAGTGGGAG AGCAATGGGCAGCCGGAGAACAACTACAAGAC CACGCCTCCCGTGCTGGACTCCGACGGCTCCTTC TTCCTCTATAGCAAGCTCACCGTGGACAAGAGC AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC GTGATGCATGAGGCTCTGCACAACCACTACACG CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA	SEQ ID NO: 2111	
	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQAPGKGLEWVAVIWYDASNKYYEDSVKG RFTISRDNSKNTLFLQVNSLRAEDTAVYYCARGITI FGHGFEYWGQGTLVTVSSASTKGPSVFPLAPSSKS TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK	

			FNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP GK
		SEQ ID NO: 384	SEQ ID NO: 541
iPS:361172	2G10_LC1.003	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTG TCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCC TGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGCAGCCACCAGGGCC ACTGGTATCCCAGCCAGGTTCAGTGGCAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGCAGTCTGAAGATTTTGCAGTTTATTACTGTC AGCAGTATAATAACTGGCCTCTCACTTTCGGCG GAGGGACCAAGGTGGAGATCAAACGAACGGTG GCTGCACCATCTGTCTTCATCTTCCCGCCATCTG ATGAGCAGTTGAAATCTGGAACTGCCTCTGTTG TGTGCCTGCTGAATAACTTCTATCCCAGAGAGG CCAAAGTACAGTGGAAGGTGGATAACGCCCTCC AATCGGGTAACTCCCAGGAGAGTGTCACAGAGC AGGACAGCAAGGACAGCACCTACAGCCTCAGC AGCACCCTGACGCTGAGCAAAGCAGACTACGAG AAACACAAAGTCTACGCCTGCGAAGTCACCCAT CAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTC AACAGGGGAGAGTGT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACCTTCAGTAACTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCGAGGGG CTGGAGTGGGTGGCAGCTATATGGTTTGATGCA AGTGATAAATACTATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGAGACAACTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGGCGATTTTTGGAGTGGTCCCGACTACTGG GGCCAGGGAACCCTGGTCACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC GAACCGGTGACGGTGTCGTGGAACTCAGGCGCC CTGACCAGCGGCGTGCACACCTTCCCGGCTGTC CTACAGTCCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCCACC GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATG CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA GGTGCATAATGCCAAGACAAAGCCGCGTGTGAGGA GCAGTACGGCAGCACGTACCGTGTGGTCAGCGT CCTCACCGTCCTGCACCAGGACTGGCTGAATGG

iPS:361178	2G10_LC1.004	NA	AA	
				CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
				CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
				AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
				ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
				AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
				GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
				AGAGCAATGGGCAGCCGGAGAACAACTACAAG
				ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
				TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
				AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
				TCCGTGATGCATGAGGCTCTGCACAACCACTAC
				ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
			SEQ ID NO: 1955	SEQ ID NO: 2112
			EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGM
			YQQKPGQAPRLLIYGAATRATGIPARFSGSGSGTE	HWVRQAPGEGLEWVAAIWFDASDKYYADAVKG
			FTLTISSLQSEDFAVYYCQQYNNWPLTFGGGTKVE	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQ
			IKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP	AIFGVVPDYWGQGTLVTVSSASTKGPSVFPLAPSS
			REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL	KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG
			SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN	VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV
			RGEC	NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG
				GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
				VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV
				LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
				KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP
				SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
				LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS
				LSPGK
			SEQ ID NO: 385	SEQ ID NO: 542
			GAAATAGTGATGACGCAGTCTCCAGCCACCCTG	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
			TCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCC	GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			TGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTA	GCAGCATCTGGATTCACCTTCAGTAACTATGGC
			GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC	ATGCACTGGGTCCGCCAGGCTCCAGGCGAGGGG
			AGGCTCCTCATCTATGGTGCAGCCACCAGGGCC	CTGGAGTGGGTGGCAGCTATATGGTTTGATGCA
			ACTGGTATCCCAGCCAGGTTCAGTGGCAGTGGG	AGTGATAAATACTATGCAGACTCCGTGAAGGGC
			TCTGGGACAGAGTTCACTCTCACCATCAGCAGC	CGATTCACCATCTCCAGAGACAACTCCAAGAAC
			CTGCAGTCTGAAGATTTTGCAGTTTATTACTGTC	ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC

AGCAGTATAATAACTGGCCTCTCACTTTCGGCG	GAGGACACGGCTGTGTATTACTGTGCGAGAGAT
GAGGGACCAAGGTGGAGATCAAACGAACGGTG	CAGGCGATTTTTGGAGTGGTCCCCGACTACTGG
GCTGCACCATCTGTCTTCATCTTCCCGCCATCTG	GGCCAGGGAACCCTGGTCACCGTCTCCTCAGCC
ATGAGCAGTTGAAATCTGGAACTGCCTCTGTTG	TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA
TGTGCCTGCTGAATAACTTCTATCCCAGAGAGG	CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG
CCAAAGTACAGTGGAAGGTGGATAACGCCCTCC	GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC
AATCGGGTAACTCCCAGGAGAGTGTCACAGAGC	GAACCGGTGACGGTGTCGTGGAACTCAGGCGCC
AGGACAGCAAGGACAGCACCTACAGCCTCAGC	CTGACCAGCGGCGTGCACACCTTCCCGGCTGTC
AGCACCCTGACGCTGAGCAAAGCAGACTACGAG	CTACAGTCCTCAGGACTCTACTCCCTCAGCAGC
AAACACAAAGTCTACGCCTGCGAAGTCACCCAT	GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
CAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTC	CAGACCTACATCTGCAACGTGAATCACAAGCCC
AACAGGGGAGAGTGT	AGCAACACCAAGGTGGACAAGAAAGTTGAGCC
	CAAATCTTGTGACAAAACTCACACATGCCCACC
	GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC
	AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC
	CCTCATGATCTCCCGGACCCCTGAGGTCACATG
	CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA
	GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
	GGTGCATAATGCCAAGACAAAGCCGCGTGTGAGGA
	GCAGTACGGCAGCACGTACCGTGTGGTCAGCGT
	CCTCACCGTCCTGCACCAGGACTGGCTGAATGG
	CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
	CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
	AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
	ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
	AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
	GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
	AGAGCAATGGGCAGCCGGAGAACAACTACAAG
	ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
	TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
	AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
	TCCGTGATGCATGAGGCTCTGCACAACCACTAC
	ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
SEQ ID NO: 1956	SEQ ID NO: 2113
AA	
EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGM
YQQKPGQAPRLLIYGAATRATGIPARFSGSGSGTE	HWVRQAPGEGLEWVAAIWFDASDKYYADSVKG

iPS:361185		
2G10_LC1.005		
NA		
FTLTISSLQSEDFAVYYCQQYNNWPLTFGGGTKVE IKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC	SEQ ID NO: 386	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGTLVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
	SEQ ID NO: 543	
	GAAATAGTGATGACGCAGTCTCCAGCCACCCTG TCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCC TGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGCAGCCACCAGGGCC ACTGGTATCCCAGCCAGGTTCAGTGGCAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGCAGTCTGAAGATTTTGCAGTTTATTACTGTC AGCAGTATAATAACTGGCCTCTCACTTTCGGCG GAGGGACCAAGGTGGAGATCAAACGAACGGTG GCTGCACCATCTGTCTTCATCTTCCCGCCATCTG ATGAGCAGTTGAAATCTGGAACTGCCTCTGTTG TGTGCCTGCTGAATAACTTCTATCCCAGAGAGG CCAAAGTACAGTGGAAGGTGGATAACGCCCTCC AATCGGGTAACTCCCAGGAGAGTGTCACAGAGC AGGACAGCAAGGACAGCACCTACAGCCTCAGC AGCACCCTGACGCTGAGCAAAGCAGACTACGAG AAACACAAAGTCTACGCCTGCGAAGTCACCCAT CAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTC AACAGGGGAGAGTGT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACCTTCAGTAACTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCGAGGGG CTGGAGTGGGTGGCAGCTATATGGTTTGATGGA AGTGATAAATACTATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGAGACAACTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGGCGATTTTTGGAGTGGTCCCCGACTACTGG GGCCAGGGAACCCTGGTCACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC GAACCGGTGACGGTGTCGTGGAACTCAGGCGCC CTGACCAGCGGCGTGCACACCTTCCCGGCTGTC CTACAGTCCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCCACC GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC AGTCTTCCTCTTCCCCCCAAAACCCAAGGACAC

CCTCATGATCTCCCGGACCCCCTGAGGTCACATG CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT CCTCACCGTCCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT ACACCCTGCCCCCATCCCGGGAGGAGATGACCA AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGAACAACTACAAG ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA	SEQ ID NO: 2114
	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGM HWVRQAPGEGLEWVAAIWFDGSDKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGTLVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
	SEQ ID NO: 1957
	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGAATRATGIPARFSGSGSGTE FTLTISSLQSEDFAVYYCQQYNNWPLTFGGGTKVE IKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC
	AA

SEQ ID NO: 387		SEQ ID NO: 544
GAAATAGTGATGACGCAGTCTCCAGCCACCCTG		CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
TCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCC		GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
TGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTA		GCAGCATCTGGATTCACCTTCAGTAACTATGGC
GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC		ATGCACTGGGTCCGCCAGGCTCCAGGCGAGGGG
AGGCTCCTCATCTATGGTGCAGCCACCAGGGCC		CTGGAGTGGGTGGCAGCTATATGGTTTGATGCA
ACTGGTATCCCAGCCAGGGTCAGTGGCAGTGGG		AGTGATAAATACTATGCAGACGCCGTGAAGGGC
TCTGGGACAGAGTTCACTCTCACCATCAGCAGC		CGATTCACCATCTCCAGAGACAACTCCAAGAAC
CTGCAGTCTGAAGATTTTGCAGTTTATTACTGTC		ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC
AGCAGTATAATAACTGGCCTCTCACTTTCGGCG		GAGGACACGGCTGTGTATTACTGTGCGAGAGAT
GAGGGACCAAGGTGGAGATCAAACGAACGGTG		CAGGCGATTTTTGGAGTGGTCCCCGACTACTGG
GCTGCACCATCTGTCTTCATCTTCCCGCCATCTG		GGCCAGGGAACCCTGGTCACCGTCTCCTCAGCC
ATGAGCAGTTGAAATCTGGAACTGCCTCTGTTG		TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA
TGTGCCTGCTGAATAACTTCTATCCCAGAGAGG		CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG
CCAAAGTACAGTGGAAGGTGGATAACGCCCTCC		GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC
AATCGGGTAACTCCCAGGAGAGTGTCACAGAGC		GAACCGGTGACGGTGTCGTGGAACTCAGGCGCC
AGGACAGCAAGGACAGCACCTACAGCCTCAGC		CTGACCAGCGGCGTGCACACCTTCCCGGCTGTC
AGCACCCTGACGCTGAGCAAAGCAGACTACGAG		CTACAGTCCTCAGGACTCTACTCCCTCAGCAGC
AAACACAAAGTCTACGCCTGCGAAGTCACCCAT		GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
CAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTC		CAGACCTACATCTGCAACGTGAATCACAAGCCC
AACAGGGGAGAGTGT		AGCAACACCAAGGTGGACAAGAAAGTTGAGCC
		CAAATCTTGTGACAAAACTCACACATGCCCACC
		GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC
		AGTCTTCCTCTTCCCCCCAAAACCCAAGGACAC
		CCTCATGATCTCCCGGACCCCTGAGGTCACATG
		CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA
		GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
		GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA
		GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT
		CCTCACCGTCCTGCACCAGGACTGGCTGAATGG
		CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
		CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
		AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
		ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
		AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
		GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG

		AGAGCAATGGGCAGCCGGAGAACAACTACAAG
		ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
		TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
		AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
		TCCGTGATGCATGAGGCTCTGCACAACCACTAC
		ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1958	SEQ ID NO: 2115
AA	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGAATRATGIPARVSGSGSGTE FTLTISSLQSEDFAVYYCQQYNNWPLTFGGGTKVE IKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGM HWVRQAPGEGLEWVAAIWFDASDKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGTLVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
	SEQ ID NO: 388	SEQ ID NO: 545
NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTG TCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCC TGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGCAGCCACCAGGGCC ACTGGTATCCCAGCCAGGTTCAGTGGCAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGGAGCCTGAAGATTTTGCAGTTTATTACTGTC AGCAGTATAATAACTTCCCTCTCACTTTCGGCGG AGGGACCAAGGTGGAGATCAAACGAACGGTGG CTGCACCATCTGTCTTCATCTTCCCGCCATCTGA TGAGCAGTTGAAATCTGGAACTGCCTCTGTTGT GTGCCTGCTGAATAACTTCTATCCCAGAGAGGC CAAAGTACAGTGGAAGGTGGATAACGCCCTCCA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACCTTCAGTAACTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGCTATATGGTTTGATGCA AGTGATAAATACTATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGAGACAACTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGGCGATTTTTGGAGTGGTCCCCGACTACTGG GGCCAGGGAACCCTGGTCACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC

ATCGGGTAACTCCCAGGAGAGTGTCACAGAGCA GGACAGCAAGGACAGCACCTACAGCCTCAGCA GCACCCTGACGCTGAGCAAAGCAGACTACGAGA AACACAAAGTCTACGCCTGCGAAGTCACCCATC AGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCA ACAGGGGAGAGTGT	GAACCGGTGACGGTGTCGTGGAACTCAGGCGCC CTGACCAGCGGCGTGCACACCTTCCCGGCTGTC CTACAGTCCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCCACC GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATG CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT CCTCACCGTCCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT ACACCCTGCCCCCATCCCGGGAGGAGATGACCA AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGAACAACTACAAG ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
SEQ ID NO: 1959	SEQ ID NO: 2116
AA	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGAATRATGIPARFSGSGSGTE FTLTISSLEPEDFAVYYCQQYNNFPLTFGGGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGM HWVRQAPGKGLEWVAAIWFDASDKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGTLVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE

		VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
		SEQ ID NO: 546
	NA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACCTTCAGTAACTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGCTATATGGTTTGATGCA AGTGATAAATACTATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGAGACAACTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGGCGATTTTTGGAGTGGTCCCCGACTACTGG GGCCAGGGAACCCTGGTCACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC GAACCGGTGACGGTGTCGTGGAACTCAGGCGCC CTGACCAGCGGCGTGCACACCTTCCCGGCTGTC CTACAGTCCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCCC CAAATCTTGTGACAAAACTCACACATGCCCACC GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATG CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA GGTGCATAATGCCAAGACAAAGCCGCGTGTGAGGA GCAGTACGGCAGCACGTACCGTGTGGTCAGCGT CCTCACCGTCCTGCACCAGGACTGGCTGAATGG
		SEQ ID NO: 389
		GAAATAGTGATGACGCAGTCTCCAGCCACCCTG TCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCC TGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGCAGCCACCAGGGCC ACTGGTATCCCAGCCAGGTTCAGTGGCAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGGAGCCTGAAGATTTTGCAGTTTATTACTGTC AGCAGTATAATAACTATCCTCTCACTTTCGGCGG AGGGACCAAGGTGGAGATCAAACGAACGGTGG CTGCACCATCTGTCTTCATCTTCCCGCCATCTGA TGAGCAGTTGAAATCTGGAACTGCCTCTGTTGT GTGCCTGCTGAATAACTTCTATCCCAGAGAGGC CAAAGTACAGTGGAAGGTGGATAACGCCCTCCA ATCGGGTAACTCCCAGGAGAGTGTCACAGAGCA GGACAGCAAGGACAGCACCTACAGCCTCAGCA GCACCCTGACGCTGAGCAAAGCAGACTACGAGA AACACAAAGTCTACGCCTGCGAAGTCACCCATC AGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCA ACAGGGGAGAGTGT
	2G10_LC1.008	
	iPS:359615	

			CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
			CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
			AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
			ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
			AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
			GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
			AGAGCAATGGGCAGCCGGAGAACAACTACAAG
			ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
			TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
			AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
			TCCGTGATGCATGAGGCTCTGCACAACCACTAC
			ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
		SEQ ID NO: 1960	SEQ ID NO: 2117
	AA	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGAATRATGIPARFSGSGSGTE FTLTISSLEPEDFAVYYCQQYNNYPLTFGGGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGM HWVRQAPGKGLEWVAAIWFDASDKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGTLVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
	NA	SEQ ID NO: 390	SEQ ID NO: 547
		GAAATAGTGATGACGCAGTCTCCAGCCACCCTG TCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCC TGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGCAGCCACCAGGGCC ACTGGTATCCCAGCCAGGTTCAGTGGCAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGGAGCCTGAAGATTTTGCAGTTTATTACTGTC	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACCTTCAGTAACTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCGAGGGG CTGGAGTGGGTGGCAGCTATATGGTTTGATGCA AGTGATAAATACTATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGAGACAACTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC

iPS:361196	
2G10_LC1.009	

AGCAGTATAATAACTGGCCTCTCACTTTCGGCG	GAGGACACGGCTGTGTATTACTGTGCGAGAGAT
GAGGGACCAAGGTGGAGATCAAACGAACGGTG	CAGGCGATTTTTGGAGTGGTCCCCGACTACTGG
GCTGCACCATCTGTCTTCATCTTCCCGCCATCTG	GGCCAGGGAACCCTGGTCACCGTCTCCTCAGCC
ATGAGCAGTTGAAATCTGGAACTGCCTCTGTTG	TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA
TGTGCCTGCTGAATAACTTCTATCCCAGAGAGG	CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG
CCAAAGTACAGTGGAAGGTGGATAACGCCCTCC	GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC
AATCGGGTAACTCCCAGGAGAGTGTCACAGAGC	GAACCGGTGACGGTGTCGTGGAACTCAGGCGCC
AGGACAGCAAGGACAGCACCTACAGCCTCAGC	CTGACCAGCGGCGTGCACACCTTCCCGGCTGTC
AGCACCCTGACGCTGAGCAAAGCAGACTACGAG	CTACAGTCCTCAGGACTCTACTCCCTCAGCAGC
AAACACAAAGTCTACGCCTGCGAAGTCACCCAT	GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
CAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTC	CAGACCTACATCTGCAACGTGAATCACAAGCCC
AACAGGGGAGAGTGT	AGCAACACCAAGGTGGACAAGAAAGTTGAGCC
	CAAATCTTGTGACAAAACTCACACATGCCCACC
	GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC
	AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC
	CCTCATGATCTCCCGGACCCCTGAGGTCACATG
	CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA
	GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
	GGTGCATAATGCCAAGACAAAGCCGCGTGTGAGGA
	GCAGTACGGCAGCACCGTACCGTCCTGTGTCAGCGT
	CCTCACCGTCCTGCACCAGGACTGGCTGAATGG
	CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
	CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
	AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
	ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
	AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
	GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
	AGAGCAATGGGCAGCCGGAGAACAACTACAAG
	ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
	TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
	AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
	TCCGTGATGCATGAGGCTCTGCACAACCACTAC
	ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
SEQ ID NO: 1961	SEQ ID NO: 2118
AA	
EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGM
YQQKPGQAPRLLIYGAATRATGIPARFSGSGSGTE	HWVRQAPGEGLEWVAAIWFDASDKYYADAVKG

iPS:361202		
2G10_LC1.010		
NA		
FTLTISSLEPEDFAVYYCQQYNNWPLTFGGGTKVE IKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC	SEQ ID NO: 391	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGTLVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
	GAAATAGTGATGACGCAGTCTCCAGCCACCCTG TCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCC TGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGCAGCCACCAGGGCC ACTGGTATCCCAGCCAGGTTCAGTGGCAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGGAGCCTGAAGATTTTGCAGTTTATTACTGTC AGCAGTATAATAACTGGCCTCTCACTTTCGGCG GAGGGACCAAGGTGGAGATCAAACGAACGGTG GCTGCACCATCTGTCTTCATCTTCCCGCCATCTG ATGAGCAGTTGAAATCTGGAACTGCCTCTGTTG TGTGCCTGCTGAATAACTTCTATCCCAGAGAGG CCAAAGTACAGTGGAAGGTGGATAACGCCCTCC AATCGGGTAACTCCCAGGAGAGTGTCACAGAGC AGGACAGCAAGGACAGCACCTACAGCCTCAGC AGCACCCTGACGCTGAGCAAAGCAGACTACGAG AAACACAAAGTCTACGCCTGCGAAGTCACCCAT CAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTC AACAGGGGAGAGTGT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACCTTCAGTAACTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGCTATATGGTTTGATGCA AGTGATAAATACTATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGAGACAACTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGGCGATTTTTGGAGTGGTCCCCGACTACTGG GGCCAGGGAACCCTGGTCACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC GAACCGGTGACGGTGTCGTGGAACTCAGGCGCC CTGACCAGCGGCGTGCACACCTTCCCGGCTGTC CTACAGTCCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCCACC GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC

		CCTCATGATCTCCCGGACCCCCTGAGGTCACATG
		CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA
		GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
		GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA
		GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT
		CCTCACCGTCCTGCACCAGGACTGGCTGAATGG
		CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
		CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
		AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
		ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
		AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
		GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
		AGAGCAATGGGCAGCCGGAGAACAACTACAAG
		ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
		TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
		AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
		TCCGTGATGCATGAGGCTCTGCACAACCACTAC
		ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1962	SEQ ID NO: 2119
	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGM
	YQQKPGQAPRLLIYGAATRATGIPARFSGSGSGTE	HWVRQAPGKGLEWVAAIWFDASDKYYADAVKG
	FTLTISSLEPEDFAVYYCQQYNNWPLTFGGGTKVE	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQ
	IKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP	AIFGVVPDYWGQGTLVTVSSASTKGPSVFPLAPSS
	REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL	KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG
	SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN	VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV
	RGEC	NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG
AA		GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
		VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV
		LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
		KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP
		SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
		LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS
		LSPGK

iPS:359644		SEQ ID NO: 549
18E3.002		CAGGTGCAGTTGCAGGAGTCGGGCCCAGGACTG
NA		GTGAAGCCTTCAGAGACCCTGTCCCTCACCTGC
SEQ ID NO: 392	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTG	ACTGTCTCTGGTGACTCCATCAGCAGTGGTGGTT
	TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT	ACTACTGGAGCTGGATCCGCCAGCCCCCAGGGA
	GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT	AGGGCCTGGAGTGGATTGGGTACATCTATTACA
	TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC	GTGGGAGCACCTACTACAACCCGTCCCTCAAGA
	CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG	GTCGAGTTACCATATCAGTAGACACCGTCTAAGA
	CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG	ACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC
	GGTCTGGGACAGACTTCACTCTCACCATCAGCA	CGCGGACACGGCCGTGTATTACTGTGCGAGAGA
	GACTGGAGCCTGATGATTTTGCAGTGTATTACTG	TCGTATTACGATTTTTGGAGTGGTTATGGGGGGC
	TCAGCAGTATGGTAGTTCACCGCTCACTTTCGGC	GGTATGGACGTCTGGGGCCAAGGGACCACGGTC
	GGAGGGACCAAGGTGGAGATCAAACGAACGGT	ACCGTCTCCTCAGCCTCCACCAAGGGCCCATCG
	GGCTGCACCATCTGTCTTCATCTTCCCGCCATCT	GTCTTCCCCCCTGGCACCCTCCTCCAAGAGCACCT
	GATGAGCAGTTGAAATCTGGAACTGCCTCTGTT	CTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCA
	GTGTGCCTGCTGAATAACTTCTATCCCAGAGAG	AGGACTACTTCCCCCGAACCGGTGACGGTGTCGT
	GCCAAAGTACAGTGGAAGGTGGATAACGCCCTC	GGAACTCAGGCGCCCTGACCAGCGGCGTGCACA
	CAATCGGGTAACTCCCAGGAGAGTGTCACAGAG	CCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTA
	CAGGACAGCAAGGACAGCACCTACAGCCTCAGC	CTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAG
	AGCACCCTGACGCTGAGCAAAGCAGACTACGAG	CAGCTTGGGCACCCAGACCTACATCTGCAACGT
	AAACACAAAGTCTACGCCTGCGAAGTCACCCAT	GAATCACAAGCCCAGCAACACCAAGGTGGACA
	CAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTC	AGAAAGTTGAGCCCAAATCTTGTGACAAAACTC
	AACAGGGGAGAGTGT	ACACATGCCCACCGTGCCCAGCACCTGAACTCC
		TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAA
		ACCCAAGGACACCCTCATGATCTCCCGGACCCC
		TGAGGTCACATGCGTGGTGGTGGACGTGAGCCA
		CGAAGACCCTGAGGTCAAGTTCAACTGGTACGT
		GGACGGCGTGGAGGTGCATAATGCCAAGACAA
		AGCCGTGTGTGAGGAGCAGTACGGCAGCACGTACC
		GTTGTGTCAGCGTCCTCACCGTCCTGCACCAGG
		ACTGGCTGAATGGCAAGGAGTACAAGTGCAAG
		GTCTCCAACAAAGCCCTCCCAGCCCCCATCGAG
		AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGA
		GAACCACAGGTGTACACCCTGCCCCCATCCCGG
		GAGGAGATGACCAAGAACCAGGTCAGCCTGAC
		CTGCCTGGTCAAAGGCTTCTATCCCAGCGACAT

		CGCCGTGGAGTGGGAGAGCAATGGGCAGCCGG AGAACAACTACAAGACCACGCCTCCCGTGCTGG ACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCT CACCGTGGACAAGAGCAGGTGGCAGCAGGGGA ACGTCTTCTCATGCTCCGTGATGCATGAGGCTCT GCACAACCACTACACGCAGAAGAGCCTCTCCCT GTCTCCGGGTAAA
	SEQ ID NO: 1963	SEQ ID NO: 2120
AA	EIVLTQSPGTLSLSPGERATLSCRASQSISYSYLAW YQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF TLTISRLEPDDFAVYYCQQYGSSPLTFGGGTKVEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR GEC	QVQLQESGPGLVKPSETLSLTCTVSGDSISSGGYY WSWIRQPPGKGLEWIGYIYYSGSTYYNPSLKSRVT ISVDTSKNQFSLKLSSVTAADTAVYYCARDRITIFG VVMGGGMDVWGQGTTVTVSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
	SEQ ID NO: 393	SEQ ID NO: 550
NA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG GGTCTGGGACAGACTTCACTCTCACCATCAGCA GACAGGAGCCTGATGATTTTGCAGTGTATTACT GTCAGCAGTATGGTAGTTCACCGCTCACTTTCGG CGGAGGGACCAAGGTGGAGATCAAACGAACGG TGGCTGCACCATCTGTCTTCATCTTCCCGCCATC TGATGAGCAGTTGAAATCTGGAACTGCCTCTGT TGTGTGCCTGCTGAATAACTTCTATCCCAGAGA	CAGGTGCAGTTGCAGGAGTCGGGCCCAGGACTG GTGAAGCCTTCAGAGACCCTGTCCCTCACCTGC ACTGTCTCTCTGGTGACTCCATCAGCAGTGGTGGTT ACTACTGGAGCTGGATCCGCCAGCCCCCAGGGA AGGGCCTGGAGTGGATTGGGTACATCTATTACA GTGGGAGCACCTACTACAACCCGTCCCTCAAGA GTCGAGTTACCATATCAGTAGACACGTCTAAGA ACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC CGCGGACACGGCCGTGTATTACTGTGCGAGAGA TCGTATTACGATTTTTGGAGTGGTTATGGGGGGC GGTATGGACGTCTGGGGCCAAGGGACCACGGTC ACCGTCTCCTCAGCCTCCACCAAGGGCCCATCG GTCTTCCCCCCTGGCACCCTCCTCCAAGAGCACCT

GGCCAAAGTACAGTGGAAGGTGGATAACGCCCT CCAATCGGGTAACTCCCAGGAGAGTGTCACAGA GCAGGACAGCAAGGACAGCACCTACAGCCTCA GCAGCACCCTGACGCTGAGCAAAGCAGACTACG AGAAACACAAAGTCTACGCCTGCGAAGTCACCC ATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCT TCAACAGGGGAGAGTGT	SEQ ID NO: 1964	CTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCA AGGACTACTTCCCCGAACCGGTGACGGTGTCGT GGAACTCAGGCGCCCTGACCAGCGGCGTGCACA CCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTA CTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAG CAGCTTGGGCACCCAGACCTACATCTGCAACGT GAATCACAAGCCCAGCAACACCAAGGTGGACA AGAAAGTTGAGCCCAAATCTTGTGACAAAACTC ACACATGCCCACCGTGCCCAGCACCTGAACTCC TGGGGGGACCGTCAGTCTTCCTCTTCCCCCAAA ACCCAAGGACACCCTCATGATCTCCCGGACCCC TGAGGTCACATGCGTGGTGGTGGACGTGAGCCA CGAAGACCCTGAGGTCAAGTTCAACTGGTACGT GGACGGCGTGGAGGTGCATAATGCCAAGACAA AGCCGTGTGAGGAGCAGTACGGCAGCACGTACC GTTGTGTCAGCGTCCTCACCGTCCTGCACCAGG ACTGGCTGAATGGCAAGGAGTACAAGTGCAAG GTCTCCAACAAAGCCCTCCCAGCCCCCATCGAG AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGA GAACCACAGGTGTACACCCTGCCCCCATCCCGG GAGGAGATGACCAAGAACCAGGTCAGCCTGAC CTGCCTGGTCAAAGGCTTCTATCCCAGCGACAT CGCCGTGGAGTGGGAGAGCAATGGGCAGCCGG AGAACAACTACAAGACCACGCCTCCCGTGCTGG ACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCT CACCGTGGACAAGAGCAGGTGGCAGCAGGGGA ACGTCTTCTCATGCTCCGTGATGCATGAGGCTCT GCACAACCACACTACACGCAGAAGAGCCTCTCCCT GTCTCCGGGTAAA
	SEQ ID NO: 2121	
AA	EIVLTQSPGTLSLSPGERATLSCRASQSISYSYLAW YQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF TLTISRQEPDDFAVYYCQQYGSSPLTFGGGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS	QVQLQESGPGLVKPSETLSLTCTVSGDSISSGGYY WSWIRQPPGKGLEWIGYIYYSGSTYYNPSLKSRVT ISVDTSKNQFSLKLSSVTAADTAVYYCARDRITIFG VVMGGGMDVWGQGTTVTVSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN

	iPS:359628	
	18E3.004	
	NA	
STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC	SEQ ID NO: 394	VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
	SEQ ID NO: 394	SEQ ID NO: 551
	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTG	CAGGTGCAGTTGCAGGAGTCGGGCCCAGGACTG
	TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT	GTGAAGCCTTCACAGACCCTGTCCCTCACCTGC
	GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT	ACTGTCTCTGGTGACTCCATCAGCAGTGGTGGTT
	TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC	ACTACTGGAGGCTGGATCCGCCAGCCCCCAGGGA
	CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG	AGGGCCTGGAGTGGATTGGGTACATCTATTACA
	CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG	GTGGGAGCACCTACTACAACCCGTCCCTCAAGA
	GGTCTGGGACAGACTTCACTCTCACCATCAGCA	GTCGAGTTACCATATCAGTAGACACGTCTAAGA
	GACTGGAGCCTGATGATTTTGCAGTGTATTACTG	ACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC
	TCAGCAGTATGGTAGTTCACCGCTCACTTTCGGC	CGCGGACACGGCCGTGTATTACTGTGCGAGAGA
	GGAGGGACCAAGGTGGAGATCAAACGAACGGT	TCGTATTACGATTTTTGGAGTGGTTATGGGGGGC
	GGCTGCACCATCTGTCTTCATCTTCCCGCCATCT	GGTATGGACGTCTGGGGCCAAGGGACCACGGTC
	GATGAGCAGTTGAAATCTGGAACTGCCTCTGTT	ACCGTCTCCTCAGCCTCCACCAAGGGCCCATCG
	GTGTGCCTGCTGAATAACTTCTATCCCAGAGAG	GTCTTCCCCCCTGGCACCCTCCTCCTCCAAGAGCACCT
	GCCAAAGTACAGTGGAAGGTGGATAACGCCCTC	CTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCA
	CAATCGGGTAACTCCCAGGAGAGTGTCACAGAG	AGGACTACTTCCCCCGAACCGGTGACGGTGTCGT
	CAGGACAGCAAGGACAGCACCTACAGCCTCAGC	GGAACTCAGGCGCCCTGACCAGCGGCGTGCACA
	AGCACCCTGACGCTGAGCAAAGCAGACTACGAG	CCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTA
	AAACACAAAGTCTACGCCTGCGAAGTCACCCAT	CTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAG
	CAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTC	CAGCTTGGGCACCCAGACCTACATCTGCAACGT
	AACAGGGGAGAGTGT	GAATCACAAGCCCAGCAACACCAAGGTGGACA
		AGAAAGTTGAGCCCAAATCTTGTGACAAAACTC
		ACACATGCCCACCGTGCCCAGCACCTGAACTCC
		TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAA
		ACCCAAGGACACCCTCATGATCTCCCGGACCCC
		TGAGGTCACATGCGTGGTGGTGGACGTGAGCCA
		CGAAGACCCTGAGGTCAAGTTCAACTGGTACGT
		GGACGGCGTGGAGGTGCATAATGCCAAGACAA

			AGCCGTGTGAGGAGCAGTACGGCAGCACGTACC
			GTTGTGTCAGCGTCCTCACCGTCCTGCACCAGG
			ACTGGCTGAATGGCAAGGAGTACAAGTGCAAG
			GTCTCCAACAAAGCCCTCCCAGCCCCCATCGAG
			AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGA
			GAACCACAGGTGTACACCCTGCCCCCATCCCGG
			GAGGAGATGACCAAGAACCAGGTCAGCCTGAC
			CTGCCTGGTCAAAGGCTTCTATCCCAGCGACAT
			CGCCGTGGAGTGGGAGAGCAATGGGCAGCCGG
			AGAACAACTACAAGACCACGCCTCCCGTGCTGG
			ACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCT
			CACCGTGGACAAGAGCAGGTGGCAGCAGGGGA
			ACGTCTTCTCATGCTCCGTGATGCATGAGGCTCT
			GCACAACCACACTACACGCAGAAGAGCCTCTCCCT
			GTCTCCGGGTAAA
		SEQ ID NO: 1965	SEQ ID NO: 2122
	AA	EIVLTQSPGTLSLSPGERATLSCRASQSISYSYLAW	QVQLQESGPGLVKPSQTLSLTCTVSGDSISSGGYY
		YQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF	WSWIRQPPGKGLEWIGYIYYSGSTYYNPSLKSRVT
		TLTISRLEPDDFAVYYCQQYGSSPLTFGGGTKVEIK	ISVDTSKNQFSLKLSSVTAADTAVYYCARDRITIFG
		RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE	VVMGGGMDVWGQGTTVTVSSASTKGPSVFPLAP
		AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS	SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS
		TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR	GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN
		GEC	VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL
			GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED
			PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV
			SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK
			AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF
			YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
			SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS
			LSLSPGK
		SEQ ID NO: 395	SEQ ID NO: 552
	NA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTG	CAGGTGCAGTTGCAGGAGTCGGGCCCAGGACTG
		TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT	GTGAAGCCTTCAGAGACCCTGTCCCTCACCTGC
		GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT	ACTGTCTCTGGTGACTCCATCAGCAGTGGTGGTT
		TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC	ACTACTGGAGCTGGATCCGCCAGCACCCAGGGA
		CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG	AGGGCCTGGAGTGGATTGGGTACATCTATTACA

GTGGGAGCACCTACTACAACCCGTCCCTCAAGA	CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG		
GTCGAGTTACCATATCAGTAGACACGTCTAAGA	GGTCTGGGACAGACTTCACTCTCACCATCAGCA		
ACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC	GACTGGAGCCTGATGATTTTGCAGTGTATTACTG		
CGCGGACACGGCCGTGTATTACTGTGCGAGAGA	TCAGCAGTATGGTAGTTCACCGCTCACTTTCGGC		
TCGTATTACGATTTTTGGAGTGGTTATGGGGGGC	GGAGGGACCAAGGTGGAGATCAAACGAACGGT		
GGTATGGACGTCTGGGGCCAAGGGACCACGGTC	GGCTGCACCATCTGTCTTCATCTTCCCGCCATCT		
ACCGTCTCCTCAGCCTCCACCAAGGGCCCATCG	GATGAGCAGTTGAAATCTGGAACTGCCTCTGTT		
GTCTTCCCCCCTGGCACCCTCCTCCAAGAGCACCT	GTGTGCCTGCTGAATAACTTCTATCCCAGAGAG		
CTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCA	GCCAAAGTACAGTGGAAGGTGGATAACGCCCTC		
AGGACTACTTCCCCGAACCGGTGACGGTGTCGT	CAATCGGGTAACTCCCAGGAGAGTGTCACAGAG		
TGAGGTCACATGCGTGGTGGTGGACGTGAGCCA	CAGGACAGCAAGGACAGCACCTACAGCCTCAGC		
CGAAGACCCTGAGGTCAAGTTCAACTGGTACGT	AGCACCCTGACGCTGAGCAAAGCAGACTACGAG		
GGACGGCGTGGAGGTGCATAATGCCAAGACAA	AAACACAAAGTCTACGCCTGCGAAGTCACCCAT		
AGCCGTGTGAGGAGCAGTACGGCAGCACGTACC	CAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTC		
GTTGTGTCAGCGTCCTCACCGTCCTGCACCAGG	AACAGGGGAGAGTGT		
ACTGGCTGAATGGCAAGGAGTACAAGTGCAAG			
GTCTCCAACAAAGCCCTCCCAGCCCCCATCGAG			
AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGA			
GAACCACAGGTGTACACCCTGCCCCCATCCCGG			
GAGGAGATGACCAAGAACCAGGTCAGCCTGAC			
CTGCCTGGTCAAAGGCTTCTATCCCAGCGACAT			
CGCCGTGGAGTGGGAGAGCAATGGGCAGCCGG			
AGAACAACTACAAGACCACGCCTCCCGTGCTGG			
ACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCT			
CACCGTGGACAAGAGCAGGTGGCAGCAGGGGA			
ACGTCTTCTCATGCTCCGTGATGCATGAGGCTCT			

		GCACAACCACTACACGCAGAAGAGCCTCTCCCT GTCTCCGGGTAAA
	AA	SEQ ID NO: 1966
		EIVLTQSPGTLSLSPGERATLSCRASQSISYSYLAW YQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF TLTISRLEPDDFAVYYCQQYGSSPLTFGGGTKVEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR GEC
		SEQ ID NO: 396
	NA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG GGTCTGGGACAGACTTCACTCTCACCATCAGCA GACTGGAGCCTGATGATTTTGCAGTGTATTACTG TCAGCAGTATGGTAGTTCACCGCTCACTTTCGGC GGAGGGACCAAGGTGGAGATCAAACGAACGGT GGCTGCACCATCTGTCTTCATCTTCCCGCCATCT GATGAGCAGTTGAAATCTGGAACTGCCTCTGTT GTGTGCCTGCTGAATAACTTCTATCCCAGAGAG GCCAAAGTACAGTGGAAGGTGGATAACGCCCTC CAATCGGGTAACTCCCAGGAGAGTGTCACAGAG CAGGACAGCAAGGACAGCACCTACAGCCTCAGC AGCACCCTGACGCTGAGCAAAGCAGACTACGAG AAACACAAAGTCTACGCCTGCGAAGTCACCCAT	SEQ ID NO: 553 CAGGTGCAGTTGCAGGAGTCGGGCCCAGGACTG GTGAAGCCTTCACAGACCCTGTCCCTCACCTGC ACTGTCTCTCTGGTGACTCCATCAGCAGTGGTGGTTT ACTACTGGAGCTGGATCCGCCAGCACCCAGGGA AGGGCCTGGAGTGGATTGGGTACATCTATTACA GTGGGAGCACCTACTACAACCCGTCCCTCAAGA GTCGAGTTACCATATCAGTAGACACGTCTAAGA ACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC CGCGGACACGGCCGTGTATTACTGTGCGAGAGA TCGTATTACGATTTTTGGAGTGGTTATGGGGGGC GGTATGGACGTCTGGGGCCAAGGGACCACGGTC ACCGTCTCCTCAGCCTCCACCAAGGGCCCATCG GTCTTCCCCCCTGGCACCCTCCTCCAAGAGCACCT CTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCA AGGACTACTTCCCCGAACCGGTGACGGTGTCGT GGAACTCAGGCGCCCTGACCAGCGGCGTGCACA CCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTA CTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAG
		18E3.006
		iPS:361210

CAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTC AACAGGGGAGAGTGT		CAGCTTGGGCACCCAGACCTACATCTGCAACGT GAATCACAAGCCCAGCAACACCAAGGTGGACA AGAAAGTTGAGCCCAAATCTTGTGACAAAACTC ACACATGCCCACCGTGCCCAGCACCTGAACTCC TGGGGGGACCGTCAGTCTTCCTCTTCCCCCAAA ACCCAAGGACACCCTCATGATCTCCCGGACCCC TGAGGTCACATGCGTGGTGGTGGACGTGAGCCA CGAAGACCCTGAGGTCAAGTTCAACTGGTACGT GGACGGCGTGGAGGTGCATAATGCCAAGACAA AGCCGTGTGAGGAGCAGTACGGCAGCACGTACC GTTGTGTCAGCGTCCTCACCGTCCTGCACCAGG ACTGGCTGAATGGCAAGGAGTACAAGTGCAAG GTCTCCAACAAAGCCCTCCCAGCCCCCATCGAG AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGA GAACCACAGGTGTACACCCTGCCCCCATCCCGG GAGGAGATGACCAAGAACCAGGTCAGCCTGAC CTGCCTGGTCAAAGGCTTCTATCCCAGCGACAT CGCCGTGGAGTGGGAGAGCAATGGGCAGCCGG AGAACAACTACAAGACCACGCCTCCCGTGCTGG ACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCT CACCGTGGACAAGAGCAGGTGGCAGCAGGGGA ACGTCTTCTCATGCTCCGTGATGCATGAGGCTCT GCACAACCACTACACGCAGAAGAGCCTCTCCCT GTCTCCGGGTAAA
	SEQ ID NO: 1967	SEQ ID NO: 2124
	EIVLTQSPGTLSLSPGERATLSCRASQSISYSYLAW YQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF TLTISRLEPDDFAVYYCQQYGSSPLTFGGGTKVEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR GEC	QVQLQESGPGLVKPSQTLSLTCTVSGDSISSGGYY WSWIRQHPGKGLEWIGYIYYSGSTYYNPSLKSRVT ISVDTSKNQFSLKLSSVTAADTAVYYCARDRITIFG VVMGGGMDVWGQGTTVTVSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF
	AA	

		YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
	SEQ ID NO: 397	SEQ ID NO: 554
	NA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTG
		TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT
		GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT
		TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC
		CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG
		CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG
		GGTCTGGGACAGACTTCACTCTCACCATCAGCA
		GACAGGAGCCTGATGATTTTGCAGTGTATTACT
		GTCAGCAGTATGGTAGTTCACCGCTCACTTTCGG
		CGGAGGGACCAAGGTGGAGATCAAACGAACGG
		TGGCTGCACCATCTGTCTTCATCTTCCCGCCATC
		TGATGAGCAGTTGAAATCTGGAACTGCCTCTGT
		TGTGTGCCTGCTGAATAACTTCTATCCCAGAGA
		GGCCAAAGTACAGTGGAAGGTGGATAACGCCCT
		CCAATCGGGTAACTCCCAGGAGAGTGTCACAGA
		GCAGGACAGCAAGGACAGCACCTACAGCCTCA
		GCAGCACCCTGACGCTGAGCAAAGCAGACTACG
		AGAAACACAAAGTCTACGCCTGCGAAGTCACCC
		ATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCT
		TCAACAGGGGAGAGTGT

		CAGGTGCAGTTGCAGGAGTCGGGCCCAGGACTG
		GTGAAGCCTTCAGAGACCCTGTCCCTCACCTGC
		ACTGTCTCTGGTGACTCCATCAGCAGTGGTGGTT
		ACTACTGGAGCTGGATCCGCCAGCACCCAGGGA
		AGGGCCTGGAGTGGATTGGGTACATCTATTACA
		GTGGGAGCACCTACTACAACCCGTCCCTCAAGA
		GTCGAGTTACCATATCAGTAGACACGTCTAAGA
		ACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC
		CGCGGACACGGCCGTGTATTACTGTGCGAGAGA
		TCGTATTACGATTTTTGGAGTGGTTATGGGGGGC
		GGTATGGACGTCTGGGGCCAAGGGACCACGGTC
		ACCGTCTCCTCAGCCTCCACCAAGGGCCCATCG
		GTCTTCCCCCCTGGCACCCTCCTCCAAGAGCACCT
		CTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCA
		AGGACTACTTCCCCGAACCGGTGACGGTGTCGT
		GGAACTCAGGCGCCCTGACCAGCGGCGTGCACA
		CCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTA
		CTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAG
		CAGCTTGGGCACCCAGACCTACATCTGCAACGT
		GAATCACAAGCCCAGCAACACCAAGGTGGACA
		AGAAAGTTGAGCCCAAATCTTGTGACAAAACTC
		ACACATGCCCACCGTGCCCAGCACCTGAACTCC
		TGGGGGGACCGTCAGTCTTCCTCTTCCCCCAAA
		ACCCAAGGACACCCTCATGATCTCCCGGACCCC
		TGAGGTCACATGCGTGGTGGTGGACGTGAGCCA
		CGAAGACCCTGAGGTCAAGTTCAACTGGTACGT
		GGACGGCGTGGAGGTGCATAATGCCAAGACAA
		AGCCGTGTGAGGAGCAGTACGGCAGCACGTACC
		GTTGTGTCAGCGTCCTCACCGTCCTGCACCAGG
		ACTGGCTGAATGGCAAGGAGTACAAGTGCAAG
		GTCTCCAACAAAGCCCTCCCAGCCCCCATCGAG
		AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGA

			GAACCACAGGTGTACACCCTGCCCCCATCCCGG
			GAGGAGATGACCAAGAACCAGGTCAGCCTGAC
			CTGCCTGGTCAAAGGCTTCTATCCCAGCGACAT
			CGCCGTGGAGTGGGAGAGCAATGGGCAGCCGG
			AGAACAACTACAAGACCACGCCTCCCGTGCTGG
			ACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCT
			CACCGTGGACAAGAGCAGGTGGCAGCAGGGGA
			ACGTCTTCTCATGCTCCGTGATGCATGAGGCTCT
			GCACAACCACTACACGCAGAAGAGCCTCTCCCT
			GTCTCCGGGTAAA
		SEQ ID NO: 1968	SEQ ID NO: 2125
	AA	EIVLTQSPGTLSLSPGERATLSCRASQSISYSYLAW YQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF TLTISRQEPDDFAVYYCQQYGSSPLTFGGGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC	QVQLQESGPGLVKPSETLSLTCTVSGDSISSGGYY WSWIRQHPGKGLEWIGYIYYSGSTYYNPSLKSRVT ISVDTSKNQFSLKLSSVTAADTAVYYCARDRITIFG VVMGGGMDVWGQGTTVTVSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
	NA	SEQ ID NO: 398	SEQ ID NO: 555
		GAAATTGTGTTGACGCAGTCTCCAGGCACCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG GGTCTGGGACAGACTTCACTCTCACCATCAGCA GACAGGAGCCTGATGATTTTGCAGTGTATTACT GTCAGCAGTATGGTAGTTCACCGCTCACTTTCGG CGGAGGGACCAAGGTGGAGATCAAACGAACGG	CAGGTGCAGTTGCAGGAGTCGGGCCCAGGACTG GTGAAGCCTTCACAGACCCTGTCCCTCACCTGC ACTGTCTCTGGTGACTCCATCAGCAGTGGTGGTT ACTACTGGAGCTGGATCCGCCAGCCCCCAGGGA AGGGCCTGGAGTGGATTGGGTACATCTATTACA GTGGGAGCACCTACTACAACCCGTCCCTCAAGA GTCGAGTTACCATATCAGTAGACACCGTCTAAGA ACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC CGCGGACACGGCCGTGTATTACTGTGCGAGAGA TCGTATTACGATTTTTGGAGTGGTTATGGGGGGC
		18E3.008	
		iPS:361218	

TGGCTGCACCATCTGTCTTCATCTTCCCGCCATC	GGTATGGACGTCTGGGGCCAAGGGACCACGGTC
TGATGAGCAGTTGAAATCTGGAACTGCCTCTGT	ACCGTCTCCTCAGCCTCCACCAAGGGCCCATCG
TGTGTGCCTGCTGAATAACTTCTATCCCAGAGA	GTCTTCCCCCCTGGCACCCTCCTCCAAGAGCACCT
GGCCAAAGTACAGTGGAAGGTGGATAACGCCCT	CTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCA
CCAATCGGGTAACTCCCAGGAGAGTGTCACAGA	AGGACTACTTCCCCCGAACCGGTGACGGTGTCGT
GCAGGACAGCAAGGACAGCACCTACAGCCTCA	GGAACTCAGGCGCCCTGACCAGCGGCGTGCACA
GCAGCACCCTGACGCTGAGCAAAGCAGACTACG	CCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTA
AGAAACACAAAGTCTACGCCTGCGAAGTCACCC	CTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAG
ATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCT	CAGCTTGGGCACCCAGACCTACATCTGCAACGT
TCAACAGGGGAGAGTGT	GAATCACACAAGCCCAGCAACACCAAGGTGGACA
	AGAAAGTTGAGCCCAAATCTTGTGACAAAACTC
	ACACATGCCCACCGTGCCCAGCACCTGAACTCC
	TGGGGGGACCGTCAGTCTTCCTCTTCCCCCAAA
	ACCCAAGGACACCCTCATGATCTCCCGGACCCC
	TGAGGTCACATGCGTGGTGGTGGACGTGAGCCA
	CGAAGACCCTGAGGTCAAGTTCAACTGGTACGT
	GGACGGCGTGGAGGTGCATAATGCCAAGACAA
	AGCCGTGTGAGGAGCAGTACGGCAGCACGTACC
	GTTGTGTCAGCGTCCTCACCGTCCTGCACCAGG
	ACTGGCTGAATGGCAAGGAGTACAAGTGCAAG
	GTCTCCAACAAAGCCCTCCCAGCCCCCATCGAG
	AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGA
	GAACCACAGGTGTACACCCTGCCCCCATCCCGG
	GAGGAGATGACCAAGAACCAGGTCAGCCTGAC
	CTGCCTGGTCAAAGGCTTCTATCCCAGCGACAT
	CGCCGTGGAGTGGGAGAGCAATGGGCAGCCGG
	AGAACAACTACAAGACCACGCCTCCCGTGCTGG
	ACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCT
	CACCGTGGACAAGAGCAGGTGGCAGCAGGGGA
	ACGTCTTCTCATGCTCCGTGATGCATGAGGCTCT
	GCACAACCACTACACGCAGAAGAGCCTCTCCCT
	GTCTCCGGGTAAA
SEQ ID NO: 1969	SEQ ID NO: 2126
AA	
EIVLTQSPGTLSLSPGERATLSCRASQSISYSYLAW	QVQLQESGPGLVKPSQTLSLTCTVSGDSISSGGYY
YQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF	WSWIRQPPGKGLEWIGYIYYSGSTYYNPSLKSRVT
TLTISRQEPDDFAVYYCQQYGSSPLTFGGGTKVEI	ISVDTSKNQFSLKLSSVTAADTAVYYCARDRITIFG

KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC	SEQ ID NO: 399	VVMGGGMDVWGQGTTVTVSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
	NA	
	5C2.006	
	iPS:361222	

ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC AGCGTCCTCACCGTCCTGCACCAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCCAGCCCCCATCGAGAAAACCATC TCCAAAGCCAAAGGGCAGCCCCGAGAACCACA GGTGTACACCCTGCCCCCATCCCGGGAGGAGAT GACCAAGAACCAGGTCAGCCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGCAGCCGGAGAACAACT ACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG TAAA	SEQ ID NO: 1970	SEQ ID NO: 2127
	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK NYIAWYQQPGHPPKLLIYWASTRESGVPDRFSGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC	
AA		
		SEQ ID NO: 400	SEQ ID NO: 557

iPS:361229	5C2.007	NA		
CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG			GACATCGTGATGACCCAGTCTCCAGACTCCCTG	
AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC			GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC	
AAGGCTTCTGGATACACCTTCACCGGCTACTAT			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC	
ATCCACTGGGTGCGACAGGCCCCTGGACAAGGG			AACAATAAGAACTACATAGCTTGGTACCAGCAG	
CTTGAGTGGATGGGGGTGGATCAACCCTGAAAGT			CAACCAGGACATCCTCCTAAGCTGCTCATTTACT	
GGTGGCACAGACTATTCACAGAGGTTTCAGGGC			GGGCATCTACCCGGGGAATCCGGGGTCCCTGACC	
AGGTTCACCATGACCAGGGACACGTCCATCAGC			GATTCAGTGGCAGCGGGTCTGGGACAGATTTCA	
ACAGCCTACATGGAACTGAACAGGCTGAGATCT			CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG	
GACGACACGGCCGTGTATTACTGTGCGAGAGAG			TGGCAGTTTTTTACTGTCAACAATATTATAGTAC	
GCCACGATTTTTGGAATGGTTATTGTACCGTTTG			TCCGTGGACGTTCGGCCAAGGGACCAAGGTGGA	
ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT			AATCAAACGAACGGTGGCTGCACCATCTGTCTT	
CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC			CATCTTCCCGCCATCTGATGAGCAGTTGAAATCT	
CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGG			GGAACTGCCTCTGTTGTGTGCCTGCTGAATAACT	
CACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA			TCTATCCCAGAGAGGCCAAAGTACAGTGGAAGG	
CTTCCCCGAACCGGTGACGGTGTCGTGGAACTC			TGGATAACGCCCTCCAATCGGGTAACTCCCAGG	
AGGCGCCCTGACCAGCGGCGTGCACACCTTCCC			AGAGTGTCACAGAGCAGGACAAGGGACAGC	
GGCTGTCTCCTACAGTCCTCAGGACTCTACTCCCTC			ACCTACAGCCTCAGCAGCACCCTGACGCTGAGC	
AGCAGGCGTGGTGACCGTGCCCTCCAGCAGCTTG			AAAGCAGACTACGAGAAACACAAAGTCTACGCC	
GGCACCCAGACCTACATCTGCAACGTGAATCAC			CTGCGAAGTCACCCATCAGGGCCTGAGCTCGCC	
AAGCCCAGCAACACCAAGGTGGACAAGAAAGT			CGTCACAAAGAGCTTCAACAGGGGAGAGTGT	
TGAGCCCAAATCTTGTGACAAAACTCACACATG				
CCCACCGTGCCCAGCACCTGAACTCCTGGGGGG				
ACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAG				
GACACCCTCATGATCTCCCGGACCCCTGAGGTC				
ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC				
CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC				
GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT				
GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC				
AGCGTCCTCACCGTCCTGCACCAGGACTGGCTG				
AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC				
AAAGCCCTCCCAGCCCCCATCGAGAAAACCATC				
TCCAAAGCCAAAGGGCAGCCCCGAGAACCACA				
GGTGTACACCCTGCCCCCATCCCGGGAGGAGAT				
GACCAAGAACCAGGTCAGCCTGACCTGCCTGGT				
CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA				
GTGGGAGAGCAATGGGCAGCCGGAGAACAACT				

		ACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG TAAA
	SEQ ID NO: 1971	SEQ ID NO: 2128
AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK NYIAWYQQPGHPPKLLIYWASTRESGVPDRFSGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWINPESGGTDYSQRFQGR FTMTRDTSISTAYMELNRLRSDDTAVYYCAREATI FGMVIVPFDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
	SEQ ID NO: 401	SEQ ID NO: 558
NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAGCAG CAACCAGGACATCCTCCTCTAAGCTGCTCATTTACT GGGCATCTACCCGGGAATCCGGGGTCCCTGACC GATTCAGTGGCAGCGGGTCTGGGACAGATTTCA CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCGGCCAAGGGACCAAGGTGGA AATCAAACGAACGGTGGCTGCACCATCTGTCTT CATCTTCCCGCCATCTGATGAGCAGTTGAAATCT GGAACTGCCTCTGTTGTGCCTGCTGAATAACT TCTATCCCAGAGAGGCCAAAGTACAGTGGAAGG	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCGGCTACTAT ATCCACTGGGTGCGACAGGCCCCTGGACAAGGG CTTGAGTGGATGGGGGTGGATCAACCCTGACGCT GGTGGCACAGACTATTCACAGAGGTTTCAGGGC AGGGTCACCATGACCAGGGACACGTCCATCAGC ACAGCCTACATGGAACTGAACAGGCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGAG GCCACGATTTTTGGAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGG CACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA
	5C2.008	
	iPS:361236	

TGGATAACGCCCTCCAATCGGGTAACTCCCAGG AGAGTGTCACAGAGCAGGACAGCAAGGACAGC ACCTACAGCCTCAGCAGCACCCTGACGCTGAGC AAAGCAGACTACGAGAAACACAAAGTCTACGC CTGCGAAGTCACCCATCAGGGCCTGAGCTCGCC CGTCACAAAGAGCTTCAACAGGGGAGAGTGT	CTTCCCCGAACCGGTGACGGTGTCGTGGAACTC AGGCGCCCTGACCAGCGGCGTGCACACCTTCCC GGCTGTCCTACAGTCCTCAGGAACTCTACTCCCTC AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCCAGCAACACCAAGGTGGACAAGAAAGT TGAGCCCAAATCTTGTGACAAAACTCACACATG CCCACCGTGCCCAGCACCTGAACTCCTGGGGGG ACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAG GACACCCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT GAGGAGCAGTACGGCAGCACCGTACCGTTGTGTC AGCGTCCTCACCGTCCTGCACCAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCCAGCCCCCATCGAGAAAACCATC TCCAAAGCCAAAGGGCAGCCCCGAGAACCACA GGTGTACACCCTGCCCCCATCCCGGGAGGAGAT GACCAAGAACCAGGTCAGCCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGCAGCCGGAGAACAACT ACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG TAAA	
SEQ ID NO: 1972	SEQ ID NO: 2129	
AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK NYIAWYQQQPGHPPKLLIYWASTRESGVPDRFSGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWINPDAGGTDYSQRFQG RVTMTRDTSISTAYMELNRLRSDDTAVYYCAREA TIFGMVIVPFDYWGQGTLVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL

LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK SLSLSPGK	SEQ ID NO: 559	CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCGGCTACTAT ATCCACTGGGTGCGACAGGCCCCTGGACAAGGG CTTGAGTGGATGGGGGTGGATCAACCCTGACGCT GGTGGCACAGACTATTCACAGAGGTTTCAGGGC AGGTTCACCATGACCAGGGACACGTCCATCAGC ACAGCCTACATGGAACTGAACAGGCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGAG GCCACGATTTTTGGAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGG CACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTCGTGGAACTC AGGCGCCCTGACCAGCGGCGTGCACACCTTCCC GGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCCAGCAACACCAAGGTGGACAAGAAAGT TGAGCCCAAATCTTGTGACAAAACTCACACATG CCCACCGTGCCCAGCACCTGAACTCCTGGGGGG ACCGTCAGTCTTCCTCTTCCCCCAAAACCCAAG GACACCCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC
	SEQ ID NO: 402	GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAGCAG CAACCAGGACATCCTCCTCAAGCTGCTCATTTACT GGGCATCTACCCGGGAATCCGGGGTCCCTGACC GATTCAGTGGCAGCGGGTCTGGGACAGATTTCA CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCGGCCAAGGGACCAAGGTGGA AATCAAACGAACGGTGGCTGCACCATCTGTCTT CATCTTCCCGCCATCTGATGAGCAGTTGAAATCT GGAACTGCCTCTGTTGTGCCTGCTGAATAACT TCTATCCCAGAGAGGCCAAAGTACAGTGGAAGG TGGATAACGCCCTCCAATCGGGTAACTCCCAGG AGAGTGTCACAGAGCAGGACAGCAAGGACAGC ACCTACAGCCTCAGCAGCACCCTGACGCTGAGC AAAGCAGACTACGAGAAACACAAAGTCTACGC CTGCGAAGTCACCCATCAGGGCCTGAGCTCGCC CGTCACAAAGAGCTTCAACAGGGGAGAGTGT
	NA	
	5C2.009	
	iPS:359685	

		AGCGTCCTCACCGTCCTGCACCAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCCAGCCCCCATCGAGAAAACCATC TCCAAAGCCAAAGGGCAGCCCCGAGAACCACA GGTGTACACCCTGCCCCCATCCCGGGAGGAGAT GACCAAGAACCAGGTCAGCCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGCAGCCGGAGAACAACT ACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG TAAA
	SEQ ID NO: 1973	SEQ ID NO: 2130
AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK NYIAWYQQQPGHPPKLLIYWASTRESGVPDRFSGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWINPDAGGTDYSQRFQG RFTMTRDTSISTAYMELNRLRSDDTAVYYCAREA TIFGMVIVPFDYWGQGTLVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK SLSLSPGK
	SEQ ID NO: 403	SEQ ID NO: 560
NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAGCAG CAACCAGGACATCCTCCTAAGCTGCTCATTTACT GGGCATCTACCCGGGAATCCGGGGTCCCTGACC	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCGGCTACTAT ATCCACTGGGTGCGACAGGCCCCTGGACAAGGG CTTGAGTGGATGGGGGTGGATCAACCCTGACAGT GGTGGCACAGACTATTTCACAGAGGTTTCAGGGC
5C2.010		
iPS:361240		

AGGGTCACCATGACCAGGGACACGTCCATCAGC ACAGCCTACATGGAACTGAACAGGCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGAG GCCACGATTTTTGGAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGG CACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTCGTGGAACTC AGGCGCCCTGACCAGCGGCGTGCACACCTTCCC GGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCCAGCAACACCAAGGTGGACAAGAAAGT TGAGCCCAAATCTTGTGACAAAACTCACACATG CCCACCGTGCCCAGCACCTGAACTCCTGGGGGG ACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAG GACACCCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC AGCGTCCTCACCGTCCTGCACCAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCCAGCCCCCATCGAGAAAACCATC TCCAAAGCCAAAGGGCAGCCCCGAGAACCACA GGTGTACACCCTGCCCCCATCCCGGGAGGAGAT GACCAAGAACCAGGTCAGCCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGCAGCCGGAGAACAACT ACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG TAAA	GATTCAGTGGCAGCGGGTCTGGGACAGATTTCA CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCGGCCAAGGGACCAAGGTGGA AATCAAACGAACGGTGGCTGCACCATCTGTCTT CATCTTCCCGCCATCTGATGAGCAGTTGAAATCT GGAACTGCCTCTGTTGTGCCTGCTGAATAACT TCTATCCCAGAGAGGCCAAAGTACAGTGGAAGG TGGATAACGCCCTCCAATCGGGTAACTCCCAGG AGAGTGTCACAGAGCAGGACAGCAAGGACAGC ACCTACAGCCTCAGCAGCACCCTGACGCTGAGC AAAGCAGACTACGAGAAACACAAAGTCTACGCC CTGCGAAGTCACCCATCAGGGCCTGAGCTCGCC CGTCACAAAGAGCTTCAACAGGGGAGAGTGT		

		iPS:361247	
		5C2.011	
AA	SEQ ID NO: 1974	NA	SEQ ID NO: 404
	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK		GACATCGTGATGACCCAGTCTCCAGACTCCCTG
	NYIAWYQQPGHPPKLLIYWASTRESGVPDRFSGS		GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
	GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ		TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
	GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL		AACAATAAGAACTACATAGCTTGGTACCAGCAG
	NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK		CAACCAGGACATCCTCCTAAGCTGCTCATTTACT
	DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSP		GGGCATCTACCCGGGAATCCGGGGTCCCTGACC
	VTKSFNRGEC		GATTCAGTGGCAGCGGGTCTGGGACAGATTTCA
			CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG
			TGGCAGTTTTTTACTGTCAACAATATTATAGTAC
			TCCGTGGACGTTCGGCCAAGGGACCAAGGGTGGA
			AATCAAACGAACGGTGGCTGCACCATCTGTCTT
			CATCTTCCCGCCATCTGATGAGCAGTTGAAATCT
			GGAACTGCCTCTGTTGTGTGCCTGCTGAATAACT
			TCTATCCCAGAGAGGCCAAAGTACAGTGGAAGG
			TGGATAACGCCCTCCAATCGGGTAACTCCCAGG
			AGAGTGTCACAGAGCAGGACAGCAAGGACAGC
			ACCTACAGCCTCAGCAGCACCCTGACGCTGAGC
			AAAGCAGACTACGAGAAAACACAAAGTCTACGC
			CTGCGAAGTCACCCATCAGGGCCTGAGCTCGCC
			CGTCACAAAGAGCTTCAACAGGGGAGAGTGT
	SEQ ID NO: 2131		SEQ ID NO: 561
	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYI		CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTG
	HWVRQAPGQGLEWMGWINPDSGGTDYSQRFQGR		AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
	VTMTRDTSISTAYMELNRLRSDDTAVYYCAREATI		AAGGCTTCTGGATACACCTTCACCGGCTACTAT
	FGMVIVPFDYWGQGTLVTVSSASTKGPSVFPLAPS		ATCCACTGGGTGCGACAGGCCCCTGGACAAGGG
	SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS		CTTGAGTGGATGGGGGTGGATCAACCCTGACAGT
	GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN		GGTGGCACAGACTATTTCACAGAGGTTTCAGGGC
	VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL		AGGTTCACCATGACCAGGGACACGTCCATCAGC
	GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED		ACAGCCTACATGGAACTGAACAGGCTGAGATCT
	PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV		GACGACACGGCCGTGTATTACTGTGCGAGAGAG
	SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK		GCCACGATTTTTGGAATGGTTATTGTACCGTTTG
	AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF		ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
	YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY		CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC
	SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS		CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGG
	LSLSPGK		CACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA
			CTTCCCCGAACCGGTGACGGTGTCGTGGAACTC
			AGGCGCCCTGACCAGCGGCGTGCACACCTTCCC
			GGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC
			AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG
			GGCACCCAGACCTACATCTGCAACGTGAATCAC
			AAGCCCAGCAACACCAAGGTGGACAAGAAAGT

TGAGCCCAAATCTTGTGACAAAACTCACACATG CCCACCGTGCCCAGCACCTGAACTCCTGGGGGG ACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAG GACACCCTCATGATCTCCCGGACCCCCTGAGGTC ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC AGCGTCCTCACCGTCCTGCACCAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCCAGCCCCCATCGAGAAAACCATC TCCAAAGCCAAAGGGCAGCCCCGAGAACCACA GGTGTACACCCTGCCCCCATCCCGGGAGGAGAT GACCAAGAACCAGGTCAGCCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGCAGCCGGAGAACAACT ACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG TAAA	SEQ ID NO: 2132	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWINPDSGGTDYSQRFQGR FTMTRDTSISTAYMELNRLRSDDTAVYYCAREATI FGMVIVPFDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
		AA

		SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
	SEQ ID NO: 405	SEQ ID NO: 562
iPS:361254	NA	CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG
		AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
		AAGGCTTCTGGATACACCTTCACCGGCTACTAT
		ATCCACTGGGTGCGACAGGCCCCTGGACAAGGG
		CTTGAGTGGATGGGGTGGATCAACCCTGACAGT
		GGTGGCACAGACTATTTCACAGAGGTTTCAGGGC
		AGGGTCACCATGACCAGGGACACGTCCATCAGC
		ACAGCCTACATGGAACTGAACAGGCTGAGATCT
		GACGACACGGCCGTGTATTACTGTGCGAGAAG
		GCCACGATTTTTGGAATGGTTATTGTACCGTTTG
		ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
		CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC
		CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGG
		CACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA
		CTTCCCCGAACCGGTGACGGTGTCGTGGAACTC
		AGGCGCCCTGACCAGCGGCGTGCACACCTTCCC
		GGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC
		AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG
		GGCACCCAGACCTACATCTGCAACGTGAATCAC
		AAGCCCAGCAACACCAAGGTGGACAAGAAAGT
		TGAGCCCAAATCTTGTGACAAAACTCACACATG
		CCCACCGTGCCCAGCACCTGAACTCCTGGGGGG
		ACCGTCAGTCTTCCTCTTCCCCCAAAACCCAAG
		GACACCCTCATGATCTCCCGGACCCCTGAGGTC
		ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC
		CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC
		GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT
		GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC
		AGCGTCCTCACCGTCCTGCACCAGGACTGGCTG
		AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC
		AAAGCCCTCCCAGCCCCCATCGAGAAAACCATC
		TCCAAAGCCAAAGGGCAGCCCCGAGAACCACA
		GGTGTACACCCTGCCCCCATCCCGGGAGGAGAT

iPS:361261	5C2.013		
	NA		GACCAAGAACCAGGTCAGCCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGCAGCCGGAGAACAACT ACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG TAAA
	AA	SEQ ID NO: 1976	SEQ ID NO: 2133
		DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK NYIAWYQQPGHPPKLLIYWASTRESGVPDRFSGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWINPDSGGTDYSQRFQGR VTMTRDTSISTAYMELNRLRSDDTAVYYCAREATI FGMVIVPFDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
	NA	SEQ ID NO: 406	SEQ ID NO: 563
		GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAGCAG CAACCAGGACATCCTCCTAAGCTGCTCATTTACT GGGCATCTACCCGGGAATCCGGGGTCCCTGACC GATTCAGTGGCAGCGGGTCTGGGACAGATTTCA CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCGGCCAAGGGACCAAGGTGGA AATCAAACGAACGGTGGCTGCACCATCTGTCTT	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCGGCTACTAT ATCCACTGGGTGCGACAGGCCCCTGGACAAGGG CTTGAGTGGATGGGGGTGGATCAACCCTGACGCT GGTGGCACACAGACTATTCACAGAGGTTTCAGGGC AGGTTCACCATGACCAGGGACACGTCCATCAGC ACAGCCTACATGGAACTGAACAGGCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGAG GCCACGATTTTTGGAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT

	CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC
	CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGG
	CACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA
	CTTCCCCGAACCGGTGACGGTGTCGTGGAACTC
	AGGCGCCCTGACCAGCGGCGTGCACACCTTCCC
	GGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC
	AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG
	GGCACCCAGACCTACATCTGCAACGTGAATCAC
	AAGCCCAGCAACACCAAGGTGGACAAGAAAGT
	TGAGCCCAAATCTTGTGACAAAACTCACACATG
	CCCACCGTGCCCAGCACCTGAACTCCTGGGGGG
	ACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAG
	GACACCCTCATGATCTCCCGGACCCCTGAGGTC
	ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC
	CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC
	GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT
	GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC
	AGCGTCCTCACCGTCCTGCACCAGGACTGGCTG
	AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC
	AAAGCCCTCCCAGCCCCCATCGAGAAAACCATC
	TCCAAAGCCAAAGGGCAGCCCCGAGAACCACA
	GGTGTACACCCTGCCCCCATCCCGGGAGGAGAT
	GACCAAGAACCAGGTCAGCCTGACCTGCCTGGT
	CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA
	GTGGGAGAGCAATGGGCAGCCGGAGAACAACT
	ACAAGACCACGCCTCCCGTGCTGGACTCCGACG
	GCTCCTTCTTCCTCTCTATAGCAAGCTCACCGTGGA
	CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC
	ATGCTCCGTGATGCATGAGGCTCTGCACAACCA
	CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG
	TAAA
	SEQ ID NO: 2134
AA	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
	HWVRQAPGQGLEWMGWINPDAGGTDYSQRFQG
	RFTMTRDTSISTAYMELNRLRSDDTAVYYCAREA
	TIFGMVIVPFDYWGQGTLVTVSSASTKGPSVFPLA

	CATCTTCCCGCCATCTGATGAGCAGTTGAAATCT
	GGAACTGCCTCTGTTGTGCCTGCTGAATAACT
	TCTATCCCAGAGAGGCCAAAGTACAGTGGAAGG
	TGGATAACGCCCTCCAATCGGGTAACTCCCAGG
	AGAGTGTCACAGAGCAGGACAGCAAGGACAGC
	ACCTACAGCCTCAGCAGCACCCTGACGCTGAGC
	AAAGCAGACTACGAGAAACACAAAGTCTACGC
	CTGCGAAGTCACCCATCAGGGCCTGAGCTCGCC
	CGTCACAAAGAGCTTCAACAGGGGAGAGTGT
	SEQ ID NO: 1977
AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK
	NYIAWYQQPGHPPKLLIYWASTRESGVPDRFSGS
	GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ
	GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL

NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC		PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK SLSLSPGK
	SEQ ID NO: 407	SEQ ID NO: 564
	NA	
	GACATCGTGATGACCCAGTCTCCAGACTCCCTG	CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG
	GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC	AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
	TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC	AAGGCTTCTGGATACACCTTCACCGGCTACTAT
	AACAATAAGAACTACATAGCTTGGTACCAGCAG	ATCCACTGGGTGCGACAGGCCCCTGGACAAGGG
	CAACCAGGACATCCTCCTAAGCTGCTCATTTACT	CTTGAGTGGATGGGGGTGGATCAACCCTGACGCT
	GGGCATCTACCCGGGAATCCGGGGTCCCTGACC	GGTGGCACACAGACTATTTCACAGAGGTTTCAGGGC
	GATTCAGTGGCAGCGGGTCTGGGACAGATTTCA	AGGGTCACCATGACCAGGGACACCGTCCATCAGC
	CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG	ACAGCCTACATGGAACTGAACAGGCTGAGATCT
	TGGCAGTTTTTTACTGTCAACAATATTATAGTAC	GACGACACGGCCGTGTATTACTGTGCGAGAGAG
	TCCGTGGACGTTCGGCCAAGGGACCAAGGTGGA	GCCACGATTTTTGGAATGGTTATTGTACCGTTTG
	AATCAAACGAACGGTGGCTGCACCATCTGTCTT	ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
	CATCTTCCCGCCATCTGATGAGCAGTTGAAATCT	CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC
	GGAACTGCCTCTGTTGTGTGCCTGCTGAATAACT	CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGG
	TCTATCCCAGAGAGGCCAAAGTACAGTGGAAGG	CACAGCGGCCCCTGGGCTGCCTGGTCAAGGACTA
	TGGATAACGCCCTCCAATCGGGTAACTCCCAGG	CTTCCCCGAACCGGTGACGGTGTCGTGGAACTC
	AGAGTGTCACAGAGCAGGACAGCAAGGACAGC	AGGCGCCCTGACCAGCGGCGTGCACACCTTCCC
	ACCTACAGCCTCAGCAGCACCCTGACGCTGAGC	GGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC
	AAAGCAGACTACGAGAAACACAAAGTCTACGC	AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG
	CTGCGAAGTCACCCATCAGGGCCTGAGCTCGCC	GGCACCCAGACCTACATCTGCAACGTGAATCAC
	CGTCACAAAGAGCTTCAACAGGGGAGAGTGT	AAGCCCAGCAACACCAAGGTGGACAAGAAAGT
		TGAGCCCAAATCTTGTGACAAAACTCACACATG
		CCCACCGTGCCCAGCACCTGAACTCCTGGGGGG
		ACCGTCAGTCTTCCTCTTCCCCCAAAACCCAAG
		GACACCCTCATGATCTCCCGGACCCCTGAGGTC
		ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC

CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC AGCGTCCTCACCGTCCTGCACCAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCCAGCCCCCATCGAGAAAACCATC TCCAAAGCCAAAGGGCAGCCCCGAGAACCACA GGTGTACACCCTGCCCCCATCCCGGGAGGAGAT GACCAAGAACCAGGTCAGCCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGCAGCCGGAGAACAACT ACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG TAAA	SEQ ID NO: 1978	SEQ ID NO: 2135
	AA	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWINPDAGGTDYSQRFQG RVTMTRDTSISTAYMELNRLRSDDTAVYYCAREA TIFGMVIVPFDYWGQGTLVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK SLSLSPGK

iPS:359669		SEQ ID NO: 408	SEQ ID NO: 565
5C2.015		GACATCGTGATGACCCAGTCTCCAGACTCCCTG	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTG
		GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC	AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
		TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC	AAGGCTTCTGGATACACCTTCACCGGCTACTAT
		AACAATAAGAACTACATAGCTTGGTACCAGCAG	ATCCACTGGGTGCGACAGGCCCCTGGACAAGGG
		AAACCAGGACAACCTCCTAAGCTGCTCATTTAC	CTTGAGTGGATGGGGGTGGATCAACCCTGACGCT
		TGGGCATCTACCCGGGAATCCGGGTCCCTGAC	GGTGGCACAGACTATTTCACAGAGGTTTCAGGGC
		CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC	AGGGTCACCATGACCAGGGACACGTCCATCAGC
		ACTCTCACCATCAGCAGCCTGCAGGCTGAAGAT	ACAGCCTACATGGAACTGAACAGCCTGAGATCT
		GTGGCAGTTTTTTACTGTCAACAATATTATAGTA	GACGACACGGCCGTGTATTACTGTGCGAGAGAG
		CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG	GCCACGATTTTTGGAATGGTTATTGTACCGTTTG
		AAATCAAACGAACGGTGGCTGCACCATCTGTCT	ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
		TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC	CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC
		TGGAACTGCCTCTGTTGTGCCTGCTGAATAAC	CCTGGCACCCTCCTCCTCCAAGAGCACCTCTGGGGG
		TTCTATCCCAGAGAGGCCAAAGTACAGTGGAAG	CACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA
		GTGGATAACGCCCTCCAATCGGGTAACTCCCAG	CTTCCCCGAACCGGTGACGGTGTCGTGGAACTC
		GAGAGTGTCACAGAGCAGGACAGCAAGGACAG	AGGCGCCCTGACCAGCGGCGTGCACACCTTCCC
		CACCTACAGCCTCAGCAGCACCCTGACGCTGAG	GGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC
		CAAAGCAGACTACGAGAAACACAAAGTCTACG	AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG
		CCTGCGAAGTCACCCATCAGGGCCTGAGCTCGC	GGCACCCAGACCTACATCTGCAACGTGAATCAC
		CCGTCACAAAGAGCTTCAACAGGGGAGAGTGT	AAGCCCAGCAACACCAAGGTGGACAAGAAAGT
			TGAGCCCAAATCTTGTGACAAAACTCACACATG
			CCCACCGTGCCCAGCACCTGAACTCCTGGGGGGG
			ACCGTCAGTCTTCCTCTTCCCCCAAAACCCAAG
			GACACCCTCATGATCTCCCGGACCCCTGAGGTC
			ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC
			CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC
			GTGGAGGTGCATAATGCCAAGACAAAGCCGCGT
			GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC
			AGCGTCCTCACCGTCCTGCACCAGGACTGGCTG
			AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC
			AAAGCCCTCCCAGCCCCCATCGAGAAAACCATC
			TCCAAAGCCAAAGGGCAGCCCCGAGAACCACA
			GGTGTACACCCTGCCCCCATCCCGGGAGGAGAT
			GACCAAGAACCAGGTCAGCCTGACCTGCCTGGT
			CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA

		GTGGGAGAGCAATGGGCAGCCGGAGAACAACT ACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG TAAA
	SEQ ID NO: 1979	SEQ ID NO: 2136
AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK NYIAWYQQKPGQPPKLLIYWASTRESGVPDRFSGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWINPDAGGTDYSQRFQG RVTMTRDTSISTAYMELNSLRSDDTAVYYCAREA TIFGMVIVPFDYWGQGTLVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK SLSLSPGK
	SEQ ID NO: 409	SEQ ID NO: 566
NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAGCAG AAACCAGGACAACCTCCTAAGCTGCTCATTTAC TGGGCATCTACCCGGGAATCCGGGGTCCCTGAC CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGAT GTGGCAGTTTTTACTGTCAACAATATTATAGTA CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG AAATCAAACGAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC TGGAACTGCCTCTGTTGTGCCTGCTGAATAAC	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCGGCTACTAT ATCCACTGGGTGCGACAGGCCCCTGGACAAGGG CTTGAGTGGATGGGGGTGGATCAACCCTGAAAGT GGTGGCACAGACTATTCACAGAGGTTTCAGGGC AGGGTCACCATGACCAGGGACACGTCCATCAGC ACAGCCTACATGGAACTGAACAGCCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGAG GCCACGATTTTTGGAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGG

TTCTATCCCAGAGAGGCCAAAGTACAGTGGAAG GTGGATAACGCCCTCCAATCGGGTAACTCCCAG GAGAGTGTCACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCCTGACGCTGAG CAAAGCAGACTACGAGAAACACAAAGTCTACG CCTGCGAAGTCACCCATCAGGGCCTGAGCTCGC CCGTCACAAAGAGCTTCAACAGGGGAGAGTGT	SEQ ID NO: 1980	CACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTCGTGGAACTC AGGCGCCCTGACCAGCGGCGTGCACACCTTCCC GGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCCAGCAACACCAAGGTGGACAAGAAAGT TGAGCCCAAATCTTGTGACAAAACTCACACATG CCCACCGTGCCCAGCACCTGAACTCCTGGGGGG ACCGTCAGTCTTCCTCTTCCCCCAAAACCCAAG GACACCCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC AGCGTCCTCACCGTCCTGCACCAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCCAGCCCCCATCGAGAAAACCATC TCCAAAGCCAAAGGGCAGCCCCGAGAACCACA GGTGTACACCCTGCCCCCATCCCGGGAGGAGAT GACCAAGAACCAGGTCAGCCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGCAGCCGGAGAACAACT ACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG TAAA
	SEQ ID NO: 1980	SEQ ID NO: 2137
AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK NYIAWYQQKPGQPPKLLIYWASTRESGVPDRFSGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWINPESGGTDYSQRFQGR VTMTRDTSISTAYMELNSLRSDDTAVYYCAREATI FGMVIVPFDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN

iPS:361275		
11C1.002		
NA	DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC	VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
	SEQ ID NO: 410	SEQ ID NO: 567
	GACATCGTGATGACCCAGTCTCCAGACTCCCTG	CAGGTGCCGCTGGTACAGTCTGGGGCTGAGGTG
	TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC	AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
	TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC	AAGGCTTCTGGATACACCTTCACCGGCTACTAT
	AACAATAAGAACTACTTAGCTTGGTACCAACAG	ATACACTGGGGTGCGTCAGGCCCCTGGACAAGGG
	AAACCAGGACAGCCTCCTAACCTGCTCATTTAC	CTTGTGTGGATGGGGTGGATCAGCCCTAACAGT
	TGGACTTCTACCCGAGAATCCGGGGTCCCTGAC	GGTGAAACAAGCTATGCACAGAAGTTTCAGGAC
	CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC	AGGGTCACCATGACCAGGGACACGTCCATCAGC
	ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT	ACAGCCTATATGGAGCTGAGCAGACTGAGATCT
	GTGGCTGTTTATTACTGTCAGCAATATTATCGTA	GACGACACGGCCGTGTATTTCTGTGCGAGAGAG
	CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG	GCCACGATTTTTGGAATGCTTATTGTACCATTTG
	AAATCAAACGAACGGTGGCTGCACCATCTGTCT	ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
	TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC	CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC
	TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAAC	CCTGGCACCCTCCTCCTCCAAGAGCACCTCTGGGGG
	TTCTATCCCAGAGAGGCCAAAGTACAGTGGAAG	CACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA
	GTGGATAACGCCCTCCAATCGGGTAACTCCCAG	CTTCCCCGAACCGGTGACGGTGTCGTGGAACTC
	GAGAGTGTCACAGAGCAGGACAGCAAGGACAG	AGGCGCCCTGACCAGCGGCGTGCACACCTTCCC
	CACCTACAGCCTCAGCAGCACCCTGACGCTGAG	GGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC
	CAAAGCAGACTACGAGAAACACAAAGTCTACG	AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG
	CCTGCGAAGTCACCCATCAGGGCCTGAGCTCGC	GGCACCCAGACCTACATCTGCAACGTGAATCAC
	CCGTCACAAAGAGCTTCAACAGGGGAGAGTGT	AAGCCCAGCAACACCAAGGTGGACAAGAAAGT
		TGAGCCCAAATCTTGTGACAAAACTCACACATG
		CCCACCGTGCCCAGCACCTGAACTCCTGGGGGG
		ACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAG
		GACACCCTCATGATCTCCCGGACCCCTGAGGTC
		ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC
		CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC
		GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT

			GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC AGCGTCCTCACCGTCCTGCACCAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCCAGCCCCCATCGAGAAAACCATC TCCAAAGCCAAAGGGCAGCCCCGAGAACCACA GGTGTACACCCTGCCCCCATCCCGGGAGGAGAT GACCAAGAACCAGGTCAGCCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGCAGCCGGAGAACAACT ACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG TAAA
		SEQ ID NO: 1981	SEQ ID NO: 2138
	AA	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK NYLAWYQQKPGQPPNLLIYWTSTRESGVPDRFSG SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC	
	NA		GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC AACAATAAGAACTACTTAGCTTGGTACCAACAG AAACCAGGACAGCCTCCTAACCTGCTCATTTAC
	11C1.003		
	iPS:36128 2		

GGTGACACAAGCTATGCACAGAAGTTTCAGGAC	TGGACTTCTACCCGAGAATCCGGGGTCCCTGAC		
AGGGTCACCATGACCAGGGACACGTCCATCAGC	CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC		
ACAGCCTATATGGAGCTGAGCAGACTGAGATCT	ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT		
GACGACACGGCCGTGTATTTCTGTGCGAGAGAG	GTGGCTGTTTATTACTGTCAGCAATATTATCGTA		
GCCACGATTTTTGGAATGCTTATTGTACCATTTG	CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG		
ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT	AAATCAAACGAACGGTGGCTGCACCATCTGTCT		
CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC	TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC		
CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGG	TGGAACTGCCTCTGTTGTGCCTGCTGAATAAC		
CACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA	TTCTATCCCAGAGAGGCCAAAGTACAGTGGAAG		
CTTCCCCGAACCGGTGACGGTGTCGTGGAACTC	GTGGATAACGCCCTCCAATCGGGTAACTCCCAG		
AGGCGCCCTGACCAGCGGCGTGCACACCTTCCC	GAGAGTGTCACAGAGCAGGACAGGACAAGGACAG		
GGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC	CACCTACAGCCTCAGCAGCACCCTGACGCTGAG		
AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG	CAAAGCAGACTACGAGAAACACACAAAGTCTACG		
GGCACCCAGACCTACATCTGCAACGTGAATCAC	CCTGCGAAGTCACCCATCAGGGCCTGAGCTCGC		
AAGCCCAGCAACACCAAGGTGGACAAGAAAGT	CCGTCACAAAGAGCTTCAACAGGGGAGAGTGT		
TGAGCCCAAATCTTGTGACAAAACTCACACATG			
CCCACCGTGCCCAGCACCTGAACTCCTGGGGGG			
ACCGTCAGTCTTCCTCTTCCCCCAAAACCCAAG			
GACACCCTCATGATCTCCCGGACCCCCTGAGGTC			
ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC			
CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC			
GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT			
GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC			
AGCGTCCTCACCGTCCTGCACCAGGACTGGCTG			
AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC			
AAAGCCCTCCCAGCCCCCATCGAGAAAACCATC			
TCCAAAGCCAAAGGGCAGCCCCGAGAACCACA			
GGTGTACACCCTGCCCCCATCCCGGGAGGAGAT			
GACCAAGAACCAGGTCAGCCTGACCTGCCTGGT			
CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA			
GTGGGAGAGCAATGGGCAGCCGGAGAACAACT			
ACAAGACCACGCCTCCCGTGCTGGACTCCGACG			
GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA			
CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC			
ATGCTCCGTGATGCATGAGGCTCTGCACAACCA			

		CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG TAAA
	SEQ ID NO: 1982	SEQ ID NO: 2139
AA	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK NYLAWYQQKPGQPPNLLIYWTSTRESGVPDRFSG SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLVWMGWISPNSGDTSYAQKFQDR VTMTRDTSISTAYMELSRLRSDDTAVYFCAREATI FGMLIVPFDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
	SEQ ID NO: 412	SEQ ID NO: 569
NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC AACAATAAGAACTACTTAGCTTGGTACCAACAG AAACCAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTCAGCAATATTATCGTA CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG AAATCAAACGAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAAC TTCTATCCCAGAGAGGCCAAAGTACAGTGGAAG GTGGATAACGCCCTCCAATCGGGTAACTCCCAG GAGAGTGTCACAGAGGACAGGACAAGGACAG CACCTACAGCCTCAGCAGCACCCTGACGCTGAG CAAAGCAGACTACGAGAAACACAAAGTCTACG	CAGGTGCCGCTGGTACAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCGGCTACTAT ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG CTTGTGTGGATGGGGTGGATCAGCCCTAACAGT GGTGAAACAAGCTATGCACAGAAGTTTCAGGAC AGGGTCACCATGACCAGGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGACTGAGATCT GACGACACGGCCGTGTATTTCTGTGCGAGAGAG GCCACGATTTTTGGAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGG CACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTCGTGGAACTC AGGCGCCCTGACCAGCGGCGTGCACACCTTCCC GGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG

CCTGCGAAGTCACCCATCAGGGCCTGAGCTCGC CCGTCACAAAGAGCTTCAACAGGGGAGAGTGT		GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCCAGCAACACCAAGGTGGACAAGAAAGT TGAGCCCAAATCTTGTGACAAAACTCACACATG CCCACCGTGCCCAGCACCTGAACTCCTGGGGGG ACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAG GACACCCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT GAGGAGCAGTACGGCAGCACCGTACCGTTGTGTC AGCGTCCTCACCGTCCTGCACCAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCCAGCCCCCATCGAGAAAACCATC TCCAAAGCCAAAGGGCAGCCCCGAGAACCACA GGTGTACACCCTGCCCCCATCCCGGGAGGAGAT GACCAAGAACCAGGTCAGCCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGCAGCCGGAGAACAACT ACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG TAAA
	SEQ ID NO: 1983	SEQ ID NO: 2140
	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK NYLAWYQQKPGQPPNLLIYWTSTRDSGVPDRFSG SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLVWMGWISPNSGETSYAQKFQDR VTMTRDTSISTAYMELSRLRSDDTAVYFCAREATI FGMLIVPFDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF
	AA	

		YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
	SEQ ID NO: 413	SEQ ID NO: 570
	NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC AACAATAAGAACTACTTAGCTTGGTACCAACAG AAACCAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGAATCCGGGGTCCCTGAC CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTCAGCAATATTATCGTA CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG AAATCAAACGAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC TGGAACTGCCTCTGTTGTGCCTGCTGAATAAC TTCTATCCCAGAGAGGCCAAAGTACAGTGGAAG GTGGATAACGCCCTCCAATCGGGTAACTCCCAG GAGAGTGTCACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCCTGACGCTGAG CAAAGCAGACTACGAGAAACACAAAGTCTACG CCTGCGAAGTCACCCATCAGGGCCTGAGCTCGC CCGTCACAAAGAGCTTCAACAGGGGAGAGTGT
		11C1.005
		iPS:359712

		GGTGTACACCCTGCCCCCATCCCGGGAGGAGAT
		GACCAAGAACCAGGTCAGCCTGACCTGCCTGGT
		CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA
		GTGGGAGAGCAATGGGCAGCCGGAGAACAACT
		ACAAGACCACGCCTCCCGTGCTGGACTCCGACG
		GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA
		CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC
		ATGCTCCGTGATGCATGAGGCTCTGCACAACCA
		CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG
		TAAA
	SEQ ID NO: 1984	SEQ ID NO: 2141
AA	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK NYLAWYQQKPGQPPNLLIYWTSTRESGVPDRFSG SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLVWMGWISPNSGETSYAQKFQDR VTMTRDTSISTAYMELSRLRSDDTAVYFCTREATI FGMLIVPFDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
	SEQ ID NO: 414	SEQ ID NO: 571
NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC AACAATAAGAACTACTTAGCTTGGTACCAACAG AAACCAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGAATCCGGGGTCCCTGAC CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTCAGCAATATTATCGTA CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG	CAGGTGCCGCTGGTACAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCGGCTACTAT ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG CTTGTGTGGATGGGGTGGATCAGCCCTAACAGT GGTGACACAAGCTATGCACAGAAGTTTCAGGAC AGGGTCACCATGACCAGGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGACTGAGATCT GACGACACGGCCGTGTATTTCTGTACGAGAGAG GCCACGATTTTTGGAATGCTTATTGTACCATTTG
11C1.006		
iPS:361293		

AAATCAAACGAACGGTGGCTGCACCATCTGTCT	ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC	CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC
TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAAC	CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGG
TTCTATCCCAGAGAGGCCAAAGTACAGTGGAAG	CACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA
GTGGATAACGCCCTCCAATCGGGTAACTCCCAG	CTTCCCCGAACCGGTGACGGTGTCGTGGAACTC
GAGAGTGTCACAGAGCAGGACAGCAAGGACAG	AGGCGCCCTGACCAGCGGCGTGCACACCTTCCC
CACCTACAGCCTCAGCAGCACCCTGACGCTGAG	GGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC
CAAAGCAGACTACGAGAAACACAAAGTCTACG	AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG
CCTGCGAAGTCACCCATCAGGGCCTGAGCTCGC	GGCACCCAGACCTACATCTGCAACGTGAATCAC
CCGTCACAAAGAGCTTCAACAGGGGAGAGTGT	AAGCCCAGCAACACCAAGGTGGACAAGAAAGT
	TGAGCCCAAATCTTGTGACAAAACTCACACATG
	CCCACCGTGCCCAGCACCTGAACTCCTGGGGGG
	ACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAG
	GACACCCTCATGATCTCCCGGACCCCTGAGGTC
	ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC
	CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC
	GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT
	GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC
	AGCGTCCTCACCGTCCTGCACCAGGACTGGCTG
	AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC
	AAAGCCCTCCCAGCCCCCATCGAGAAAACCATC
	TCCAAAGCCAAAGGGCAGCCCCGAGAACCACA
	GGTGTACACCCTGCCCCCATCCCGGGAGGAGAT
	GACCAAGAACCAGGTCAGCCTGACCTGCCTGGT
	CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA
	GTGGGAGAGCAATGGGCAGCCGGAGAACAACT
	ACAAGACCACGCCTCCCGTGCTGGACTCCGACG
	GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA
	CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC
	ATGCTCCGTGATGCATGAGGCTCTGCACAACCA
	CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG
	TAAA
SEQ ID NO: 1985	SEQ ID NO: 2142
AA	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK NYLAWYQQKPGQPPNLLIYWTSTRESGVPDRFSG SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLVWMGWISPNSGDTSYAQKFQDR VTMTRDTSISTAYMELSRLRSDDTAVYFCTREATI

iPS;361297	11C1.007	NA	FGMLIVPFDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK	SEQ ID NO: 572	CAGGTGCCGCTGGTACAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCGGCTACTAT ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG CTTGTGTGGATGGGGTGGATCAGCCCTAACAGT GGTGAAACAAGCTATGCACAGAAGTTTCAGGAC AGGGTCACCATGACCAGGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGACTGAGATCT GACGACACGGCCGTGTATTTCTGTACGAGAGAG GCCACGATTTTTGGAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGG CACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTCGTGGAACTC AGGCGCCCTGACCAGCGGCGTGCACACCTTCCC GGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCCAGCAACACCAAGGTGGACAAGAAAGT TGAGCCCAAATCTTGTGACAAAACTCACACATG CCCACCGTGCCCAGCACCTGAACTCCTGGGGGG ACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAG GACACCCTCATGATCTCCCGGACCCCTGAGGTC

	ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC AGCGTCCTCACCGTCCTGCACCAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCCAGCCCCCATCGAGAAAACCATC TCCAAAGCCAAAGGGCAGCCCCGAGAACCACA GGTGTACACCCTGCCCCCATCCCGGGAGGAGAT GACCAAGAACCAGGTCAGCCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGCAGCCGGAGAACAACT ACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG TAAA
	SEQ ID NO: 1986
AA	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK NYLAWYQQKPGQPPNLLIYWTSTRDSGVPDRFSG SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC
	SEQ ID NO: 2143
	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLVWMGWISPNSGETSYAQKFQDR VTMTRDTSISTAYMELSRLRSDDTAVYFCTREATI FGMLIVPFDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
	SEQ ID NO: 416
	SEQ ID NO: 573

iPS:361301	11C1.008	NA		
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG	CAGGTGCCGCTGGTACAGTCTGGGGCTGAGGTG
			TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC	AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC	AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			AACAATAAGAACTACTTAGCTTGGTACCAACAG	ATACACTGGGGTGCGTCAGGCCCCTGGACAAGGG
			AAACCAGGACAGCCTCCTAACCTGCTCATTTAC	CTTGTGTGGATGGGGTGGATCAGCCCTAACAGT
			TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC	GGTGACACAAGCTATGCACAGAAGTTTCAGGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC	AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT	ACAGCCTATATGGAGCTGAGCAGACTGAGATCT
			GTGGCTGTTTATTACTGTCAGCAATATTATCGTA	GACGACACGGCCGTGTATTTCTGTGCGAGAGAG
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG	GCCACGATTTTTGGAATGCTTATTGTACCATTTG
			AAATCAAACGAACGGTGGCTGCACCATCTGTCT	ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC	CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC
			TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAAC	CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGG
			TTCTATCCCAGAGAGGCCAAAGTACAGTGGAAG	CACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA
			GTGGATAACGCCCTCCAATCGGGTAACTCCCAG	CTTCCCCGAACCGGTGACGGTGTCGTGGAACTC
			GAGAGTGTCACAGAGCAGGACAAGGACAGCAG	AGGCGCCCTGACCAGCGGCGTGCACACCTTCCC
			CACCTACAGCCTCAGCAGCACCCTGACGCTGAG	GGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC
			CAAAGCAGACTACGAGAAACACAAAGTCTACG	AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG
			CCTGCGAAGTCACCCATCAGGGCCTGAGCTCGC	GGCACCCAGACCTACATCTGCAACGTGAATCAC
			CCGTCACAAAGAGCTTCAACAGGGGAGAGTGT	AAGCCCAGCAACACCAAGGTGGACAAGAAAGT
				TGAGCCCAAATCTTGTGACAAAACTCACACATG
				CCCACCGTGCCCAGCACCTGAACTCCTGGGGGG
				ACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAG
				GACACCCTCATGATCTCCCGGACCCCCTGAGGTC
				ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC
				CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC
				GTGGAGGTGCATAATGCCAAGACAAAGCCGCGT
				GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC
				AGCGTCCTCACCGTCCTGCACCAGGACTGGCTG
				AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC
				AAAGCCCTCCCAGCCCCCATCGAGAAAACCATC
				TCCAAAGCCAAAGGGCAGCCCCGAGAACCACA
				GGTGTACACCCTGCCCCCATCCCGGGAGGAGAT
				GACCAAGAACCAGGTCAGCCTGACCTGCCTGGT
				CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA
				GTGGGAGAGCAATGGGCAGCCGGAGAACAACT

		ACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG TAAA
	SEQ ID NO: 1987	SEQ ID NO: 2144
AA	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK NYLAWYQQKPGQPPNLLIYWTSTRDSGVPDRFSG SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLVWMGWISPNSGDTSYAQKFQDR VTMTRDTSISTAYMELSRLRSDDTAVYFCAREATI FGMLIVPFDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
	SEQ ID NO: 417	SEQ ID NO: 574
NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC AACAATAAGAACTACTTAGCTTGGTACCAACAG AAACCAGGACAGCCTCCTAAACTGCTCATTTAC TGGACTTCTACCCGAGAATCCGGGGTCCCTGAC CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTCAGCAATATTATCGTA CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG AAATCAAACGAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC TGGAACTGCCTCTGTTGTGCCTGCTGAATAAC TTCTATCCCAGAGAGGCCAAAGTACAGTGGAAG	CAGGTGCAGCTGGTACAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCGGCTACTAT ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG CTTGAGTGGATGGGGGTGGATCAGCCCTAACAGT GGTGAAACAAGCTATGCACAGAAGTTTCAGGAC AGGGTCACCATGACCAGGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGCCTGAGATCT GACGACACGGCCGTGTATTTCTGTGCGAGAGAG GCCACGATTTTTGGAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGG CACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA
	11C1.009	
	iPS:359703	

GTGGATAACGCCCTCCAATCGGGTAACTCCCAG	CTTCCCCGAACCGGTGACGGTGTCGTGGAACTC	
GAGAGTGTCACAGAGCAGGACAGCAAGGACAG	AGGCGCCCTGACCAGCGGCGTGCACACCTTCCC	
CACCTACAGCCTCAGCAGCACCCTGACGCTGAG	GGCTGTCCTACAGTCCTCAGGAACTCTACTCCCTC	
CAAAGCAGACTACGAGAAACACAAAGTCTACG	AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG	
CCTGCGAAGTCACCCATCAGGGCCTGAGCTCGC	GGCACCCAGACCTACATCTGCAACGTGAATCAC	
CCGTCACAAAGAGCTTCAACAGGGGAGAGTGT	AAGCCCAGCAACACCAAGGTGGACAAGAAAGT	
	TGAGCCCAAATCTTGTGACAAAACTCACACATG	
	CCCACCGTGCCCAGCACCTGAACTCCTGGGGGG	
	ACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAG	
	GACACCCTCATGATCTCCCGGACCCCTGAGGTC	
	ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC	
	CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC	
	GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT	
	GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC	
	AGCGTCCTCACCGTCCTGCACCAGGACTGGCTG	
	AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC	
	AAAGCCCTCCCAGCCCCCATCGAGAAAACCATC	
	TCCAAAGCCAAAGGGCAGCCCCGAGAACCACA	
	GGTGTACACCCTGCCCCCATCCCGGGAGGAGAT	
	GACCAAGAACCAGGTCAGCCTGACCTGCCTGGT	
	CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA	
	GTGGGAGAGCAATGGGCAGCCGGAGAACAACT	
	ACAAGACCACGCCTCCCGTGCTGGACTCCGACG	
	GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA	
	CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC	
	ATGCTCCGTGATGCATGAGGCTCTGCACAACCA	
	CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG	
	TAAA	
SEQ ID NO: 1988	SEQ ID NO: 2145	
DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYI	
NYLAWYQQKPGQPPKLLIYWTSTRESGVPDRFSG	HWVRQAPGQGLEWMGWISPNSGETSYAQKFQDR	
SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF	VTMTRDTSISTAYMELSSLRSDDTAVYFCAREATI	
GQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVC	FGMLIVPFDYWGQGTLVTVSSASTKGPSVFPLAPS	
LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS	SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS	
KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSS	GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN	
PVTKSFNRGEC	VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL	

	iPS:361305	GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED
	11C1.010	PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV
	NA	SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK
		AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF
		YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
		SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS
		LSLSPGK
	SEQ ID NO: 418	SEQ ID NO: 575
	GACATCGTGATGACCCAGTCTCCAGACTCCCTG	CAGGTGCAGCTGGTACAGTCTGGGGCTGAGGTG
	TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC	AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
	TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC	AAGGCTTCTGGATACACCTTCACCGGCTACTAT
	AACAATAAGAACTACTTAGCTTGGTACCAACAG	ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
	AAACCAGGACAGCCTCCTAACCTGCTCATTTAC	CTTGAGTGGATGGGGGTGGATCAGCCCTAACAGT
	TGGACTTCTACCCGAGAATCCGGGGTCCCTGAC	GGTGAAACAAGCTATGCACAGAAGTTTCAGGAC
	CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC	AGGGTCACCATGACCAGGGACACGTCCATCAGC
	ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT	ACAGCCTATATGGAGCTGAGCAGACTGAGATCT
	GTGGCTGTTTATTACTGTCAGCAATATTATCGTA	GACGACACGGCCGTGTATTTCTGTGCGAGAGAG
	CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG	GCCACGATTTTTGGAATGCTTATTGTACCATTTG
	AAATCAAACGAACGGTGGCTGCACCATCTGTCT	ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
	TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC	CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC
	TGGAACTGCCTCTGTTGTGCCTGCTGAATAAC	CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGG
	TTCTATCCCAGAGAGGCCAAAGTACAGTGGAAG	CACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA
	GTGGATAACGCCCTCCAATCGGGTAACTCCCAG	CTTCCCCGAACCGGTGACGGTGTCGTGGAACTC
	GAGAGTGTCACAGAGCAGGACAGCAAGGACAG	AGGCGCCCTGACCAGCGGCGTGCACACCTTCCC
	CACCTACAGCCTCAGCAGCACCCTGACGCTGAG	GGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC
	CAAAGCAGACTACGAGAAACACAAAGTCTACG	AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG
	CCTGCGAAGTCACCCATCAGGGCCTGAGCTCGC	GGCACCCAGACCTACATCTGCAACGTGAATCAC
	CCGTCACAAAGAGCTTCAACAGGGGAGAGTGT	AAGCCCAGCAACACCAAGGTGGACAAGAAAGT
		TGAGCCCAAATCTTGTGACAAAACTCACACATG
		CCCACCGTGCCCAGCACCTGAACTCCTGGGGGG
		ACCGTCAGTCTTCCTCTTCCCCCAAAACCCAAG
		GACACCCTCATGATCTCCCGGACCCCTGAGGTC
		ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC
		CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC
		GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT
		GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC

		AGCGTCCTCACCGTCCTGCACCAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCCAGCCCCCATCGAGAAAACCATC TCCAAAGCCAAAGGGCAGCCCCGAGAACCACA GGTGTACACCCTGCCCCCATCCCGGGAGGAGAT GACCAAGAACCAGGTCAGCCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGCAGCCGGAGAACAACT ACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG TAAA
	SEQ ID NO: 1989	SEQ ID NO: 2146
AA	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK NYLAWYQQKPGQPPNLLIYWTSTRESGVPDRFSG SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWISPNSGETSYAQKFQDR VTMTRDTSISTAYMELSRLRSDDTAVYFCAREATI FGMLIVPFDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
	SEQ ID NO: 419	SEQ ID NO: 576
NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAGCAG AAACCAGGACATCCTCCTAAGCTGCTCATTTACT GGGCATCTACCCGGGAATCCGGGTCCCTGACC	CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCGGCTACTAT ATCCACTGGGTGCGACAGGCCCCTGGACAAGGA CTTGAGTGGATGGGGGTGGATCAACCCTGAAAGT GGTGGCACAGACTATTTCACAGAGGTTTCAGGGC
13H12.002		
iPS:361312		

AGGGTCACCATGACCAGGGACACGTCCATCAGC ACAGCCTACATGGAACTGAGCAGGCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGAG GCCACGATTTTTGGAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGG CACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTCGTGGAACTC AGGCGCCCTGACCAGCGGCGTGCACACCTTCCC GGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCCAGCAACACCAAGGTGGACAAGAAAGT TGAGCCCAAATCTTGTGACAAAACTCACACATG CCCACCGTGCCCAGCACCTGAACTCCTGGGGGG ACCGTCAGTCTTCCTCTTCCCCCAAAACCCAAG GACACCCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC AGCGTCCTCACCGTCCTGCACCAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCCAGCCCCCATCGAGAAAACCATC TCCAAAGCCAAAGGGCAGCCCCGAGAACCACA GGTGTACACCCTGCCCCCATCCCGGGAGGAGAT GACCAAGAACCAGGTCAGCCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGCAGCCGGAGAACAACT ACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG TAAA	GATTCAGTGGCAGCGGGTCTGGGACAGATTTCA CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCGGCCAAGGGACCAAGGTGGA AATCAAACGAACGGTGGCTGCACCATCTGTCTT CATCTTCCCGCCATCTGATGAGCAGTTGAAATCT GGAACTGCCTCTGTTGTGCCTGCTGAATAACT TCTATCCCAGAGAGGCCAAAGTACAGTGGAAGG TGGATAACGCCCTCCAATCGGGTAACTCCCAGG AGAGTGTCACAGAGCAGGACAGCAAGGACAGC ACCTACAGCCTCAGCAGCACCCTGACGCTGAGC AAAGCAGACTACGAGAAACACAAAGTCTACGCC CTGCGAAGTCACCCATCAGGGCCTGAGCTCGCC CGTCACAAAGAGCTTCAACAGGGGAGAGTGT		

	AA	SEQ ID NO: 1990	SEQ ID NO: 2147
		DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
		NYIAWYQQKPGHPPKLLIYWASTRESGVPDRFSGS	HWVRQAPGQGLEWMGWINPESGGTDYSQRFQGR
		GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ	VTMTRDTSISTAYMELSRLRSDDTAVYYCAREATI
		GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL	FGMVIVPFDYWGQGTLVTVSSASTKGPSVFPLAPS
		NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK	SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS
		DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSP	GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN
		VTKSFNRGEC	VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL
			GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED
			PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV
			SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK
			AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF
			YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
			SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS
			LSLSPGK
	NA	SEQ ID NO: 420	SEQ ID NO: 577
		GACATCGTGATGACCCAGTCTCCAGACTCCCTG	CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG
		GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC	AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
		TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC	AAGGCTTCTGGATACACCTTCACCGGCTACTAT
		AACAATAAGAACTACATAGCTTGGTACCAGCAG	ATCCACTGGGTGCGACAGGCCCCTGGACAAGGA
		AAACCAGGACATCCTCCTAAGCTGCTCATTTACT	CTTGAGTGGATGGGGGTGGATCAACCCTGAAAGT
		GGGCATCTACCCGGGAATCCGGGGTCCCTGACC	GGTGGCACAGACTATTTCACAGAGGTTTCAGGGC
		GATTCAGTGGCAGCGGGTCTGGGACAGATTTCA	AGGTTCACCATGACCAGGGACACGTCCATCAGC
		CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG	ACAGCCTACATGGAACTGAGCAGGCTGAGATCT
		TGGCAGTTTTTTACTGTCAACAATATTATAGTAC	GACGACACGGCCGTGTATTACTGTGCGAGAGAG
		TCCGTGGACGTTCGGCCAAGGGACCAAGGTGGA	GCCACGATTTTTGGAATGGTTATTGTACCGTTTG
		AATCAAACGAACGGTGGCTGCACCATCTGTCTT	ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
		CATCTTCCCGCCATCTGATGAGCAGTTGAAATCT	CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC
		GGAACTGCCTCTGTTGTGTGCCTGCTGAATAACT	CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGG
		TCTATCCCAGAGAGGCCAAAGTACAGTGGAAGG	CACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA
		TGGATAACGCCCTCCAATCGGGTAACTCCCAGG	CTTCCCCGAACCGGTGACGGTGTCGTGGAACTC
		AGAGTGTCACAGAGCAGGACAGCAAGGACAGC	AGGCGCCCTGACCAGCGGCGTGCACACCTTCCC
		ACCTACAGCCTCAGCAGCACCCTGACGCTGAGC	GGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC
		AAAGCAGACTACGAGAAACACAAAGTCTACGC	AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG
		CTGCGAAGTCACCCATCAGGGCCTGAGCTCGCC	GGCACCCAGACCTACATCTGCAACGTGAATCAC
		CGTCACAAAGAGCTTCAACAGGGGAGAGTGT	AAGCCCAGCAACACCAAGGTGGACAAGAAAGT

TGAGCCCAAATCTTGTGACAAAACTCACACATG CCCACCGTGCCCAGCACCTGAACTCCTGGGGGG ACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAG GACACCCTCATGATCTCCCGGACCCCCTGAGGTC ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC AGCGTCCTCACCGTCCTGCACCAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCCAGCCCCCATCGAGAAAACCATC TCCAAAGCCAAAGGGCAGCCCCGAGAACCACA GGTGTACACCCTGCCCCCATCCCGGGAGGAGAT GACCAAGAACCAGGTCAGCCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGCAGCCGGAGAACAACT ACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG TAAA	SEQ ID NO: 2148
	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWINPESGGTDYSQRFQGR FTMTRDTSISTAYMELSRLRSDDTAVYYCAREATI FGMVIVPFDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
AA	

		SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
	SEQ ID NO: 421	SEQ ID NO: 578
iPS:361319	GACATCGTGATGACCCAGTCTCCAGACTCCCTG	CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG
	GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC	AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
	TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC	AAGGCTTCTGGATACACCTTCACCGGCTACTAT
	AACAATAAGAACTACATAGCTTGGTACCAGCAG	ATCCACTGGGTGCGACAGGCCCCTGGACAAGGA
	AAACCAGGACATCCTCCTCTAAGCTGCTCATTTACT	CTTGAGTGGATGGGGGTGGATCAACCCTGACAGT
	GGGCATCTACCCGGGAATCCGGGGTCCCTGACC	GGTGGCACAGACTATTCACAGAGGTTTCAGGGC
	GATTCAGTGGCAGCGGGTCTGGGACAGATTTCA	AGGGTCACCATGACCAGGGACACGTCCATCAGC
	CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG	ACAGCCTACATGGAACTGAGCAGGCTGAGATCT
	TGGCAGTTTTTTACTGTCAACAATATTATAGTAC	GACGACACGGCCGTGTATTACTGTGCGAGAAG
	TCCGTGGACGTTCGGCCAAGGGACCAAGGTGGA	GCCACGATTTTTGGAATGGTTATTGTACCGTTTG
	AATCAAACGAACGGTGGCTGCACCATCTGTCTT	ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
	CATCTTCCCGCCATCTGATGAGCAGTTGAAATCT	CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC
	GGAACTGCCTCTGTTGTGTGCCTGCTGAATAACT	CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGG
	TCTATCCCAGAGAGGCCAAAGTACAGTGGAAGG	CACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA
	TGGATAACGCCCTCCAATCGGGTAACTCCCAGG	CTTCCCCGAACCGGTGACGGTGTCGTGGAACTC
	AGAGTGTCACAGAGCAGGACAGCAAGGACAGC	AGGCGCCCTGACCAGCGGCGTGCACACCTTCCC
	ACCTACAGCCTCAGCAGCACCCTGACGCTGAGC	GGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC
	AAAGCAGACTACGAGAAACACAAAGTCTACGC	AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG
	CTGCGAAGTCACCCATCAGGGCCTGAGCTCGCC	GGCACCCAGACCTACATCTGCAACGTGAATCAC
	CGTCACAAAGAGCTTCAACAGGGGAGAGTGT	AAGCCCAGCAACACCAAGGTGGACAAGAAAGT
		TGAGCCCAAATCTTGTGACAAAACTCACACATG
		CCCACCGTGCCCAGCACCTGAACTCCTGGGGGG
		ACCGTCAGTCTTCCTCTTCCCCCAAAACCCAAG
		GACACCCTCATGATCTCCCGGACCCCTGAGGTC
		ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC
		CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC
		GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT
		GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC
		AGCGTCCTCACCGTCCTGCACCAGGACTGGCTG
		AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC
		AAAGCCCTCCCAGCCCCCATCGAGAAAACCATC
		TCCAAAGCCAAAGGGCAGCCCCGAGAACCACA
		GGTGTACACCCTGCCCCCATCCCGGGAGGAGAT

			GACCAAGAACCAGGTCAGCCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGCAGCCGGAGAACAACT ACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG TAAA
	AA	SEQ ID NO: 1992	SEQ ID NO: 2149
		DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK NYIAWYQQKPGHPPKLLIYWASTRESGVPDRFSGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWINPDSGGTDYSQRFQGR VTMTRDTSISTAYMELSRLRSDDTAVYYCAREATI FGMVIVPFDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
	NA	SEQ ID NO: 422	SEQ ID NO: 579
		GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAGCAG AAACCAGGACAACCTCCTAAGCTGCTCATTTAC TGGGCATCTACCCGGGAATCCGGGGTCCCTGAC CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGAT GTGGCAGTTTTTACTGTCAACAATATTATAGTA CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG AAATCAAACGAACGGTGGCTGCACCATCTGTCT	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCGGCTACTAT ATCCACTGGGTGCGACAGGCCCCTGGACAAGGA CTTGAGTGGATGGGGGTGGATCAACCCTGAAAGT GGTGGCACACAGACTATTCACAGAGGTTTCAGGGC AGGGTCACCATGACCAGGGACACGTCCATCAGC ACAGCCTACATGGAACTGAGCAGCCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGAG GCCACGATTTTTGGAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT

TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC TGGAACTGCCTCTGTTGTGCCTGCTGAATAAC TTCTATCCCAGAGAGGCCAAAGTACAGTGGAAG GTGGATAACGCCCTCCAATCGGGTAACTCCCAG GAGAGTGTCACAGAGCAGGACAGGACAAGGACAG CACCTACAGCCTCAGCAGCACCCTGACGCTGAG CAAAGCAGACTACGAGAAACACAAAGTCTACG CCTGCGAAGTCACCCATCAGGGCCTGAGCTCGC CCGTCACAAAGAGCTTCAACAGGGGAGAGTGT	SEQ ID NO: 1993	CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGG CACAGCGGCCCTGGCTGCCTGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTCGTGGAACTC AGGCGCCCTGACCAGCGGCGTGCACACCTTCCC GGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCCAGCAACACCAAGGTGGACAAGAAAGT TGAGCCCAAATCTTGTGACAAAACTCACACATG CCCACCGTGCCCAGCACCTGAACTCCTGGGGGG ACCGTCAGTCTTCCTCTTCCCCCAAAACCCAAG GACACCCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC AGCGTCCTCACCGTCCTGCACCAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCCAGCCCCCATCGAGAAAACCATC TCCAAAGCCAAAGGGCAGCCCCGAGAACCACA GGTGTACACCCTGCCCCCATCCCGGGAGGAGAT GACCAAGAACCAGGTCAGCCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGCAGCCGGAGAACAACT ACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCTCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG TAAA
AA	SEQ ID NO: 2150	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWINPESGGTDYSQRFQGR VTMTRDTSISTAYMELSSLRSDDTAVYYCAREATI FGMVIVPFDYWGQGTLVTVSSASTKGPSVFPLAPS

NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC	SEQ ID NO: 423	SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
	NA	SEQ ID NO: 580
	13H12.006	GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAGCAG AAACCAGGACAACCTCCTAAGCTGCTCATTTAC TGGGCATCTACCCGGGAATCCGGGGTCCCTGAC CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGAT GTGGCAGTTTTTACTGTCAACAATATTATAGTA CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG AAATCAAACGAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAAC TTCTATCCCAGAGAGGCCAAAGTACAGTGGAAG GTGGATAACGCCCTCCAATCGGGTAACTCCCAG GAGAGTGTCACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCCTGACGCTGAG CAAAGCAGACTACGAGAAACACAAAGTCTACG CCTGCGAAGTCACCCATCAGGGCCTGAGCTCGC CCGTCACAAAGAGCTTCAACAGGGGAGAGTGT	CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCGGCTACTAT ATCCACTGGGTGCGACAGGCCCCTGGACAAGGA CTTGAGTGGATGGGGGTGGATCAACCCTGAAAGT GGTGGCACACAGACTATTCACAGAGGTTTCAGGGC AGGGTCACCATGACCAGGGACACCGTCCATCAGC ACAGCCTACATGGAACTGAGCAGGCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGAG GCCACGATTTTTGGAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGG CACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTCGTGGAACTC AGGCGCCCTGACCAGCGGCGTGCACACCTTCCC GGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCCAGCAACACCAAGGTGGACAAGAAAGT TGAGCCCAAATCTTGTGACAAAACTCACACATG CCCACCGTGCCCAGCACCTGAACTCCTGGGGGG ACCGTCAGTCTTCCTCTTCCCCCAAAACCCAAG GACACCCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC

	CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC
	GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT
	GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC
	AGCGTCCTCACCGTCCTGCACCAGGACTGGCTG
	AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC
	AAAGCCCTCCCAGCCCCCATCGAGAAAACCATC
	TCCAAAGCCAAAGGGCAGCCCCGAGAACCACA
	GGTGTACACCCTGCCCCCATCCCGGGAGGAGAT
	GACCAAGAACCAGGTCAGCCTGACCTGCCTGGT
	CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA
	GTGGGAGAGCAATGGGCAGCCGGAGAACAACT
	ACAAGACCACGCCTCCCGTGCTGGACTCCGACG
	GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA
	CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC
	ATGCTCCGTGATGCATGAGGCTCTGCACAACCA
	CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG
	TAAA
SEQ ID NO: 1994	SEQ ID NO: 2151
DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK NYIAWYQQKPGQPPKLLIYWASTRESGVPDRFSGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWINPESGGTDYSQRFQGR VTMTRDTSISTAYMELSRLRSDDTAVYYCAREATI FGMVIVPFDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
AA	
SEQ ID NO: 424	SEQ ID NO: 581

iPS:361330	12H11.002	NA		
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG	CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG
			TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC	AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC	AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			AACAATAAGAACTACTTAGCTTGGTACCAGCAG	ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
			AAACCAGGACAGCCTCCTAACCTGCTCATTTAC	CTTGAGTGGATGGGGGTGGATAAGCCCTAACCAA
			TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC	GGTGAAACAAACTATGCACAGAAGTTTCAGGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC	AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT	ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT
			GTGGCTGTTTATTACTGTCAGCAATATTATCGTA	GACGACACGGCCGTGTATTACTGTGCGAGAGAG
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG	GCCACGATTTTTGGAATGCTTATTGTACCATTTG
			AAATCAAACGAACGGTGGCTGCACCATCTGTCT	ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC	CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC
			TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAAC	CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGG
			TTCTATCCCAGAGAGGCCAAAGTACAGTGGAAG	CACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA
			GTGGATAACGCCCTCCAATCGGGTAACTCCCAG	CTTCCCCGAACCGGTGACGGTGTCGTGGAACTC
			GAGAGTGTCACAGAGCAGGACAGCAAGGACAG	AGGCGCCCTGACCAGCGGCGTGCACACCTTCCC
			CACCTACAGCCTCAGCAGCACCCTGACGCTGAG	GGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC
			CAAAGCAGACTACGAGAAACACAAAGTCTACG	AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG
			CCTGCGAAGTCACCCATCAGGGCCTGAGCTCGC	GGCACCCAGACCTACATCTGCAACGTGAATCAC
			CCGTCACAAAGAGCTTCAACAGGGGAGAGTGT	AAGCCCAGCAACACCAAGGTGGACAAGAAAGT
				TGAGCCCAAATCTTGTGACAAAACTCACACATG
				CCCACCGTGCCCAGCACCTGAACTCCTGGGGGG
				ACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAG
				GACACCCTCATGATCTCCCGGACCCCTGAGGTC
				ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC
				CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC
				GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT
				GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC
				AGCGTCCTCACCGTCCTGCACCAGGACTGGCTG
				AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC
				AAAGCCCTCCCAGCCCCCATCGAGAAAACCATC
				TCCAAAGCCAAAGGGCAGCCCCGAGAACCACA
				GGTGTACACCCTGCCCCCATCCCGGGAGGAGAT
				GACCAAGAACCAGGTCAGCCTGACCTGCCTGGT
				CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA
				GTGGGAGAGCAATGGGCAGCCGGAGAACAACT

		ACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG TAAA
	SEQ ID NO: 1995	SEQ ID NO: 2152
AA	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK NYLAWYQQKPGQPPNLLIYWTSTRDSGVPDRFSG SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWISPNQGETNYAQKFQD RVTMTRDTSISTAYMELSRLRSDDTAVYYCAREA TIFGMLIVPFDYWGQGTLVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK SLSLSPGK
	SEQ ID NO: 425	SEQ ID NO: 582
NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC AACAATAAGAACTACTTAGCTTGGTACCAGCAG AAACCAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTCAGCAATATTATCGTA CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG AAATCAAACGAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAAC TTCTATCCCAGAGAGGCCAAAGTACAGTGGAAG	CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCGGCTACTAT ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG CTTGAGTGGATGGGGGTGGATAAGCCCTAACCAA GGTGACACAAACTATGCACAGAAGTTTCAGGAC AGGGTCACCATGACCAGGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGAG GCCACGATTTTTGGAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGG CACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA
	12H11.003	
	iPS:361337	

GTGGATAACGCCCTCCAATCGGGTAACTCCCAG	CTTCCCCGAACCGGTGACGGTGTCGTGGAACTC	
GAGAGTGTCACAGAGCAGGACAGGACAAGGACAG	AGGCGCCCTGACCAGCGGCGTGCACACCTTCCC	
CACCTACAGCCTCAGCAGCACCCTGACGCTGAG	GGCTGTCCTACAGTCCTCAGGAACTCTACTCCCTC	
CAAAGCAGACTACGAGAAACACACAAAGTCTACG	AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG	
CCTGCGAAGTCACCCATCAGGGCCTGAGCTCGC	GGCACCCAGACCTACATCTGCAACGTGAATCAC	
CCGTCACAAAGAGCTTCAACAGGGGGAGAGTGT	AAGCCCAGCAACACCAAGGTGGACAAGAAAGT	
	TGAGCCCAAATCTTGTGACAAAACTCACACATG	
	CCCACCGTGCCCAGCACCTGAACTCCTGGGGGG	
	ACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAG	
	GACACCCTCATGATCTCCCGGACCCCTGAGGTC	
	ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC	
	CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC	
	GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT	
	GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC	
	AGCGTCCTCACCGTCCTGCACCAGGACTGGCTG	
	AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC	
	AAAGCCCTCCCAGCCCCCATCGAGAAAACCATC	
	TCCAAAGCCAAAGGGCAGCCCCGAGAACCACA	
	GGTGTACACCCTGCCCCCATCCCGGGAGGAGAT	
	GACCAAGAACCAGGTCAGCCTGACCTGCCTGGT	
	CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA	
	GTGGGAGAGCAATGGGCAGCCGGAGAACAACT	
	ACAAGACCACGCCTCCCGTGCTGGACTCCGACG	
	GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA	
	CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC	
	ATGCTCCGTGATGCATGAGGCTCTGCACAACCA	
	CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG	
	TAAA	
SEQ ID NO: 1996	SEQ ID NO: 2153	
DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI	
NYLAWYQQKPGQPPNLLIYWTSTRDSGVPDRFSG	HWVRQAPGQGLEWMGWISPNQGDTNYAQKFQD	
SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF	RVTMTRDTSISTAYMELSRLRSDDTAVYYCAREA	
GQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVC	TIFGMLIVPFDYWGQGTLVTVSSASTKGPSVFPLA	
LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS	PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT	
KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSS	SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC	
PVTKSFNRGEC	NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL	

		LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK SLSLSPGK
	SEQ ID NO: 426	SEQ ID NO: 583
		GACATCGTGATGACCCAGTCTCCAGACTCCCTG
		TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
		TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
		AACAATAAGAACTACTTAGCTTGGTACCAGCAG
		AAACCAGGACAGCCTCCTAACCTGCTCATTTAC
		TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC
		CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC
		ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT
		GTGGCTGTTTATTACTGTCAGCAATATTATCGTA
		CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG
		AAATCAAACGAACGGTGGCTGCACCATCTGTCT
		TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC
		TGGAACTGCCTCTGTTGTGCCTGCTGAATAAC
		TTCTATCCCAGAGAGGCCAAAGTACAGTGGAAG
		GTGGATAACGCCCTCCAATCGGGTAACTCCCAG
		GAGAGTGTCACAGAGGACAGGACAAGGACAG
		CACCTACAGCCTCAGCAGCACCCTGACGCTGAG
		CAAAGCAGACTACGAGAAACACAAAGTCTACG
		CCTGCGAAGTCACCCATCAGGGCCTGAGCTCGC
		CCGTCACAAAGAGCTTCAACAGGGGAGAGTGT
		CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG
		AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
		AAGGCTTCTGGATACACCTTCACCGGCTACTAT
		ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
		CTTGAGTGGATGGGGGTGGATAAGCCCTAACCAA
		GGTGAAACAAACTATGCACAGAAGTTTCAGGAC
		AGGGTCACCATGACCAGGGACACGTCCATCAGC
		ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT
		GACGACACGGCCGTGTATTACTGTACGAGAGAG
		GCCACGATTTTTGGAATGCTTATTGTACCATTTG
		ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
		CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC
		CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGG
		CACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA
		CTTCCCCGAACCGGTGACGGTGTCGTGGAACTC
		AGGCGCCCTGACCAGCGGCGTGCACACCTTCCC
		GGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC
		AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG
		GGCACCCAGACCTACATCTGCAACGTGAATCAC
		AAGCCCAGCAACACCAAGGTGGACAAGAAAGT
		TGAGCCCAAATCTTGTGACAAAACTCACACATG
		CCCACCGTGCCCAGCACCTGAACTCCTGGGGGG
		ACCGTCAGTCTTCCTCTTCCCCCAAAACCCAAG
		GACACCCTCATGATCTCCCGGACCCCTGAGGTC
		ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC
		CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC
		GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT
		GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC
	NA	
	12H11.004	
	iPS:361344	

		AGCGTCCTCACCGTCCTGCACCAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCCAGCCCCCATCGAGAAAACCATC TCCAAAGCCAAAGGGCAGCCCCGAGAACCACA GGTGTACACCCTGCCCCCATCCCGGGAGGAGAT GACCAAGAACCAGGTCAGCCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGCAGCCGGAGAACAACT ACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG TAAA
	SEQ ID NO: 1997	SEQ ID NO: 2154
AA	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK NYLAWYQQKPGQPPNLLIYWTSTRDSGVPDRFSG SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWISPNQGETNYAQKFQD RVTMTRDTSISTAYMELSRLRSDDTAVYYCTREA TIFGMLIVPFDYWGQGTLVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK SLSLSPGK
	SEQ ID NO: 427	SEQ ID NO: 584
NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC AACAATAAGAACTACTTAGCTTGGTACCAGCAG AAACCAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC	CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCGGCTACTAT ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG CTTGAGTGGATGGGGGTGGATAAGCCCTAACAAT GGTGAAACAAACTATGCACAGAAGTTTCAGGAC
12H11.005		
iPS:361351		

AGGGTCACCATGACCAGGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGAG GCCACGATTTTTGGAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGG CACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTCGTGGAACTC AGGCGCCCTGACCAGCGGCGTGCACACCTTCCC GGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCCAGCAACACCAAGGTGGACAAGAAAGT TGAGCCCAAATCTTGTGACAAAACTCACACATG CCCACCGTGCCCAGCACCTGAACTCCTGGGGGG ACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAG GACACCCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC AGCGTCCTCACCGTCCTGCACCAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCCAGCCCCCATCGAGAAAACCATC TCCAAAGCCAAAGGGCAGCCCCGAGAACCACA GGTGTACACCCTGCCCCCATCCCGGGAGGAGAT GACCAAGAACCAGGTCAGCCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGCAGCCGGAGAACAACT ACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG TAAA	CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTCAGCAATATTATCGTA CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG AAATCAAACGAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC TGGAACTGCCTCTGTTGTGCCTGCTGAATAAC TTCTATCCCAGAGAGGCCAAAGTACAGTGGAAG GTGGATAACGCCCTCCAATCGGGTAACTCCCAG GAGAGTGTCACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCCTGACGCTGAG CAAAGCAGACTACGAGAAACACAAAGTCTACG CCTGCGAAGTCACCCATCAGGGCCTGAGCTCGC CCGTCACAAAGAGCTTCAACAGGGGAGAGTGT		

AA	SEQ ID NO: 1998	SEQ ID NO: 2155	
	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK NYLAWYQQKPGQPPNLLIYWTSTRDSGVPDRFSG SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWISPNNGETNYAQKFQD RVTMTRDTSISTAYMELSRLRSDDTAVYYCAREA TIFGMLIVPFDYWGQGTLVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK SLSLSPGK
	SEQ ID NO: 428	SEQ ID NO: 585	
NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC AACAATAAGAACTACTTAGCTTGGTACCAGCAG AAACCAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTCAGCAATATTATCGTA CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG AAATCAAACGAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAAC TTCTATCCCAGAGAGGCCAAAGTACAGTGGAAG GTGGATAACGCCCTCCAATCGGGTAACTCCCAG GAGAGTGTCACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCCTGACGCTGAG CAAAGCAGACTACGAGAAACACAAAGTCTACG CCTGCGAAGTCACCCATCAGGGCCTGAGCTCGC CCGTCACAAAGAGCTTCAACAGGGGAGAGTGT	CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCGGCTACTAT ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG CTTGAGTGGATGGGGGTGGATAAGCCCTAACAAT GGTGACACAAACTATGCACAGAAGTTTCAGGAC AGGGTCACCATGACCAGGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGAG GCCACGATTTTTGGAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGG CACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTCGTGGAACTC AGGCGCCCTGACCAGCGGCGTGCACACCTTCCC GGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCCAGCAACACCAAGGTGGACAAGAAAGT

	TGAGCCCAAATCTTGTGACAAAACTCACACATG CCCACCGTGCCCAGCACCTGAACTCCTGGGGGG ACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAG GACACCCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC AGCGTCCTCACCGTCCTGCACCAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCCAGCCCCCATCGAGAAAACCATC TCCAAAGCCAAAGGGCAGCCCCGAGAACCACA GGTGTACACCCTGCCCCCATCCCGGGAGGAGAT GACCAAGAACCAGGTCAGCCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGCAGCCGGAGAACAACT ACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG TAAA	SEQ ID NO: 2156	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWISPNNGDTNYAQKFQD RVTMTRDTSISTAYMELSRLRSDDTAVYYCAREA TIFGMLIVPFDYWGQGTLVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL
		AA	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK NYLAWYQQKPGQPPNLLIYWTSTRDSGVPDRFSG SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC

		YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK SLSLSPGK
	SEQ ID NO: 429	SEQ ID NO: 586
NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG	CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG
	TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC	AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
	TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC	AAGGCTTCTGGATACACCTTCACCGGCTACTAT
	AACAATAAGAACTACTTAGCTTGGTACCAGCAG	ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
	AAACCAGGACAGCCTCCTAACCTGCTCATTTAC	CTTGAGTGGATGGGGGTGGATAAGCCCTAACCAA
	TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC	GGTGACACAAACTATGCACAGAAGTTTCAGGAC
	CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC	AGGGTCACCATGACCAGGGACACGTCCATCAGC
	ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT	ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT
	GTGGCTGTTTATTACTGTCAGCAATATTATCGTA	GACGACACGGCCGTGTATTACTGTACGAGAGAG
	CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG	GCCACGATTTTTGGAATGCTTATTGTACCATTTG
	AAATCAAACGAACGGTGGCTGCACCATCTGTCT	ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
	TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC	CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC
	TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAAC	CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGG
	TTCTATCCCAGAGAGGCCAAAGTACAGTGGAAG	CACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA
	GTGGATAACGCCCTCCAATCGGGTAACTCCCAG	CTTCCCCGAACCGGTGACGGTGTCGTGGAACTC
	GAGAGTGTCACAGAGGACAGGACAAGGACAG	AGGCGCCCTGACCAGCGGCGTGCACACCTTCCC
	CACCTACAGCCTCAGCACCCTGACGCTGAG	GGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC
	CAAAGCAGACTACGAGAAACACAAAGTCTACG	AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG
	CCTGCGAAGTCACCCATCAGGGCCTGAGCTCGC	GGCACCCAGACCTACATCTGCAACGTGAATCAC
	CCGTCACAAAGAGCTTCAACAGGGGAGAGTGT	AAGCCCAGCAACACCAAGGTGGACAAGAAAGT
		TGAGCCCAAATCTTGTGACAAAACTCACACATG
		CCCACCGTGCCCAGCACCTGAACTCCTGGGGGG
		ACCGTCAGTCTTCCTCTTCCCCCAAAACCCAAG
		GACACCCTCATGATCTCCCGGACCCCTGAGGTC
		ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC
		CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC
		GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT
		GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC
		AGCGTCCTCACCGTCCTGCACCAGGACTGGCTG
		AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC
		AAAGCCCTCCCAGCCCCCATCGAGAAAACCATC
		TCCAAAGCCAAAGGGCAGCCCCGAGAACCACA
		GGTGTACACCCTGCCCCCATCCCGGGAGGAGAT

		GACCAAGAACCAGGTCAGCCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGCAGCCGGAGAACAACT ACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG TAAA
	SEQ ID NO: 2000	SEQ ID NO: 2157
AA	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK NYLAWYQQKPGQPPNLLIYWTSTRDSGVPDRFSG SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWISPNQGDTNYAQKFQD RVTMTRDTSISTAYMELSRLRSDDTAVYYCTREA TIFGMLIVPFDYWGQGTLVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK SLSLSPGK
	SEQ ID NO: 430	SEQ ID NO: 587
NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC AACAATAAGAACTACTTAGCTTGGTACCAGCAG AAACCAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTCAGCAATATTATCGTA CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG AAATCAAACGAACGGTGGCTGCACCATCTGTCT	CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCGGCTACTAT ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG CTTGAGTGGATGGGGGTGGATAAGCCCTAACAAT GGTGAAACAAACTATGCACAGAAGTTTCAGGAC AGGGTCACCATGACCAGGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT GACGACACGGCCGTGTATTACTGTACGAGAGAG GCCACGATTTTTGGAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
	12H11.008	
	iPS:361372	

TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC	CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC
TGGAACTGCCTCTGTTGTGCCTGCTGAATAAC	CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGG
TTCTATCCCAGAGAGGCCAAAGTACAGTGGAAG	CACAGCGGCCCTGGCTGCCTGGTCAAGGACTA
GTGGATAACGCCCTCCAATCGGGTAACTCCCAG	CTTCCCCGAACCGGTGACGGTGTCGTGGAACTC
GAGAGTGTCACAGAGCAGGACAGGCAAGGACAG	AGGCGCCCTGACCAGCGGCGTGCACACCTTCCC
CACCTACAGCCTCAGCAGCACCCTGACGCTGAG	GGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC
CAAAGCAGACTACGAGAAACACAAAGTCTACG	AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG
CCTGCGAAGTCACCCATCAGGGCCTGAGCTCGC	GGCACCCAGACCTACATCTGCAACGTGAATCAC
CCGTCACAAAGAGCTTCAACAGGGGAGAGTGT	AAGCCCAGCAACACCAAGGTGGACAAGAAAGT
	TGAGCCCAAATCTTGTGACAAAACTCACACATG
	CCCACCGTGCCCAGCACCTGAACTCCTGGGGGG
	ACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAG
	GACACCCTCATGATCTCCCGGACCCCTGAGGTC
	ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC
	CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC
	GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT
	GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC
	AGCGTCCTCACCGTCCTGCACCAGGACTGGCTG
	AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC
	AAAGCCCTCCCAGCCCCCATCGAGAAAACCATC
	TCCAAAGCCAAAGGGCAGCCCCGAGAACCACA
	GGTGTACACCCTGCCCCCATCCCGGGAGGAGAT
	GACCAAGAACCAGGTCAGCCTGACCTGCCTGGT
	CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA
	GTGGGAGAGCAATGGGCAGCCGGAGAACAACT
	ACAAGACCACGCCTCCCGTGCTGGACTCCGACG
	GCTCCTTCTTCCTCTCTATAGCAAGCTCACCGTGGA
	CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC
	ATGCTCCGTGATGCATGAGGCTCTGCACAACCA
	CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG
	TAAA
SEQ ID NO: 2001	SEQ ID NO: 2158
AA	
DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
NYLAWYQQKPGQPPNLLIYWTSTRDSGVPDRFSG	HWVRQAPGQGLEWMGWISPNNGETNYAQKFQD
SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF	RVTMTRDTSISTAYMELSRLRSDDTAVYYCTREA
GQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVC	TIFGMLIVPFDYWGQGTLVTVSSASTKGPSVFPLA

		PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT
		SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC
		NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL
		LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
		DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC
		VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
		KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG
		FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL
		YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK
		SLSLSPGK
LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS	SEQ ID NO: 431	SEQ ID NO: 588
KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSS		
PVTKSFNRGEC		
		GACATCGTGATGACCCAGTCTCCAGACTCCCTG
		TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
		TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
		AACAATAAGAACTACTTAGCTTGGTACCAGCAG
		AAACCAGGACAGCCTCCTAACCTGCTCATTTAC
		TGGACTTCTACCCGAGAATCCGGGGTCCCTGAC
		CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC
		ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT
		GTGGCTGTTTATTACTGTCAGCAATATTATCGTA
		CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG
		AAATCAAACGAACGGTGGCTGCACCATCTGTCT
		TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC
NA		TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAAC
		TTCTATCCCAGAGAGGCCAAAGTACAGTGGAAG
		GTGGATAACGCCCTCCAATCGGGTAACTCCCAG
		GAGAGTGTCACAGAGCAGGACAGCAAGGACAG
		CACCTACAGCCTCAGCAGCACCCTGACGCTGAG
		CAAAGCAGACTACGAGAAACACAAAGTCTACG
		CCTGCGAAGTCACCCATCAGGGCCTGAGCTCGC
		CCGTCACAAAGAGCTTCAACAGGGGAGAGTGT
12H11.009		
iPS:361379		

	CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC AGCGTCCTCACCGTCCTGCACCAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCCAGCCCCCATCGAGAAAACCATC TCCAAAGCCAAAGGGCAGCCCCGAGAACCACA GGTGTACACCCTGCCCCCATCCCGGGAGGAGAT GACCAAGAACCAGGTCAGCCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGCAGCCGGAGAACAACT ACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG TAAA
	SEQ ID NO: 2159
	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWISPNQGETNYAQKFQD RVTMTRDTSISTAYMELSRLRSDDTAVYYCAREA TIFGMLIVPFDYWGQGTLVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK SLSLSPGK
AA	SEQ ID NO: 432
	SEQ ID NO: 589

iPS:361383	12H11.010	NA		
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG	CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG
			TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC	AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC	AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			AACAATAAGAACTACTTAGCTTGGTACCAGCAG	ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
			AAACCAGGACAGCCTCCTAACCTGCTCATTTAC	CTTGAGTGGATGGGGGTGGATAAGCCCTAACAAT
			TGGACTTCTACCCGAGAATCCGGGGTCCCTGAC	GGTGACACAAACTATGCACAGAAGTTTCAGGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC	AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT	ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT
			GTGGCTGTTTATTACTGTCAGCAATATTATCGTA	GACGACACGGCCGTGTATTACTGTGCGAGAGAG
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG	GCCACGATTTTTGGAATGCTTATTGTACCATTTG
			AAATCAAACGAACGGTGGCTGCACCATCTGTCT	ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC	CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC
			TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAAC	CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGG
			TTCTATCCCAGAGAGGCCAAAGTACAGTGGAAG	CACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA
			GTGGATAACGCCCTCCAATCGGGTAACTCCCAG	CTTCCCCGAACCGGTGACGGTGTCGTGGAACTC
			GAGAGTGTCACAGAGCAGGACAAGGACAGCAG	AGGCGCCCTGACCAGCGGCGTGCACACCTTCCC
			CACCTACAGCCTCAGCAGCACCCTGACGCTGAG	GGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC
			CAAAGCAGACTACGAGAAACACAAAGTCTACG	AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG
			CCTGCGAAGTCACCCATCAGGGCCTGAGCTCGC	GGCACCCAGACCTACATCTGCAACGTGAATCAC
			CCGTCACAAAGAGCTTCAACAGGGGAGAGTGT	AAGCCCAGCAACACCAAGGTGGACAAGAAAGT
				TGAGCCCAAATCTTGTGACAAAACTCACACATG
				CCCACCGTGCCCAGCACCTGAACTCCTGGGGGG
				ACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAG
				GACACCCTCATGATCTCCCGGACCCCCTGAGGTC
				ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC
				CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC
				GTGGAGGTGCATAATGCCAAGACAAAGCCGCGT
				GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC
				AGCGTCCTCACCGTCCTGCACCAGGACTGGCTG
				AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC
				AAAGCCCTCCCAGCCCCCATCGAGAAAACCATC
				TCCAAAGCCAAAGGGCAGCCCCGAGAACCACA
				GGTGTACACCCTGCCCCCATCCCGGGAGGAGAT
				GACCAAGAACCAGGTCAGCCTGACCTGCCTGGT
				CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA
				GTGGGAGAGCAATGGGCAGCCGGAGAACAACT

		ACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG TAAA
AA	SEQ ID NO: 2003	SEQ ID NO: 2160
	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK NYLAWYQQKPGQPPNLLIYWTSTRESGVPDRFSG SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWISPNNGDTNYAQKFQD RVTMTRDTSISTAYMELSRLRSDDTAVYYCAREA TIFGMLIVPFDYWGQGTLVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK SLSLSPGK
NA	SEQ ID NO: 433	SEQ ID NO: 590
	GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC AACAATAAGAACTACTTAGCTTGGTACCAGCAG AAACCAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGAATCCGGGGTCCCTGAC CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTCAGCAATATTATCGTA CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG AAATCAAACGAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC TGGAACTGCCTCTGTTGTGCCTGCTGAATAAC TTCTATCCCAGAGAGGCCAAAGTACAGTGGAAG	CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCGGCTACTAT ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG CTTGAGTGGATGGGGGTGGATAAGCCCTAACCAA GGTGACACAAAACTATGCACAGAAGTTTCAGGAC AGGGTCACCATGACCAGGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGAG GCCACGATTTTTGGAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGG CACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA
	12H11.011	
	iPS:361387	

GTGGATAACGCCCTCCAATCGGGTAACTCCCAG	CTTCCCCGAACCGGTGACGGTGTCGTGGAACTC
GAGAGTGTCACAGAGCAGGACAGGACAAGGACAG	AGGCGCCCTGACCAGCGGCGTGCACACCTTCCC
CACCTACAGCCTCAGCAGCACCCTGACGCTGAG	GGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC
CAAAGCAGACTACGAGAAACACAAAGTCTACG	AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG
CCTGCGAAGTCACCCATCAGGGCCTGAGCTCGC	GGCACCCAGACCTACATCTGCAACGTGAATCAC
CCGTCACAAAGAGCTTCAACAGGGGAGAGTGT	AAGCCCAGCAACACCAAGGTGGACAAGAAAGT
	TGAGCCCAAATCTTGTGACAAAACTCACACATG
	CCCACCGTGCCCAGCACCTGAACTCCTGGGGGG
	ACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAG
	GACACCCTCATGATCTCCCGGACCCCTGAGGTC
	ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC
	CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC
	GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT
	GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC
	AGCGTCCTCACCGTCCTGCACCAGGACTGGCTG
	AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC
	AAAGCCCTCCCAGCCCCCATCGAGAAAACCATC
	TCCAAAGCCAAAGGGCAGCCCCGAGAACCACA
	GGTGTACACCCTGCCCCCATCCCGGGAGGAGAT
	GACCAAGAACCAGGTCAGCCTGACCTGCCTGGT
	CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA
	GTGGGAGAGCAATGGGCAGCCGGAGAACAACT
	ACAAGACCACGCCTCCCGTGCTGGACTCCGACG
	GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA
	CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC
	ATGCTCCGTGATGCATGAGGCTCTGCACAACCA
	CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG
	TAAA
SEQ ID NO: 2004	SEQ ID NO: 2161
DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
NYLAWYQQKPGQPPNLLIYWTSTRESGVPDRFSG	HWVRQAPGQGLEWMGWISPNQGDTNYAQKFQD
SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF	RVTMTRDTSISTAYMELSRLRSDDTAVYYCAREA
GQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVC	TIFGMLIVPFDYWGQGTLVTVSSASTKGPSVFPLA
LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS	PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT
KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSS	SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC
PVTKSFNRGEC	NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL

		LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
		DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC
		VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
		KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG
		FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL
		YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK
		SLSLSPGK
	SEQ ID NO: 434	SEQ ID NO: 591
	GACATCGTGATGACCCAGTCTCCAGACTCCCTG	CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG
	TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC	AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
	TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC	AAGGCTTCTGGATACACCTTCACCGGCTACTAT
	AACAATAAGAACTACTTAGCTTGGTACCAGCAG	ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
	AAACCAGGACAGCCTCCTAACCTGCTCATTTAC	CTTGAGTGGATGGGGGTGGATAAGCCCTAACAAT
	TGGACTTCTACCCGAGAATCCGGGGTCCCTGAC	GGTGAAACAAACTATGCACAGAAGTTTCAGGAC
	CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC	AGGGTCACCATGACCAGGGACACGTCCATCAGC
	ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT	ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT
	GTGGCTGTTTATTACTGTCAGCAATATTATCGTA	GACGACACGGCCGTGTATTACTGTGCGAGAGAG
	CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG	GCCACGATTTTTGGAATGCTTATTGTACCATTTG
	AAATCAAACGAACGGTGGCTGCACCATCTGTCT	ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
	TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC	CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC
	TGGAACTGCCTCTGTTGTGCCTGCTGAATAAC	CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGG
	TTCTATCCCAGAGAGGCCAAAGTACAGTGGAAG	CACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA
	GTGGATAACGCCCTCCAATCGGGTAACTCCCAG	CTTCCCCGAACCGGTGACGGTGTCGTGGAACTC
	GAGAGTGTCACAGAGGACAGGACAAGGACAG	AGGCGCCCTGACCAGCGGCGTGCACACCTTCCC
	CACCTACAGCCTCAGCAGCACCCTGACGCTGAG	GGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC
	CAAAGCAGACTACGAGAAACACAAAGTCTACG	AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG
	CCTGCGAAGTCACCCATCAGGGCCTGAGCTCGC	GGCACCCAGACCTACATCTGCAACGTGAATCAC
	CCGTCACAAAGAGCTTCAACAGGGGAGAGTGT	AAGCCCAGCAACACCAAGGTGGACAAGAAAGT
		TGAGCCCAAATCTTGTGACAAAACTCACACATG
		CCCACCGTGCCCAGCACCTGAACTCCTGGGGGG
		ACCGTCAGTCTTCCTCTTCCCCCAAAACCCAAG
		GACACCCTCATGATCTCCCGGACCCCTGAGGTC
		ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC
		CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC
		GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT
		GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC

		iPS:361391
		12H11.012
	SEQ ID NO: 434	NA

		AGCGTCCTCACCGTCCTGCACCAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCCAGCCCCCATCGAGAAAACCATC TCCAAAGCCAAAGGGCAGCCCCGAGAACCACA GGTGTACACCCTGCCCCCATCCCGGGAGGAGAT GACCAAGAACCAGGTCAGCCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGCAGCCGGAGAACAACT ACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG TAAA
	SEQ ID NO: 2005	SEQ ID NO: 2162
AA	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK NYLAWYQQKPGQPPNLLIYWTSTRESGVPDRFSG SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWISPNNGETNYAQKFQD RVTMTRDTSISTAYMELSRLRSDDTAVYYCAREA TIFGMLIVPFDYWGQGTLVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK SLSLSPGK
	SEQ ID NO: 435	SEQ ID NO: 592
NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC AACAATAAGAACTACTTAGCTTGGTACCAGCAG AAACCAGGACAGCCTCCTAAACTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCGGCTACTAT ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG CTTGAGTGGATGGGGGTGGATAAGCCCTAACCAA GGTGAAACAAACTATGCACAGAAGTTTCAGGAC
	12H11.013	
	iPS:361395	

AGGGTCACCATGACCAGGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGCCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGAG GCCACGATTTTTGGAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGG CACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTCGTGGAACTC AGGCGCCCTGACCAGCGGCGTGCACACCTTCCC GGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCCAGCAACACCAAGGTGGACAAGAAAGT TGAGCCCAAATCTTGTGACAAAACTCACACATG CCCACCGTGCCCAGCACCTGAACTCCTGGGGGG ACCGTCAGTCTTCCTCTTCCCCCAAAACCCAAG GACACCCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC AGCGTCCTCACCGTCCTGCACCAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCCAGCCCCCATCGAGAAAACCATC TCCAAAGCCAAAGGGCAGCCCCGAGAACCACA GGTGTACACCCTGCCCCCATCCCGGGAGGAGAT GACCAAGAACCAGGTCAGCCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGCAGCCGGAGAACAACT ACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG TAAA	CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTCAGCAATATTATCGTA CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG AAATCAAACGAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC TGGAACTGCCTCTGTTGTGCCTGCTGAATAAC TTCTATCCCAGAGAGGCCAAAGTACAGTGGAAG GTGGATAACGCCCTCCAATCGGGTAACTCCCAG GAGAGTGTCACAGAGCAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCCTGACGCTGAG CAAAGCAGACTACGAGAAACACAAAGTCTACG CCTGCGAAGTCACCCATCAGGGCCTGAGCTCGC CCGTCACAAAGAGCTTCAACAGGGGAGAGTGT	

		iPS:361402	12H11.014
AA	SEQ ID NO: 2006	NA	SEQ ID NO: 436
	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK		GACATCGTGATGACCCAGTCTCCAGACTCCCTG
	NYLAWYQQKPGQPPKLLIYWTSTRDSGVPDRFSG		GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
	SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF		TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
	GQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVC		AACAATAAGAACTACTTAGCTTGGTACCAGCAG
	LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS		AAACCAGGACAGCCTCCTAAACTGCTCATTTAC
	KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSS		TGGACTTCTACCCGAGAATCCGGGGTCCCTGAC
	PVTKSFNRGEC		CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC
			ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT
			GTGGCTGTTTATTACTGTCAGCAATATTATCGTA
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG
			AAATCAAACGAACGGTGGCTGCACCATCTGTCT
			TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC
			TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAAC
			TTCTATCCCAGAGAGGCCAAAGTACAGTGGAAG
			GTGGATAACGCCCTCCAATCGGGTAACTCCCAG
			GAGAGTGTCACAGAGCAGGACAGCAAGGACAG
			CACCTACAGCCTCAGCAGCACCCTGACGCTGAG
			CAAAGCAGACTACGAGAAACACAAAGTCTACG
			CCTGCGAAGTCACCCATCAGGGCCTGAGCTCGC
			CCGTCACAAAGAGCTTCAACAGGGGAGAGTGT
			CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGGGTGGATAAGCCCTAACCAA
			GGTGAAACAAACTATGCACAGAAGTTTCAGGAC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTATATGGAGCTGAGCAGCCTGAGATCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGAG
			GCCACGATTTTTGGAATGCTTATTGTACCATTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC
			CCTGGCACCCTCCTCCTCCAAGAGCACCTCTGGGGG
			CACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA
			CTTCCCCGAACCGGTGACGGTGTCGTGGAACTC
			AGGCGCCCTGACCAGCGGCGTGCACACCTTCCC
			GGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC
			AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG
			GGCACCCAGACCTACATCTGCAACGTGAATCAC
			AAGCCCAGCAACACCAAGGTGGACAAGAAAGT

TGAGCCCAAATCTTGTGACAAAACTCACACATG CCCACCGTGCCCAGCACCTGAACTCCTGGGGGG ACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAG GACACCCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC AGCGTCCTCACCGTCCTGCACCAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCCAGCCCCCATCGAGAAAACCATC TCCAAAGCCAAAGGGCAGCCCCGAGAACCACA GGTGTACACCCTGCCCCCATCCCGGGAGGAGAT GACCAAGAACCAGGTCAGCCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGCAGCCGGAGAACAACT ACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG TAAA	SEQ ID NO: 2164 QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWISPNQGETNYAQKFQD RVTMTRDTSISTAYMELSSLRSDDTAVYYCAREA TIFGMLIVPFDYWGQGTLVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL
	AA

		YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK SLSLSPGK
	SEQ ID NO: 437	SEQ ID NO: 594
iPS:361406	NA	CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG
		AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
		AAGGCTTCCGGATACACCTTCACCGGCTACTAT
		ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG
		CTTGAGTGGATGGGATGGAACCCTAACAGT
		GGTGGCACAAACTATGCACAGAAGTTTCAGGGC
		AGGGTCACCATGACCAGGGACACGTCCATCAGT
		ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT
		GACGACACGGCCGTGTATTACTGTGCGAGAGGG
		GGGGATTACGTTTGGGGGACTTATCGGCCTCAC
		TACTACTACGGTATGGACGTCTGGGGCCAAGGG
		ACCACGGTCACCGTCTCCTCAGCCTCCACCAAG
		GGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCA
		AGAGCACCTCTGGGGGCACAGCGGCCCTGGGCT
		GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA
		CGGTGTCGTGGAACTCAGGCGCCCTGACCAGCG
		GCGTGCACACCTTCCCGGCTGTCCTACAGTCCTC
		AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT
		GCCCTCCAGCAGCTTGGGCACCCAGACCTACAT
		CTGCAACGTGAATCACAAGCCCAGCAACACCAA
		GGTGGACAAGAAAGTTGAGCCCAAATCTTGTGA
		CAAAACTCACACATGCCCACCGTGCCCAGCACC
		TGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTC
		CCCCCAAAACCCAAGGACACCCTCATGATCTCC
		CGGACCCCTGAGGTCACATGCGTGGTGGTGGAC
		GTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC
		TGGTACGTGGACGGCGTGGAGGTGCATAATGCC
		AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG
		CACGTACCGTTGTGTCAGCGTCCTCACCGTCCTG
		CACCAGGACTGGCTGAATGGCAAGGAGTACAA
		GTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCC
		CATCGAGAAAACCATCTCCAAAGCCAAAGGGCA
		GCCCCGAGAACCACAGGTGTACACCCTGCCCCC

		ATCCCGGGAGGAGATGACCAAGAACCAGGTCA
		GCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA
		GCGACATCGCCGTGGAGTGGGAGAGCAATGGG
		CAGCCGGAGAACAACTACAAGACCACGCCTCCC
		GTGCTGGACTCCGACGGCTCCTTCTTCCTCTATA
		GCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
		CAGGGGAACGTCTTCTCATGCTCCGTGATGCAT
		GAGGCTCTGCACAACCACTACACGCAGAAGAGC
		CTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 2008	SEQ ID NO: 2165
AA	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSQTVNW YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDESLSGPVFGGGTK LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD FYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKY AASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV APTECS	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG GDYVWGTYRPHYYYGMDVWGQGTTVTVSSAST KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK
	SEQ ID NO: 438	SEQ ID NO: 595
NA	CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT CTGGAAGTAGCTCCAACATCGGAAGTCAAACTG TAAACTGGTACCAGCACCTCCCAGGAACGGCCC CCAAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATGAAAGCCTGCAAGGTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCCTAGGTC AGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCC	CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCCGGATACACCTTCACCGGCTACTAT ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG CTTGAGTGGATGGGATGGAACCCTAACAGT GGTGGCACAAACTATGCACAGAAGTTTCAGGGC AGGGTCACCATGACCAGGGACACCGTCCATCAGT ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT GACGACACGGCCGTGTATTACTGTGCGAGAGGG GGGGATTACGTTTGGGGGACTTATCGGCCTCAC TACTACTACGGTATGGACGTCTGGGGCCAAGGG
2C2.005.002		
iPS:361412		

			ACCACGGTCACCGTCTCCTCAGCCTCCACCAAG
			GGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCA
			AGAGCACCTCTGGGGGCACAGCGGCCCTGGGCT
			GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA
			CGGTGTCGTGGAACTCAGGCGCCCTGACCAGCG
			GCGTGCACACCTTCCCGGCTGTCCTACAGTCCTC
			AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT
			GCCCTCCAGCAGCTTGGGCACCCAGACCTACAT
			CTGCAACGTGAATCACAAGCCCAGCAACACCAA
			GGTGGACAAGAAAGTTGAGCCCAAATCTTGTGA
			CAAAACTCACACATGCCCACCGTGCCCAGCACC
			TGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTC
			CCCCCAAAACCCAAGGACACCCTCATGATCTCC
			CGGACCCCTGAGGTCACATGCGTGGTGGTGGAC
			GTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC
			TGGTACGTGGACGGCGTGGAGGTGCATAATGCC
			AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG
			CACGTACCGTTGTGTCAGCGTCCTCACCGTCCTG
			CACCAGGACTGGCTGAATGGCAAGGAGTACAA
			GTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCC
			CATCGAGAAAACCATCTCCAAAGCCAAAGGGCA
			GCCCCGAGAACCACAGGTGTACACCCTGCCCCC
			ATCCCGGGAGGAGATGACCAAGAACCAGGTCA
			GCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA
			GCGACATCGCCGTGGAGTGGGAGAGCAATGGG
			CAGCCGGAGAACAACTACAAGACCACGCCTCCC
			GTGCTGGACTCCGACGGCTCCTTCTTCCTCTATA
			GCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
			CAGGGGAACGTCTTCTCATGCTCCGTGATGCAT
			GAGGCTCTGCACAACCACTACACGCAGAAGAGC
			CTCTCCCTGTCTCCGGGTAAA
		SEQ ID NO: 2009	SEQ ID NO: 2166
AA		QSVLTQPPSASGTPGQRVTISCSGSSSNIGSQTVNW	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY
		YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS	MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ
		ASLAISGLQSEDEADYFCATFDESLQGPVFGGGTK	GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG
		LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD	GDYVWGTYRPHYYYGMDVWGQGTTVTVSSAST

		KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT
		VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPS
		SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH
		TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT
		CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE
		EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK
		ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ
		VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
		LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA
		LHNHYTQKSLSLSPGK
	SEQ ID NO: 439	SEQ ID NO: 596
iPS:361418	NA	CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG
		AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
		AAGGCTTCCGGATACACCTTCACCGGCTACTAT
		ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG
		CTTGAGTGGATGGGATGGATCAACCCTAACAGT
		GGTGGCACAAACTATGCACAGAAGTTTCAGGGC
		AGGGTCACCATGACCAGGGACACCGTCCATCAGT
		ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT
		GACGACACGGCCGTGTATTACTGTGCGAGAGGG
		GGGGATTACGTTTGGGGGACTTATCGGCCTCAC
		TACTACTACGGTATGGACGTCTGGGGCCAAGGG
		ACCACGGTCACCGTCTCCTCAGCCTCCACCAAG
		GGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCA
		AGAGCACCTCTGGGGGCACAGCGGCCCTGGGCT
		GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA
		CGGTGTCGTGGAACTCAGGCGCCCTGACCAGCG
		GCGTGCACACCTTCCCGGCTGTCCTACAGTCCTC
		AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT
		GCCCTCCAGCAGCTTGGGCACCCAGACCTACAT
		CTGCAACGTGAATCACAAGCCCAGCAACACCAA
		GGTGGACAAGAAAGTTGAGCCCAAATCTTGTGA
		CAAAACTCACACATGCCCACCGTGCCCAGCACC
		TGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTC
		CCCCCAAAACCCAAGGACACCCTCATGATCTCC
		CGGACCCCTGAGGTCACATGCGTGGTGGTGGAC

	GTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC
	TGGTACGTGGACGGCGTGGAGGTGCATAATGCC
	AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG
	CACGTACCGTTGTGTCAGCGTCCTCACCGTCCTG
	CACCAGGACTGGCTGAATGGCAAGGAGTACAA
	GTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCC
	CATCGAGAAAACCATCTCCAAAGCCAAAGGGCA
	GCCCCGAGAACCACAGGTGTACACCCTGCCCCC
	ATCCCGGGAGGAGATGACCAAGAACCAGGTCA
	GCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA
	GCGACATCGCCGTGGAGTGGGAGAGCAATGGG
	CAGCCGGAGAACAACTACAAGACCACGCCTCCC
	GTGCTGGACTCCGACGGCTCCTTCTTCCTCTATA
	GCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
	CAGGGGAACGTCTTCTCATGCTCCGTGATGCAT
	GAGGCTCTGCACAACCACTACACGCAGAAGAGC
	CTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 2167
SEQ ID NO: 2010	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY
QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNYVNW	MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ
YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS	GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG
ASLAISGLQSEDEADYFCATFDESLSGPVFGGGTK	GDYVWGTYRPHYYYGMDVWGQGTTVTVSSAST
LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD	KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT
FYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKY	VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPS
AASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV	SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH
APTECS	TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT
	CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE
	EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK
	ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ
	VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
	LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA
	LHNHYTQKSLSLSPGK
AA	SEQ ID NO: 440

iPS:361424	2C2.005.004	NA	CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG	CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG
			GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT	AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			CTGGAAGTAGCTCCAACATCGGAAGTAATTATG	AAGGCTTCCGGATACACCTTCACCGGCTACTAT
			TAAACTGGTACCAGCACCTCCCAGGAACGGCCC	ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG
			CCAAACTCCTCATCTATACTAATAATCAGCGGC	CTTGAGTGGATGGGATGGATCAACCCTAACAGT
			CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA	GGTGGCACAAACTATGCACAGAAGTTTCAGGGC
			GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG	AGGGTCACCATGACCAGGGACACGTCCATCAGT
			CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG	ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT
			CAACATTCGATGAAAGCCTGCAAGGTCCGGTAT	GACGACACGGCCGTGTATTACTGTGCGAGAGGG
			TCGGCGGAGGGACCAAGCTGACCGTCCTAGGTC	GGGGATTACGTTTGGGGGACTTATCGGCCTCAC
			AGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCC	TACTACTACGGTATGGACGTCTGGGGCCAAGGG
			GCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGC	ACCACGGTCACCGTCTCCTCAGCCTCCACCAAG
			CACACTGGTGTGTCTCATAAGTGACTTCTACCCG	GGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCA
			GGAGCCGTGACAGTGGCCTGGAAGGCAGATAG	AGAGCACCTCTGGGGGGCACAGCGGCCCTGGGCT
			CAGCCCCGTCAAGGCGGGAGTGGAGACCACCAC	GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA
			ACCCTCCAAACAAAGCAACAACAAGTACGCGGC	CGGTGTCGTGGAACTCAGGCGCCCTGACCAGCG
			CAGCAGCTATCTGAGCCTGACGCCTGAGCAGTG	GCGTGCACACCTTCCCGGCTGTCCTACAGTCCTC
			GAAGTCCCACAGAAGCTACAGCTGCCAGGTCAC	AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT
			GCATGAAGGGAGCACCGTGGAGAAGACAGTGG	GCCCTCCAGCAGCTTGGGCACCCAGACCTACAT
			CCCCTACAGAATGTTCA	CTGCAACGTGAATCACAAGCCCAGCAACACCAA
				GGTGGACAAGAAAGTTGAGCCCAAATCTTGTGA
				CAAAACTCACACATGCCCACCGTGCCCAGCACC
				TGAACTCCTGGGGGGGACCGTCAGTCTTCCTCTTC
				CCCCCAAAACCCAAGGACACCCTCATGATCTCC
				CGGACCCCTGAGGTCACATGCGTGGTGGTGGAC
				GTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC
				TGGTACGTGGACGGCGTGGAGGTGCATAATGCC
				AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG
				CACGTACCGTTGTGTCAGCGTCCTCACCGTCCTG
				CACCAGGACTGGCTGAATGGCAAGGAGTACAA
				GTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCC
				CATCGAGAAAACCATCTCCAAAGCCAAAGGGCA
				GCCCCGAGAACCACAGGTGTACACCCTGCCCCC
				ATCCCGGGAGGAGATGACCAAGAACCAGGTCA
				GCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA
				GCGACATCGCCGTGGAGTGGGAGAGCAATGGG

		CAGCCGGAGAACAACTACAAGACCACGCCTCCC
		GTGCTGGACTCCGACGGCTCCTTCTTCCTCTATA
		GCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
		CAGGGGAACGTCTTCTCATGCTCCGTGATGCAT
		GAGGCTCTGCACAACCACTACACGCAGAAGAGC
		CTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 2011	SEQ ID NO: 2168
AA	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNYVNW YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDESLQGPVFGGGTK LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD FYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKY AASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV APTECS	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG GDYVWGTYRPHYYYGMDVWGQGTTVTVSSAST KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK
	SEQ ID NO: 441	SEQ ID NO: 598
NA	CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG GGACCCCGGGCAGAGGGTCACCATCTCTTGTT CTGGAAGTAGCTCCAACATCGGAAGTCAAACTG TAAACTGGTACCAGCACCTCCCAGGAACGGCCC CCAAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATGACAGCCTGAATGGTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCCTAGGTC AGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCC GCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGC CACACTGGTGTGTCTCATAAGTGACTTCTACCCG GGAGCCGTGACAGTGGCCTGGAAGGCAGATAG	CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCCGGATACACCTTCACCGGCTACTAT ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG CTTGAGTGGATGGGATGGGATCAACCCTAACAGT GGTGGCACAAACTATGCACAGAAGTTTCAGGGC AGGGTCACCATGACCAGGGACACGTCCATCAGT ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT GACGACACGGCCGTGTATTACTGTGCGAGAGGG GGGGATTACGTTTGGGGGACTTATCGGCCTCAC TACTACTACGGTATGGACGTCTGGGGCCAAGGG ACCACGGTCACCGTCTCCTCAGCCTCCACCAAG GGCCCATCGGTCTTCCCCCTGGCACCCTCTCCA AGAGCACCTCTGGGGGCACAGCGGCCCTGGGCT
	2C2.005.005	
	iPS:361430	

CAGCCCCGTCAAGGCGGGAGTGGAGACCACCAC ACCCTCCAAACAAAGCAACAACAAGTACGCGGC CAGCAGCTATCTGAGCCTGACGCCTGAGCAGTG GAAGTCCCACAGAAGCTACAGCTGCCAGGTCAC GCATGAAGGGAGCACCGTGGAGAAGACAGTGG CCCCTACAGAATGTTCA	SEQ ID NO: 2012	GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA CGGTGTCGTGGAACTCAGGCGCCCTGACCAGCG GCGTGCACACCTTCCCGGCTGTCCTACAGTCCTC AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT GCCCTCCAGCAGCTTGGGCACCCAGACCTACAT CTGCAACGTGAATCACAAGCCCAGCAACACCAA GGTGGACAAGAAAGTTGAGCCCAAATCTTGTGA CAAAACTCACACATGCCCACCGTGCCCAGCACC TGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTC CCCCCAAAACCCAAGGACACCCTCATGATCTCC CGGACCCCTGAGGTCACATGCGTGGTGGTGGAC GTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC TGGTACGTGGACGGCGTGGAGGTGCATAATGCC AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG CACGTACCGTTGTGTCAGCGTCCTCACCGTCCTG CACCAGGACTGGCTGAATGGCAAGGAGTACAA GTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCC CATCGAGAAAACCATCTCCAAAGCCAAAGGGCA GCCCCGAGAACCACAGGTGTACACCCTGCCCCC ATCCCGGGAGGAGATGACCAAGAACCAGGTCA GCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA GCGACATCGCCGTGGAGTGGGAGAGCAATGGG CAGCCGGAGAACAACTACAAGACCACGCCTCCC GTGCTGGACTCCGACGGCTCCTTCTTCCTCTATA GCAAGCTCACCGTGGACAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAACCACTACACGCAGAAGAGC CTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 2169	
AA	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSQTVNW YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDDSLNGPVFGGGTK LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD FYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKY AASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV APTECS	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG GDYVWGTYRPHYYYGMDVWGQGTTVTVSSAST KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH

		TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT
		CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE
		EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK
		ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ
		VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
		LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA
		LHNHYTQKSLSLSPGK
	SEQ ID NO: 442	SEQ ID NO: 599
	CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG	CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG
	GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT	AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
	CTGGAAGTAGCTCCAACATCGGAAGTAATTATG	AAGGCTTCCGGATACACCTTCACCGGCTACTAT
	TAAACTGGTACCAGCACACCTCCCAGGAACGGCCC	ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG
	CCAAACTCCTCATCTATACTAATAATCAGCGGC	CTTGAGTGGATGGGATGGATCAACCCTAACAGT
	CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA	GGTGGCACAAACTATGCACAGAAGTTTCAGGGC
	GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG	AGGGTCACCATGACCAGGGACACCGTCCATCAGT
	CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG	ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT
	CAACATTCGATGACAGCCTGAATGGTCCGGTAT	GACGACACGGCCGTGTATTACTGTGCGAGAGGG
	TCGGCGGAGGGACCAAGCTGACCGTCCTAGGTC	GGGGATTACGTTTGGGGGACTTTATCGGCCTCAC
	AGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCC	TACTACTACGGTATGGACGTCTGGGGCCAAGGG
	GCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGC	ACCACGGTCACCGTCTCCTCAGCCTCCACCAAG
	CACACTGGTGTGTCTCATAAGTGACTTCTACCCG	GGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCA
	GGAGCCGTGACAGTGGCCTGGAAGGCAGATAG	AGAGCACCTCTGGGGGCACAGCGGCCCTGGGCT
	CAGCCCCGTCAAGGCGGGAGTGGAGACCCACCAC	GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA
	ACCCTCCAAACAAAGCAACAACAAGTACGCGGGC	CGGTGTCGTGGAACTCAGGCGCCCTGACCAGCG
	CAGCAGCTATCTGAGCCTGACGCCTGAGCAGTG	GCGTGCACACCTTCCCGGCTGTCCTACAGTCCTC
	GAAGTCCCACAGAAGCTACAGCTGCCAGGTCAC	AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT
	GCATGAAGGGAGCACCGTGGAGAAGACAGTGG	GCCCTCCAGCAGCTTGGGCACCCAGACCTACAT
	CCCCTACAGAATGTTCA	CTGCAACGTGAATCACAAGCCCAGCAACACCAA
		GGTGGACAAGAAAGTTGAGCCCAAATCTTGTGA
		CAAAACTCACACATGCCCACCGTGCCCAGCACC
		TGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTC
		CCCCCAAAACCCAAGGACACCCTCATGATCTCC
		CGGACCCCTGAGGTCACATGCGTGGTGGTGGAC
		GTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC
		TGGTACGTGGACGGCGTGGAGGTGCATAATGCC
		AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG

		CACGTACCGTTGTGTCAGCGTCCTCACCGTCCTG CACCAGGACTGGCTGAATGGCAAGGAGTACAA GTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCC CATCGAGAAAACCATCTCCAAAGCCAAAGGGCA GCCCCGAGAACCACAGGTGTACACCCTGCCCCC ATCCCGGGAGGAGATGACCAAGAACCAGGTCA GCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA GCGACATCGCCGTGGAGTGGGAGAGCAATGGG CAGCCGGAGAACAACTACAAGACCACGCCTCCC GTGCTGGACTCCGACGGCTCCTTCTTCCTCTATA GCAAGCTCACCGTGGACAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAACCACTACACGCAGAAGAGC CTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 2013	
AA	QSVLTQPPSASGTPGQRVTISCSGSSNIGSNYVNW YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDDSLNGPVFGGGTK LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD FYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKY AASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV APTECS	
	SEQ ID NO: 443	
NA	CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT CTGGAAGTAGCTCCAACATCGGAAGTAATACTG TAAACTGGTACCAGCACCTCCCAGGAACGGCCC CCAAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA	CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCCGGATACACCTTCACCGGCTACTAT ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG CTTGAGTGGATGGGATGGATCAACCCTAACAGT GGTGGCACAAACTATGCACAGAAGTTTCAGGGC
2C2.005.007		
iPS:361442		

GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG	AGGGTCACCATGACCAGGGACACGTCCATCAGT		
CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG	ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT		
CAACATTCGATGAAAGCCTGAATGGTCCGGTAT	GACGACACGGCCGTGTATTACTGTGCGAGAGGG		
TCGGCGGAGGGACCAAGCTGACCGTCCTAGGTC	GGGGATTACGTTTGGGGGACTTATCGGCCTCAC		
AGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCC	TACTACTACGGTATGGACGTCTGGGGCCAAGGG		
GCCCTCCTCTGAGGAGCTTCAAGCCAACACAAGGC	ACCACGGTCACCGTCTCCTCAGCCTCCACCAAG		
CACACTGGTGTGTCTCATAAGTGACTTCTACCCG	GGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCA		
GGAGCCGTGACAGTGGCCTGGAAGGCAGATAG	AGAGCACCTCTGGGGGCACAGCGGCCCTGGGCT		
CAGCCCCGTCAAGGCGGGAGTGGAGACCACCAC	GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA		
ACCCTCCAAACAAAGCAACAACAAGTACGCGGC	CGGTGTCGTGGAACTCAGGCGCCCTGACCAGCG		
CAGCAGCTATCTGAGCCTGACGCCTGAGCAGTG	GCGTGCACACCTTCCCGGCTGTCCTACAGTCCTC		
GAAGTCCCACAGAAGCTACAGCTGCCAGGTCAC	AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT		
GCATGAAGGGAGCACCGTGGAGAAGACAGTGG	GCCCTCCAGCAGCTTGGGCACCCAGACCTACAT		
CCCCTACAGAATGTTCA	CTGCAACGTGAATCACAAGCCCAGCAACACCAA		
	GGTGGACAAGAAAGTTGAGCCCAAATCTTGTGA		
	CAAAACTCACACATGCCCACCGTGCCCAGCACC		
	TGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTC		
	CCCCCAAAACCCAAGGACACCCTCATGATCTCC		
	CGGACCCCTGAGGTCACATGCGTGGTGGTGGAC		
	GTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC		
	TGGTACGTGGACGGCGTGGAGGTGCATAATGCC		
	AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG		
	CACGTACCGTTGTGTCAGCGTCCTCACCGTCCTG		
	CACCAGGACTGGCTGAATGGCAAGGAGTACAA		
	GTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCC		
	CATCGAGAAAACCATCTCCAAAGCCAAAGGGCA		
	GCCCCGAGAACCACAGGTGTACACCCTGCCCCC		
	ATCCCGGGAGGAGATGACCAAGAACCAGGTCA		
	GCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA		
	GCGACATCGCCGTGGAGTGGGAGAGCAATGGG		
	CAGCCGGAGAACAACTACAAGACCACGCCTCCC		
	GTGCTGGACTCCGACGGCTCCTTCTTCCTCTATA		
	GCAAGCTCACCGTGGACAAGAGCAGGTGGCAG		
	CAGGGGAACGTCTTCTCATGCTCCGTGATGCAT		
	GAGGCTCTGCACAACCACTACACGCAGAAGAGC		
	CTCTCCCTGTCTCCGGGTAAA		

		SEQ ID NO: 2171
AA	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNW YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDESLNGPVFGGGTK LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD FYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKY AASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV APTECS	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG GDYVWGTYRPHYYYGMDVWGQGTTVTVSSAST KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK
		SEQ ID NO: 601
NA	CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT CTGGAAGTAGCTCCAACATCGGAAGTAATACTG TAAACTGGTACCAGCACCTCCCAGGAACGGCCC CCAAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATGACAGCCTGCAAGGTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCCTAGGTC AGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCC GCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGC CACACTGGTGTGTCTCATAAGTGACTTCTACCCG GGAGCCGTGACAGTGGCCTGGAAGGCAGATAG CAGCCCCGTCAAGGCGGGAGTGGAGACCACCAC ACCCTCCAAACAAAGCAACAACAAGTACGCGGC CAGCAGCTATCTGAGCCTGACGCCTGAGCAGTG GAAGTCCCACAGAAGCTACAGCTGCCAGGTCAC GCATGAAGGGAGCACCGTGGAGAAGACAGTGG CCCCTACAGAATGTTCA	CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCCGGATACACCTTCACCGGCTACTAT ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG CTTGAGTGGATGGGATGGAACCCTAACAGT GGTGGCACAAACTATGCACAGAAGTTTCAGGGC AGGGTCACCATGACCAGGGACACCGTCCATCAGT ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT GACGACACGGCCGTGTATTACTGTGCGAGAGGG GGGGATTACGTTTGGGGGACTTTATCGGCCTCAC TACTACTACGGTATGGACGTCTGGGGCCAAGGG ACCACGGTCACCGTCTCCTCAGCCTCCACCAAG GGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCA AGAGCACCTCTGGGGGGCACAGCGGCCCTGGGCT GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA CGGTGTCGTGGAACTCAGGCGCCCTGACCAGCG GCGTGCACACCTTCCCGGCTGTCCTACAGTCCTC AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT GCCCTCCAGCAGCTTGGGCACCCAGACCTACAT CTGCAACGTGAATCACAAGCCCAGCAACACCAA

GGTGGACAAGAAAGTTGAGCCCAAATCTTGTGA CAAAACTCACACATGCCCACCGTGCCCAGCACC TGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTC CCCCCAAAACCCAAGGACACCCTCATGATCTCC CGGACCCCTGAGGTCACATGCGTGGTGGTGGAC GTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC TGGTACGTGGACGGCGTGGAGGTGCATAATGCC AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG CACGTACCGTTGTGTCAGCGTCCTCACCGTCCTG CACCAGGACTGGCTGAATGGCAAGGAGTACAA GTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCC CATCGAGAAAACCATCTCCAAAGCCAAAGGGCA GCCCCGAGAACCACAGGTGTACACCCTGCCCCC ATCCCGGGAGGAGATGACCAAGAACCAGGTCA GCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA GCGACATCGCCGTGGAGTGGGAGAGCAATGGG CAGCCGGAGAACAACTACAAGACCACGCCTCCC GTGCTGGACTCCGACGGCTCCTTCTTCCTCTATA GCAAGCTCACCGTGGACAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAACCACTACACGCAGAAGAGC CTCTCCCTGTCTCCGGGTAAA	SEQ ID NO: 2172
	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG GDYVWGTYRPHYYYGMDVWGQGTTVTVSSAST KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
AA	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNW YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDDSLQGPVFGGGTK LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD FYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKY AASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV APTECS

		LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK
	SEQ ID NO: 445	SEQ ID NO: 602
NA	CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG	CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG
	GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT	AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
	CTGGAAGTAGCTCCAACATCGGAAGTAATACTG	AAGGCTTCCGGATACACCTTCACCGGCTACTAT
	TAAACTGGTACCAGCACACCTCCCAGGAACGGCCC	ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG
	CCAAACTCCTCATCTATACTAATAATCAGCGGC	CTTGAGTGGATGGGATGGATCAACCCTAACAGT
	CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA	GGTGGCACAAACTATGCACAGAAGTTTCAGGGC
	GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG	AGGGTCACCATGACCAGGGACACGTCCATCAGT
	CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG	ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT
	CAACATTCGATGACAGCCTGAGTGGTCCGGTAT	GACGACACGGCCGTGTATTACTGTGCGAGAGGG
	TCGGCGGAGGGACCAAGCTGACCGTCCTAGGTC	GGGGATTACGTTTGGGGGACTTATCGGCCTCAC
	AGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCC	TACTACTACGGTATGGACGTCTGGGGCCAAGGG
	GCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGC	ACCACGGTCACCGTCTCCTCAGCCTCCACCAAG
	CACACTGGTGTGTCTCATAAGTGACTTCTACCCG	GGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCA
	GGAGCCGTGACAGTGGCCTGGAAGGCAGATAG	AGAGCACCTCTGGGGGCACAGCGGCCCTGGGCT
	CAGCCCCGTCAAGGCGGGAGTGGAGACCACCAC	GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA
	ACCCTCCAAACAAAGCAACAACAAGTACGCGGC	CGGTGTCGTGGAACTCAGGCGCCCTGACCAGCG
	CAGCAGCTATCTGAGCCTGACGCCTGAGCAGTG	GCGTGCACACCTTCCCGGCTGTCCTACAGTCCTC
	GAAGTCCCACAGAAGCTACAGCTGCCAGGTCAC	AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT
	GCATGAAGGGAGCACCGTGGAGAAGACAGTGG	GCCCTCCAGCAGCTTGGGCACCCAGACCTACAT
	CCCCTACAGAATGTTCA	CTGCAACGTGAATCACAAGCCCAGCAACACCAA
		GGTGGACAAGAAAGTTGAGCCCAAATCTTGTGA
		CAAAACTCACACATGCCCACCGTGCCCAGCACC
		TGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTC
		CCCCCAAAACCCAAGGACACCCTCATGATCTCC
		CGGACCCCTGAGGTCACATGCGTGGTGGTGGAC
		GTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC
		TGGTACGTGGACGGCGTGGAGGTGCATAATGCC
		AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG
		CACGTACCGTTGTGTCAGCGTCCTCACCGTCCTG
		CACCAGGACTGGCTGAATGGCAAGGAGTACAA
		GTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCC
		CATCGAGAAAACCATCTCCAAAGCCAAAGGGCA
		GCCCCGAGAACCACAGGTGTACACCCTGCCCCC

		ATCCCGGGAGGAGATGACCAAGAACCAGGTCA
		GCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA
		GCGACATCGCCGTGGAGTGGGAGAGCAATGGG
		CAGCCGGAGAACAACTACAAGACCACGCCTCCC
		GTGCTGGACTCCGACGGCTCCTTCTTCCTCTATA
		GCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
		CAGGGGAACGTCTTCTCATGCTCCGTGATGCAT
		GAGGCTCTGCACAACCACTACACGCAGAAGAGC
		CTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 2016	SEQ ID NO: 2173
AA	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNW YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDDSLSGPVFGGGTK LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD FYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKY AASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV APTECS	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG GDYVWGTYRPHYYYGMDVWGQGTTVTVSSAST KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK
	SEQ ID NO: 446	SEQ ID NO: 603
NA	CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT CTGGAAGTAGCTCCAACATCGGAAGTAATACTG TAAACTGGTACCAGCACCTCCCAGGAACGGCCC CCAAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATGACAGCCTGAATGCTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCCTAGGTC AGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCC	CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCCGGATACACCTTCACCGGCTACTAT ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG CTTGAGTGGATGGGATGGAACCCTAACAGT GGTGGCACAAACTATGCACAGAAGTTTCAGGGC AGGGTCACCATGACCAGGGACACCGTCCATCAGT ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT GACGACACGGCCGTGTATTACTGTGCGAGAGGG GGGGATTACGTTTGGGGGACTTATCGGCCTCAC TACTACTACGGTATGGACGTCTGGGGCCAAGGG
	2C2.005.010	
	iPS:361460	

GCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGC	ACCACGGTCACCGTCTCCTCAGCCTCCACCAAG
CACACTGGTGTGTCTCATAAGTGACTTCTACCCG	GGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCA
GGAGCCGTGACAGTGGCCTGGAAGGCAGATAG	AGAGCACCTCTGGGGGCACAGCGGCCCTGGGCT
CAGCCCCGTCAAGGCGGGAGTGGAGACCACCAC	GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA
ACCCTCCAAACAAAGCAACAACAAGTACGCGGC	CGGTGTCGTGGAACTCAGGCGCCCTGACCAGCG
CAGCAGCTATCTGAGCCTGACGCCTGAGCAGTG	GCGTGCACACCTTCCCGGCTGTCCTACAGTCCTC
GAAGTCCCACAGAAGCTACAGCTGCCAGGTCAC	AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT
GCATGAAGGGAGCACCGTGGAGAAGACAGTGG	GCCCTCCAGCAGCTTGGGCACCCAGACCTACAT
CCCCTACAGAATGTTCA	CTGCAACGTGAATCACAAGCCCAGCAACACCAA
	GGTGGACAAGAAAGTTGAGCCCAAATCTTGTGA
	CAAAACTCACACATGCCCACCGTGCCCAGCACC
	TGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTC
	CCCCCAAAACCCAAGGACACCCTCATGATCTCC
	CGGACCCCTGAGGTCACATGCGTGGTGGTGGAC
	GTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC
	TGGTACGTGGACGGCGTGGAGGTGCATAATGCC
	AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG
	CACGTACCGTTGTGTCAGCGTCCTCACCGTCCTG
	CACCAGGACTGGCTGAATGGCAAGGAGTACAA
	GTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCC
	CATCGAGAAAACCATCTCCAAAGCCAAAGGGCA
	GCCCCGAGAACCACAGGTGTACACCCTGCCCCCC
	ATCCCGGGAGGAGATGACCAAGAACCAGGTCA
	GCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA
	GCGACATCGCCGTGGAGTGGGAGAGCAATGGG
	CAGCCGGAGAACAACTACAAGACCACGCCTCCC
	GTGCTGGACTCCGACGGCTCCTTCTTCCTCTATA
	GCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
	CAGGGGAACGTCTTCTCATGCTCCGTGATGCAT
	GAGGCTCTGCACAACCACTACACGCAGAAGAGC
	CTCTCCCTGTCTCCGGGTAAA
SEQ ID NO: 2017	SEQ ID NO: 2174
AA	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNW
	YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
	ASLAISGLQSEDEADYFCATFDDSLNAPVFGGGTK
	LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD
	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY
	MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ
	GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG
	GDYVWGTYRPHYYYGMDVWGQGTTVTVSSAST

		KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT
		VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPS
		SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH
		TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT
		CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE
		EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK
		ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ
		VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
		LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA
		LHNHYTQKSLSLSPGK
	SEQ ID NO: 447	SEQ ID NO: 604
iPS:361466	NA	CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG
		AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
		AAGGCTTCCGGATACACCTTCACCGGCTACTAT
		ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG
		CTTGAGTGGATGGGATGGATCAACCCTAACAGT
		GGTGGCACAAACTATGCACAGAAGTTTCAGGGC
		AGGGTCACCATGACCAGGGACACCGTCCATCAGT
		ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT
		GACGACACGGCCGTGTATTACTGTGCGAGAGGG
		GGGGATTACGTTTGGGGGACTTTATCGGCCTCAC
		TACTACTACGGTATGGACGTCTGGGGCCAAGGG
		ACCACGGTCACCGTCTCCTCAGCCTCCACCAAG
		GGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCA
		AGAGCACCTCTGGGGGCACAGCGGCCCTGGGCT
		GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA
		CGGTGTCGTGGAACTCAGGCGCCCTGACCAGCG
		GCGTGCACACCTTCCCGGCTGTCCTACAGTCCTC
		AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT
		GCCCTCCAGCAGCTTGGGCACCCAGACCTACAT
		CTGCAACGTGAATCACAAGCCCAGCAACACCAA
		GGTGGACAAGAAAGTTGAGCCCAAATCTTGTGA
		CAAAACTCACACATGCCCACCGTGCCCAGCACC
		TGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTC
		CCCCCAAAACCCAAGGACACCCTCATGATCTCC
		CGGACCCCTGAGGTCACATGCGTGGTGGTGGAC

		GTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC
		TGGTACGTGGACGGCGTGGAGGTGCATAATGCC
		AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG
		CACGTACCGTTGTGTCAGCGTCCTCACCGTCCTG
		CACCAGGACTGGCTGAATGGCAAGGAGTACAA
		GTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCC
		CATCGAGAAAACCATCTCCAAAGCCAAAGGGCA
		GCCCCGAGAACCACAGGTGTACACCCTGCCCCC
		ATCCCGGGAGGAGATGACCAAGAACCAGGTCA
		GCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA
		GCGACATCGCCGTGGAGTGGGAGAGCAATGGG
		CAGCCGGAGAACAACTACAAGACCACGCCTCCC
		GTGCTGGACTCCGACGGCTCCTTCTTCCTCTATA
		GCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
		CAGGGGAACGTCTTCTCATGCTCCGTGATGCAT
		GAGGCTCTGCACAACCACTACACGCAGAAGAGC
		CTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 2018	SEQ ID NO: 2175
AA	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNW YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDSSLNGPVFGGGTK LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD FYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKY AASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV APTECS	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG GDYVWGTYRPHYYYGMDVWGQGTTVTVSSAST KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK
	SEQ ID NO: 448	SEQ ID NO: 605
NA	CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG GGACCCCCGGGCAGAGGTCACCATCTCTTGTT CTGGAAGTAGCTCCAACATCGGAAGTAATTATG	CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCCGGATACACCTTCACCGGCTACTAT

ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG	TAAACTGGTACCAGCACCTCCCAGGAACGGCCC		
CTTGAGTGGATGGGATGGATCAACCCTAACAGT	CCAAACTCCTCATCTATACTAATAATCAGCGGC		
GGTGGCACAAACTATGCACAGAAGTTTCAGGGC	CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA		
AGGGTCACCATGACCAGGGACACGTCCATCAGT	GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG		
ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT	CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG		
GACGACACGGCCGTGTATTACTGTGCGAGAGGG	CAACATTCGATAGCAGCCTGAATGCTCCGGTAT		
GGGGATTACGTTTGGGGACTTTATCGGCCTCAC	TCGGCGGAGGGACCAAGCTGACCGTCCTAGGTC		
TACTACTACGGTATGGACGTCTGGGGCCAAGGG	AGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCC		
ACCACGGTCACCGTCTCCTCAGCCTCCACCAAG	GCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGC		
GGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCA	CACACTGGTGTGTCTCATAAGTGACTTCTACCCG		
AGAGCACCTCTGGGGGGCACAGCGGCCCTGGGCT	GGAGCCGTGACAGTGGCCTGGAAGGCAGATAG		
GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA	CAGCCCCGTCAAGGCGGGAGTGGAGACCACCAC		
CGGTGTCGTGGAACTCAGGCGCCCTGACCAGCG	ACCCTCCAAACAAAGCAACAACAAGTACGCGGC		
GCGTGCACACCTTCCCGGCTGTCCTACAGTCCTC	CAGCAGCTATCTGAGCCTGACGCCTGAGCAGTG		
AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT	GAAGTCCCACAGAAGCTACAGCTGCCAGGTCAC		
GCCCTCCAGCAGCTTGGGCACCCAGACCTACAT	GCATGAAGGGAGCACCGTGGAGAAGACAGTGG		
CTGCAACGTGAATCACAAGCCCAGCAACACCAA	CCCCTACAGAATGTTCA		
GGTGGACAAGAAAGTTGAGCCCAAATCTTGTGA			
CAAAACTCACACATGCCCACCGTGCCCAGCACC			
TGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTC			
CCCCCAAAACCCAAGGACACCCTCATGATCTCC			
CGGACCCCCTGAGGTCACATGCGTGGTGGTGGAC			
GTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC			
TGGTACGTGGACGGCGTGGAGGTGCATAATGCC			
AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG			
CACGTACCGTTGTGTCAGCGTCCTCACCGTCCTG			
CACCAGGACTGGCTGAATGGCAAGGAGTACAA			
GTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCC			
CATCGAGAAAACCATCTCCAAAGCCAAAGGGCA			
GCCCCGAGAACCACAGGTGTACACCCTGCCCCC			
ATCCCGGGAGGAGATGACCAAGAACCAGGTCA			
GCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA			
GCGACATCGCCGTGGAGTGGGAGAGCAATGGG			
CAGCCGGAGAACAACTACAAGACCACGCCTCCC			
GTGCTGGACTCCGACGGCTCCTTCTTCCTCTATA			
GCAAGCTCACCGTGGACAAGAGCAGGTGGCAG			

		CAGGGGAACGTCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAACCACTACACGCAGAAGAGC CTCTCCCTGTCTCCGGGTAAA
AA	SEQ ID NO: 2019	SEQ ID NO: 2176
	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNYVNW YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDSSLNAPVFGGGTK LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD FYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKY AASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV APTECS	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG GDYVWGTYRPHYYYGMDVWGQGTTVTVSSAST KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK
NA	SEQ ID NO: 449	SEQ ID NO: 606
	CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT CTGGAAGTAGCTCCAACATCGGAAGTAATTATG TAAACTGGTACCAGCACCTCCCAGGAACGGCCC CCAAACTCCTCATCTATACTAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATAGCAGCCTGAATGCTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCCTAGGTC AGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCC GCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGC CACACTGGTGTGTCTCATAAGTGACTTCTACCCG GGAGCCGTGACAGTGGCCTGGAAGGCAGATAG CAGCCCCGTCAAGGCGGGAGTGGAGACCACCAC ACCCTCCAAACAAAGCAACAACAAGTACGCGGC CAGCAGCTATCTGAGCCTGACGCCTGAGCAGTG	CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCCGGATACACCTTCACCGGCTACTAT ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG CTTGAGTGGATGGGATGGATCAACCCTAACAGT GGTGGCACAAACTATGCACAGAAGTTTCAGGGC AGGGTCACCATGACCAGGGACACGTCCATCAGT ACAGCCTACATGGAGCTGAGCAGCCTGAGGTCT GACGACACGGCCGTGTATTACTGTGCGAGAGGG GGGGATTACGTTTTCGGGACTTATCGGCCTCACT ACTACTACGGTATGGACGTCTGGGGCCAAGGGA CCACGGTCACCGTCTCCTCAGCCTCCACCAAGG GCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAA GAGCACCTCTGGGGGCACAGCGGCCCTGGGCTG CCTGGTCAAGGACTACTTCCCCGAACCGGTGAC GGTGTCGTGGAACTCAGGCGCCCTGACCAGCGG CGTGCACACCTTCCCGGCTGTCCTACAGTCCTCA

GAAGTCCCACAGAAGCTACAGCTGCCAGGTCAC GCATGAAGGGAGCACCGTGGAGAAGACAGTGG CCCCTACAGAATGTTCA		GGACTCTACTCCCTCAGCAGCGTGGTGACCGTG CCCTCCAGCAGCTTGGGCACCCAGACCTACATC TGCAACGTGAATCACAAGCCCAGCAACACCAAG GTGGACAAGAAAGTTGAGCCCAAATCTTGTGAC AAAACTCACACATGCCCACCGTGCCCAGCACCT GAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCC CCCCAAAACCCAAGGACACCCTCATGATCTCCC GGACCCCTGAGGTCACATGCGTGGTGGTGGACG TGAGCCACGAAGACCCTGAGGTCAAGTTCAACT GGTACGTGGACGGCGTGGAGGTGCATAATGCCA AGACAAAGCCGTGTGAGGAGCAGTACGGCAGC ACGTACCGTTGTGTCAGCGTCCTCACCGTCCTGC ACCAGGACTGGCTGAATGGCAAGGAGTACAAGT GCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCA TCGAGAAAACCATCTCCAAAGCCAAAGGGCAGC CCCGAGAACCACAGGTGTACACCCTGCCCCCAT CCCGGGAGGAGATGACCAAGAACCAGGTCAGC CTGACCTGCCTGGTCAAAGGCTTCTATCCCAGC GACATCGCCGTGGAGTGGGAGAGCAATGGGCA GCCGGAGAACAACTACAAGACCACGCCTCCCGT GCTGGACTCCGACGGCTCCTTCTTCCTCTATAGC AAGCTCACCGTGGACAAGAGCAGGTGGCAGCA GGGGAACGTCTTCTCATGCTCCGTGATGCATGA GGCTCTGCACAACCACTACACGCAGAAGAGCCT CTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 2020	SEQ ID NO: 2177
	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNYVNW YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDSSLNAPVFGGGTK LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD FYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKY AASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV APTECS	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSSLRSDDTAVYYCARG GDYVFGTYRPHYYYGMDVWGQGTTVTVSSASTK GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSS SLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEE QYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKA
AA		

		LPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK
	SEQ ID NO: 450	SEQ ID NO: 607
	NA	CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCCGGATACACCTTCACCGGCTACTAT ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG CTTGAGTGGATGGGATGGATCAACCCTAACAGT GGTGGCACAAACTATGCACAGAAGTTTCAGGGC AGGGTCACCATGACCAGGGACACGTCCATCAGT ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT GACGACACGGCCGTGTATTACTGTGCGAGAGGG GGGGATTACGTTTTCGGGGACTTATCGGCCTCACT ACTACTACGGTATGGACGTCTGGGGCCAAGGGA CCACGGTCACCGTCTCCTCAGCCTCCACCAAGG GCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAA GAGCACCTCTCTGGGGGCACAGCGGCCCTGGGCTG CCTGGTCAAGGACTACTTCCCCGAACCGGTGAC GGTGTCGTGGAACTCAGGCGCCCTGACCAGCGG CGTGCACACCTTCCCGGCTGTCCTACAGTCCTCA GGACTCTACTCCCTCAGCAGCGTGGTGACCGTG CCCTCCAGCAGCTTGGGCACCCAGACCTACATC TGCAACGTGAATCACAAGCCCAGCAACACCAAG GTGGACAAGAAAGTTGAGCCCAAATCTTGTGAC AAAACTCACACATGCCCACCGTGCCCAGCACCT GAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCC CCCCAAAACCCAAGGACACCCTCATGATCTCCC GGACCCCTGAGGTCACATGCGTGGTGGTGGACG TGAGCCACGAAGACCCTGAGGTCAAGTTCAACT GGTACGTGGACGGCGTGGAGGTGCATAATGCCA AGACAAAGCCGTGTGAGGAGCAGTACGGCAGC ACGTACCGTTGTGTCAGCGTCCTCACCGTCCTGC ACCAGGACTGGCTGAATGGCAAGGAGTACAAGT GCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCA
		CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT CTGGAAGTAGCTCCAACATCGGAAGTCAAACTG TAAACTGGTACCAGCACCTCCCAGGAACGGCCC CCAAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATGAAAGCCTGAGTGGTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCCTAGGTC AGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCC GCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGC CACACTGGTGTGTCTCATAAGTGACTTCTACCCG GGAGCCGTGACAGTGGCCTGGAAGGCAGATAG CAGCCCCGTCAAGGCGGGAGTGGAGACCACCAC ACCCTCCAAACAAAGCAACAACAAGTACGCGGC CAGCAGCTATCTGAGCCTGACGCCTGAGCAGTG GAAGTCCCACAGAAGCTACAGCTGCCAGGTCAC GCATGAAGGGAGCACCGTGGAGAAGACAGTGG CCCCTACAGAATGTTCA

		TCGAGAAAACCATCTCCAAAGCCAAAGGGCAGC
		CCCGAGAACCACAGGTGTACACCCTGCCCCCAT
		CCCGGGAGGAGATGACCAAGAACCAGGTCAGC
		CTGACCTGCCTGGTCAAAGGCTTCTATCCCAGC
		GACATCGCCGTGGAGTGGGAGAGCAATGGGCA
		GCCGGAGAACAACTACAAGACCACGCCTCCCGT
		GCTGGACTCCGACGGCTCCTTCTTCCTCTATAGC
		AAGCTCACCGTGGACAAGAGCAGGTGGCAGCA
		GGGGAACGTCTTCTCATGCTCCGTGATGCATGA
		GGCTCTGCACAACCACTACACGCAGAAGAGCCT
		CTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 2021	SEQ ID NO: 2178
AA	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSQTVNW YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDESLSGPVFGGGTK LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD FYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKY AASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV APTECS	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG GDYVFGTYRPHYYYGMDVWGQGTTVTVSSASTK GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSS SLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEE QYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK
	SEQ ID NO: 451	SEQ ID NO: 608
NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCAACAGAAACCAGGGAAAGCCCCTA AGCGCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCAA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTGATGCAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATA
18F2.013		
iPS:361845		

GGACGATCTTTGGAGTGGTCTTGGGGGACTACT	GGACCAAAGTGGATATCAAACGAACGGTGGCT
GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG	GCACCATCTGTCTTCATCTTCCCGCCATCTGATG
CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC	AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT
ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC	GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA
GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC	AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT
CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC	CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG
CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT	ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA
CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC	CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC
GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC	ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG
CAGACCTACATCTGCAACGTGAATCACAAGCCC	GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA
AGCAACACCAAGGTGGACAAGAAAGTTGAGCC	GGGGAGAGTGT
CAAATCTTGTGACAAAACTCACACATGCCCACC	
GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC	
AGTCTTCCTCTTCCCCCCAAAACCCAAGGACAC	
CCTCATGATCTCCCGGACCCCTGAGGTCACATG	
CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA	
GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA	
GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA	
GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT	
CCTCACCGTCCTGCACCAGGACTGGCTGAATGG	
CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC	
CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA	
AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT	
ACACCCTGCCCCCATCCCGGGAGGAGATGACCA	
AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG	
GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG	
AGAGCAATGGGCAGCCGGAGAACAACTACAAG	
ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC	
TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG	
AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC	
TCCGTGATGCATGAGGCTCTGCACAACCACTAC	
ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA	
SEQ ID NO: 2179	SEQ ID NO: 2022
QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW
HWVRQAPGKGLEWVAVIWYDASNENYADAVKG	YQQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTE
RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR	FTLTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDI
AA	

KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC	SEQ ID NO: 452	TIFGVVLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
	NA	
	6H1.009	
	iPS:361851	

	CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA
	GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
	GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA
	GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT
	CCTCACCGTCCTGCACCAGGACTGGCTGAATGG
	CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
	CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
	AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
	ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
	AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
	GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
	AGAGCAATGGGCAGCCGGAGAACAACTACAAG
	ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
	TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
	AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
	TCCGTGATGCATGAGGCTCTGCACAACCACTAC
	ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
SEQ ID NO: 2023	SEQ ID NO: 2180
DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR GEC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVLLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
AA	
SEQ ID NO: 453	SEQ ID NO: 610

iPS:361855	2C2.005.015	NA	
			CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCCGGATACACCTTCACCGGCTACTAT
			ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGATGGATCAACCCTAACAGT
			GGTGGCACAAACTATGCACAGAAGTTTCAGGGC
			AGGGTCACCATGACCAGGGACACGTCCATCAGT
			ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGGG
			GGGGATTACGTTTGGGGGACTTATCGGCCTCAC
			TACTACTACGGTATGGACGTCTGGGGCCAAGGG
			ACCACGGTCACCGTCTCCTCAGCCTCCACCAAG
			GGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCA
			AGAGCACCTCTGGGGGCACAGCGGCCCTGGGCT
			GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA
			CGGTGTCGTGGAACTCAGGCGCCCTGACCAGCG
			GCGTGCACACCTTCCCGGCTGTCCTACAGTCCTC
			AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT
			GCCCTCCAGCAGCTTGGGCACCCAGACCTACAT
			CTGCAACGTGAATCACAAGCCCAGCAACACCAA
			GGTGGACAAGAAAGTTGAGCCCAAATCTTGTGA
			CAAAACTCACACATGCCCACCGTGCCCAGCACC
			TGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTC
			CCCCCAAAACCCAAGGACACCCTCATGATCTCC
			CGGACCCCTGAGGTCACATGCGTGGTGGTGGAC
			GTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC
			TGGTACGTGGACGGCGTGGAGGTGCATAATGCC
			AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG
			CACGTACCGTTGTGTCAGCGTCCTCACCGTCCTG
			CACCAGGACTGGCTGAATGGCAAGGAGTACAA
			GTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCC
			CATCGAGAAAACCATCTCCAAAGCCAAAGGGCA
			GCCCCGAGAACCACAGGTGTACACCCTGCCCCC
			ATCCCGGGAGGAGATGACCAAGAACCAGGTCA
			GCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA
			GCGACATCGCCGTGGAGTGGGAGAGCAATGGG

		CAGCCGGAGAACAACTACAAGACCACGCCTCCC
		GTGCTGGACTCCGACGGCTCCTTCTTCCTCTATA
		GCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
		CAGGGGAACGTCTTCTCATGCTCCGTGATGCAT
		GAGGCTCTGCACAACCACTACACGCAGAAGAGC
		CTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 2024	SEQ ID NO: 2181
AA	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNW YQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDSSLSGPVFGGGTK LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD FYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKY AASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV APTECS	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG GDYVWGTYRPHYYYGMDVWGQGTTVTVSSAST KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK
	SEQ ID NO: 454	SEQ ID NO: 611
NA	GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACTATCACTT GCCGGGCAAGTCAGACCATTAGCAGGTTTTTAA ATTGGTATCAGCAGAAACCTGGGAAAGCCCCTG AGCTCCTGATCTATGTTGCATCCAGTTTGCAAAG TGGGGTCCCATCAAGATTCAGTGGCAGTGGTTC TGGGACAGATTTCACTCTCACCATCAGCAGTCT GCAACCTGAAGATTTTGCAACTTACTACTGTCA ACAGAGTTACAGTACCCTGATCAGTTTTGGCCA GGGGACCAAGCTGGAGATCACACGAACGGTGG CTGCACCATCTGTCTTCATCTTCCCGCCATCTGA TGAGCAGTTGAAATCTGGAACTGCCTCTGTTGT GTGCCTGCTGAATAACTTCTATCCCAGAGAGGC CAAAGTACAGTGGAAGGTGGATAACGCCCTCCA	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT ACAGCGTCTGGATTCACCTTCAGTAGCTATGGC ATACACTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGTTATATGGTATGATGGA AGTAATAAGTTCCATGCAGACTCCGTGAAGGGC CGATTCACCATCTCCAGAGACAATTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA AAAGTGGCTGGTATGCCTGAAGCTTTTGAAATC TGGGGCCAAGGGACAAAGGTCACCGTCTCTTCA GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTG GCACCCTCCTCCAAGAGCACCTCTGGGGGCACA GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTC

	CCCGAACCGGTGACGGTGTCGTGGAACTCAGGC
	GCCCTGACCAGCGGCGTGCACACCTTCCCGGCT
	GTCCTACAGTCCTCAGGACTCTACTCCCTCAGCA
	GCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCA
	CCCAGACCTACATCTGCAACGTGAATCACAAGC
	CCAGCAACACCAAGGTGGACAAGAAAGTTGAG
	CCCAAATCTTGTGACAAAACTCACACATGCCCA
	CCGTGCCCAGCACCTGAACTCCTGGGGGGACCG
	TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACA
	CCCTCATGATCTCCCGGACCCCTGAGGTCACAT
	GCGTGGTGGTGGACGTGAGCCACGAAGACCCTG
	AGGTCAAGTTCAACTGGTACGTGGACGGCGTGG
	AGGTGCATAATGCCAAGACAAAGCCGTGTGAGG
	AGCAGTACGGCAGCACGTACCGTTGTGTCAGCG
	TCCTCACCGTCCTGCACCAGGACTGGCTGAATG
	GCAAGGAGTACAAGTGCAAGGTCTCCAACAAA
	GCCCTCCCAGCCCCCATCGAGAAAACCATCTCC
	AAAGCCAAAGGGCAGCCCCGAGAACCACAGGT
	GTACACCCTGCCCCCATCCCGGGAGGAGATGAC
	CAAGAACCAGGTCAGCCTGACCTGCCTGGTCAA
	AGGCTTCTATCCCAGCGACATCGCCGTGGAGTG
	GGAGAGCAATGGGCAGCCGGAGAACAACTACA
	AGACCACGCCTCCCGTGCTGGACTCCGACGGCT
	CCTTCTTCCTCTATAGCAAGCTCACCGTGGACAA
	GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATG
	CTCCGTGATGCATGAGGCTCTGCACAACCACTA
	CACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAA
	A
	SEQ ID NO: 2182
AA	QVQLVESGGGVVQPGRSLRLSCTASGFTFSSYGIH
AA	WVRQAPGKGLEWVAVIWYDGSNKFHADSVKGRF
AA	TISRDNSKNTLYLQMNSLRAEDSAMYFCARGKVA
AA	GMPEAFEIWGQGTKVTVSSASTKGPSVFPLAPSSK
AA	STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV
AA	HTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
AA	HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP
	ATCGGGTAACTCCCAGGAGAGTGTCACAGAGCA
	GGACAGCAAGGACAGCACCTACAGCCTCAGCA
	GCACCCTGACGCTGAGCAAAGCAGACTACGAGA
	AACACAAAGTCTACGCCTGCGAAGTCACCCATC
	AGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCA
	ACAGGGGAGAGTGT
	SEQ ID NO: 2025
AA	DIQLTQSPSSLSASVGDRVTITCRASQTISRFLNWY
AA	QQKPGKAPELLIYVASSLQSGVPSRFSGSGSGTDFT
AA	LTISSLQPEDFATYYCQQSYSTLISFGQGTKLEITRT
AA	VAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA
AA	KVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST
AA	LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG
AA	EC

		SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
		KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVL
		TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
		GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS
		DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL
		TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL
		SPGK
	SEQ ID NO: 455	SEQ ID NO: 612
	CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTG	CAAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG
	CGGCCCCAGGACAGAAGGTCACCATCTCCTGCT	AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
	CTGGAAGCAGCTCCAACATTGGAAATAATTATG	AAGGCTTCTGGATACACCTTCACCAGTTATGAT
	TATCCTGGTATGAGCAGTTCCCAGGAACAGCCC	ATCAACTGGGTGCGACAGGCCACTGGACAAGGG
	CCAAACTCCTCATTTATGACAATAATAAGCGAC	CTTGAGTGGATGGGATGGAACCCTAACAGT
	CCTCAGGGATTCCTGACCGATTCTCTGGCTCCAA	GGTAACACAGGCTATGCACAGAAGTTCCAGGGC
	GTCTGGCACGTCAGCCACCCTGGGCATCACCGG	AGAGTCACCATGACCAGGGACACCTCCATAAGC
	ACTCCAGACTGGGGACGAGGCCGATTATTACTG	ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT
	CGGAACATGGGATAGCAGCCTGAGTGCTGTGGT	CAGGACACGGCCGTGTATTACTGTGCGAGAGGG
	ATTCGGCGGAGGGACCAAACTGACCGTCCTAGG	GGTGATTACGTTTGGGGGAGTTATCGTCCCTACT
	TCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTC	ACTACTACTACGGTATGGACGTCTGGGGCCAAG
	CCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAG	GGACCACGGTCACCGTCTCCTCAGCCTCCACCA
	GCCACACTGGTGTGTCTCATAAGTGACTTCTACC	AGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTC
	CGGGAGCCGTGACAGTGGCCTGGAAGGCAGAT	CAAGAGCACCTCTGGGGGCACAGCGGCCCTGGG
	AGCAGCCCCGTCAAGGCGGGAGTGGAGACCAC	CTGCCTGGTCAAGGACTACTTCCCCGAACCGGT
	CACACCCTCCAAACAAAGCAACAACAAGTACGC	GACGGTGTCGTGGAACTCAGGCGCCCTGACCAG
	GGCCAGCAGCTATCTGAGCCTGACGCCTGAGCA	CGGCGTGCACACCTTCCCGGCTGTCCTACAGTCC
	GTGGAAGTCCCACAGAAGCTACAGCTGCCAGGT	TCAGGACTCTACTCCCTCAGCAGCGTGGTGACC
	CACGCATGAAGGGAGCACCGTGGAGAAGACAG	GTGCCCTCCAGCAGCTTGGGCACCCAGACCTAC
	TGGCCCCTACAGAATGTTCA	ATCTGCAACGTGAATCACAAGCCCAGCAACACC
		AAGGTGGACAAGAAAGTTGAGCCCAAATCTTGT
		GACAAAACTCACACATGCCCACCGTGCCCAGCA
		CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCT
		TCCCCCCAAAACCCAAGGACACCCTCATGATCT
		CCCGGACCCCTGAGGTCACATGCGTGGTGGTGG
		ACGTGAGCCACGAAGACCCTGAGGTCAAGTTCA
		ACTGGTACGTGGACGGCGTGGAGGTGCATAATG
		CCAAGACAAAGCCGTGTGAGGAGCAGTACGGC

		AGCACGTACCGTTGTGTCAGCGTCCTCACCGTCC
		TGCACCAGGACTGGCTGAATGGCAAGGAGTACA
		AGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCC
		CCATCGAGAAAACCATCTCCAAAGCCAAAGGGC
		AGCCCCGAGAACCACAGGTGTACACCCTGCCCC
		CATCCCGGGAGGAGATGACCAAGAACCAGGTC
		AGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC
		AGCGACATCGCCGTGGAGTGGGAGAGCAATGG
		GCAGCCGGAGAACAACTACAAGACCACGCCTCC
		CGTGCTGGACTCCGACGGCTCCTTCTTCCTCTAT
		AGCAAGCTCACCGTGGACAAGAGCAGGTGGCA
		GCAGGGGAACGTCTTCTCATGCTCCGTGATGCA
		TGAGGCTCTGCACAACCACTACACGCAGAAGAG
		CCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 2026	SEQ ID NO: 2183
AA	QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVS	QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDI
	WYEQFPGTAPKLLIYDNNKRPSGIPDRFSGSKSGTS	NWVRQATGQGLEWMGWMNPNSGNTGYAQKFQ
	ATLGITGLQTGDEADYYCGTWDSSLSAVVFGGGT	GRVTMTRDTSISTAYMELSSLRSQDTAVYYCARG
	KLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLIS	GDYVWGSYRPYYYYYGMDVWGQGTTVTVSSAS
	DFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNK	TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV
	YAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKT	TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP
	VAPTECS	SSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH
		TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT
		CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE
		EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK
		ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ
		VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
		LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA
		LHNHYTQKSLSLSPGK
	SEQ ID NO: 456	SEQ ID NO: 613
NA	GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTG
	CTGCATCTGTAGGAGACAGAGTCACTATCACTT	GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
	GCCGGGCAAGTCAGACCATTAGCAGGTTTTTAA	GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC
	ATTGGTATCAGCAGAAACCTGGGAAAGCCCCTG	ATACACTGGGTCCGCCAGGCTCCAGGCAAGGGG
	AGCTCCTGATCTATGTTGCATCCAGTTTGCAAAG	CTGGAGTGGGTGGCAGTTATATGGTATGATGCA
	TGGGGTCCCATCAAGATTCAGTGGCAGTGGTTC	AGTAATAAGTTCCATGCAGACGCCGTGAAGGGC

CGATTCACCATCTCCAGAGACAATTCCAAGAAC	TGGGACAGATTTCACTCTCACCATCAGCAGTCT		
ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC	GCAACCTGAAGATTTTGCAACTTACTACTGTCA		
GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA	ACAGAGTTACAGTACCCTGATCAGTTTTGGCCA		
AAAGTGGCTGGTATGCCTGAAGCTTTTGAAATC	GGGGACCAAGCTGGAGATCAAACGAACGGTGG		
TGGGGCCAAGGGACAAAGGTCACCGTCTCTTCA	CTGCACCATCTGTCTTCATCTTCCCGCCATCTGA		
GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTG	TGAGCAGTTGAAATCTGGAACTGCCTCTGTTGT		
GCACCCTCCTCCAAGAGCACCTCTGGGGGCACA	GTGCCTGCTGAATAACTTCTATCCCAGAGAGGC		
GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTC	CAAAGTACAGTGGAAGGTGGATAACGCCCTCCA		
CCCGAACCGGTGACGGTGTCGTGGAACTCAGGC	ATCGGGTAACTCCCAGGAGAGTGTCACAGAGCA		
GCCCTGACCAGCGGCGTGCACACCTTCCCGGCT	GGACAGCAAGGACAGCACCTACAGCCTCAGCA		
GTCCTACAGTCCTCAGGACTCTACTCCCTCAGCA	GCACCCTGACGCTGAGCAAAGCAGACTACGAGA		
GCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCA	AACACAAAGTCTACGCCTGCGAAGTCACCCATC		
CCCAGACCTACATCTGCAACGTGAATCACAAGC	AGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCA		
CCAGCAACACCAAGGTGGACAAGAAAGTTGAG	ACAGGGGAGAGTGT		
CCCAAATCTTGTGACAAAACTCACACATGCCCA			
CCGTGCCCAGCACCTGAACTCCTGGGGGGACCG			
TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACA			
CCCTCATGATCTCCCGGACCCCTGAGGTCACAT			
GCGTGGTGGTGGACGTGAGCCACGAAGACCCTG			
AGGTCAAGTTCAACTGGTACGTGGACGGCGTGG			
AGGTGCATAATGCCAAGACAAAGCCGTGTGAGG			
AGCAGTACGGCAGCACGTACCGTTGTGTCAGCG			
TCCTCACCGTCCTGCACCAGGACTGGCTGAATG			
GCAAGGAGTACAAGTGCAAGGTCTCCAACAAA			
GCCCTCCCAGCCCCCATCGAGAAAACCATCTCC			
AAAGCCAAAGGGCAGCCCCGAGAACCACAGGT			
GTACACCCTGCCCCCATCCCGGGAGGAGATGAC			
CAAGAACCAGGTCAGCCTGACCTGCCTGGTCAA			
AGGCTTCTATCCCAGCGACATCGCCGTGGAGTG			
GGAGAGCAATGGGCAGCCGGAGAACAACTACA			
AGACCACGCCTCCCGTGCTGGACTCCGACGGCT			
CCTTCTTCCTCTATAGCAAGCTCACCGTGGACAA			
GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATG			
CTCCGTGATGCATGAGGCTCTGCACAACCACTA			
CACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAA			
A			

		iPS;361136	
		5G12.006.002	
AA	SEQ ID NO: 2027	NA	SEQ ID NO: 457
	DIQLTQSPSSLSASVGDRVTITCRASQTISRFLNWY		GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT
	QQKPGKAPELLIYVASSLQSGVPSRFSGSGSGTDFT		CTGCATCTGTAGGAGACAGAGTCACTATCACTT
	LTISSLQPEDFATYYCQQSYSTLISFGQGTKLEIKRT		GCCGGGCAAGTCAGACCATTAGCAGGTTTTTAA
	VAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA		ATTGGTATCAGCAGAAACCTGGGAAAGCCCCTG
	KVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST		AGCTCCTGATCTATGTTGCATCCAGTTTGCAAAG
	LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG		TGGGGTCCCATCAAGATTCAGTGGCAGTGGTTC
	EC		TGGGACAGATTTCACTCTCACCATCAGCAGTCT
	SEQ ID NO: 2184		SEQ ID NO: 614
	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGIH		CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTG
	WVRQAPGKGLEWVAVIWYDASNKFHADAVKGR		GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
	FTISRDNSKNTLYLQMNSLRAEDSAMYFCARGKV		ACAGCGTCTGGATTCACCTTCAGTAGCTATGGC
	AGMPEAFEIWGQGTKVTVSSASTKGPSVFPLAPSS		ATACACTGGGTCCGCCAGGCTCCAGGCAAGGGG
	KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG		CTGGAGTGGGTGGCAGTTATATGGTATGATGCA
	VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV		AGTAATAAGTTCCATGCAGACGCCGTGAAGGGC
	NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG		CGATTCACCATCTCCAGAGACAATTCCAAGAAC
	GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE		ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC
	VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV		GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA
	LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA		AAAGTGGCTGGTATGCCTGAAGCTTTTGAAATC
	KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP		TGGGGCCAAGGGACAAAGGTCACCGTCTCTTCA
	SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK		GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTG
	LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS		GCACCCTCCTCCAAGAGCACCTCTGGGGGCACA
	LSPGK		GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTC
			CCCGAACCGGTGACGGTGTCGTGGAACTCAGGC
			GCCCTGACCAGCGGCGTGCACACCTTCCCGGCT
			GTCCTACAGTCCTCAGGACTCTACTCCCTCAGCA
			GCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCA
			CCCAGACCTACATCTGCAACGTGAATCACAAGC
			CCAGCAACACCAAGGTGGACAAGAAAGTTGAG

CCCAAATCTTGTGACAAAACTCACACATGCCCA CCGTGCCCAGCACCTGAACTCCTGGGGGGACCG TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACA CCCTCATGATCTCCCGGACCCCTGAGGTCACAT GCGTGGTGGTGGACGTGAGCCACGAAGACCCTG AGGTCAAGTTCAACTGGTACGTGGACGGCGTGG AGGTGCATAATGCCAAGACAAAGCCGTGTGAGG AGCAGTACGGCAGCACGTACCGTTGTGTCAGCG TCCTCACCGTCCTGCACCAGGACTGGCTGAATG GCAAGGAGTACAAGTGCAAGGTCTCCAACAAA GCCCTCCCAGCCCCCATCGAGAAAACCATCTCC AAAGCCAAAGGGCAGCCCCGAGAACCACAGGT GTACACCCTGCCCCCATCCCGGGAGGAGATGAC CAAGAACCAGGTCAGCCTGACCTGCCTGGTCAA AGGCTTCTATCCCAGCGACATCGCCGTGGAGTG GGAGAGCAATGGGCAGCCGGAGAACAACTACA AGACCACGCCTCCCGTGCTGGACTCCGACGGCT CCTTCTTCCTCTATAGCAAGCTCACCGTGGACAA GAGCAGGTGGCAGCAGGGGAACCGTCTTCTCATG CTCCGTGATGCATGAGGCTCTGCACAACCACTA CACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAA A	SEQ ID NO: 2185	QVQLVESGGGVVQPGRSLRLSCTASGFTFSSYGIH WVRQAPGKGLEWVAVIWYDASNKFHADAVKGR FTISRDNSKNTLYLQMNSLRAEDSAMYFCARGKV AGMPEAFEIWGQGTKVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK

		LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
	SEQ ID NO: 458	SEQ ID NO: 615
iPS:361140		
5G12.006.003		
NA	GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACTATCACTT GCCGGGCAAGTCAGACCATTAGCAGGTTTTTAA ATTGGTATCAGCAGAAACCTGGGAAAGCCCCTG AGCTCCTGATCTATGTTGCATCCAGTTTGCAAAG TGGGGTCCCATCAAGATTCAGTGGCAGTGGTTC TGGGACAGATTTCACTCTCACCATCAGCAGTCT GCAACCTGAAGATTTTGCAACTTACTACTGTCA ACAGAGTTACAGTACCCTGATCAGTTTTGGCCA GGGGACCAAGCTGGAGATCACACGAACGGTGG CTGCACCATCTGTCTTCATCTTCCCGCCATCTGA TGAGCAGTTGAAATCTGGAACTGCCTCTGTTGT GTGCCTGCTGAATAACTTCTATCCCAGAGAGGC CAAAGTACAGTGGAAGGTGGATAACGCCCTCCA ATCGGGTAACTCCCAGGAGAGTGTCACAGAGCA GGACAGCAAGGACAGCACCTACAGCCTCAGCA GCACCCTGACGCTGAGCAAAGCAGACTACGAGA AACACAAAGTCTACGCCTGCGAAGTCACCCATC AGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCA ACAGGGGAGAGTGT	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC ATACACTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGTTATATGGTATGATGCA AGTAATAAGTTCCATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGAGACAATTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA AAAGTGGCTGGTATGCCTGAAGCTTTTGAAATC TGGGGCCAAGGGACAAAGGTCACCGTCTCTTCA GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTG GCACCCTCCTCCTCCAAGAGCACCTCTGGGGGCACA GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTC CCCGAACCGGTGACGGTGTCGTGGAACTCAGGC GCCCTGACCAGCGGCGTGCACACCTTCCCGGCT GTCCTACAGTCCTCAGGACTCTACTCCCTCAGCA GCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCA CCCAGACCTACATCTGCAACGTGAATCACAAGC CCAGCAACACCAAGGTGGACAAGAAAGTTGAG CCCAAATCTTGTGACAAAACTCACACATGCCCA CCGTGCCCAGCACCTGAACTCCTGGGGGGACCG TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACA CCCTCATGATCTCCCGGACCCCTGAGGTCACAT GCGTGGTGGTGGACGTGAGCCACGAAGACCCTG AGGTCAAGTTCAACTGGTACGTGGACGGCGTGG AGGTGCATAATGCCAAGACAAAGCCGCGTGTGAGG AGCAGTACGGCAGCACGTACCGTTGTGTCAGCG TCCTCACCGTCCTGCACCAGGACTGGCTGAATG GCAAGGAGTACAAGTGCAAGGTCTCCAACAAA GCCCTCCCAGCCCCCATCGAGAAAACCATCTCC

			AAAGCCAAAGGGCAGCCCCGAGAACCACAGGT GTACACCCTGCCCCCATCCCGGGAGGAGATGAC CAAGAACCAGGTCAGCCTGACCTGCCTGGTCAA AGGCTTCTATCCCAGCGACATCGCCGTGGAGTG GGAGAGCAATGGGCAGCCGGAGAACAACTACA AGACCACGCCTCCCGTGCTGGACTCCGACGGCT CCTTCTTCCTCTATAGCAAGCTCACCGTGGACAA GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATG CTCCGTGATGCATGAGGCTCTGCACAACCACTA CACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAA A
		SEQ ID NO: 2029	SEQ ID NO: 2186
	AA	DIQLTQSPSSLSASVGDRVTITCRASQTISRFLNWY QQKPGKAPELLIYVASSLQSGVPSRFSGSGSGTDFT LTISSLQPEDFATYYCQQSYSTLISFGQGTKLEITRT VAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGIH WVRQAPGKGLEWVAVIWYDASNKFHADAVKGR FTISRDNSKNTLYLQMNSLRAEDSAMYFCARGKV AGMPEAFEIWGQGTKVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
		SEQ ID NO: 459	SEQ ID NO: 616
	NA	GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACTATCACTT GCCGGGCAAGTCAGACCATTAGCAGGTTTTTAA ATTGGTATCAGCAGAAACCTGGGAAAGCCCCTA AGCTCCTGATCTATGTTGCATCCAGTTTGCAAAG TGGGGTCCCATCAAGATTCAGTGGCAGTGGTTC TGGGACAGATTTCACTCTCACCATCAGCAGTCT GCAACCTGAAGATTTTGCAACTTACTACTGTCA ACAGAGTTACAGTACCCTGATCAGTTTTGGCCA	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC ATACACTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGTTATATGGTATGATGCA AGTAATAAGTTCCATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGAGACAATTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA
	5G12.006.004		
	iPS:359919		

GGGGACCAAGCTGGAGATCAAACGAACGGTGG CTGCACCATCTGTCTTCATCTTCCCGCCATCTGA TGAGCAGTTGAAATCTGGAACTGCCTCTGTTGT GTGCCTGCTGAATAACTTCTATCCCAGAGAGGC CAAAGTACAGTGGAAGGTGGATAACGCCCTCCA ATCGGGTAACTCCCAGGAGAGTGTCACAGAGCA GGACAGCAAGGACAGCACCTACAGCCTCAGCA GCACCCTGACGCTGAGCAAAGCAGACTACGAGA AACACAAAGTCTACGCCTGCGAAGTCACCCATC AGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCA ACAGGGGAGAGTGT	AAAGTGGCTGGTATGCCTGAAGCTTTTGAAATC TGGGGCCAAGGGACATTGGTCACCGTCTCTTCA GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTG GCACCCTCCTCCAAGAGCACCTCTGGGGGCACA GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTC CCCGAACCGGTGACGGTGTCGTGGAACTCAGGC GCCCTGACCAGCGGCGTGCACACCTTCCCGGCT GTCCTACAGTCCTCAGGACTCTACTCCCTCAGCA GCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCA CCCAGACCTACATCTGCAACGTGAATCACAAGC CCAGCAACACCAAGGTGGACAAGAAAGTTGAG CCCAAATCTTGTGACAAAACTCACACATGCCCA CCGTGCCCAGCACCTGAACTCCTGGGGGGACCG TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACA CCCTCATGATCTCCCGGACCCCTGAGGTCACAT GCGTGGTGGTGGACGTGAGCCACGAAGACCCTG AGGTCAAGTTCAACTGGTACGTGGACGGCGTGG AGGTGCATAATGCCAAGACAAAGCCGTGTGAGG AGCAGTACGGCAGCACGTACCGTTGTGTCAGCG TCCTCACCGTCCTGCACCAGGACTGGCTGAATG GCAAGGAGTACAAGTGCAAGGTCTCCAACAAA GCCCTCCCAGCCCCCATCGAGAAAACCATCTCC AAAGCCAAAGGGCAGCCCCGAGAACCACAGGT GTACACCCTGCCCCCATCCCGGGAGGAGATGAC CAAGAACCAGGTCAGCCTGACCTGCCTGGTCAA AGGCTTCTATCCCAGCGACATCGCCGTGGAGTG GGAGAGCAATGGGCAGCCGGAGAACAACTACA AGACCACGCCTCCCGTGCTGGACTCCGACGGCT CCTTCTTCCTCTATAGCAAGCTCACCGTGGACAA GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATG CTCCGTGATGCATGAGGCTCTGCACAACCACTA CACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAA A	SEQ ID NO: 2187
DIQLTQSPSSLSASVGDRVTITCRASQTISRFLNWY QQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDF	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGIH WVRQAPGKGLEWVAVIWYDASNKFHADAVKGR	

TLTISSLQPEDFATYYCQQSYSTLISFGQGTKLEIKR TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC	SEQ ID NO: 460	FTISRDNSKNTLYLQMNSLRAEDSAMYFCARGKV AGMPEAFEIWGQGTLVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
	NA	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC ATACACTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGTTATATGGTATGATGCA AGTAATAAGTTCCATGCAGACTCCGTGAAGGGC CGATTCACCATCTCCAGAGACAATTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA AAAGTGGCTGGTATGCCTGAAGCTTTTGAAATC TGGGGCCAAGGGACAAAGGTCACCGTCTCTTCA GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTG GCACCCTCCTCCAAGAGCACCTCTGGGGGCACA GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTC CCCGAACCGGTGACGGTGTCGTGGAACTCAGGC GCCCTGACCAGCGGCGTGCACACCTTCCCGGCT GTCCTACAGTCCTCAGGACTCTACTCCCTCAGCA GCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCA CCCAGACCTACATCTGCAACGTGAATCACAAGC CCAGCAACACCAAGGTGGACAAGAAAGTTGAG CCCAAATCTTGTGACAAAACTCACACATGCCCA CCGTGCCCAGCACCTGAACTCCTGGGGGGACCG TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACA

CCCTCATGATCTCCCGGACCCCCTGAGGTCACAT GCGTGGTGGTGGACGTGAGCCACGAAGACCCTG AGGTCAAGTTCAACTGGTACGTGGACGGCGTGG AGGTGCATAATGCCAAGACAAAGCCGTGTGAGG AGCAGTACGGCAGCACGTACCGTTGTGTCAGCG TCCTCACCGTCCTGCACCAGGACTGGCTGAATG GCAAGGAGTACAAGTGCAAGGTCTCCAACAAA GCCCTCCCAGCCCCCATCGAGAAAACCATCTCC AAAGCCAAAGGGCAGCCCCGAGAACCACAGGT GTACACCCTGCCCCCATCCCGGGAGGAGATGAC CAAGAACCAGGTCAGCCTGACCTGCCTGGTCAA AGGCTTCTATCCCAGCGACATCGCCGTGGAGTG GGAGAGCAATGGGCAGCCGGAGAACAACTACA AGACCACGCCTCCCGTGCTGGACTCCGACGGCT CCTTCTTCCTCTATAGCAAGCTCACCGTGGACAA GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATG CTCCGTGATGCATGAGGCTCTGCACAACCACTA CACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAA A	SEQ ID NO: 2188
	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGIH WVRQAPGKGLEWVAVIWYDASNKFHADSVKGRF TISRDNSKNTLYLQMNSLRAEDSAMYFCARGKVA GMPEAFEIWGQGTKVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVL TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL SPGK
	SEQ ID NO: 618
	SEQ ID NO: 461
	SEQ ID NO: 2031
	DIQLTQSPSSLSASVGDRVTITCRASQTISRFLNWY QQKPGKAPELLIYVASSLQSGVPSRFSGSGSGTDFT LTISSLQPEDFATYYCQQSYSTLISFGQGTKLEIKRT VAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC
AA	

iPS:361151	5G12.006.006	NA	
			GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTGTAGGAGACAGAGTCACTATCACTT
			GCCGGGCAAGTCAGACCATTAGCAGGTTTTTAA
			ATTGGTATCAGCAGAAACCTGGGAAAGCCCCTG
			AGCTCCTGATCTATGTTGCATCCAGTTTGCAAAG
			TGGGGTCCCATCAAGATTCAGTGGCAGTGGTTC
			TGGGACAGATTTCACTCTCACCATCAGCAGTCT
			GCAACCTGAAGATTTTGCAACTTACTACTGTCA
			ACAGAGTTACAGTACCCTGATCAGTTTTGGCCA
			GGGGACCAAGCTGGAGATCAAACGAACGGTGG
			CTGCACCATCTGTCTTCATCTTCCCGCCATCTGA
			TGAGCAGTTGAAATCTGGAACTGCCTCTGTTGT
			GTGCCTGCTGAATAACTTCTATCCCAGAGAGGC
			CAAAGTACAGTGGAAGGTGGATAACGCCCTCCA
			ATCGGGTAACTCCCAGGAGAGTGTCACAGAGCA
			GGACAGCAAGGACAGCACCTACAGCCTCAGCA
			GCACCCTGACGCTGAGCAAAGCAGACTACGAGA
			AACACAAAGTCTACGCCTGCGAAGTCACCCATC
			AGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCA
			ACAGGGGAGAGTGT
			CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTG
			GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC
			ATACACTGGGTCCGCCAGGCTCCAGGCAAGGGG
			CTGGAGTGGGTGGCAGTTATATGGTATGATGGA
			AGTAATAAGTTCCATGCAGACGCCGTGAAGGGC
			CGATTCACCATCTCCAGAGACAATTCCAAGAAC
			ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC
			GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA
			AAAGTGGCTGGTATGCCTGAAGCTTTTGAAATC
			TGGGGCCAAGGGACAAAGGTCACCGTCTCTTCA
			GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTG
			GCACCCTCCTCCAAGAGCACCTCTGGGGGCACA
			GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTC
			CCCGAACCGGTGACGGTGTCGTGGAACTCAGGC
			GCCCTGACCAGCGGCGTGCACACCTTCCCGGCT
			GTCCTACAGTCCTCAGGACTCTACTCCCTCAGCA
			GCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCA
			CCCAGACCTACATCTGCAACGTGAATCACAAGC
			CCAGCAACACCAAGGTGGACAAGAAAGTTGAG
			CCCAAATCTTGTGACAAAACTCACACATGCCCA
			CCGTGCCCAGCACCTGAACTCCTGGGGGGACCG
			TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACA
			CCCTCATGATCTCCCGGACCCCTGAGGTCACAT
			GCGTGGTGGTGGACGTGAGCCACGAAGACCCTG
			AGGTCAAGTTCAACTGGTACGTGGACGGCGTGG
			AGGTGCATAATGCCAAGACAAAGCCGTGTGAGG
			AGCAGTACGGCAGCACGTACCGTTGTGTCAGCG
			TCCTCACCGTCCTGCACCAGGACTGGCTGAATG
			GCAAGGAGTACAAGTGCAAGGTCTCCAACAAA
			GCCCTCCCAGCCCCCATCGAGAAAACCATCTCC
			AAAGCCAAAGGGCAGCCCCGAGAACCACAGGT
			GTACACCCTGCCCCCATCCCGGGAGGAGATGAC
			CAAGAACCAGGTCAGCCTGACCTGCCTGGTCAA
			AGGCTTCTATCCCAGCGACATCGCCGTGGAGTG
			GGAGAGCAATGGGCAGCCGGAGAACAACTACA

		AGACCACGCCTCCCGTGCTGGACTCCGACGGCT CCTTCTTCCTCTATAGCAAGCTCACCGTGGACAA GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATG CTCCGTGATGCATGAGGCTCTGCACAACCACTA CACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAA A
	SEQ ID NO: 2032	SEQ ID NO: 2189
	AA	DIQLTQSPSSLSASVGDRVTITCRASQTISRFLNWY QQKPGKAPELLIYVASSLQSGVPSRFSGSGSGTDFT LTISSLQPEDFATYYCQQSYSTLISFGQGTKLEIKRT VAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC
	SEQ ID NO: 462	SEQ ID NO: 619
iPS:361491	NA	CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTG CGGCCCCAGGACAGAAGGTCACCATCTCCTGCT CTGGAAGCAGCTCCAACATTGGAAATAATTATG TATCCTGGTATCAGCAGCTCCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCCTGACCGATTCTCTGGCTCCAA GTCTGGCACGTCAGCCACCCTGGGCATCACCGG ACTCCAGACTGGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGCTGTGGT ATTCGGCGGAGGGACCAAACTGACCGTCCTAGG TCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTC CCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAG GCCACACTGGTGTGTCTCATAAGTGACTTCTACC CGGGAGCCGTGACAGTGGCCTGGAAGGCAGAT
17B11.002.001		

AGCAGCCCCGTCAAGGCGGGAGTGGAGACCAC CACACCCTCCAAACAAAGCAACAACAAGTACGC GGCCAGCAGCTATCTGAGCCTGACGCCTGAGCA GTGGAAGTCCCACAGAAGCTACAGCTGCCAGGT CACGCATGAAGGGAGCACCGTGGAGAAGACAG TGGCCCCTACAGAATGTTCA	CTGCCTGGTCAAGGACTACTTCCCCGAACCGGT GACGGTGTCGTGGAACTCAGGCGCCCTGACCAG CGGCGTGCACACCTTCCCGGCTGTCCTACAGTCC TCAGGACTCTACTCCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCACCCAGACCTAC ATCTGCAACGTGAATCACAAGCCCAGCAACACC AAGGTGGACAAGAAAGTTGAGCCCAAATCTTGT GACAAAACTCACACATGCCCACCGTGCCCAGCA CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCT TCCCCCCAAAACCCAAGGACACCCTCATGATCT CCCGGACCCCTGAGGTCACATGCGTGGTGGTGG ACGTGAGCCACGAAGACCCTGAGGTCAAGTTCA ACTGGTACGTGGACGGCGTGGAGGTGCATAATG CCAAGACAAAGCCGTGTGAGGAGCAGTACGGC AGCACGTACCGTTGTGTCAGCGTCCTCACCGTCC TGCACCAGGACTGGCTGAATGGCAAGGAGTACA AGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCC CCATCGAGAAAACCATCTCCAAAGCCAAAGGGC AGCCCCGAGAACCACAGGTGTACACCCTGCCCC CATCCCGGGAGGAGATGACCAAGAACCAGGTC AGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC AGCGACATCGCCGTGGAGTGGGAGAGCAATGG GCAGCCGGAGAACAACTACAAGACCACGCCTCC CGTGCTGGACTCCGACGGCTCCTTCTTCCTCTAT AGCAAGCTCACCGTGGACAAGAGCAGGTGGCA GCAGGGGAACGTCTTCTCATGCTCCGTGATGCA TGAGGCTCTGCACAACCACTACACGCAGAAGAG CCTCTCCCTGTCTCCGGGTAAA
SEQ ID NO: 2033	SEQ ID NO: 2190
QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLGITGLQTGDEADYYCGTWDSSLSAVVFGGG TKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNN KYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK TVAPTECS	QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDI NWVRQATGQGLEWMGWMNPNSGGTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSQDTAVYYCARG GDYVWGSYRPYYYYYGMDVWGQGTTVTVSSAS TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP SSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH
AA	

		TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT
		CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE
		EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK
		ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ
		VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
		LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA
		LHNHYTQKSLSLSPGK
	SEQ ID NO: 463	SEQ ID NO: 620
	CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTG	CAAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG
	CGGCCCCAGGACAGAAGGTCACCATCTCCTGCT	AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
	CTGGAAGCAGCTCCAACATTGGAAATAATTATG	AAGGCTTCTGGATACACCTTCACCAGTTATGAT
	TATCCTGGTATCAGCAGCTCCCAGGAACAGCCC	ATCAACTGGGTGCGACAGGCCACTGGACAAGGG
	CCAAACTCCTCATTTATGACAATAATAAGCGAC	CTTGAGTGGATGGGATGGAACCCTAACAGT
	CCTCAGGGATTCCTGACCGATTCTCTGGCTCCAA	GGTAACACAGGCTATGCACAGAAGTTCCAGGGC
	GTCTGGCACGTCAGCCACCCTGGGCATCACCGG	AGAGTCACCATGACCAGGGACACCTCCATAAGC
	ACTCCAGACTGGGGACGAGGCCGATTATTACTG	ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT
	CGGAACATGGGATAGCAGCCTGAGTGCTGTGGT	CAGGACACGGCCGTGTATTACTGTGCGAGAGGG
	ATTCGGCGGAGGGACCAAACTGACCGTCCTAGG	GGTGATTACGTTTGGGGGAGTTATCGTCCCTACT
	TCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTC	ACTACTACTACGGTATGGACGTCTGGGGCCAAG
	CCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAG	GGACCACGGTCACCGTCTCCTCAGCCTCCACCA
	GCCACACTGGTGTGTCTCATAAGTGACTTCTACC	AGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTC
	CGGGAGCCGTGACAGTGGCCTGGAAGGCAGAT	CAAGAGCACCTCTGGGGGCACAGCGGCCCTGGG
	AGCAGCCCCGTCAAGGCGGGAGTGGAGACCAC	CTGCCTGGTCAAGGACTACTTCCCCGAACCGGT
	CACACCCTCCAAACAAAGCAACAACAAGTACGC	GACGGTGTCGTGGAACTCAGGCGCCCTGACCAG
	GGCCAGCAGCTATCTGAGCCTGACGCCTGAGCA	CGGCGTGCACACCTTCCCGGCTGTCCTACAGTCC
	GTGGAAGTCCCACAGAAGCTACAGCTGCCAGGT	TCAGGACTCTACTCCCTCAGCAGCGTGGTGACC
	CACGCATGAAGGGAGCACCGTGGAGAAGACAG	GTGCCCTCCAGCAGCTTGGGCACCCAGACCTAC
	TGGCCCCTACAGAATGTTCA	ATCTGCAACGTGAATCACAAGCCCAGCAACACC
		AAGGTGGACAAGAAAGTTGAGCCCAAATCTTGT
		GACAAAACTCACACATGCCCACCGTGCCCAGCA
		CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCT
		TCCCCCCAAAACCCAAGGACACCCTCATGATCT
		CCCGGACCCCTGAGGTCACATGCGTGGTGGTGG
		ACGTGAGCCACGAAGACCCTGAGGTCAAGTTCA
		ACTGGTACGTGGACGGCGTGGAGGTGCATAATG
		CCAAGACAAAGCCGTGTGAGGAGCAGTACGGC
	NA	
	17B11.002.002	
	iPS:361499	

	AGCACGTACCGTTGTGTCAGCGTCCTCACCGTCC
	TGCACCAGGACTGGCTGAATGGCAAGGAGTACA
	AGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCC
	CCATCGAGAAAACCATCTCCAAAGCCAAAGGGC
	AGCCCCGAGAACCACAGGTGTACACCCTGCCCC
	CATCCCGGGAGGAGATGACCAAGAACCAGGTC
	AGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC
	AGCGACATCGCCGTGGAGTGGGAGAGCAATGG
	GCAGCCGGAGAACAACTACAAGACCACGCCTCC
	CGTGCTGGACTCCGACGGCTCCTTCTTCCTCTAT
	AGCAAGCTCACCGTGGACAAGAGCAGGTGGCA
	GCAGGGGAACGTCTTCTCATGCTCCGTGATGCA
	TGAGGCTCTGCACAACCACTACACGCAGAAGAG
	CCTCTCCCTGTCTCCGGGTAAA
SEQ ID NO: 2034	SEQ ID NO: 2191
QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVS	QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDI
WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT	NWVRQATGQGLEWMGWMNPNSGNTGYAQKFQ
SATLGITGLQTGDEADYYCGTWDSSLSAVVFGGG	GRVTMTRDTSISTAYMELSSLRSQDTAVYYCARG
TKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI	GDYVWGSYRPYYYYYGMDVWGQGTTVTVSSAS
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNN	TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV
KYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK	TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP
TVAPTECS	SSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH
	TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT
	CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE
	EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK
	ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ
	VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
	LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA
	LHNHYTQKSLSLSPGK
SEQ ID NO: 464	SEQ ID NO: 621
CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTG	CAAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG
CGGCCCCAGGACAGAAGGTCACCATCTCCTGCT	AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
CTGGAAGCAGCTCCAACATTGGAAATAATTATG	AAGGCTTCTGGATACACCTTCACCAGTTATGAT
TATCCTGGTATGAGCAGTTCCCAGGAACAGCCC	ATCAACTGGGTGCGACAGGCCACTGGACAAGGG
CCAAACTCCTCATTTATGACAATAATAAGCGAC	CTTGAGTGGATGGGATGGAACCCTAACAGT
CCTCAGGGATTCCTGACCGATTCTCTGGCTCCAA	GGTGGCACAGGCTATGCACAGAAGTTCCAGGGC

iPS:361503	
17B11.002.00 3	
NA	
AA	

AGAGTCACCATGACCAGGGACACCTCCATAAGC	GTCTGGCACGTCAGCCACCCTGGGCATCACCGG		
ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT	ACTCCAGACTGGGGACGAGGCCGATTATTACTG		
CAGGACACGGCCGTGTATTACTGTGCGAGAGGG	CGGAACATGGGATAGCAGCCTGAGTGCTGTGGT		
GGTGATTACGTTTGGGGGAGTTATCGTCCCTACT	ATTCGGCGGAGGGACCAAACTGACCGTCCTAGG		
ACTACTACTACGGTATGGACGTCTGGGGCCAAG	TCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTC		
GGACCACGGTCACCGTCTCCTCAGCCTCCACCA	CCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAG		
AGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTC	GCCACACTGGTGTGTCTCATAAGTGACTTCTACC		
CAAGAGCACCTCTGGGGGCACAGCGGCCCTGGG	CGGGAGCCGTGACAGTGGCCTGGAAGGCAGAT		
CTGCCTGGTCAAGGACTACTTCCCCGAACCGGT	AGCAGCCCCGTCAAGGCGGGAGTGGAGACCAC		
GACGGTGTCGTGGAACTCAGGCGCCCTGACCAG	CACACCCTCCAAACAAAGCAACAACAAGTACGC		
CGGCGTGCACACCTTCCCGGCTGTCCTACAGTCC	GGCCAGCAGCTATCTGAGCCTGACGCCTGAGCA		
TCAGGACTCTACTCCCTCAGCAGCGTGGTGACC	GTGGAAGTCCCACAGAAGCTACAGCTGCCAGGT		
GTGCCCTCCAGCAGCTTGGGCACCCAGACCTAC	CACGCATGAAGGGAGCACCGTGGAGAAGACAG		
ATCTGCAACGTGAATCACAAGCCCAGCAACACC	TGGCCCCTACAGAATGTTCA		
AAGGTGGACAAGAAAGTTGAGCCCAAATCTTGT			
GACAAAACTCACACATGCCCACCGTGCCCAGCA			
CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCT			
TCCCCCAAAACCCAAGGACACCCTCATGATCT			
CCCGGACCCCTGAGGTCACATGCGTGGTGGTGG			
ACGTGAGCCACGAAGACCCTGAGGTCAAGTTCA			
ACTGGTACGTGGACGGCGTGGAGGTGCATAATG			
CCAAGACAAAGCCGCGTGTGAGGAGCAGTACGGC			
AGCACGTACCGTTGTGTCAGCGTCCTCACCGTCC			
TGCACCAGGACTGGCTGAATGGCAAGGAGTACA			
AGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCC			
CCATCGAGAAAACCATCTCCAAAGCCAAAGGGC			
AGCCCCGAGAACCACACAGGTGTACACCCTGCCCC			
CATCCCGGGAGGAGATGACCAAGAACCAGGTC			
AGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC			
AGCGACATCGCCGTGGAGTGGGAGAGCAATGG			
GCAGCCGGAGAACAACTACAAGACCACGCCTCC			
CGTGCTGGACTCCGACGGCTCCTTCTTCCTCTAT			
AGCAAGCTCACCGTGGACAAGAGCAGGTGGCA			
GCAGGGGAACGTCTTCTCATGCTCCGTGATGCA			
TGAGGCTCTGCACAACCACTACACGCAGAAGAG			
CCTCTCCCTGTCTCCGGGTAAA			

		iPS:361507
		17B11.002.004
AA	SEQ ID NO: 2035	SEQ ID NO: 2192
	QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVS WYEQFPGTAPKLLIYDNNKRPSGIPDRFSGSKSGTS ATLGITGLQTGDEADYYCGTWDSSLSAVVFGGGT KLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLIS DFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNK YAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKT VAPTECS	QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDI NWVRQATGQGLEWMGWMNPNSGGTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSQDTAVYYCARG GDYVWGSYRPYYYYYGMDVWGQGTTVTVSSAS TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP SSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK
NA	SEQ ID NO: 465	SEQ ID NO: 622
	CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTG CGGCCCCAGGACAGAAGGTCACCATCTCCTGCT CTGGAAGCAGCTCCAACATTGGAAATAATTATG TATCCTGGTATCAGCAGCTCCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAAGCGAC CCTCAGGGATTCCTGACCGATTCTCTGGCTCCAA GTCTGGCACGTCAGCCACCCTGGCCATCACCGG ACTCCAGACTGGGGACGAGGCCGATTATTACTG CGGAACATTCGAAAGCAGCCTGAGTGCTGTGGT ATTCGGCGGAGGGACCAAACTGACCGTCCTAGG TCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTC CCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAG GCCACACTGGTGTGTCTCATAAGTGACTTCTACC CGGGAGCCGTGACAGTGGCCTGGAAGGCAGAT AGCAGCCCCGTCAAGGCGGGAGTGGAGACCAC CACACCCTCCAAACAAAGCAACAACAAGTACGC GGCCAGCAGCTATCTGAGCCTGACGCCTGAGCA GTGGAAGTCCCACAGAAGCTACAGCTGCCAGGT CACGCATGAAGGGAGCACCGTGGAGAAGACAG TGGCCCCTACAGAATGTTCA	CAAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCAGTTATGAT ATCAACTGGGTGCGACAGGCCCCTGGACAAGGG CTTGAGTGGATGGGATGGAACCCTAACAGT GGTGGCACAGGCTATGCACAGAAGTTCCAGGGC AGAGTCACCATGACCAGGGACACCTCCATAAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGGG GGTGATTACGTTTGGGGGAGTTATCGTCCCTACT ACTACTACTACGGTATGGACGTCTGGGGCCAAG GGACCACGGTCACCGTCTCCTCAGCCTCCACCA AGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTC CAAGAGCACCTCTGGGGGCACAGCGGCCCTGGG CTGCCTGGTCAAGGACTACTTCCCCGAACCGGT GACGGTGTCGTGGAACTCAGGCGCCCTGACCAG CGGCGTGCACACCTTCCCGGCTGTCCTACAGTCC TCAGGACTCTACTCCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCACCCAGACCTAC ATCTGCAACGTGAATCACAAGCCCAGCAACACC

AAGGTGGACAAGAAAGTTGAGCCCAAATCTTGT GACAAAACTCACACATGCCCACCGTGCCCAGCA CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCT TCCCCCAAAACCCAAGGACACCCTCATGATCT CCCGGACCCCTGAGGTCACATGCGTGGTGGTGG ACGTGAGCCACGAAGACCCTGAGGTCAAGTTCA ACTGGTACGTGGACGGCGTGGAGGTGCATAATG CCAAGACAAAGCCGTGTGAGGAGCAGTACGGC AGCACGTACCGTTGTGTCAGCGTCCTCACCGTCC TGCACCAGGACTGGCTGAATGGCAAGGAGTACA AGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCC CCATCGAGAAAACCATCTCCAAAGCCAAAGGGC AGCCCCGAGAACCACAGGTGTACACCCTGCCCC CATCCCGGGAGGAGATGACCAAGAACCAGGTC AGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC AGCGACATCGCCGTGGAGTGGGAGAGCAATGG GCAGCCGGAGAACAACTACAAGACCACGCCTCC CGTGCTGGACTCCGACGGCTCCTTCTTCCTCTAT AGCAAGCTCACCGTGGACAAGAGCAGGTGGCA GCAGGGGAACGTCTTCTCATGCTCCGTGATGCA TGAGGCTCTGCACAACCACTACACGCAGAAGAG CCTCTCCCTGTCTCCGGGTAAA	SEQ ID NO: 2193
	SEQ ID NO: 2036
AA	QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLAITGLQTGDEADYYCGTFESSLSAVVFGGGT KLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLIS DFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNK YAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKT VAPTECS
	QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDI NWVRQAPGQGLEWMGWMNPNSGGTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSDDTAVYYCARG GDYVWGSYRPYYYYYGMDVWGQGTTVTVSSAS TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP SSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV

		LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK
	SEQ ID NO: 466	SEQ ID NO: 623
	CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTG	CAAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG
	CGGCCCCAGGACAGAAGGTCACCATCTCCTGCT	AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
	CTGGAAGCAGCTCCAACATTGGAAATAATTATG	AAGGCTTCTGGATACACCTTCACCAGTTATGAT
	TATCCTGGTATCAGCAGCTCCCAGGAACAGCCC	ATCAACTGGGTGCGACAGGCCACTGGACAAGGG
	CCAAACTCCTCATTTATGACAATAATAAGCGAC	CTTGAGTGGATGGGATGGAACCCTAACAGT
	CCTCAGGGATTCCTGACCGATTCTCTGGCTCCAA	GGTGGCACAGGCTATGCACAGAAGTTCCAGGGC
	GTCTGGCACGTCAGCCACCCTGGCCATCACCGG	AGAGTCACCATGACCAGGGACACCTCCATAAGC
	ACTCCAGACTGGGGACGAGGCCGATTATTACTG	ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT
	CGGAACATGGGATAGCAGCCTGAGTGCTGTGGT	CAGGACACGGCCGTGTATTACTGTGCGAGAGGG
	ATTCGGCGGAGGGACCAAACTGACCGTCCTAGG	GGTGATTACGTTTGGGGGAGTTATCGTCCCTACT
	TCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTC	ACTACTACTACGGTATGGACGTCTGGGGCCAAG
	CCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAG	GGACCACGGTCACCGTCTCCTCAGCCTCCACCA
	GCCACACTGGTGTGTCTCATAAGTGACTTCTACC	AGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTC
	CGGGAGCCGTGACAGTGGCCTGGAAGGCAGAT	CAAGAGCACCTCTGGGGGCACAGCGGCCCTGGG
	AGCAGCCCCGTCAAGGCGGGAGTGGAGACCAC	CTGCCTGGTCAAGGACTACTTCCCCGAACCGGT
	CACACCCTCCAAACAAAGCAACAACAAGTACGC	GACGGTGTCGTGGAACTCAGGCGCCCTGACCAG
	GGCCAGCAGCTATCTGAGCCTGACGCCTGAGCA	CGGCGTGCACACCTTCCCGGCTGTCCTACAGTCC
	GTGGAAGTCCCACAGAAGCTACAGCTGCCAGGT	TCAGGACTCTACTCCCTCAGCAGCGTGGTGACC
	CACGCATGAAGGGAGCACCGTGGAGAAGACAG	GTGCCCTCCAGCAGCTTGGGCACCCAGACCTAC
	TGGCCCCTACAGAATGTTCA	ATCTGCAACGTGAATCACAAGCCCAGCAACACC
		AAGGTGGACAAGAAAGTTGAGCCCAAATCTTGT
		GACAAAACTCACACATGCCCACCGTGCCCAGCA
		CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCT
		TCCCCCCAAAACCCAAGGACACCCTCATGATCT
		CCCGGACCCCTGAGGTCACATGCGTGGTGGTGG
		ACGTGAGCCACGAAGACCCTGAGGTCAAGTTCA
		ACTGGTACGTGGACGGCGTGGAGGTGCATAATG
		CCAAGACAAAGCCGTGTGAGGAGCAGTACGGC
		AGCACGTACCGTTGTGTCAGCGTCCTCACCGTCC
		TGCACCAGGACTGGCTGAATGGCAAGGAGTACA
		AGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCC
		CCATCGAGAAAACCATCTCCAAAGCCAAAGGGC
		AGCCCCGAGAACCACAGGTGTACACCCTGCCCCC

			CATCCCGGGAGGAGATGACCAAGAACCAGGTC
			AGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC
			AGCGACATCGCCGTGGAGTGGGAGAGCAATGG
			GCAGCCGGAGAACAACTACAAGACCACGCCTCC
			CGTGCTGGACTCCGACGGCTCCTTCTTCCTCTAT
			AGCAAGCTCACCGTGGACAAGAGCAGGTGGCA
			GCAGGGGAACGTCTTCTCATGCTCCGTGATGCA
			TGAGGCTCTGCACAACCACTACACGCAGAAGAG
			CCTCTCCCTGTCTCCGGGTAAA
		SEQ ID NO: 2037	SEQ ID NO: 2194
	AA	QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLAITGLQTGDEADYYCGTWDSSLSAVVFGGG TKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNN KYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK TVAPTECS	QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDI NWVRQATGQGLEWMGWMNPNSGGTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSQDTAVYYCARG GDYVWGSYRPYYYYYGMDVWGQGTTVTVSSAS TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP SSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK
		SEQ ID NO: 467	SEQ ID NO: 624
	NA	CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTG CGGCCCCAGGACAGAAGGTCACCATCTCCTGCT CTGGAAGCAGCTCCAACATTGGAAATAATTATG TATCCTGGTATCAGCAGCTCCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAAGCGAC CCTCAGGGATTCCTGACCGATTCTCTGGCTCCAA GTCTGGCACGTCAGCCACCCTGGCCATCACCGG ACTCCAGACTGGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGCTGTGGT ATTCGGCGGAGGGACCAAACTGACCGTCCTAGG TCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTC	CAAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCAGTTATGAT ATCAACTGGGTGCGACAGGCCCCTGGACAAGGG CTTGAGTGGATGGGATGGAACCCTAACAGT GGTAACACAGGCTATGCACAGAAGTTCCAGGGC AGAGTCACCATGACCAGGGACACCTCCATAAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGGG GGTGATTACGTTTGGGGGAGTTATCGTCCCTACT ACTACTACTACGGTATGGACGTCTGGGGCCAAG
	17B11.002.006		
	iPS:360582		

CCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAG		GGACCACGGTCACCGTCTCCTCAGCCTCCACCA
GCCACACTGGTGTGTCTCATAAGTGACTTCTACC		AGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTC
CGGGAGCCGTGACAGTGGCCTGGAAGGCAGAT		CAAGAGCACCTCTGGGGGCACAGCGGCCCTGGG
AGCAGCCCCGTCAAGGCGGGAGTGGAGACCAC		CTGCCTGGTCAAGGACTACTTCCCCGAACCGGT
CACACCCTCCAAACAAAGCAACAACAAGTACGC		GACGGTGTCGTGGAACTCAGGCGCCCTGACCAG
GGCCAGCAGCTATCTGAGCCTGACGCCTGAGCA		CGGCGTGCACACCTTCCCGGCTGTCCTACAGTCC
GTGGAAGTCCCACAGAAGCTACAGCTGCCAGGT		TCAGGACTCTACTCCCTCAGCAGCGTGGTGACC
CACGCATGAAGGGAGCACCGTGGAGAAGACAG		GTGCCCTCCAGCAGCTTGGGCACCCAGACCTAC
TGGCCCCTACAGAATGTTCA		ATCTGCAACGTGAATCACAAGCCCAGCAACACC
		AAGGTGGACAAGAAAGTTGAGCCCAAATCTTGT
		GACAAAACTCACACATGCCCACCGTGCCCAGCA
		CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCT
		TCCCCCCAAAACCCAAGGACACCCTCATGATCT
		CCCGGACCCCTGAGGTCACATGCGTGGTGGTGG
		ACGTGAGCCACGAAGACCCTGAGGTCAAGTTCA
		ACTGGTACGTGGACGGCGTGGAGGTGCATAATG
		CCAAGACAAAGCCGTGTGAGGAGCAGTACGGC
		AGCACGTACCGTTGTGTCAGCGTCCTCACCGTCC
		TGCACCAGGACTGGCTGAATGGCAAGGAGTACA
		AGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCC
		CCATCGAGAAAACCATCTCCAAAGCCAAAGGGC
		AGCCCCGAGAACCACAGGTGTACACCCTGCCCCC
		CATCCCGGGAGGAGATGACCAAGAACCAGGTC
		AGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC
		AGCGACATCGCCGTGGAGTGGGAGAGCAATGG
		GCAGCCGGAGAACAACTACAAGACCACGCCTCC
		CGTGCTGGACTCCGACGGCTCCTTCTTCCTCTAT
		AGCAAGCTCACCGTGGACAAGAGCAGGTGGCA
		GCAGGGGAACGTCTTCTCATGCTCCGTGATGCA
		TGAGGCTCTGCACAACCACTACACGCAGAAGAG
		CCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 2038	SEQ ID NO: 2195
AA	QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVS	QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDI
	WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT	NWVRQAPGQGLEWMGWMNPNSGNTGYAQKFQ
	SATLAITGLQTGDEADYYCGTWDSSLSAVVFGGG	GRVTMTRDTSISTAYMELSSLRSDDTAVYYCARG
	TKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI	GDYVWGSYRPYYYYYGMDVWGQGTTVTVSSAS

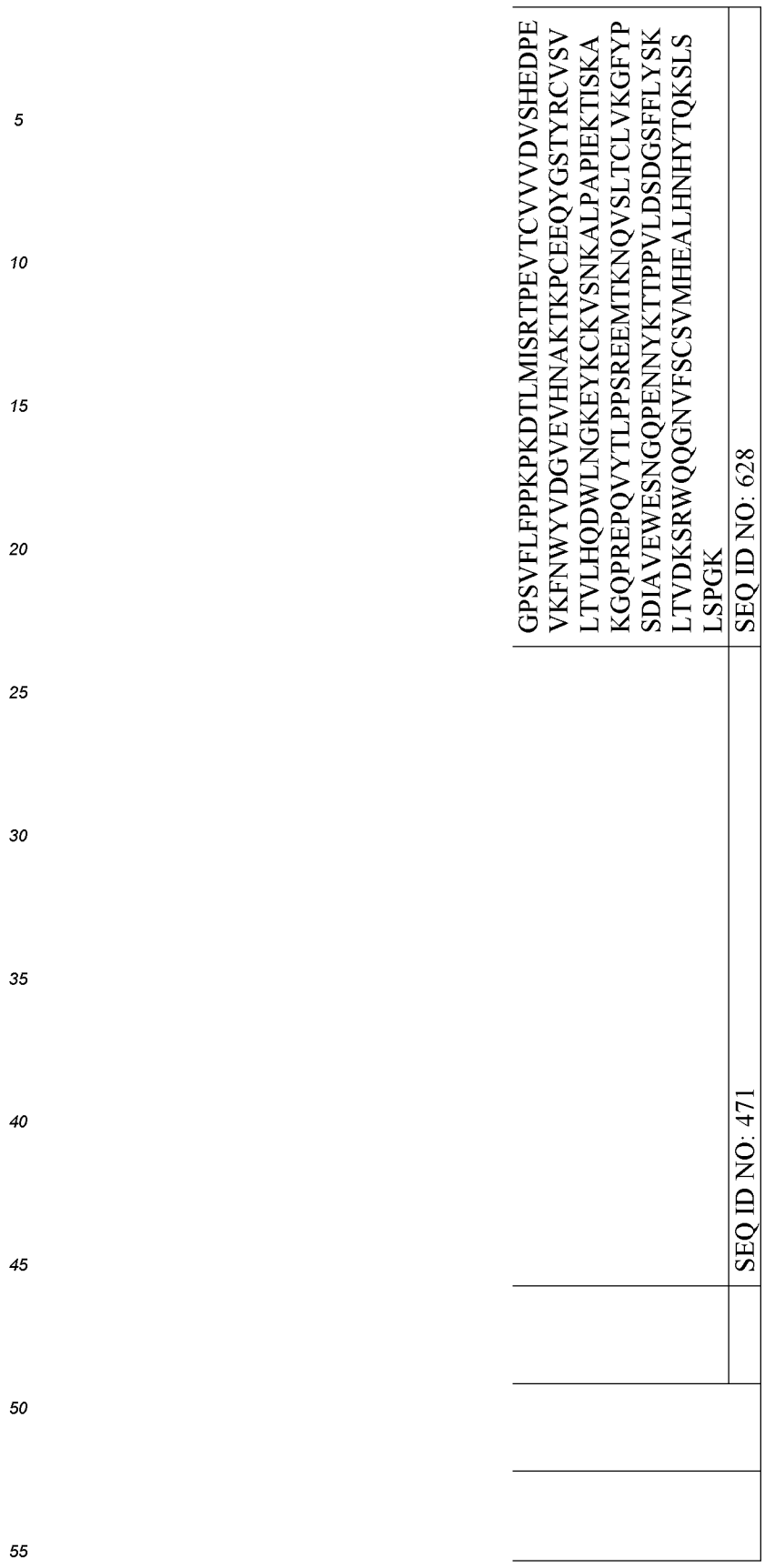
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNN KYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK TVAPTECS		TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP SSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK
SEQ ID NO: 468		SEQ ID NO: 625
NA		CAAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCAGTTATGAT ATCAACTGGGTGCGACAGGCCACTGGACAAGGG CTTGAGTGGATGGGATGGAACCCTAACAGT GGTGGCACAGGCTATGCACAGAAGTTCCAGGGC AGAGTCACCATGACCAGGGACACCTCCATAAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT CAGGACACGGCCGTGTATTACTGTGCGAGAGGG GGTGATTACGTTTTCGGGAGTTATCGTCCCTACT ACTACTACTACGGTATGGACGTCTGGGGCCAAG GGACCACGGTCACCGTCTCCTCAGCCTCCACCA AGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTC CAAGAGCACCTCTGGGGGCACAGCGGCCCTGGG CTGCCTGGTCAAGGACTACTTCCCCGAACCGGT GACGGTGTCGTGGAACTCAGGCGCCCTGACCAG CGGCGTGCACACCTTCCCGGCTGTCCTACAGTCC TCAGGACTCTACTCCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCACCCAGACCTAC ATCTGCAACGTGAATCACAAGCCCAGCAACACC AAGGTGGACAAGAAAGTTGAGCCCAAATCTTGT GACAAAACTCACACATGCCCACCGTGCCCAGCA CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCT TCCCCCCAAAACCCAAGGACACCCTCATGATCT CCCGGACCCCTGAGGTCACATGCGTGGTGGTGG

		ACGTGAGCCACGAAGACCCTGAGGTCAAGTTCA ACTGGTACGTGGACGGCGTGGAGGTGCATAATG CCAAGACAAAGCCGTGTGAGGAGCAGTACGGC AGCACGTACCGTTGTGTCAGCGTCCTCACCGTCC TGCACCAGGACTGGCTGAATGGCAAGGAGTACA AGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCC CCATCGAGAAAACCATCTCCAAAGCCAAAGGGC AGCCCCGAGAACCACAGGTGTACACCCTGCCCC CATCCCGGGAGGAGATGACCAAGAACCAGGTC AGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC AGCGACATCGCCGTGGAGTGGGAGAGCAATGG GCAGCCGGAGAACAACTACAAGACCACGCCTCC CGTGCTGGACTCCGACGGCTCCTTCTTCCTCTAT AGCAAGCTCACCGTGGACAAGAGCAGGTGGCA GCAGGGGAACGTCTTCTCATGCTCCGTGATGCA TGAGGCTCTGCACAACCACTACACGCAGAAGAG CCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 2039	SEQ ID NO: 2196
AA	QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLGITGLQTGDEADYYCGTWDSSLSAVVFGGG TKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNN KYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK TVAPTECS	QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDI NWVRQATGQGLEWMGWMNPNSGGTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSQDTAVYYCARG GDYVFGSYRPYYYYYGMDVWGQGTTVTVSSAST KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK
	SEQ ID NO: 469	SEQ ID NO: 626

iPS:360570	17B11.002.008	NA	CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTG CGGCCCCAGGACAGAAGGTCACCATCTCCTGCT CTGGAAGCAGCTCCAACATTGGAAATAATTATG TATCCTGGTATCAGCAGCTCCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCCTGACCGATTCTCTGGCTCCAA GTCTGGCACGTCAGCCACCCTGGCCATCACCGG ACTCCAGACTGGGGACGAGGCCGATTATTACTG CGGAACATTCGAAAGCAGCCTGAGTGCTGTGGT ATTCGGCGGAGGGACCAAACTGACCGTCCTAGG TCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTC CCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAG GCCACACTGGTGTGTCTCATAAGTGACTTCTACC CGGGAGCCGTGACAGTGGCCTGGAAGGCAGAT AGCAGCCCCGTCAAGGCGGGAGTGGAGACCAC CACACCCTCCAAACAAAGCAACACAAGTACGC GGCCAGCAGCTATCTGAGCCTGACGCCTGAGCA GTGGAAGTCCCACAGAAGCTACAGCTGCCAGGT CACGCATGAAGGGAGCACCGTGGAGAAGACAG TGGCCCCTACAGAATGTTCA	CAAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCAGTTATGAT ATCAACTGGGTGCGACAGGCCCCTGGACAAGGG CTTGAGTGGATGGGATGGAACCCTAACAGT GGTGGCACAGGCTATGCACAGAAGTTCCAGGGC AGAGTCACCATGACCAGGGACACCTCCATAAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGG GGTGATTACGTTTTCGGGAGTTATCGTCCCTACT ACTACTACTACGGTATGGACGTCTGGGGCCAAG GGACCACGGTCACCGTCTCCTCAGCCTCCACCA AGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTC CAAGAGCACCTCTGGGGGCACAGCGGCCCTGGG CTGCCTGGTCAAGGACTACTTCCCCGAACCGGT GACGGTGTCGTGGAACTCAGGCGCCCTGACCAG CGGCGTGCACACCTTCCCGGCTGTCCTACAGTCC TCAGGACTCTACTCCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCACCCAGACCTAC ATCTGCAACGTGAATCACAAGCCCAGCAACACC AAGGTGGACAAGAAAGTTGAGCCCAAATCTTGT GACAAAACTCACACATGCCCACCGTGCCCAGCA CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCT TCCCCCCAAAACCCAAGGACACCCTCATGATCT CCCGGACCCCCTGAGGTCACATGCGTGGTGGTGG ACGTGAGCCACGAAGACCCTGAGGTCAAGTTCA ACTGGTACGTGGACGGCGTGGAGGTGCATAATG CCAAGACAAAGCCGTGTGAGGAGCAGTACGGC AGCACGTACCGTTGTGTCAGCGTCCTCACCGTCC TGCACCAGGACTGGCTGAATGGCAAGGAGTACA AGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCC CCATCGAGAAAACCATCTCCAAAGCCAAAGGGC AGCCCCGAGAACCACAGGTGTACACCCTGCCCC CATCCCGGGAGGAGATGACCAAGAACCAGGTC AGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC AGCGACATCGCCGTGGAGTGGGAGAGCAATGG

		GCAGCCGGAGAACAACTACAAGACCACGCCTCC
		CGTGCTGGACTCCGACGGCTCCTTCTTCCTCTAT
		AGCAAGCTCACCGTGGACAAGAGCAGGTGGCA
		GCAGGGGAACGTCTTCTCATGCTCCGTGATGCA
		TGAGGCTCTGCACAACCACTACACGCAGAAGAG
		CCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 2040	SEQ ID NO: 2197
AA	QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLAITGLQTGDEADYYCGTFESSLSAVVFGGGT KLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLIS DFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNK YAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKT VAPTECS	QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDI NWVRQAPGQGLEWMGWMNPNSGGTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSDDTAVYYCARG GDYVFGSYRPYYYYYGMDVWGQGTTVTVSSAST KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK
	SEQ ID NO: 470	SEQ ID NO: 627
NA	GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACTATCACTT GCCGGGCAAGTCAGACCATTAGCAGGTTTTTAA ATTGGTATCAGCAGAAACCTGGGAAAGCCCCTA AGCTCCTGATCTATGTTGCATCCAGTTTGCAAAG TGGGGTCCCATCAAGATTCAGTGGCAGTGGTTC TGGGACAGATTTCACTCTCACCATCAGCAGTCT GCAACCTGAAGATTTTGCAACTTACTACTGTCA ACAGAGTTACAGTACCCTGCTCAGTTTTGGCCA GGGGACCAAGCTGGAGATCAAACGAACGGTGG CTGCACCATCTGTCTTCATCTTCCCGCCATCTGA TGAGCAGTTGAAATCTGGAACTGCCTCTGTTGT GTGCCTGCTGAATAACTTCTATCCCAGAGAGGC CAAAGTACAGTGGAAGGTGGATAACGCCCTCCA	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC ATACACTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGTTATATGGTATGATGCA AGTAATAAGTTCCATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGAGACAATTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA AAAGTGGCTGGTATGCCTGAAGCTTTTGAAATC TGGGGCCAAGGGACATTGGTCACCGTCTCTTCA GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTG GCACCCTCCTCCAAGAGCACCTCTGGGGGCACA GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTC

ATCGGGTAACTCCCAGGAGAGTGTCACAGAGCA GGACAGCAAGGACAGCACCTACAGCCTCAGCA GCACCCTGACGCTGAGCAAAGCAGACTACGAGA AACACAAAGTCTACGCCTGCGAAGTCACCCATC AGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCA ACAGGGGAGAGTGT	SEQ ID NO: 2041	CCCGAACCGGTGACGGTGTCGTGGAACTCAGGC GCCCTGACCAGCGGCGTGCACACCTTCCCGGCT GTCCTACAGTCCTCAGGACTCTACTCCCTCAGCA GCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCA CCCAGACCTACATCTGCAACGTGAATCACAAGC CCAGCAACACCAAGGTGGACAAGAAAGTTGAG CCCAAATCTTGTGACAAAACTCACACATGCCCA CCGTGCCCAGCACCTGAACTCCTGGGGGGACCG TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACA CCCTCATGATCTCCCGGACCCCTGAGGTCACAT GCGTGGTGGTGGACGTGAGCCACGAAGACCCTG AGGTCAAGTTCAACTGGTACGTGGACGGCGTGG AGGTGCATAATGCCAAGACAAAGCCGTGTGAGG AGCAGTACGGCAGCACGTACCGTTGTGTCAGCG TCCTCACCGTCCTGCACCAGGACTGGCTGAATG GCAAGGAGTACAAGTGCAAGGTCTCCAACAAA GCCCTCCCAGCCCCCATCGAGAAAACCATCTCC AAAGCCAAAGGGCAGCCCCGAGAACCACAGGT GTACACCCTGCCCCCATCCCGGGAGGAGATGAC CAAGAACCAGGTCAGCCTGACCTGCCTGGTCAA AGGCTTCTATCCCAGCGACATCGCCGTGGAGTG GGAGAGCAATGGGCAGCCGGAGAACAACTACA AGACCACGCCTCCCGTGCTGGACTCCGACGGCT CCTTCTTCCTCTATAGCAAGCTCACCGTGGACAA GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATG CTCCGTGATGCATGAGGCTCTGCACAACCACTA CACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAA A
	SEQ ID NO: 2198	
AA	DIQLTQSPSSLSASVGDRVTITCRASQTISRFLNWY QQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDF TLTISSLQPEDFATYYCQQSYSTLLSFGQGTKLEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR GEC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGIH WVRQAPGKGLEWVAVIWYDASNKFHADAVKGR FTISRDNSKNTLYLQMNSLRAEDSAMYFCARGKV AGMPEAFEIWGQGTLVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG



[0138] In one embodiment the antibody or fragment thereof comprises a light chain variable region comprising a sequence selected from the group consisting of SEQ ID NOs: 1-157 and a heavy chain variable region comprising a

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

[0139] 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 variable region comprising SEQ ID NO: 176; a light chain variable region comprising SEQ ID NO: 20 and a heavy chain variable region comprising SEQ ID NO: 177; a light chain variable region comprising SEQ ID NO: 21 and a heavy chain variable region comprising SEQ ID NO: 178; a light chain variable region comprising SEQ ID NO: 22 and a heavy chain variable region comprising SEQ ID NO: 179; a light chain variable region comprising SEQ ID NO: 23 and a heavy chain variable region comprising SEQ ID NO: 180; a light chain variable region comprising SEQ ID NO: 24 and a heavy chain variable region comprising SEQ ID NO: 181; a light chain variable region comprising SEQ ID NO: 25 and a heavy chain variable region comprising SEQ ID NO: 182; a light chain variable region comprising SEQ ID NO: 26 and a heavy chain variable region comprising SEQ ID NO: 183; a light chain variable region comprising SEQ ID NO: 27 and a heavy chain variable region comprising SEQ ID NO: 184; a light chain variable region comprising SEQ ID NO: 28 and a heavy chain variable region comprising SEQ ID NO: 185; a light chain variable region comprising SEQ ID NO: 29 and a heavy chain variable region comprising SEQ ID NO: 186; a light chain variable region comprising SEQ ID NO: 30 and a heavy chain variable region comprising SEQ ID NO: 187; a light chain variable region comprising SEQ ID NO: 31 and a heavy chain variable region comprising SEQ ID NO: 188; a light chain variable region comprising SEQ ID NO: 32 and a heavy chain variable region comprising SEQ ID NO: 189; a light chain variable region comprising SEQ ID NO: 33 and a heavy chain variable region comprising SEQ ID NO: 190; a light chain variable region comprising SEQ ID NO: 34 and a heavy chain variable region comprising SEQ ID NO: 191; a light chain variable region comprising SEQ ID NO: 35 and a heavy chain variable region comprising SEQ ID NO: 192; a light chain variable region comprising SEQ ID NO: 36 and a heavy chain variable region comprising SEQ ID NO: 193; a light chain variable region comprising SEQ ID NO: 37 and a heavy chain variable region comprising SEQ ID NO: 194; a light chain variable region comprising SEQ ID NO: 38 and a heavy chain variable region comprising SEQ ID NO: 195; a light chain variable region comprising SEQ ID NO: 39 and a heavy chain variable region comprising SEQ ID NO: 196; a light chain variable region comprising SEQ ID NO: 40 and a heavy chain variable region comprising SEQ ID NO: 197; a light chain variable region comprising SEQ ID NO: 41 and a heavy chain variable region comprising SEQ ID NO: 198; a light chain variable region comprising SEQ ID NO: 42 and a heavy chain variable region comprising SEQ ID NO: 199; a light chain variable region comprising SEQ ID NO: 43 and a heavy chain variable region comprising SEQ ID NO: 200; a light chain variable region comprising SEQ ID NO: 44 and a heavy chain variable region comprising SEQ ID NO: 201; a light chain variable region comprising SEQ ID NO: 45 and a heavy chain variable region comprising SEQ ID NO: 202; a light chain variable region comprising SEQ ID NO: 46 and a heavy chain variable region comprising SEQ ID NO: 203; a light chain variable region comprising SEQ ID NO: 47 and a heavy chain variable region comprising SEQ ID NO: 204; a light chain variable region comprising SEQ ID NO: 48 and a heavy chain variable region comprising SEQ ID NO: 205; a light chain variable region comprising SEQ ID NO: 49 and a heavy chain variable region comprising SEQ ID NO: 206; a light chain variable region comprising SEQ ID NO: 50 and a heavy chain variable region comprising SEQ ID NO: 207; a light chain variable region comprising SEQ ID NO: 51 and a heavy chain variable region comprising SEQ ID NO: 208; a light chain variable region comprising SEQ

ID NO: 52 and a heavy chain variable region comprising SEQ ID NO: 209; a light chain variable region comprising SEQ ID NO: 53 and a heavy chain variable region comprising SEQ ID NO: 210; a light chain variable region comprising SEQ ID NO: 54 and a heavy chain variable region comprising SEQ ID NO: 211; a light chain variable region comprising SEQ ID NO: 55 and a heavy chain variable region comprising SEQ ID NO: 212; a light chain variable region comprising SEQ ID NO: 56 and a heavy chain variable region comprising SEQ ID NO: 213; a light chain variable region comprising SEQ ID NO: 57 and a heavy chain variable region comprising SEQ ID NO: 214; a light chain variable region comprising SEQ ID NO: 58 and a heavy chain variable region comprising SEQ ID NO: 215; a light chain variable region comprising SEQ ID NO: 59 and a heavy chain variable region comprising SEQ ID NO: 216; a light chain variable region comprising SEQ ID NO: 60 and a heavy chain variable region comprising SEQ ID NO: 217; a light chain variable region comprising SEQ ID NO: 61 and a heavy chain variable region comprising SEQ ID NO: 218; a light chain variable region comprising SEQ ID NO: 62 and a heavy chain variable region comprising SEQ ID NO: 219; a light chain variable region comprising SEQ ID NO: 63 and a heavy chain variable region comprising SEQ ID NO: 220; a light chain variable region comprising SEQ ID NO: 64 and a heavy chain variable region comprising SEQ ID NO: 221; a light chain variable region comprising SEQ ID NO: 65 and a heavy chain variable region comprising SEQ ID NO: 222; a light chain variable region comprising SEQ ID NO: 66 and a heavy chain variable region comprising SEQ ID NO: 223; a light chain variable region comprising SEQ ID NO: 67 and a heavy chain variable region comprising SEQ ID NO: 224; a light chain variable region comprising SEQ ID NO: 68 and a heavy chain variable region comprising SEQ ID NO: 225; a light chain variable region comprising SEQ ID NO: 69 and a heavy chain variable region comprising SEQ ID NO: 226; a light chain variable region comprising SEQ ID NO: 70 and a heavy chain variable region comprising SEQ ID NO: 227; a light chain variable region comprising SEQ ID NO: 71 and a heavy chain variable region comprising SEQ ID NO: 228; a light chain variable region comprising SEQ ID NO: 72 and a heavy chain variable region comprising SEQ ID NO: 229; a light chain variable region comprising SEQ ID NO: 73 and a heavy chain variable region comprising SEQ ID NO: 230; a light chain variable region comprising SEQ ID NO: 74 and a heavy chain variable region comprising SEQ ID NO: 231; a light chain variable region comprising SEQ ID NO: 75 and a heavy chain variable region comprising SEQ ID NO: 232; a light chain variable region comprising SEQ ID NO: 76 and a heavy chain variable region comprising SEQ ID NO: 233; a light chain variable region comprising SEQ ID NO: 77 and a heavy chain variable region comprising SEQ ID NO: 234; a light chain variable region comprising SEQ ID NO: 78 and a heavy chain variable region comprising SEQ ID NO: 235; a light chain variable region comprising SEQ ID NO: 79 and a heavy chain variable region comprising SEQ ID NO: 236; a light chain variable region comprising SEQ ID NO: 80 and a heavy chain variable region comprising SEQ ID NO: 237; a light chain variable region comprising SEQ ID NO: 81 and a heavy chain variable region comprising SEQ ID NO: 238; a light chain variable region comprising SEQ ID NO: 82 and a heavy chain variable region comprising SEQ ID NO: 239; a light chain variable region comprising SEQ ID NO: 83 and a heavy chain variable region comprising SEQ ID NO: 240; a light chain variable region comprising SEQ ID NO: 84 and a heavy chain variable region comprising SEQ ID NO: 241; a light chain variable region comprising SEQ ID NO: 85 and a heavy chain variable region comprising SEQ ID NO: 242; a light chain variable region comprising SEQ ID NO: 86 and a heavy chain variable region comprising SEQ ID NO: 243; a light chain variable region comprising SEQ ID NO: 87 and a heavy chain variable region comprising SEQ ID NO: 244; a light chain variable region comprising SEQ ID NO: 88 and a heavy chain variable region comprising SEQ ID NO: 245; a light chain variable region comprising SEQ ID NO: 89 and a heavy chain variable region comprising SEQ ID NO: 246; a light chain variable region comprising SEQ ID NO: 90 and a heavy chain variable region comprising SEQ ID NO: 247; a light chain variable region comprising SEQ ID NO: 91 and a heavy chain variable region comprising SEQ ID NO: 248; a light chain variable region comprising SEQ ID NO: 92 and a heavy chain variable region comprising SEQ ID NO: 249; a light chain variable region comprising SEQ ID NO: 93 and a heavy chain variable region comprising SEQ ID NO: 250; a light chain variable region comprising SEQ ID NO: 94 and a heavy chain variable region comprising SEQ ID NO: 251; a light chain variable region comprising SEQ ID NO: 95 and a heavy chain variable region comprising SEQ ID NO: 252; a light chain variable region comprising SEQ ID NO: 96 and a heavy chain variable region comprising SEQ ID NO: 253; a light chain variable region comprising SEQ ID NO: 97 and a heavy chain variable region comprising SEQ ID NO: 254; a light chain variable region comprising SEQ ID NO: 98 and a heavy chain variable region comprising SEQ ID NO: 255; a light chain variable region comprising SEQ ID NO: 99 and a heavy chain variable region comprising SEQ ID NO: 256; a light chain variable region comprising SEQ ID NO: 100 and a heavy chain variable region comprising SEQ ID NO: 257; a light chain variable region comprising SEQ ID NO: 101 and a heavy chain variable region comprising SEQ ID NO: 258; a light chain variable region comprising SEQ ID NO: 102 and a heavy chain variable region comprising SEQ ID NO: 259; a light chain variable region comprising SEQ ID NO: 103 and a heavy chain variable region comprising SEQ ID NO: 260; a light chain variable region comprising SEQ ID NO: 104 and a heavy chain variable region comprising SEQ ID NO: 261; a light chain variable region comprising SEQ ID NO: 105 and a heavy chain variable region comprising SEQ ID NO: 262; a light chain variable region comprising SEQ ID NO: 106 and a heavy chain variable region comprising SEQ ID NO: 263; a light chain variable region comprising SEQ ID NO: 107 and a heavy chain variable region comprising SEQ ID NO: 264; a light chain variable region comprising SEQ ID NO: 108 and a heavy chain variable region comprising SEQ ID NO: 265; a light chain variable region comprising SEQ ID NO: 109 and a heavy chain variable region comprising SEQ ID NO: 266; a light chain variable region comprising

SEQ ID NO: 110 and a heavy chain variable region comprising SEQ ID NO: 267; a light chain variable region comprising SEQ ID NO: 111 and a heavy chain variable region comprising SEQ ID NO: 268; a light chain variable region comprising SEQ ID NO: 112 and a heavy chain variable region comprising SEQ ID NO: 269; a light chain variable region comprising SEQ ID NO: 113 and a heavy chain variable region comprising SEQ ID NO: 270; a light chain variable region comprising SEQ ID NO: 114 and a heavy chain variable region comprising SEQ ID NO: 271; a light chain variable region comprising SEQ ID NO: 115 and a heavy chain variable region comprising SEQ ID NO: 272; a light chain variable region comprising SEQ ID NO: 116 and a heavy chain variable region comprising SEQ ID NO: 273; a light chain variable region comprising SEQ ID NO: 117 and a heavy chain variable region comprising SEQ ID NO: 274; a light chain variable region comprising SEQ ID NO: 118 and a heavy chain variable region comprising SEQ ID NO: 275; a light chain variable region comprising SEQ ID NO: 119 and a heavy chain variable region comprising SEQ ID NO: 276; a light chain variable region comprising SEQ ID NO: 120 and a heavy chain variable region comprising SEQ ID NO: 277; a light chain variable region comprising SEQ ID NO: 121 and a heavy chain variable region comprising SEQ ID NO: 278; a light chain variable region comprising SEQ ID NO: 122 and a heavy chain variable region comprising SEQ ID NO: 279; a light chain variable region comprising SEQ ID NO: 123 and a heavy chain variable region comprising SEQ ID NO: 280; a light chain variable region comprising SEQ ID NO: 124 and a heavy chain variable region comprising SEQ ID NO: 281; a light chain variable region comprising SEQ ID NO: 125 and a heavy chain variable region comprising SEQ ID NO: 282; a light chain variable region comprising SEQ ID NO: 126 and a heavy chain variable region comprising SEQ ID NO: 283; a light chain variable region comprising SEQ ID NO: 127 and a heavy chain variable region comprising SEQ ID NO: 284; a light chain variable region comprising SEQ ID NO: 128 and a heavy chain variable region comprising SEQ ID NO: 285; a light chain variable region comprising SEQ ID NO: 129 and a heavy chain variable region comprising SEQ ID NO: 286; a light chain variable region comprising SEQ ID NO: 130 and a heavy chain variable region comprising SEQ ID NO: 287; a light chain variable region comprising SEQ ID NO: 131 and a heavy chain variable region comprising SEQ ID NO: 288; a light chain variable region comprising SEQ ID NO: 132 and a heavy chain variable region comprising SEQ ID NO: 289; a light chain variable region comprising SEQ ID NO: 133 and a heavy chain variable region comprising SEQ ID NO: 290; a light chain variable region comprising SEQ ID NO: 134 and a heavy chain variable region comprising SEQ ID NO: 291; a light chain variable region comprising SEQ ID NO: 135 and a heavy chain variable region comprising SEQ ID NO: 292; a light chain variable region comprising SEQ ID NO: 136 and a heavy chain variable region comprising SEQ ID NO: 293; a light chain variable region comprising SEQ ID NO: 137 and a heavy chain variable region comprising SEQ ID NO: 294; a light chain variable region comprising SEQ ID NO: 138 and a heavy chain variable region comprising SEQ ID NO: 295; a light chain variable region comprising SEQ ID NO: 139 and a heavy chain variable region comprising SEQ ID NO: 296; a light chain variable region comprising SEQ ID NO: 140 and a heavy chain variable region comprising SEQ ID NO: 297; a light chain variable region comprising SEQ ID NO: 141 and a heavy chain variable region comprising SEQ ID NO: 298; a light chain variable region comprising SEQ ID NO: 142 and a heavy chain variable region comprising SEQ ID NO: 299; a light chain variable region comprising SEQ ID NO: 143 and a heavy chain variable region comprising SEQ ID NO: 300; a light chain variable region comprising SEQ ID NO: 144 and a heavy chain variable region comprising SEQ ID NO: 301; a light chain variable region comprising SEQ ID NO: 145 and a heavy chain variable region comprising SEQ ID NO: 302; a light chain variable region comprising SEQ ID NO: 146 and a heavy chain variable region comprising SEQ ID NO: 303; a light chain variable region comprising SEQ ID NO: 147 and a heavy chain variable region comprising SEQ ID NO: 304; a light chain variable region comprising SEQ ID NO: 148 and a heavy chain variable region comprising SEQ ID NO: 305; a light chain variable region comprising SEQ ID NO: 149 and a heavy chain variable region comprising SEQ ID NO: 306; a light chain variable region comprising SEQ ID NO: 150 and a heavy chain variable region comprising SEQ ID NO: 307; a light chain variable region comprising SEQ ID NO: 151 and a heavy chain variable region comprising SEQ ID NO: 308; a light chain variable region comprising SEQ ID NO: 152 and a heavy chain variable region comprising SEQ ID NO: 309; a light chain variable region comprising SEQ ID NO: 153 and a heavy chain variable region comprising SEQ ID NO: 310; a light chain variable region comprising SEQ ID NO: 154 and a heavy chain variable region comprising SEQ ID NO: 311; a light chain variable region comprising SEQ ID NO: 155 and a heavy chain variable region comprising SEQ ID NO: 312; a light chain variable region comprising SEQ ID NO: 156 and a heavy chain variable region comprising SEQ ID NO: 313; and a light chain variable region comprising SEQ ID NO: 157 and a heavy chain variable region comprising SEQ ID NO: 314, wherein the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s) selected from the group consisting of D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455, E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, and T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612.

[0140] In one embodiment the antibody or fragment thereof comprises a light chain variable region encoded by a polynucleotide sequence selected from the group consisting of SEQ ID NOs: 1571-1727 and a heavy chain variable region encoded by a polynucleotide sequence selected from the group consisting of SEQ ID NOs: 1728-1884, wherein the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s) selected from the group consisting of D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455, E276 of the antibody heavy chain relative to reference sequence SEQ ID NO:

612, and T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612.

[0141] 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 light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1575 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1732; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1576 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1733; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1577 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1734; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1578 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1735; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1579 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1736; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1580 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1737; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1581 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1738; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1582 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1739; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1583 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1740; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1584 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1741; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1585 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1742; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1586 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1743; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1587 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1744; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1588 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1745; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1589 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1746; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1590 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1747; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1591 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1748; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1592 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1749; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1593 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1750; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1594 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1751; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1595 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1752; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1596 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1753; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1597 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1754; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1598 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1755; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1599 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1756; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1600 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1757; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1601 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1758; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1602 and a heavy chain variable region encoded by a

polynucleotide sequence comprising SEQ ID NO: 1759; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1603 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1760; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1604 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1761; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1605 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1762; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1606 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1763; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1607 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1764; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1608 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1765; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1609 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1766; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1610 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1767; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1611 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1768; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1612 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1769; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1613 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1770; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1614 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1771; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1615 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1772; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1616 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1773; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1617 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1774; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1618 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1775; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1619 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1776; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1620 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1777; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1621 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1778; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1622 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1779; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1623 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1780; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1624 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1781; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1625 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1782; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1626 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1783; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1627 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1784; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1628 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1785; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1629 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1786; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1630 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1787; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1631 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1788; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1632 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1789; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1633 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1790; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1634 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1791; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1635 and a heavy chain variable region encoded by a polynucleotide sequence

comprising SEQ ID NO: 1792; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1636 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1793; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1637 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1794; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1638 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1795; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1639 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1796; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1640 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1797; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1641 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1798; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1642 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1799; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1643 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1800; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1644 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1801; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1645 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1802; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1646 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1803; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1647 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1804; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1648 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1805; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1649 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1806; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1650 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1807; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1651 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1808; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1652 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1809; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1653 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1810; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1654 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1811; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1655 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1812; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1656 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1813; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1657 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1814; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1658 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1815; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1659 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1816; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1660 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1817; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1661 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1818; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1662 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1819; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1663 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1820; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1664 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1821; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1665 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1822; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1666 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1823; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1667 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1824; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1668 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1825; a

light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1669 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1826; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1670 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1827; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1671 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1828; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1672 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1829; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1673 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1830; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1674 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1831; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1675 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1832; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1676 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1833; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1677 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1834; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1678 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1835; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1679 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1836; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1680 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1837; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1681 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1838; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1682 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1839; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1683 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1840; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1684 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1841; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1685 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1842; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1686 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1843; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1687 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1844; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1688 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1845; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1689 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1846; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1690 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1847; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1691 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1848; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1692 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1849; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1693 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1850; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1694 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1851; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1695 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1852; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1696 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1853; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1697 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1854; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1698 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1855; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1699 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1856; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1700 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1857; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1701 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1858; a light chain variable region

encoded by a polynucleotide sequence comprising SEQ ID NO: 1702 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1859; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1703 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1860; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1704 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1861; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1705 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1862; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1706 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1863; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1707 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1864; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1708 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1865; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1709 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1866; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1710 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1867; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1711 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1868; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1712 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1869; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1713 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1870; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1714 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1871; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1715 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1872; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1716 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1873; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1717 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1874; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1718 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1875; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1719 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1876; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1720 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1877; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1721 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1878; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1722 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1879; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1723 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1880; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1724 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1881; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1725 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1882; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1726 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1883; and a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1727 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1884, wherein the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s) selected from the group consisting of D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455, E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, and T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612.

[0142] The present invention relates to a composition comprising an anti-GIPR antigen binding protein having at least one conjugation site. The conjugation site must be amenable to conjugation of an additional functional moiety (e.g., a GLP-1 receptor agonist) by a defined conjugation chemistry through the side chain of an amino acid residue at the conjugation site. Achieving highly selective, site-specific conjugation to the anti-GIPR antigen binding protein, in accordance with the present invention, requires consideration of a diverse variety of design criteria. First, a preferred conjugation or coupling chemistry must be defined or predetermined. Functional moieties such as, GLP-1 receptor agonists, can be conjugated or coupled to the selected conjugation site of the anti-GIPR antigen binding protein through an assortment of different conjugation chemistries known in the art. For example, a maleimide-activated conjugation partner targeting

an accessible cysteine thiol on the anti-GIPR antigen binding protein is one embodiment, but numerous conjugation or coupling chemistries targeting the side chains of either canonical or non-canonical, e.g., unnatural amino acids in the anti-GIPR antigen binding protein sequence, can be employed in accordance with the present invention.

[0143] Chemistries for the chemoselective conjugation include: copper(I)-catalyzed azide-alkyne [3+2] dipolar cycloadditions, Staudinger ligation, other acyl transfers processes (S→N; X→N), oximations, hydrazone bonding formation and other suitable organic chemistry reactions such as cross-couplings using water-soluble palladium catalysts. (E.g., Bong et al., Chemoselective Pd(0)-catalyzed peptide coupling in water, Organic Letters 3(16):2509-11 (2001); Dibowski et al., Bioconjugation of peptides by palladium-catalyzed C-C cross-coupling in water, Angew. Chem. Int. Ed. 37(4):476-78 (1998); DeVasher et al., Aqueous-phase, palladium-catalyzed cross-coupling of aryl bromides under mild conditions, using water-soluble, sterically demanding alkylphosphines, J. Org. Chem. 69:7919-27 (2004); Shaugnessy et al., J.Org. Chem, 2003, 68, 6767-6774; Prescher, JA and Bertozzi CR, Chemistry in living system, Nature Chemical Biology 1(1); 13-21 (2005)).

[0144] As mentioned above, the conjugation (or covalent binding) to the anti-GIPR antigen binding protein is through the side chain of an amino acid residue at the conjugation site, for example, but not limited to, a cysteinyl residue. The amino acid residue, for example, a cysteinyl residue, at the internal conjugation site that is selected can be one that occupies the same amino acid residue position in a native Fc domain sequence, or the amino acid residue can be engineered into the Fc domain sequence by substitution or insertion..

[0145] Other examples of unnatural amino acid residues that can be particularly useful as the conjugation site in some embodiments of the inventive processes and compositions of matter include: azido-containing amino acid residues, e.g., azidohomoalanine, p-azido-phenylalanine; keto-containing amino acid residues, e.g., p-acetyl-phenylalanine; alkyne-containing amino acid residues, e.g., p-ethynylphenylalanine, homopropargylglycine, p-(prop-2-ynyl)-tyrosine; alkene-containing amino acid residues e.g., homoallylglycine; aryl halide- containing amino acid residues e.g. p-iodophenylalanine, p-bromophenylalanine; and 1,2-aminothiol containing amino acid residues.

[0146] The non-canonical amino acid residues can be incorporated by amino acid substitution or insertion. Non-canonical amino acid residues can be incorporated into the peptide by chemical peptide synthesis rather than by synthesis in biological systems, such as recombinantly expressing cells, or alternatively the skilled artisan can employ known techniques of protein engineering that use recombinantly expressing cells. (See, e.g., Link et al., Non-canonical amino acids in protein engineering, Current Opinion in Biotechnology, 14(6):603-609 (2003); Schultz et al., In vivo incorporation of unnatural amino acids, U.S. Patent No. 7,045,337).

[0147] The selection of the placement of the conjugation site in the overall anti-GIPR antigen binding protein is another important facet of selecting an internal conjugation site in accordance with the present invention. Any of the exposed amino acid residues on the anti-GIPR antigen binding protein can be potentially useful conjugation sites and can be mutated to cysteine or some other reactive amino acid for site-selective coupling, if not already present at the selected conjugation site of the anti-GIPR antigen binding protein sequence. However, this approach does not take into account potential steric constraints that may perturb the activity of the conjugated partner or limit the reactivity of the engineered mutation.

[0148] The anti-GIPR antigen binding protein of the invention is an antibody or functional fragment thereof. The anti-GIPR antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s). The conjugation site(s) can be essentially on any residue of the antigen binding protein. In certain embodiments the conjugation site is located within the CL, CH1, CH2 or CH3 region of an antibody or functional fragment thereof. In certain embodiments the conjugation site(s) are selected from the group consisting of D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455; E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612; and T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612. For sake of clarity, "D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455" is the same substitution site as AHo position D88 of the light chain of antibody 5G12.006 and Kabat position D70 of the light chain of antibody 5G12.006; "E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612" is the same substitution site as AHo position E384 of the heavy chain of antibody 5G12.006 and Kabat position E285 of the heavy chain of antibody 5G12.006; and "T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612" is the same substitution site as AHo position T487 of the heavy chain of antibody 5G12.006 and Kabat position T382 of the heavy chain of antibody 5G12.006.

[0149] 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.

[0150] 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).

[0151] 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.

[0152] The various combinations of heavy chain variable regions may be combined with any of the various combinations of light chain variable regions.

[0153] 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 IgG_1-, IgG_2-IgG_3- or IgG_4-type.

[0154] 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.

[0155] 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.

[0156] 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.

[0157] In one embodiment the antibody or fragment thereof comprises a CDRL1, a CDRL2, a CDRL3, a CDRH1, a CDRH2, and a CDRH3, wherein the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s) selected from the group consisting of D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455, E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, and T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612. 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, SEQID NO: 951, SEQID NO: 1108,

SEQID 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 NO: 668, SEQ ID NO: 825, SEQ ID NO: 982, SEQ ID NO: 1139, SEQ ID NO: 1296, and SEQ ID NO: 1453; SEQ ID NO: 669, SEQ ID NO: 826, SEQ ID NO: 983, SEQ ID NO: 1140, SEQ ID NO: 1297, and SEQ ID NO: 1454; SEQ ID NO: 670, SEQ ID NO: 827, SEQ ID NO: 984, SEQ ID NO: 1141, SEQ ID NO: 1298, and SEQ ID NO: 1455; SEQ ID NO: 671, SEQ ID NO: 828, SEQ ID NO: 985, SEQ ID NO: 1142, SEQ ID NO: 1299, and SEQ ID NO: 1456; SEQ ID NO: 672, SEQ ID NO: 829, SEQ ID NO: 986, SEQ ID NO: 1143, SEQ ID NO: 1300, and SEQ ID NO: 1457; SEQ ID NO: 673, SEQ ID NO: 830, SEQ ID NO: 987, SEQ ID NO: 1144, SEQ ID NO: 1301, and SEQ ID NO: 1458; SEQ ID NO: 674, SEQ ID NO: 831, SEQ ID NO: 988, SEQ ID NO: 1145, SEQ ID NO: 1302, and SEQ ID NO: 1459; SEQ ID NO: 675, SEQ ID NO: 832, SEQ ID NO: 989, SEQ ID NO: 1146, SEQ ID NO: 1303, and SEQ ID NO: 1460; SEQ ID NO: 676, SEQ ID NO: 833, SEQ ID NO: 990, SEQ ID NO: 1147, SEQ ID NO: 1304, and SEQ ID NO: 1461; SEQ ID NO: 677, SEQ ID NO: 834, SEQ ID NO: 991, SEQ ID NO: 1148, SEQ ID NO: 1305, and SEQ ID NO: 1462; SEQ ID NO: 678, SEQ ID NO: 835, SEQ ID NO: 992, SEQ ID NO: 1149, SEQ ID NO: 1306, and SEQ ID NO: 1463; SEQ ID NO: 679, SEQ ID NO: 836, SEQ ID NO: 993, SEQ ID NO: 1150, SEQ ID NO: 1307, and SEQ ID NO: 1464; SEQ ID NO: 680, SEQ ID NO: 837, SEQ ID NO: 994, SEQ ID NO: 1151, SEQ ID NO: 1308, and SEQ ID NO: 1465; SEQ ID NO: 681, SEQ ID NO: 838, SEQ ID NO: 995, SEQ ID NO: 1152, SEQ ID NO: 1309, and SEQ ID NO: 1466; SEQ ID NO: 682, SEQ ID NO: 839, SEQ ID NO: 996, SEQ ID NO: 1153, SEQ ID NO: 1310, and SEQ ID NO: 1467; SEQ ID NO: 683, SEQ ID NO: 840, SEQ ID NO: 997, SEQ ID NO: 1154, SEQ ID NO: 1311, and SEQ ID NO: 1468; SEQ ID NO: 684, SEQ ID NO: 841, SEQ ID NO: 998, SEQ ID NO: 1155, SEQ ID NO: 1312, and SEQ ID NO: 1469; SEQ ID NO: 685, SEQ ID NO: 842, SEQ ID NO: 999, SEQ ID NO: 1156, SEQ ID NO: 1313, and SEQ ID NO: 1470; SEQ ID NO: 686, SEQ ID NO: 843, SEQ ID NO: 1000, SEQ ID NO: 1157, SEQ ID NO: 1314, and SEQ ID NO: 1471; SEQ ID NO: 687, SEQ ID NO: 844, SEQ ID NO: 1001, SEQ ID NO: 1158, SEQ ID NO: 1315, and SEQ ID NO: 1472; SEQ ID NO: 688, SEQ ID NO: 845, SEQ ID NO: 1002, SEQ ID NO: 1159, SEQ ID NO: 1316, and SEQ ID NO: 1473; SEQ ID NO: 689, SEQ ID NO: 846, SEQ ID NO: 1003, SEQ ID NO: 1160, SEQ ID NO: 1317, and SEQ ID NO: 1474; SEQ ID NO: 690, SEQ ID NO: 847, SEQ ID NO: 1004, SEQ ID NO: 1161, SEQ ID NO: 1318, and SEQ ID NO: 1475; SEQ ID NO: 691, SEQ ID NO: 848, SEQ ID NO: 1005, SEQ ID NO: 1162, SEQ ID NO: 1319, and SEQ ID NO: 1476; SEQ ID NO: 692, SEQ ID NO: 849, SEQ ID NO: 1006, SEQ ID NO: 1163, SEQ ID NO: 1320, and SEQ ID NO: 1477; SEQ ID NO: 693, SEQ ID NO: 850, SEQ ID NO: 1007, SEQ ID NO: 1164, SEQ ID NO: 1321, and SEQ ID NO: 1478; SEQ ID NO: 694, SEQ ID NO: 851, SEQ ID NO: 1008, SEQ ID NO: 1165, SEQ ID NO: 1322, and SEQ ID NO: 1479; SEQ ID NO: 695, SEQ ID NO: 852, SEQ ID NO: 1009, SEQ ID NO: 1166, SEQ ID

NO: 1323, and SEQ ID NO: 1480; SEQ ID NO: 696, SEQ ID NO: 853, SEQ ID NO: 1010, SEQ ID NO: 1167, SEQ ID NO: 1324, and SEQ ID NO: 1481; SEQ ID NO: 697, SEQ ID NO: 854, SEQ ID NO: 1011, SEQ ID NO: 1168, SEQ ID NO: 1325, and SEQ ID NO: 1482; SEQ ID NO: 698, SEQ ID NO: 855, SEQ ID NO: 1012, SEQ ID NO: 1169, SEQ ID NO: 1326, and SEQ ID NO: 1483; SEQ ID NO: 699, SEQ ID NO: 856, SEQ ID NO: 1013, SEQ ID NO: 1170, SEQ ID NO: 1327, and SEQ ID NO: 1484; SEQ ID NO: 700, SEQ ID NO: 857, SEQ ID NO: 1014, SEQ ID NO: 1171, SEQ ID NO: 1328, and SEQ ID NO: 1485; SEQ ID NO: 701, SEQ ID NO: 858, SEQ ID NO: 1015, SEQ ID NO: 1172, SEQ ID NO: 1329, and SEQ ID NO: 1486; SEQ ID NO: 702, SEQ ID NO: 859, SEQ ID NO: 1016, SEQ ID NO: 1173, SEQ ID NO: 1330, and SEQ ID NO: 1487; SEQ ID NO: 703, SEQ ID NO: 860, SEQ ID NO: 1017, SEQ ID NO: 1174, SEQ ID NO: 1331, and SEQ ID NO: 1488; SEQ ID NO: 704, SEQ ID NO: 861, SEQ ID NO: 1018, SEQ ID NO: 1175, SEQ ID NO: 1332, and SEQ ID NO: 1489; SEQ ID NO: 705, SEQ ID NO: 862, SEQ ID NO: 1019, SEQ ID NO: 1176, SEQ ID NO: 1333, and SEQ ID NO: 1490; SEQ ID NO: 706, SEQ ID NO: 863, SEQ ID NO: 1020, SEQ ID NO: 1177, SEQ ID NO: 1334, and SEQ ID NO: 1491; SEQ ID NO: 707, SEQ ID NO: 864, SEQ ID NO: 1021, SEQ ID NO: 1178, SEQ ID NO: 1335, and SEQ ID NO: 1492; SEQ ID NO: 708, SEQ ID NO: 865, SEQ ID NO: 1022, SEQ ID NO: 1179, SEQ ID NO: 1336, and SEQ ID NO: 1493; SEQ ID NO: 709, SEQ ID NO: 866, SEQ ID NO: 1023, SEQ ID NO: 1180, SEQ ID NO: 1337, and SEQ ID NO: 1494; SEQ ID NO: 710, SEQ ID NO: 867, SEQ ID NO: 1024, SEQ ID NO: 1181, SEQ ID NO: 1338, and SEQ ID NO: 1495; SEQ ID NO: 711, SEQ ID NO: 868, SEQ ID NO: 1025, SEQ ID NO: 1182, SEQ ID NO: 1339, and SEQ ID NO: 1496; SEQ ID NO: 712, SEQ ID NO: 869, SEQ ID NO: 1026, SEQ ID NO: 1183, SEQ ID NO: 1340, and SEQ ID NO: 1497; SEQ ID NO: 713, SEQ ID NO: 870, SEQ ID NO: 1027, SEQ ID NO: 1184, SEQ ID NO: 1341, and SEQ ID NO: 1498; SEQ ID NO: 714, SEQ ID NO: 871, SEQ ID NO: 1028, SEQ ID NO: 1185, SEQ ID NO: 1342, and SEQ ID NO: 1499; SEQ ID NO: 715, SEQ ID NO: 872, SEQ ID NO: 1029, SEQ ID NO: 1186, SEQ ID NO: 1343, and SEQ ID NO: 1500; SEQ ID NO: 716, SEQ ID NO: 873, SEQ ID NO: 1030, SEQ ID NO: 1187, SEQ ID NO: 1344, and SEQ ID NO: 1501; SEQ ID NO: 717, SEQ ID NO: 874, SEQ ID NO: 1031, SEQ ID NO: 1188, SEQ ID NO: 1345, and SEQ ID NO: 1502; SEQ ID NO: 718, SEQ ID NO: 875, SEQ ID NO: 1032, SEQ ID NO: 1189, SEQ ID NO: 1346, and SEQ ID NO: 1503; SEQ ID NO: 719, SEQ ID NO: 876, SEQ ID NO: 1033, SEQ ID NO: 1190, SEQ ID NO: 1347, and SEQ ID NO: 1504; SEQ ID NO: 720, SEQ ID NO: 877, SEQ ID NO: 1034, SEQ ID NO: 1191, SEQ ID NO: 1348, and SEQ ID NO: 1505; SEQ ID NO: 721, SEQ ID NO: 878, SEQ ID NO: 1035, SEQ ID NO: 1192, SEQ ID NO: 1349, and SEQ ID NO: 1506; SEQ ID NO: 722, SEQ ID NO: 879, SEQ ID NO: 1036, SEQ ID NO: 1193, SEQ ID NO: 1350, and SEQ ID NO: 1507; SEQ ID NO: 723, SEQ ID NO: 880, SEQ ID NO: 1037, SEQ ID NO: 1194, SEQ ID NO: 1351, and SEQ ID NO: 1508; SEQ ID NO: 724, SEQ ID NO: 881, SEQ ID NO: 1038, SEQ ID NO: 1195, SEQ ID NO: 1352, and SEQ ID NO: 1509; SEQ ID NO: 725, SEQ ID NO: 882, SEQ ID NO: 1039, SEQ ID NO: 1196, SEQ ID NO: 1353, and SEQ ID NO: 1510; SEQ ID NO: 726, SEQ ID NO: 883, SEQ ID NO: 1040, SEQ ID NO: 1197, SEQ ID NO: 1354, and SEQ ID NO: 1511; SEQ ID NO: 727, SEQ ID NO: 884, SEQ ID NO: 1041, SEQ ID NO: 1198, SEQ ID NO: 1355, and SEQ ID NO: 1512; SEQ ID NO: 728, SEQ ID NO: 885, SEQ ID NO: 1042, SEQ ID NO: 1199, SEQ ID NO: 1356, and SEQ ID NO: 1513; SEQ ID NO: 729, SEQ ID NO: 886, SEQ ID NO: 1043, SEQ ID NO: 1200, SEQ ID NO: 1357, and SEQ ID NO: 1514; SEQ ID NO: 730, SEQ ID NO: 887, SEQ ID NO: 1044, SEQ ID NO: 1201, SEQ ID NO: 1358, and SEQ ID NO: 1515; SEQ ID NO: 731, SEQ ID NO: 888, SEQ ID NO: 1045, SEQ ID NO: 1202, SEQ ID NO: 1359, and SEQ ID NO: 1516; SEQ ID NO: 732, SEQ ID NO: 889, SEQ ID NO: 1046, SEQ ID NO: 1203, SEQ ID NO: 1360, and SEQ ID NO: 1517; SEQ ID NO: 733, SEQ ID NO: 890, SEQ ID NO: 1047, SEQ ID NO: 1204, SEQ ID NO: 1361, and SEQ ID NO: 1518; SEQ ID NO: 734, SEQ ID NO: 891, SEQ ID NO: 1048, SEQ ID NO: 1205, SEQ ID NO: 1362, and SEQ ID NO: 1519; SEQ ID NO: 735, SEQ ID NO: 892, SEQ ID NO: 1049, SEQ ID NO: 1206, SEQ ID NO: 1363, and SEQ ID NO: 1520; SEQ ID NO: 736, SEQ ID NO: 893, SEQ ID NO: 1050, SEQ ID NO: 1207, SEQ ID NO: 1364, and SEQ ID NO: 1521; SEQ ID NO: 737, SEQ ID NO: 894, SEQ ID NO: 1051, SEQ ID NO: 1208, SEQ ID NO: 1365, and SEQ ID NO: 1522; SEQ ID NO: 738, SEQ ID NO: 895, SEQ ID NO: 1052, SEQ ID NO: 1209, SEQ ID NO: 1366, and SEQ ID NO: 1523; SEQ ID NO: 739, SEQ ID NO: 896, SEQ ID NO: 1053, SEQ ID NO: 1210, SEQ ID NO: 1367, and SEQ ID NO: 1524; SEQ ID NO: 740, SEQ ID NO: 897, SEQ ID NO: 1054, SEQ ID NO: 1211, SEQ ID NO: 1368, and SEQ ID NO: 1525; SEQ ID NO: 741, SEQ ID NO: 898, SEQ ID NO: 1055, SEQ ID NO: 1212, SEQ ID NO: 1369, and SEQ ID NO: 1526; SEQ ID NO: 742, SEQ ID NO: 899, SEQ ID NO: 1056, SEQ ID NO: 1213, SEQ ID NO: 1370, and SEQ ID NO: 1527; SEQ ID NO: 743, SEQ ID NO: 900, SEQ ID NO: 1057, SEQ ID NO: 1214, SEQ ID NO: 1371, and SEQ ID NO: 1528; SEQ ID NO: 744, SEQ ID NO: 901, SEQ ID NO: 1058, SEQ ID NO: 1215, SEQ ID NO: 1372, and SEQ ID NO: 1529; SEQ ID NO: 745, SEQ ID NO: 902, SEQ ID NO: 1059, SEQ ID NO: 1216, SEQ ID NO: 1373, and SEQ ID NO: 1530; SEQ ID NO: 746, SEQ ID NO: 903, SEQ ID NO: 1060, SEQ ID NO: 1217, SEQ ID NO: 1374, and SEQ ID NO: 1531; SEQ ID NO: 747, SEQ ID NO: 904, SEQ ID NO: 1061, SEQ ID NO: 1218, SEQ ID NO: 1375, and SEQ ID NO: 1532; SEQ ID NO: 748, SEQ ID NO: 905, SEQ ID NO: 1062, SEQ ID NO: 1219, SEQ ID NO: 1376, and SEQ ID NO: 1533; SEQ ID NO: 749, SEQ ID NO: 906, SEQ ID NO: 1063, SEQ ID NO: 1220, SEQ ID NO: 1377, and SEQ ID NO: 1534; SEQ ID NO: 750, SEQ ID NO: 907, SEQ ID NO: 1064, SEQ ID NO: 1221, SEQ ID NO: 1378, and SEQ ID NO: 1535; SEQ ID NO: 751, SEQ ID NO: 908, SEQ ID NO: 1065, SEQ ID NO: 1222, SEQ ID NO: 1379, and SEQ ID NO: 1536; SEQ ID NO: 752, SEQ ID NO: 909, SEQ ID NO: 1066, SEQ ID NO: 1223, SEQ ID NO: 1380, and SEQ ID NO: 1537; SEQ ID NO: 753, SEQ ID NO: 910, SEQ ID NO: 1067, SEQ ID NO: 1224, SEQ ID

NO: 1381, and SEQ ID NO: 1538; SEQ ID NO: 754, SEQ ID NO: 911, SEQ ID NO: 1068, SEQ ID NO: 1225, SEQ ID NO: 1382, and SEQ ID NO: 1539; SEQ ID NO: 755, SEQ ID NO: 912, SEQ ID NO: 1069, SEQ ID NO: 1226, SEQ ID NO: 1383, and SEQ ID NO: 1540; SEQ ID NO: 756, SEQ ID NO: 913, SEQ ID NO: 1070, SEQ ID NO: 1227, SEQ ID NO: 1384, and SEQ ID NO: 1541; SEQ ID NO: 757, SEQ ID NO: 914, SEQ ID NO: 1071, SEQ ID NO: 1228, SEQ ID NO: 1385, and SEQ ID NO: 1542; SEQ ID NO: 758, SEQ ID NO: 915, SEQ ID NO: 1072, SEQ ID NO: 1229, SEQ ID NO: 1386, and SEQ ID NO: 1543; SEQ ID NO: 759, SEQ ID NO: 916, SEQ ID NO: 1073, SEQ ID NO: 1230, SEQ ID NO: 1387, and SEQ ID NO: 1544; SEQ ID NO: 760, SEQ ID NO: 917, SEQ ID NO: 1074, SEQ ID NO: 1231, SEQ ID NO: 1388, and SEQ ID NO: 1545; SEQ ID NO: 761, SEQ ID NO: 918, SEQ ID NO: 1075, SEQ ID NO: 1232, SEQ ID NO: 1389, and SEQ ID NO: 1546; SEQ ID NO: 762, SEQ ID NO: 919, SEQ ID NO: 1076, SEQ ID NO: 1233, SEQ ID NO: 1390, and SEQ ID NO: 1547; SEQ ID NO: 763, SEQ ID NO: 920, SEQ ID NO: 1077, SEQ ID NO: 1234, SEQ ID NO: 1391, and SEQ ID NO: 1548; SEQ ID NO: 764, SEQ ID NO: 921, SEQ ID NO: 1078, SEQ ID NO: 1235, SEQ ID NO: 1392, and SEQ ID NO: 1549; SEQ ID NO: 765, SEQ ID NO: 922, SEQ ID NO: 1079, SEQ ID NO: 1236, SEQ ID NO: 1393, and SEQ ID NO: 1550; SEQ ID NO: 766, SEQ ID NO: 923, SEQ ID NO: 1080, SEQ ID NO: 1237, SEQ ID NO: 1394, and SEQ ID NO: 1551; SEQ ID NO: 767, SEQ ID NO: 924, SEQ ID NO: 1081, SEQID NO: 1238, SEQID NO: 1395, and SEQ ID NO: 1552; SEQID NO: 768, SEQ ID NO: 925, SEQ ID NO: 1082, SEQ ID NO: 1239, SEQ ID NO: 1396, and SEQ ID NO: 1553; SEQ ID NO: 769, SEQ ID NO: 926, SEQ ID NO: 1083, SEQ ID NO: 1240, SEQ ID NO: 1397, and SEQ ID NO: 1554; SEQ ID NO: 770, SEQ ID NO: 927, SEQ ID NO: 1084, SEQ ID NO: 1241, SEQ ID NO: 1398, and SEQ ID NO: 1555; SEQ ID NO: 771, SEQ ID NO: 928, SEQ ID NO: 1085, SEQ ID NO: 1242, SEQ ID NO: 1399, and SEQ ID NO: 1556; SEQ ID NO: 772, SEQ ID NO: 929, SEQ ID NO: 1086, SEQ ID NO: 1243, SEQ ID NO: 1400, and SEQ ID NO: 1557; SEQ ID NO: 773, SEQ ID NO: 930, SEQ ID NO: 1087, SEQ ID NO: 1244, SEQ ID NO: 1401, and SEQ ID NO: 1558; SEQ ID NO: 774, SEQ ID NO: 931, SEQ ID NO: 1088, SEQ ID NO: 1245, SEQ ID NO: 1402, and SEQ ID NO: 1559; SEQ ID NO: 775, SEQ ID NO: 932, SEQ ID NO: 1089, SEQ ID NO: 1246, SEQ ID NO: 1403, and SEQ ID NO: 1560; SEQ ID NO: 776, SEQ ID NO: 933, SEQ ID NO: 1090, SEQ ID NO: 1247, SEQ ID NO: 1404, and SEQ ID NO: 1561; SEQ ID NO: 777, SEQ ID NO: 934, SEQ ID NO: 1091, SEQ ID NO: 1248, SEQ ID NO: 1405, and SEQ ID NO: 1562; SEQ ID NO: 778, SEQ ID NO: 935, SEQ ID NO: 1092, SEQ ID NO: 1249, SEQ ID NO: 1406, and SEQ ID NO: 1563; SEQ ID NO: 779, SEQ ID NO: 936, SEQ ID NO: 1093, SEQ ID NO: 1250, SEQ ID NO: 1407, and SEQ ID NO: 1564; SEQ ID NO: 780, SEQ ID NO: 937, SEQ ID NO: 1094, SEQ ID NO: 1251, SEQ ID NO: 1408, and SEQ ID NO: 1565; SEQ ID NO: 781, SEQ ID NO: 938, SEQ ID NO: 1095, SEQ ID NO: 1252, SEQ ID NO: 1409, and SEQ ID NO: 1566; SEQ ID NO: 782, SEQ ID NO: 939, SEQ ID NO: 1096, SEQ ID NO: 1253, SEQ ID NO: 1410, and SEQ ID NO: 1567; SEQ ID NO: 783, SEQ ID NO: 940, SEQ ID NO: 1097, SEQ ID NO: 1254, SEQ ID NO: 1411, and SEQ ID NO: 1568; SEQ ID NO: 784, SEQ ID NO: 941, SEQ ID NO: 1098, SEQ ID NO: 1255, SEQ ID NO: 1412, and SEQ ID NO: 1569; and SEQ ID NO: 785, SEQ ID NO: 942, SEQ ID NO: 1099, SEQ ID NO: 1256, SEQ ID NO: 1413, and SEQ ID NO: 1570, wherein the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s) selected from the group consisting of D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455, E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, and T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612.

[0158] In one embodiment the antibody or fragment thereof comprises a CDRL1, a CDRL2, a CDRL3, a CDRH1, a CDRH2, and a CDRH3, wherein the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s) selected from the group consisting of D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455, E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, and T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, encoded by a polynucleotide. In one embodiment the antibody or fragment thereof comprises a CDRL1, a CDRL2, a CDRL3, a CDRH1, a CDRH2, and a CDRH3, wherein the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s) selected from the group consisting of D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455, E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, and T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, wherein each CDRL1, CDRL2, CDRL3, CDRH1, CDRH2, and CDRH3, respectively, is encoded by a sequence selected from the group consisting of SEQ ID NO: 2199, SEQ ID NO: 2356, SEQ ID NO: 2513, SEQ ID NO: 2670, SEQ ID NO: 2827, and SEQ ID NO: 2984 ; SEQ ID NO: 2200, SEQ ID NO: 2357, SEQ ID NO: 2514, SEQ ID NO: 2671, SEQ ID NO: 2828, and SEQ ID NO: 2985 ; SEQ ID NO: 2201, SEQ ID NO: 2358, SEQ ID NO: 2515, SEQ ID NO: 2672, SEQ ID NO: 2829, and SEQ ID NO: 2986 ; SEQ ID NO: 2202, SEQ ID NO: 2359, SEQ ID NO: 2516, SEQ ID NO: 2673, SEQ ID NO: 2830, and SEQ ID NO: 2987 ; SEQ ID NO: 2203, SEQ ID NO: 2360, SEQ ID NO: 2517, SEQ ID NO: 2674, SEQ ID NO: 2831, and SEQ ID NO: 2988 ; SEQ ID NO: 2204, SEQ ID NO: 2361, SEQ ID NO: 2518, SEQ ID NO: 2675, SEQ ID NO: 2832, and SEQ ID NO: 2989 ; SEQ ID NO: 2205, SEQ ID NO: 2362, SEQ ID NO: 2519, SEQ ID NO: 2676, SEQ ID NO: 2833, and SEQ ID NO: 2990 ; SEQ ID NO: 2206, SEQ ID NO: 2363, SEQ ID NO: 2520, SEQ ID NO: 2677, SEQ ID NO: 2834, and SEQ ID NO: 2991 ; SEQ ID NO: 2207, SEQ ID NO: 2364, SEQ ID NO: 2521, SEQ ID NO: 2678, SEQ ID NO: 2835, and SEQ ID NO: 2992 ; SEQ ID NO: 2208, SEQ ID NO: 2365, SEQ ID NO: 2522,

SEQ ID NO: 2679, SEQ ID NO: 2836, and SEQ ID NO: 2993 ; SEQ ID NO: 2209, SEQ ID NO: 2366, SEQ ID NO: 2523,
SEQ ID NO: 2680, SEQ ID NO: 2837, and SEQ ID NO: 2994 ; SEQ ID NO: 2210, SEQ ID NO: 2367, SEQ ID NO: 2524,
SEQ ID NO: 2681, SEQ ID NO: 2838, and SEQ ID NO: 2995 ; SEQ ID NO: 2211, SEQ ID NO: 2368, SEQ ID NO: 2525,
SEQ ID NO: 2682, SEQ ID NO: 2839, and SEQ ID NO: 2996 ; SEQ ID NO: 2212, SEQ ID NO: 2369, SEQ ID NO: 2526,
SEQ ID NO: 2683, SEQ ID NO: 2840, and SEQ ID NO: 2997 ; SEQ ID NO: 2213, SEQ ID NO: 2370, SEQ ID NO: 2527,
SEQ ID NO: 2684, SEQ ID NO: 2841, and SEQ ID NO: 2998 ; SEQ ID NO: 2214, SEQ ID NO: 2371, SEQ ID NO: 2528,
SEQ ID NO: 2685, SEQ ID NO: 2842, and SEQ ID NO: 2999 ; SEQ ID NO: 2215, SEQ ID NO: 2372, SEQ ID NO: 2529,
SEQ ID NO: 2686, SEQ ID NO: 2843, and SEQ ID NO: 3000 ; SEQ ID NO: 2216, SEQ ID 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 SEQ ID NO: 3007 ; SEQ ID NO: 2223, SEQ ID NO: 2380, SEQ ID NO: 2537,
SEQ ID NO: 2694, SEQ ID NO: 2851, and SEQ ID NO: 3008 ; SEQ ID NO: 2224, SEQ ID NO: 2381, SEQ ID NO: 2538,
SEQ ID NO: 2695, SEQ ID NO: 2852, and SEQ ID NO: 3009 ; SEQ ID NO: 2225, SEQ ID NO: 2382, SEQ ID NO: 2539,
SEQ ID NO: 2696, SEQ ID NO: 2853, and SEQ ID NO: 3010 ; SEQ ID NO: 2226, SEQ ID NO: 2383, SEQ ID NO: 2540,
SEQ ID NO: 2697, SEQ ID NO: 2854, and SEQ ID NO: 3011 ; SEQ ID NO: 2227, SEQ ID NO: 2384, SEQ ID NO: 2541,
SEQ ID NO: 2698, SEQ ID NO: 2855, and SEQ ID NO: 3012 ; SEQ ID NO: 2228, SEQ ID NO: 2385, SEQ ID NO: 2542,
SEQ ID NO: 2699, SEQ ID NO: 2856, and SEQ ID NO: 3013 ; SEQ ID NO: 2229, SEQ ID NO: 2386, SEQ ID NO: 2543,
SEQ ID NO: 2700, SEQ ID NO: 2857, and SEQ ID NO: 3014 ; SEQ ID NO: 2230, SEQ ID NO: 2387, SEQ ID NO: 2544,
SEQ ID NO: 2701, SEQ ID NO: 2858, and SEQ ID NO: 3015 ; SEQ ID NO: 2231, SEQ ID NO: 2388, SEQ ID NO: 2545,
SEQ ID NO: 2702, SEQ ID NO: 2859, and SEQ ID NO: 3016 ; SEQ ID NO: 2232, SEQ ID NO: 2389, SEQ ID NO: 2546,
SEQ ID NO: 2703, SEQ ID NO: 2860, and SEQ ID NO: 3017 ; SEQ ID NO: 2233, SEQ ID NO: 2390, SEQ ID NO: 2547,
SEQ ID NO: 2704, SEQ ID NO: 2861, and SEQ ID NO: 3018 ; SEQ ID NO: 2234, SEQ ID NO: 2391, SEQ ID NO: 2548,
SEQ ID NO: 2705, SEQ ID NO: 2862, and SEQ ID NO: 3019 ; SEQ ID NO: 2235, SEQ ID NO: 2392, SEQ ID NO: 2549,
SEQ ID NO: 2706, SEQ ID NO: 2863, and SEQ ID NO: 3020 ; SEQ ID NO: 2236, SEQ ID NO: 2393, SEQ ID NO: 2550,
SEQ ID NO: 2707, SEQ ID NO: 2864, and SEQ ID NO: 3021 ; SEQ ID NO: 2237, SEQ ID NO: 2394, SEQ ID NO: 2551,
SEQ ID NO: 2708, SEQ ID NO: 2865, and SEQ ID NO: 3022 ; SEQ ID NO: 2238, SEQ ID NO: 2395, SEQ ID NO: 2552,
SEQ ID NO: 2709, SEQ ID NO: 2866, and SEQ ID NO: 3023 ; SEQ ID NO: 2239, SEQ ID NO: 2396, SEQ ID NO: 2553,
SEQ ID NO: 2710, SEQ ID NO: 2867, and SEQ ID NO: 3024 ; SEQ ID NO: 2240, SEQ ID NO: 2397, SEQ ID NO: 2554,
SEQ ID NO: 2711, SEQ ID NO: 2868, and SEQ ID NO: 3025 ; SEQ ID NO: 2241, SEQ ID NO: 2398, SEQ ID NO: 2555,
SEQ ID NO: 2712, SEQ ID NO: 2869, and SEQ ID NO: 3026 ; SEQ ID NO: 2242, SEQ ID NO: 2399, SEQ ID NO: 2556,
SEQ ID NO: 2713, SEQ ID NO: 2870, and SEQ ID NO: 3027 ; SEQ ID NO: 2243, SEQ ID NO: 2400, SEQ ID NO: 2557,
SEQ ID NO: 2714, SEQ ID NO: 2871, and SEQ ID NO: 3028 ; SEQ ID NO: 2244, SEQ ID NO: 2401, SEQ ID NO: 2558,
SEQ ID NO: 2715, SEQ ID NO: 2872, and SEQ ID NO: 3029 ; SEQ ID NO: 2245, SEQ ID NO: 2402, SEQ ID NO: 2559,
SEQ ID NO: 2716, SEQ ID NO: 2873, and SEQ ID NO: 3030 ; SEQ ID NO: 2246, SEQ ID NO: 2403, SEQ ID NO: 2560,
SEQ ID NO: 2717, SEQ ID NO: 2874, and SEQ ID NO: 3031 ; SEQ ID NO: 2247, SEQ ID NO: 2404, SEQ ID NO: 2561,
SEQ ID NO: 2718, SEQ ID NO: 2875, and SEQ ID NO: 3032 ; SEQ ID NO: 2248, SEQ ID NO: 2405, SEQ ID NO: 2562,
SEQ ID NO: 2719, SEQ ID NO: 2876, and SEQ ID NO: 3033 ; SEQ ID NO: 2249, SEQ ID NO: 2406, SEQ ID NO: 2563,
SEQ ID NO: 2720, SEQ ID NO: 2877, and SEQ ID NO: 3034 ; SEQ ID NO: 2250, SEQ ID NO: 2407, SEQ ID NO: 2564,
SEQ ID NO: 2721, SEQ ID NO: 2878, and SEQ ID NO: 3035 ; SEQ ID NO: 2251, SEQ ID NO: 2408, SEQ ID NO: 2565,
SEQ ID NO: 2722, SEQ ID NO: 2879, and SEQ ID NO: 3036 ; SEQ ID NO: 2252, SEQ ID NO: 2409, SEQ ID NO: 2566,
SEQ ID NO: 2723, SEQ ID NO: 2880, and SEQ ID NO: 3037 ; SEQ ID NO: 2253, SEQ ID NO: 2410, SEQ ID NO: 2567,
SEQ ID NO: 2724, SEQ ID NO: 2881, and SEQ ID NO: 3038 ; SEQ ID NO: 2254, SEQ ID NO: 2411, SEQ ID NO: 2568,
SEQ ID NO: 2725, SEQ ID NO: 2882, and SEQ ID NO: 3039 ; SEQ ID NO: 2255, SEQ ID NO: 2412, SEQ ID NO: 2569,
SEQ ID NO: 2726, SEQ ID NO: 2883, and SEQ ID NO: 3040 ; SEQ ID NO: 2256, SEQ ID NO: 2413, SEQ ID NO: 2570,
SEQ ID NO: 2727, SEQ ID NO: 2884, and SEQ ID NO: 3041 ; SEQ ID NO: 2257, SEQ ID NO: 2414, SEQ ID NO: 2571,
SEQ ID NO: 2728, SEQ ID NO: 2885, and SEQ ID NO: 3042 ; SEQ ID NO: 2258, SEQ ID NO: 2415, SEQ ID NO: 2572,
SEQ ID NO: 2729, SEQ ID NO: 2886, and SEQ ID NO: 3043 ; SEQ ID NO: 2259, SEQ ID NO: 2416, SEQ ID NO: 2573,
SEQ ID NO: 2730, SEQ ID NO: 2887, and SEQ ID NO: 3044 ; SEQ ID NO: 2260, SEQ ID NO: 2417, SEQ ID NO: 2574,
SEQ ID NO: 2731, SEQ ID NO: 2888, and SEQ ID NO: 3045 ; SEQ ID NO: 2261, SEQ ID NO: 2418, SEQ ID NO: 2575,
SEQ ID NO: 2732, SEQ ID NO: 2889, and SEQ ID NO: 3046 ; SEQ ID NO: 2262, SEQ ID NO: 2419, SEQ ID NO: 2576,
SEQ ID NO: 2733, SEQ ID NO: 2890, and SEQ ID NO: 3047 ; SEQ ID NO: 2263, SEQ ID NO: 2420, SEQ ID NO: 2577,
SEQ ID NO: 2734, SEQ ID NO: 2891, and SEQ ID NO: 3048 ; SEQ ID NO: 2264, SEQ ID NO: 2421, SEQ ID NO: 2578,
SEQ ID NO: 2735, SEQ ID NO: 2892, and SEQ ID NO: 3049 ; SEQ ID NO: 2265, SEQ ID NO: 2422, SEQ ID NO: 2579,
SEQ ID NO: 2736, SEQ ID NO: 2893, and SEQ ID NO: 3050 ; SEQ ID NO: 2266, SEQ ID NO: 2423, SEQ ID NO: 2580,

SEQ ID NO: 2737, SEQ ID NO: 2894, and SEQ ID NO: 3051 ; SEQ ID NO: 2267, SEQ ID NO: 2424, SEQ ID NO: 2581,
SEQ ID NO: 2738, SEQ ID NO: 2895, and SEQ ID NO: 3052 ; SEQ ID NO: 2268, SEQ ID NO: 2425, SEQ ID NO: 2582,
SEQ ID NO: 2739, SEQ ID NO: 2896, and SEQ ID NO: 3053 ; SEQ ID NO: 2269, SEQ ID NO: 2426, SEQ ID NO: 2583,
SEQ ID NO: 2740, SEQ ID NO: 2897, and SEQ ID NO: 3054 ; SEQ ID NO: 2270, SEQ ID NO: 2427, SEQ ID NO: 2584,
SEQ ID NO: 2741, SEQ ID NO: 2898, and SEQ ID NO: 3055 ; SEQ ID NO: 2271, SEQ ID NO: 2428, SEQ ID NO: 2585,
SEQ ID NO: 2742, SEQ ID NO: 2899, and SEQ ID NO: 3056 ; SEQ ID NO: 2272, SEQ ID NO: 2429, SEQ ID NO: 2586,
SEQ ID NO: 2743, SEQ ID NO: 2900, and SEQ ID NO: 3057 ; SEQ ID NO: 2273, SEQ ID NO: 2430, SEQ ID NO: 2587,
SEQ ID NO: 2744, SEQ ID NO: 2901, and 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.

[0159] 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.

[0160] 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.

[0161] In one embodiment the antibody or fragment thereof comprises a light chain comprising a sequence selected from the group consisting of SEQ ID NOs: 472-628 and a heavy chain comprising a sequence selected from the group consisting of SEQ ID NOs: 472-628, wherein the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s) selected from the group consisting of D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455, E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, and T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612. In one embodiment the antibody or fragment thereof comprises a combination of a light chain and a heavy chain selected from the group consisting of a light chain comprising SEQ ID NO: 315 and a heavy chain comprising SEQ ID NO: 472; a light chain comprising SEQ ID NO: 316 and a heavy chain comprising SEQ ID NO: 473; a light chain comprising SEQ ID NO: 317 and a heavy chain comprising SEQ ID NO: 474; a light chain comprising SEQ ID NO: 318 and a heavy chain comprising SEQ ID NO: 475; a light chain comprising SEQ ID NO: 319 and a heavy chain comprising SEQ ID NO: 476; a light chain comprising SEQ ID NO: 320 and a heavy chain comprising SEQ ID NO: 477; a light chain

comprising SEQ ID NO: 321 and a heavy chain comprising SEQ ID NO: 478; a light chain comprising SEQ ID NO: 322 and a heavy chain comprising SEQ ID NO: 479; a light chain comprising SEQ ID NO: 323 and a heavy chain comprising SEQ ID NO: 480; a light chain comprising SEQ ID NO: 324 and a heavy chain comprising SEQ ID NO: 481; a light chain comprising SEQ ID NO: 325 and a heavy chain comprising SEQ ID NO: 482; a light chain comprising SEQ ID NO: 326 and a heavy chain comprising SEQ ID NO: 483; a light chain comprising SEQ ID NO: 327 and a heavy chain comprising SEQ ID NO: 484; a light chain comprising SEQ ID NO: 328 and a heavy chain comprising SEQ ID NO: 485; a light chain comprising SEQ ID NO: 329 and a heavy chain comprising SEQ ID NO: 486; a light chain comprising SEQ ID NO: 330 and a heavy chain comprising SEQ ID NO: 487; a light chain comprising SEQ ID NO: 331 and a heavy chain comprising SEQ ID NO: 488; a light chain comprising SEQ ID NO: 332 and a heavy chain comprising SEQ ID NO: 489; a light chain comprising SEQ ID NO: 333 and a heavy chain comprising SEQ ID NO: 490; a light chain comprising SEQ ID NO: 334 and a heavy chain comprising SEQ ID NO: 491; a light chain comprising SEQ ID NO: 335 and a heavy chain comprising SEQ ID NO: 492; a light chain comprising SEQ ID NO: 336 and a heavy chain comprising SEQ ID NO: 493; a light chain comprising SEQ ID NO: 337 and a heavy chain comprising SEQ ID NO: 494; a light chain comprising SEQ ID NO: 338 and a heavy chain comprising SEQ ID NO: 495; a light chain comprising SEQ ID NO: 339 and a heavy chain comprising SEQ ID NO: 496; a light chain comprising SEQ ID NO: 340 and a heavy chain comprising SEQ ID NO: 497; a light chain comprising SEQ ID NO: 341 and a heavy chain comprising SEQ ID NO: 498; a light chain comprising SEQ ID NO: 342 and a heavy chain comprising SEQ ID NO: 499; a light chain comprising SEQ ID NO: 343 and a heavy chain comprising SEQ ID NO: 500; a light chain comprising SEQ ID NO: 344 and a heavy chain comprising SEQ ID NO: 501; a light chain comprising SEQ ID NO: 345 and a heavy chain comprising SEQ ID NO: 502; a light chain comprising SEQ ID NO: 346 and a heavy chain comprising SEQ ID NO: 503; a light chain comprising SEQ ID NO: 347 and a heavy chain comprising SEQ ID NO: 504; a light chain comprising SEQ ID NO: 348 and a heavy chain comprising SEQ ID NO: 505; a light chain comprising SEQ ID NO: 349 and a heavy chain comprising SEQ ID NO: 506; a light chain comprising SEQ ID NO: 350 and a heavy chain comprising SEQ ID NO: 507; a light chain comprising SEQ ID NO: 351 and a heavy chain comprising SEQ ID NO: 508; a light chain comprising SEQ ID NO: 352 and a heavy chain comprising SEQ ID NO: 509; a light chain comprising SEQ ID NO: 353 and a heavy chain comprising SEQ ID NO: 510; a light chain comprising SEQ ID NO: 354 and a heavy chain comprising SEQ ID NO: 511; a light chain comprising SEQ ID NO: 355 and a heavy chain comprising SEQ ID NO: 512; a light chain comprising SEQ ID NO: 356 and a heavy chain comprising SEQ ID NO: 513; a light chain comprising SEQ ID NO: 357 and a heavy chain comprising SEQ ID NO: 514; a light chain comprising SEQ ID NO: 358 and a heavy chain comprising SEQ ID NO: 515; a light chain comprising SEQ ID NO: 359 and a heavy chain comprising SEQ ID NO: 516; a light chain comprising SEQ ID NO: 360 and a heavy chain comprising SEQ ID NO: 517; a light chain comprising SEQ ID NO: 361 and a heavy chain comprising SEQ ID NO: 518; a light chain comprising SEQ ID NO: 362 and a heavy chain comprising SEQ ID NO: 519; a light chain comprising SEQ ID NO: 363 and a heavy chain comprising SEQ ID NO: 520; a light chain comprising SEQ ID NO: 364 and a heavy chain comprising SEQ ID NO: 521; a light chain comprising SEQ ID NO: 365 and a heavy chain comprising SEQ ID NO: 522; a light chain comprising SEQ ID NO: 366 and a heavy chain comprising SEQ ID NO: 523; a light chain comprising SEQ ID NO: 367 and a heavy chain comprising SEQ ID NO: 524; a light chain comprising SEQ ID NO: 368 and a heavy chain comprising SEQ ID NO: 525; a light chain comprising SEQ ID NO: 369 and a heavy chain comprising SEQ ID NO: 526; a light chain comprising SEQ ID NO: 370 and a heavy chain comprising SEQ ID NO: 527; a light chain comprising SEQ ID NO: 371 and a heavy chain comprising SEQ ID NO: 528; a light chain comprising SEQ ID NO: 372 and a heavy chain comprising SEQ ID NO: 529; a light chain comprising SEQ ID NO: 373 and a heavy chain comprising SEQ ID NO: 530; a light chain comprising SEQ ID NO: 374 and a heavy chain comprising SEQ ID NO: 531; a light chain comprising SEQ ID NO: 375 and a heavy chain comprising SEQ ID NO: 532; a light chain comprising SEQ ID NO: 376 and a heavy chain comprising SEQ ID NO: 533; a light chain comprising SEQ ID NO: 377 and a heavy chain comprising SEQ ID NO: 534; a light chain comprising SEQ ID NO: 378 and a heavy chain comprising SEQ ID NO: 535; a light chain comprising SEQ ID NO: 379 and a heavy chain comprising SEQ ID NO: 536; a light chain comprising SEQ ID NO: 380 and a heavy chain comprising SEQ ID NO: 537; a light chain comprising SEQ ID NO: 381 and a heavy chain comprising SEQ ID NO: 538; a light chain comprising SEQ ID NO: 382 and a heavy chain comprising SEQ ID NO: 539; a light chain comprising SEQ ID NO: 383 and a heavy chain comprising SEQ ID NO: 540; a light chain comprising SEQ ID NO: 384 and a heavy chain comprising SEQ ID NO: 541; a light chain comprising SEQ ID NO: 385 and a heavy chain comprising SEQ ID NO: 542; a light chain comprising SEQ ID NO: 386 and a heavy chain comprising SEQ ID NO: 543; a light chain comprising SEQ ID NO: 387 and a heavy chain comprising SEQ ID NO: 544; a light chain comprising SEQ ID NO: 388 and a heavy chain comprising SEQ ID NO: 545; a light chain comprising SEQ ID NO: 389 and a heavy chain comprising SEQ ID NO: 546; a light chain comprising SEQ ID NO: 390 and a heavy chain comprising SEQ ID NO: 547; a light chain comprising SEQ ID NO: 391 and a heavy chain comprising SEQ ID NO: 548; a light chain comprising SEQ ID NO: 392 and a heavy chain comprising SEQ ID NO: 549; a light chain comprising SEQ ID NO: 393 and a heavy chain comprising SEQ ID NO: 550; a light chain comprising SEQ ID NO: 394 and a heavy chain comprising SEQ ID NO: 551; a light chain comprising SEQ ID NO: 395 and a heavy chain comprising SEQ ID NO: 552; a light chain comprising SEQ ID NO: 396 and a heavy chain comprising SEQ ID NO: 553; a light chain comprising SEQ ID NO: 397 and a heavy chain comprising SEQ ID NO: 554; a light chain comprising SEQ ID NO: 398

and a heavy chain comprising SEQ ID NO: 555; a light chain comprising SEQ ID NO: 399 and a heavy chain comprising SEQ ID NO: 556; a light chain comprising SEQ ID NO: 400 and a heavy chain comprising SEQ ID NO: 557; a light chain comprising SEQ ID NO: 401 and a heavy chain comprising SEQ ID NO: 558; a light chain comprising SEQ ID NO: 402 and a heavy chain comprising SEQ ID NO: 559; a light chain comprising SEQ ID NO: 403 and a heavy chain comprising SEQ ID NO: 560; a light chain comprising SEQ ID NO: 404 and a heavy chain comprising SEQ ID NO: 561; a light chain comprising SEQ ID NO: 405 and a heavy chain comprising SEQ ID NO: 562; a light chain comprising SEQ ID NO: 406 and a heavy chain comprising SEQ ID NO: 563; a light chain comprising SEQ ID NO: 407 and a heavy chain comprising SEQ ID NO: 564; a light chain comprising SEQ ID NO: 408 and a heavy chain comprising SEQ ID NO: 565; a light chain comprising SEQ ID NO: 409 and a heavy chain comprising SEQ ID NO: 566; a light chain comprising SEQ ID NO: 410 and a heavy chain comprising SEQ ID NO: 567; a light chain comprising SEQ ID NO: 411 and a heavy chain comprising SEQ ID NO: 568; a light chain comprising SEQ ID NO: 412 and a heavy chain comprising SEQ ID NO: 569; a light chain comprising SEQ ID NO: 413 and a heavy chain comprising SEQ ID NO: 570; a light chain comprising SEQ ID NO: 414 and a heavy chain comprising SEQ ID NO: 571; a light chain comprising SEQ ID NO: 415 and a heavy chain comprising SEQ ID NO: 572; a light chain comprising SEQ ID NO: 416 and a heavy chain comprising SEQ ID NO: 573; a light chain comprising SEQ ID NO: 417 and a heavy chain comprising SEQ ID NO: 574; a light chain comprising SEQ ID NO: 418 and a heavy chain comprising SEQ ID NO: 575; a light chain comprising SEQ ID NO: 419 and a heavy chain comprising SEQ ID NO: 576; a light chain comprising SEQ ID NO: 420 and a heavy chain comprising SEQ ID NO: 577; a light chain comprising SEQ ID NO: 421 and a heavy chain comprising SEQ ID NO: 578; a light chain comprising SEQ ID NO: 422 and a heavy chain comprising SEQ ID NO: 579; a light chain comprising SEQ ID NO: 423 and a heavy chain comprising SEQ ID NO: 580; a light chain comprising SEQ ID NO: 424 and a heavy chain comprising SEQ ID NO: 581; a light chain comprising SEQ ID NO: 425 and a heavy chain comprising SEQ ID NO: 582; a light chain comprising SEQ ID NO: 426 and a heavy chain comprising SEQ ID NO: 583; a light chain comprising SEQ ID NO: 427 and a heavy chain comprising SEQ ID NO: 584; a light chain comprising SEQ ID NO: 428 and a heavy chain comprising SEQ ID NO: 585; a light chain comprising SEQ ID NO: 429 and a heavy chain comprising SEQ ID NO: 586; a light chain comprising SEQ ID NO: 430 and a heavy chain comprising SEQ ID NO: 587; a light chain comprising SEQ ID NO: 431 and a heavy chain comprising SEQ ID NO: 588; a light chain comprising SEQ ID NO: 432 and a heavy chain comprising SEQ ID NO: 589; a light chain comprising SEQ ID NO: 433 and a heavy chain comprising SEQ ID NO: 590; a light chain comprising SEQ ID NO: 434 and a heavy chain comprising SEQ ID NO: 591; a light chain comprising SEQ ID NO: 435 and a heavy chain comprising SEQ ID NO: 592; a light chain comprising SEQ ID NO: 436 and a heavy chain comprising SEQ ID NO: 593; a light chain comprising SEQ ID NO: 437 and a heavy chain comprising SEQ ID NO: 594; a light chain comprising SEQ ID NO: 438 and a heavy chain comprising SEQ ID NO: 595; a light chain comprising SEQ ID NO: 439 and a heavy chain comprising SEQ ID NO: 596; a light chain comprising SEQ ID NO: 440 and a heavy chain comprising SEQ ID NO: 597; a light chain comprising SEQ ID NO: 441 and a heavy chain comprising SEQ ID NO: 598; a light chain comprising SEQ ID NO: 442 and a heavy chain comprising SEQ ID NO: 599; a light chain comprising SEQ ID NO: 443 and a heavy chain comprising SEQ ID NO: 600; a light chain comprising SEQ ID NO: 444 and a heavy chain comprising SEQ ID NO: 601; a light chain comprising SEQ ID NO: 445 and a heavy chain comprising SEQ ID NO: 602; a light chain comprising SEQ ID NO: 446 and a heavy chain comprising SEQ ID NO: 603; a light chain comprising SEQ ID NO: 447 and a heavy chain comprising SEQ ID NO: 604; a light chain comprising SEQ ID NO: 448 and a heavy chain comprising SEQ ID NO: 605; a light chain comprising SEQ ID NO: 449 and a heavy chain comprising SEQ ID NO: 606; a light chain comprising SEQ ID NO: 450 and a heavy chain comprising SEQ ID NO: 607; a light chain comprising SEQ ID NO: 451 and a heavy chain comprising SEQ ID NO: 608; a light chain comprising SEQ ID NO: 452 and a heavy chain comprising SEQ ID NO: 609; a light chain comprising SEQ ID NO: 453 and a heavy chain comprising SEQ ID NO: 610; a light chain comprising SEQ ID NO: 454 and a heavy chain comprising SEQ ID NO: 611; a light chain comprising SEQ ID NO: 455 and a heavy chain comprising SEQ ID NO: 612; a light chain comprising SEQ ID NO: 456 and a heavy chain comprising SEQ ID NO: 613; a light chain comprising SEQ ID NO: 457 and a heavy chain comprising SEQ ID NO: 614; a light chain comprising SEQ ID NO: 458 and a heavy chain comprising SEQ ID NO: 615; a light chain comprising SEQ ID NO: 459 and a heavy chain comprising SEQ ID NO: 616; a light chain comprising SEQ ID NO: 460 and a heavy chain comprising SEQ ID NO: 617; a light chain comprising SEQ ID NO: 461 and a heavy chain comprising SEQ ID NO: 618; a light chain comprising SEQ ID NO: 462 and a heavy chain comprising SEQ ID NO: 619; a light chain comprising SEQ ID NO: 463 and a heavy chain comprising SEQ ID NO: 620; a light chain comprising SEQ ID NO: 464 and a heavy chain comprising SEQ ID NO: 621; a light chain comprising SEQ ID NO: 465 and a heavy chain comprising SEQ ID NO: 622; a light chain comprising SEQ ID NO: 466 and a heavy chain comprising SEQ ID NO: 623; a light chain comprising SEQ ID NO: 467 and a heavy chain comprising SEQ ID NO: 624; a light chain comprising SEQ ID NO: 468 and a heavy chain comprising SEQ ID NO: 625; a light chain comprising SEQ ID NO: 469 and a heavy chain comprising SEQ ID NO: 626; a light chain comprising SEQ ID NO: 470 and a heavy chain comprising SEQ ID NO: 627; and a light chain comprising SEQ ID NO: 471 and a heavy chain comprising SEQ ID NO: 628, wherein the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s) selected from the group consisting of D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455, E276 of the antibody heavy chain relative to

reference sequence SEQ ID NO: 612, and T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612.

[0162] In one embodiment the antibody or fragment thereof comprises a light chain encoded by a polynucleotide sequence selected from the group consisting of SEQ ID NOs: 1885-2014 and a heavy chain comprising a sequence selected from the group consisting of SEQ ID NOs: 2042-2198, wherein the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s) selected from the group consisting of D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455, E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, and T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612. In one embodiment the antibody or fragment thereof comprises a combination of a light chain and a heavy chain, wherein the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s) selected from the group consisting of D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455, E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, and T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, selected from the group consisting of a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1885 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2042; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1886 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2043; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1887 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2044; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1888 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2045; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1889 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2046; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1890 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2047; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1891 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2048; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1892 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2049; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1893 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2050; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1894 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2051; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1895 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2052; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1896 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2053; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1897 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2054; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1898 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2055; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1899 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2056; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1900 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2057; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1901 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2058; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1902 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2059; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1903 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2060; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1904 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2061; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1905 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2062; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1906 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2063; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1907 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2064; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1908 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2065; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1909 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2066; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1910 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2067; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1911 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2068; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1912 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2069; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1913 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2070; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1914 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2071; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1915 and a heavy chain encoded by a polynucleotide sequence comprising

SEQ ID NO: 2072; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1916 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2073; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1917 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2074; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1918 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2075; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1919 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2076; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1920 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2077; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1921 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2078; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1922 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2079; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1923 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2080; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1924 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2081; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1925 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2082; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1926 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2083; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1927 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2084; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1928 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2085; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1929 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2086; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1930 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2087; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1931 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2088; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1932 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2089; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1933 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2090; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1934 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2091; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1935 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2092; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1936 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2093; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1937 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2094; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1938 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2095; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1939 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2096; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1940 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2097; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1941 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2098; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1942 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2099; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1943 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2100; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1944 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2101; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1945 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2102; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1946 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2103; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1947 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2104; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1948 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2105; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1949 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2106; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1950 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2107; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1951 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2108; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1952 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2109; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1953 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2110; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1954 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2111; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1955 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2112; a light chain

encoded by a polynucleotide sequence comprising SEQ ID NO: 1956 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2113; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1957 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2114; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1958 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2115; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1959 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2116; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1960 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2117; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1961 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2118; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1962 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2119; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1963 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2120; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1964 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2121; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1965 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2122; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1966 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2123; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1967 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2124; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1968 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2125; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1969 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2126; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1970 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2127; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1971 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2128; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1972 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2129; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1973 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2130; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1974 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2131; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1975 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2132; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1976 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2133; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1977 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2134; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1978 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2135; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1979 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2136; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1980 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2137; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1981 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2138; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1982 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2139; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1983 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2140; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1984 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2141; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1985 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2142; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1986 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2143; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1987 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2144; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1988 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2145; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1989 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2146; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1990 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2147; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1991 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2148; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1992 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2149; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1993 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2150; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1994 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2151; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1995 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2152; a light chain encoded by a poly-

nucleotide sequence comprising SEQ ID NO: 1996 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2153; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1997 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2154; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1998 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2155; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1999 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2156; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2000 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2157; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2001 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2158; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2002 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2159; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2003 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2160; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2004 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2161; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2005 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2162; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2006 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2163; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2007 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2164; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2008 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2165; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2009 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2166; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2010 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2167; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2011 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2168; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2012 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2169; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2013 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2170; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2014 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2171; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2015 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2172; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2016 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2173; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2017 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2174; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2018 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2175; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2019 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2176; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2020 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2177; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2021 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2178; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2022 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2179; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2023 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2180; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2024 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2181; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2025 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2182; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2026 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2183; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2027 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2184; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2028 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2185; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2029 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2186; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2030 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2187; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2031 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2188; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2032 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2189; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2033 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2190; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2034 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2191; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2035 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2192; a light chain encoded by a polynucleotide sequence comprising

SEQ ID NO: 2036 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2193; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2037 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2194; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2038 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2195; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2039 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2196; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2040 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2197; and a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2041 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2198.

[0163] 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.

[0164] In another embodiment, the antigen binding protein consists of a just a light or a heavy chain polypeptide as set forth in TABLE 5.

[0165] 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.

[0166] 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.

[0167] 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:

all 6 of the CDRs listed for any antibody listed in TABLES 4A and 4B;
a VH and a VL listed for any antibody listed in TABLE 3; or
two light chains and two heavy chains as specified for any antibody listed in TABLE 5.

[0168] 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.

[0169] 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.

[0170] 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.

[0171] 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. 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.

[0172] 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.

[0173] 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).

[0174] 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.

[0175] In certain embodiments, constant regions from species other than human can be used along with the human variable region(s) to produce hybrid antibodies.

[0176] 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.

[0177] 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.

[0178] 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.YAcad. Sci. 764:536-546). The preparation of HuMab mice is described in detail in Taylor et al., 1992, Nucleic Acids Research 20:6287-6295; Chen et al., 1993, International Immunology 5:647-656; Tuaillon et al., 1994, J. Immunol. 152:2912-2920; Lonberg et al., 1994, Nature 368:856-859; Lonberg, 1994, Handbook of Exp. Pharmacology 113:49-101; Taylor et al., 1994, International Immunology 6:579-591; Lonberg and Huszar, 1995, Intern. Rev. Immunol. 13:65-93; Harding and Lonberg, 1995, Ann. N.YAcad. Sci. 764:536-546; Fishwild et al., 1996, Nature Biotechnology 14:845-851. *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. 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. 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.

[0179] 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.

[0180] 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.

[0181] 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.

[0182] 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.

[0183] Naturally-occurring amino acids may be divided into classes based on common side chain properties:

1) hydrophobic: norleucine, Met, Ala, Val, Leu, Ile;
2) neutral hydrophilic: Cys, Ser, Thr, Asn, Gln;
3) acidic: Asp, Glu;
4) basic: His, Lys, Arg;
5) residues that influence chain orientation: Gly, Pro; and
6) aromatic: Trp, Tyr, Phe.

[0184] 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.

[0185] 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.

[0186] 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).

[0187] 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.

[0188] 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.

[0189] The following hydrophilicity values have been assigned to these amino acid residues: arginine (+3.0); lysine (+3.0); aspartate (+3.0±1); glutamate (+3.0±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."

[0190] 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, He
Phe	Met, Leu, Tyr
Ser	Thr
Thr	Ser
Trp	Tyr
Tyr	Trp, Phe
Val	Ile, Leu

[0191] 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.

[0192] 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.

[0193] 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.

[0194] A number of scientific publications have been devoted to the prediction of secondary structure. *See,* Moult, 1996, Curr. Op. in Biotech. 7:422-427; Chou et al., 1974, Biochem. 13:222-245; Chou et al., 1974, Biochemistry 113:211-222; Chou et al., 1978, Adv. Enzymol. Relat. Areas Mol. Biol. 47:45-148; Chou et al., 1979, Ann. Rev. Biochem. 47:251-276; and Chou et al., 1979, Biophys. J. 26:367-384. Moreover, computer programs are currently available to assist with predicting secondary structure. One method of predicting secondary structure is based upon homology modeling. For example, two polypeptides or proteins that have a sequence identity of greater than 30%, or similarity greater than 40% can have similar structural topologies. The recent growth of the protein structural database (PDB) has provided enhanced predictability of secondary structure, including the potential number of folds within a polypeptide's or protein's structure. *See,* Holm et al., 1999, Nucl. Acid. Res. 27:244-247. It has been suggested (Brenner et al., 1997, Curr. Op. Struct. Biol. 7:369-376) that there are a limited number of folds in a given polypeptide or protein and that once a critical number of structures have been resolved, structural prediction will become dramatically more accurate.

[0195] 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*).

[0196] 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.

[0197] 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.

[0198] 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).

[0199] 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. 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: $-CH_2NH-$, $-CH_2S-$, $-CH_2-CH_2-$, -CH-CH-(cis and trans), $-COCH_2-$, $-CH(OH)CH_2-$, and $-CH_2SO-$, 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)), for example, by adding internal cysteine residues capable of forming intramolecular disulfide bridges which cyclize the peptide.

[0200] 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, propropylene glycol homopolymers, polypropylene oxide/ethylene oxide co-polymers, polyoxyethylated polyols and polyvinyl alcohols.

[0201] 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).

[0202] 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.*, ^{3}H, ^{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.

[0203] 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.*, ^{3}H, ^{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.

[0204] 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.

[0205] 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" fluores, or proteinaceous fluores.

[0206] 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.

[0207] 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).

[0208] 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.

[0209] 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.

[0210] 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.

[0211] 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.

[0212] 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.

[0213] 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.

[0214] 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.

[0215] 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.

[0216] 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.

[0217] 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.

[0218] 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.

[0219] 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. *Semetabolice, 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).

[0220] 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 bacte-

riophage 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.

[0221] 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. The heavy or light chain constant region may be 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). Vectors may be used that employ protein-fragment complementation assays using protein reporters, such as dihydrofolate reductase (*see,* for example, U.S. Pat. No. 6,270,964). 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. Additional suitable expression vectors are discussed, for example, in Methods Enzymol., vol. 185 (D. V. Goeddel, ed.), 1990, New York: Academic Press.

[0222] 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.

[0223] 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 (hemaglutinin 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.

[0224] 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.

[0225] 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.

[0226] 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.

[0227] 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 stomatitus 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).

[0228] 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.

[0229] 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.

[0230] 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.

[0231] 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.

[0232] 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.

[0233] 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.

[0234] 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.

[0235] 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 ele-

ments 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.

[0236] In one embodiment the leader sequence comprises SEQ ID NO: 3157 (MDMRVPAQLL GLLLLWLRGA RC) which is encoded by SEQ ID NO: 3158 (atggacatga gagtgcctgc acagctgctg ggcctgctgc 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 ctcactcagg gcacagggtc ctgggcc).

[0237] 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.

[0238] 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.*

[0239] 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.

[0240] 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.

[0241] 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.

[0242] 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.

[0243] In certain embodiments, the pharmaceutical composition may contain formulation materials for modifying, maintaining or preserving, for example, the pH, osmolarity, viscosity, clarity, color, isotonicity, odor, sterility, stability, rate of dissolution or release, adsorption or penetration of the composition. In such embodiments, suitable formulation materials include, but are not limited to, amino acids (such as glycine, glutamine, asparagine, arginine or lysine); antimicrobials; antioxidants (such as ascorbic acid, sodium sulfite or sodium hydrogen-sulfite); buffers (such as borate, bicarbonate, Tris-HCl, citrates, phosphates or other organic acids); bulking agents (such as mannitol or glycine); chelating agents (such as ethylenediamine tetraacetic acid (EDTA)); complexing agents (such as caffeine, polyvinylpyrrolidone, beta-cyclodextrin or hydroxypropyl-beta-cyclodextrin); fillers; monosaccharides; disaccharides; and other carbohydrates (such as glucose, mannose or dextrins); proteins (such as serum albumin, gelatin or immunoglobulins); coloring, flavoring and diluting agents; emulsifying agents; hydrophilic polymers (such as polyvinylpyrrolidone); low molecular weight polypeptides; salt-forming counterions (such as sodium); preservatives (such as benzalkonium chloride, benzoic acid, salicylic acid, thimerosal, phenethyl alcohol, methylparaben, propylparaben, chlorhexidine, sorbic acid or hydrogen peroxide); solvents (such as glycerin, propylene glycol or polyethylene glycol); sugar alcohols (such as mannitol or

sorbitol); suspending agents; surfactants or wetting agents (such as pluronics, PEG, sorbitan esters, polysorbates such as polysorbate 20, polysorbate, triton, tromethamine, lecithin, cholesterol, tyloxapal); stability enhancing agents (such as sucrose or sorbitol); tonicity enhancing agents (such as alkali metal halides, preferably sodium or potassium chloride, mannitol sorbitol); delivery vehicles; diluents; excipients and/or pharmaceutical adjuvants. REMINGTON'S PHARMACEUTICAL SCIENCES, 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.

[0244] 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.

[0245] 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.

[0246] 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.

[0247] 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.

[0248] 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 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.

[0249] 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.

[0250] 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 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), copolymers of L-glutamic acid and gamma ethyl-L-glutamate (Sidman et al., 1983, Biopolymers 2:547-556), poly (2-hydroxyethyl-inethacr-

ylate) (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.

[0251] 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.

[0252] 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).

[0253] 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.

[0254] 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.

[0255] 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.

[0256] 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.

[0257] 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.

[0258] 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).

[0259] 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, phospatidylcholine to sphingomyelin, or HDL-C levels.

[0260] 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.

[0261] In one aspect the present invention is directed to a composition as claimed for use in a method of treating a subject with a metabolic disorder, the method comprising administering to the subject the composition as claimed. In one embodiment the GIPR antagonist inhibits GIP binding to GIPR.

[0262] In one aspect the present invention is directed to composition as claimed for use in a method of treating a subject with a metabolic disorder, the method comprising administering to the subject a composition comprising the antibody or functional fragment thereof and the GLP-1 receptor agonist.

[0263] In one aspect the present invention is directed to a method of promoting GIPR and GLP-1R internalization into the cell upon which they are co-expressed by administering a GIPR antagonist conjugated to a GLP-1 receptor agonist to the cell. In one embodiment, the GIPR and GLP-1R are co-localized while being internalized.

[0264] In one aspect the present invention is directed to a method of stimulating calcium flux in a cell by administering a GIPR antagonist conjugated to a GLP-1 receptor agonist to the cell.

[0265] In one aspect the present invention is directed to a method of promoting beta-arrestin recruitment in a cell by administering a GIPR antagonist conjugated to a GLP-1 receptor agonist to the cell.

[0266] In one aspect the present invention is directed to a method of stimulating insulin secretion from a cell by administering a GIPR antagonist conjugated to a GLP-1 receptor agonist to the cell. In one embodiment the cell is a human pancreatic microislet.

[0267] 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.

[0268] The term "exendin" includes naturally occurring (or synthetic versions of naturally occurring) exendin peptides that are found in the salivary secretions of the Gila monster. Exendins of particular interest include exendin-3 and exendin-4. The exendins, exendin analogs, and exendin agonists for use in the methods described herein may optionally be amidated, and may also be in an acid form, pharmaceutically acceptable salt form, or any other physiologically active form of the molecule.

[0269] In one embodiment, the GLP-1 receptor agonist is GLP-1(7-37) or a GLP-1(7-37) analog.

[0270] In one embodiment, the GLP-1 receptor agonist is selected from the group consisting of exenatide, liraglutide, lixisenatide, albiglutide, dulaglutide, semaglutide, and taspoglutide.

[0271] In one aspect the present invention is directed to a composition comprising a) an antibody or functional fragment thereof that specifically binds to human GIPR, wherein the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid substitution at one or more conjugation site(s), and wherein the antibody or functional fragment thereof is a GIPR antagonist; and a GLP-1 receptor agonist, wherein the GLP-1 receptor agonist is conjugated to the antibody or functional fragment thereof through the sidechain of the cysteine residue or non-canonical amino acid residue substituted at the one or more conjugation site(s), for use in a method of treatment comprising administering to a subject a therapeutically effective amount of at least one GLP-1 receptor agonist in combination with administration of at least one GIPR antagonist, wherein the GIPR antagonist is conjugated to the GLP-1 receptor agonist, which upon administration to a subject with symptoms of a metabolic disorder provides sustained beneficial effects.

[0272] 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.

[0273] 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.

[0274] In one embodiment, the therapeutically effective amounts of the GLP-1 receptor agonist and the GIPR antagonist are administered to the subject sequentially.

[0275] In one embodiment, the therapeutically effective amounts of a GLP-1 receptor agonist and a GIPR antagonist are synergistically effective amounts.

[0276] Exendin-4 (HGEGTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGAPPPS-NH_2 (SEQ ID NO: 3163)) is a peptide found in the saliva of the Gila monster, *Heloderma suspectum;* and exendin-3 (HSDGTFTSDLSKQMEEEA-VRLFIEWLKNGGPSSGAPPPS-NH_2(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).

[0277] 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.

[0278] "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). Preferably, the exendin analogs will bind in such assays with an affinity of less than 1 μM, and more preferably with an affinity of less than 3 nM, less than 1 nM, or less than 0.1 nM. The term "exendin analog" may also be referred to as "exendin agonist". In a preferred embodiment, the exendin analog is an exendin-4 analog.

[0279] 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.

[0280] Exemplary exendins and exendin analogs exendin-4 (SEQ ID NO: 3163); exendin-3 (SEQ ID NO: 3164); Leu^{14}-exendin-4 (SEQ ID NO: 3165); Leu^{14},Phe^{25}-exendin-4 (SEQ ID NO: 3166); Leu^{14},Ala^{19},Phe^{25}-exendin-4 (SEQ ID NO: 3167); exendin-4(1~30) (SEQ ID NO: 3168); Leu^{14}-exendin-4(1-30) (SEQ ID NO: 3169); Leu^{14},Phe^{25}-exendin-4(1-30) (SEQ ID NO: 3170); Leu^{14},Ala^{19},Phe^{25}-exendin-4(1-30) (SEQ ID NO: 3171), exendin-4(1-28) (SEQ ID NO: 3172); Leu^{14}-exendin-4(1-28) (SEQ ID NO: 3173); Leu^{14},Phe^{25}-exendin-4(1-28) (SEQ ID NO: 3174); Leu^{14},Ala^{19},Phe^{25}-exendin-4 (1-28) (SEQ ID NO: 3175); Leu^{14},$Lys^{17,20}$,Ala^{19},Glu^{21},Phe^{25},Gln^{28}-exendin-4 (SEQ ID NO: 3176); Leu^{14},$Lys^{17,20}$,Ala^{19},Glu^{21},Gln^{28}-exendin-4 (SEQ ID NO: 3177); octylGly^{14},Gln^{28}-exendin-4 (SEQ ID NO: 3178), Leu^{14},Gln^{28},octylGly^{34}-exendin-4 (SEQ ID NO: 3179), Phe^{4},Leu^{14},Gln^{28},Lys^{33},Glu^{34}, Ile,^{11,36}, Ser^{37}-exendin-4(1-37) (SEQ ID NO: 3180); Phe^{4},Leu^{14},$Lys^{17,20}$,Ala^{19},Glu^{21},Gln^{28}-exendin-4 (SEQ ID NO: 3181); Val^{11},Ile^{13},$Leu^{14}Ala^{16}$,Lys^{21},Phe^{25}-exendin-4 (SEQ ID NO: 3182); exendin-4-Lys^{40} (SEQ ID NO: 3183); lixisenatide (Sanofi-Aventis/Zealand Pharma); CJC-1134 (ConjuChem, Inc.), [N^{e}-(17-carboxyheptadecanoic acid)Lys^{20}]exendin-4-NH_2 (SEQ ID NO: 3208); [N^{e}-(17-carboxyhepta-decanoyl)Lys^{32}]exendin-4-NH_2 (SEQ ID NO: 3209); [desamino-His^{1},N^{e}-(17-carboxyheptadecanoyl)Lys^{20}]exendin-4-NH_2 (SEQ ID NO: 3210), [$Arg^{12,27}$,NLe^{14},N^{e}-(17-carboxy-heptadecanoyl)Lys^{32}]exendin-4-NH_2 (SEQ ID NO: 32(1); [N^{e}-(19-carboxy-nonadecanoylamino)Lys^{20}]-exendin-4-NH_2 (SEQ ID NO: 32(2); [N^{e}-(15-carboxypentadecanoylamino)Lys^{20}]-exendin-4-NH_2(SEQ ID NO: 3213); [N^{e}-(13-carboxytridecanoylamino)Lys^{20}]exendin-4-NH_2 (SEQ ID NO: 3214); [N^{e}-(11-carboxy-undecanoyl-amino)Lys^{20}]exendin-4-NH_2 (SEQ ID NO: 3215); exendin-4-Lys^{40}(e-MPA)-NH_2 (SEQ ID NO: 3216); exendin-4-Lys^{40}(e-AEEA-AEEA-MPA)-NH_2 (SEQ ID NO: 3217); exendin-4-Lys^{40}(e-AEEA-MPA)-NH_2 (SEQ ID NO: 3218); exendin-4-Lys^{40}(e-MPA)-albumin (SEQ ID NO: 3219); exendin-4-Lys^{40}(e-AEEA-AEEA-MPA)-albumin (SEQ ID NO: 3220); exendin-4-Lys^{40}(e-AEEA-MPA)-albumin (SEQ ID NO: 3221); and the like. AEEA refers to [2-(2-amino)ethoxy)]acetic acid. EDA refers to ethylenediamine. MPA refers to maleimidopropionic acid. The exendins and exendin analogs may optionally be amidated.

[0281] 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).

[0282] Other exendins and exendin analogs useful in the methods described herein include those described in WO 98/05351; WO 99/07404; WO 99/25727; WO 99/25728; WO 99/40788; WO 00/41546; WO 00/41548; WO 00/73331; WO 01/51078; WO 03/099314; U.S. Pat. No. 6,956,026; U.S. Pat. No. 6,506,724; U.S. Pat. No. 6,703,359; U.S. Pat. No. 6,858,576; U.S. Pat. No. 6,872,700; U.S. Pat. No. 6,902,744; U.S. Pat. No. 7,157,555; U.S. Pat. No. 7,223,725; U.S. Pat. No. 7,220,721; US Publication No. 2003/0036504; and US Publication No. 2006/0094652.

[0283] "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). 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)-NH_2. GLP-1(7-37) analogs include the amidated forms, the acid form, the pharmaceutically acceptable salt form, and any other physiologically active form of the molecule. In some embodiments a simple nomenclature is used to describe the GLP-1 receptor agonist, e.g., [Aib8] GLP-1(7-37) designates an analogue

of GLP-1(7-37) wherein the naturally occurring Ala in position 8 has been substituted with Aib.

[0284] Exemplary GLP-1(7-37) and GLP-1(7-37) analogs include GLP-1(7-37) (SEQ ID NO: 3184); GLP-1(7-36)-NH_2(SEQ ID NO: 3185); liraglutide (VICTOZA® from Novo Nordisk); albiglutide (SYNCRIA® from GlaxoSmith-Kline), taspoglutide (Hoffman La-Roche); dulaglutide (also known LY2189265; Eli Lilly and Company); LY2428757 (Eli Lilly and Company), 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); desamino-His^7,Arg^{26},Lys^{34}(N^{ε}-octanoyl)-GLP-1(7-37) (SEQ ID NO: 3223); $Arg^{26,34}$,Lys^{38}(N^{ε}-((ω-carboxypentadecanoyl))-GLP-1(7-38) (SEQ ID NO: 3224); $Arg^{26,34}$,Lys^{36}(N^{ε}-(γ-Glu(N-α-hexadecanoyl)))-GLP-1(7-36) (core peptide disclosed as SEQ ID NO: 3225); $Aib^{8,35}$,$Arg^{26,34}$,Phe^{31}-GLP-1(7-36) (SEQ ID NO: 3186); $HXaa_8EGTFTSDVSSYLEXaa_{22}Xaa_{23}AAKEFIXaa_{30}WLXaa_{33}Xaa_{34}G\ Xaa_{36}Xaa_{37}$; wherein Xaa_3 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 (SEQ ID NO: 3187); Arg^{34}-GLP-1(7-37) (SEQ ID NO: 3188); Glu^{30}-GLP-1(7-37) (SEQ ID NO: 3189); Lys^{22}-GLP-1(7-37) (SEQ ID NO: 3190); $Gly^{8,36}$,Glu^{22}-GLP-1(7-37) (SEQ ID NO: 3191); Val^8,Glu^{22},Gly^{36}-GLP-1(7-37) (SEQ ID NO: 3192), $Gly^{8,36}$,Glu^{22},Lys^{33},Asn^{34}-GLP-1(7-37) (SEQ ID NO: 3193); Val^8,Glu^{22},Lys^{33},Asn^{34},Gly^{36}-GLP-1(7-37) (SEQ ID NO: 3194); $Gly^{8,36}$,Glu^{22},Pro^{37}-GLP-1(7-37) (SEQ ID NO: 3195); Val^8,Glu^{22},$Gly^{36}Pro^{37}$-GLP-1(7-37) (SEQ ID NO: 3196); $Gly^{8,36}$,Glu^{22},Lys^{33}, Asn^{34},Pro^{37}-GLP-1(7-37) (SEQ ID NO: 3197); Val^8,$Glu2^{22}Lys^{33}$,Asn^{34},Gly^{36},Pro^{37}-GLP-1(7-37) (SEQ ID NO: 3198); $Gly^{8,36}$,Glu^{22}-GLP-1(7-36) (SEQ ID NO: 3199); Val^8,Glu^{22},Gly^{36}-GLP-1(7-36) (SEQ ID NO: 3200); Val^8,Glu^{22},Asn^{34},Gly^{36}-GLP-1(7-36) (SEQ ID NO: 3201); $Gly^{8,36}$, Glu^{22},$Asr,^{34}$-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.

[0285] The GLP-1 receptor agonists of the inventive composition of matter can also be chemically derivatized at one or more amino acid residues by known organic chemistry techniques. "Chemical derivative" or "chemically derivatized" refers to a subject peptide having one or more residues chemically derivatized by reaction of a functional side group. Such derivatized molecules include, for example, those molecules in which free amino groups have been derivatized to form amine hydrochlorides, p-toluene sulfonyl groups, carbobenzoxy groups, t-butyloxycarbonyl groups, chloroacetyl groups or formyl groups. Free carboxyl groups may be derivatized to form salts, methyl and ethyl esters or other types of esters or hydrazides. Free hydroxyl groups may be derivatized to form O-acyl or O-alkyl derivatives. The imidazole nitrogen of histidine may be derivatized to form N-im-benzylhistidine. Also included as chemical derivatives are those peptides which contain one or more naturally occurring amino acid derivatives of the twenty canonical amino acids, whether in L- or D- form. For example, 4-hydroxyproline may be substituted for proline; 5-hydroxylysine maybe substituted for lysine; 3-methylhistidine may be substituted for histidine; homoserine may be substituted for serine; and ornithine may be substituted for lysine.

[0286] Useful derivatizations include, in some embodiments, those in which the amino terminal of the peptide is chemically blocked so that conjugation with the vehicle will be prevented from taking place at an N-terminal free amino group. There may also be other beneficial effects of such a modification, for example a reduction in the toxin peptide analog's susceptibility to enzymatic proteolysis. The N-terminus can be acylated or modified to a substituted amine, or derivatized with another functional group, such as an aromatic moiety (e.g., an indole acid, benzyl (Bzl or Bn), dibenzyl (DiBzl or Bn_2), or benzyloxycarbonyl (Cbz or Z)), *N*-*N*-dimethylglycine or creatine. For example, in some embodiments, an acyl moiety, such as, but not limited to, a formyl, acetyl (Ac), propanoyl, butanyl, heptanyl, hexanoyl, octanoyl, or nonanoyl, can be covalently linked to the N-terminal end of the peptide, which can prevent undesired side reactions during conjugation of the vehicle to the peptide. Other exemplary N-terminal derivative groups include -NRR^1 (other than -NH_2), -$NRC(O)R^1$, -$NRC(O)OR^1$, -$NRS(O)_2R^1$, -$NHC(O)NHR^1$, succinimide, or benzyloxycarbonyl-NH- (Cbz-NH-), wherein R and R^1 are each independently hydrogen or lower alkyl and wherein the phenyl ring may be substituted with 1 to 3 substituents selected from C_1-C_4 alkyl, C_1-C_4 alkoxy, chloro, and bromo.

[0287] In some embodiments, one or more peptidyl [-C(O)NR-] linkages (bonds) between amino acid residues can be replaced by a non-peptidyl linkage. Exemplary non-peptidyl linkages are -CH_2-carbamate [-CH_2-OC(O)NR-], phosphonate, -CH_2-sulfonamide [-CH_2-$S(O)_2$NR-], urea [-NHC(O)NH-], -CH_2-secondary amine, and alkylated peptide [-C(O)NR^6-wherein R^6 is lower alkyl].

[0288] In some embodiments, one or more individual amino acid residues can be derivatized. Various derivatizing agents are known to react specifically with selected sidechains or terminal residues, as described in detail below by way of example.

[0289] Lysinyl residues and amino terminal residues may be reacted with succinic or other carboxylic acid anhydrides, which reverse the charge of the lysinyl residues. Other suitable reagents for derivatizing alpha-amino-containing residues include imidoesters such as methyl picolinimidate; pyridoxal phosphate; pyridoxal; chloroborohydride; trinitrobenzenesulfonic acid; O-methylisourea; 2,4 pentanedione; and transaminase-catalyzed reaction with glyoxylate.

[0290] Arginyl residues may be modified by reaction with any one or combination of several conventional reagents, including phenylglyoxal, 2,3-butanedione, 1,2-cyclohexanedione, and ninhydrin. Derivatization of arginyl residues requires that the reaction be performed in alkaline conditions because of the high pKa of the guanidine functional group. Furthermore, these reagents may react with the groups of lysine as well as the arginine epsilon-amino group.

[0291] Specific modification of tyrosyl residues has been studied extensively, with particular interest in introducing

spectral labels into tyrosyl residues by reaction with aromatic diazonium compounds or tetranitromethane. Most commonly, N-acetylimidizole and tetranitromethane are used to form O-acetyl tyrosyl species and 3-nitro derivatives, respectively.

[0292] Carboxyl sidechain groups (aspartyl or glutamyl) may be selectively modified by reaction with carbodiimides (R'-N=C=N-R') such as 1-cyclohexyl-3-(2-morpholinyl-(4-ethyl) carbodiimide or 1-ethyl-3-(4-azonia-4,4-dimethylpentyl) carbodiimide. Furthermore, aspartyl and glutamyl residues may be converted to asparaginyl and glutaminyl residues by reaction with ammonium ions.

[0293] Glutaminyl and asparaginyl residues may be deamidated to the corresponding glutamyl and aspartyl residues. Alternatively, these residues are deamidated under mildly acidic conditions. Either form of these residues falls within the scope of this invention.

[0294] Cysteinyl residues can be replaced by amino acid residues or other moieties either to eliminate disulfide bonding or, conversely, to stabilize cross-linking. (See, e.g., Bhatnagar et al., J. Med. Chem., 39:3814-3819 (1996)).

[0295] Other possible modifications include hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, oxidation of the sulfur atom in Cys, methylation of the alpha-amino groups of lysine, arginine, and histidine side chains. Creighton, Proteins: Structure and Molecule Properties (W. H. Freeman & Co., San Francisco), 79-86 (1983).

[0296] The above examples of derivatizations are not intended to be an exhaustive treatment, but merely illustrative

[0297] 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:
AESKYGPPCPPCPAPXaa$_{16}$Xaa$_{17}$Xaa$_{18}$GGPSWLFPPKPKDTLMISRTPEVTCVVVDVSQ
EDPEVQFNWYVOGVEVHNAKTKPREEQFXaa$_{80}$STYRVVSVLTVLHQDWLNGKEYK
CKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMEALHN HYTQKSLSLSLGXaa$_{230}$;
wherein Xaa$_{16}$ is P or E; Xaa$_{17}$ is F, V or A; Xaa$_{18}$ is L, E or A; Xaa$_{80}$ is N or A, and Xaa$_{230}$ is K or absent (SEQ ID NO: 3203). The linking group may be any chemical moiety (e.g., amino acids and/or chemical groups). In one embodiment, the linking group is (-GGGGS-)$_x$(SEQ ID NO: 3204) where x is 1, 2, 3, 4, 5 or 6; preferably 2, 3 or 4; more preferably 3. In one embodiment, the GLP-1(7-37) analog covalently linked to the Fc portion of an immunoglobulin comprises the amino acid sequence:

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

[0298] 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: HXaa$_{8E}$GTFTSDVS SYLEXaa$_{22}$QAAKEFIAWLXaa$_{33}$KGGPSSGAPPPC$_{45}$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$_2$, (SEQ ID NO: 3206), 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$_{46}$. In one embodiment, the GLP-1(7-37) analog is HVEGTFTSDVSSYLEEQAAKEFI AWLIKGGPSSGAPPPC$_{45}$C$_{46}$-NH$_2$ (SEQ ID NO: 3207) and, optionally, wherein (i) one polyethylene glycol moiety is covalently attached to C$_4$, (ii) one polyethylene glycol moiety is covalently attached to C$_{46}$, or (iii) one polyethylene glycol moiety is attached to C$_{45}$ and one polyethylene glycol moiety is attached to C$_{46}$.

[0299] GLP-1 recpetor agonist amino acid residues that can provide a primary amine moiety for conjugation include residues of lysine, homolysine, ornithine, α, β-diaminopropionic acid (Dap), α, β-diaminopropionoic acid (Dpr), and α, γ-diaminobutyric acid (Dab), aminobutyric acid (Abu), and α-amino-isobutyric acid (Aib). The polypeptide N-terminus also provides a useful α-amino group for conjugation as does an amidated polypeptide C-terminus. In certain embodiments, the GLP-1(7-37) or GLP-1(7-37) analog is conjugated to the antibody or fragment thereof at a residue that corresponds to K26 (position 20 of SEQ ID NO: 3184), K34 (position 28 of SEQ ID NO: 3184), K36 (position 30 of SEQ

ID NO: 3184; *e.g.,* via a R36K mutation), K37 (position 31 of SEQ ID NO: 3184; *e.g.,* via a G37K mutation), K39 (*e.g.,* via addition of two amino acids to the GLP-1(7-37) or GLP-1(7-37) analog with lysine at position 39) or a C-terminal amine group of said analog. Amino acid residues that can provide a secondary amine moiety include ε-N-alkyl lysine, α-N-alkyl lysine, δ-N-alkyl ornithine, α-N-alkyl ornithine, or an N-terminal proline, where the alkyl is C_1 to C_6.

[0300] A "linker moiety" as used herein refers to a biologically acceptable peptidyl or non-peptidyl organic group that is covalently bound to an amino acid residue of a toxin peptide analog or other polypeptide chain (e.g., an immunoglobulin HC or LC or immunoglobulin Fc domain) contained in the inventive composition, which linker moiety covalently joins or conjugates the toxin peptide analog or other polypeptide chain to another peptide or polypeptide chain in the composition, or to a half-life extending moiety. In some embodiments of the composition, a half-life extending moiety, as described herein, is conjugated, i.e., covalently bound directly to an amino acid residue of the toxin peptide analog itself, or optionally, to a peptidyl or non-peptidyl linker moiety (including but not limited to aromatic or aryl linkers) that is covalently bound to an amino acid residue of the toxin peptide analog. The presence of any linker moiety is optional. When present, its chemical structure is not critical, since it serves primarily as a spacer to position, join, connect, or optimize presentation or position of one functional moiety in relation to one or more other functional moieties of a molecule of the inventive composition. The presence of a linker moiety can be useful in optimizing pharamcologial activity of some embodiments of the inventive composition. The linker, if present, can be made up of amino acids linked together by peptide bonds. The linker moiety, if present, can be independently the same or different from any other linker, or linkers, that may be present in the inventive composition. In some embodiments the linker can be a multivalent linker that facilitates multivalent display of toxin peptide analogs of the present invention; multivalent display of such biologically active compounds can increase binding affinity and/or potency through avidity. The in vivo properties of a therapuetic can be altered (i.e., specific targeting, half-life extension, distribution profile, etc.) through conjugation to a polymer or protein.

[0301] Peptidyl linkers. As stated above, the linker moiety, if present (whether within the primary amino acid sequence of the toxin peptide analog, or as a linker for attaching a half-life extending moiety to the toxin peptide analog), can be "peptidyl" in nature (i.e., made up of amino acids linked together by peptide bonds) and made up in length, preferably, of from 1 up to about 40 amino acid residues, more preferably, of from 1 up to about 20 amino acid residues, and most preferably of from 1 to about 10 amino acid residues. Preferably, but not necessarily, the amino acid residues in the linker are from among the twenty canonical amino acids, more preferably, cysteine, glycine, alanine, proline, asparagine, glutamine, and /or serine. Even more preferably, a peptidyl linker is made up of a majority of amino acids that are sterically unhindered, such as glycine, serine, and alanine linked by a peptide bond. It is also desirable that, if present, a peptidyl linker be selected that avoids rapid proteolytic turnover in circulation *in vivo.* Some of these amino acids may be glycosylated, as is well understood by those in the art. For example, a useful linker sequence constituting a sialylation site is $X_1X_2NX_4X_5G$ (SEQ ID NO: 3250), wherein X_1, X_2,X_4 and X_5 are each independently any amino acid residue.

[0302] In other embodiments, the 1 to 40 amino acids of the peptidyl linker moiety are selected from glycine, alanine, proline, asparagine, glutamine, and lysine. Preferably, a linker is made up of a majority of amino acids that are sterically unhindered, such as glycine and alanine. Thus, preferred linkers include polyglycines, polyserines, and polyalanines, or combinations of any of these. Some exemplary peptidyl linkers are poly$(Gly)_{1-8}$, particularly $(Gly)_3$ (SEQ ID NO:3251), $(Gly)_4$(SEQ ID NO:480), $(Gly)_5$ (SEQ ID NO:3251) and $(Gly)_7$ (SEQ ID NO:3252), as well as, GlySer and poly$(Gly)_4$Ser, such as "L15" (GGGGSGGGGSGGGGS; SEQ ID NO:3253), poly(Gly-Ala)$_{2-4}$ and poly$(Ala)_{1-8}$. Other specific examples of peptidyl linkers include (Gly)sLys (SEQ ID NO:3254), and (Gly)sLysArg (SEQ ID NO:3255). Other examples of useful peptidyl linkers are: Other examples of useful peptidyl linkers are:

$(Gly)_3Lys(Gly)_4$ (SEQ ID NO:3256);
$(Gly)_3AsnGlySer(Gly)_2$ (SEQ ID NO:3257);
$(Gly)_3Cys(Gly)_4$ (SEQ ID NO:3258); and
GlyProAsnGlyGly (SEQ ID NO:3259).

[0303] To explain the above nomenclature, for example, $(Gly)_3Lys(Gly)_4$ means Gly-Gly-Gly-Lys-Gly-Gly-Gly-Gly (SEQ ID NO:3260). Other combinations of Gly and Ala are also useful.

[0304] Other preferred linkers are those identified herein as "L5" (GGGGS; or "G_4S"; SEQ ID NO:3261), "L10" (GGGGSGGGGS; SEQ ID NO:3262); "L20" (GGGGSGGGGSGGGGSGGGGS; SEQ ID NO:3263) ; "L25" (GGGGSGGGGSGGGGSGGGGSGGGGS; SEQ ID NO:3264) and any linkers used in the working examples hereinafter.

[0305] In some embodiments of the compositions of this invention, which comprise a peptide linker moiety, acidic residues, for example, glutamate or aspartate residues, are placed in the amino acid sequence of the linker moiety. Examples include the following peptide linker sequences:

GGEGGG (SEQ ID NO:3265);
GGEEEGGG (SEQ ID NO:3266);
GEEEG (SEQ ID NO:3267);

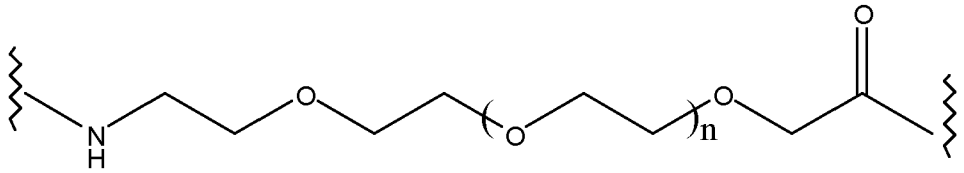
GEEE (SEQ ID NO:3268);
GGDGGG (SEQ ID NO:3269);
GGDDDGG (SEQ ID NO:3270);
GDDDG (SEQ ID NO:3271);
GDDD (SEQ ID NO:3272);
GGGGSDDSDEGSDGEDGGGGS (SEQ ID NO:3273);
WEWEW (SEQ ID NO:3274);
FEFEF (SEQ ID NO:3275);
EEEWWW (SEQ ID NO:3276);
EEEFFF (SEQ ID NO:3277);
WWEEEWW (SEQ ID NO:3278); or
FFEEEFF (SEQ ID NO:3279).

[0306] In other embodiments, the linker constitutes a phosphorylation site, e.g., $X_1X_2YX_4X_5G$ (SEQ ID NO:3280), wherein X_1, X_2, X_4, and X_5 are each independently any amino acid residue; $X_1X_2SX_4X_5G$ (SEQ ID NO:3281), wherein X_1, X_2,X_4 and X_5 are each independently any amino acid residue; or $X_1X_2TX_4X_5G$ (SEQ ID NO:3282), wherein X_1, X_2, X_4 and X_5 are each independently any amino acid residue.

[0307] The linkers shown here are exemplary; peptidyl linkers within the scope of this invention may be much longer and may include other residues. A peptidyl linker can contain, e.g., a cysteine, another thiol, or nucleophile for conjugation with a half-life extending moiety. In another embodiment, the linker contains a cysteine or homocysteine residue, or other 2-amino-ethanethiol or 3-amino-propanethiol moiety for conjugation to maleimide, iodoacetaamide or thioester, functionalized half-life extending moiety.

[0308] Another useful peptidyl linker is a large, flexible linker comprising a random Gly/Ser/Thr sequence, for example: GSGSATGGSGSTASSGSGSATH (SEQ ID NO:3283) or HGSGSATGGSGSTASSGSGSAT (SEQ ID NO:3284), that is estimated to be about the size of a 1 kDa PEG molecule. Alternatively, a useful peptidyl linker may be comprised of amino acid sequences known in the art to form rigid helical structures (e.g., Rigid linker: - AEAAAKEAAAKEAAAKAGG-// SEQ ID NO:3285). Additionally, a peptidyl linker can also comprise a non-peptidyl segment such as a 6 carbon aliphatic molecule of the formula - CH_2-CH_2-CH_2-CH_2-CH_2-CH_2-. The peptidyl linkers can be altered to form derivatives as described herein.

[0309] Non-peptidyl linkers. Optionally, a non-peptidyl linker moiety is also useful for conjugating the half-life extending moiety to the peptide portion of the half-life extending moiety-conjugated toxin peptide analog. For example, alkyl linkers such as -NH-$(CH_2)_s$-C(O)-, wherein s = 2-20 can be used. These alkyl linkers may further be substituted by any non-sterically hindering group such as lower alkyl (e.g., C_1-C_6) lower acyl, halogen (e.g., Cl, Br), CN, NH_2, phenyl, *etc.* Exemplary non-peptidyl linkers are PEG linkers (e.g., shown below):



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

[0310] In one embodiment, the non-peptidyl linker is aryl. The linkers may be altered to form derivatives in the same manner as described herein. "Aryl" is phenyl or phenyl vicinally-fused with a saturated, partially-saturated, or unsaturated 3-, 4-, or 5 membered carbon bridge, the phenyl or bridge being substituted by 0, 1, 2 or 3 substituents selected from C_{1-8} alkyl, C_{1-4} haloalkyl or halo. "Heteroaryl" is an unsaturated 5 , 6 or 7 membered monocyclic or partially-saturated or unsaturated 6-, 7-, 8-, 9-, 10- or 11 membered bicyclic ring, wherein at least one ring is unsaturated, the monocyclic and the bicyclic rings containing 1, 2, 3 or 4 atoms selected from N, O and S, wherein the ring is substituted by 0, 1, 2 or 3 substituents selected from C_{1-8} alkyl, C_{1-4} haloalkyl and halo.

[0311] Non-peptide portions of the inventive composition of matter, such as non-peptidyl linkers or non-peptide half-life extending moieties can be synthesized by conventional organic chemistry reactions.

[0312] Other embodiments of the multivalent linker comprise a rigid polyheterocyclic core of controlled length. The linkers are chemically differentiated on either end to accommodate orthogonal coupling chemistries (i.e. azide "Click", amide coupling, thioether formation by alkylation with maleimide or haloacetamide, oxime formation, reductive amination, etc.).

[0313] The above is merely illustrative and not an exhaustive treatment of the kinds of linkers that can optionally be

employed in accordance with the present invention.

[0314] 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).

[0315] 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.

Table 7. Examples of GLP-1 receptor agonist Sequences

SEQ ID NO:	Sequence	Description
3163	HGEGTFTSDLSKQMEEEAVRLFIEWLKN GGPSSGAPPPS	Exendin-4
3164	HSDGTFTSDLSKQMEEEAVRLFIEWLKN GGPSSGAPPPS	Exendin-3
3165	HGEGTFTSDLSKQLEEEAVRLFIEWLKN GGPSSGAPPPS	Leu^{14}-exendin-4
3166	HGEGTFTSDLSKQLEEEAVRLFIEFLKN GGPSSGAPPPS	Leu^{14},Phe^{25}-exendin-4
3167	HGEGTFTSDLSKQLEEEAARLFIEFLKN GGPSSGAPPPS	Leu^{14},Ala,^{19},Phe^{25}-exendin-4
3168	HGEGTFTSDLSKQMEEEAVRLFIEWLKN GG	exendin-4(1-30)
3169	HGEGTFTSDLSKQLEEEAVRLFIEWLKN GG	Leu^{14}-exendin-4(1-30)
3170	HGEGTFTSDLSKQLEEEAVRLFIEFLKN GG	Leu^{14},Phe^{25}-exendin-4(1-30)
3171	HGEGTFTSDLSKQLEEEAARLFIEFLKN GG	Leu^{14},Ala^{19} ,Phe^{25} -exendin-4 (1-30)
3172	HGEGTFTSDLSKQMEEEAVRLFIEWLKN	exendin-4(1-28)
3173	HGEGTFTSDLSKQLEEEAVRLFIEWLKN	Leu^{14}-exendin-4(1-28)
3174	HGEGTFTSDLSKQLEEEAVRLFIEFLKN	Leu^{14},Phe^{25}-exendin-4(1-28)
3175	HGEGTFTSDLSKQLEEEAARLFIEFLKN	Leu^{14},Ala^{19},Phe^{25}-exendin-4 (1-28)
3176	HGEGTFTSDLSKQLEEKAAKEFIEFLKQ GGPSSGAPPPS	Leu^{14},$Lys^{17,20}$,Ala^{19},Glu^{21},Phe^{25}, Gl n^{28}-exendin-4
3177	HGEGTFTSDLSKQLEEKAAKEFIEWLKQ GGPSSGAPPPS	Leu^{14},$Lys^{17,20}$,Ala^{19},Glu^{21}, Gln^{28}-exendin-4
3178	HGEGTFTSDLSKQ(octylG)EEEAVRL FIEWLKQGGPSSGAPPPS	octylGly^{14},Gln^{28}-exendin-4

(continued)

SEQ ID NO:	Sequence	Description
3179	HGEGTFTSDLSKQLEEEAVRLFIEWLKQ GGPSS(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}, Gl n^{28}-exendin-4
3182	HGEGTFTSDLVKILEAEAVRKFIEFLKN GGPSSGAPPPS	Val^{11},Ile^{13},Leu^{14},Ala^{16},Lys^{21}, Phe^{25} -exendin-4
3183	HGEGTFTSDLSKQMEEEAVRLFIEWLKN GGPSSGAPPPSK	exendin-4-Lys^{40}
3184	HAEGTFTSDVSSYLEGQAAKEFIAWLVK GRG	GLP-1(7-37)
3185	HAEGTFTSDVSSYLEGQAAKEFIAWLVK GR	GLP-1(7-36)-NH_2
3186	H(Aib)EGTFTSDVSSYLEGQAAREFIA FLVR(Aib)R	Alb^{8,35},Arg^{26,34},Phe^{31}-GLP-1 (7-36))
3187	HXaa$_8$EGTFTSDVSSYLEXaa$_{22}$Xaa$_{23}$AA KEFI Xaa$_{30}$WLXaa$_{33}$Xaa$_{34}$ GXaa$_{36}$Xaa$_{37}$ wherein Xaa$_8$ is A, V, or G Xaa$_{22}$ is G, K, or E Xaa$_{23}$ is Q or K Xaa$_{30}$ is A or E Xaa$_{33}$ is V or K Xaa$_{34}$ is K, N, or R Xaa$_{36}$ is R or G and Xaa$_{37}$ is G, H, P, or absent	HXaa$_8$EGTFTSDVSSYLEXaa$_{22}$X aa$_{23}$AAKEFIXaa$_{30}$WLXaa$_{33}$Xaa$_{34}$ G Xaa$_{36}$Xaa$_{37}$ wherein Xaa$_8$ is A, V, or G Xaa$_{22}$ is G, K, or E Xaa$_{23}$ is Q or K Xaa$_{30}$ is A or E Xaa$_{33}$ is V or K Xaa$_{34}$ is K, N, or R Xaa$_{36}$ is R or G and Xaa$_{37}$ is G, H, P, or absent
3188	HAEGTFTSDVSSYLEGQAAKEFIAWLVR GRG	Arg^{34}-GLP-1 (7-37)
3189	HAEGTFTSDVSSYLEGQAAKEFIEWLVK GRG	Glu^{30}-GLP-1(7-37)
3190	HAEGTFTSDVSSYLEKQAAKEFIAWLVK GRG	Lys^{22}-GLP-1(7-37)
3191	HGEGTFTSDVSSYLEEQAAKEFIAWLVK GGG	Gly^{8,36},Glu^{22}-GLP-1(7-37)
3192	HVEGTFTSDVSSYLEEQAAKEFIAWLVK GGG	Val^{8},Glu^{22},Gly^{36}-GLP-1(7-37)
3193	HGEGTFTSDVSSYLEEQAAKEFIAWLKN GGG	Gly^{8,36},Glu^{22},Lys^{33},Asn^{34}-GLP-1 (7-37)

(continued)

SEQ ID NO:	Sequence	Description
3194	HVEGTFTSDVSSYLEEQAAKEFIAWLKN GGG	Val8,Glu^{22},Lys^{33},Asn^{34}, Gly^{36}-GLP-1(7-37)
3195	HGEGTFTSDVSSYLEEQAAKEFIAWLVK GGP	Gly^{8,36},Glu^{22},Pro^{37}-GLP-1(7-37)
3196	HVEGTFTSDVSSYLEEQAAKEFIAWLVK GGP	Val^{8},Glu^{22},Gly^{36},Pro^{37}-GLP-1 (7-37)
3197	HGEGTFTSDVSSYLEEQAAKEFIAWLKN GGP	Gly^{8,36},Glu^{22},Lys^{33}, Asn^{34}, Pro^{37}-GLP-1(7-37)
3198	HVEGTFTSDVSSYLEEQAAKEFIAWLKN GGP	Val^{8},Glu^{22},Lys^{33},Asn^{34},Gly^{36}, Pro^{37} -GLP-1(7-37)
3199	HGEGTFTSDVSSYLEEQAAKEFIAWLVK GG	Gly^{8,36},Glu^{22}-GLP-1(7-36)
3200	HVEGTFTSDVSSYLEEQAAKEFIAWLVK 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	AESKYGPPCPPCPAPXaa$_{16}$Xaa$_{17}$Xaa$_{18}$ GGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSQEDPEVQFNWYVDGVEVHNAKTKP REEQFXaa$_{80}$STYRVVSVLTVLHQDWLNG KEYKCKVSNKGLPSSIEKTISKAKGQPR EPQVYTLPPSQEEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDS DGSFFLYSRLTVDKSRWQEGNVFSCSVM HEALHNHYTQKSLSLSLGXaa$_{230}$ wherein Xaa$_{16}$ is P or E Xaa$_{17}$ is F, V or A. Xaa$_{18}$ is L, E or A Xaa$_{80}$ is N or A and Xaa$_{230}$ is K or absent	Fc portion of an immunoglobulin
3204	(-GGGGS-)$_x$ where x is 1, 2, 3, 4, 5 or 6	Linker

(continued)

SEQ ID NO:	Sequence	Description
3205	HGEGTFTSDVSSYLEEQAAKEFIAWLVK GGGGGGGSGGGGSGGGGSAESKYGPPCP PCPAPEAAGGPSVFLFPPKPKDTLMISR TPEVTCVVVDVSQEDPEVQFNWYVDGVE VHNAKTKPREEQFNSTYRVVSVLTVLHQ DWLNGKEYKCKVSNKGLPSSIEKTISKA KGQPREPQVYTLPPSQEEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSR LTVDKSRWQEGNVFSCSVMHEALHNHYT QKSLSLSLG	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 polythylene glycol moiety is attached to C$_{46}$.	GLP-1 analog
3207	HVEGTFTSDVSSYLEEQAAKEFIAWLIK GGPSSGAPPC$_{45}$C$_{46}$-NH$_2$ and, , optionally, wherein (i) one polyethylene glycol moiety is covalently attached to C$_4$, (ii) one polyethylene glycol moiety is covalently attached to C$_{46}$, or (iii) one polyethylene to C$_{46}$, or (iii) one polyethyleneglycol moiety is attached to C$_{45}$ and one polyethylene glycol moiety is attached to C$_{46}$	GLP-1 analog
3208	HGEGTFTSDLSKQMEEEAVKLFIEWLKN GGPSSGAPPPS	[N^e-(17-carboxyheptadecanoic acid)Lys^{20}]exendin-4-NH$_2$
3209	HGEGTFTSDLSKQMEEEAVRLFIEWLKN GGPKSGAPPPS	[N^e-(17-carboxyhepta-decanoyl) Lys^{32}]exendin-4-NH$_2$
3210	GEGTFTSDLSKQMEEEAVKLFIEWLKNG GPSSGAPPPS	[desamino-His^1,N^e-(17-carboxyheptadecanoyl)Lys^{20}]exendin-4-NH$_2$
3211	HGEGTFTSDLSRQNorLeEEEAVRLFIE WLRNGGPKSGAPPPS	[Arg^{12,27},NLe^{14},N^e-(17-carboxy-heptadecanoyl)Lys^{32}]exendin-4-NH$_2$
3212	HGEGTFTSDLSKQMEEEAVKLFIEWLKN GGPSSGAPPPS	[N^e-(19-carboxy-nonadecanoylamino) Lys^{20}]-exendin-4-NH$_2$

(continued)

SEQ ID NO:	Sequence	Description
3213	HGEGTFTSDLSKQMEEEAVKLFIEWLKN GGPSSGAPPPS	[N^e-(15-carboxypentadecanoylamino) Lys^{20}]-exendin-4-NH_2
3214	HGEGTFTSDLSKQMEEEAVKLFIEWLKN GGPSSGAPPPS	[N^e-(13-carboxytridecanoylamino) Lys^{20}]ex endin-4-NH_2
3215	HGEGTFTSDLSKQMEEEAVKLFIEWLKN GGPSSGAPPPS	[N^e-(11-carboxy-undecanoyl-amino)Lys^{20}]exendin-4-NH_2
3216	HGEGTFTSDLSKQMEEEAVRLFIEWLKN GGPSSGAPPPSK	exendin-4-Lys^{40}(e-MPA)-NH_2
3217	HGEGTFTSDLSKQMEEEAVRLFIEWLKN GGPSSGAPPPSK	exendin-4-Lys^{40}(e-AEEA-AEEA-MPA)-NH_2
3218	HGEGTFTSDLSKQMEEEAVRLFIEWLKN GGPSSGAPPPSK	exendin-4-Lys^{40}(e-AEEA-MPA)-NH_2
3219	HGEGTFTSDLSKQMEEEAVRLFIEWLKN GGPSSGAPPPSK	exendin-4-Lys^{40}(e-MPA)-albumin
3220	HGEGTFTSDLSKQMEEEAVRLFIEWLKN GGPSSGAPPPSK	exendin-4-Lys^{40}(e-AEEA-AEEA-MPA)-albumin
3221	HGEGTFTSDLSKQMEEEAVRLFIEWLKN GGPSSGAPPPSK	exendin-4-Lys^{40}(e-AEEA-MPA)-albumin
3222	AEGTFTSDVSSYLEGQAAREFIAWLVKG RG	desamino-His^7,Arg^{26},$Lys^{34}N^{\varepsilon}$-(γ-Glu(N-α-hexadecanoyl)))-GLP-1 (7-37) (core peptide disclosed as SEQ ID NO: 3222)
3223	AEGTFTSDVSSYLEGQAAREFIAWLVKG RG	desamino-His^7,Arg^{26},Lys^{34} (N^{ε}-octanoyl)-GLP-1(7-37)
3224	HAEGTFTSDVSSYLEGQAAREFIAWLVR GRGK	$Arg^{26,34}$,Lys^{38}(N^{ε}-(ω carboxypentadecanoyl))-GLP-1 (7-38)
3225	HAEGTFTSDVSSYLEGQAAREFIAWLVR GRGK	$Arg^{26,34}$,Lys^{36}(N^{ε}-(γ-Glu(N-α-hexad ecanoyl)))-GLP-1 (7-3 6) (core peptide disclosed as SEQ ID NO: 3225)
3226	H[Aib]EGTFTSDVSSYLEGQAAKEFIA WLVKGRK	[Aib^8;Lys^{37}]GLP-1_(7-37)
3227	H[Aib]EGTFTSDVSSYLEGQAAKEFIA WLVKGKG	[Aib^8, Lys^{36}]GLP-1_(7-37)
3228	H[Aib]EGTFTSDVSSYLE[Aib]QAAK EFIAWLVKGK	[$Aib^{8,22}$;Lys^{36}]GLP-1(7-36)-Amide
3229	H[Aib]EGTFTSDVSSYLE[Aib]QAAK EFIAW[BLeu]VKGK	[$Aib^{8,22}$;$BLeu^{32}$;Lys^{36}]GLP-1 (7-36)-Amide

(continued)

SEQ ID NO:	Sequence	Description
3230	H[Aib]EGTFTSDVSSYLE[Aib]QAAK EFIAWLVKGRK	[Aib^{8,22};Lys^{37}]GLP-1(7-37)-Amide
3231	H[Aib]EGTFTSDVSSYLE[Aib]QAAK EFIAW[BLeu]VKGRK	[Aib^{8,22};BLeu^{32};Lys^{37}]GLP-1 (7-37)-Amide
3232	H[Aib]EGTFTSDVSSYLE[Aib]QAAK EFIAW[aMeLeu]VKGRK	[Aib^{8,22},aMeLeu^{32};Lys^{37}]GLP-1 (7-37)-Amide
3233	H[Aib]EGT[AMEF]TSDVSSYLE[Aib]QAAKEFIAWLVKGRK	[Aib^{8,22};AMEF^{12};Lys^{37}]GLP-1 (7-37)-Amide
3234	H[Aib]EGTFTSD[BLeu]SSYLE[Aib]QAAKEFIAWLVKGRK	[Aib^{8,22};BLeu^{16};Lys^{37}]GLP-1 (7-37)-Amide
3235	H[Aib]EGTFTSDVSSYLE[Aib]QAAK EFIAWLVKGGK	[Aib^{8,22};Gly^{36};Lys^{37}]GLP-1 (7-37)-Amide
3236	H[Aib]EGTFTSDVSSYLE[Aib]QAAK EFIAWLKNGGK	[Aib^{8,22};LyS^{33,37};Asn^{34};Gly^{36}] GLP-1(7-37)-Amide
3237	H[Aib]EGTFTSDVSSYLE[Aib]QAAK EFIAWLKNGG[Aeea]	[Aib^{8,22};Lys^{33};Asn^{34};Gly^{36};Aeea^{37}] GLP-1(7-37)-Aeea-Lys-Amide
3238	H[Aib]EGTFTSDVSSYLE[Aib]QAAK EFIAWLVKGGG	Gly^{36}]GLP-1(7-37)
3239	H[Aib]EGTFTSDVSSYLEGEAAKKFIA WLVKGGG	cyclo[E^{23}-K^{27}][Aib^{8};Gly^{36}]GLP-1 (7-37)
3240	H[Aib]EGTFTSDVSSYLEEQAAKEKFI AWLVKGGK	cyclo[E^{22}-K^{26}][Aib^{8};Gly^{36};Lys^{37}] GLP-1(7-37)-Amide
3241	H[Aib]EGTFTSDVSSYLE[Aib]EAVR LFIEWLKNGGPSSGAPPPS	[Aib^{8,22}]-GLP-1(7-22)-Ex4(17-39)
3242	HGEGTFTSDVSSYLEEQAAKEFIAWLVK GGG	[Gly^{8,36};Glu^{22}]GLP-1(7-37)
3243	H[Aib]EGTFTSDVSSYLEEQAAKEFIA WLVKGGG	[Aib^{8};Glu^{22};Gly^{36}]GLP-1 (7-37)-Amide
3244	H[Aib]EGTFTSDYSSYLEEQAAKEFIA WLVKGGG	[Aib^{8};Tyr^{16};(Glu^{22};Gly^{36}]GLP-1 (7-37)
3245	H[Aib]EGTFTSDVSKYLEEEAVRLFIE WLKNGGG	[Aib^{8};Lys^{18,33};Glu^{22,23,30};Val^{25};Arg ^{26};Leu^{27};Asn^{34};Gly^{36}]GLP-1(7-3 7)
3246	H[Aib]EGTFTSDVSKYLEEEAAKLFIE WLKNGGG	[Aib^{8};Lys^{18,33};Glu^{22,23,30}Leu^{27}; Asn ^{34};Gly^{36}]GLP-1(7-37)
3247	H[Aib]EGTFTSDVSKYLEEEAAKLFIE WLVKGGG	[Aib^{8};Lys^{18};Glu^{22,23,30};Leu^{27}; Gly^{36}] GLP-1(7-37)
3248	H[Aib]IGTFTSDVSSYLE[Aib]QAAK EFIAWLVKGG	[Aib^{8,22};Ile^{9};Gly^{36}]GLP-1_(7-36)

(continued)

SEQ ID NO:	Sequence	Description
3249	H[Aib]EGTFTSEVSSYLE[Aib]QAAK EFIAWLVKGG	[Aib^{8,22};Glu^{15};Gly^{36}]GLP-1_(7-36)
3286	{H2}H[Aib]EGTFTSDVSSYLE[Aib] QAAKEFIAWLKNGG[Aeea][Aeea]K{ CONH2}	
3287	{H2}H[Aib]EGTFTSDVSSYLE[Aib] QAAKEFIAWLVKGGG	
3288	{H2}H[Aib]EGTFTSDVSSYLEGEAAK KFIAWLVKGGG	
3289	{H2}H[Aib]EGTFTSDVSSYLEEQAAK EFIAWLVKGGK{CONH2}	
3290	{H2}H[Aib]EGTFTSDVSSYLE[Aib] EAVRLFIEWLKNGGPSSGAPPPS	
3291	{H2}HGEGTFTSDVSSYLEEQAAKEFIA WLVKGGG	
3292	{H2}H[Aib]EGTFTSDVSSYLEEQAAK EFIAWLVKGGG	
3293	{H2}H[Aib]EGTFTSDYSSYLEEQAAK EFIAWLVKGGG	
3294	{H2}H[Aib]EGTFTSDVSKYLEEEAVR LFIEWLKNGGG	
3295	{H2}H[Aib]EGTFTSDVSKYLEEEAAK LFIEWLKNGGG	
3296	{H2}H[Aib]EGTFTSDVSKYLEEEAAK LFIEWLVKGGG	
3297	{H2}H[Aib]IGTFTSDVSSYLE[Aib] QAAKEFIAWLVKGG	
3298	{H2}H[Aib]EGTFTSEVSSYLE[Aib] QAAKEFIAWLVKGG	
3299	{H2}H[Aib]AGTFTSDVSSYLE[Aib] QAAKEFIAWLVKGG	
3300	{H2}H[Aib]EGTFTSDVSSYLE[Aib] QAAKEFAAWLVKGG	
3301	{H2}H[Aib]EGTFTSDVSSYLE[Aib] QAAKEFIAALVKGG	
3302	{H2}H[Aib]TGTFTSDVSSYLE[Aib] QAAKEFIAWLVKGGG	

(continued)

SEQ ID NO:	Sequence	Description
3303	{H2}H[Aib]EGTFTSEVSSYLE[Aib] QAAKEFIAALVKGGG	
3304	{H2}H[Aib]EGTFTSDVSSYLE[Aib] QAAKEFIAALVKGGG	
3305	{H2}H[Aib]EGTFTSDVSSYLEEEAVR LFIEWLKNGGPSSGAPPPS	
3306	{H2}H[Aib]EGTFTSDYSSYLE[Aib] QAAKEFIAWLVKGGG	
3307	{H2}H[Aib]EGTFTSDVSSYLE[Aib] QAAKEFIAWLVKGGG{CONH2}	
3308	{Dmia}SQGTFTSDYSKYLDERRAKDFV QWLMNT	
3309	{H2}HGEGTFTSDLSKQMEEEAVRLFIE WLKNGGPSSGAPPPS	
AEEA refers to [2-(2-amino)ethoxy)]acetic acid EDA refers to ethylenediamine. MPA refers to maleimidopropionic acid.		

[0316] 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.

[0317] 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.

[0318] 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.

[0319] 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.

[0320] 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.

[0321] 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.

[0322] 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.

[0323] 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.

[0324] 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.*

[0325] 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).

[0326] 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.*, ^{3}H, ^{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.

[0327] 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.

[0328] 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.

[0329] 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.

[0330] 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.

[0331] 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.

[0332] 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.

[0333] 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.

[0334] 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 compostion comprising a GIPR binding protein include rosiglitizone, pioglitizone, repaglinide, nateglitinide, metformin, exenatide, stiagliptin, pramlintide, glipizide, glimepriridеacarbose, and miglitol.

Example 1

Generation of bis-cysteamine-capped anti-GIPR cys mAb (2 g scale)

[0335] The reaction scheme for the generation of anti-GIPR/GLP-1 peptide conjugates is shown in Figure 1. Anti-GIPR monoclonal antibodies with specific cysteine mutation (anti-GIPR cys mAb, 2 g) was incubated with 800 mL solution of 2.5 mM cystamine and 2.5 mM cysteamine in 40 mM HEPES buffer, pH 7.5-8.5 for 15-20 h. The reaction mixture was filtered using 0.22 μm filter, and diluted in 1200 mL of 100 mM sodium acetate buffer pH 5. Cation exchange chromatography was used to purify the bis-cysteamine-capped anti-GIPR cys mAb from the reaction mixture. First, 2 L of reaction mixture diluted in 100 mM sodium acetate buffer pH 5 was loaded onto 240 mL SP HP column at 20 mL/min. The column was washed with 2 column volumes of 100 mM sodium acetate pH 5, followed by a 0-20% gradient of 100 mM sodium acetate with 1.2 M NaCl pH 5. The main peak containing bis-cysteamine-capped anti-GIPR cys mAb was

collected and buffer exchanged to 10 mM sodium acetate with 9% sucrose pH 5.2 using tangential flow filtration.

Example 2

Generation of anti-GIPR/GLP-1 peptide conjugates

[0336] Bis-cysteamine-capped anti-GIPR cys mAb (6 mg/mL in 10 mM sodium acetate with 9% sucrose) was partially reduced using 3-4 equivalents of tris(2-carboxyethyl)phosphine (TCEP) at RT for 60-90 min. TCEP was removed, and partially reduced cys mAb was buffer exchanged to 50 mM sodium phosphate buffer containing 2 mM ethylenediaminetetraacetic acid (EDTA) pH 7.5. To the partially reduced cys mAb was added 6-10 equivalents of dehydroascorbic acid (DHAA), and oxidation was carried out at RT until only trace amount of partially reduced mAb species were observed (30-120 min). Without removing dhAA, 3-8 equivalents of bromoacetyl-GLP-1 peptides was added to the reaction mixture and incubated at RT for 15-20 h. All the reagents were removed, and the anti-GIPR/GLP-1 peptide conjugate product was buffer exchanged to final formulation using spin concentration or tangential flow filtration.

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

Conjugate#	Description	Peptide information	Site/linker	hGLP-1 IC_{50} (nM)	hGIPR IC50 (nM)
3159936#1	5G12-D88C-3156820	[Aib8,Lys26(SGGAcBr)]GLP-1 (7-37)	Lys26/SGG	0.167	81.9
1140-1	5G12-D88C-3156820	[Aib8,Lys26(SGGAcBr)]GLP-1 (7-37)	Lys26/SGG	0.059	101.6
1109-1	5G12-E384C-3156820 DAR1	[Aib8,Lys26(SGGAcBr)]GLP-1 (7-37)	Lys26/SGG	0.622	44.9
1110-1	5G12-E384C-3156820	[Aib8,Lys26(SGGAcBr)]GLP-1 (7-37)	Lys26/SGG	0.159	47.0
1118-1	5G12 SEFL2 D88C-3156820 DAR1	[Aib8,Lys26(SGGAcBr)]GLP-1 (7-37)	Lys26/SGG	0.143	61.2
1135-1	5G12 T487C-3156820	[Aib8,Lys26(SGGAcBr)]GLP-1 (7-37)	Lys26/SGG	0.065	50.6
1143-1	5G12-E384C-3161655	[Aib8,22;Gly36;Lys37(PEG11AcBr)] GLP-1(7-37)-Amide	Lys37/PEG11	0.047	37.0
1144-1	5G12-E384C-3161021	[Aib8,22;Lys36(SGGACBr)]GLP-1 (7-36)-Amide	Lys36/SGG	0.036	37.9
1159-1	5G12-D88C-3166119	[Aib8,22;Gly36]GLP-1(7-37) [GGGGSGGGGSGGGGSK(BrAc)]	C-term/ (GGGGS)3	0.044	152.1
1160-1	5G12-E384C-3166119	[Aib8,22;Gly36]GLP-1(7-37) [GGGGSGGGGSGGGGSK(BrAc)]	C-term/ (GGGGS)3	0.171	43.5
1161-1	5G12-T4874C-3166119	[Aib8,22;Gly36]GLP-1(7-37) [GGGGSGGGGSGGGGSK(BrAc)]	C-term/ (GGGGS)3	0.032	41.3
1163-1	5G12-D88C-3157736	[Aib8;Glu22-Lys26;Gly36]GLP-1(7-37) [GGGGSGGGGSGGGGSK(BrAc)]	C-term/ (GGGGS)3	0.01	275.5
1164-1	5G12-E384C-3157736	[Aib8;Glu22-Lys26;Gly36]GLP-1(7-37) [GGGGSGGGGSGGGGSK(BrAc)]	C-term/ (GGGGS)3	0.053	26.8
1165-1	5G12-T487C-3157736	[Aib8;Glu22-Lys26;Gly36]GLP-1(7-37) [GGGGSGGGGSGGGGSK(BrAc)]	C-term/ (GGGGS)3	0.014	34
1172-1	5G12-E384C-3169019	cyclo[E22-K26][Aib8;Lys(NPeg11-BrAc)37]GLP-1(7-37)-Amide	Lys37/PEG11	0.044	50

(continued)

Conjugate#	Description	Peptide information	Site/linker	hGLP-1 IC_{50} (nM)	hGIPR IC50 (nM)
1198-1	5G12-E384C-3169018	[Aib8,22;Gly36;Lys(NPeg27-BrAc)37] GLP-1(7-37)-Amide	Lys37/PEG27	0.0329	98.5
1199-1	5G12-T487C-3169018	[Aib8,22;Gly36;Lys(NPeg27-BrAc)37] GLP-1(7-37)-Amide	Lys37/PEG27	0.006	84
1200-1	5G12-E384C-3172563	[Aib8;Glu23-Lys27;Gly36]GLP-1(7-37) [GGGGSGGGGSGGGGSK(BrAc)]	C-term/ (GGGGS)3	0.045	40.4
1201-1	5G12-T487C-3172563-DAR2	[Aib8;Glu23-Lys27;Gly36]GLP-1(7-37) [GGGGSGGGGSGGGGSK(BrAc)]	C-term/ (GGGGS)3	0.011	35
1202-1	5G12-T487C-3172563-DAR1	[Aib8;Glu23-Lys27;Gly36]GLP-1(7-37) [GGGGSGGGGSGGGGSK(BrAc)]	C-term/ (GGGGS)3	0.01	30
1203-1	5G12-T487C-3167736-DAR1	[Aib8;Glu22-Lys26;Gly36]GLP-1(7-37) [GGGGSGGGGSGGGGSK(BrAc)]	C-term/ (GGGGS)3	0.0072	45.4
1227-1	5G12-E384C-3173043	[Aib8,22]-GLP-1(7-22)-Ex4(17-39) [GGGGSGGGGSGGGGSK(BrAc)]	C-term/ (GGGGS)3	0.0236	96.5
1228-1	5G12-E384C-3173044	[Aib8,22;Gly36]GLP-1(7-37)-1K2015-Lys(BrAc)	C-term/lKmod	0.0306	103.8
1229-1	5G12-E384C-3340181	Exendin-4(1-39) [GGGGSGGGGSGGGGSK(BrAc)]	C-term/ (GGGGS)3	0.013	84.9
1230-1	5G12-E384C-3340577	[Gly8,36;Glu22]GLP-1(7-37) [GGGGSGGGGSGGGGSK(BrAc)]	C-term/ (GGGGS)3	0.0376	92.2
1231-1	5G12-E384C-3340578	[Aib8;Glu22;Gly36]GLP-1(7-37) [GGGGSGGGGSGGGGSK(BrAc)]	C-term/ (GGGGS)3	0.0297	101.9
1233-1	aGIPR 5G12 E384C Ab-3342048	[Aib8,22;Glu15;Gly36;Lys]GLP-1 (7-37)-(G4S)3K(BrAc)-amide	C-term/ (GGGGS)3	0.118	121
1234-1	aGIPR 5G12 E384C Ab-3341281	[Aib8,22;Gly36]GLP-1(7-37)-(G4S)2K (BrAc)-amide	Lys37(C-term) /(GGGGS)2	0.0446	108
1235-1	aGIPR 5G12 E384C Ab-3341282	[Aib8,22;Gly36]GLP-1(7-37)-AS(AP) 5GSK(BrAc)-amide	C-term/AS (AP)5GS	0.0311	122
1237-1	aGIPR 5G12 SEFL2 E384C-3341284	[Aib8,22;Gly36]GLP-1_(7-37)-Pro-Ser-Ser-Gly-Ala-Pro-Pro-Pro-Ser-(G4S)2K (AcBr)	C-term/ (GGGGS)2	0.0226	83.5
1238-1	aGIPR 5G12 SEFL2 E384C-3341285	[Aib8;Tyr16;Glu22;Gly36]GLP-1_ (7-37)-(G4S)3-K(AcBr)	C-term/ (GGGGS)3	0.0046	82.8
1239-1	aGIPR 6H1 SEFL2 E384C-3166119	[Aib8,22;Gly36]GLP-1(7-37)-G4S3-Lys (BrAc)	C-term/ (GGGGS)3	0.126	34.3
1240-1	aGIPR 5G12 SEFL2 E384C-3342047	[Aib8,22;Ile9;Gly36]GLP-1_ (7-36)-(G4S)3-K(AcBr)	C-term/ (GGGGS)3	0.0552	111

(continued)

Conjugate#	Description	Peptide information	Site/linker	hGLP-1 IC_{50} (nM)	hGlPR IC50 (nM)
1241-1	aGIPR 5G12 SEFL2 E384C-3342049	[Aib8,22;Ala9;Gly36]GLP-1_ (7-36)-(G4S)3-K(AcBr)	C-term/ (GGGGS)3	0.0549	92.3
1242-1	aGIPR 5G12 SEFL2 E384C-3342050	[Aib8,22;Ala29;Gly36]GLP-1_ (7-36)-(G4S)3-K(AcBr)	C-term/ (GGGGS)3	0.173	92.4
1243-1	aGIPR 5G12 SEFL2 E384C-3342051	[Aib8,22;Ala31;Gly36]GLP-1_ (7-36)-(G4S)3-K(AcBr)	C-term/ (GGGGS)3	1.147	75.9
1248-1	aGIPR 2G10 SEFL2 E384C-3166119	[Aib8,22;Gly36]GLP-1(7-37) [GGGGSGGGGSGGGGS(BrAc)]	C-term/ (GGGGS)3	0.015	68.9
1250-1	aGIPR 5G12 SEFL2 E384C-3343106	[Aib8,22;Tbr9;Gly36]GLP-1_ (7-37)-(G4S)3-K(AcBr)	C-term/ (GGGGS)3	0.069	85
1251-1	aGIPR 5G12 SEFL2 E384C-3343109	[Aib8,22;Glu15;Ala31;Gly36]GLP-1_ (7-37)-(G4S)3-K(AcBr)	C-term/ (GGGGS)3	0.32	85
1252-1	aGIPR 5G12 SEFL2 E384C-3343110	[Aib8,22;Ala31;Gly36]GLP-1_ (7-37)-(G4S)3-K(AcBr)	C-term/ (GGGGS)3	0.2	78.8
1253-1	aGIPR 5G12 SEFL2 E384C-3343906	[Aib8,22;LysG4S3G(AcBr)26;Gly36] GLP-1_(7-37)	Lys26/ (GGGGS)3	0.0013	77.4
1253-2	aGIPR 5G12 SEFL2 E384C-3343906	[Aib8,22;LysG4S3G(AcBr)26;Gly36] GLP-1_(7-37)	Lys26/ (GGGGS)3	0.0084	51.4
1254-1	aGIPR 5G12 SEFL2 E384C-3343905	[Aib8,22;Tyr16;Gly36]GLP-1_ (7-37)-(G4S)3-K(AcBr)	C-term/ (GGGGS)3	0.0058	73.8
1255-1	aGIPR 2G10 SEFL2 E384C-3341281	[Aib8,22;Gly36]GLP-1(7-37)-G4S2K (BrAc)	C-term/ (GGGGS)2	0.026	56.4
1256-1	aGIPR 2G10 SEFL2 E384C-3343106	[Aib8,22;Thr9;Gly36]GLP-1 (7-37)-G4S2K(BrAc)	C-term/ (GGGGS)3	0.104	66
1257-1	aGIPR 2G10 SEFL2 E384C-3340578	[Aib8,Glu22;Gly36]GLP-1(7-37)-G4S3-K(BrAc)	C-term/ (GGGGS)3	0.011	66
1258-1	2G10 SEFL2 E384C-3343109	[Aib8,22;Glu15;Ala31;Gly36]GLP-1_ (7-37)-(G4S)3-K(AcBr)	C-term/ (GGGGS)3	3.58	53.9
1261-1	2G10 SEFL2 E384C-3343110	[Aib8,22;Ala31;Gly36]GLP-1_ (7-37)-(G4S)3-K(AcBr)	C-term/ (GGGGS)3	0.096	41.9

(continued)

Conjugate#	Description	Peptide information	Site/linker	hGLP-1 IC_{50} (nM)	hGlPR IC50 (nM)
1262-1	aGIPR 2G10 SEFL2 E384C-3343905	[Aib8,22;Tyr16;Gly36]GLP-1_ (7-37)-(G4S)3-K(AcBr)	C-term/ (GGGGS)3	0.0347	52.9
1263-1	aGIPR 2G10 SEFL2 E384C-3343906	[Aib8,22;LysG4S3G(AcBr)26;Gly36] GLP-1_(7-37)	Lys26/ (GGGGS)3	0.0143	48.7
1264-1	2G10 SEFL2 E384C-3344713	[Aib8,22;Glu15;Gly36]GLP-1_ (7-37)-(G4S)3-K(AcBr)	C-term/ (GGGGS)3	0.0459	48.6
1264-2	2G10 SEFL2 E384C-3344713	[Aib8,22;Glu15;Gly36]GLP-1_ (7-37)-(G4S)3-K(AcBr)	C-term/ (GGGGS)3	0.112	40.3
1265-1	2G10 SEFL2 E384C-3344748	[Aib8,22;Tyr16;Gly36]GLP-1_ (7-37)-(GGGGSGG)-K(AcBr)	C-term/ GGGGSGG	0.0439	50.4
1265-2	2G10 SEFL2 E384C-3344748	[Aib8,22;Tyr16;Gly36]GLP-1_ (7-37)-(GGGGSGG)-K(AcBr)	C-term/ GGGGSGG	0.177	50.4
1267-1	aGIPR 2G10 SEFL2 E384C-3169019	cyclo[E22-K26][Aib8;(NPeg11-BrAc)37] GLP-1(7-37)-Amide	Lys37/PEG11	0.004	49.3
1269-1	aGIPR 5G12 SEFL2-E384C-3344713	[Aib8,22;Glu15;Gly36]GLP-1_ (7-37)-(G4S)3-K(AcBr)	C-term/ (GGGGS)3	0.0169	57.4
1270-1	aGIPR 5G12 SEFL2-E384C-3344748	[Aib8,22;Tyr16;Gly36]GLP-1_ (7-37)-(GGGGSGG)-K(AcBr)	C-term/ (GGGGS)3	0.0298	50.9
1272-1	aGIPR 2G10 SEFL2-E384C-3161655	[Aib8,22;Gly36]GLP-1_(7-37)-PEG11-AcBr	Lys37/PEG11	0.055	53
1273-1	aGIPR 2G10 SEFL2-E384C-3341285	[Aib8;Tyr16;Glu22;Gly36]GLP-1_ (7-37)-(GGGGSGG)-K(AcBr)	C-term/ (GGGGS)3	0.061	42.3
1274-1	aGIPR 2G10 SEFL2-E384C-3345837	[Aib8,22]-GLP-1(7-22)-Ex4 (17-39)-(G4S)K-BrAc	C-term/ (GGGGS)	0.199	36.4
1281-1	aGIPR 2G10 SEFL2-E384C-3345836	[Aib8,22]-GLP-1(7-22)-Ex4 (17-39)-(G4S)2K-BrAc	C-term/ (GGGGS)2	0.177	47.9
1282-1	aGIPR 2G10 SEFL2-E384C-3173043	[Aib8,22]-GLP-1(7-22)-Ex4 (17-39)-(G4S)3K-BrAc	C-term/ (GGGGS)3	0.094	43.9
1283-1	aGIPR 5G12 SEFL2-E384C-3345836	[Aib8,22]-GLP-1(7-22)-Ex4 (17-39)-(G4S)2K-BrAc	C-term/ (GGGGS)2	0.139	67.8
1284-1	aGIPR 5G12 SEFL2-E384C-3345837	[Aib8,22]-GLP-1(7-22)-Ex4 (17-39)-(G4S)K-BrAc	C-term/ (GGGGS)	0.154	63.8

Example 3

Methods for In vitro and in vivo assay

GLP-1 receptor agonist activity

[0337] CHOK1 cells stably expressing the human GLP-1R alone or both GLP-1R and GIPR (M1) were used to measure peptide/conjugate-induced cAMP production in a homogeneous time-resolved fluorescence (HTRF) assay (CISBIO, cat# 62AM4PEJ). Serial diluted peptides/conjugates (3×10^{-7} M - 3×10^{-14} M) were incubated with 40,000 cells in assay buffer (0.1% BSA, 500 uM IBMX in F12 media) for 15 min at 37°C. Cells were then lysed with lysis buffer containing cAMP-d2 and cAMP cryptate (CISBIO) and incubated for 1 hour at room temperature before measured in Evision plate reader (PerkinElmer). The cAMP levels are expressed as a fluorescence ratio of 665/620 nm and shown in Figures 2A-2E and Figure 3.

Example 4

GIPR antagonist activity

[0338] HEK 293T cells stably expressing the human GIPR were used to measure peptide/conjugate-induced cAMP generation in HTRF assay (Cisbio, cat# 62AM4PEJ). Serial diluted conjugates or GIPR antibody (3×10^{-6} M - 1×10^{-11} M) were incubated with 30,000 cells in assay buffer (0.1% BSA, 500 uM IBMX in F12 media) for 30 min at 37°C before being treated with GIP at final concentration of 0.05 nM. Cells were incubated for 30 min at 37°C and then lysed in lysis buffer containing cAMP-d2 and cAMP cryptate (CISBIO) for 1 hour at room temperature. The fluorescence was measured in Evision plate reader (PerkinElmer) and the cAMP levels are expressed as a ratio of 665/620 nm and shown in Figures 2A-2E and Figure.

Example 5

Materials and Methods for Bispecific-mouse *in vivo*

[0339] Diabetic mice were selected primarily to screen for GLP-1 activity of the bispecific molecules. Molecules were selected based on their potential to reduce plasma glucose levels at different time points post injection. In addition, body weight loss or inhibition of body weight gain was also measured indicative of GLP-1 activity, GIPR inhibition, or a combination of both, either from co-administration of each or from the bispecific molecule as shown in Figures 4A-4I. Male db/db mice (#642) were obtained from Jackson Laboratories (Bar Harbor, ME) and delivered at 8-9 weeks of age. Upon arrival, mice were group-housed at four per cage and maintained in controlled environmental conditions with 12 hour light (6:30 AM - 6:30 PM) and dark cycles (6:30 PM - 6:30 AM). Mice were fed a standard rodent chow diet (2020x Harlan Teklad) with free-access to drinking water.

[0340] In other studies, glucose tolerance test was used to rank the potency of GLP-1 analogs (Figures 5A-5C). C57Bl6 mice were acclimated to environment conditions for one to two weeks. Prior to dosing, mice were handled and body weight measurements were taken. One day prior to dosing, conscious mice were bled from the retro-orbital sinus for plasma glucose measurement using a handheld glucometer designed for rodent plasma. On the day of dosing, baseline plasma glucose and body weight measurements were taken. The cage mean for plasma glucose and body weight were used to stratify cages into treatment groups. Mice were maintained in their home cages. Following administration of test article, plasma glucose was measured at various time points at (1, 3, and 6hr) or (4hr) and plasma glucose and body weight measurements were taken every 24hrs thereafter. Plasma glucose levels were measured until levels returned to near baseline levels and body weight measurements were taken until the rate of body weight gain was similar to Vehicle-treated control group.

[0341] Diet-induced obese mice (DIO) were also used as a model to measure weight loss effects from treatment with different molecules as shown in Figure 6.

[0342] Male c57bl6 mice were obtained from Harlan Laboratories and delivered at 26 days of age. Mice were group-housed with littermates consisting between two to four mice per cage. Following one week of acclimation, mice were started on a feeding regimen of high-fat diet (HFD: D12492, Research Diets, New Brunswick, NJ) or continued on standard rodent diet (2020x, Harlan Laboratories). After 12 weeks of feeding, single-housed mice were acclimated to routine handling, food intake measurement, and daily saline injections (IP). Blood was collected from the retro orbital sinus of conscious DIO mice. A small volume of blood was immediately placed on a handheld glucometer designed for rodent plasma and the remaining blood was placed in EDTA filled collection tubes with a protease-inhibitor cocktail (Roche Diagnostics, Indianapolis, IN). Following centrifugation, plasma was stored at -80C. Mice were stratified into

treatment groups based on body weight, and plasma glucose measurements. Mice were treated with Vehicle (Q3D), GIPR Ab (2.5 or 10 mg/kg, Q3D), GLP-1 Peptide (0.06 mg/kg, QD), Dulaglutide (1 mg/kg, Q3D), or bispecific conjugate (2.5 or 10 mg/kg, Q3D). 2 additional groups of mice received a combination treatment of GLP-1 and GIPR Ab with the above dosage and dose frequency (GIPR 2.5 mg/kg + GLP-1 Peptide and GIPR 2.5 mg/kg + Dulaglutide). Aside from the GLP-1 Peptide dosed groups, all other mice were injected with saline when not dosed with their respective test article. Body weight was measured daily and cumulative food intake over three days was averaged for a daily food intake value. Food intake was measured between study days 0-3 and days 6-9. A blood collection was taken on study Day 9, 1 hour post injection and a terminal blood collection was taken on study Day 12, 1 or 3 days post the previous test article injection.

[0343] Plasma insulin was measured with a mouse ELISA kit following manufacturer's instructions (ALPCO, Salem, NH). Plasma glucose, cholesterol, triglyceride, non-esterified fatty acids, AST, and ALT were measured using an Olympus AU400e Chemistry Analyzer (Olympus America, Center Valley, PA).

Example 6

Materials and Methods for Bispecific-cyno *in vivo*

[0344] Naive male spontaneously obese cynomolgus monkeys (age 9-14 years) were acclimated/trained to experimental procedures prior to study initiation and were sorted into 7 treatment groups with n=10 monkeys each with equal distribution among groups for all sorting parameters (body weight and blood chemistries). Monkeys were then injected once weekly for 6 weeks with vehicle or GLP-1R-GIPR conjugates (1264, 1273, 1248 or 1257). After the 6 week treatment period, monkeys went through a 4 week washout phase. During training/treatment/washout phases of study, total energy intake was monitored daily; body weight, blood chemistries and drug exposure were monitored weekly or every other week as shown in Figures 7-21.

Example 7

Materials and Methods for GIP and GLP-1 Radioligand Competition Binding Assay

[0345] Membranes were prepared from mammalian cell lines overexpressing hu GIPR and hu GLP-1R and were typically stored at -80°C in Assay Buffer: 50 mM HEPES (7.4), 5 mM $MgCl_2$, 1mM $CaCl_2$, 0.2% BSA and Protease Inhibitor Tablets "EDTA Free". Unlabeled GIP and GLP-1 peptides were obtained from Phoenix Pharmaceuticals and Radiolabeled ^{125}I-GIP and ^{125}I-GLP-1 were ordered from Perkin Elmer. Primary reactions were conducted for 2h at room temperature with shaking in 96 well cell culture round bottom plates (Costar). Cell membrane concentration was fixed at 0.6 mg/mL and radioligands were used at a concentration of 0.1 nM. Test articles were titrated at six concentrations in duplicate. The primary plate was harvested after two hours with ice cold 50 mM TRIS (pH 7.4) using a Filtermate Harvester (Perkin Elmer) and cell membranes were captured on PEI-treated GF/C UniFilter plates (Perkin Elmer). Plates were dried for 15 min using a vacuum oven and Microscint 20 was added to each well before counting in a Perkin Elmer TopCount NXT HTS instrument. Specific binding was determined by taking the difference of total and non-specific counts. Non-specific wells contained 1 μM cold ligand. Data was analyzed and plotted using GraphPad Prism 7 as shown in Figure 22.

Example 8

Internalization assay

[0346] GLP-1R and GIPR internalization were assessed in CHOK1 cells expressing both human GLP-1R and GIPR. Cells were plated at a density of 25,000 cells/well in 96 well plates and cultured overnight at 37°C, 5% CO_2. Cells were serum starved in F12 media (Thermo Fisher) with 0.1% BSA for 4 hours prior to treatment. Cells were treated with 20nM or dose titrations of GLP-1, GIP or bispecific conjugates for 30minutes or the specified time in the respective figures. Cells were washed and fixed with 4% formaldehyde and permeabilized with 0.1% triton-X 100. To detect GIPR or GLP-1R, cells were first blocked with Odyssey blocking buffer (LiCor) for 1 hour at room temperature and incubated with 2μg/ml of mouse anti-human GLP-1R (R&D systems) or 5μg/ml of anti-human GIPR antibody (R&D Systems) at 4°C overnight followed by AlexaFluor-555 or Alexa-Fluor 647 conjugated anti-mouse secondary antibody (Thermo Fisher) for GLP-1R or GIPR detection, respectively. Images (Figure 23) were captured using Operetta high content Imaging system (Perkin Elmer) and analyzed by using the Harmony software (Perkin Elmer) to quantify the intracellular GLP-1R content (total spot area) as the readout parameter for the degree of internalization (Figure 24).

Example 9

GLP-1R, GIPR and bispecific conjugate are co-localized upon internalization

[0347] U2OS cells expressing GIPR and SNAP-GLP-1R were plated at a density of 15,000 cells per well in 96 well plate and cultured overnight at 37°C with 5% CO_2. Prior to treatment, cells were starved for 3.5 hours in McCoy's 5A media (Thermo Fisher) with 0.1% BSA. Prior to treatment, GLP-1R on the surface of U2OS cells were labeled with Alexa-Fluor 564 by incubating with SNAP-Surface Alexa-fluor 564 substrate (New England Biolabs) for 30 minutes. Cells were then washed to remove excess label and treated with 5nM bispecific conjugates for 30 minutes. After 3 washes, cells were fixed with 4% formaldehyde and permeabilized with 0.1% triton-X 100 in PBS. For GIPR detection, cells were first blocked with Odyssey blocking buffer (LiCor) for 1 hour at room temperature and then incubated with 5μg/ml of mouse anti-human GIPR (R&D Systems) at 4°C overnight followed by incubation with Alexa-Fluor 647 conjugated anti-mouse secondary antibody (Thermo Fisher) for 1 hour at room temperature. Bispecific conjugate was detected using Alexa-Fluor labeled anti-Human Fc antibody. Hoechst 33342 were used for nuclei detection (Thermo Fisher). Images were captured using Operetta CLS high content Imaging system (Perkin Elmer) as shown in Figure 25.

Example 10

GloSensor cAMP assay

[0348] The GloSensor cAMP assay was conducted per manufacturer's protocol (Promega). In brief, ChoK1 human GLP-1R/GIPR-expressing cells were seeded at 15,000 cells per well in a 96 well plate and incubated for 16 hours in a humidified 37°C, 5% CO_2 incubator. Cells were transiently transfected with 100 ng pGloSensor -22F cAMP plasmid using FuGENE HD for 24 hours. Cells were then equilibrated with 0.1% BSA, 2% GloSensor cAMP reagent in CO_2 independent media (Invitrogen) for 2 hours at room temperature. Cells were preincubated for 15 min with or without 0.43 M sucrose (Sigma). Basal luminescence measurements were taken for 10 minutes prior to addition of 1248 in conditions with or without sucrose. Immediately following addition of 1248, kinetic luminescence was measured using an integration time of 0.1-1 second every 60 seconds. Data were analyzed using GraphPad Prism software and presented in Figure 26.

Example 11

FACS analysis

[0349] CHOK1-GLP-1R H20, 293T-GIPR clone 10 and CHOK1-GLP-1R/GIPR cells were suspended at a density of 1×10^6 cells in 100ul of F12 assay media containing 1% FBS, 0.05% sodium azide and incubated with 10ug/ml of indicated antibodies or anti-GIPR/GLP-1R bispecific conjugates for 1 hr at 4°C. Cells were washed one time with assay buffer and then incubated with 10ug/ml of Alexa Fluor 647-goat anti-human Fc (Jackson) for 30min at 4°C. The Fluorescence was measured using BD LSR II Flow Cytometer (BD Biosciences) and shown in Figure 27.

Example 12

Calcium flux assay

[0350] CHOK1 cells expressing GIPR and GLP-1-R were plated at a density of 30,000 cells per well in 96 well black clear bottom plate and cultured overnight at 37°C with 5% CO_2. Cells were serum starved in F12 media (Thermo Fisher) with 20mM HEPES for 2 hours. Cells were then loaded with buffer containing the calcium-sensitive dye (BD Biosciences) and incubated for 1 hour at room temperature before being treated with dose titrations of GLP-1 or bispecific conjugates. Changes in intracellular calcium content were monitored for using a FLIPR (Molecular Devices). Maximum peak height in each well was recorded as representing calcium influx as shown in Figure 28.

Example 13

Beta- arrestin assay

[0351] CHOK1 Pathhunter cells expressing ProLink™ tagged GLP-1R and GIPR from DiscoverX were transfected with un-tagged GIPR or GLP-1R, respectively. Cells were plated at a density of 20,000 cells per well in assay media (F12/0.1%BSA) and incubated at 37°C overnight. Cells were treated with dose titrations of GLP-1, GIP or bispecific conjugates for 90 minutes. The working detection solution (DiscoverX) were then added to the cells and incubated for

60 min at room temp in the dark. Chemiluminescent signal representing beta-arrestin recruitments were measured using Envision and shown in Figure 29.

Example 14

Human pancreatic islet microtissues glucose stimulated insulin secretion (GSIS) assay

[0352] Human pancreatic islet microtissues were purchased from InSphero in 96 well format. Microtissues were incubated for 16 hours in InSphero assay media. They were then treated for 1 hour with fresh KREBS buffer (129 mM NaCl, 4.8 mM KCl, 1.2 mM KH_2PO_4, 1.2 mM $MgSO_4$-$7H_2O$, 10 mM HEPES, 1.3 mM $CaCl_2$, 0.5% BSA, pH 7.4) with 2.8 mM glucose. Following 2 KREBS buffer washes, they were then incubated with KREBS buffer alone, 2.8 mM or 11 mM glucose in KREBS buffer with or without GLP-1 (Phoenix Pharmaceuticals) and a dose response of 1248 for 16 hours. Supernatant was collected and analyzed for insulin secretion according to manufacturer's protocol (Mercodia). Optical density was read at 450 nm on a TECAN microplate reader and shown in Figure 30.

REFERENCES CITED IN THE DESCRIPTION

Cited references

This list of references cited by the applicant is for the reader's convenience only. It does not form part of the European patent document. Even though great care has been taken in compiling the references, errors or omissions cannot be excluded and the EPO disclaims all liability in this regard.

Patent documents cited in the description

- WO8801649A [0069]
- US4946778A [0069]
- US5260203A [0069]
- US7045337B [0146]
- US4816567A [0171]
- US6180370B [0171]
- US5693762A [0171] [0173]
- US5693761A [0171]
- US5585089A [0171] [0173]
- US5530101A [0171]
- WO9633735A [0177]
- WO9402602A [0177]
- US5545807A [0177] [0177] [0178]
- US6713610B [0177]
- US6673986B [0177]
- US6162963A [0177]
- US6300129B [0177]
- US6255458B [0177]
- US5877397A [0177] [0178]
- US5874299A [0177] [0178]
- US5545806A [0177] [0178]
- WO9110741A [0177]
- WO9004036A [0177]
- EP546073B1 [0177]
- EP546073A1 [0177]
- US5569825A [0178]
- US5625126A [0178]
- US5633425A [0178]
- US5789650A [0178]
- US5661016A [0178]
- US5814318A [0178]
- US5770429A [0178]
- WO931227A [0178]
- WO9222646A [0178]
- WO9203918A [0178]
- WO9824893A [0178]
- WO9910494A [0180]
- US5011912A [0201]
- WO9215673A [0207]
- WO9507463A [0207]
- WO9814605A [0207]
- WO9826277A [0207]
- WO9949019A [0207]
- US5292658A [0207]
- US5418155A [0207]
- US5683888A [0207]
- US5741668A [0207]
- US5777079A [0207]
- US5804387A [0207]
- US5874304A [0207]
- US5876995A [0207]
- US5925558A [0207]
- US4399216A [0220]
- US4912040A [0220]

- US4740461A [0220]
- US4959455A [0220]
- US6270964B [0221]
- US4965195A [0235]
- EP0367566A [0235]
- US4968607A [0235]
- EP0460846A [0235]
- US94001875W [0248]
- US9300829W [0250]
- US3773919A [0250]
- EP058481A [0250]
- EP133988A [0250]
- EP036676A [0250]
- EP088046A [0250]
- EP143949A [0250]
- WO2005102293A [0277] [0316]
- WO9805351A [0282]
- WO9907404A [0282]
- WO9925727A [0282]
- WO9925728A [0282]
- WO9940788A [0282]
- WO0041546A [0282]
- WO0041548A [0282]
- WO0073331A [0282]
- WO0151078A [0282]
- WO03099314A [0282]
- US6956026B [0282]
- US6506724B [0282]
- US6703359B [0282]
- US6858576B [0282]
- US6872700B [0282]
- US6902744B [0282]
- US7157555B [0282]
- US7223725B [0282]
- US7220721B [0282]
- US20030036504A [0282]
- US20060094652A [0282]
- US7521423B [0316] [0321]
- US7456254B [0316] [0321]
- WO2000037098A [0316]
- WO2005021022A [0316]
- WO2006068910A [0316] [0321]
- WO2006125763A [0316] [0321]
- WO2009068910A [0316]
- US20040106547A [0316] [0321]

Non-patent literature cited in the description

- INAGAKI et al.Mol Endocrinol, 1989, vol. 3, 1014-1021 [0002]
- FEHMANN et al.Endocr Rev., 1995, vol. 16, 390-410 [0002]
- NAUCK et al.J. Cline. Invest., 1993, vol. 91, 301-307 [0003]
- USDIN et al.Endocrinology., 1993, vol. 133, 2861-2870 [0004]
- GREMLICH et al.Diabetes., 1995, vol. 44, 1202-8 [0004]

- VOLZ et al.FEBS Lett., 1995, vol. 373, 23-29 [0004] [0098]
- YAMADA et al.Diabetes, 2006, vol. 55, S86- [0005]
- MIYAWAKI et al.Nature Med., 2002, vol. 8, 738-742 [0005]
- 44th EASD Annual meeting posterDiabetologia, 2008, vol. 51, S373 [0005]
- Diabetes, 2004, vol. 53, S3205-214 [0007]
- Diabetes Care, 2003, vol. 26, 102929-2940 [0007]
- Endocrinology., 1993, vol. 133, 41907-10 [0007]
- Bioorg. Med. Chem.Lett, 2013, vol. 23, 4011-4018 [0007]
- PETER RAVN et al.Structural and pharmacological characterization of novel potent and selective monoclonal antibody antagonists of glucose-dependent insulinotropic polypeptide receptorThe Journal of Biological Chemistry, 2013, vol. 288, 27 [0008]
- SULEIMAN AL-SABAHMolecular Pharmacology of the Incretin ReceptorsMedical Principles and Practice, 2015, vol. 25, 1 [0009]
- PAULA L. MCCLEAN et al.GIP receptor antagonism reverses obesity, insulin resistance, and associated metabolic disturbances induced in mice by prolonged consumption of high-fat dietAmerican Journal of Physiology: Endocrinology and Metabolism, 2007, vol. 293, [0010]
- DOMINIK SCHUMACHER et al.Current Status: Site-Specific Antibody Drug ConjugatesJournal of Clinical immunology, 2016, vol. 36, 1 [0011]
- CHRISTOPHER R BEHRENSBIN LIUMethods for site-specific drug conjugation to antibodiesMABS, 2014, vol. 6, 1 [0012]
- JAMIE T. LEWIS et al.Glucose dependent Insulinotropic Polypeptide Confers Early Phase Insulin Release to Oral Glucose in Rats: Demonstration by a Receptor AntagonistEndocrinology, 2000, vol. 141, 10 [0013]
- SAMBROOK et al.Molecular Cloning: A Laboratory ManualCold Spring Harbor Laboratory Press19890000 [0024]
- Current Protocols in Molecular BiologyGreen Publishers Inc. and Wiley and Sons19940000 [0024]
- SAMBROOK et al.Molecular Cloning: A Laboratory ManualCold Spring Harbor Laboratory Press20010000 [0027]
- AUSUBEL et al.Current Protocols in Molecular BiologyGreene Publishing Associates19920000 [0027]
- HARLOWLANEAntibodies: A Laboratory ManualCold Spring Harbor Laboratory Press19900000 [0027]
- Computational Molecular BiologyOxford University Press19880000 [0039]
- Biocomputing Informatics and Genome ProjectsAcademic Press19930000 [0039]
- Computer Analysis of Sequence DataHumana Press19940000 [0039]
- VON HEINJE, G.Sequence Analysis in Molecular BiologyAcademic Press19870000 [0039]
- Sequence Analysis PrimerStockton Press19910000 [0039]
- CARILLO et al.SIAM J. Applied Math.19880000vol. 48, 1073- [0039]
- DEVEREUX et al.Nucl. Acid Res., 1984, vol. 12, 387- [0040]
- MADISON, WIGenetics Computer GroupUniversity of Wisconsin [0040]
- DAYHOFF et al.Atlas of Protein Sequence and Structure, 1978, vol. 5, 345-352 [0040]
- HENIKOFF et al.Proc. Natl. Acad. Sci. U.S.A., 1992, vol. 89, 10915-10919 [0040]
- NEEDLEMAN et al.J. Mol. Biol., 1970, vol. 48, 443-453 [0041]
- Biochemical and Biophysical Research Communications, 2002, vol. 290, 1420-1426 [0046] [0046]
- Biochimica et Biophysica Acta, 2001, vol. 1547, 143-155 [0047]
- SONGSIVILAILACHMANNClin. Exp. Immunol., 1990, vol. 79, 315-321 [0073]
- KOSTELNY et al.J. Immunol., 1992, vol. 148, 1547-1553 [0073]
- STAHLI et al.Methods in Enzymology, 1983, vol. 9, 242-253 [0074]
- KIRKLAND et al.J. Immunol., 1986, vol. 137, 3614-3619 [0074]
- HARLOWLANEAntibodies, A Laboratory ManualCold Spring Harbor Press19880000 [0074]
- MOREL et al.Molec. Immunol., 1988, vol. 25, 7-15 [0074]
- CHEUNG et al.Virology, 1990, vol. 176, 546-552 [0074]
- MOLDENHAUER et al.Scand. J. Immunol., 1990, vol. 32, 77-82 [0074]
- GREMLICH et al.Diabetes, 1995, vol. 44, 1202-8 [0100]
- VASSILATIS et al.PNAS USA, 2003, vol. 100, 4903-4908 [0101]
- GERHARD et al.Genome Res, 2004, vol. 14, 2121-2127 [0102]
- CREIGHTONPROTEINS: STRUCTURE AND MOLECULAR PROPERTIESW.H. Freeman and Company.19840000 [0106]
- SAMBROOK, J.FRITSH, E. F.MANIATIS, T.Molecular Cloning: A Laboratory ManualCold Spring Harbor Laboratory Press19890000 [0110]
- VAN HEEKESCHUSTERJ. Biol. Chem., 1989, vol. 264, 5503-5509 [0112]

- BOOTCOV MRProc. Natl. Acad. Sci. USA, 1997, vol. 94, 11514-9 [0119]
- FAIRLIE WDGene, 2000, vol. 254, 67-76 [0119]
- Fundamental ImmunologyRaven Press19890000 [0133]
- KABATSequences of Proteins of Immunological InterestNIH, Bethesda19870000 [0134]
- CHOTHIALESKJ. Mol. Biol.19870000vol. 196, 901-917 [0134]
- CHOTHIA et al.Nature, 1989, vol. 342, 878-883 [0134]
- BONG et al.Chemoselective Pd(0)-catalyzed peptide coupling in waterOrganic Letters, 2001, vol. 3, 162509-11 [0143]
- DIBOWSKI et al.Bioconjugation of peptides by palladium-catalyzed C-C cross-coupling in waterAngew. Chem. Int. Ed., 1998, vol. 37, 4476-78 [0143]
- DEVASHER et al.Aqueous-phase, palladium-catalyzed cross-coupling of aryl bromides under mild conditions, using water-soluble, sterically demanding alkylphosphinesJ. Org. Chem., 2004, vol. 69, 7919-27 [0143]
- SHAUGNESSY et al.J.Org. Chem, 2003, vol. 68, 6767-6774 [0143]
- Chemistry in living systemPRESCHER, JABERTOZZI CRNature Chemical Biology120050000vol. 1, 13-21 [0143]
- LINK et al.Non-canonical amino acids in protein engineeringCurrent Opinion in Biotechnology, 2003, vol. 14, 6603-609 [0146]
- KABAT et al.Sequences of Proteins of Immunological InterestUS Dept. of Health and Human Services, PHS, NIH, NIH Publication19910000 [0155]
- KABAT et al.Sequences of Proteins of Immunological InterestPublic Health Service N.I.H.19910000 [0156]
- CHOTHIALESKJ. Mol. Biol., 1987, vol. 196, 901-917 [0156]
- CHOTHIA et al.Nature, 1989, vol. 342, 877-883 [0156]
- Proc. Natl. Acad. Sci. USA, vol. 81, 6851-6855 [0171]
- JONES et al.Nature, 1986, vol. 321, 522-525 [0173]
- RIECHMANN et al.Nature, 1988, vol. 332, 323-27 [0173]
- VERHOEYEN et al.Science, 1988, vol. 239, 1534-1536 [0173]
- JAKOBOVITS et al.Proc. Natl. Acad. Sci. USA, 1993, vol. 90, 2551-2555 [0177]
- JAKOBOVITS et al.Nature, 1993, vol. 362, 255-258 [0177]
- BRUGGERMANN et al.Year in Immunol., 1993, vol. 7, 33- [0177]
- LONBERG et al.Nature, 1994, vol. 368, 856-859 [0178] [0178]
- LONBERGHUSZARIntern. Rev. Immunol., 1995, vol. 13, 65-93 [0178] [0178]
- HARDINGLONBERGAnn. N.YAcad. Sci., 1995, vol. 764, 536-546 [0178] [0178]
- TAYLOR et al.Nucleic Acids Research, 1992, vol. 20, 6287-6295 [0178]
- CHEN et al.International Immunology, 1993, vol. 5, 647-656 [0178]
- TUAILLON et al.J. Immunol., 1994, vol. 152, 2912-2920 [0178]
- LONBERGHandbook of Exp. Pharmacology, 1994, vol. 113, 49-101 [0178]
- TAYLOR et al.International Immunology, 1994, vol. 6, 579-591 [0178]
- FISHWILD et al.Nature Biotechnology, 1996, vol. 14, 845-851 [0178]
- MENDEZ et al.Nature Genetics, 1997, vol. 15, 146-156 [0178]
- HOOGENBOOM et al.J. Mol. Biol., 1991, vol. 227, 381- [0180]
- MARKS et al.J. Mol. Biol., 1991, vol. 222, 581- [0180]
- KYTE et al.J. Mol. Biol., 1982, vol. 157, 105-131 [0187]
- MOULTCurr. Op. in Biotech., 1996, vol. 7, 422-427 [0194]
- CHOU et al.Biochem., 1974, vol. 13, 222-245 [0194]
- CHOU et al.Biochemistry, 1974, vol. 113, 211-222 [0194]
- CHOU et al.Adv. Enzymol. Relat. Areas Mol. Biol., 1978, vol. 47, 45-148 [0194]
- CHOU et al.Ann. Rev. Biochem., 1979, vol. 47, 251-267 [0194]
- CHOU et al.Biophys. J., 1979, vol. 26, 367-384 [0194]
- HOLM et al.Nucl. Acid. Res., 1999, vol. 27, 244-247 [0194]
- BRENNER et al.Curr. Op. Struct. Biol., 1997, vol. 7, 369-376 [0194]
- JONESCurr. Opin. Struct. Biol., 1997, vol. 7, 377-387 [0195]
- SIPPL et al.Structure, 1996, vol. 4, 15-19 [0195]
- BOWIE et al.Science, 1991, vol. 253, 164-170 [0195]
- GRIBSKOV et al.Meth. Enzym., 1990, vol. 183, 146-159 [0195]
- GRIBSKOV et al.Proc. Nat. Acad. Sci., 1987, vol. 84, 4355-4358 [0195]
- Proteins, Structures and Molecular PrinciplesFreeman and Company19840000 [0196]
- Introduction to Protein StructureGarland Publishing19910000 [0196]

- THORNTON et al.Nature19910000vol. 354, 105- [0196]
- FAUCHEREAdv. Drug Res., 1986, vol. 15, 29 [0199]
- VEBERFREIDINGERTINS, 1985, 392- [0199]
- EVANS et al.J. Med. Chem., 1987, vol. 30, 1229- [0199]
- RIZOGIERASCHAnn. Rev. Biochem., 1992, vol. 61, 387- [0199]
- HOPP et al.Bio/Technology, 1988, vol. 6, 1204- [0201]
- CHALFIE et al.Science, 1994, vol. 263, 802-805 [0207]
- STAUBERBiotechniques, 1998, vol. 24, 462-471 [0207]
- HEIM et al.Curr. Biol., 1996, vol. 6, 178-182 [0207]
- ICHIKI et al.J. Immunol., 1993, vol. 150, 5408-5417 [0207]
- NOLAN et al.Proc. Natl. Acad. Sci. U.S.A., 1988, vol. 85, 2603-2607 [0207]
- Current Protocols in Molecular BiologyJohn Wiley & Sons19890000 [0210]
- SAMBROOKFRITSCHMANIATISMolecular Cloning: A Laboratory ManualCold Spring Harbor Laboratory Press20010000 [0211]
- Current Protocols in Molecular BiologyJohn Wiley & Sons, Inc.19950000 [0211]
- VOSS et al.Trends Biochem. Sci., 1986, vol. 11, 287- [0216]
- MANIATIS et al.Science, 1987, vol. 236, 1237- [0216]
- Monoclonal Antibodies, Hybridomas: A New Dimension in Biological AnalysesPlenum Press19800000 [0219]
- Antibodies: A Laboratory ManualCold Spring Harbor Laboratory Press19880000 [0219]
- BIANCHIMCGREWBiotech. Biotechnol. Bioeng., 2003, vol. 84, 439-44 [0221]
- Methods Enzymol.Academic Press19900000vol. 185, [0221]
- COSMAN et al.Nature, 1984, vol. 312, 768- [0235]
- REMINGTON'S PHARMACEUTICAL SCIENCESMack Publishing Company19900000 [0243]
- SIDMAN et al.Biopolymers, 1983, vol. 2, 547-556 [0250]
- LANGER et al.J. Biomed. Mater. Res., 1981, vol. 15, 167-277 [0250]
- LANGERChem. Tech., 1982, vol. 12, 98-105 [0250]
- EPPSTEIN et al.Proc. Natl. Acad. Sci. U.S.A., 1985, vol. 82, 3688-3692 [0250]
- NIELSEN et al.Current Opinion in Investigational Drugs, 2003, vol. 4, 4401-405 [0276]
- HARGROVE et al.Regulatory Peptides,, 2007, vol. 141, 113-119 [0278]
- HARGROVE et al.Regulatory Peptides, 2007, vol. 141, 113-119 [0283]
- BHATNAGAR et al.J. Med. Chem., 1996, vol. 39, 3814-3819 [0294]
- CREIGHTONProteins: Structure and Molecule PropertiesW. H. Freeman & Co.1983000079-86 [0295]
- TIJSSENPractice and Theory of Enzyme ImmunoassaysElsevier19930000vol. 15, [0324]
- ZOLAMonoclonal Antibodies: A Manual of Techniques,CRC Press, Inc19870000147-158 [0324]
- JALKANEN et al.J. Cell. Biol., 1985, vol. 101, 976-985 [0324]
- JALKANEN et al.J. Cell Biol., 1987, vol. 105, 3087-3096 [0324]
- HARLOWLANEAntibodies: A Laboratory Manual,Cold Spring Harbor19880000 [0327]
- Current Protocols In ImmunologyJohn Wiley & Sons19930000 [0327]
- American Diabetes AssociationDiabetes Care, 2010, vol. 34, 1S11-S61 [0329]

Patentkrav

1. Sammensætning, som omfatter
a) et antistof eller et funktionelt fragment deraf, der specifikt binder til human GIPR, hvor antistoffet eller det funktionelle fragment deraf omfatter en cystein eller ikke-kanonisk aminosyresubstitution i et eller flere konjugationssted(er); og
b) en GLP-1-receptoragonist, hvor GLP-1-receptoragonisten er konjugeret til antistoffet eller det funktionelle fragment deraf via sidekæden på cysteinresten eller den ikke-kanoniske aminosyrerest, der er substitueret i det ene eller de flere konjugationssted(er),
hvor antistoffet eller det funktionelle fragment deraf er en antagonist for GIPR.

2. Sammensætning ifølge krav 1, hvor den humane GIPR har en sekvens, der omfatter en sekvens valgt fra gruppen, der består af SEQ ID NO: 3141, SEQ ID NO: 3143 og SEQ ID NO: 3145.

3. Sammensætning ifølge krav 1 eller 2, hvor antistoffet er et monoklonalt antistof, et rekombinant antistof, et humant antistof, et humaniseret antistof, et kimært antistof eller et multispecifikt antistof, eller hvor det funktionelle fragment er et funktionelt fragment af et monoklonalt antistof, et rekombinant antistof, et humant antistof, et humaniseret antistof, et kimært antistof eller et multispecifikt antistof.

4. Sammensætning ifølge krav 3, hvor antistoffragmentet er et Fab-fragment, et Fab'-fragment, eller et F(ab')2-fragment,
hvor antistoffet eller det funktionelle fragment deraf er et humant antistof,
hvor antistoffet eller det funktionelle fragment deraf er et monoklonalt antistof,
hvor antistoffet eller det funktionelle fragment deraf er af IgG1-, IgG2- IgG3- eller IgG4-typen,
hvor fortrinsvis antistoffet eller det funktionelle fragment deraf er af IgG1- eller the IgG2-typen, eller

hvor antistoffet eller det funktionelle fragment deraf hæmmer binding af GIP til den extracellulære del af human GIPR.

5. Sammensætning ifølge krav 3, hvor antistoffet omfatter en CDRL1, en CDRL2, en CDRL3, en CDRH1, en CDRH2 og en CDRH3, hvor CDRL1 omfatter en sekvens valgt fra gruppen, der består af SEQ ID NO: 629-785; CDRL2 omfatter en sekvens valgt fra gruppen, der består af SEQ ID NO: 786-942; CDRL3 omfatter en sekvens valgt fra gruppen, der består af SEQ ID NO: 943-1099; CDRH1 omfatter en sekvens valgt fra gruppen, der består af SEQ ID NO: 1100-1256; CDRH2 omfatter en sekvens valgt fra gruppen, der består af SEQ ID NO: 1257-1413; og CDRH3 omfatter en sekvens valgt fra gruppen, der består af SEQ ID NO: 1414-1570, hvor
antistoffet eller det funktionelle fragment deraf omfatter en cystein eller ikke-kanonisk aminosyresubstitution i et eller flere konjugationssted(er) valgt fra gruppen, der består af
D70 i antistoffets lette kæde i forhold til referencesekvens SEQ ID NO: 455,
E276 i antistoffets tunge kæde i forhold til referencesekvens SEQ ID NO: 612 og
T363 i antistoffets tunge kæde i forhold til referencesekvens SEQ ID NO: 612.

6. Sammensætning ifølge krav 3, hvor antistoffet omfatter en CDRL1, en CDRL2, en CDRL3, en CDRH1, en CDRH2 og en CDRH3, og hvor kombinationen af CDRL1, CDRL2, CDRL3, CDRH1, CDRH2 og CDRH3 er valgt fra gruppen af kombinationer, der består af:

Kombination	CDRL1 (SEQ ID NO)	CDRL2 (SEQ ID NO)	CDRL3 (SEQ ID NO)	CDRH1 (SEQ ID NO)	CDRH2 (SEQ ID NO)	CDRH3 (SEQ ID NO)
2C2.005	629	786	943	1100	1257	1414
4B1	630	787	944	1101	1258	1415
6H1	631	788	945	1102	1259	1416
2F11	632	789	946	1103	1260	1417
5C2	633	790	947	1104	1261	1418
13H12	634	791	948	1105	1262	1419

Kombination	CDRL1 (SEQ ID NO)	CDRL2 (SEQ ID NO)	CDRL3 (SEQ ID NO)	CDRH1 (SEQ ID NO)	CDRH2 (SEQ ID NO)	CDRH3 (SEQ ID NO)
11C1	635	792	949	1106	1263	1420
12H11	636	793	950	1107	1264	1421
18E3	637	794	951	1108	1265	1422
2G10_LC1	638	795	952	1109	1266	1423
4H9.004	639	796	953	1110	1267	1424
6A5.004	640	797	954	1111	1268	1425
17H11.004	641	798	955	1112	1269	1426
17H11.004.001	642	799	956	1113	1270	1427
4H9.004.001	643	800	957	1114	1271	1428
4H9.004.002	644	801	958	1115	1272	1429
4H9.004.003	645	802	959	1116	1273	1430
4H9.004.004	646	803	960	1117	1274	1431
4H9.004.005	647	804	961	1118	1275	1432
4H9.004.006	648	805	962	1119	1276	1433
4B1.010	649	806	963	1120	1277	1434
4B1.011	650	807	964	1121	1278	1435
4B1.012	651	808	965	1122	1279	1436
4B1.013	652	809	966	1123	1280	1437
4B1.014	653	810	967	1124	1281	1438
4B1.015	654	811	968	1125	1282	1439
4B1.016	655	812	969	1126	1283	1440
18F2	656	813	970	1127	1284	1441
18F2.002	657	814	971	1128	1285	1442
18F2.003	658	815	972	1129	1286	1443
18F2.004	659	816	973	1130	1287	1444
18F2.005	660	817	974	1131	1288	1445

Kombination	CDRL1 (SEQ ID NO)	CDRL2 (SEQ ID NO)	CDRL3 (SEQ ID NO)	CDRH1 (SEQ ID NO)	CDRH2 (SEQ ID NO)	CDRH3 (SEQ ID NO)
18F2.006	661	818	975	1132	1289	1446
18F2.007	662	819	976	1133	1290	1447
18F2.008	663	820	977	1134	1291	1448
18F2.009	664	821	978	1135	1292	1449
18F2.010	665	822	979	1136	1293	1450
18F2.011	666	823	980	1137	1294	1451
18F2.012	667	824	981	1138	1295	1452
2F11.002	668	825	982	1139	1296	1453
2F11.003	669	826	983	1140	1297	1454
2F11.004	670	827	984	1141	1298	1455
2F11.005	671	828	985	1142	1299	1456
2F11.006	672	829	986	1143	1300	1457
2F11.007	673	830	987	1144	1301	1458
2F11.008	674	831	988	1145	1302	1459
2F11.009	675	832	989	1146	1303	1460
2F11.010	676	833	990	1147	1304	1461
6H1.002	677	834	991	1148	1305	1462
6H1.003	678	835	992	1149	1306	1463
6H1.004	679	836	993	1150	1307	1464
6H1.005	680	837	994	1151	1308	1465
6H1.006	681	838	995	1152	1309	1466
6H1.007	682	839	996	1153	1310	1467
6H1.008	683	840	997	1154	1311	1468
6A5.004.001	684	841	998	1155	1312	1469
6A5.004.002	685	842	999	1156	1313	1470
6A5.004.003	686	843	1000	1157	1314	1471

Kombination	CDRL1 (SEQ ID NO)	CDRL2 (SEQ ID NO)	CDRL3 (SEQ ID NO)	CDRH1 (SEQ ID NO)	CDRH2 (SEQ ID NO)	CDRH3 (SEQ ID NO)
6A5.004.004	687	844	1001	1158	1315	1472
6A5.004.005	688	845	1002	1159	1316	1473
6A5.004.006	689	846	1003	1160	1317	1474
6A5.004.007	690	847	1004	1161	1318	1475
6A5.004.008	691	848	1005	1162	1319	1476
6A5.004.009	692	849	1006	1163	1320	1477
6A5.004.010	693	850	1007	1164	1321	1478
6A5.004.011	694	851	1008	1165	1322	1479
2A11.002	695	852	1009	1166	1323	1480
2A11.003	696	853	1010	1167	1324	1481
2A11.004	697	854	1011	1168	1325	1482
2A11.005	698	855	1012	1169	1326	1483
2G10_LC1.003	699	856	1013	1170	1327	1484
2G10_LC1.004	700	857	1014	1171	1328	1485
2G10_LC1.005	701	858	1015	1172	1329	1486
2G10_LC1.006	702	859	1016	1173	1330	1487
2G10_LC1.007	703	860	1017	1174	1331	1488
2G10_LC1.008	704	861	1018	1175	1332	1489
2G10_LC1.009	705	862	1019	1176	1333	1490
2G10_LC1.010	706	863	1020	1177	1334	1491
18E3.002	707	864	1021	1178	1335	1492
18E3.003	708	865	1022	1179	1336	1493
18E3.004	709	866	1023	1180	1337	1494
18E3.005	710	867	1024	1181	1338	1495
18E3.006	711	868	1025	1182	1339	1496
18E3.007	712	869	1026	1183	1340	1497

Kombination	CDRL1 (SEQ ID NO)	CDRL2 (SEQ ID NO)	CDRL3 (SEQ ID NO)	CDRH1 (SEQ ID NO)	CDRH2 (SEQ ID NO)	CDRH3 (SEQ ID NO)
18E3.008	713	870	1027	1184	1341	1498
5C2.006	714	871	1028	1185	1342	1499
5C2.007	715	872	1029	1186	1343	1500
5C2.008	716	873	1030	1187	1344	1501
5C2.009	717	874	1031	1188	1345	1502
5C2.010	718	875	1032	1189	1346	1503
5C2.011	719	876	1033	1190	1347	1504
5C2.012	720	877	1034	1191	1348	1505
5C2.013	721	878	1035	1192	1349	1506
5C2.014	722	879	1036	1193	1350	1507
5C2.015	723	880	1037	1194	1351	1508
5C2.016	724	881	1038	1195	1352	1509
11C1.002	725	882	1039	1196	1353	1510
11C1.003	726	883	1040	1197	1354	1511
11C1.004	727	884	1041	1198	1355	1512
11C1.005	728	885	1042	1199	1356	1513
11C1.006	729	886	1043	1200	1357	1514
11C1.007	730	887	1044	1201	1358	1515
11C1.008	731	888	1045	1202	1359	1516
11C1.009	732	889	1046	1203	1360	1517
11C1.010	733	890	1047	1204	1361	1518
13H12.002	734	891	1048	1205	1362	1519
13H12.003	735	892	1049	1206	1363	1520
13H12.004	736	893	1050	1207	1364	1521
13H12.005	737	894	1051	1208	1365	1522
13H12.006	738	895	1052	1209	1366	1523

Kombination	CDRL1 (SEQ ID NO)	CDRL2 (SEQ ID NO)	CDRL3 (SEQ ID NO)	CDRH1 (SEQ ID NO)	CDRH2 (SEQ ID NO)	CDRH3 (SEQ ID NO)
12H11.002	739	896	1053	1210	1367	1524
12H11.003	740	897	1054	1211	1368	1525
12H11.004	741	898	1055	1212	1369	1526
12H11.005	742	899	1056	1213	1370	1527
12H11.006	743	900	1057	1214	1371	1528
12H11.007	744	901	1058	1215	1372	1529
12H11.008	745	902	1059	1216	1373	1530
12H11.009	746	903	1060	1217	1374	1531
12H11.010	747	904	1061	1218	1375	1532
12H11.011	748	905	1062	1219	1376	1533
12H11.012	749	906	1063	1220	1377	1534
12H11.013	750	907	1064	1221	1378	1535
12H11.014	751	908	1065	1222	1379	1536
2C2.005.001	752	909	1066	1223	1380	1537
2C2.005.002	753	910	1067	1224	1381	1538
2C2.005.003	754	911	1068	1225	1382	1539
2C2.005.004	755	912	1069	1226	1383	1540
2C2.005.005	756	913	1070	1227	1384	1541
2C2.005.006	757	914	1071	1228	1385	1542
2C2.005.007	758	915	1072	1229	1386	1543
2C2.005.008	759	916	1073	1230	1387	1544
2C2.005.009	760	917	1074	1231	1388	1545
2C2.005.010	761	918	1075	1232	1389	1546
2C2.005.011	762	919	1076	1233	1390	1547
2C2.005.012	763	920	1077	1234	1391	1548
2C2.005.013	764	921	1078	1235	1392	1549

Kombination	CDRL1 (SEQ ID NO)	CDRL2 (SEQ ID NO)	CDRL3 (SEQ ID NO)	CDRH1 (SEQ ID NO)	CDRH2 (SEQ ID NO)	CDRH3 (SEQ ID NO)
2C2.005.014	765	922	1079	1236	1393	1550
18F2.013	766	923	1080	1237	1394	1551
6H1.009	767	924	1081	1238	1395	1552
2C2.005.015	768	925	1082	1239	1396	1553
5G12.006	769	926	1083	1240	1397	1554
17B11.002	770	927	1084	1241	1398	1555
5G12.006.001	771	928	1085	1242	1399	1556
5G12.006.002	772	929	1086	1243	1400	1557
5G12.006.003	773	930	1087	1244	1401	1558
5G12.006.004	774	931	1088	1245	1402	1559
5G12.006.005	775	932	1089	1246	1403	1560
5G12.006.006	776	933	1090	1247	1404	1561
17B11.002.001	777	934	1091	1248	1405	1562
17B11.002.002	778	935	1092	1249	1406	1563
17B11.002.003	779	936	1093	1250	1407	1564
17B11.002.004	780	937	1094	1251	1408	1565
17B11.002.005	781	938	1095	1252	1409	1566
17B11.002.006	782	939	1096	1253	1410	1567
17B11.002.007	783	940	1097	1254	1411	1568
17B11.002.008	784	941	1098	1255	1412	1569
5G12.005.001	785	942	1099	1256	1413	1570

hvor

antistoffet eller det funktionelle fragment deraf omfatter en cystein eller ikke-kanonisk aminosyresubstitution i et eller flere konjugationssted(er) valgt fra gruppen, der består af

D70 i antistoffets lette kæde i forhold til referencesekvens SEQ ID NO: 455,

E276 i antistoffets tunge kæde i forhold til referencesekvens

SEQ ID NO: 612 og
T363 i antistoffets tunge kæde i forhold til referencesekvens SEQ ID NO: 612.

7. Sammensætning ifølge krav 3, hvor antistoffet eller fragmentet deraf omfatter en variabel region af let kæde, der omfatter en sekvens valgt fra gruppen, der består af SEQ ID NO: 1-157, og en variabel region af tung kæde, der omfatter en sekvens valgt fra gruppen, der består af SEQ ID NO: 158-314, hvor
antistoffet eller det funktionelle fragment deraf omfatter en cystein eller ikke-kanonisk aminosyresubstitution i et eller flere konjugationssted(er) valgt fra gruppen, der består af
D70 i antistoffets lette kæde i forhold til referencesekvens SEQ ID NO: 455,
E276 i antistoffets tunge kæde i forhold til referencesekvens SEQ ID NO: 612 og
T363 i antistoffets tunge kæde i forhold til referencesekvens SEQ ID NO: 612.

8. Sammensætning ifølge krav 3, hvor antistoffet eller fragmentet deraf omfatter en kombination af en variabel region af let kæde og en variabel region af tung kæde valgt fra gruppen, der består af en variabel region af let kæde, der omfatter SEQ ID NO: 1, og en variabel region af tung kæde, der omfatter SEQ ID NO: 158; en variabel region af let kæde, der omfatter SEQ ID NO: 2, og en variabel region af tung kæde, der omfatter SEQ ID NO: 159; en variabel region af let kæde, der omfatter SEQ ID NO: 3, og en variabel region af tung kæde, der omfatter SEQ ID NO: 160; en variabel region af let kæde, der omfatter SEQ ID NO: 4, og en variabel region af tung kæde, der omfatter SEQ ID NO: 161; en variabel region af let kæde, der omfatter SEQ ID NO: 5, og en variabel region af tung kæde, der omfatter SEQ ID NO: 162; en variabel region af let kæde, der omfatter SEQ ID NO: 6, og en variabel region af tung kæde, der omfatter SEQ ID NO: 163; en variabel region af let kæde, der omfatter SEQ ID NO: 7, og en variabel region af tung kæde, der omfatter SEQ ID NO: 164; en variabel region af let kæde, der omfatter SEQ ID NO: 8, og

en variabel region af tung kæde, der omfatter SEQ ID NO: 165;
en variabel region af let kæde, der omfatter SEQ ID NO: 9, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 166;
en variabel region af let kæde, der omfatter SEQ ID NO: 10, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 167;
en variabel region af let kæde, der omfatter SEQ ID NO: 11, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 168;
en variabel region af let kæde, der omfatter SEQ ID NO: 12, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 169;
en variabel region af let kæde, der omfatter SEQ ID NO: 13, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 170;
en variabel region af let kæde, der omfatter SEQ ID NO: 14, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 171;
en variabel region af let kæde, der omfatter SEQ ID NO: 15, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 172;
en variabel region af let kæde, der omfatter SEQ ID NO: 16, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 173;
en variabel region af let kæde, der omfatter SEQ ID NO: 17, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 174;
en variabel region af let kæde, der omfatter SEQ ID NO: 18, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 175;
en variabel region af let kæde, der omfatter SEQ ID NO: 19, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 176;
en variabel region af let kæde, der omfatter SEQ ID NO: 20, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 177;
en variabel region af let kæde, der omfatter SEQ ID NO: 21, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 178;
en variabel region af let kæde, der omfatter SEQ ID NO: 22, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 179;
en variabel region af let kæde, der omfatter SEQ ID NO: 23, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 180;
en variabel region af let kæde, der omfatter SEQ ID NO: 24, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 181;
en variabel region af let kæde, der omfatter SEQ ID NO: 25, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 182;
en variabel region af let kæde, der omfatter SEQ ID NO: 26, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 183;
en variabel region af let kæde, der omfatter SEQ ID NO: 27, og

en variabel region af tung kæde, der omfatter SEQ ID NO: 184;
en variabel region af let kæde, der omfatter SEQ ID NO: 28, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 185;
en variabel region af let kæde, der omfatter SEQ ID NO: 29, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 186;
en variabel region af let kæde, der omfatter SEQ ID NO: 30, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 187;
en variabel region af let kæde, der omfatter SEQ ID NO: 31, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 188;
en variabel region af let kæde, der omfatter SEQ ID NO: 32, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 189;
en variabel region af let kæde, der omfatter SEQ ID NO: 33, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 190;
en variabel region af let kæde, der omfatter SEQ ID NO: 34, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 191;
en variabel region af let kæde, der omfatter SEQ ID NO: 35, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 192;
en variabel region af let kæde, der omfatter SEQ ID NO: 36, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 193;
en variabel region af let kæde, der omfatter SEQ ID NO: 37, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 194;
en variabel region af let kæde, der omfatter SEQ ID NO: 38, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 195;
en variabel region af let kæde, der omfatter SEQ ID NO: 39, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 196;
en variabel region af let kæde, der omfatter SEQ ID NO: 40, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 197;
en variabel region af let kæde, der omfatter SEQ ID NO: 41, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 198;
en variabel region af let kæde, der omfatter SEQ ID NO: 42, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 199;
en variabel region af let kæde, der omfatter SEQ ID NO: 43, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 200;
en variabel region af let kæde, der omfatter SEQ ID NO: 44, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 201;
en variabel region af let kæde, der omfatter SEQ ID NO: 45, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 202;
en variabel region af let kæde, der omfatter SEQ ID NO: 46, og

en variabel region af tung kæde, der omfatter SEQ ID NO: 203;
en variabel region af let kæde, der omfatter SEQ ID NO: 47, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 204;
en variabel region af let kæde, der omfatter SEQ ID NO: 48, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 205;
en variabel region af let kæde, der omfatter SEQ ID NO: 49, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 206;
en variabel region af let kæde, der omfatter SEQ ID NO: 50, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 207;
en variabel region af let kæde, der omfatter SEQ ID NO: 51, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 208;
en variabel region af let kæde, der omfatter SEQ ID NO: 52, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 209;
en variabel region af let kæde, der omfatter SEQ ID NO: 53, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 210;
en variabel region af let kæde, der omfatter SEQ ID NO: 54, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 211;
en variabel region af let kæde, der omfatter SEQ ID NO: 55, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 212;
en variabel region af let kæde, der omfatter SEQ ID NO: 56, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 213;
en variabel region af let kæde, der omfatter SEQ ID NO: 57, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 214;
en variabel region af let kæde, der omfatter SEQ ID NO: 58, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 215;
en variabel region af let kæde, der omfatter SEQ ID NO: 59, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 216;
en variabel region af let kæde, der omfatter SEQ ID NO: 60, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 217;
en variabel region af let kæde, der omfatter SEQ ID NO: 61, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 218;
en variabel region af let kæde, der omfatter SEQ ID NO: 62, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 219;
en variabel region af let kæde, der omfatter SEQ ID NO: 63, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 220;
en variabel region af let kæde, der omfatter SEQ ID NO: 64, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 221;
en variabel region af let kæde, der omfatter SEQ ID NO: 65, og

en variabel region af tung kæde, der omfatter SEQ ID NO: 222;
en variabel region af let kæde, der omfatter SEQ ID NO: 66, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 223;
en variabel region af let kæde, der omfatter SEQ ID NO: 67, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 224;
en variabel region af let kæde, der omfatter SEQ ID NO: 68, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 225;
en variabel region af let kæde, der omfatter SEQ ID NO: 69, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 226;
en variabel region af let kæde, der omfatter SEQ ID NO: 70, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 227;
en variabel region af let kæde, der omfatter SEQ ID NO: 71, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 228;
en variabel region af let kæde, der omfatter SEQ ID NO: 72, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 229;
en variabel region af let kæde, der omfatter SEQ ID NO: 73, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 230;
en variabel region af let kæde, der omfatter SEQ ID NO: 74, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 231;
en variabel region af let kæde, der omfatter SEQ ID NO: 75, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 232;
en variabel region af let kæde, der omfatter SEQ ID NO: 76, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 233;
en variabel region af let kæde, der omfatter SEQ ID NO: 77, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 234;
en variabel region af let kæde, der omfatter SEQ ID NO: 78, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 235;
en variabel region af let kæde, der omfatter SEQ ID NO: 79, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 236;
en variabel region af let kæde, der omfatter SEQ ID NO: 80, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 237;
en variabel region af let kæde, der omfatter SEQ ID NO: 81, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 238;
en variabel region af let kæde, der omfatter SEQ ID NO: 82, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 239;
en variabel region af let kæde, der omfatter SEQ ID NO: 83, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 240;
en variabel region af let kæde, der omfatter SEQ ID NO: 84, og

en variabel region af tung kæde, der omfatter SEQ ID NO: 241;
en variabel region af let kæde, der omfatter SEQ ID NO: 85, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 242;
en variabel region af let kæde, der omfatter SEQ ID NO: 86, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 243;
en variabel region af let kæde, der omfatter SEQ ID NO: 87, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 244;
en variabel region af let kæde, der omfatter SEQ ID NO: 88, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 245;
en variabel region af let kæde, der omfatter SEQ ID NO: 89, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 246;
en variabel region af let kæde, der omfatter SEQ ID NO: 90, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 247;
en variabel region af let kæde, der omfatter SEQ ID NO: 91, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 248;
en variabel region af let kæde, der omfatter SEQ ID NO: 92, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 249;
en variabel region af let kæde, der omfatter SEQ ID NO: 93, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 250;
en variabel region af let kæde, der omfatter SEQ ID NO: 94, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 251;
en variabel region af let kæde, der omfatter SEQ ID NO: 95, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 252;
en variabel region af let kæde, der omfatter SEQ ID NO: 96, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 253;
en variabel region af let kæde, der omfatter SEQ ID NO: 97, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 254;
en variabel region af let kæde, der omfatter SEQ ID NO: 98, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 255;
en variabel region af let kæde, der omfatter SEQ ID NO: 99, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 256;
en variabel region af let kæde, der omfatter SEQ ID NO: 100, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 257;
en variabel region af let kæde, der omfatter SEQ ID NO: 101, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 258;
en variabel region af let kæde, der omfatter SEQ ID NO: 102, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 259;
en variabel region af let kæde, der omfatter SEQ ID NO: 103, og

en variabel region af tung kæde, der omfatter SEQ ID NO: 260;
en variabel region af let kæde, der omfatter SEQ ID NO: 104, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 261;
en variabel region af let kæde, der omfatter SEQ ID NO: 105, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 262;
en variabel region af let kæde, der omfatter SEQ ID NO: 106, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 263;
en variabel region af let kæde, der omfatter SEQ ID NO: 107, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 264;
en variabel region af let kæde, der omfatter SEQ ID NO: 108, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 265;
en variabel region af let kæde, der omfatter SEQ ID NO: 109, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 266;
en variabel region af let kæde, der omfatter SEQ ID NO: 110, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 267;
en variabel region af let kæde, der omfatter SEQ ID NO: 111, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 268;
en variabel region af let kæde, der omfatter SEQ ID NO: 112, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 269;
en variabel region af let kæde, der omfatter SEQ ID NO: 113, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 270;
en variabel region af let kæde, der omfatter SEQ ID NO: 114, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 271;
en variabel region af let kæde, der omfatter SEQ ID NO: 115, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 272;
en variabel region af let kæde, der omfatter SEQ ID NO: 116, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 273;
en variabel region af let kæde, der omfatter SEQ ID NO: 117, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 274;
en variabel region af let kæde, der omfatter SEQ ID NO: 118, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 275;
en variabel region af let kæde, der omfatter SEQ ID NO: 119, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 276;
en variabel region af let kæde, der omfatter SEQ ID NO: 120, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 277;
en variabel region af let kæde, der omfatter SEQ ID NO: 121, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 278;
en variabel region af let kæde, der omfatter SEQ ID NO: 122, og

en variabel region af tung kæde, der omfatter SEQ ID NO: 279;
en variabel region af let kæde, der omfatter SEQ ID NO: 123, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 280;
en variabel region af let kæde, der omfatter SEQ ID NO: 124, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 281;
en variabel region af let kæde, der omfatter SEQ ID NO: 125, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 282;
en variabel region af let kæde, der omfatter SEQ ID NO: 126, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 283;
en variabel region af let kæde, der omfatter SEQ ID NO: 127, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 284;
en variabel region af let kæde, der omfatter SEQ ID NO: 128, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 285;
en variabel region af let kæde, der omfatter SEQ ID NO: 129, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 286;
en variabel region af let kæde, der omfatter SEQ ID NO: 130, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 287;
en variabel region af let kæde, der omfatter SEQ ID NO: 131, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 288;
en variabel region af let kæde, der omfatter SEQ ID NO: 132, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 289;
en variabel region af let kæde, der omfatter SEQ ID NO: 133, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 290;
en variabel region af let kæde, der omfatter SEQ ID NO: 134, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 291;
en variabel region af let kæde, der omfatter SEQ ID NO: 135, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 292;
en variabel region af let kæde, der omfatter SEQ ID NO: 136, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 293;
en variabel region af let kæde, der omfatter SEQ ID NO: 137, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 294;
en variabel region af let kæde, der omfatter SEQ ID NO: 138, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 295;
en variabel region af let kæde, der omfatter SEQ ID NO: 139, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 296;
en variabel region af let kæde, der omfatter SEQ ID NO: 140, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 297;
en variabel region af let kæde, der omfatter SEQ ID NO: 141, og

en variabel region af tung kæde, der omfatter SEQ ID NO: 298;
en variabel region af let kæde, der omfatter SEQ ID NO: 142, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 299;
en variabel region af let kæde, der omfatter SEQ ID NO: 143, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 300;
en variabel region af let kæde, der omfatter SEQ ID NO: 144, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 301;
en variabel region af let kæde, der omfatter SEQ ID NO: 145, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 302;
en variabel region af let kæde, der omfatter SEQ ID NO: 146, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 303;
en variabel region af let kæde, der omfatter SEQ ID NO: 147, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 304;
en variabel region af let kæde, der omfatter SEQ ID NO: 148, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 305;
en variabel region af let kæde, der omfatter SEQ ID NO: 149, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 306;
en variabel region af let kæde, der omfatter SEQ ID NO: 150, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 307;
en variabel region af let kæde, der omfatter SEQ ID NO: 151, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 308;
en variabel region af let kæde, der omfatter SEQ ID NO: 152, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 309;
en variabel region af let kæde, der omfatter SEQ ID NO: 153, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 310;
en variabel region af let kæde, der omfatter SEQ ID NO: 154, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 311;
en variabel region af let kæde, der omfatter SEQ ID NO: 155, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 312;
en variabel region af let kæde, der omfatter SEQ ID NO: 156, og
en variabel region af tung kæde, der omfatter SEQ ID NO: 313;,
og en variabel region af let kæde, der omfatter SEQ ID NO: 157,
og en variabel region af tung kæde, der omfatter SEQ ID NO: 314,
hvor
antistoffet eller det funktionelle fragment deraf omfatter en cystein eller ikke-kanonisk aminosyresubstitution i et eller flere konjugationssted(er) valgt fra gruppen, der består af D70 i antistoffets lette kæde i forhold til referencesekvens SEQ

ID NO: 455,
E276 i antistoffets tunge kæde i forhold til referencesekvens SEQ ID NO: 612 og
T363 i antistoffets tunge kæde i forhold til referencesekvens SEQ ID NO: 612.

9. Sammensætning ifølge krav 3, hvor antistoffet eller det funktionelle fragment deraf er et antistof, hvor antistoffet omfatter en let kæde, der omfatter en sekvens valgt fra gruppen, der består af SEQ ID NO: 315-471, og en tung kæde, der omfatter en sekvens valgt fra gruppen, der består af SEQ ID NO: 472-628, hvor
antistoffet eller det funktionelle fragment deraf omfatter en cystein eller ikke-kanonisk aminosyresubstitution i et eller flere konjugationssted(er) valgt fra gruppen, der består af
D70 i antistoffets lette kæde i forhold til referencesekvens SEQ ID NO: 455,
E276 i antistoffets tunge kæde i forhold til referencesekvens SEQ ID NO: 612 og
T363 i antistoffets tunge kæde i forhold til referencesekvens SEQ ID NO: 612.

10. Sammensætning ifølge krav 3, hvor antistoffet eller det funktionelle fragment deraf er et antistof, hvor antistoffet omfatter en kombination af en let kæde og en tung kæde valgt fra gruppen, der består af en let kæde, der omfatter SEQ ID NO: 315, og en tung kæde, der omfatter SEQ ID NO: 472; en let kæde, der omfatter SEQ ID NO: 316, og en tung kæde, der omfatter SEQ ID NO: 473; en let kæde, der omfatter SEQ ID NO: 317, og en tung kæde, der omfatter SEQ ID NO: 474; en let kæde, der omfatter SEQ ID NO: 318, og en tung kæde, der omfatter SEQ ID NO: 475; en let kæde, der omfatter SEQ ID NO: 319, og en tung kæde, der omfatter SEQ ID NO: 476; en let kæde, der omfatter SEQ ID NO: 320, og en tung kæde, der omfatter SEQ ID NO: 477; en let kæde, der omfatter SEQ ID NO: 321, og en tung kæde, der omfatter SEQ ID NO: 478; en let kæde, der omfatter SEQ ID NO: 322, og en tung kæde, der omfatter SEQ ID NO: 479; en let kæde, der omfatter SEQ ID NO: 323, og en tung kæde, der omfatter SEQ ID NO: 480; en let kæde,

der omfatter SEQ ID NO: 324, og en tung kæde, der omfatter SEQ ID NO: 481; en let kæde, der omfatter SEQ ID NO: 325, og en tung kæde, der omfatter SEQ ID NO: 482; en let kæde, der omfatter SEQ ID NO: 326, og en tung kæde, der omfatter SEQ ID NO: 483; en let kæde, der omfatter SEQ ID NO: 327, og en tung kæde, der omfatter SEQ ID NO: 484; en let kæde, der omfatter SEQ ID NO: 328, og en tung kæde, der omfatter SEQ ID NO: 485; en let kæde, der omfatter SEQ ID NO: 329, og en tung kæde, der omfatter SEQ ID NO: 486; en let kæde, der omfatter SEQ ID NO: 330, og en tung kæde, der omfatter SEQ ID NO: 487; en let kæde, der omfatter SEQ ID NO: 331, og en tung kæde, der omfatter SEQ ID NO: 488; en let kæde, der omfatter SEQ ID NO: 332, og en tung kæde, der omfatter SEQ ID NO: 489; en let kæde, der omfatter SEQ ID NO: 333, og en tung kæde, der omfatter SEQ ID NO: 490; en let kæde, der omfatter SEQ ID NO: 334, og en tung kæde, der omfatter SEQ ID NO: 491; en let kæde, der omfatter SEQ ID NO: 335, og en tung kæde, der omfatter SEQ ID NO: 492; en let kæde, der omfatter SEQ ID NO: 336, og en tung kæde, der omfatter SEQ ID NO: 493; en let kæde, der omfatter SEQ ID NO: 337, og en tung kæde, der omfatter SEQ ID NO: 494; en let kæde, der omfatter SEQ ID NO: 338, og en tung kæde, der omfatter SEQ ID NO: 495; en let kæde, der omfatter SEQ ID NO: 339, og en tung kæde, der omfatter SEQ ID NO: 496; en let kæde, der omfatter SEQ ID NO: 340, og en tung kæde, der omfatter SEQ ID NO: 497; en let kæde, der omfatter SEQ ID NO: 341, og en tung kæde, der omfatter SEQ ID NO: 498; en let kæde, der omfatter SEQ ID NO: 342, og en tung kæde, der omfatter SEQ ID NO: 499; en let kæde, der omfatter SEQ ID NO: 343, og en tung kæde, der omfatter SEQ ID NO: 500; en let kæde, der omfatter SEQ ID NO: 344, og en tung kæde, der omfatter SEQ ID NO: 501; en let kæde, der omfatter SEQ ID NO: 345, og en tung kæde, der omfatter SEQ ID NO: 502; en let kæde, der omfatter SEQ ID NO: 346, og en tung kæde, der omfatter SEQ ID NO: 503; en let kæde, der omfatter SEQ ID NO: 347, og en tung kæde, der omfatter SEQ ID NO: 504; en let kæde, der omfatter SEQ ID NO: 348, og en tung kæde, der omfatter SEQ ID NO: 505; en let kæde, der omfatter SEQ ID NO: 349, og en tung kæde, der omfatter SEQ ID NO: 506; en let kæde, der omfatter SEQ ID NO: 350, og en tung kæde, der omfatter SEQ ID NO: 507; en let kæde, der omfatter SEQ ID NO: 351, og en tung kæde, der omfatter

SEQ ID NO: 508; en let kæde, der omfatter SEQ ID NO: 352, og en tung kæde, der omfatter SEQ ID NO: 509; en let kæde, der omfatter SEQ ID NO: 353, og en tung kæde, der omfatter SEQ ID NO: 510; en let kæde, der omfatter SEQ ID NO: 354, og en tung kæde, der omfatter SEQ ID NO: 511; en let kæde, der omfatter SEQ ID NO: 355, og en tung kæde, der omfatter SEQ ID NO: 512; en let kæde, der omfatter SEQ ID NO: 356, og en tung kæde, der omfatter SEQ ID NO: 513; en let kæde, der omfatter SEQ ID NO: 357, og en tung kæde, der omfatter SEQ ID NO: 514; en let kæde, der omfatter SEQ ID NO: 358, og en tung kæde, der omfatter SEQ ID NO: 515; en let kæde, der omfatter SEQ ID NO: 359, og en tung kæde, der omfatter SEQ ID NO: 516; en let kæde, der omfatter SEQ ID NO: 360, og en tung kæde, der omfatter SEQ ID NO: 517; en let kæde, der omfatter SEQ ID NO: 361, og en tung kæde, der omfatter SEQ ID NO: 518; en let kæde, der omfatter SEQ ID NO: 362, og en tung kæde, der omfatter SEQ ID NO: 519; en let kæde, der omfatter SEQ ID NO: 363, og en tung kæde, der omfatter SEQ ID NO: 520; en let kæde, der omfatter SEQ ID NO: 364, og en tung kæde, der omfatter SEQ ID NO: 521; en let kæde, der omfatter SEQ ID NO: 365, og en tung kæde, der omfatter SEQ ID NO: 522; en let kæde, der omfatter SEQ ID NO: 366, og en tung kæde, der omfatter SEQ ID NO: 523; en let kæde, der omfatter SEQ ID NO: 367, og en tung kæde, der omfatter SEQ ID NO: 524; en let kæde, der omfatter SEQ ID NO: 368, og en tung kæde, der omfatter SEQ ID NO: 525; en let kæde, der omfatter SEQ ID NO: 369, og en tung kæde, der omfatter SEQ ID NO: 526; en let kæde, der omfatter SEQ ID NO: 370, og en tung kæde, der omfatter SEQ ID NO: 527; en let kæde, der omfatter SEQ ID NO: 371, og en tung kæde, der omfatter SEQ ID NO: 528; en let kæde, der omfatter SEQ ID NO: 372, og en tung kæde, der omfatter SEQ ID NO: 529; en let kæde, der omfatter SEQ ID NO: 373, og en tung kæde, der omfatter SEQ ID NO: 530; en let kæde, der omfatter SEQ ID NO: 374, og en tung kæde, der omfatter SEQ ID NO: 531; en let kæde, der omfatter SEQ ID NO: 375, og en tung kæde, der omfatter SEQ ID NO: 532; en let kæde, der omfatter SEQ ID NO: 376, og en tung kæde, der omfatter SEQ ID NO: 533; en let kæde, der omfatter SEQ ID NO: 377, og en tung kæde, der omfatter SEQ ID NO: 534; en let kæde, der omfatter SEQ ID NO: 378, og en tung kæde, der omfatter SEQ ID NO: 535; en let kæde, der omfatter SEQ ID NO:

379, og en tung kæde, der omfatter SEQ ID NO: 536; en let kæde, der omfatter SEQ ID NO: 380, og en tung kæde, der omfatter SEQ ID NO: 537; en let kæde, der omfatter SEQ ID NO: 381, og en tung kæde, der omfatter SEQ ID NO: 538; en let kæde, der omfatter SEQ ID NO: 382, og en tung kæde, der omfatter SEQ ID NO: 539; en let kæde, der omfatter SEQ ID NO: 383, og en tung kæde, der omfatter SEQ ID NO: 540; en let kæde, der omfatter SEQ ID NO: 384, og en tung kæde, der omfatter SEQ ID NO: 541; en let kæde, der omfatter SEQ ID NO: 385, og en tung kæde, der omfatter SEQ ID NO: 542; en let kæde, der omfatter SEQ ID NO: 386, og en tung kæde, der omfatter SEQ ID NO: 543; en let kæde, der omfatter SEQ ID NO: 387, og en tung kæde, der omfatter SEQ ID NO: 544; en let kæde, der omfatter SEQ ID NO: 388, og en tung kæde, der omfatter SEQ ID NO: 545; en let kæde, der omfatter SEQ ID NO: 389, og en tung kæde, der omfatter SEQ ID NO: 546; en let kæde, der omfatter SEQ ID NO: 390, og en tung kæde, der omfatter SEQ ID NO: 547; en let kæde, der omfatter SEQ ID NO: 391, og en tung kæde, der omfatter SEQ ID NO: 548; en let kæde, der omfatter SEQ ID NO: 392, og en tung kæde, der omfatter SEQ ID NO: 549; en let kæde, der omfatter SEQ ID NO: 393, og en tung kæde, der omfatter SEQ ID NO: 550; en let kæde, der omfatter SEQ ID NO: 394, og en tung kæde, der omfatter SEQ ID NO: 551; en let kæde, der omfatter SEQ ID NO: 395, og en tung kæde, der omfatter SEQ ID NO: 552; en let kæde, der omfatter SEQ ID NO: 396, og en tung kæde, der omfatter SEQ ID NO: 553; en let kæde, der omfatter SEQ ID NO: 397, og en tung kæde, der omfatter SEQ ID NO: 554; en let kæde, der omfatter SEQ ID NO: 398, og en tung kæde, der omfatter SEQ ID NO: 555; en let kæde, der omfatter SEQ ID NO: 399, og en tung kæde, der omfatter SEQ ID NO: 556; en let kæde, der omfatter SEQ ID NO: 400, og en tung kæde, der omfatter SEQ ID NO: 557; en let kæde, der omfatter SEQ ID NO: 401, og en tung kæde, der omfatter SEQ ID NO: 558; en let kæde, der omfatter SEQ ID NO: 402, og en tung kæde, der omfatter SEQ ID NO: 559; en let kæde, der omfatter SEQ ID NO: 403, og en tung kæde, der omfatter SEQ ID NO: 560; en let kæde, der omfatter SEQ ID NO: 404, og en tung kæde, der omfatter SEQ ID NO: 561; en let kæde, der omfatter SEQ ID NO: 405, og en tung kæde, der omfatter SEQ ID NO: 562; en let kæde, der omfatter SEQ ID NO: 406, og en tung kæde, der omfatter SEQ ID NO: 563; en let

kæde, der omfatter SEQ ID NO: 407, og en tung kæde, der omfatter SEQ ID NO: 564; en let kæde, der omfatter SEQ ID NO: 408, og en tung kæde, der omfatter SEQ ID NO: 565; en let kæde, der omfatter SEQ ID NO: 409, og en tung kæde, der omfatter SEQ ID NO: 566; en let kæde, der omfatter SEQ ID NO: 410, og en tung kæde, der omfatter SEQ ID NO: 567; en let kæde, der omfatter SEQ ID NO: 411, og en tung kæde, der omfatter SEQ ID NO: 568; en let kæde, der omfatter SEQ ID NO: 412, og en tung kæde, der omfatter SEQ ID NO: 569; en let kæde, der omfatter SEQ ID NO: 413, og en tung kæde, der omfatter SEQ ID NO: 570; en let kæde, der omfatter SEQ ID NO: 414, og en tung kæde, der omfatter SEQ ID NO: 571; en let kæde, der omfatter SEQ ID NO: 415, og en tung kæde, der omfatter SEQ ID NO: 572; en let kæde, der omfatter SEQ ID NO: 416, og en tung kæde, der omfatter SEQ ID NO: 573; en let kæde, der omfatter SEQ ID NO: 417, og en tung kæde, der omfatter SEQ ID NO: 574; en let kæde, der omfatter SEQ ID NO: 418, og en tung kæde, der omfatter SEQ ID NO: 575; en let kæde, der omfatter SEQ ID NO: 419, og en tung kæde, der omfatter SEQ ID NO: 576; en let kæde, der omfatter SEQ ID NO: 420, og en tung kæde, der omfatter SEQ ID NO: 577; en let kæde, der omfatter SEQ ID NO: 421, og en tung kæde, der omfatter SEQ ID NO: 578; en let kæde, der omfatter SEQ ID NO: 422, og en tung kæde, der omfatter SEQ ID NO: 579; en let kæde, der omfatter SEQ ID NO: 423, og en tung kæde, der omfatter SEQ ID NO: 580; en let kæde, der omfatter SEQ ID NO: 424, og en tung kæde, der omfatter SEQ ID NO: 581; en let kæde, der omfatter SEQ ID NO: 425, og en tung kæde, der omfatter SEQ ID NO: 582; en let kæde, der omfatter SEQ ID NO: 426, og en tung kæde, der omfatter SEQ ID NO: 583; en let kæde, der omfatter SEQ ID NO: 427, og en tung kæde, der omfatter SEQ ID NO: 584; en let kæde, der omfatter SEQ ID NO: 428, og en tung kæde, der omfatter SEQ ID NO: 585; en let kæde, der omfatter SEQ ID NO: 429, og en tung kæde, der omfatter SEQ ID NO: 586; en let kæde, der omfatter SEQ ID NO: 430, og en tung kæde, der omfatter SEQ ID NO: 587; en let kæde, der omfatter SEQ ID NO: 431, og en tung kæde, der omfatter SEQ ID NO: 588; en let kæde, der omfatter SEQ ID NO: 432, og en tung kæde, der omfatter SEQ ID NO: 589; en let kæde, der omfatter SEQ ID NO: 433, og en tung kæde, der omfatter SEQ ID NO: 590; en let kæde, der omfatter SEQ ID NO: 434, og en tung kæde, der

omfatter SEQ ID NO: 591; en let kæde, der omfatter SEQ ID NO: 435, og en tung kæde, der omfatter SEQ ID NO: 592; en let kæde, der omfatter SEQ ID NO: 436, og en tung kæde, der omfatter SEQ ID NO: 593; en let kæde, der omfatter SEQ ID NO: 437, og en tung kæde, der omfatter SEQ ID NO: 594; en let kæde, der omfatter SEQ ID NO: 438, og en tung kæde, der omfatter SEQ ID NO: 595; en let kæde, der omfatter SEQ ID NO: 439, og en tung kæde, der omfatter SEQ ID NO: 596; en let kæde, der omfatter SEQ ID NO: 440, og en tung kæde, der omfatter SEQ ID NO: 597; en let kæde, der omfatter SEQ ID NO: 441, og en tung kæde, der omfatter SEQ ID NO: 598; en let kæde, der omfatter SEQ ID NO: 442, og en tung kæde, der omfatter SEQ ID NO: 599; en let kæde, der omfatter SEQ ID NO: 443, og en tung kæde, der omfatter SEQ ID NO: 600; en let kæde, der omfatter SEQ ID NO: 444, og en tung kæde, der omfatter SEQ ID NO: 601; en let kæde, der omfatter SEQ ID NO: 445, og en tung kæde, der omfatter SEQ ID NO: 602; en let kæde, der omfatter SEQ ID NO: 446, og en tung kæde, der omfatter SEQ ID NO: 603; en let kæde, der omfatter SEQ ID NO: 447, og en tung kæde, der omfatter SEQ ID NO: 604; en let kæde, der omfatter SEQ ID NO: 448, og en tung kæde, der omfatter SEQ ID NO: 605; en let kæde, der omfatter SEQ ID NO: 449, og en tung kæde, der omfatter SEQ ID NO: 606; en let kæde, der omfatter SEQ ID NO: 450, og en tung kæde, der omfatter SEQ ID NO: 607; en let kæde, der omfatter SEQ ID NO: 451, og en tung kæde, der omfatter SEQ ID NO: 608; en let kæde, der omfatter SEQ ID NO: 452, og en tung kæde, der omfatter SEQ ID NO: 609; en let kæde, der omfatter SEQ ID NO: 453, og en tung kæde, der omfatter SEQ ID NO: 610; en let kæde, der omfatter SEQ ID NO: 454, og en tung kæde, der omfatter SEQ ID NO: 611; en let kæde, der omfatter SEQ ID NO: 455, og en tung kæde, der omfatter SEQ ID NO: 612; en let kæde, der omfatter SEQ ID NO: 456, og en tung kæde, der omfatter SEQ ID NO: 613; en let kæde, der omfatter SEQ ID NO: 457, og en tung kæde, der omfatter SEQ ID NO: 614; en let kæde, der omfatter SEQ ID NO: 458, og en tung kæde, der omfatter SEQ ID NO: 615; en let kæde, der omfatter SEQ ID NO: 459, og en tung kæde, der omfatter SEQ ID NO: 616; en let kæde, der omfatter SEQ ID NO: 460, og en tung kæde, der omfatter SEQ ID NO: 617; en let kæde, der omfatter SEQ ID NO: 461, og en tung kæde, der omfatter SEQ ID NO: 618; en let kæde, der omfatter SEQ

ID NO: 462, og en tung kæde, der omfatter SEQ ID NO: 619; en let kæde, der omfatter SEQ ID NO: 463, og en tung kæde, der omfatter SEQ ID NO: 620; en let kæde, der omfatter SEQ ID NO: 464, og en tung kæde, der omfatter SEQ ID NO: 621; en let kæde, der omfatter SEQ ID NO: 465, og en tung kæde, der omfatter SEQ ID NO: 622; en let kæde, der omfatter SEQ ID NO: 466, og en tung kæde, der omfatter SEQ ID NO: 623; en let kæde, der omfatter SEQ ID NO: 467, og en tung kæde, der omfatter SEQ ID NO: 624; en let kæde, der omfatter SEQ ID NO: 468, og en tung kæde, der omfatter SEQ ID NO: 625; en let kæde, der omfatter SEQ ID NO: 469, og en tung kæde, der omfatter SEQ ID NO: 626; en let kæde, der omfatter SEQ ID NO: 470, og en tung kæde, der omfatter SEQ ID NO: 627; og en let kæde, der omfatter SEQ ID NO: 471, og en tung kæde, der omfatter SEQ ID NO: 628, hvor
antistoffet eller det funktionelle fragment deraf omfatter en cystein eller ikke-kanonisk aminosyresubstitution i et eller flere konjugationssted(er) valgt fra gruppen, der består af
D70 i antistoffets lette kæde i forhold til referencesekvens SEQ ID NO: 455,
E276 i antistoffets tunge kæde i forhold til referencesekvens SEQ ID NO: 612 og
T363 i antistoffets tunge kæde i forhold til referencesekvens SEQ ID NO: 612.

11. Sammensætning ifølge et hvilket som helst af kravene 1-10, hvor GLP-1-receptoragonisten er valgt fra gruppen, der består af SEQ ID NO: 3184; SEQ ID NO: 3185; liraglutid; albiglutid; taspoglutid; dulaglutid; semaglutid; LY2428757; SEQ ID NO: 3163; SEQ ID NO: 3164; SEQ ID NO: 3165; SEQ ID NO: 3166; SEQ ID NO: 3167; SEQ ID NO: 3168; SEQ ID NO: 3169; SEQ ID NO: 3170; SEQ ID NO: 3171; SEQ ID NO: 3172; SEQ ID NO: 3173; SEQ ID NO: 3174; SEQ ID NO: 3175; SEQ ID NO: 3176; SEQ ID NO: 3177; SEQ ID NO: 3178; SEQ ID NO: 3179; SEQ ID NO: 3180; SEQ ID NO: 3181; SEQ ID NO: 3182; SEQ ID NO: 3183; SEQ ID NO: 3184; SEQ ID NO: 3185; SEQ ID NO: 3186; SEQ ID NO: 3187; SEQ ID NO: 3188; SEQ ID NO: 3189;SEQ ID NO: 3190; SEQ ID NO: 3191; SEQ ID NO: 3192; SEQ ID NO: 3193; SEQ ID NO: 3194; SEQ ID NO: 3195; SEQ ID NO: 3196; SEQ ID NO: 3197; SEQ ID NO: 3198; SEQ ID NO: 3199; SEQ ID NO: 3200; SEQ ID

NO: 3201; SEQ ID NO: 3202; SEQ ID NO: 3206; SEQ ID NO: 3207; SEQ ID NO: 3208; SEQ ID NO: 3209; SEQ ID NO: 3210; SEQ ID NO: 3211; SEQ ID NO: 3212; SEQ ID NO: 3213; SEQ ID NO: 3214; SEQ ID NO: 3215; SEQ ID NO: 3216; SEQ ID NO: 3217; SEQ ID NO: 3218; SEQ ID NO: 3219; SEQ ID NO: 3220; SEQ ID NO: 3221; SEQ ID NO: 3222; SEQ ID NO: 3223; SEQ ID NO: 3224; SEQ ID NO: 3225; SEQ ID NO: 3226; SEQ ID NO: 3227; SEQ ID NO: 3228; SEQ ID NO: 3229; SEQ ID NO: 3230; SEQ ID NO: 3231; SEQ ID NO: 3232; SEQ ID NO: 3233; SEQ ID NO: 3234; SEQ ID NO: 3235; SEQ ID NO: 3236; SEQ ID NO: 3237; SEQ ID NO: 3238; SEQ ID NO: 3239; SEQ ID NO: 3240; SEQ ID NO: 3241; SEQ ID NO: 3242; SEQ ID NO: 3243; SEQ ID NO: 3244; SEQ ID NO: 3245; SEQ ID NO: 3246; SEQ ID NO: 3247; SEQ ID NO: 3248; og SEQ ID NO: 3249, og fortrinsvis GLP-1-receptoragonisten er konjugeret til antistoffet eller fragmentet deraf i en rest, der svarer til K26, K36, K37, K39 eller en C-terminal amingruppen i analogen.

12. Sammensætning ifølge et hvilket som helst af kravene 1-10, hvor GLP-1-receptoragonisten er valgt fra gruppen, der består af exenatid, liraglutid, lixisenatid, albiglutid, dulaglutid, semaglutid og taspoglutid.

13. Sammensætning ifølge krav 1, hvor GLP-1-receptoragonisten er konjugeret til antistoffet eller fragmentet deraf via en peptidlinker, der omfatter en sekvens valgt fra gruppen, der består af $(Gly_3Ser)_2$, $(Gly_4Ser)_2$, $(Gly_3Ser)_3$, $(Gly_4Ser)_3$, $(Gly_3Ser)_4$, $(Gly_4Ser)_4$, $(Gly_3Ser)_5$, $(Gly_4Ser)_5$, $(Gly_3Ser)_6$ og $(Gly_4Ser)_6$.

14. Sammensætning ifølge krav 3,
(i) hvor antistoffet omfatter en kombination af en variabel region af let kæde og en variabel region af tung kæde, hvor den variable region af let kæde omfatter SEQ ID NO: 74, og den variable region af tung kæde omfatter SEQ ID NO: 231, og hvor antistoffet omfatter en kombination af en let kæde og en tung kæde, hvor den lette kæde omfatter SEQ ID NO: 388, og den tunge kæde omfatter SEQ ID NO: 545, og
(ii) hvor GLP-1-receptoragonisten omfatter SEQ ID NO: 3244,

hvor antistoffet omfatter en cystein i E276 i antistoffets tunge kæde i forhold til referencesekvens SEQ ID NO: 612.

15. Sammensætning ifølge et hvilket som helst af kravene 1-14 til anvendelse i en fremgangsmåde til behandling af en metabolisk forstyrrelse.

DRAWINGS

Drawing

FIG. 1

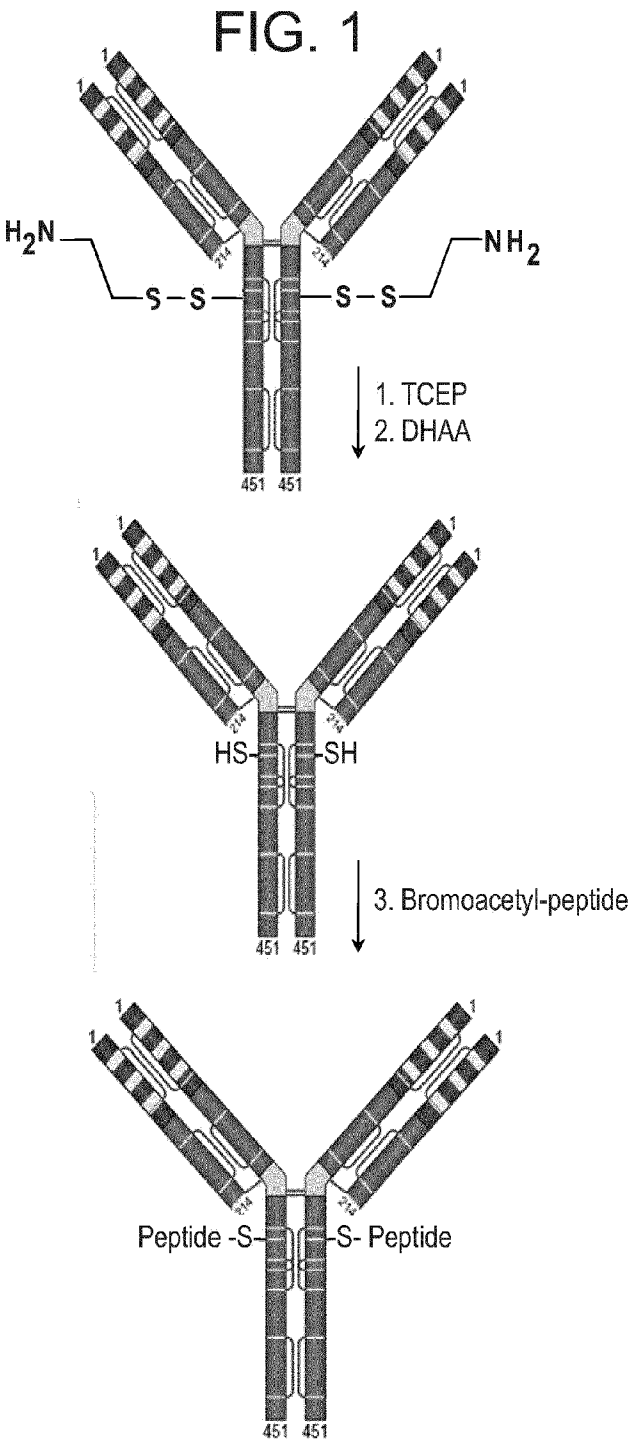


FIG. 2A

GLP1 cAMP assay in ChoK1 hGLP1R clone H20

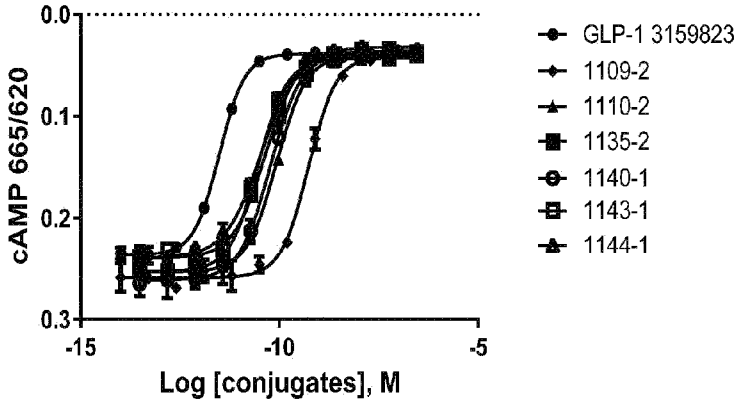


FIG. 2B

GIPR antagonist cAMP assay in 293T/huGIPR clone10

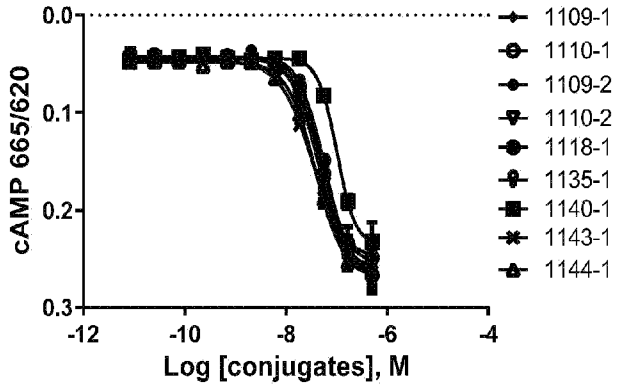


FIG. 2C

GLP1 cAMP assay in ChoK1 hGLP1R clone H20

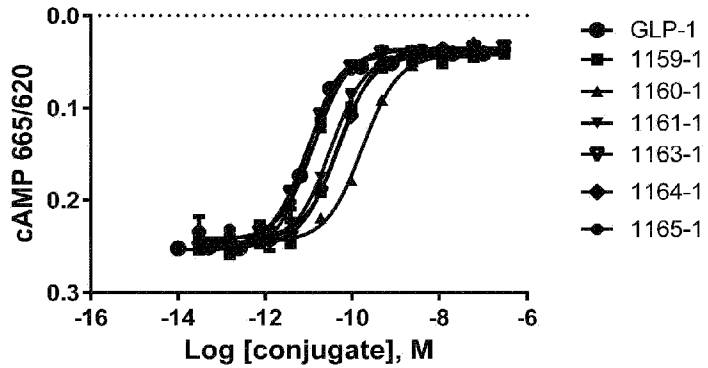


FIG. 2D

GIPR cAMP assay in 293T/huGIPR clone10

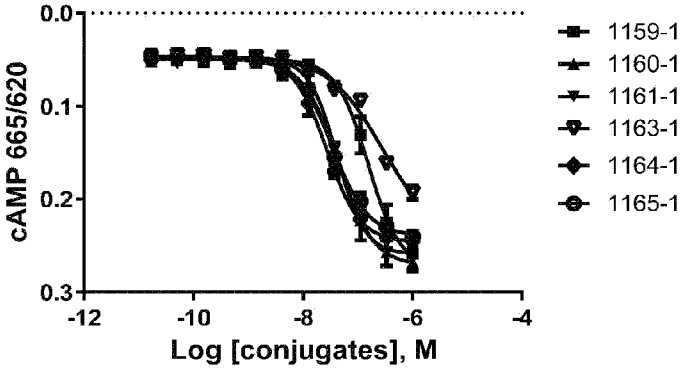


FIG. 2E

cAMP assay (GLP-1 agonist mode) in CHOK1 hGLP1R H20

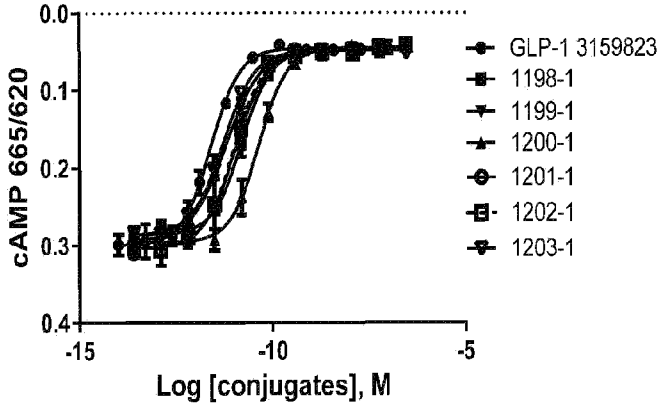


FIG. 2F

cAMP assay (GIPR antagonist mode) in 293T/hGIPR #10

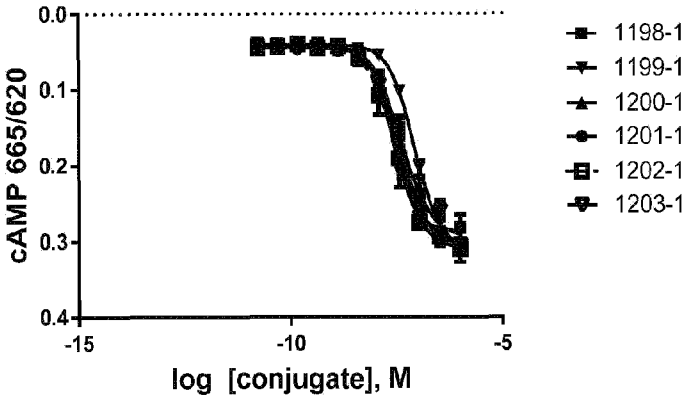


FIG. 2G

cAMP assay (GLP-1 agonist mode) in CHOK1 hGLP1R H20

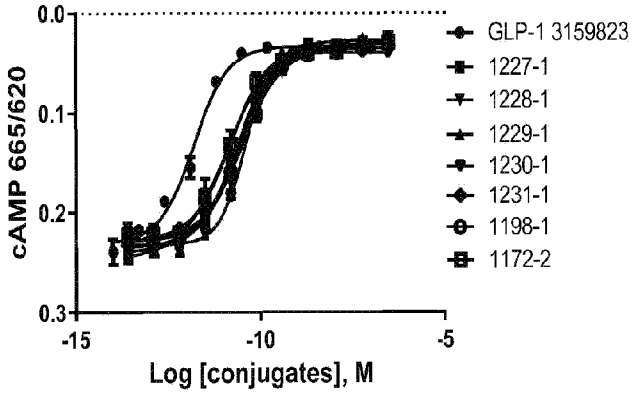
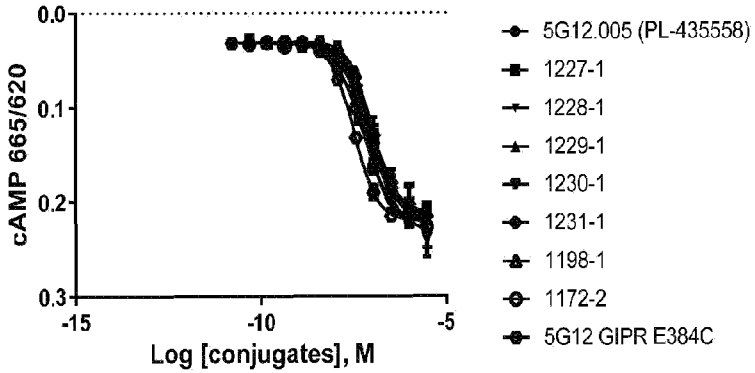


FIG. 2H

cAMP assay (GIPR antagonist mode) in 293T/hGIPR #10



DK/EP 3570885 T3

FIG. 2I

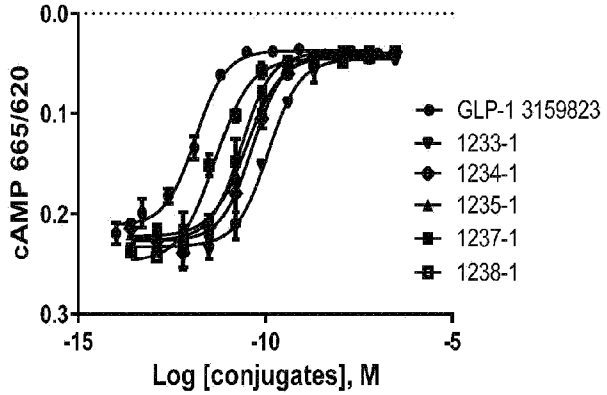


FIG. 2J

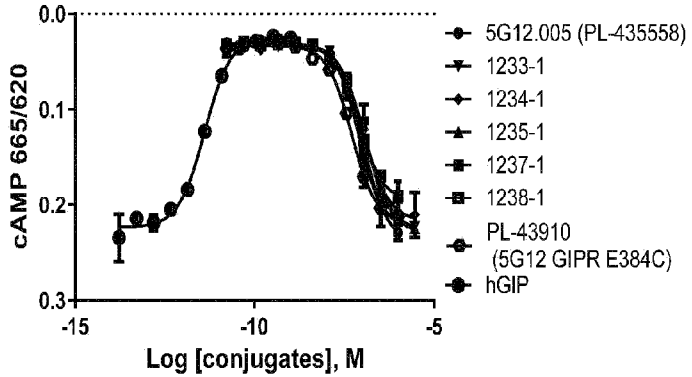


FIG. 2K

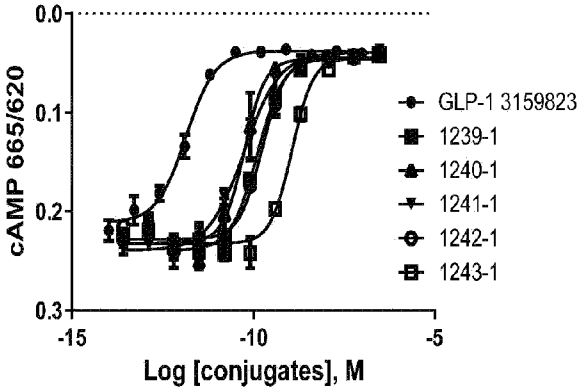


FIG. 2L

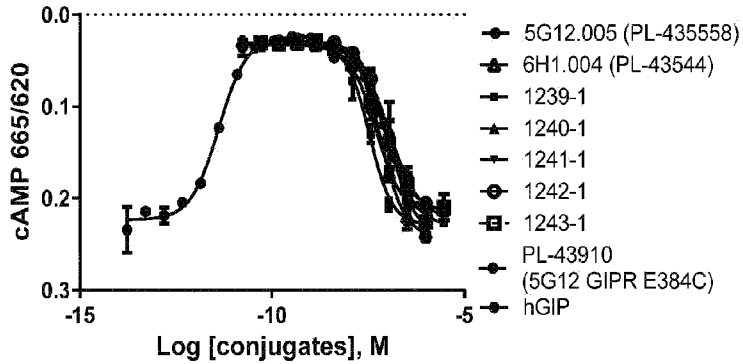


FIG. 2M

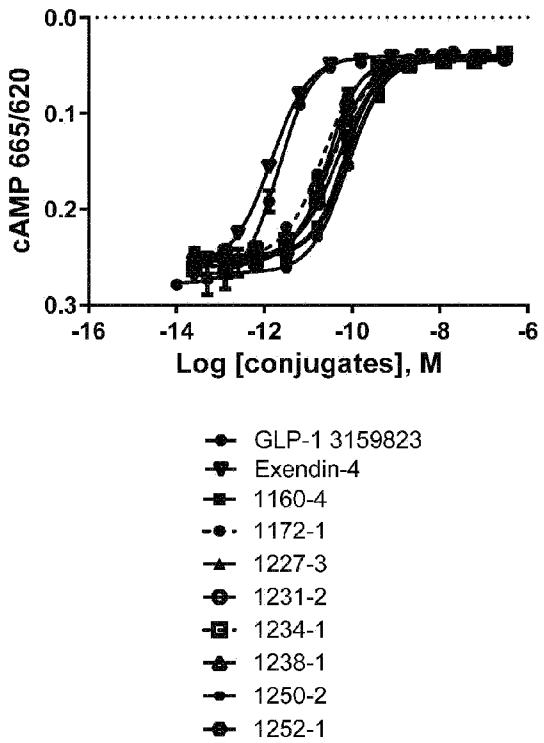

cAMP assay (GLP-1 agonist mode) in CHOK1 hGLP1R H20:
Chemical Conjugates on 5G12
cAMP 665/620
0.0
0.1
0.2
0.3
-16
-14
-12
-10
-8
-6
Log [conjugates], M
GLP-1 3159823
Exendin-4
1160-4
1172-1
1227-3
1231-2
1234-1
1238-1
1250-2
1252-1

FIG. 2N

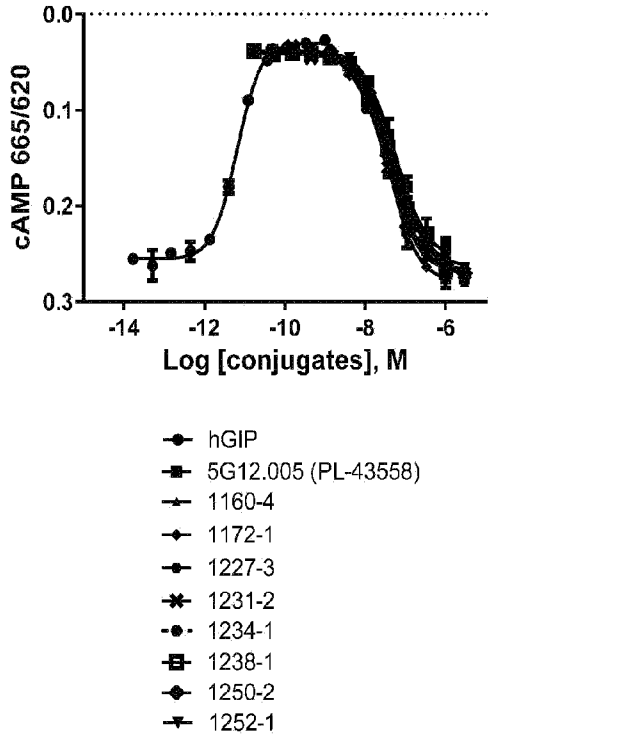

cAMP assay (GIPR antagonist mode) in 293T/hGIPR #10
Chemical Conjugates on 5G12
cAMP 665/620
0.0
0.1
0.2
0.3
-14
-12
-10
-8
-6
Log [conjugates], M
hGIP
5G12.005 (PL-43558)
1160-4
1172-1
1227-3
1231-2
1234-1
1238-1
1250-2
1252-1

FIG. 2O

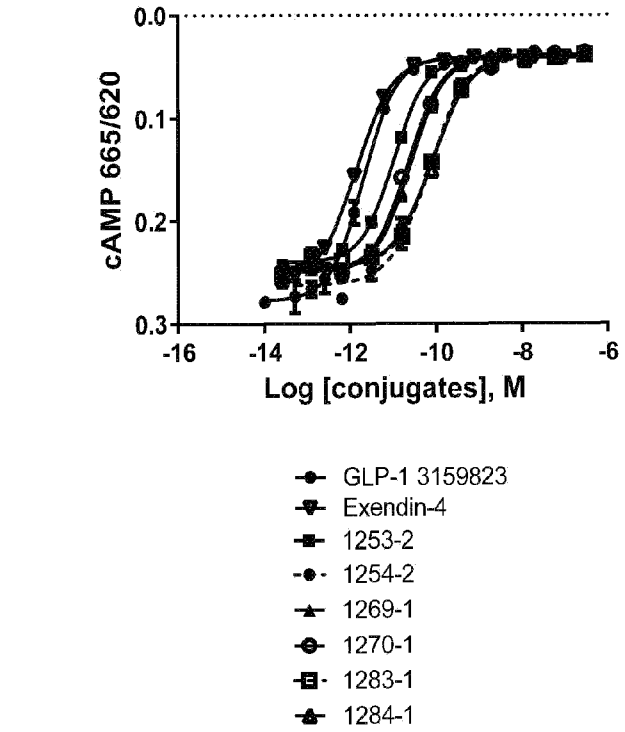

cAMP assay (GLP-1 agonist mode) in CHOK1 hGLP1R H20:
Chemical Conjugates on 5G12
cAMP 665/620
0.0
0.1
0.2
0.3
-16
-14
-12
-10
-8
-6
Log [conjugates], M
GLP-1 3159823
Exendin-4
1253-2
1254-2
1269-1
1270-1
1283-1
1284-1

FIG. 2P

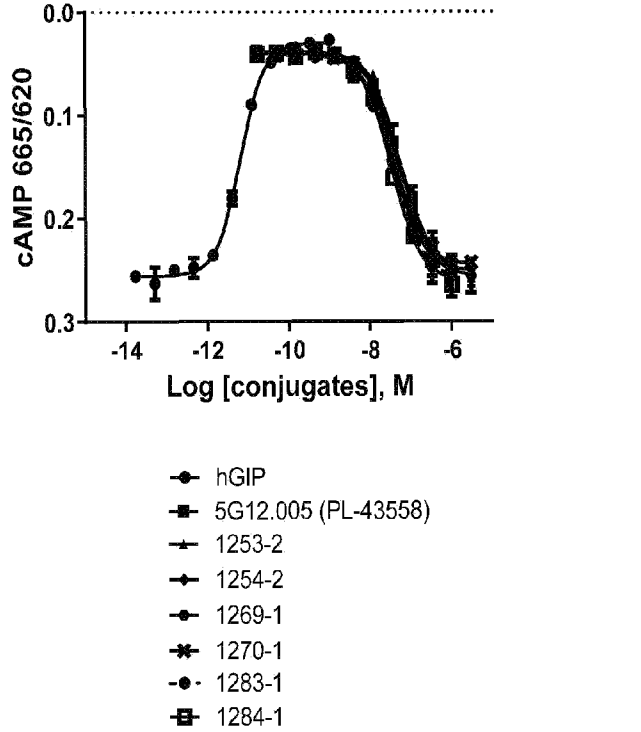

cAMP assay (GIPR antagonist mode) in 293T/hGIPR #10
Chemical Conjugates on 5G12
cAMP 665/620
0.0
0.1
0.2
0.3
-14
-12
-10
-8
-6
Log [conjugates], M
hGIP
5G12.005 (PL-43558)
1253-2
1254-2
1269-1
1270-1
1283-1
1284-1

FIG. 2Q

cAMP assay (GLP-1 agonist mode) in CHOK1 hGLP1R H20: Chemical Conjugates on 2G10

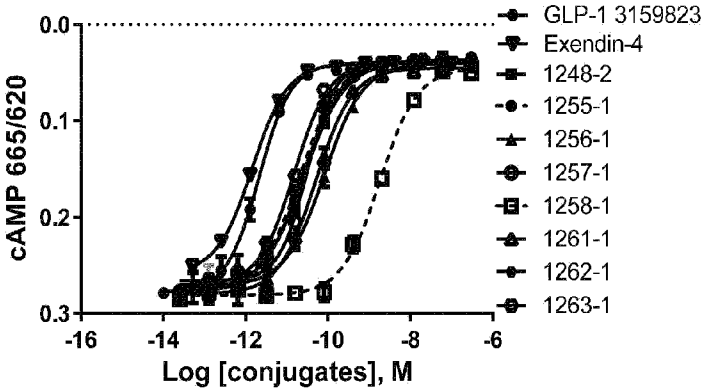


FIG. 2R

cAMP assay (GIPR antagonist mode) in 293T/hGIPR #10 Chemical Conjugates on 2G10

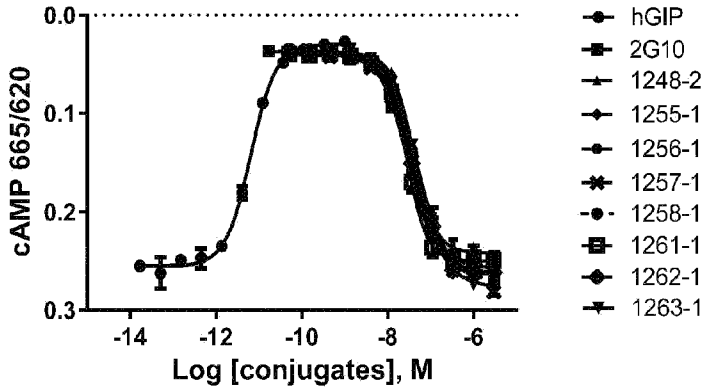


FIG. 2S

cAMP assay (GLP-1 agonist mode) in CHOK1 hGLP1R H20: Chemical Conjugates on 2G10

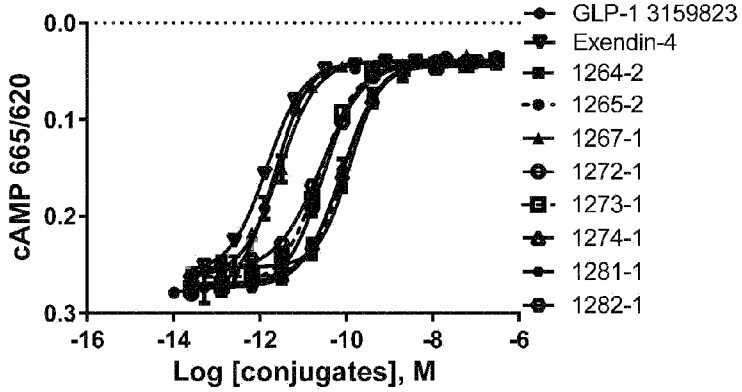


FIG. 2T

cAMP assay (GIPR antagonist mode) in 293T/hGIPR #10 Chemical Conjugates on 2G10

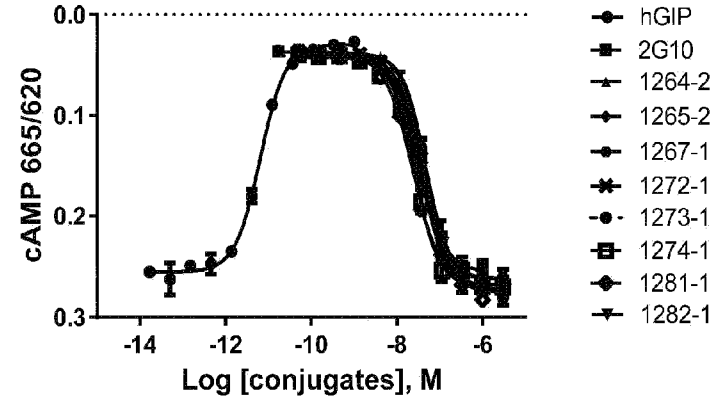
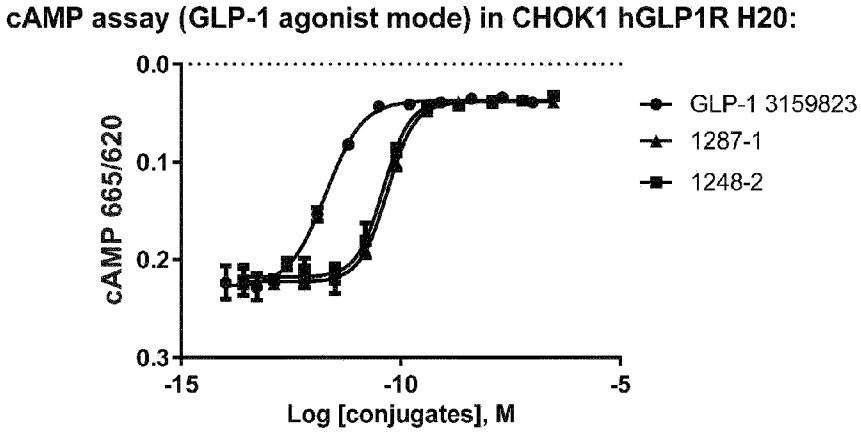


FIG. 3A

Reg #	Description	Peptide information	CHOK1 hGLP-1R	CHOK1 hGLP-1R/GlPR
1148	3166119-E384C-2G10	[Aib8,22;Gly36]GLP-1(7-37)[(G4S)3(BrAc)]	0.04 nM	0.0008 nM
1187	3166119-E384C-aDNP	[Aib8,22;Gly36]GLP-1(7-37)[(G4S)3(BrAc)]	0.05nM	0.08 nM

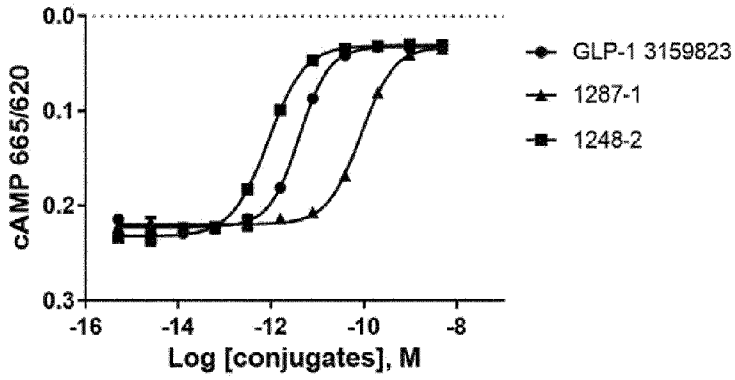
FIG. 3B



	GLP-1 3159823	1287-1	1248-2
EC50	1.990e-012	4.963e-011	4.010e-011

FIG. 3C

cAMP assay (GLP-1 agonist mode) in CHOK1 hGLP1R/hGIPR M1 :



	GLP-1 3159823	1287-1	1248-2
EC50	4.091e-012	8.573e-011	8.793e-013

FIG. 4A

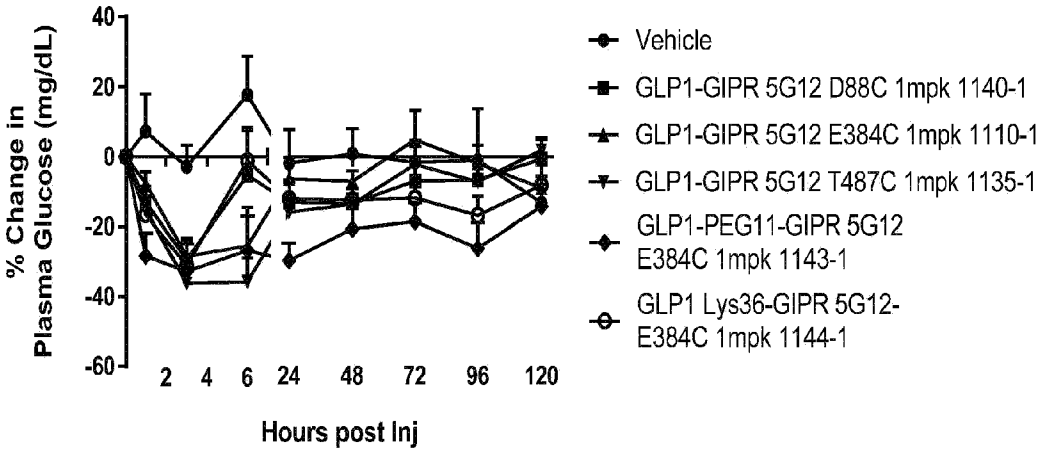

% Change in Plasma Glucose (mg/dL)
40
20
0
-20
-40
-60
2
4
6
24
48
72
96
120
Hours post Inj
Vehicle
GLP1-GIPR 5G12 D88C 1mpk 1140-1
GLP1-GIPR 5G12 E384C 1mpk 1110-1
GLP1-GIPR 5G12 T487C 1mpk 1135-1
GLP1-PEG11-GIPR 5G12 E384C 1mpk 1143-1
GLP1 Lys36-GIPR 5G12-E384C 1mpk 1144-1

FIG. 4B

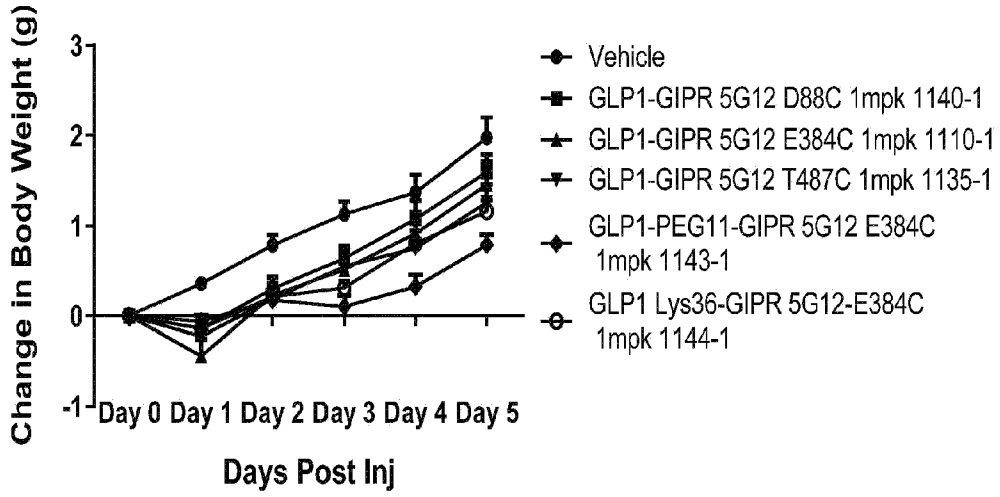

Change in Body Weight (g)
3
2
1
0
-1
Day 0
Day 1
Day 2
Day 3
Day 4
Day 5
Days Post Inj
Vehicle
GLP1-GIPR 5G12 D88C 1mpk 1140-1
GLP1-GIPR 5G12 E384C 1mpk 1110-1
GLP1-GIPR 5G12 T487C 1mpk 1135-1
GLP1-PEG11-GIPR 5G12 E384C 1mpk 1143-1
GLP1 Lys36-GIPR 5G12-E384C 1mpk 1144-1

FIG. 4C

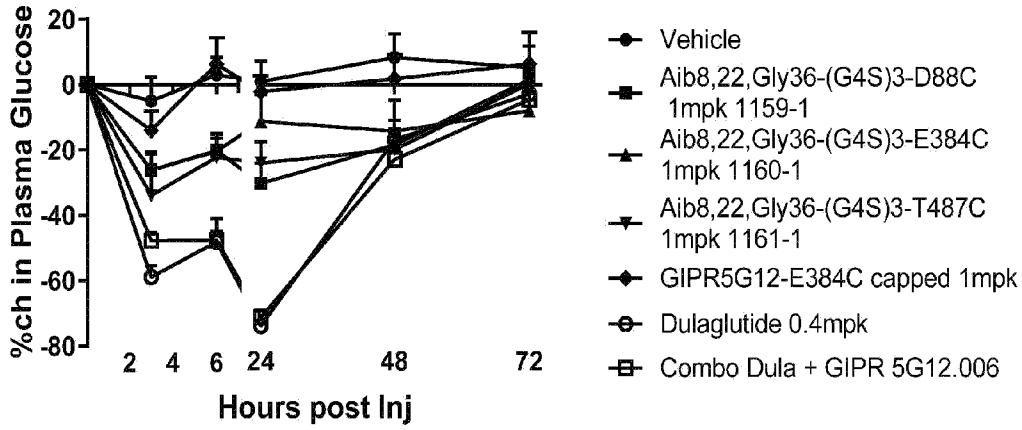

%ch in Plasma Glucose
20
0
-20
-40
-60
-80
2
4
6
24
48
72
Hours post Inj
Vehicle
Aib8,22,Gly36-(G4S)3-D88C 1mpk 1159-1
Aib8,22,Gly36-(G4S)3-E384C 1mpk 1160-1
Aib8,22,Gly36-(G4S)3-T487C 1mpk 1161-1
GIPR5G12-E384C capped 1mpk
Dulaglutide 0.4mpk
Combo Dula + GIPR 5G12.006

FIG. 4D

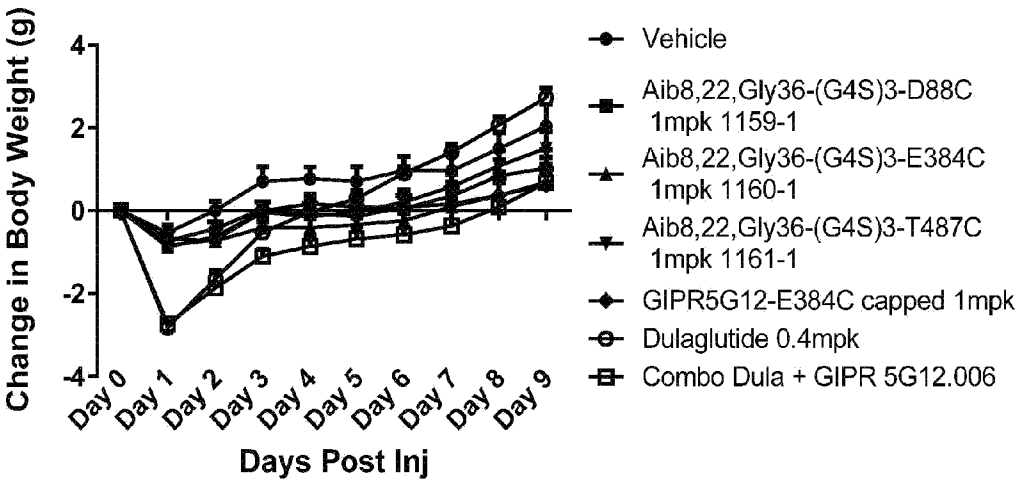

Change in Body Weight (g)
4
2
0
-2
-4
Day 0
Day 1
Day 2
Day 3
Day 4
Day 5
Day 6
Day 7
Day 8
Day 9
Days Post Inj
Vehicle
Aib8,22,Gly36-(G4S)3-D88C 1mpk 1159-1
Aib8,22,Gly36-(G4S)3-E384C 1mpk 1160-1
Aib8,22,Gly36-(G4S)3-T487C 1mpk 1161-1
GIPR5G12-E384C capped 1mpk
Dulaglutide 0.4mpk
Combo Dula + GIPR 5G12.006

FIG. 4E

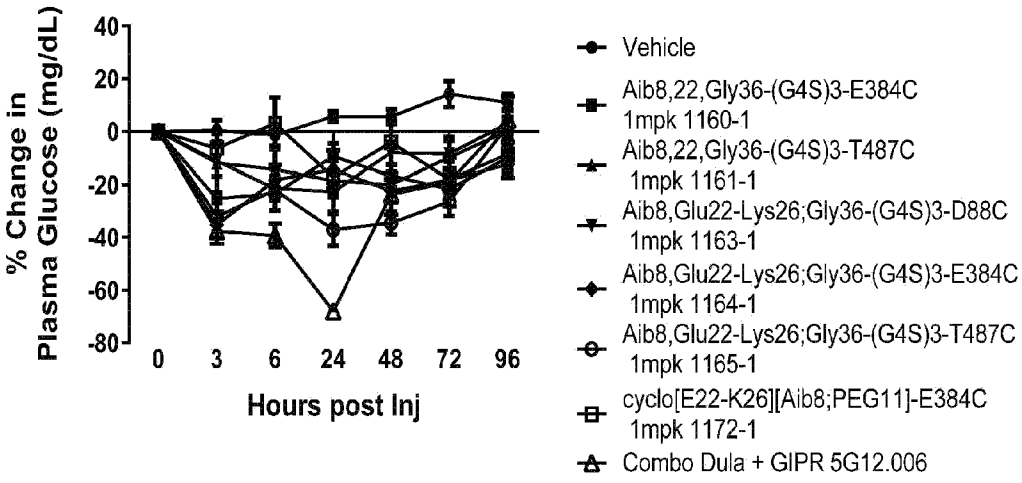

% Change in Plasma Glucose (mg/dL)
40
20
0
-20
-40
-60
-80
0
3
6
24
48
72
96
Hours post Inj
Vehicle
Aib8,22,Gly36-(G4S)3-E384C 1mpk 1160-1
Aib8,22,Gly36-(G4S)3-T487C 1mpk 1161-1
Aib8,Glu22-Lys26;Gly36-(G4S)3-D88C 1mpk 1163-1
Aib8,Glu22-Lys26;Gly36-(G4S)3-E384C 1mpk 1164-1
Aib8,Glu22-Lys26;Gly36-(G4S)3-T487C 1mpk 1165-1
cyclo[E22-K26][Aib8;PEG11]-E384C 1mpk 1172-1
Combo Dula + GIPR 5G12.006

FIG. 4F

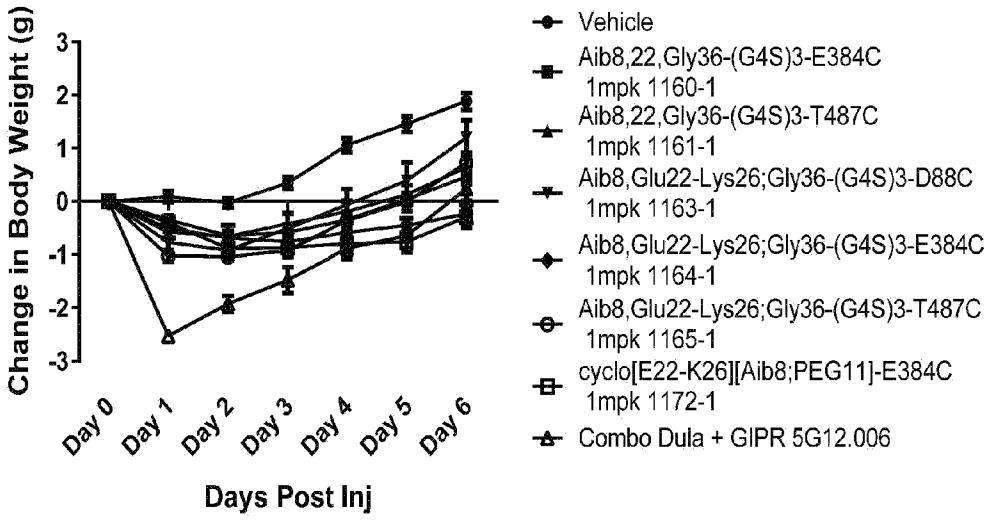

Change in Body Weight (g)
3
2
1
0
-1
-2
-3
Day 0
Day 1
Day 2
Day 3
Day 4
Day 5
Day 6
Days Post Inj
Vehicle
Aib8,22,Gly36-(G4S)3-E384C 1mpk 1160-1
Aib8,22,Gly36-(G4S)3-T487C 1mpk 1161-1
Aib8,Glu22-Lys26;Gly36-(G4S)3-D88C 1mpk 1163-1
Aib8,Glu22-Lys26;Gly36-(G4S)3-E384C 1mpk 1164-1
Aib8,Glu22-Lys26;Gly36-(G4S)3-T487C 1mpk 1165-1
cyclo[E22-K26][Aib8;PEG11]-E384C 1mpk 1172-1
Combo Dula + GIPR 5G12.006

FIG. 4G

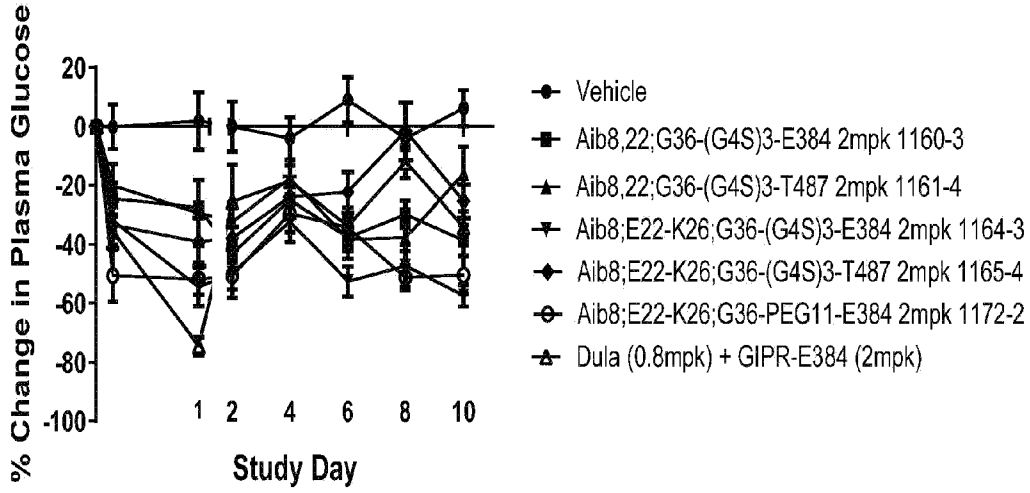

% Change in Plasma Glucose
20
0
-20
-40
-60
-80
-100
1
2
4
6
8
10
Study Day
Vehicle
Aib8,22;G36-(G4S)3-E384 2mpk 1160-3
Aib8,22;G36-(G4S)3-T487 2mpk 1161-4
Aib8;E22-K26;G36-(G4S)3-E384 2mpk 1164-3
Aib8;E22-K26;G36-(G4S)3-T487 2mpk 1165-4
Aib8;E22-K26;G36-PEG11-E384 2mpk 1172-2
Dula (0.8mpk) + GIPR-E384 (2mpk)

FIG. 4H

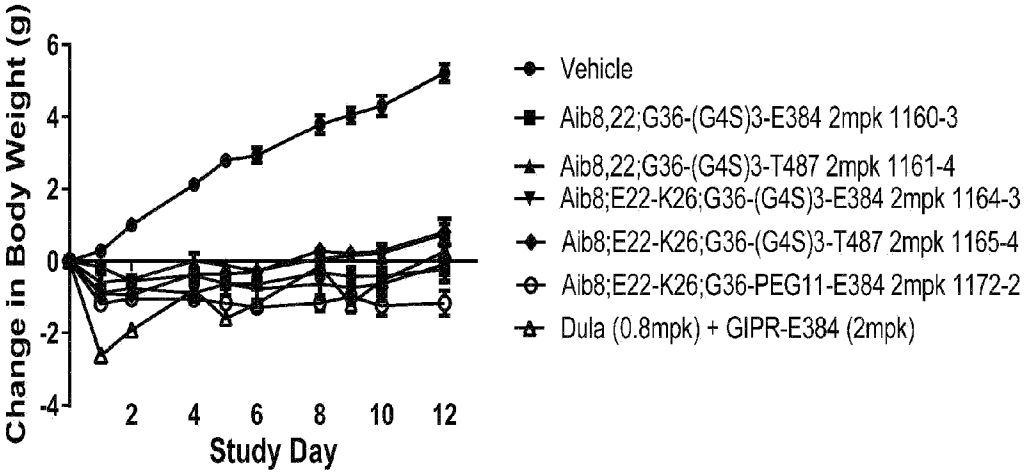

Change in Body Weight (g)
6
4
2
0
-2
-4
2
4
6
8
10
12
Study Day
Vehicle
Aib8,22;G36-(G4S)3-E384 2mpk 1160-3
Aib8,22;G36-(G4S)3-T487 2mpk 1161-4
Aib8;E22-K26;G36-(G4S)3-E384 2mpk 1164-3
Aib8;E22-K26;G36-(G4S)3-T487 2mpk 1165-4
Aib8;E22-K26;G36-PEG11-E384 2mpk 1172-2
Dula (0.8mpk) + GIPR-E384 (2mpk)

FIG. 4I

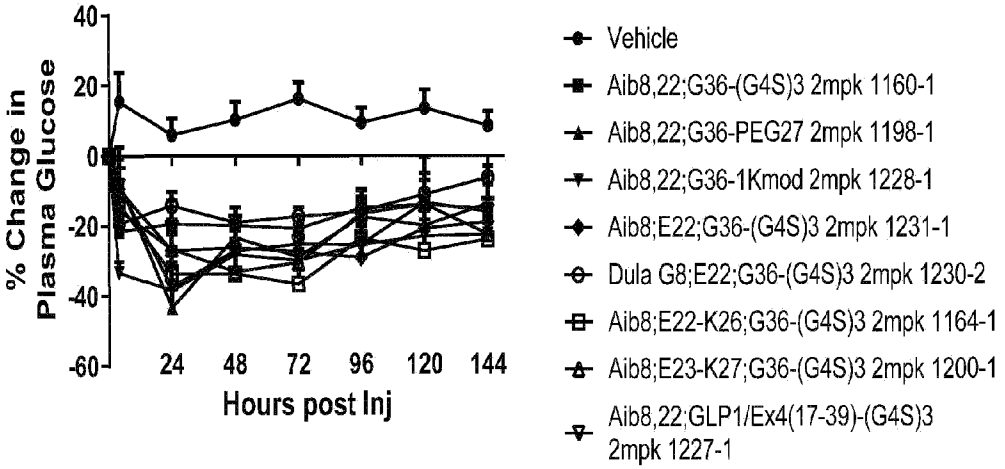

% Change in Plasma Glucose
40
20
0
-20
-40
-60
24
48
72
96
120
144
Hours post Inj
Vehicle
Aib8,22;G36-(G4S)3 2mpk 1160-1
Aib8,22;G36-PEG27 2mpk 1198-1
Aib8,22;G36-1Kmod 2mpk 1228-1
Aib8;E22;G36-(G4S)3 2mpk 1231-1
Dula G8;E22;G36-(G4S)3 2mpk 1230-2
Aib8;E22-K26;G36-(G4S)3 2mpk 1164-1
Aib8;E23-K27;G36-(G4S)3 2mpk 1200-1
Aib8,22;GLP1/Ex4(17-39)-(G4S)3 2mpk 1227-1

FIG. 4J

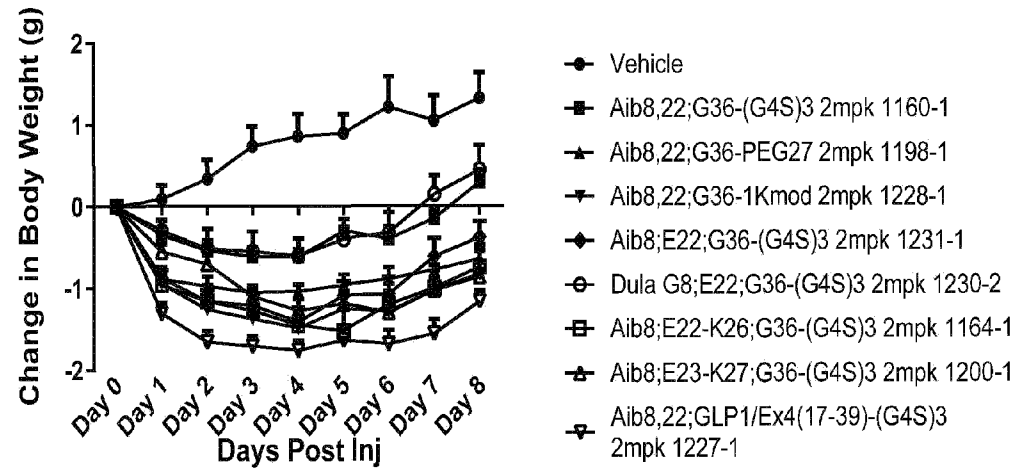

Change in Body Weight (g)
2
1
0
-1
-2
Day 0
Day 1
Day 2
Day 3
Day 4
Day 5
Day 6
Day 7
Day 8
Days Post Inj
Vehicle
Aib8,22;G36-(G4S)3 2mpk 1160-1
Aib8,22;G36-PEG27 2mpk 1198-1
Aib8,22;G36-1Kmod 2mpk 1228-1
Aib8;E22;G36-(G4S)3 2mpk 1231-1
Dula G8;E22;G36-(G4S)3 2mpk 1230-2
Aib8;E22-K26;G36-(G4S)3 2mpk 1164-1
Aib8;E23-K27;G36-(G4S)3 2mpk 1200-1
Aib8,22;GLP1/Ex4(17-39)-(G4S)3 2mpk 1227-1

FIG. 4K

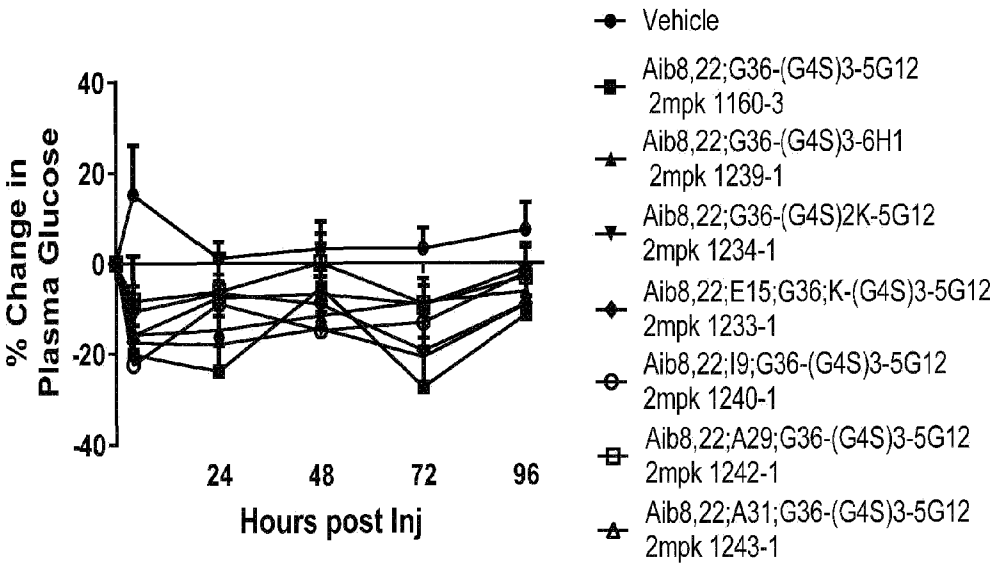

% Change in Plasma Glucose
40
20
0
-20
-40
24
48
72
96
Hours post Inj
Vehicle
Aib8,22;G36-(G4S)3-5G12 2mpk 1160-3
Aib8,22;G36-(G4S)3-6H1 2mpk 1239-1
Aib8,22;G36-(G4S)2K-5G12 2mpk 1234-1
Aib8,22;E15;G36;K-(G4S)3-5G12 2mpk 1233-1
Aib8,22;I9;G36-(G4S)3-5G12 2mpk 1240-1
Aib8,22;A29;G36-(G4S)3-5G12 2mpk 1242-1
Aib8,22;A31;G36-(G4S)3-5G12 2mpk 1243-1

FIG. 4L

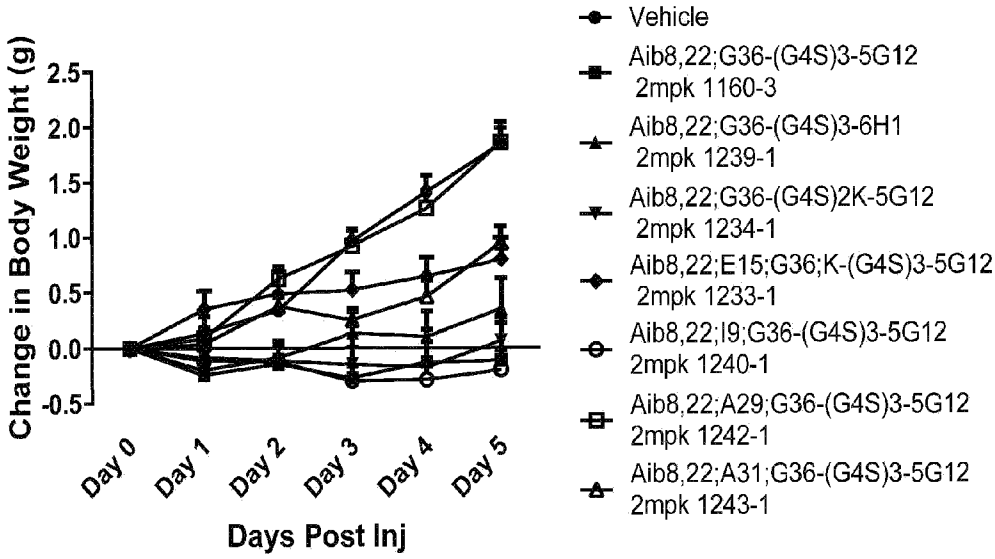

Change in Body Weight (g)
2.5
2.0
1.5
1.0
0.5
0.0
-0.5
Day 0
Day 1
Day 2
Day 3
Day 4
Day 5
Days Post Inj
Vehicle
Aib8,22;G36-(G4S)3-5G12 2mpk 1160-3
Aib8,22;G36-(G4S)3-6H1 2mpk 1239-1
Aib8,22;G36-(G4S)2K-5G12 2mpk 1234-1
Aib8,22;E15;G36;K-(G4S)3-5G12 2mpk 1233-1
Aib8,22;I9;G36-(G4S)3-5G12 2mpk 1240-1
Aib8,22;A29;G36-(G4S)3-5G12 2mpk 1242-1
Aib8,22;A31;G36-(G4S)3-5G12 2mpk 1243-1

FIG. 4M

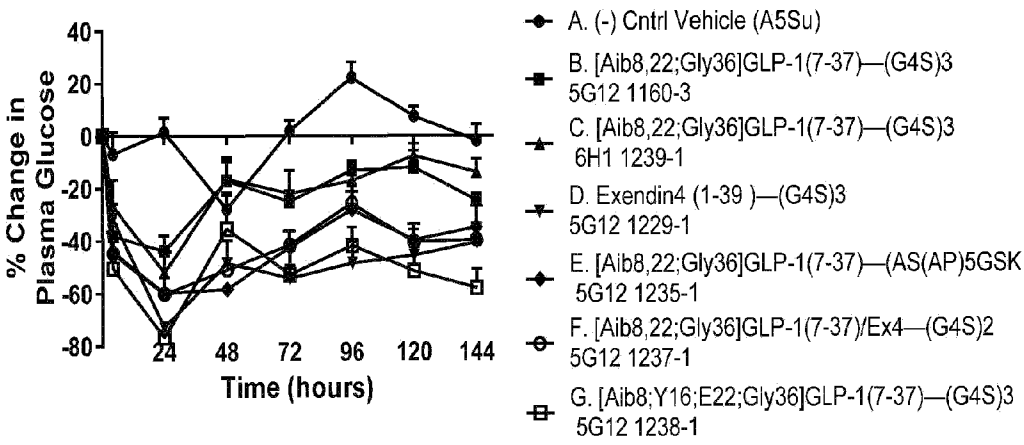

% Change in Plasma Glucose
40
20
0
-20
-40
-60
-80
24
48
72
96
120
144
Time (hours)
A. (-) Cntrl Vehicle (A5Su)
B. [Aib8,22;Gly36]GLP-1(7-37)—(G4S)3 5G12 1160-3
C. [Aib8,22;Gly36]GLP-1(7-37)—(G4S)3 6H1 1239-1
D. Exendin4 (1-39)—(G4S)3 5G12 1229-1
E. [Aib8,22;Gly36]GLP-1(7-37)—(AS(AP)5GSK 5G12 1235-1
F. [Aib8,22;Gly36]GLP-1(7-37)/Ex4—(G4S)2 5G12 1237-1
G. [Aib8;Y16;E22;Gly36]GLP-1(7-37)—(G4S)3 5G12 1238-1

FIG. 4N

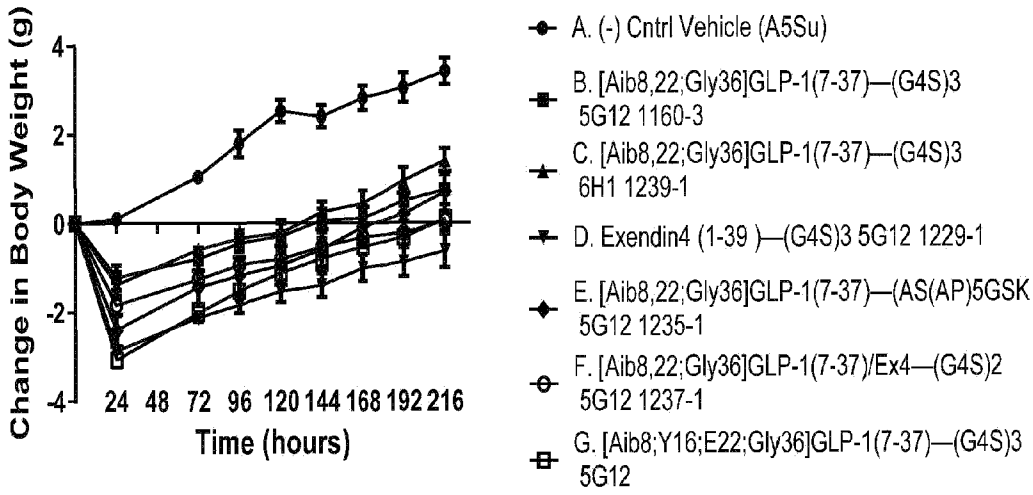

Change in Body Weight (g)
4
2
0
-2
-4
24 48 72 96 120 144 168 192 216
Time (hours)
A. (-) Cntrl Vehicle (A5Su)
B. [Aib8,22;Gly36]GLP-1(7-37)—(G4S)3 5G12 1160-3
C. [Aib8,22;Gly36]GLP-1(7-37)—(G4S)3 6H1 1239-1
D. Exendin4 (1-39)—(G4S)3 5G12 1229-1
E. [Aib8,22;Gly36]GLP-1(7-37)—(AS(AP)5GSK 5G12 1235-1
F. [Aib8,22;Gly36]GLP-1(7-37)/Ex4—(G4S)2 5G12 1237-1
G. [Aib8;Y16;E22;Gly36]GLP-1(7-37)—(G4S)3 5G12

FIG. 4O

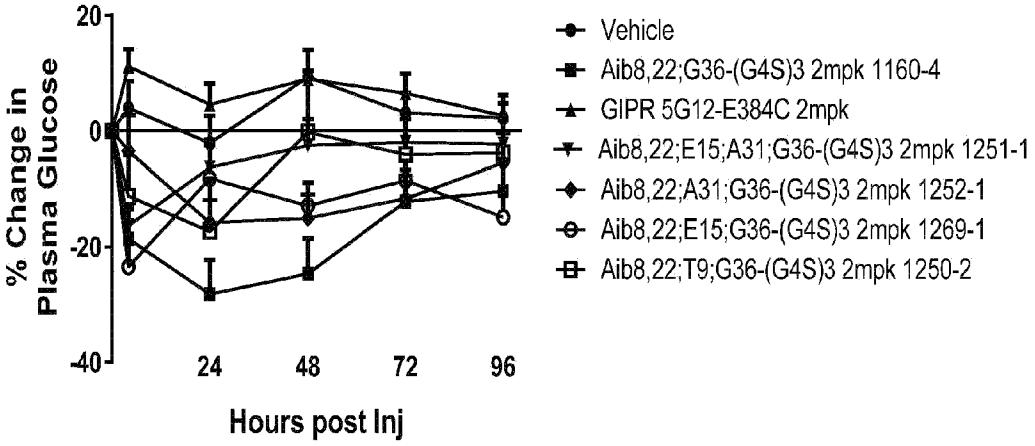

% Change in Plasma Glucose
20
0
-20
-40
24
48
72
96
Hours post Inj
Vehicle
Aib8,22;G36-(G4S)3 2mpk 1160-4
GIPR 5G12-E384C 2mpk
Aib8,22;E15;A31;G36-(G4S)3 2mpk 1251-1
Aib8,22;A31;G36-(G4S)3 2mpk 1252-1
Aib8,22;E15;G36-(G4S)3 2mpk 1269-1
Aib8,22;T9;G36-(G4S)3 2mpk 1250-2

FIG. 4P

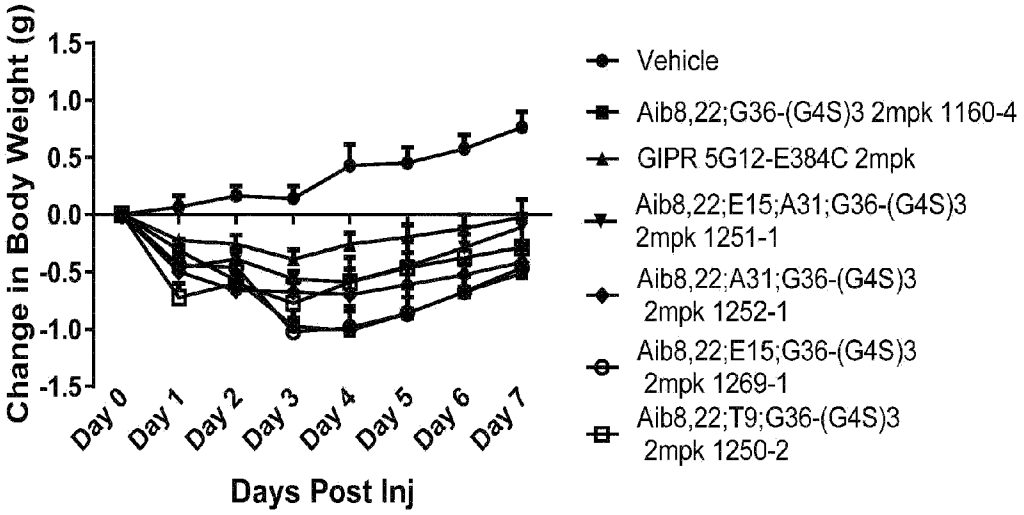

Change in Body Weight (g)
1.5
1.0
0.5
0.0
-0.5
-1.0
-1.5
Day 0
Day 1
Day 2
Day 3
Day 4
Day 5
Day 6
Day 7
Days Post Inj
Vehicle
Aib8,22;G36-(G4S)3 2mpk 1160-4
GIPR 5G12-E384C 2mpk
Aib8,22;E15;A31;G36-(G4S)3 2mpk 1251-1
Aib8,22;A31;G36-(G4S)3 2mpk 1252-1
Aib8,22;E15;G36-(G4S)3 2mpk 1269-1
Aib8,22;T9;G36-(G4S)3 2mpk 1250-2

FIG. 4Q

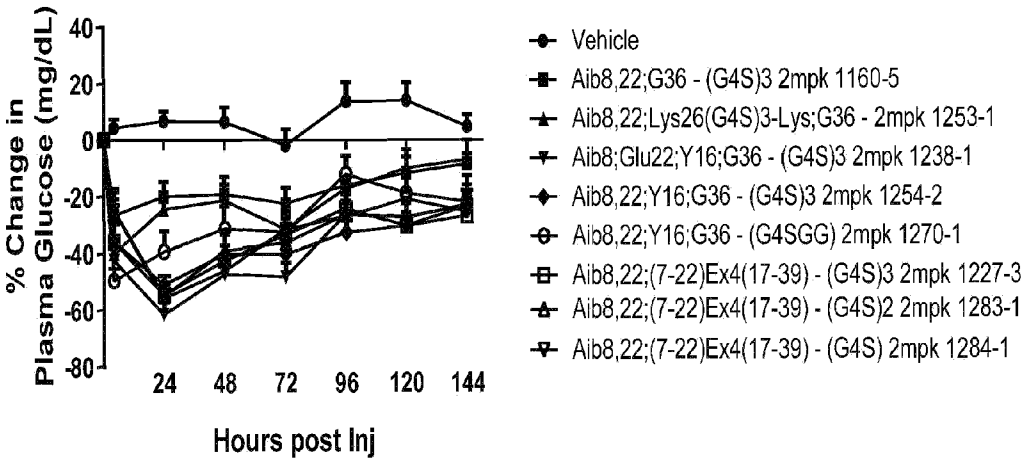

% Change in Plasma Glucose (mg/dL)
40
20
0
-20
-40
-60
-80
24
48
72
96
120
144
Hours post Inj
Vehicle
Aib8,22;G36 - (G4S)3 2mpk 1160-5
Aib8,22;Lys26(G4S)3-Lys;G36 - 2mpk 1253-1
Aib8;Glu22;Y16;G36 - (G4S)3 2mpk 1238-1
Aib8,22;Y16;G36 - (G4S)3 2mpk 1254-2
Aib8,22;Y16;G36 - (G4SGG) 2mpk 1270-1
Aib8,22;(7-22)Ex4(17-39) - (G4S)3 2mpk 1227-3
Aib8,22;(7-22)Ex4(17-39) - (G4S)2 2mpk 1283-1
Aib8,22;(7-22)Ex4(17-39) - (G4S) 2mpk 1284-1

FIG. 4R

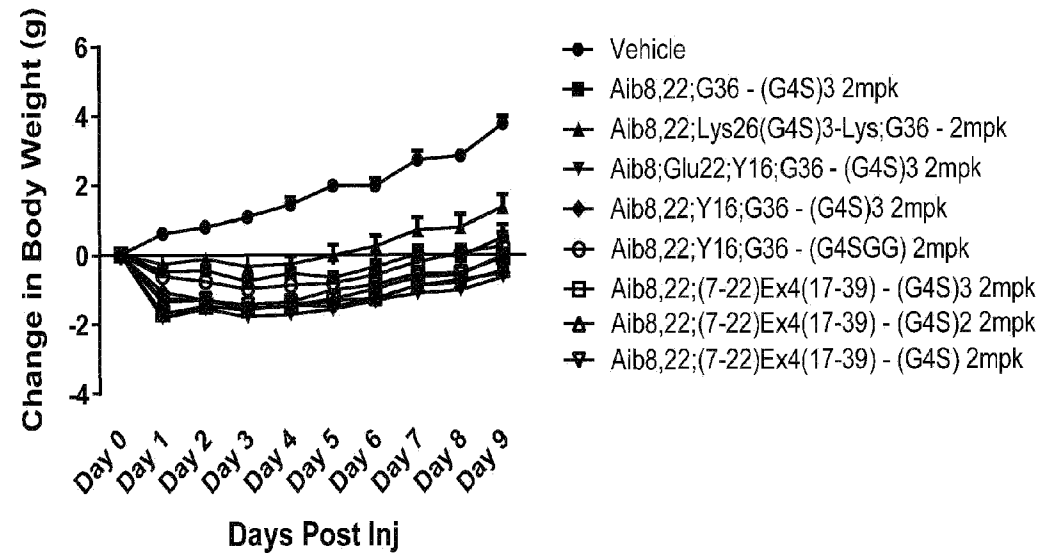

Change in Body Weight (g)
6
4
2
0
-2
-4
Day 0
Day 1
Day 2
Day 3
Day 4
Day 5
Day 6
Day 7
Day 8
Day 9
Days Post Inj
Vehicle
Aib8,22;G36 - (G4S)3 2mpk
Aib8,22;Lys26(G4S)3-Lys;G36 - 2mpk
Aib8;Glu22;Y16;G36 - (G4S)3 2mpk
Aib8,22;Y16;G36 - (G4S)3 2mpk
Aib8,22;Y16;G36 - (G4SGG) 2mpk
Aib8,22;(7-22)Ex4(17-39) - (G4S)3 2mpk
Aib8,22;(7-22)Ex4(17-39) - (G4S)2 2mpk
Aib8,22;(7-22)Ex4(17-39) - (G4S) 2mpk

FIG. 5A

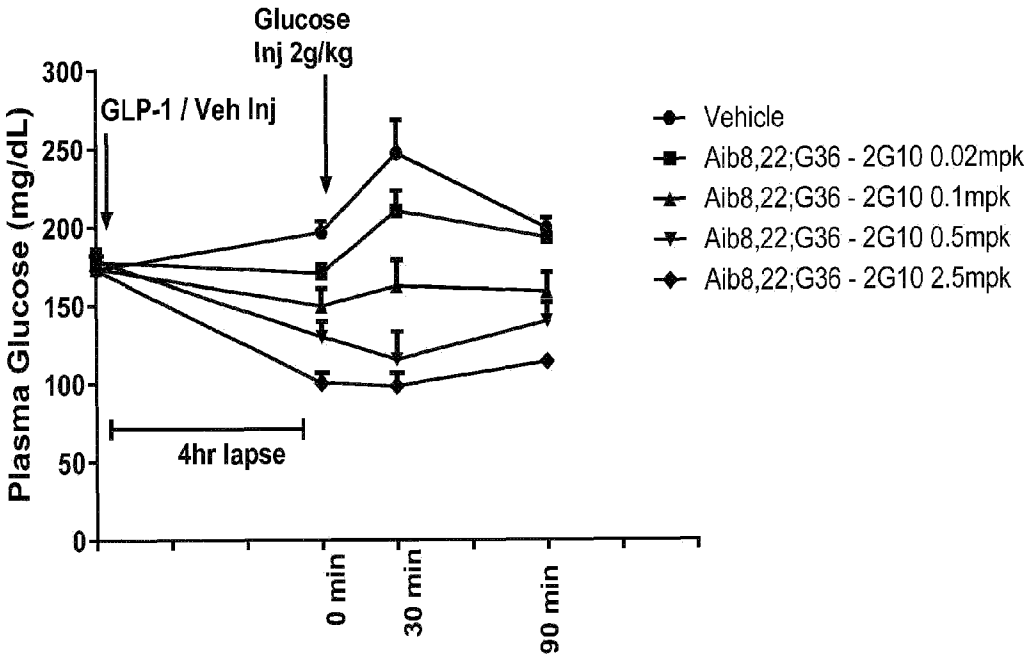

Glucose
Inj 2g/kg
GLP-1 / Veh Inj
Plasma Glucose (mg/dL)
300
250
200
150
100
50
0
4hr lapse
0 min
30 min
90 min
Vehicle
Aib8,22;G36 - 2G10 0.02mpk
Aib8,22;G36 - 2G10 0.1mpk
Aib8,22;G36 - 2G10 0.5mpk
Aib8,22;G36 - 2G10 2.5mpk

FIG. 5B

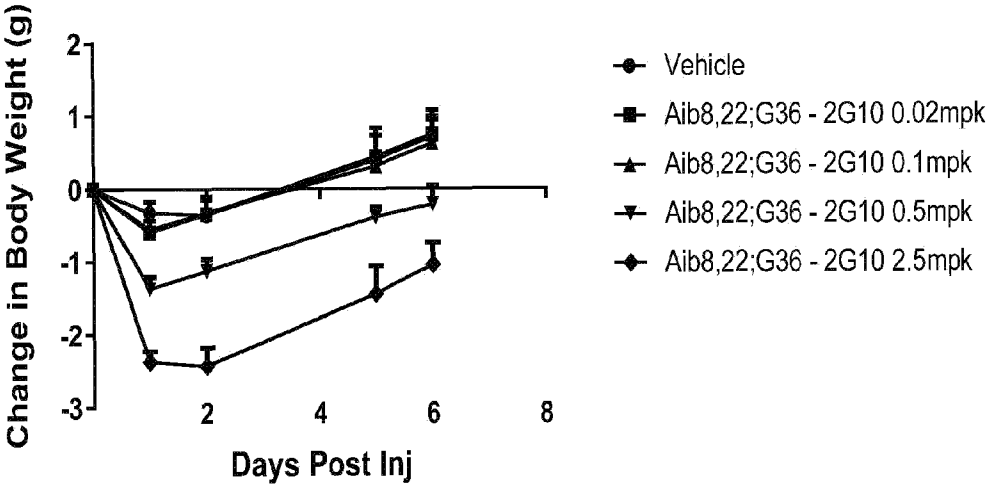

Change in Body Weight (g)
2
1
0
-1
-2
-3
2
4
6
8
Days Post Inj
Vehicle
Aib8,22;G36 - 2G10 0.02mpk
Aib8,22;G36 - 2G10 0.1mpk
Aib8,22;G36 - 2G10 0.5mpk
Aib8,22;G36 - 2G10 2.5mpk

FIG. 5C

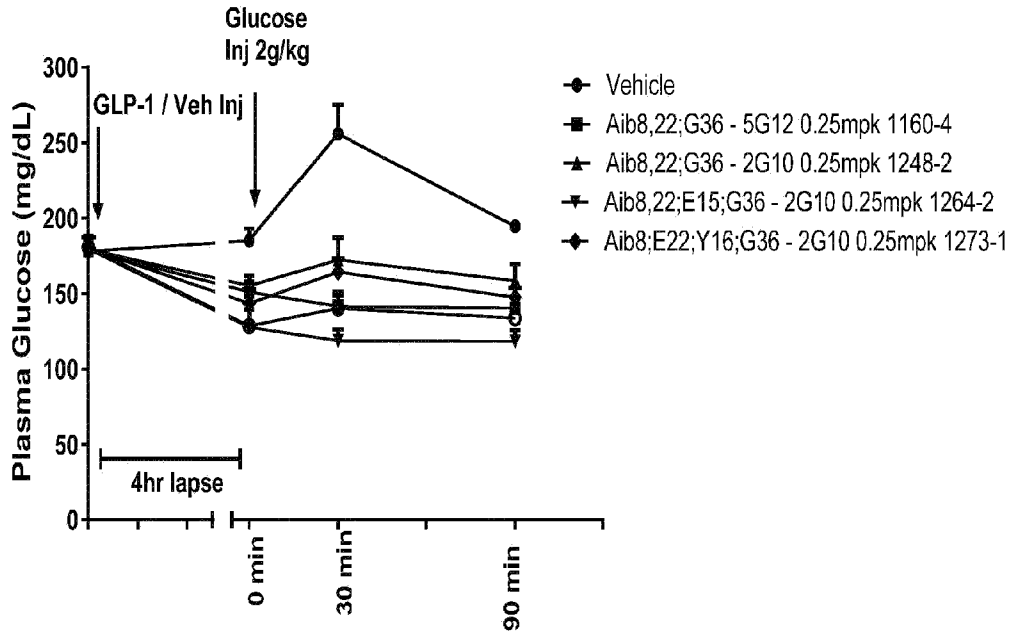

Glucose
Inj 2g/kg
GLP-1 / Veh Inj
Plasma Glucose (mg/dL)
300
250
200
150
100
50
0
4hr lapse
0 min
30 min
90 min
Vehicle
Aib8,22;G36 - 5G12 0.25mpk 1160-4
Aib8,22;G36 - 2G10 0.25mpk 1248-2
Aib8,22;E15;G36 - 2G10 0.25mpk 1264-2
Aib8;E22;Y16;G36 - 2G10 0.25mpk 1273-1

FIG. 5D

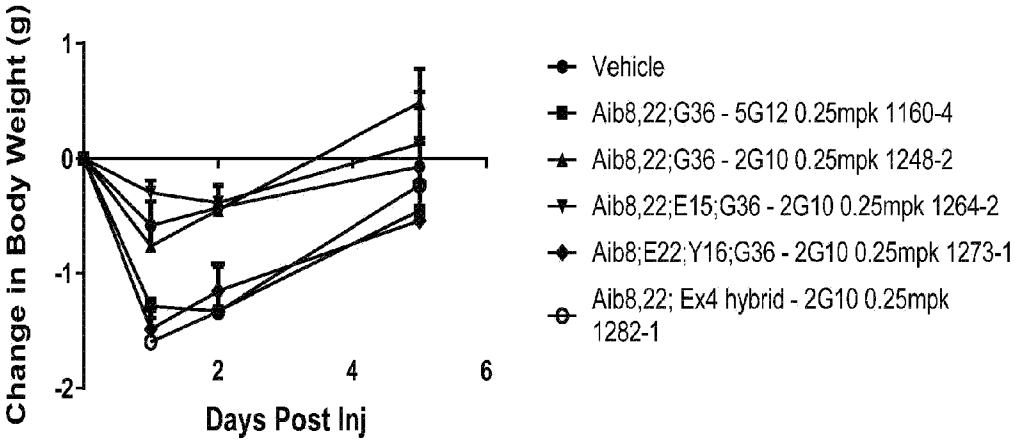

Change in Body Weight (g)
1
0
-1
-2
2
4
6
Days Post Inj
Vehicle
Aib8,22;G36 - 5G12 0.25mpk 1160-4
Aib8,22;G36 - 2G10 0.25mpk 1248-2
Aib8,22;E15;G36 - 2G10 0.25mpk 1264-2
Aib8;E22;Y16;G36 - 2G10 0.25mpk 1273-1
Aib8,22; Ex4 hybrid - 2G10 0.25mpk 1282-1

FIG. 6A

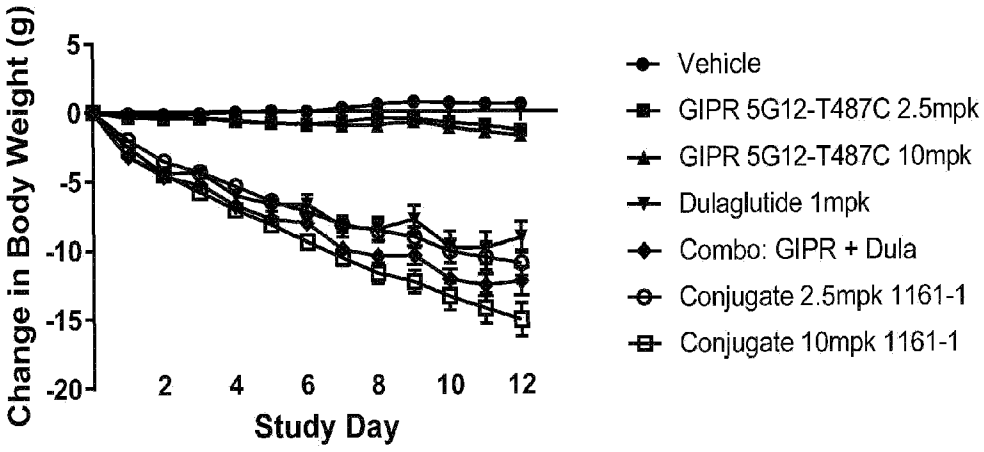

Change in Body Weight (g)
5
0
-5
-10
-15
-20
2
4
6
8
10
12
Study Day
Vehicle
GIPR 5G12-T487C 2.5mpk
GIPR 5G12-T487C 10mpk
Dulaglutide 1mpk
Combo: GIPR + Dula
Conjugate 2.5mpk 1161-1
Conjugate 10mpk 1161-1

FIG. 6B

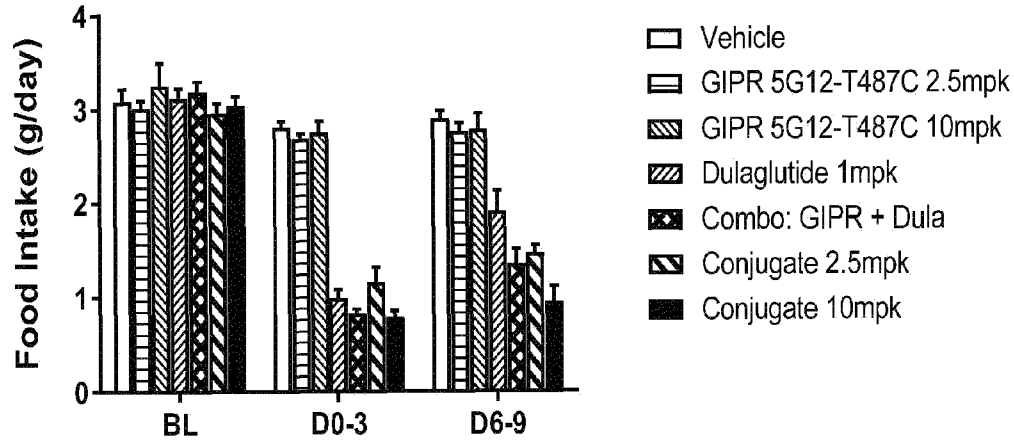
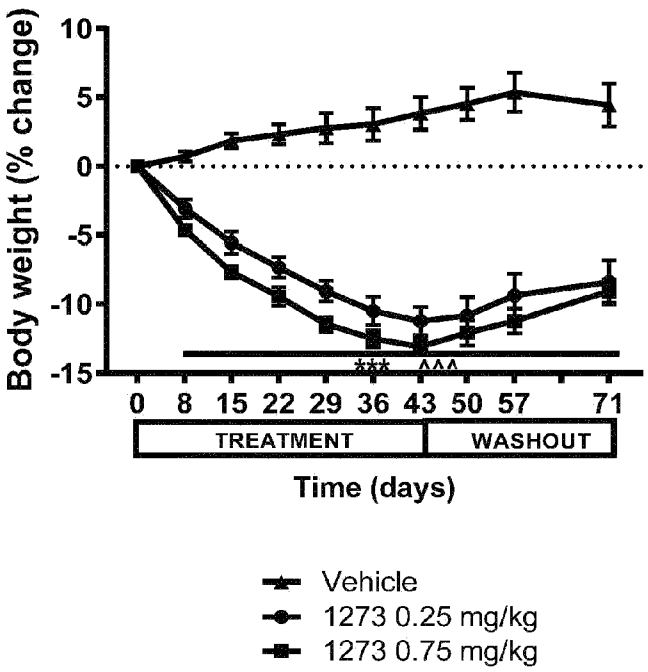
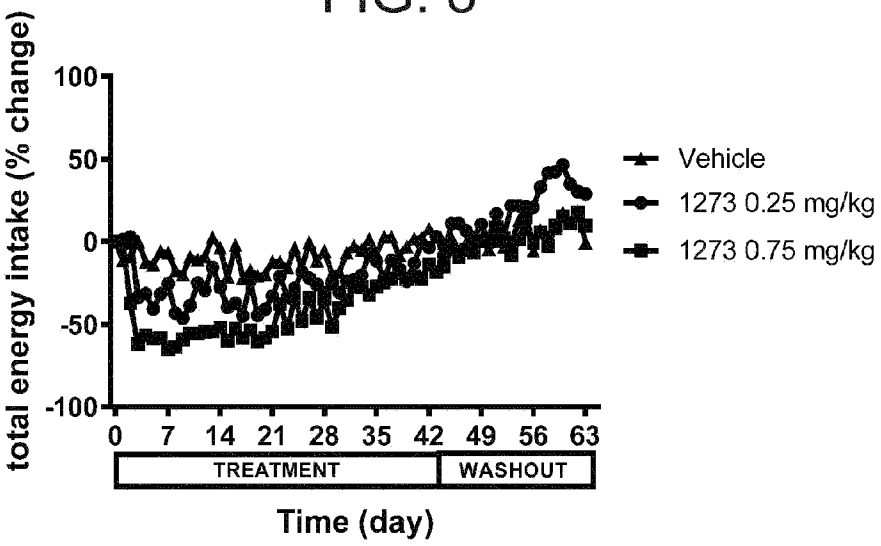

Food Intake (g/day)
4
3
2
1
0
BL
D0-3
D6-9
Vehicle
GIPR 5G12-T487C 2.5mpk
GIPR 5G12-T487C 10mpk
Dulaglutide 1mpk
Combo: GIPR + Dula
Conjugate 2.5mpk
Conjugate 10mpk

FIG. 7



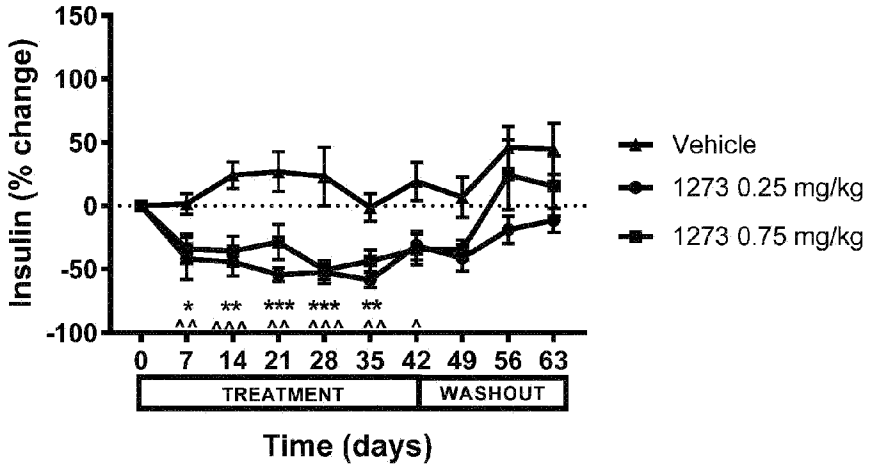
ANCOVA; ***p<0.001 vs vehicle for 0.25 mg/kg; ^^^p<0.001 vs vehicle for 0.75 mg/kg
Data represented as group mean ± SEM; n=8-9/group

FIG. 8



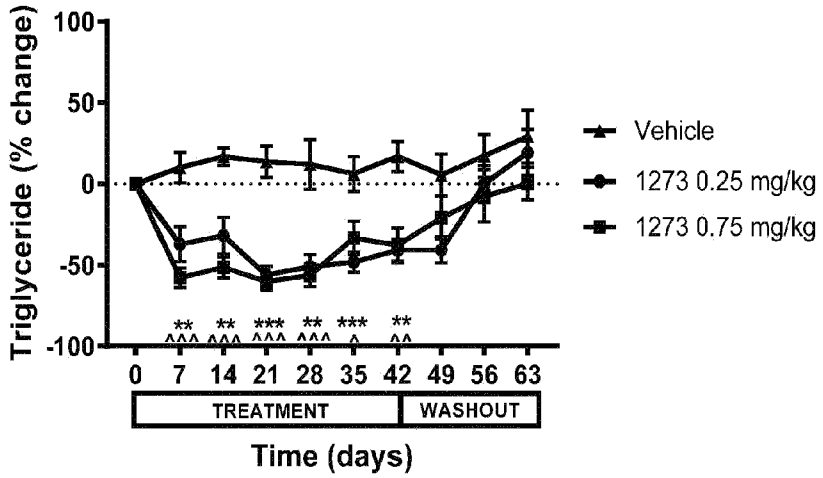
Statistical analysis not performed on total energy intake; error bars not shown; data represented as group mean; n=8-9/group

FIG. 9



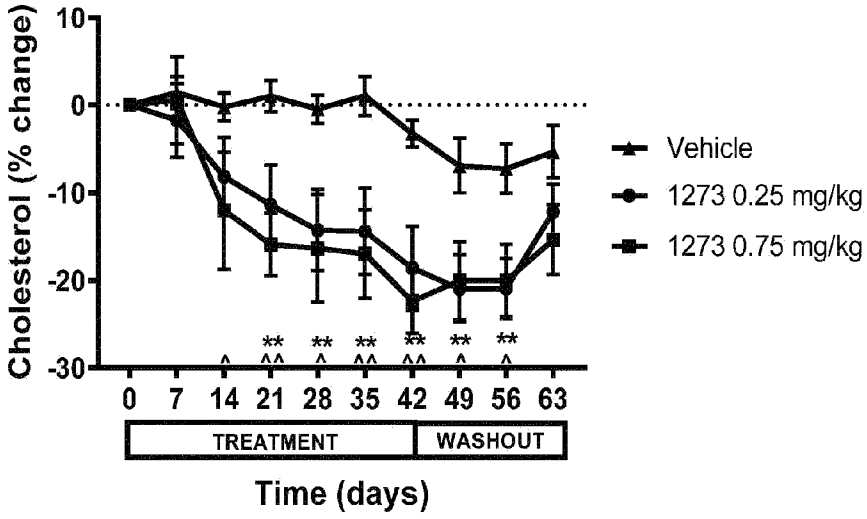
ANCOVA; *p<0.05, **p<0.01, ***p<0.001 vs vehicle for 0.25 mg/kg; ^p<0.05, ^^p<0.01, ^^^p<0.001 vs vehicle for 0.75 mg/kg Data represented as group mean ± SEM; n=8-9/group

FIG. 10



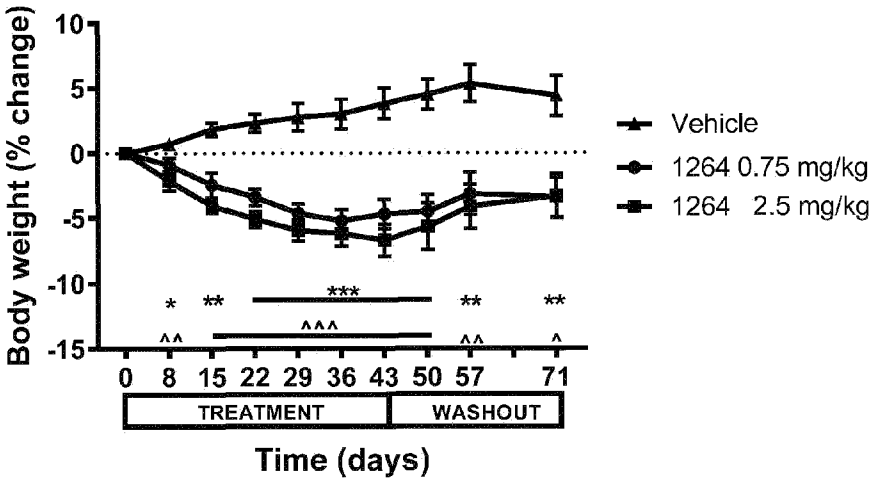
ANCOVA; **p<0.01, ***p<0.001 vs vehicle for 0.25 mg/kg; ^p<0.05, ^^p<0.01, ^^^p<0.001 vs vehicle or 0.75 mg/kg Data represented as group mean ± SEM; n=8-9/group

FIG. 11



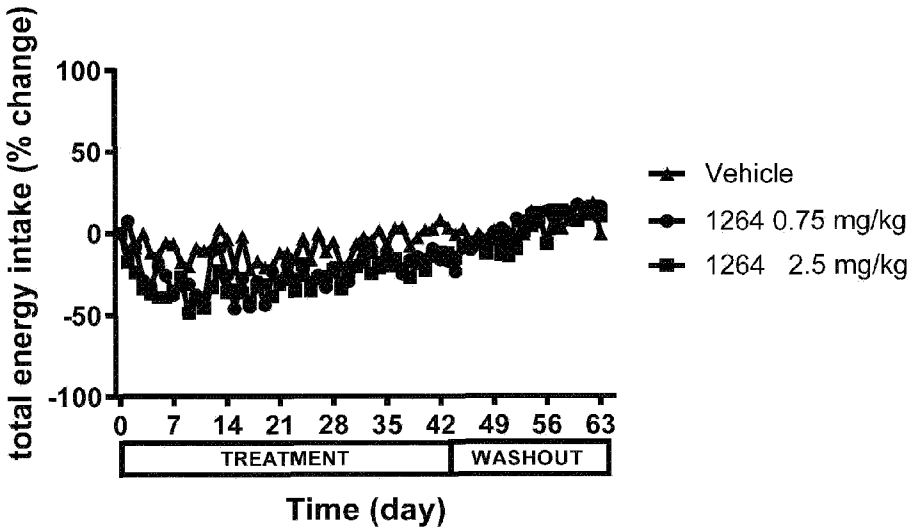
ANCOVA; **p<0.01 vs vehicle for 0.25 mg/kg; ^p<0.05, ^^p<0.01 vs vehicle for 0.75 mg/kg Data represented as group mean ± SEM; n=8-9/group

FIG. 12



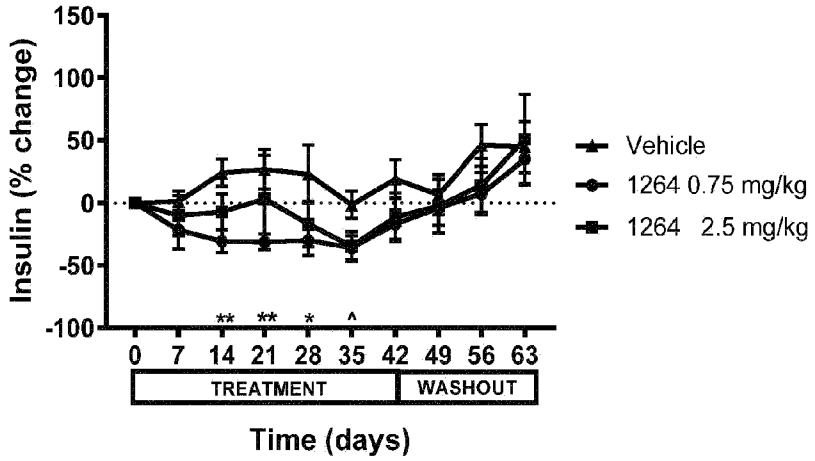
ANCOVA; *p<0.05, **p<0.01, ***p<0.001 vs vehicle for 0.75 mg/kg; ^p<0.05, ^^p<0.01, ^^^p<0.001 vs vehicle for 2.5 mg/kg Data represented as group mean ± SEM; n=9/group

FIG. 13



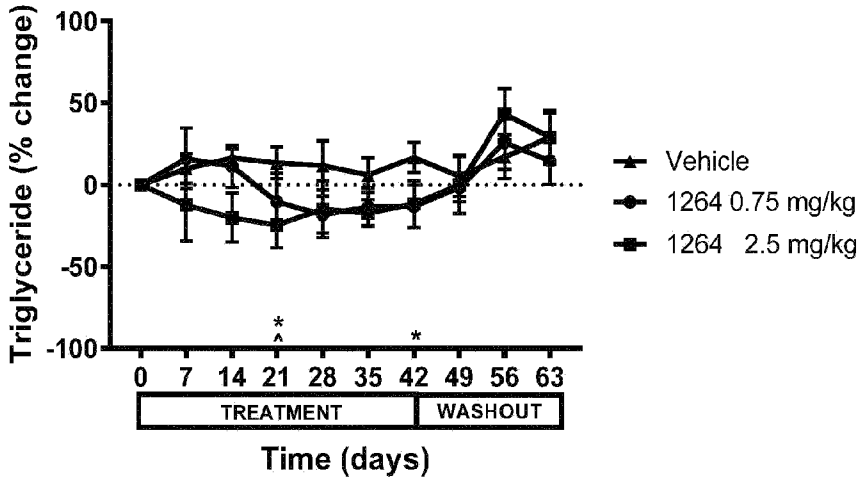
Statistical analysis not performed on total energy intake; error bars not shown; data represented as group mean; n=9/group

FIG. 14



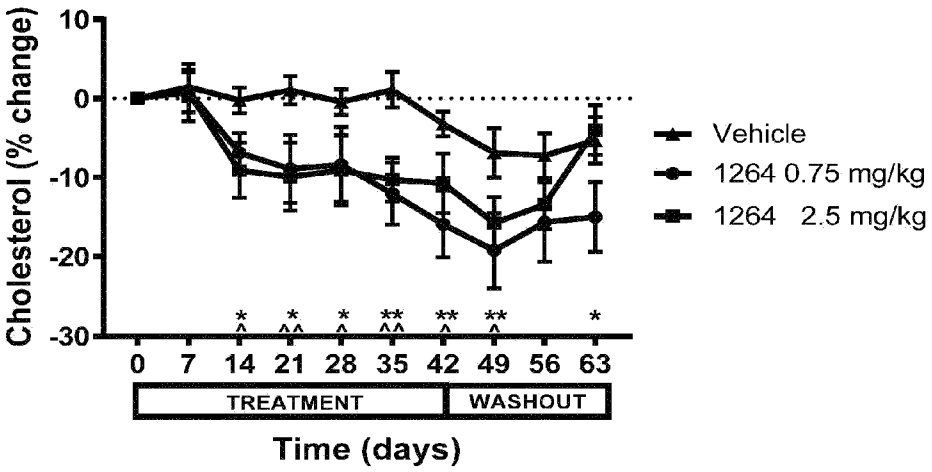
ANCOVA; *p<0.05, **p<0.01 vs vehicle for 0.75 mg/kg; ^p<0.05 vs vehicle for 2.5 mg/kg
Data represented as group mean ± SEM; n=9/group

FIG. 15



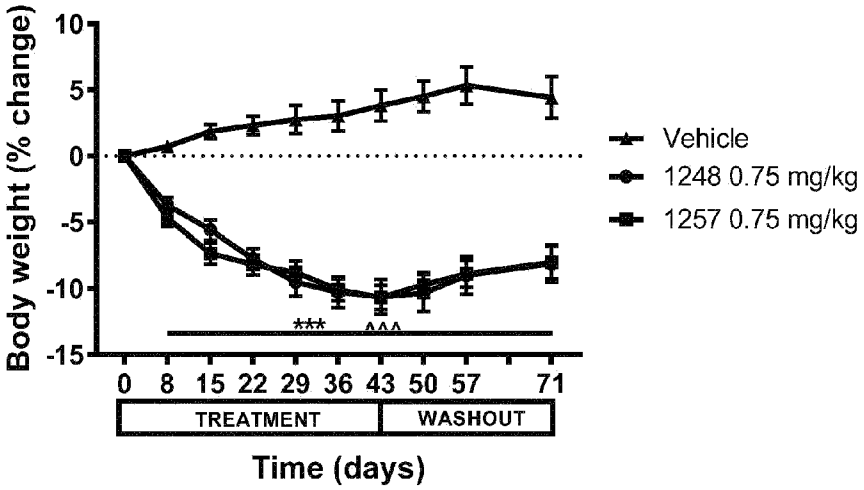
ANCOVA; *p<0.05 vs vehicle for 0.75 mg/kg; ^p<0.05 vs vehicle for 2.5 mg/kg
Data represented as group mean ± SEM; n=9/group

FIG. 16



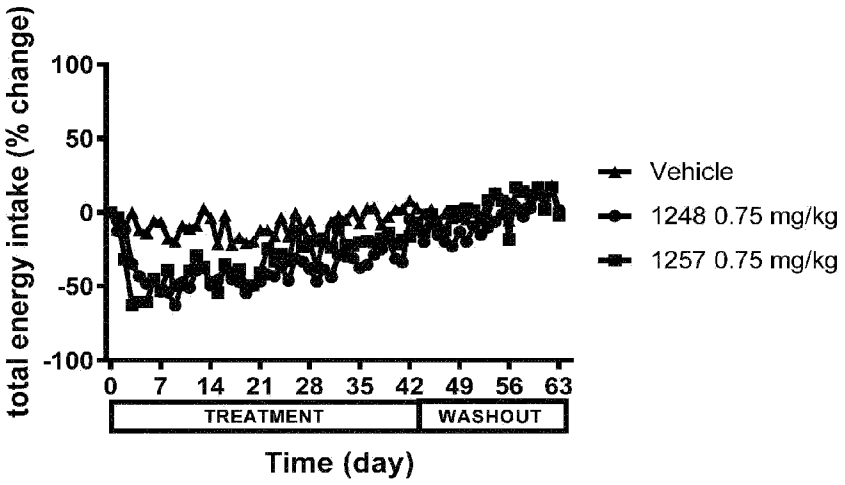
ANCOVA; *p<0.05, **p<0.01 vs vehicle for 0.75 mg/kg; ^p<0.05, ^^p<0.01 vs vehicle for 2.5 mg/kg Data represented as group mean ± SEM; n=9/group

FIG. 17



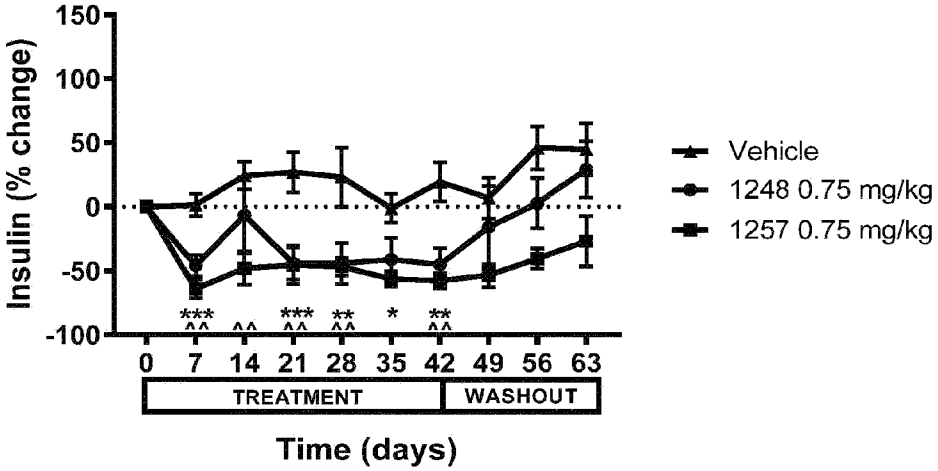
ANCOVA; ***p<0.001 vs vehicle for 1248 0.75 mg/kg; ^^^p<0.001 vs vehicle for 1257 0.75 mg/kg Data represented as group mean ± SEM; n=7-10/group

FIG. 18



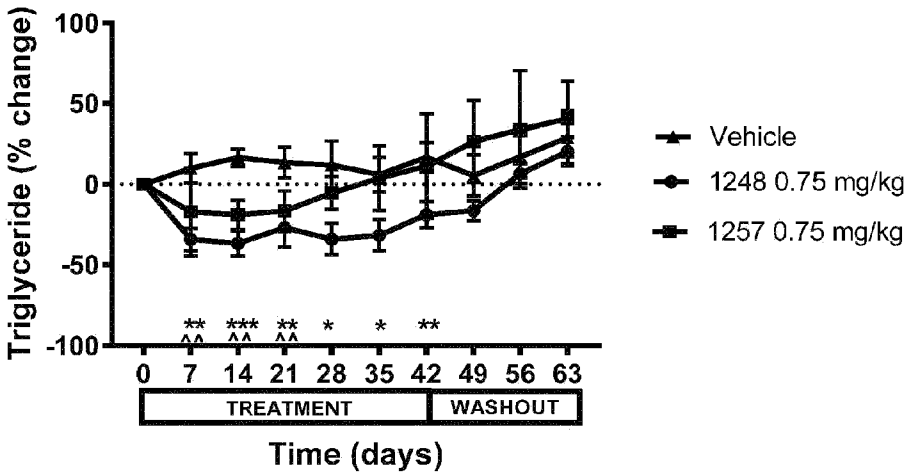
ANCOVA; ***p<0.001 vs vehicle for 1248 0.75 mg/kg; ^^^p<0.001 vs vehicle for 1257 0.75 mg/kgData represented as group mean ± SEM; n=7-10/group

FIG. 19



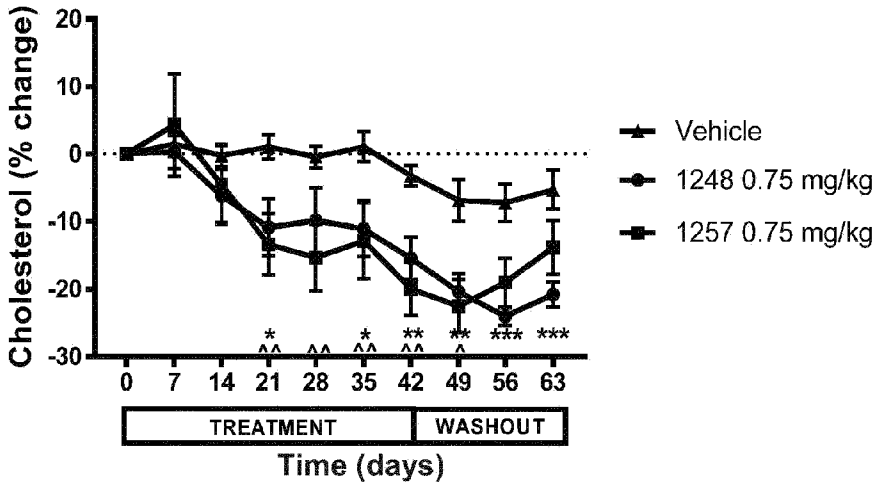
ANCOVA; *p<0.05, **p<0.01, ***p<0.001 vs vehicle for 1248 0.75 mg/kg;
^^p<0.01 vs vehicle for 1257 0.75 mg/kg
Data represented as group mean ± SEM; n=7-10/group

FIG. 20



ANCOVA; *p<0.05, **p<0.01, ***p<0.001 vs vehicle for 1248 0.75 mg/kg;
^^p<0.01 vs vehicle for 1257 0.75 mg/kg
Data represented as group mean ± SEM; n=7-10/group

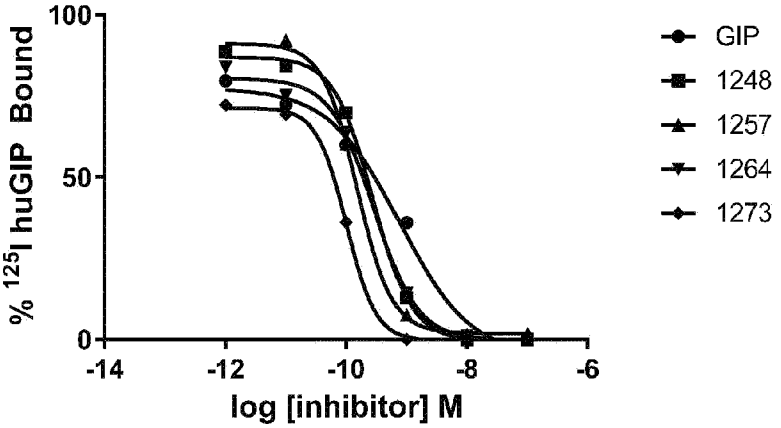
FIG. 21



ANCOVA; *p<0.05, **p<0.01, ***p<0.001 vs vehicle for 1248 0.75 mg/kg; ^p<0.05,
^^p<0.01 vs vehicle for 1257 0.75 mg/kg
Data represented as group mean ± SEM; n=7-10/group

FIG. 22A

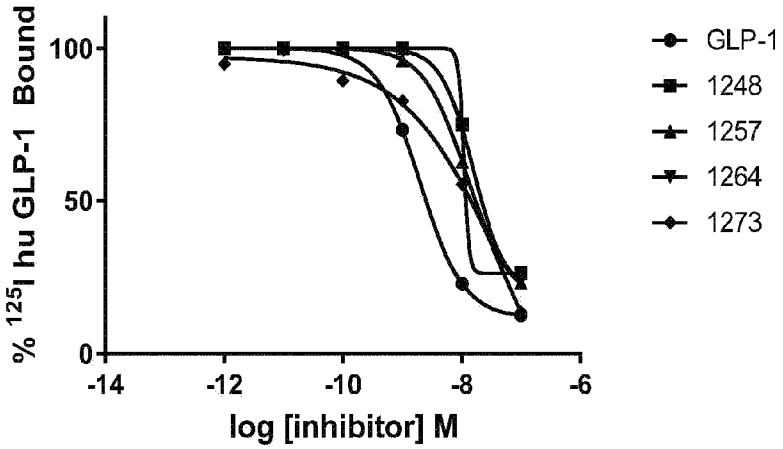
^{125}I huGIP Radioligand Binding Assay



	GIP	1248	1257	1264	1273
IC50	7.788e-010	2.806e-010	1.539e-010	2.928e-010	1.021e-010

FIG. 22B

^{125}I huGLP-1 Radioligand Binding Assay



	GLP-1	1248	1257	1264	1273
IC50	1.995e-009	1.069e-008	1.174e-008	1.548e-008	5.627e-008

FIG. 23

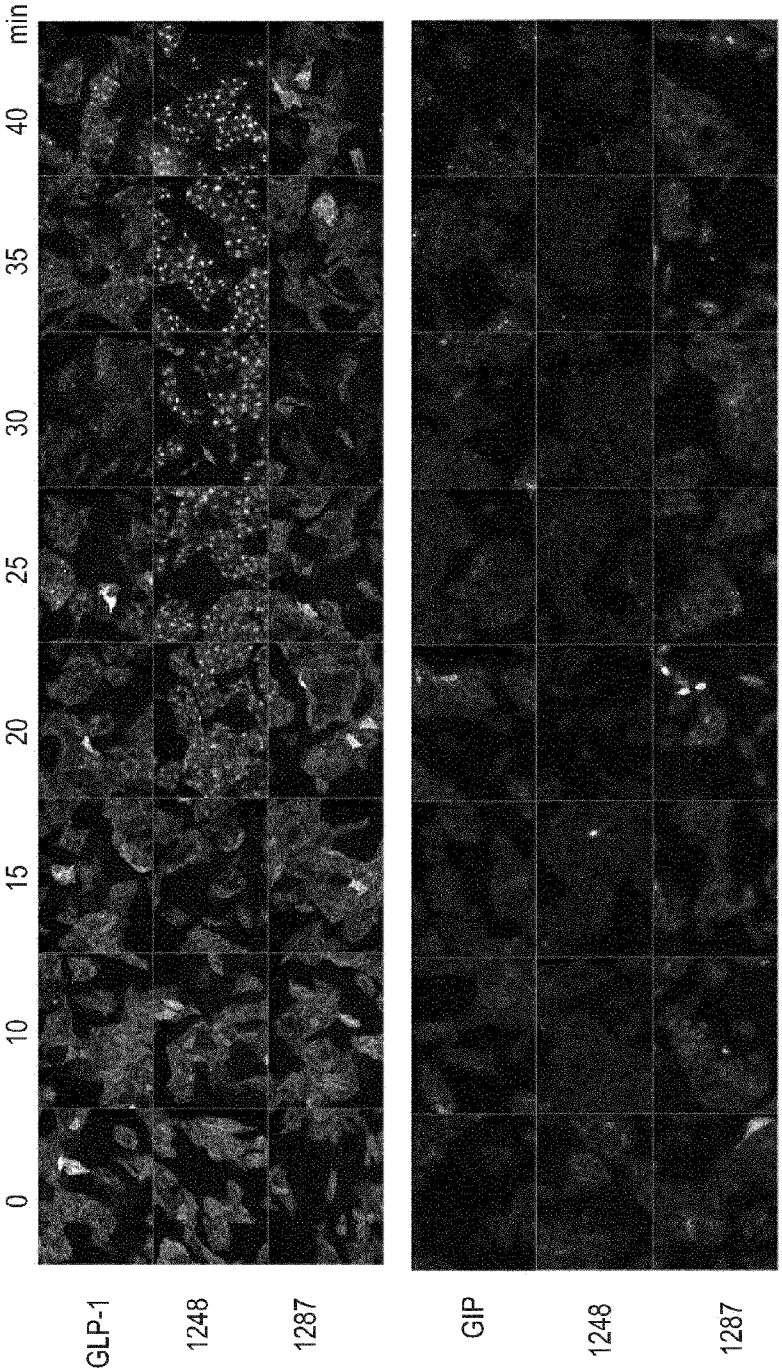


FIG. 24A

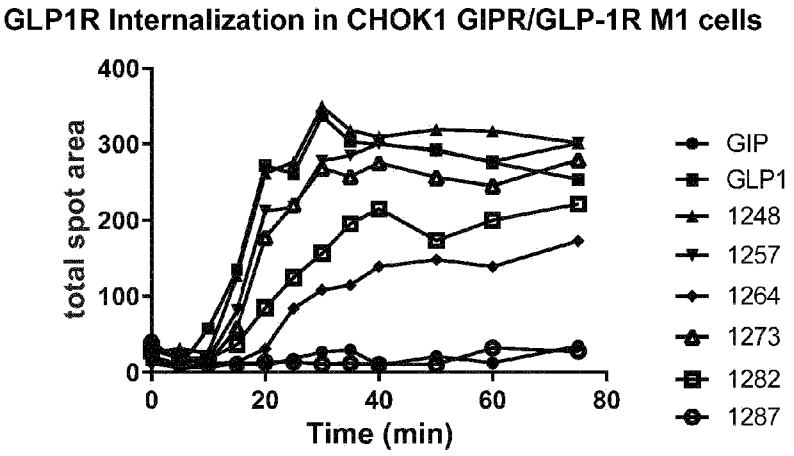
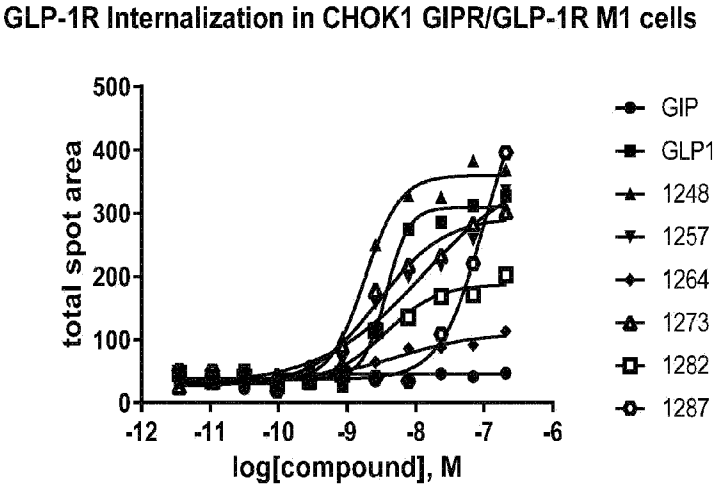


FIG. 24B



	GIP	GLP1	1248	1257	1264	1273	1282	1287
EC50	~ 9.480e-011	3.689e-009	1.834e-009	1.235e-008	5.348e-009	2.830e-009	3.606e-009	1.033e-007

FIG. 25A

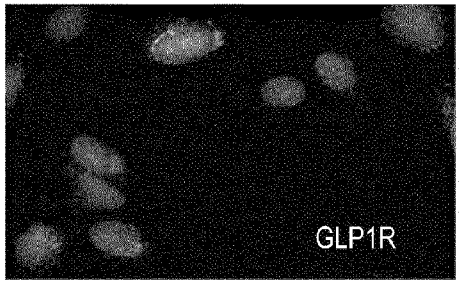


FIG. 25B

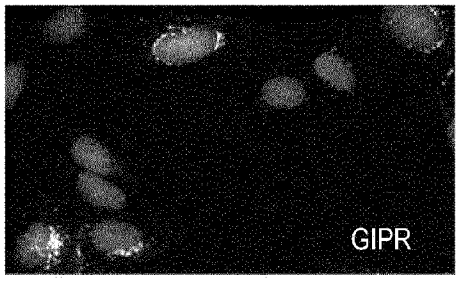


FIG. 25C

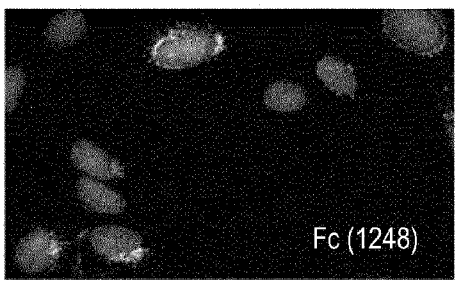


FIG. 25D

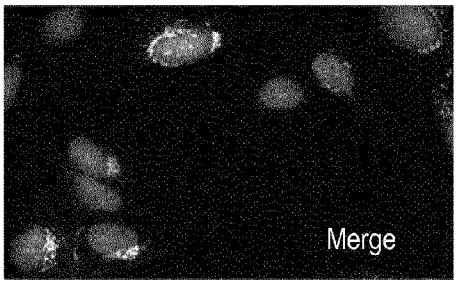


FIG. 26A

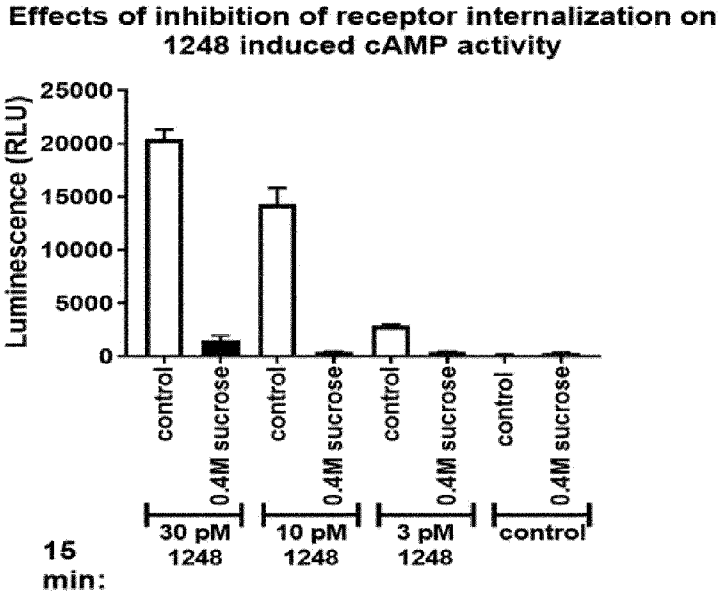


FIG. 26B

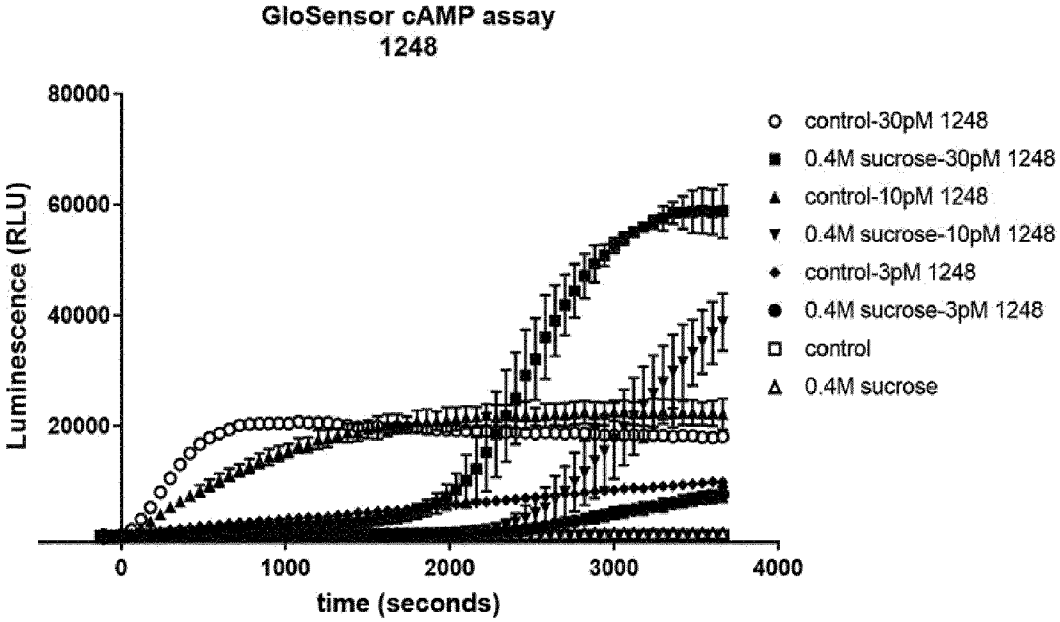


FIG. 27A

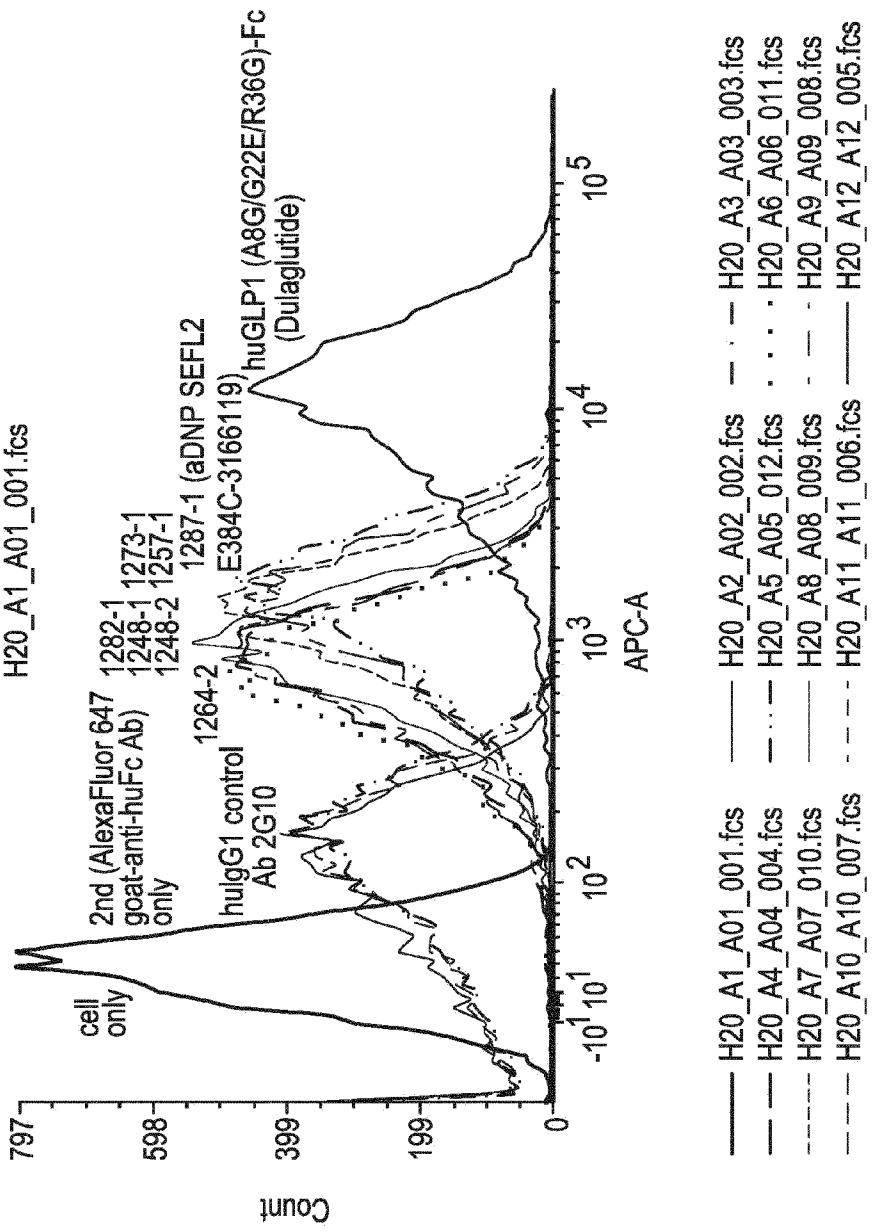

CHOK1-hGLP1R H20
H20_A1_A01_001.fcs
cell only
2nd (AlexaFluor 647 goat-anti-huFc Ab) only
hulgG1 control Ab 2G10
1264-2
1282-1
1248-1
1248-2
1273-1
1257-1
1287-1 (aDNP SEFL2 E384C-3166119)
huGLP1 (A8G/G22E/R36G)-Fc (Dulaglutide)
Count
APC-A
797
598
399
199
0
-10^1
10^1
10^2
10^3
10^4
10^5
H20_A1_A01_001.fcs
H20_A4_A04_004.fcs
H20_A7_A07_010.fcs
H20_A10_A10_007.fcs
H20_A2_A02_002.fcs
H20_A5_A05_012.fcs
H20_A8_A08_009.fcs
H20_A11_A11_006.fcs
H20_A3_A03_003.fcs
H20_A6_A06_011.fcs
H20_A9_A09_008.fcs
H20_A12_A12_005.fcs

FIG. 27B

293T-GIPR clone 10

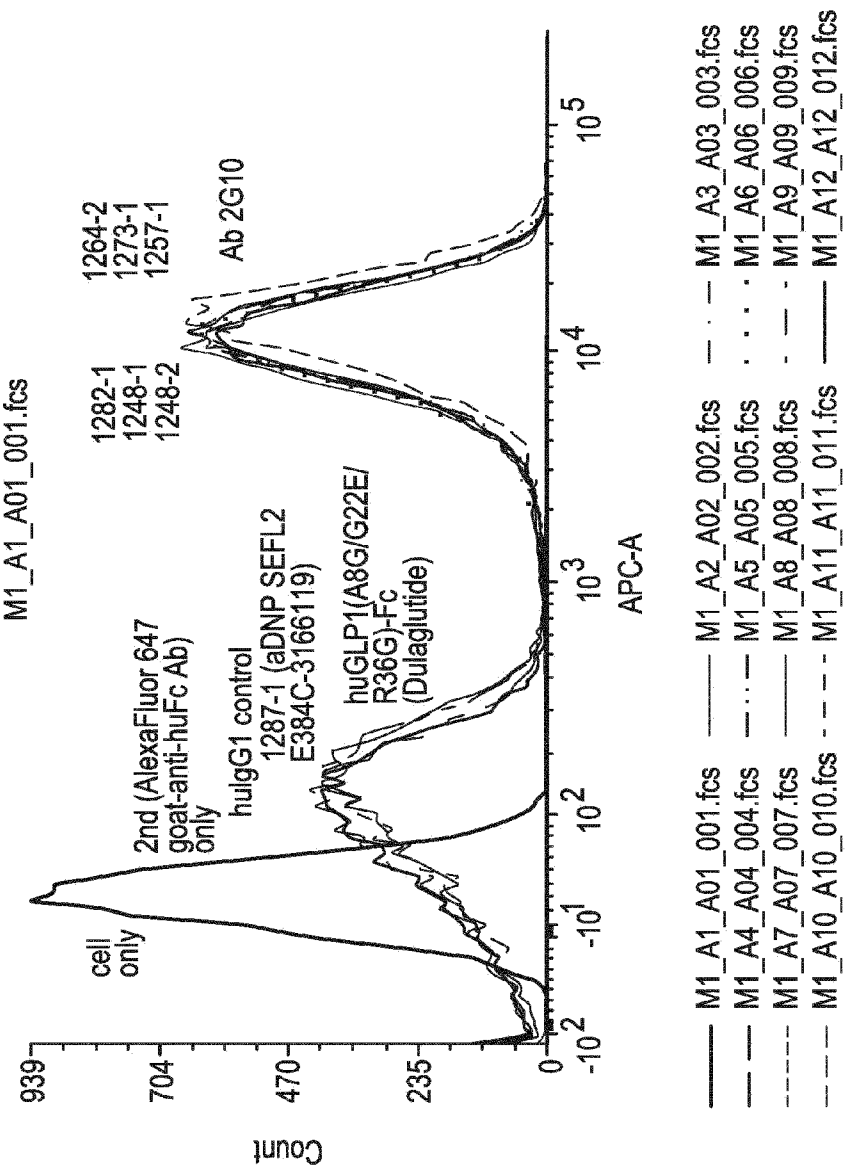


FIG. 27C

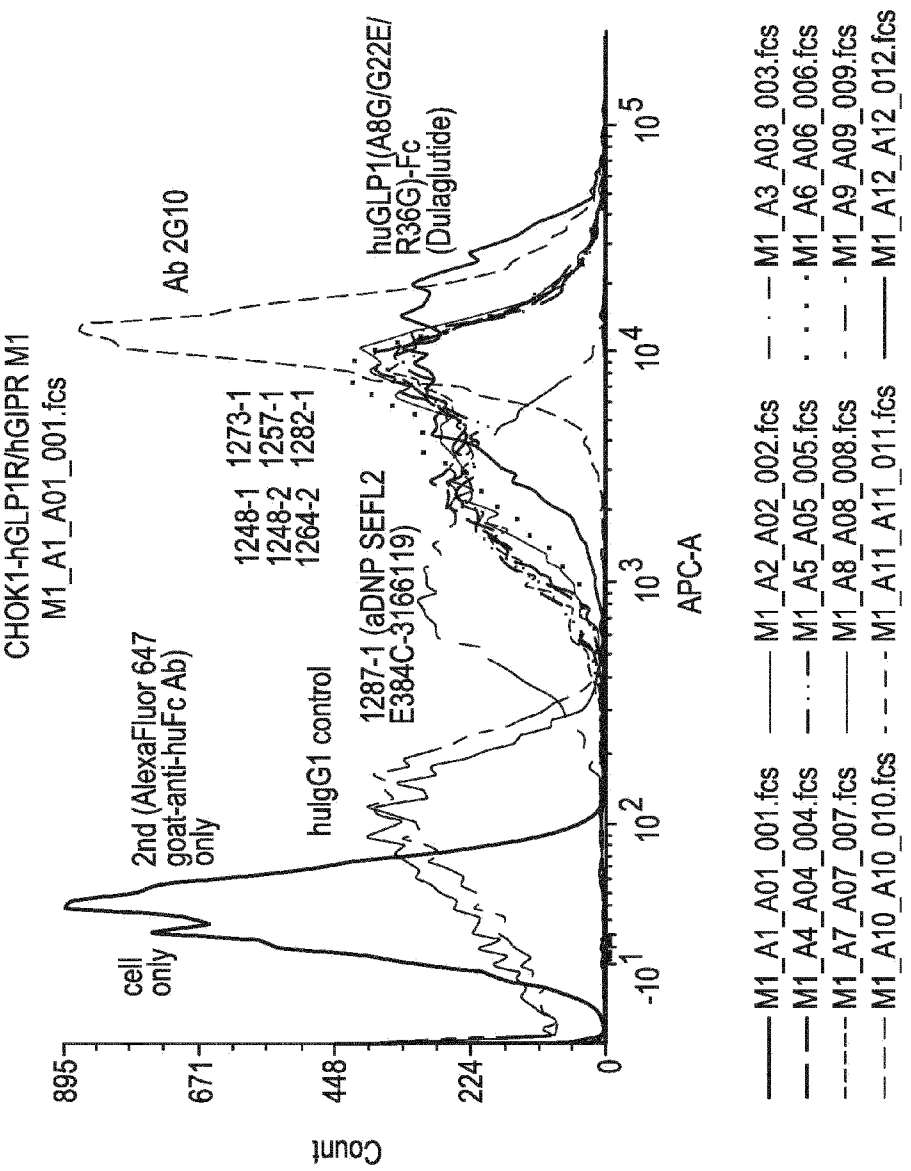
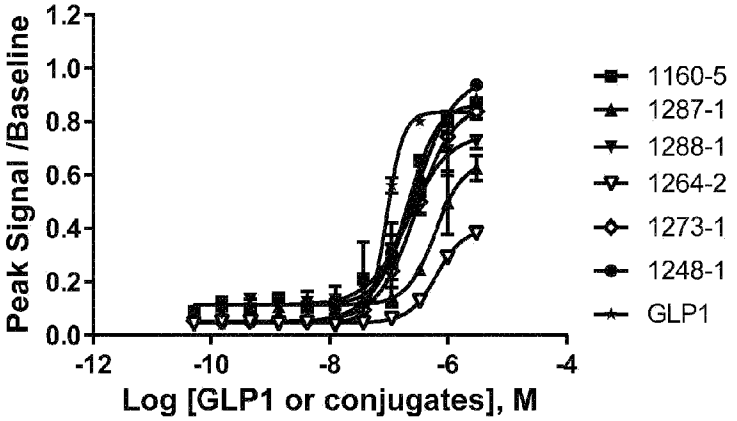

CHOK1-hGLP1R/hGIPR M1
M1_A1_A01_001.fcs
Count
895
671
448
224
0
cell only
2nd (AlexaFluor 647 goat-anti-huFc Ab) only
huIgG1 control
1287-1 (aDNP SEFL2 E384C-3166119)
1248-1 1273-1
1248-2 1257-1
1264-2 1282-1
Ab 2G10
huGLP1(A8G/G22E/R36G)-Fc (Dulaglutide)
-10^1
10^2
10^3
10^4
10^5
APC-A
M1_A1_A01_001.fcs
M1_A4_A04_004.fcs
M1_A7_A07_007.fcs
M1_A10_A10_010.fcs
M1_A2_A02_002.fcs
M1_A5_A05_005.fcs
M1_A8_A08_008.fcs
M1_A11_A11_011.fcs
M1_A3_A03_003.fcs
M1_A6_A06_006.fcs
M1_A9_A09_009.fcs
M1_A12_A12_012.fcs

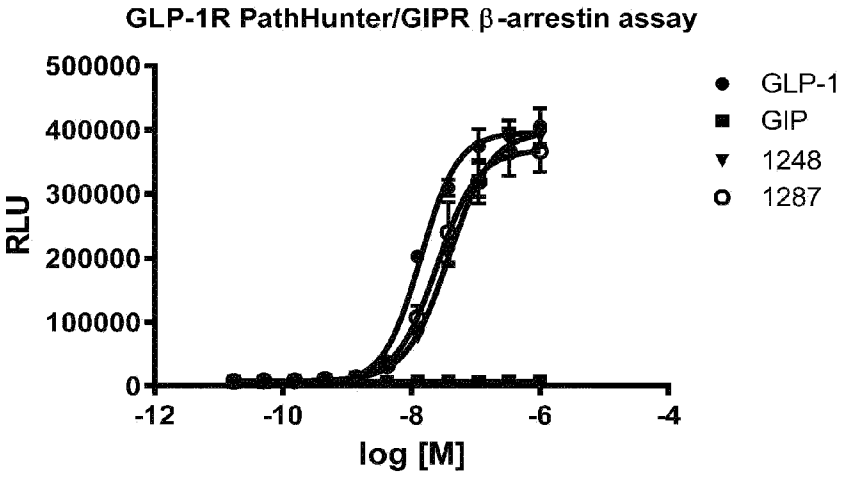
FIG. 28

Calcium Flux assay in ChoK1 GLP1R/GIPR M1 cells



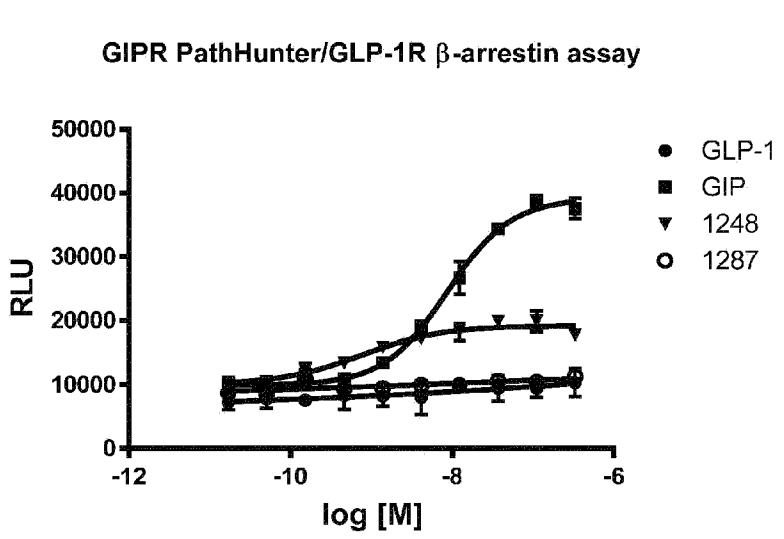
	1160-5	1287-1	1288-1	1264-2	1273-1	1248-1	GLP1
EC50	2.098e-007	6.152e-007	2.141e-007	6.485e-007	2.862e-007	2.594e-007	9.123e-008

FIG. 29A



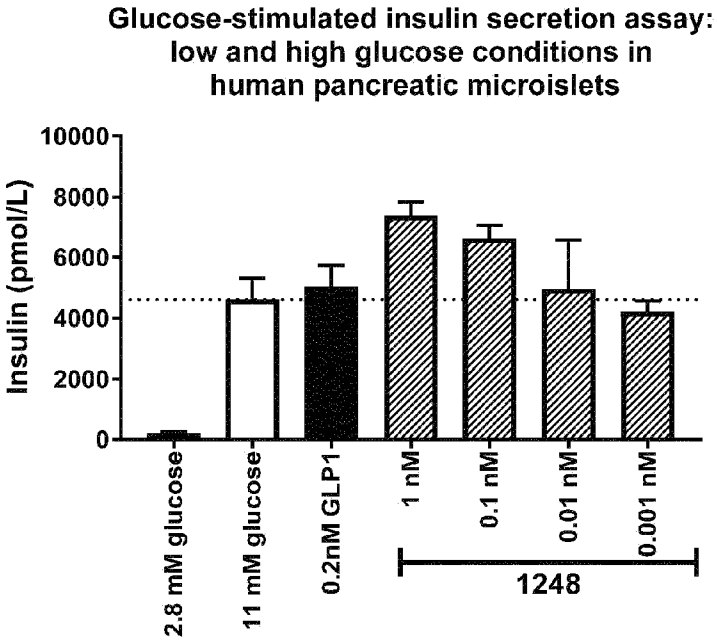
	GIP	GLP-1	1248	1287
EC50	1.974e-010	1.379e-008	3.83e-008	2.493e-008

FIG. 29B



	GLP-1	GIP	1248	1287
EC50	1.689e+017	8.702e-009	7.363e-010	~ 4.234e-006

FIG. 30


Glucose-stimulated insulin secretion assay:
low and high glucose conditions in
human pancreatic microislets
Insulin (pmol/L)
10000
8000
6000
4000
2000
0
2.8 mM glucose
11 mM glucose
0.2nM GLP1
1 nM
0.1 nM
0.01 nM
0.001 nM
1248

SEKVENSLISTE

Sekvenslisten er udeladt af skriftet og kan hentes fra det Europæiske Patent Register.

The Sequence Listing was omitted from the document and can be downloaded from the European Patent Register.