TRADUZIONE DEL BREVETTO EUROPEO N. 3570885 DAL TITOLO: "METODO PER TRATTARE O MIGLIORARE DISTURBI METABOLICI USANDO AGONISTI DEL RECETTORE DI GLP-1 CONIUGATI AD ANTAGONISTI DEL RECETTORE DEL PEPTIDE INIBITORIO GASTRICO (GIPR)"

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DESCRIZIONE

CAMPO DELL'INVENZIONE

La presente invenzione riguarda il trattamento o il miglioramento di un disturbo metabolico, come diabete di tipo 2, livelli elevati di glucosio, livelli elevati di insulina, obesità, malattia del fegato grasso non alcolica, malattie cardiovascolari o nefropatia diabetica, usando agonisti del recettore di GLP-1 coniugati a una proteina legante l'antigene specifica per il recettore del peptide inibitorio gastrico (GIPR).

STATO DELL'ARTE DELL'INVENZIONE

Il polipeptide insulinotropico glucosio-dipendente (GIP) è un singolo peptide di 42 amminoacidi secreto dalle cellule K nell'intestino tenue (duodeno e digiuno). Il GIP umano deriva dall'elaborazione di proGIP, un precursore di 153 amminoacidi che è codificato da un gene localizzato nel cromosoma 17q (Inagaki et al., Mol Endocrinol 1989; 3:1014-1021; Fehmann et al. Endocr Rev. 1995; 16:390-410). In passato, GIP era chiamato polipeptide inibitorio gastrico.

La secrezione di GIP è indotta dall'assunzione di cibo. Il GIP ha una serie di effetti fisiologici nei tessuti, tra cui la promozione

dell'accumulo di grasso negli adipociti e la promozione della funzionalità delle cellule β delle isole pancreatiche e della secrezione di insulina glucosio-dipendente. Il GIP e il polipeptide-1 simile al glucagone (GLP-1) sono noti fattori insulinotropici ("incretine"). Il GIP intatto viene rapidamente degradato dal DPPIV in una forma inattiva. L'effetto insulinotropico del GIP si perde nei pazienti con diabete di tipo 2, mentre l'effetto incretinico del GLP-1 rimane intatto (Nauck et al. J. Cline. Invest. 1993; 91:301-307).

Il recettore di GIP (GIPR) è un membro della famiglia secretina-glucagone dei recettori accoppiati alle proteine G (GPCR) aventi un N-terminale extracellulare, sette domini transmembrana e un C-terminale intracellulare. I domini extracellulari N-terminali di questa famiglia di recettori sono solitamente glicosilati e formano il dominio di riconoscimento e legame del recettore. Il GIPR è altamente espresso in numerosi tessuti, tra cui pancreas, intestino, tessuto adiposo, cuore, ipofisi, corteccia surrenale e cervello (Usdin et al., Endocrinology. 1993, 133:2861-2870). Il GIPR umano è composto da 466 amminoacidi ed è codificato da un gene situato nel cromosoma 19q13.3 (Gremlich et al., Diabetes. 1995; 44:1202-8; Volz et al., FEBS Lett. 1995, 373:23-29). Alcuni studi hanno suggerito che lo splicing alternativo dell'mRNA risulta nella produzione di varianti del recettore di GIP di differenti lunghezze negli esseri umani, nei ratti e nei topi.

I topi con knockout di GIPR ($Gipr^{-/-}$) sono resistenti all'aumento di peso indotto da una dieta ricca di grassi e hanno una sensibilità

all'insulina e profili lipidici migliorati. (Yamada et al., Diabetes. 2006, 55:S86; Miyawaki et al. Nature Med. 2002, 8:738-742). In aggiunta, un nuovo antagonista di GIPR a piccola molecola, SKL-14959, previene l'obesità e l'insulinoresistenza. (Diabetologia 2008, 51:S373, 44° poster del meeting annuale EASD).

Nel complesso, questi collegamenti con l'obesità e l'insulinoresistenza implicano che l'inibizione di GIPR sia un approccio utile per l'intervento terapeutico.

Il peptide-1 simile al glucagone è un peptide di 31 amminoacidi derivato dal gene del proglucagone. Viene secreto dalle cellule L intestinali e rilasciato in risposta all'ingestione di cibo per indurre la secrezione di insulina dalle cellule β pancreatiche (Diabetes 2004, 53:S3, 205-214). In aggiunta agli effetti incretinici, il GLP-1 diminuisce anche la secrezione di glucagone, ritarda lo svuotamento gastrico e riduce l'apporto calorico (Diabetes Care, 2003, 26(10): 2929-2940). Il GLP-1 esercita i suoi effetti mediante l'attivazione del recettore di GLP-1, che appartiene a un recettore accoppiato a proteine G di classe B (Endocrinology. 1993, 133(4):1907-10). La funzione del GLP-1 è limitata dalla rapida degradazione da parte dell'enzima DPP-IV, risultante in un'emivita di approssimativamente 2 minuti. Di recente sono stati sviluppati agonisti del recettore di GLP-1 d'azione (GLP-1 RA) a lunga durata, come exenatide, liraglutide e dulaglutide, che vengono ora usati nella clinica per migliorare il controllo glicemico nei pazienti con diabete di tipo 2. Per di più, i GLP-1RA promuovono anche la riduzione del peso

corporeo, nonché la riduzione della pressione sanguigna e dei livelli di colesterolo plasmatico nei pazienti (Bioorg. Med. Chem.Lett 2013, 23:4011-4018).

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, n. 27 (2013), concerne un anticorpo contro il recettore di GIP.

Suleiman Al-Sabah, "Molecular Pharmacology of the Incretin Receptors", Medical Principles and Practice, vol. 25, n. 1 (2015), concerne i meccanismi di segnalazione e la regolazione di GIP e GLP-1.

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) concerne gli studi sugli effetti della somministrazione di un antagonista del recettore di GIP.

Dominik Schumacher et al., "Current Status: Site-Specific Antibody Drug Conjugates", Journal of Clinical immunology, volume 36, n. 1 (2016) concerne l'attacco sito-specifico di farmaci per coniugati farmaco-anticorpo di seconda generazione.

Christopher R Behrens e Bin Liu, "Methods for site-specific drug conjugation to antibodies", MABS, volume 6, uscita 1 (2014) concerne metodi per la coniugazione sito-specifica di farmaci ad anticorpi.

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, n. 10 (2000) concerne un antagonista del recettore di GIP.

SOMMARIO DELL'INVENZIONE

L'invenzione protetta è definita nelle rivendicazioni.

I riferimenti a metodi di trattamento in questa descrizione non devono essere interpretati come protetti dalle presenti rivendicazioni in quanto tali. Piuttosto, alcune delle presenti rivendicazioni sono dirette alle composizioni della presente invenzione per uso nel trattamento di un disturbo metabolico.

In un aspetto, la presente invenzione fornisce una composizione comprendente a) un anticorpo, o suo frammento funzionale, che si lega specificamente a GIPR umano, in cui l'anticorpo, o suo frammento funzionale, comprende una sostituzione di cisteina o di amminoacido non canonico in uno o più siti di coniugazione; e b) un agonista del recettore di GLP-1, in cui l'agonista del recettore di GLP-1 è coniugato all'anticorpo, o suo frammento funzionale, attraverso la catena laterale del residuo di cisteina o del residuo di amminoacido non canonico sostituito negli uno o più siti di coniugazione, in cui l'anticorpo, o suo frammento funzionale, è un antagonista del GIPR, per uso in un metodo per trattare un soggetto con un disturbo metabolico. In una forma di realizzazione, il disturbo metabolico è un disturbo del metabolismo del glucosio. In un'altra forma di realizzazione, il disturbo del metabolismo

del glucosio comprende iperglicemia, e somministrare la proteina legante l'antigene riduce il glucosio plasmatico. In un'altra forma di realizzazione, il disturbo del metabolismo del glucosio comprende iperinsulinemia, e somministrare la proteina legante l'antigene riduce l'insulina plasmatica. In un'altra forma di realizzazione, il disturbo del metabolismo del glucosio comprende intolleranza al glucosio, e somministrare la proteina legante l'antigene riduce gli aumenti di tolleranza al glucosio. In un'altra forma di realizzazione, il disturbo del metabolismo del glucosio comprende insulinoresistenza, e somministrare la proteina legante l'antigene riduce l'insulinoresistenza. In un'altra forma di realizzazione, il disturbo del metabolismo del glucosio comprende diabete mellito. In un'altra forma di realizzazione, il soggetto è obeso. In un'altra forma di realizzazione, somministrare la composizione riduce il peso corporeo in un soggetto obeso. In un'altra forma di realizzazione, somministrare la composizione riduce un aumento di peso corporeo in un soggetto obeso. In un'altra forma di realizzazione, somministrare la composizione riduce la massa grassa in un soggetto obeso. In un'altra forma di realizzazione, il disturbo del metabolismo del glucosio comprende insulinoresistenza, e somministrare la composizione riduce l'insulinoresistenza in un soggetto obeso. In un'altra forma di realizzazione, somministrare la composizione riduce la steatosi epatica in un soggetto obeso con steatosi epatica aumentata. In un'altra forma di realizzazione, somministrare la composizione riduce il contenuto di grassi epatici in un soggetto obeso avente un contenuto di grassi epatici aumentato.

In un aspetto, la composizione comprende un anticorpo, o suo frammento funzionale, che si lega specificamente a GIPR umano, in cui l'anticorpo, o suo frammento funzionale, è un antagonista di GIPR e comprende una sostituzione di cisteina o di amminoacido non canonico in uno o più siti di coniugazione selezionati dal gruppo consistente in D70 della catena leggera di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 455; E276 della catena pesante di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 612, e T363 della catena pesante di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 612; e un agonista del recettore di GLP-1, in cui l'agonista del recettore di GLP-1 è coniugato all'anticorpo, o suo frammento funzionale, attraverso la catena laterale del residuo di cisteina o del residuo di amminoacido non canonico sostituito negli uno o più siti di coniugazione.

In una forma di realizzazione, il GIPR umano ha una sequenza comprendente una sequenza selezionata dal gruppo consistente in SEQ ID NO: 3141, SEQ ID NO: 3143, e SEQ ID NO: 3145. In una forma di realizzazione, l'anticorpo è un anticorpo monoclonale, un anticorpo ricombinante, un anticorpo umano, un anticorpo umanizzato, un anticorpo chimerico, un anticorpo multispecifico, oppure il suo frammento funzionale è un frammento funzionale di un anticorpo monoclonale, un anticorpo ricombinante, un anticorpo umano, un anticorpo umanizzato, un anticorpo chimerico, o un anticorpo multispecifico. In una forma di realizzazione, il frammento di anticorpo è un frammento Fab, un frammento Fab', o un frammento F(ab')2. In una forma di realizzazione,

l'anticorpo, o suo frammento funzionale, è del tipo IgG1, IgG2, IgG3 o IgG4. In una forma di realizzazione, l'anticorpo, o suo frammento funzionale, inibisce il legame di GIP alla porzione extracellulare di GIPR umano.

In una forma di realizzazione, l'agonista del recettore di GLP-1 è GLP-1(7-37) o un analogo di GLP-1(7-37). In una forma di realizzazione, l'agonista del recettore di GLP-1 è selezionato dal gruppo consistente in exenatide, liraglutide, lixisenatide, albiglutide, dulaglutide, semaglutide, e taspoglutide. In una forma di realizzazione, l'agonista del recettore di GLP-1 è selezionato dal gruppo consistente in GLP-1(7-37) (SEQ ID NO: 3184); GLP-1(7-36)-NH_2 (SEQ ID NO: 3185); liraglutide; albiglutide; taspoglutide, dulaglutide, semaglutide; LY2428757, Exendina-4 (SEQ ID NO: 3163); Exendina-3 (SEQ ID NO: 3164); Leu^{14}-exendina-4 (SEQ ID NO: 3165); Leu^{14},Phe^{25}-exendina-4 (SEQ ID NO: 3166); Leu^{14},Ala^{19},Phe^{25}-exendina-4 (SEQ ID NO: 3167); exendina-4(1-30) (SEQ ID NO: 3168); Leu^{14}-exendina-4(1-30) (SEQ ID NO: 3169); Leu^{14},Phe^{25}-exendina-4(1-30) (SEQ ID NO: 3170); Leu^{14},Ala^{19},Phe^{25}-exendina-4(1-30) (SEQ ID NO: 3171); exendina-4(1-28) (SEQ ID NO: 3172); Leu^{14}-exendina-4(1-28) (SEQ ID NO: 3173); Leu^{14},Phe^{25}-exendina-4(1-28) (SEQ ID NO: 3174); Leu^{14},Ala^{19},Phe^{25}-exendina-4 (1-28) (SEQ ID NO: 3175); Leu^{14},$Lys^{17,20}$,Ala^{19},Glu^{21},Phe^{25},Gln^{28}-exendina-4 (SEQ ID NO: 3176); Leu^{14},$Lys^{17,20}Ala^{19}$,$Glu^{21}Gln^{28}$-exendina-4 (SEQ ID NO: 3177); ottilGly^{14},Gln^{28}-exendina-4 (SEQ ID NO: 3178); Leu^{14},Gln^{28},ottilGly^{34}-exendina-4 (SEQ ID NO: 3179);

Phe[4],Leu[J4],Gln[28],Lys[3]3,Glu[34], Ile[35,36],Ser[37]-exendina-4(1-37) (SEQ ID NO: 3180); Phe[4],Leu[14],Lys[17,20],Ala[19],Glu[21],Gln[28]-exendina-4 (SEQ ID NO: 3181); Val[11],Ile[13],Leu[1]4,Ala[1]6,Lys[21],Phe[23]-exendina-4 (SEQ ID NO: 3182); exendina-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$_8$EGTFTSDVSSYLEXaa$_{22}$Xaa$_{23}$AAKEFIXaa$_{30}$WLXaa$_{33}$Xaa$_{34}$G Xaa$_{36}$Xaa$_{37}$; in cui Xaa$_8$ è A, V, o G; Xaa$_{22}$ è G, K, o E; Xaa$_{23}$ è Q o K; Xaa$_{30}$ è A o E; Xaa$_{33}$ è V o K; Xaa$_{34}$ è K, N, o R; Xaa$_{36}$ è R o G; e Xaa$_{37}$ è G, H, P, o assente (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],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); analogo di GLP-1 (SEQ ID NO: 3206); analogo di GLP-1 (SEQ ID NO: 3207); [N[e]-(acido 17-carbossieptadecanoico)Lys[20]]exendina-4-NH_2 (SEQ ID NO:

3208); [N^e-(17-carbossiepta-decanoil)Lys^{32}]exendina-4-NH_2 (SEQ ID NO: 3209); [desammino-His^1,N^e-(17-carbossieptadecanoil)Lys^{20}]exendina-4-NH_2 (SEQ ID NO: 3210); [$Arg^{12,27}$,NLe^{14},N^e-(17-carbossi-eptadecanoil)Lys^{32}]exendina-4-NH_2 (SEQ ID NO: 3211); [N^e-(19-carbossi-nonadecanoilammino)Lys^{20}]-exendina-4-NH_2 (SEQ ID NO: 3212); [N^e-(15-carbossipentadecanoilammino)Lys^{20}]-exendina-4-NH_2 (SEQ ID NO: 3213); [N^e-(13-carbossitridecanoilammino)Lys^{20}]exendina-4-NH_2 (SEQ ID NO: 3214); [N^e-(11-carbossi-undecanoil-ammino)Lys^{20}]exendina-4-NH_2 (SEQ ID NO: 3215); exendina-4-Lys^{40}(e-MPA)-NH_2 (SEQ ID NO: 3216); exendina-4-Lys^{40}(e-AEEA-AEEA-MPA)-NH_2 (SEQ ID NO: 3217); exendina-4-Lys^{40}(e-AEEA-MPA)-NH_2 (SEQ ID NO: 3218); exendina-4-Lys^{40}(e-MPA)-albumina (SEQ ID NO: 3219); exendina-4-Lys^{40}(e-AEEA-AEEA-MPA)-albumina (SEQ ID NO: 3220); exendina-4-Lys^{40}(e-AEEA-MPA)-albumina (SEQ ID NO: 3221); desammino-His^7, Ar^{26},Lys^{34}(N^{ε}-(γ-Glu(N-a-esadecanoil)))-GLP-1(7-37) (peptide nucleo divulgato come SEQ ID NO: 3222) (SEQ ID NO: 3222); desammino-His^7,Arg^{26},Lys^{34}(N^{ε}-ottanoil)-GLP-1(7-37) (SEQ ID NO: 3223); $Arg^{26,34}$,Lys^{38}(N^{ε}-((o-carbossipentadecanoil))-GLP-1(7-38) (SEQ ID NO: 3224); $Arg^{26,34}$,Lys^{36}(N^{ε}-(γ-Glu(N-a-esadecanoil)))-GLP-1(7-36) (peptide nucleo divulgato come 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)-ammide (SEQ ID NO: 3228); [$Aib^{8,22}$;$BLeu^{32}$;Lys^{36}]GLP-17-36)-ammide (SEQ ID NO: 3229);

[Aib^{8,22};Lys^{37}]GLP-1(7-37)-ammide (SEQ ID NO: 3230); [Aib^{8,22};BLeu^{32};Lys^{37}]GLP-1(7-37)-ammide (SEQ ID NO: 3231); [Aib^{8,22};aMeLeu^{32};Lys^{37}]GLP-1(7-37)-ammide (SEQ ID NO: 3232); [Aib^{8,22};AMEF^{12};Lys^{37}]GLP-1(7-37)-ammide (SEQ ID NO: 3233); [Aib^{8,22};BLeu^{16};Lys^{37}]GLP-1(7-37)-ammide (SEQ ID NO: 3234); [Aib^{8,22};Gly^{36};Lys^{37}]GLP-1(7-37)-ammide (SEQ ID NO: 3235); [Aib^{8,22};Lys^{33,37};Asn^{34};Gly^{36}]GLP-1(7-37)-ammide (SEQ ID NO: 3236); [Aib^{8,22};Lys^{33};Asn^{34};Gly^{36};Aeea^{37}]GLP-1(7-37)-Aeea-Lys-ammide (SEQ ID NO: 3237); [Aib^{8,22};Gly^{36}]GLP-1(7-37) (SEQ ID NO: 3238); ciclo[E^{23}-K^{27}][Aib^{8};Gly^{36}]GLP-1(7-37) (SEQ ID NO: 3239); ciclo[E^{22}-K^{26}][Aib^{8};Gly^{36};Lys^{37}]GLP-1(7-37)-ammide (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)-ammide (SEQ ID NO: 3243); [Aib^{8};Tyr^{16};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); e [Aib^{8,22};Glu^{15};Gly^{36}]GLP-1_(7-36) (SEQ ID NO: 3249).

In una forma di realizzazione, GLP-1(7-37) o l'analogo di GLP-1(7-37) è coniugato all'anticorpo, o suo frammento, in un residuo che corrisponde a K26, K36, K37, K39 o un gruppo ammina C-terminale di detto analogo.

In una forma di realizzazione, l'agonista del recettore di GLP-1 è coniugato all'anticorpo, o suo frammento, tramite un linker peptidico comprendente una sequenza selezionata dal gruppo consistente in $(Gly_3Ser)_2$, $(Gly_4Ser)_2$, $(Gly_3Ser)_3$, $(Gly_4Ser)_3$, $(Gly_3Ser)_4$, $(Gly_4Ser)_4$, $(Gly_3Ser)_5$, $(Gly_4Ser)_5$, $(Gly_3Ser)_6$, e $(Gly_4Ser)_6$.

BREVE DESCRIZIONE DEI DISEGNI

Figura 1. Schema di reazione per la generazione del coniugato di peptidi anti-GIPR/GLP-1

Figure 2A-2T. Attività di agonista del recettore di GLP-1 in cellule ricombinanti CHOK1-GLP-1R H20 e attività di antagonista di GIPR in cellule ricombinanti 293 HEK-GIPR #10

Figure 3A-3C. L'attività di agonista di GLP-1 del coniugato 2G10 è più potente in cellule esprimenti sia GLP-1R che GIPR (CHOK1 hGLP-1R/hGIPR M1) rispetto a cellule esprimenti solo GLP-1R (CHOK1 hGLP-1R H20)

Figure 4A-4R. Attività in vivo: effetti del glucosio e del peso corporeo in topi db/db

Figure 5A-5D. Attività di agonista del recettore di GLP-1 e di antagonista di GIPR in vivo dei coniugati chimici SG12 e 2G10 in topi C57Bl6 (test di tolleranza al glucosio)

Figure 6A-6B. Attività di agonista del recettore di GLP-1 e di antagonista di GIPR in vivo dei coniugati chimici SG12 e 2G10 in topi DIO (glucosio plasmatico e cambiamento di peso corporeo)

Figura 7. Il coniugato bispecifico GLP-1R-GIPR 1273 riduce il peso corporeo in scimmie cinomolgo spontaneamente obese maschio (% di cambiamento rispetto al basale)

Figura 8. Il coniugato bispecifico GLP-1R-GIPR 1273 riduce l'apporto di energia totale in scimmie cinomolgo spontaneamente obese maschio (% di cambiamento rispetto al basale)

Figura 9. Il coniugato bispecifico GLP-1R-GIPR 1273 riduce l'insulina a digiuno in scimmie cinomolgo spontaneamente obese maschio (% di cambiamento rispetto al basale)

Figura 10. Il coniugato bispecifico GLP-1R-GIPR 1273 riduce i trigliceridi a digiuno in scimmie cinomolgo spontaneamente obese maschio (% di cambiamento rispetto al basale)

Figura 11. Il coniugato bispecifico GLP-1R-GIPR 1273 riduce il colesterolo totale a digiuno in scimmie cinomolgo spontaneamente obese maschio (% di cambiamento rispetto al basale)

Figura 12. Il coniugato bispecifico GLP-1R-GIPR 1264 riduce il peso corporeo in scimmie cinomolgo spontaneamente obese maschio (% di cambiamento rispetto al basale)

Figura 13. Il coniugato bispecifico GLP-1R-GIPR 1264 riduce l'apporto di energia totale in scimmie cinomolgo spontaneamente obese maschio (% di cambiamento rispetto al basale)

Figura 14. Il coniugato bispecifico GLP-1R-GIPR 1264 riduce l'insulina a digiuno in scimmie cinomolgo spontaneamente obese maschio (% di cambiamento rispetto al basale)

Figura 15. Il coniugato bispecifico GLP-1R-GIPR 1264 riduce i trigliceridi a digiuno in scimmie cinomolgo spontaneamente obese maschio (% di cambiamento rispetto al basale)

Figura 16. Il coniugato bispecifico GLP-1R-GIPR 1264 riduce il colesterolo totale a digiuno in scimmie cinomolgo spontaneamente obese maschio (% di cambiamento rispetto al basale)

Figura 17. I coniugati bispecifici GLP-1R-GIPR 1248 e 1257 riducono il peso corporeo in scimmie cinomolgo spontaneamente obese maschio (% di cambiamento rispetto al basale)

Figura 18. I coniugati bispecifici GLP-1R-GIPR 1248 e 1257 riducono l'apporto di energia totale in scimmie cinomolgo spontaneamente obese maschio (% di cambiamento rispetto al basale)

Figura 19. I coniugati bispecifici GLP-1R-GIPR 1248 e 1257 riducono l'insulina a digiuno in scimmie cinomolgo spontaneamente obese (% di cambiamento rispetto al basale)

Figura 20. I coniugati bispecifici GLP-1R-GIPR 1248 e 1257 riducono i trigliceridi a digiuno in scimmie cinomolgo spontaneamente obese maschio (% di cambiamento rispetto al basale)

Figura 21. I coniugati bispecifici GLP-1R-GIPR 1248 e 1257 riducono il colesterolo a digiuno in scimmie cinomolgo spontaneamente obese maschio (% di cambiamento rispetto al basale)

Figure 22A-22B. Affinità di legame di coniugati bispecifici anti-GIPR/GLP-1R

Figura 23. Il coniugato bispecifico anti-GIPR/GLP-1R 1248 promuove una forte internalizzazione di GLP-1R e GIPR in cellule esprimenti sia GLP-1R che GIPR

Figure 24A-24B. Andamento temporale e risposta alla dose di coniugati bispecifici anti-GIPR/GLP-1R in un saggio di internalizzazione di GLP-1R

Figure 25A-25D. GLP-1R, GIPR e coniugato bispecifico si co-localizzano dopo l'internalizzazione

Figure 26A-26B. L'inibizione dell'internalizzazione del recettore riduce la generazione di cAMP indotta da 1248

Figure 27A-27C. I coniugati bispecifici mostrano il legame a GLP-1R e GIPR in un'analisi FACS

Figura 28. I coniugati bispecifici anti-GIPR/GLP-1R stimolano il flusso di calcio

Figure 29A-29B. Il coniugato bispecifico anti-GIPR/GLP-1R 1248 promuove il reclutamento della beta-arrestina attraverso le vie di GLP-1R e GIPR

Figura 30. Il coniugato bispecifico anti-GIPR/GLP-1R 1248 stimola la secrezione di insulina in micro-isole pancreatiche umane.

DESCRIZIONE DETTAGLIATA DELL'INVENZIONE

La presente invenzione riguarda una composizione comprendente a) un anticorpo, o suo frammento funzionale, che si lega specificamente a GIPR umano, in cui l'anticorpo, o suo frammento funzionale, comprende una sostituzione di cisteina o di amminoacido non

canonico in uno o più siti di coniugazione; e un agonista del recettore di GLP-1, in cui l'agonista del recettore di GLP-1 è coniugato all'anticorpo, o suo frammento funzionale, attraverso la catena laterale del residuo di cisteina o del residuo di amminoacido non canonico sostituito negli uno o più siti di coniugazione, in cui l'anticorpo, o suo frammento funzionale, è un antagonista di GIPR, per uso in un metodo per trattare un disturbo metabolico, come un disturbo del metabolismo del glucosio (ad esempio diabete di tipo 2, livelli elevati di glucosio, livelli elevati di insulina, dislipidemia, sindrome metabolica (sindrome X o sindrome da insulinoresistenza), glicosuria, acidosi metabolica, neuropatia diabetica, nefropatia diabetica, retinopatia diabetica, cardiomiopatia diabetica, diabete di tipo 1, obesità e condizioni esacerbate dall'obesità) bloccando o interferendo con l'attività biologica di GIP. Vengono inoltre forniti metodi di somministrazione ed erogazione.

I metodi con polipeptidi ricombinanti e acidi nucleici usati nella presente, inclusi gli esempi, sono generalmente quelli esposti in Sambrook et al., Molecular Cloning: A Laboratory Manual (Cold Spring Harbor Laboratory Press, 1989) o Current Protocols in Molecular Biology (Ausubel et al., curatori, Green Publishers Inc. e Wiley and Sons 1994).

Le intestazioni di sezione usate nella presente sono soltanto a scopo organizzativo e non devono essere interpretate come limitanti l'argomento in oggetto descritto.

Se non diversamente definito nella presente, i termini scientifici e tecnici usati in relazione alla presente domanda avranno i significati

comunemente compresi dai comuni tecnici del ramo. Inoltre, se non richiesto diversamente dal contesto, i termini singolari includeranno i plurali e i termini plurali includeranno il singolare.

Generalmente, le nomenclature usate in connessione con, e le tecniche di, coltura di cellule e tessuti, biologia molecolare, immunologia, microbiologia, genetica e chimica e ibridazione di proteine e acidi nucleici descritte nella presente sono quelle ben note e comunemente usate nell'arte. I metodi e le tecniche della presente domanda sono generalmente eseguiti secondo metodi convenzionali ben noti nell'arte e come descritto in vari riferimenti generali e più specifici che sono menzionati e discussi nella presente descrizione, salvo indicato diversamente. Si veda, ad esempio, Sambrook et al., Molecular Cloning: A Laboratory Manual, 3a ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (2001), Ausubel et al., Current Protocols in Molecular Biology, Greene Publishing Associates (1992), e Harlow e Lane Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1990). Le reazioni enzimatiche e le tecniche di purificazione vengono eseguite secondo le indicazioni del produttore, come comunemente realizzato nell'arte o come descritto nella presente. La terminologia usata in connessione con, e le procedure e le tecniche di, laboratorio di chimica analitica, chimica organica sintetica e chimica medicinale e farmaceutica descritte nella presente sono quelle ben note e comunemente usate nell'arte. Tecniche standard possono essere usate

per le sintesi chimiche, le analisi chimiche, la preparazione farmaceutica, la formulazione, l'erogazione, e il trattamento dei pazienti.

Resta inteso che questa invenzione non è limitata alla metodologia, ai protocolli, ai reagenti, eccetera, particolari descritti nella presente, e, di fatto, può variare. La terminologia usata nella presente ha lo scopo di descrivere solo particolari forme di realizzazione e non intende limitare la portata di quanto divulgato, che è definita esclusivamente dalle rivendicazioni.

Salvo quanto previsto negli esempi operativi, o laddove diversamente indicato, tutti i numeri esprimenti quantitativi di ingredienti o condizioni di reazione usati nella presente devono essere intesi come modificati in tutte le esemplificazioni dal termine "circa". Il termine "circa", quando usato in relazione alle percentuali, può significare ±1%.

Per convenzione, secondo l'uso fattone nella presente, i termini "un/una/un'/uno" significano "uno o più", salvo diversa indicazione specifica.

Secondo l'uso fattone nella presente, i termini "amminoacido" e "residuo" sono intercambiabili e, quando usati nel contesto di un peptide o di un polipeptide, si riferiscono sia ad amminoacidi presenti in natura sia ad amminoacidi sintetici, nonché ad analoghi di amminoacidi, mimetici di amminoacidi e amminoacidi non presenti in natura che sono chimicamente simili agli amminoacidi presenti in natura.

Un "amminoacido presente in natura" è un amminoacido che è codificato dal codice genetico, così come gli amminoacidi che sono

codificati dal codice genetico che vengono modificati dopo la sintesi, ad esempio idrossiprolina, γ-carbossiglutammato, e O-fosfoserina. Un analogo di amminoacido è un composto che ha la stessa struttura chimica di base di un amminoacido presente in natura, ossia un carbonio α che è legato a un idrogeno, un gruppo carbossile, un gruppo ammino, e un gruppo R, ad esempio omoserina, norleucina, metionina solfossido, metionina metilsolfonio. Tali analoghi possono avere gruppi R modificati (ad esempio, norleucina) o scheletri di peptide modificati, ma manterranno la stessa struttura chimica di base di un amminoacido presente in natura.

Un "mimetico di amminoacido" è un composto chimico che ha una struttura che è differente dalla struttura chimica generale di un amminoacido, ma che funziona in modo simile a un amminoacido presente in natura. Esempi includono un derivato di metacriloile o acriloile di un'ammide, β-, γ-, δ-imminoacidi (come acido piperidin-4-carbossilico), e simili.

Un "amminoacido non presente in natura" è un composto che ha la stessa struttura chimica di base di un amminoacido presente in natura, ma non è incorporato in una catena di polipeptide in crescita dal complesso di traduzione. "Amminoacido non presente in natura" include anche, ma senza limitarvisi, amminoacidi che si verificano mediante modifica (ad esempio, modifiche post-traduzionali) di un amminoacido codificato naturalmente (inclusi, ma senza limitarvisi, i 20 amminoacidi comuni) ma che non sono essi stessi incorporati naturalmente in una

catena di polipeptide in crescita dal complesso di traduzione. Un elenco non limitativo di esempi di amminoacidi non presenti in natura che possono essere inseriti in una sequenza di polipeptide o sostituiti con un residuo di tipo selvatico in una sequenza di polipeptide include β-amminoacidi, omoamminoacidi, amminoacidi ciclici e amminoacidi con catene laterali derivatizzate. Esempi includono (nella forma L o D; abbreviati come tra parentesi): citrullina (Cit), omocitrullina (hCit), Nα-metilcitrullina (NMeCit), Nα-metilomocitrullina (Nα-MeHoCit), ornitina (Orn), Nα-metilornitina (Nα-MeOrn o NMeOrn), sarcosina (Sar), omolisina (hLys o hK), omoarginina (hArg o hR), omoglutammina (hQ), Nα-metilarginina (NMeR), Nα-metilleucina (Nα-MeL o NMeL), N-metilomolisina (NMeHoK), Nα-metilglutammina (NMeQ), norleucina (Nle), norvalina (Nva), 1,2,3,4-tetraidroisochinolina (Tic), acido ottaidroindolo-2-carbossilico (Oic), 3-(1-naftil)alanina (1-Nal), 3-(2-naftil)alanina (2-Nal), 1,2,3,4-tetraidroisochinolina (Tic), 2-indanilglicina (IgI), para-iodofenilalanina (pI-Phe), para-amminofenilalanina (4AmP o 4-Ammino-Phe), 4-guanidino fenilalanina (Guf), glicillisina (abbreviato "K(Nε-glicile)" o "K(glicile)" o "K(gly)"), nitrofenilalanina (nitrofe), amminofenilalanina (amminofe o Ammino-Phe), benzilfenilalanina (benzilfe), acido γ-carbossiglutammico (γ-carbossiglu), idrossiprolina (idrossipro), p-carbossil-fenilalanina (Cpa), acido α-amminoadipico (Aad), Nα-metil valina (NMeVal), N-α-metil leucina (NMeLeu), Nα-metilnorleucina (NMeNle), ciclopentilglicina (Cpg), cicloesilglicina (Chg), acetilarginina (acetilarg), acido α, β-diamminopropionoico (Dpr), acido α,

γ-diamminobutirrico (Dab), acido diamminopropionico (Dap), cicloesilalanina (Cha), 4-metil-fenilalanina (MePhe), β, β-difenil-alanina (BiPhA), acido amminobutirrico (Abu), 4-fenil-fenilalanina (o bifenilalanina; 4Bip), acido α-ammino-isobutirrico (Aib), beta-alanina, acido beta-amminopropionico, acido piperidinico, acido amminocaprioico, acido amminoeptanoico, acido amminopimelico, desmosina, acido diamminopimelico, N-etilglicina, N-etilaspargina, idrossilisina, allo-idrossilisina, isodesmosina, alloisoleucina, N-metilglicina, N-metilisoleucina, N-metilvalina, 4-idrossiprolina (Hyp), γ-carbossiglutammato, ε-N,N,N-trimetillisina, ε-N-acetillisina, O-fosfoserina, N-acetilserina, N-formilmetionina, 3-metilistidina, 5-idrossilisina, ω-metilarginina, acido 4-ammino-O-ftalico (4APA), e altri amminoacidi simili, e forme derivatizzate di qualsiasi di quelli specificatamente elencati.

Il termine "molecola di acido nucleico isolato" si riferisce a un polimero a singolo o doppio filamento di basi deossiribonucleotidiche o ribonucleotidiche lette dall'estremità 5' a quella 3' (ad esempio, una sequenza di acido nucleico di GIPR fornita nella presente), o un suo analogo, che è stato separato da almeno circa il 50 percento di polipeptidi, peptidi, lipidi, carboidrati, polinucleotidi o altri materiali con cui l'acido nucleico si trova naturalmente quando l'acido nucleico totale viene isolato dalle cellule di origine. Preferibilmente, una molecola di acido nucleico isolato è sostanzialmente priva di qualsiasi altra molecola di acido nucleico contaminante o di altre molecole che si trovano

nell'ambiente naturale dell'acido nucleico che potrebbero interferire con il suo uso nella produzione di polipeptidi o con il suo uso terapeutico, diagnostico, profilattico o di ricerca.

Il termine "polipeptide isolato" si riferisce a un polipeptide (ad esempio, una sequenza di polipeptide di GIPR fornita nella presente o una proteina legante l'antigene della presente invenzione) che è stato separato da almeno circa il 50 percento di polipeptidi, peptidi, lipidi, carboidrati, polinucleotidi o altri materiali con cui il polipeptide si trova naturalmente quando isolato da una cellula di origine. Preferibilmente, il polipeptide isolato è sostanzialmente privo di qualsiasi altro polipeptide contaminante o di altri contaminanti che si trovano nel suo ambiente naturale che potrebbero interferire con il suo uso terapeutico, diagnostico, profilattico o di ricerca.

Una composizione della presente invenzione che include un agonista del recettore di GLP-1 dell'invenzione collegato, attaccato o legato in modo covalente, direttamente o indirettamente attraverso una frazione linker, a un'altra proteina legante l'antigene anti-GIPR dell'invenzione è un "coniugato" o una molecola "coniugata", indipendentemente dal fatto che sia coniugata con mezzi chimici (ad esempio, post-traduzionalmente o post-sinteticamente).

Il termine "codificante" si riferisce a una sequenza polinucleotidica codificante uno o più amminoacidi. Il termine non richiede un codone di avvio o di arresto.

I termini "identico/a" e percentuale di "identità", nel contesto di due o più acidi nucleici o sequenze di polipeptide, si riferiscono a due o più sequenze o sotto-sequenze che sono le stesse sequenze. Per "percentuale di identità" significa la percentuale di residui identici tra gli amminoacidi o i nucleotidi nelle molecole confrontate e viene calcolata in base alla dimensione della più piccola delle molecole confrontate. Per questi calcoli, eventuali gap negli allineamenti (se presenti) possono essere affrontati mediante un particolare modello matematico o programma per computer (ossia un "algoritmo"). I metodi che possono essere usati per calcolare l'identità degli acidi nucleici o dei polipeptidi allineati includono quelli descritti 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, Parte I, (Griffin, A. M., e Griffin, H. G., curatori), 1994, New Jersey: Humana Press; von Heinje, G., (1987) Sequence Analysis in Molecular Biology, New York: Academic Press; Sequence Analysis Primer, (Gribskov, M. e Devereux, J., curatori), 1991, New York: M. Stockton Press; e Carillo et al., (1988) SIAM J. Applied Math. 48:1073.

Nel calcolo dell'identità percentuale, le sequenze confrontate vengono allineate in un modo che dà la massima corrispondenza tra le sequenze. Il programma per computer usato per determinare la percentuale di identità è il pacchetto di programmi GCG, che include GAP (Devereux et al., (1984) Nucl. Acid Res. 12:387; Genetics Computer

Group, University of Wisconsin, Madison, WI). L'algoritmo per computer GAP viene usato per allineare i due polipeptidi o polinucleotidi per i quali la percentuale di identità di sequenza deve essere determinata. Le sequenze vengono allineate per la corrispondenza ottimale del loro rispettivo amminoacido o nucleotide (la "copertura corrispondente", come determinato dall'algoritmo). Una penalità di apertura di gap (che viene calcolata come 3 volte la diagonale media, in cui la "diagonale media" è la media della diagonale della matrice di confronto usata; la "diagonale" è il punteggio o il numero assegnato a ogni corrispondenza perfetta di amminoacidi dalla particolare matrice di confronto) e una penalità di estensione di gap (che solitamente è 1/10 volte la penalità di apertura di gap), nonché una matrice di confronto come PAM 250 o BLOSUM 62 vengono usate unitamente all'algoritmo. In alcune forme di realizzazione, anche una matrice di confronto standard (si veda, Dayhoff et al., (1978) Atlas of Protein Sequence and Structure 5:345-352 per la matrice di confronto PAM 250; Henikoff et al., (1992) Proc. Natl. Acad. Sci. U.S.A. 89:10915-10919 per la matrice di confronto BLOSUM 62) viene usata dall'algoritmo.

I parametri consigliati per determinare la percentuale di identità per polipeptidi o sequenze di nucleotidi usando il programma GAP sono i seguenti:

Algoritmo: Needleman et al., 1970, J. Mol. Biol. 48:443-453;

Matrice di confronto: BLOSUM 62 di Henikoff et al., 1992, sopra;

Penalità gap: 12 (ma senza penalità per gap finali)

Penalità per la lunghezza dei gap: 4

Soglia di similarità: 0

Certi schemi di allineamento per allineare due sequenze di amminoacidi possono risultare in corrispondenza solo di una piccola regione delle due sequenze, e questa piccola regione allineata può avere un'identità di sequenza molto alta, anche se non vi è alcuna relazione significativa tra le due sequenze a lunghezza intera. Di conseguenza, il metodo di allineamento selezionato (ad esempio, il programma GAP) può essere regolato, se lo si desidera, per risultare in un allineamento che copra almeno 50 amminoacidi contigui del polipeptide bersaglio.

I termini "polipeptide di GIPR" e "proteina di GIPR" sono usati in modo intercambiabile e significano un polipeptide di tipo selvatico presente in natura espresso in un mammifero, come un essere umano o un topo, e include alleli presenti in natura (ad esempio, forme alleliche presenti in natura della proteina di GIPR umano). Ai fini di questa divulgazione, il termine "polipeptide di GIPR" può essere usato in modo intercambiabile per fare riferimento a qualsiasi polipeptide di GIPR a lunghezza intera, ad esempio SEQ ID NO: 3141, che consiste in 466 residui di amminoacidi e che è codificato dalla sequenza di nucleotidi SEQ ID NO: 3142, o SEQ ID NO: 3143, che consiste in 430 residui di amminoacidi e che è codificato dalla sequenza di acido nucleico SEQ ID NO: 3144, o SEQ ID NO: 3145, che consiste in 493 residui di amminoacidi ed è codificato dalla sequenza di acido nucleico SEQ ID NO: 3146, o SEQ ID NO. 3147, che consiste in 460 residui di

amminoacidi e che è codificato dalla sequenza di acido nucleico di SEQ ID NO: 3148, o SEQ ID NO. 3149, che consiste in 230 residui di amminoacidi e che è codificato dalla sequenza di acido nucleico di SEQ ID NO: 3150.

Il termine "polipeptide di GIPR" racchiude anche un polipeptide di GIPR nel quale una sequenza di polipeptide di GIPR presente in natura (ad esempio, SEQ ID NO: 3141, 3143 o 3145) è stata modificata. Tali modifiche includono, ma senza limitarvisi, una o più sostituzioni di amminoacidi, incluse sostituzioni con amminoacidi non presenti in natura, analoghi di amminoacidi non presenti in natura e mimetici di amminoacidi.

In varie forme di realizzazione, un polipeptide di GIPR comprende una sequenza di amminoacidi che è almeno circa al 90 percento identica a un polipeptide di GIPR presente in natura (ad esempio, SEQ ID NO: 3141, 3143 o 3145). In altre forme di realizzazione, un polipeptide di GIPR comprende una sequenza di amminoacidi che è almeno circa al 95, 96, 97, 98 o 99 percento identica a una sequenza di amminoacidi di polipeptide di GIPR presente in natura (ad esempio, SEQ ID NO: 3141, 3143 o 3145). Tali polipeptidi di GIPR preferibilmente, ma non necessariamente, possiedono almeno un'attività di un polipeptide di GIPR di tipo selvatico, come la capacità di legarsi a GIP. La presente invenzione racchiude anche molecole di acido nucleico codificanti tali sequenze di polipeptide di GIPR.

Il termine "saggio di attività di GIPR" (cui si fa riferimento anche come "saggio funzionale di GIPR") significa un saggio che può essere usato per misurare l'attività di GIP o di una proteina legante GIP in un contesto cellulare. In una forma di realizzazione, il saggio "di attività" (o "funzionale") può essere un saggio di cAMP in cellule esprimenti GIPR, in cui GIP può indurre un segnale di cAMP, e l'attività di una proteina legante GIP/GIPR potrebbe essere misurata in presenza/assenza del ligando GIP, in cui possono essere ottenuti IC50/EC50 e il grado di inibizione/attivazione (Biochemical and Biophysical Research Communications (2002) 290:1420-1426). In un'altra forma di realizzazione, il saggio "di attività" (o "funzionale") può essere un saggio di secrezione di insulina in cellule beta del pancreas, in cui GIP può indurre la secrezione di insulina dipendente dal glucosio, e l'attività di una proteina legante GIP/GIPR potrebbe essere misurata in presenza/assenza del ligando GIP, in cui possono essere ottenuti IC50/EC50 e il grado di inibizione/attivazione (Biochemical and Biophysical Research Communications (2002) 290:1420-1426).

Il termine "saggio di legame a GIPR" significa un saggio che può essere usato per misurare il legame di GIP a GIPR. In una forma di realizzazione, il "saggio di legame a GIPR" può essere un saggio che usa FMAT o FACS che misura il legame di GIP marcato con fluorescenza a cellule con espressione di GIPR, e l'attività della proteina legante GIP/GIPR può essere misurata per lo spostamento del legame di GIP marcato con fluorescenza alle cellule con espressione di GIPR. In

un'altra forma di realizzazione, il "saggio di legame di GIPR" può essere un saggio che misura il legame di GIP marcato con radioattività a cellule con espressione di GIPR, e l'attività della proteina legante GIP/GIPR può essere misurata per lo spostamento del legame di GIP marcato con radioattività alle cellule con espressione di GIPR (Biochimica et Biophysica Acta (2001) 1547:143-155).

I termini "GIP", "polipeptide inibitorio gastrico", "peptide insulinotropico glucosio-dipendente" e "ligando GIP" sono usati in modo intercambiabile e significano un polipeptide di tipo selvatico presente in natura espresso in un mammifero, come un essere umano o un topo, e includono alleli presenti in natura (ad esempio, forme alleliche presenti in natura della proteina di GIP umano). Ai fini di questa divulgazione, il termine "GIP" può essere usato in modo intercambiabile per riferirsi a qualsiasi polipeptide di GIP maturo.

La sequenza di 42 amminoacidi di GIP umano maturo è:

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

ed è codificata dalla sequenza di DNA:

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

La sequenza di 42 amminoacidi di GIP murino maturo è:

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

ed è codificata dalla sequenza di DNA:

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

La sequenza di 42 amminoacidi di GIP di ratto maturo è:

YAEGTFISDY SIAMDKIRQQ DFVNWLLAQK GKKNDWKHNL TQ (SEQ ID NO: 3155)

ed è codificata dalla sequenza di DNA:

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

"Antagonista di GIPR" si riferisce a composti che riducono o inibiscono l'attivazione di GIPR da parte di GIP. Tali antagonisti includono piccole molecole sintetizzate chimicamente e proteine leganti l'antigene.

"Proteina legante l'antigene", secondo l'uso fattone nella presente, si riferisce a qualsiasi proteina che si lega specificamente a un antigene bersaglio specificato, come un polipeptide di GIPR (ad esempio, un polipeptide di GIPR umano come quello fornito in SEQ ID NO: 3141, 3143 o 3145). Il termine racchiude anticorpi intatti che comprendono almeno due catene pesanti intere a lunghezza intera e due catene leggere a lunghezza intera, nonché loro derivati, varianti, frammenti e mutazioni. Esempi di frammenti di anticorpi includono frammenti Fab, Fab', $F(ab')_2$, e Fv. Una proteina legante l'antigene include anche anticorpi di dominio quali Nanobody e scFv, come descritto ulteriormente più avanti.

In generale, si dice che una proteina legante l'antigene di GIPR "si lega specificamente" al suo antigene bersaglio di GIPR quando la proteina legante l'antigene esibisce essenzialmente un legame di fondo

con molecole non GIPR. Tuttavia, una proteina legante l'antigene che si lega specificamente a GIPR può reagire in modo crociato con polipeptidi di GIPR di specie differenti. Tipicamente, una proteina legante l'antigene di GIPR si lega specificamente a GIPR umano quando la costante di dissociazione (KD) è $\leq 10^{-7}$ M, misurata tramite una tecnica di risonanza plasmonica di superficie (ad esempio, BIACore, GE-Healthcare Uppsala, Svezia) o Kinetic Exclusion Assay (KinExA, Sapidyne, Boise, Idaho). Una proteina legante l'antigene di GIPR si lega specificamente a GIPR umano con "alta affinità" quando la KD è $\leq 5 \times 10^{-9}$ M, e con "affinità molto alta" quando la KD è $\leq 5 \times 10^{-10}$ M, misurata usando i metodi descritti.

"Regione legante l'antigene" significa una proteina, o una porzione di una proteina, che si lega specificamente a un antigene specifico. Ad esempio, a quella porzione di una proteina legante l'antigene che contiene i residui di amminoacidi che interagiscono con un antigene e conferiscono alla proteina legante l'antigene la sua specificità e affinità per l'antigene si fa riferimento come "regione legante l'antigene". Una regione legante l'antigene include tipicamente una o più "regioni di legame complementari" ("CDR") di un'immunoglobulina, di un'immunoglobulina a catena singola, o di un anticorpo di camelide. Certe regioni leganti l'antigene includono anche una o più regioni "cornice". Una "CDR" è una sequenza di amminoacidi che contribuisce alla specificità e all'affinità di legame all'antigene. Le regioni "cornice" sono di ausilio nel mantenere la corretta conformazione delle CDR per promuovere il legame tra la regione legante l'antigene e un antigene.

Una "proteina ricombinante", includente una proteina legante l'antigene di GIPR ricombinante, è una proteina realizzata usando tecniche ricombinanti, ossia attraverso l'espressione di un acido nucleico ricombinante come descritto nella presente. Metodi e tecniche per la produzione di proteine ricombinanti sono ben noti nell'arte.

Il termine "anticorpo" si riferisce a un'immunoglobulina intatta di qualsiasi isotipo, o a un suo frammento che può competere con l'anticorpo intatto per il legame specifico all'antigene bersaglio, e include, ad esempio, anticorpi chimerici, umanizzati, completamente umani e bispecifici. Un "anticorpo", di fatto, è una specie di una proteina legante l'antigene. Un anticorpo intatto sarà generalmente composto da almeno due catene pesanti a lunghezza intera e due catene leggere a lunghezza intera. Gli anticorpi possono essere derivati esclusivamente da un'unica fonte oppure possono essere "chimerici", vale a dire che differenti porzioni dell'anticorpo possono essere derivate da due anticorpi differenti, come descritto ulteriormente più avanti. Le proteine leganti l'antigene, gli anticorpi o i frammenti di legame possono essere prodotti in ibridomi, mediante tecniche di DNA ricombinante, o mediante clivaggio enzimatico o chimico di anticorpi intatti.

Il termine "catena leggera", secondo l'uso fattone in relazione a un anticorpo o a suoi frammenti, include una catena leggera a lunghezza intera e suoi frammenti aventi una sequenza di regione variabile sufficiente a conferire specificità di legame. Una catena leggera a lunghezza intera include un dominio di regione variabile, VL, e un

dominio di regione costante, CL. Il dominio di regione variabile della catena leggera è all'ammino-terminale del polipeptide. Le catene leggere includono le catene kappa e le catene lambda.

Il termine "catena pesante", secondo l'uso fattone in relazione a un anticorpo o a un suo frammento, include una catena pesante a lunghezza intera e suoi frammenti aventi una sequenza di regione variabile sufficiente a conferire specificità di legame. Una catena pesante a lunghezza intera include un dominio di regione variabile, VH, e tre domini di regione costante, CH1, CH2 e CH3. Il dominio VH è all'ammino-terminale del polipeptide, e i domini CH sono al carbossi-terminale, con il dominio CH3 più vicino al carbossi-terminale del polipeptide. Le catene pesanti possono essere di qualsiasi isotipo, incluse IgG (inclusi i sottotipi IgG1, IgG2, IgG3 e IgG4), IgA (inclusi i sottotipi IgA1 e IgA2), IgM e IgE.

Il termine "frammento immunologicamente funzionale" (o semplicemente "frammento") di un anticorpo o di una catena di immunoglobulina (catena pesante o leggera), secondo l'uso fattone nella presente, è una proteina legante l'antigene comprendente una porzione (indipendentemente da come quella porzione sia ottenuta o sintetizzata) di un anticorpo che manca di almeno alcuni degli amminoacidi presenti in una catena a lunghezza intera ma che è in grado di legarsi specificamente a un antigene. Tali frammenti sono biologicamente attivi in quanto si legano specificamente all'antigene bersaglio e possono competere con altre proteine leganti l'antigene, inclusi anticorpi intatti, per il legame specifico a un dato epitopo.

Questi frammenti biologicamente attivi possono essere prodotti mediante tecniche di DNA ricombinante oppure possono essere prodotti mediante clivaggio enzimatico o chimico di proteine leganti l'antigene, inclusi anticorpi intatti. I frammenti di immunoglobulina immunologicamente funzionali includono, ma senza limitarvisi, i frammenti Fab, Fab' e $F(ab')_2$.

In un'altra forma di realizzazione, Fv, anticorpi di dominio e scFv possono essere derivati da un anticorpo della presente invenzione.

È contemplato inoltre che una frazione delle proteine leganti l'antigene divulgate nella presente, ad esempio una o più CDR, possa essere legata in modo covalente a una seconda proteina o a una piccola molecola per creare un agente terapeutico diretto a un bersaglio particolare nel corpo, possedente proprietà terapeutiche bifunzionali o avente un'emivita sierica prolungata.

Un "frammento Fab" è composto da una catena leggera e dalle regioni CH1 e variabili di una catena pesante. La catena pesante di una molecola Fab non può formare un legame disolfuro con un'altra molecola di catena pesante.

Una regione "Fc" contiene due frammenti di catena pesante comprendenti i domini CH2 e CH3 di un anticorpo. I due frammenti di catena pesante sono tenuti insieme da due o più legami disolfuro e da interazioni idrofobe dei domini CH3.

Un "frammento Fab'" contiene una catena leggera e una porzione di una catena pesante che contiene il dominio VH e il dominio

CH1 e anche la regione tra i domini CH1 e CH2, in modo tale che un legame disolfuro intercatena possa essere formato tra le due catene pesanti di due frammenti Fab' per formare una molecola $F(ab')_2$.

Un "frammento $F(ab')_2$" contiene due catene leggere e due catene pesanti contenenti una porzione della regione costante tra i domini CH1 e CH2, in modo tale che un legame disolfuro intercatena sia formato tra le due catene pesanti. Un frammento $F(ab')_2$ è perciò composto da due frammenti Fab' che sono tenuti insieme da un legame disolfuro tra le due catene pesanti.

La "regione Fv" comprende le regioni variabili delle catene pesanti e leggere, ma manca delle regioni costanti.

Gli "anticorpi a catena singola" o "scFv" sono molecole di Fv in cui le regioni variabili di catena pesante e leggera sono state connesse mediante un linker flessibile per formare una singola catena di polipeptide, che forma una regione legante l'antigene. Gli scFv sono discussi in dettaglio nella pubblicazione della domanda di brevetto internazionale n. WO 88/01649 e nei brevetti statunitensi n. 4,946,778 e n. 5,260,203.

Un "anticorpo di dominio" o "immunoglobulina a catena singola" è un frammento di immunoglobulina immunologicamente funzionale contenente solo la regione variabile di una catena pesante o la regione variabile di una catena leggera. Esempi di anticorpi di dominio includono i Nanobodies®. In alcune esemplificazioni, due o più regioni VH vengono unite in modo covalente con un linker peptidico per creare un anticorpo

di dominio bivalente. Le due regioni VH di un anticorpo di dominio bivalente possono avere come bersaglio lo stesso antigene o antigeni differenti.

Una "proteina legante l'antigene bivalente" o "anticorpo bivalente" è composta da due regioni leganti l'antigene. In alcune esemplificazioni, le due regioni di legame hanno le stesse specificità per l'antigene. Proteine leganti l'antigene bivalenti e anticorpi bivalenti possono essere bispecifici, si veda sotto.

Una "proteina legante l'antigene multispecifica" o un "anticorpo multispecifico" è una/o che ha come bersaglio più di un antigene o epitopo.

Una proteina legante l'antigene o un anticorpo" bispecifica/o", "a doppia specificità" o "bifunzionale" è una proteina legante l'antigene o un anticorpo ibrida/o, rispettivamente, avente due differenti siti leganti l'antigene. Proteine leganti l'antigene e anticorpi bispecifiche/bispecifici sono una specie di proteina legante l'antigene multispecifica o di anticorpo multispecifico e possono essere prodotti mediante una varietà di metodi, inclusi, ma senza limitarvisi, la fusione di ibridomi o il collegamento di frammenti Fab'. Si veda, ad esempio, Songsivilai e Lachmann, 1990, Clin. Exp. Immunol. 79:315-321; Kostelny et al., 1992, J. Immunol. 148:1547-1553. I due siti di legame di una proteina legante l'antigene o di un anticorpo bispecifica/o si legheranno a due epitopi differenti, che possono risiedere su bersagli di proteina uguali o differenti.

Il termine "competere", quando usato nel contesto di proteine leganti l'antigene (ad esempio anticorpi), significa che la competizione tra le proteine leganti l'antigene è determinata mediante un saggio in cui la proteina legante l'antigene (ad esempio anticorpo o suo frammento immunologicamente funzionale) sottoposta al test impedisce o inibisce il legame specifico di una proteina legante l'antigene di riferimento a un antigene comune (ad esempio GIPR o un suo frammento). Possono essere usati numerosi tipi di saggi di legame competitivo, ad esempio: saggio radioimmunologico (RIA) diretto o indiretto in fase solida, saggio immunoenzimatico (EIA) diretto o indiretto in fase solida, saggio di competizione sandwich (si veda, ad esempio, Stahli et al., 1983, Methods in Enzymology 9:242-253); EIA biotina-avidina diretto in fase solida (si veda, ad esempio, Kirkland et al., 1986, J. Immunol. 137:3614-3619), saggio con marcatura diretto in fase solida, saggio sandwich con marcatura diretto in fase solida (si veda, ad esempio, Harlow e Lane, 1988, Antibodies, A Laboratory Manual, Cold Spring Harbor Press); RIA con marcatura diretto in fase solida usando la marcatura I-125 (si veda, ad esempio, Morel et al., 1988, Molec. Immunol. 25:7-15); EIA biotina-avidina diretto in fase solida (si veda, ad esempio, Cheung, et al., 1990, Virology 176:546-552); e RIA con marcatura diretto (Moldenhauer et al., 1990, Scand. J. Immunol. 32:77-82). Tipicamente, un tale saggio comporta l'uso di un antigene purificato legato a una superficie solida o cellule che portano uno di questi, una proteina legante l'antigene del test non marcata e una proteina legante l'antigene di riferimento marcata.

L'inibizione competitiva viene misurata determinando la quantità di marcatura legata alla superficie solida o alle cellule in presenza della proteina legante l'antigene del test. Solitamente, la proteina legante l'antigene del test è presente in eccesso. Dettagli aggiuntivi sui metodi per determinare il legame competitivo sono forniti negli esempi nella presente. Solitamente, quando una proteina legante l'antigene in competizione è presente in eccesso, essa inibisce il legame specifico di una proteina legante un antigene di riferimento a un antigene comune di almeno 40%, 45%, 50%, 55%, 60%, 65%, 70% o 75%. In alcune esemplificazioni, il legame è inibito almeno di 80%, 85%, 90%, 95% o 97% o più.

Il termine "antigene" si riferisce a una molecola o a una porzione di una molecola in grado di essere legata da un agente di legame selettivo, come una proteina legante l'antigene (incluso, ad esempio, un anticorpo), e, in aggiunta, in grado di essere usata in un animale per produrre anticorpi in grado di legarsi a quell'antigene. Un antigene può possedere uno o più epitopi che sono in grado di interagire con differenti proteine leganti l'antigene, ad esempio anticorpi.

Il termine "epitopo" è la porzione di una molecola che è legata da una proteina legante l'antigene (ad esempio, un anticorpo). Il termine include qualsiasi determinante in grado di legarsi specificamente a una proteina legante l'antigene, come un anticorpo. Un epitopo può essere contiguo o non contiguo (discontinuo) (ad esempio, in un polipeptide, i residui di amminoacidi che non sono contigui tra loro nella sequenza di

polipeptide ma che nel contesto della molecola sono legati dalla proteina legante l'antigene). Un epitopo conformazionale è un epitopo che esiste all'interno della conformazione di una proteina attiva ma che non è presente in una proteina denaturata. In certe forme di realizzazione, gli epitopi possono essere mimetici in quanto comprendono una struttura tridimensionale che è simile a un epitopo usato per generare la proteina legante l'antigene, ma non comprendono nessuno, o solo alcuni, dei residui di amminoacidi trovati in quell'epitopo usato per generare la proteina legante l'antigene. Più spesso, gli epitopi risiedono nelle proteine, ma, in alcune esemplificazioni, possono risiedere anche in altri tipi di molecole, come gli acidi nucleici. I determinanti dell'epitopo possono includere raggruppamenti superficiali chimicamente attivi di molecole quali amminoacidi, catene laterali di zuccheri, gruppi fosforile o solfonile, e possono avere caratteristiche strutturali tridimensionali specifiche, e/o caratteristiche di carica specifiche. Generalmente, le proteine leganti l'antigene specifiche per un particolare antigene bersaglio riconosceranno in modo preferenziale un epitopo sull'antigene bersaglio in una miscela complessa di proteine e/o macromolecole.

Secondo l'uso fattone nella presente, "sostanzialmente puro" significa che la specie di molecola descritta è la specie predominante presente, vale a dire che, su base molare, è più abbondante di qualsiasi altra specie individuale nella stessa miscela. In certe forme di realizzazione, una molecola sostanzialmente pura è una composizione in cui la specie in oggetto comprende almeno il 50% (su base molare) di

tutte le specie macromolecolari presenti. In altre forme di realizzazione, una composizione sostanzialmente pura comprenderà almeno 80%, 85%, 90%, 95%, 96%, 97%, 98%, o 99% di tutte le specie macromolecolari presenti nella composizione. In altre forme di realizzazione, la specie in oggetto viene purificata fino a un'omogeneità essenziale, in cui specie contaminanti non possono essere rilevate nella composizione mediante metodi di rilevamento convenzionali e, perciò, la composizione consiste in una singola specie macromolecolare rilevabile.

Il termine "trattare" si riferisce a qualsiasi indizio di successo nel trattamento o nel miglioramento di una lesione, una patologia o una condizione, incluso qualsiasi parametro oggettivo o soggettivo come attenuazione; remissione; diminuzione di sintomi, resa della lesione, della patologia o della condizione più tollerabile per il paziente; rallentamento del tasso di degenerazione o declino; resa del punto finale della degenerazione meno debilitante; miglioramento del benessere fisico o mentale di un paziente. Il trattamento o il miglioramento di sintomi può basarsi su parametri oggettivi o soggettivi; inclusi i risultati di un esame fisico, esami neuropsichiatrici, e/o una valutazione psichiatrica. Ad esempio, certi metodi presentati nella presente trattano con successo una malattia cardiovascolare, come l'aterosclerosi, riducendo l'incidenza, della malattia cardiovascolare, causando remissione della malattia cardiovascolare e/o migliorando un sintomo associato alla malattia cardiovascolare.

Una "quantità efficace" è generalmente una quantità sufficiente a ridurre la gravità e/o la frequenza di sintomi, eliminare i sintomi e/o la causa sottostante, prevenire il verificarsi di sintomi e/o della loro causa sottostante e/o migliorare il, o rimediare al, danno che risulta dallo, o è associato allo, stato di malattia (ad esempio diabete, obesità, dislipidemia, livelli elevati di glucosio, livelli elevati di insulina o nefropatia diabetica). In alcune forme di realizzazione, la quantità efficace è una quantità terapeuticamente efficace o una quantità profilatticamente efficace. Una "quantità terapeuticamente efficace" è una quantità sufficiente a porre rimedio a uno stato di malattia (ad esempio aterosclerosi) o a sintomi, particolarmente uno stato o sintomi associati allo stato di malattia, o altrimenti prevenire, ostacolare, ritardare o invertire la progressione dello stato di malattia o qualsiasi altro sintomo indesiderato associato alla malattia in qualsiasi modo. Una "quantità profilatticamente efficace" è una quantità di una composizione farmaceutica che, quando somministrata a un soggetto, avrà l'effetto profilattico previsto, ad esempio prevenire o ritardare l'insorgenza (o la ricomparsa) dello stato di malattia, o ridurre la probabilità di insorgenza (o di ricomparsa) dello stato di malattia o dei sintomi associati. L'effetto terapeutico o profilattico completo non si verifica necessariamente mediante somministrazione di una dose e può verificarsi solo dopo somministrazione di una serie di dosi. Perciò, una quantità terapeuticamente o profilatticamente efficace può essere somministrata in una o più somministrazioni.

I termini "dose terapeuticamente efficace" e "quantità terapeuticamente efficace", secondo l'uso fattone nella presente, significano una quantità di una proteina legante GIPR che suscita una risposta biologica o medica in un sistema tessutale, un animale o un essere umano ricercata da un ricercatore, un medico o altro clinico, che include alleviamento o miglioramento dei sintomi della malattia o del disturbo che viene trattata/o, ossia una quantità di una proteina legante GIPR che supporta un livello osservabile di una o più risposte biologiche o mediche desiderate, ad esempio abbassando i livelli di glucosio ematico, insulina, trigliceridi o colesterolo; riducendo il peso corporeo; o migliorando la tolleranza al glucosio, il dispendio energetico, o la sensibilità all'insulina.

Il termine "polinucleotide" o "acido nucleico" include sia polimeri di nucleotidi a filamento singolo che a doppio filamento. I nucleotidi che costituiscono il polinucleotide possono essere ribonucleotidi o deossiribonucleotidi oppure una forma modificata di uno dei due tipi di nucleotide. Le modifiche includono modifiche della base come derivati di bromouridina e inosina, modifiche del ribosio come 2',3'-dideossiribosio e modifiche del collegamento internucleotidico come fosforotioato, fosforoditioato, fosforoselenoato, fosforodiselenoato, fosforanilotioato, fosforaniladato e fosforamidato.

Il termine "oligonucleotide" significa un polinucleotide comprendente 200 nucleotidi o meno. In alcune forme di realizzazione, gli oligonucleotidi hanno una lunghezza da 10 a 60 basi. In altre forme di

realizzazione, gli oligonucleotidi hanno una lunghezza di 12, 13, 14, 15, 16, 17, 18, 19 o da 20 a 40 nucleotidi. Gli oligonucleotidi possono essere a singolo filamento o a doppio filamento, ad esempio per uso nella costruzione di un gene mutante. Gli oligonucleotidi possono essere senso o antisenso. Un oligonucleotide può includere una marcatura, incluse una radiomarcatura, una marcatura fluorescente, un aptene o una marcatura antigenica, per saggi di rilevamento. Gli oligonucleotidi possono essere usati, ad esempio, come primer per PCR, primer di clonaggio o sonde di ibridazione.

"Molecola di acido nucleico isolato" significa un DNA o RNA con origine genomica, da mRNA, da cDNA o sintetica, o una combinazione di questi, che non è associato a tutto, o a una porzione di, un polinucleotide in cui il polinucleotide isolato si trova in natura, oppure è collegato a un polinucleotide al quale non è collegato in natura. Ai fini di questa divulgazione, resta inteso che "una molecola di acido nucleico comprendente" una particolare sequenza di nucleotidi non racchiude cromosomi intatti. Molecole di acido nucleico isolato "comprendenti" sequenze di acido nucleico specificate possono includere, in aggiunta alle sequenze specificate, sequenze codificanti per un massimo di dieci o anche fino a venti altre proteine, o loro porzioni, oppure possono includere sequenze regolatrici collegate funzionalmente che controllano l'espressione della regione codificante delle sequenze di acido nucleico enumerate, e/o possono includere sequenze di vettore.

Salvo diversamente specificato, l'estremità sinistra di qualsiasi sequenza polinucleotidica a singolo filamento discussa nella presente è l'estremità 5'; alla direzione sinistra delle sequenze polinucleotidiche a doppio filamento si fa riferimento come direzione 5'. Alla direzione dell'aggiunta da 5' a 3' di trascritti di RNA nascenti si fa riferimento come direzione di trascrizione; a regioni di sequenza sul filamento di DNA aventi la stessa sequenza del trascritto di RNA che sono 5' rispetto all'estremità 5' del trascritto di RNA si fa riferimento come "sequenze a monte"; a regioni di sequenza sul filamento di DNA aventi la stessa sequenza del trascritto di RNA che sono 3' rispetto all'estremità 3' del trascritto di RNA si fa riferimento come "sequenze a valle".

Il termine "sequenza di controllo" si riferisce a una sequenza polinucleotidica che può influenzare l'espressione e l'elaborazione di sequenze codificanti a cui è legata. La natura di tali sequenze di controllo può dipendere dall'organismo ospite. In particolari forme di realizzazione, le sequenze di controllo per i procarioti possono includere un promotore, un sito di legame al ribosoma, e una sequenza di terminazione della trascrizione. Ad esempio, le sequenze di controllo per gli eucarioti possono includere promotori comprendenti uno o una pluralità di siti di riconoscimento per fattori di trascrizione, sequenze di potenziatori della trascrizione, e sequenze di terminazione della trascrizione. Le "sequenze di controllo" possono includere sequenze leader e/o sequenze di partner di fusione.

Il termine "vettore" significa qualsiasi molecola o entità (ad esempio acido nucleico, plasmide, batteriofago o virus) usata per trasferire informazioni codificanti proteine in una cellula ospite.

Il termine "vettore di espressione" o "costrutto di espressione" si riferisce a un vettore che è adatto alla trasformazione di una cellula ospite e che contiene sequenze di acido nucleico che dirigono e/o controllano (unitamente alla cellula ospite) l'espressione di una o più regioni codificanti eterologhe collegate funzionalmente ad esse. Un costrutto di espressione può includere, ma senza limitarvisi, sequenze che influenzano o controllano la trascrizione, la traduzione e, se sono presenti introni, influenzano lo splicing dell'RNA di una regione codificante collegata funzionalmente ad essa.

Secondo l'uso fattone nella presente, "collegato funzionalmente" significa che i componenti a cui è applicato il termine sono in una relazione che consente loro di effettuare le loro funzioni intrinseche in condizioni adatte. Ad esempio, una sequenza di controllo in un vettore che è "collegata funzionalmente" a una sequenza codificante proteine viene legata a quest'ultima in modo che l'espressione della sequenza codificante proteine venga conseguita in condizioni compatibili con l'attività trascrizionale delle sequenze di controllo.

Il termine "cellula ospite" significa una cellula che è stata trasformata con una sequenza di acido nucleico e che quindi esprime un gene di interesse. Il termine include la progenie della cellula parentale, che la progenie sia o non sia identica per morfologia o per costituzione

genetica alla cellula parentale originaria, purché il gene di interesse sia presente.

Nella presente, i termini "polipeptide" o "proteina" sono usati in modo intercambiabile per riferirsi a un polimero di residui di amminoacidi. I termini si applicano anche a polimeri di amminoacidi in cui uno o più residui di amminoacidi sono un analogo o mimetico di un corrispondente amminoacido presente in natura, nonché a polimeri di amminoacidi presenti in natura. I termini possono anche racchiudere polimeri di amminoacidi che sono stati modificati, ad esempio mediante l'aggiunta di residui di carboidrati per formare glicoproteine, o fosforilati. Polipeptidi e proteine possono essere prodotti da una cellula presente in natura e non ricombinante; oppure possono essere prodotti da una cellula geneticamente ingegnerizzata o ricombinante, e comprendono molecole aventi la sequenza di amminoacidi della proteina nativa, o molecole aventi delezioni, aggiunte e/o sostituzioni di uno o più amminoacidi della sequenza nativa. I termini "polipeptide" e "proteina" racchiudono specificamente proteine leganti l'antigene di GIPR, anticorpi, o sequenze che hanno delezioni, aggiunte e/o sostituzioni di uno o più amminoacidi di una proteina legante l'antigene. Il termine "frammento di polipeptide" si riferisce a un polipeptide che ha una delezione ammino-terminale, una delezione carbossi-terminale e/o una delezione interna rispetto alla proteina a lunghezza intera. Tali frammenti possono anche contenere amminoacidi modificati rispetto alla proteina a lunghezza intera. In certe forme di realizzazione, i frammenti sono lunghi da cinque a 500

amminoacidi. Ad esempio, i frammenti possono essere lunghi almeno 5, 6, 8, 10, 14, 20, 50, 70, 100, 110, 150, 200, 250, 300, 350, 400 o 450 amminoacidi. Frammenti di polipeptide utili includono frammenti di anticorpi immunologicamente funzionali, inclusi domini di legame.

Il termine "proteina isolata" significa che una proteina in questione (1) è priva di almeno alcune altre proteine con cui si troverebbe normalmente, (2) è essenzialmente priva di altre proteine della stessa fonte, ad esempio della stessa specie, (3) è espressa da una cellula di una specie differente, (4) è stata separata da almeno circa il 50 percento di polinucleotidi, lipidi, carboidrati o altri materiali con cui è associata in natura, (5) è associata funzionalmente (mediante interazione covalente o non covalente) a un polipeptide con cui non è associata in natura, o (6) non è presente in natura. Tipicamente, una "proteina isolata" costituisce almeno circa il 5%, almeno circa il 10%, almeno circa il 25% o almeno circa il 50% di un dato campione. DNA genomico, cDNA, mRNA o altro RNA, di origine sintetica, o qualsiasi loro combinazione, possono codificare una tale proteina isolata. Preferibilmente, la proteina isolata è sostanzialmente priva di proteine o polipeptidi o altri contaminanti che si trovano nel suo ambiente naturale che potrebbero interferire con il suo uso terapeutico, diagnostico, profilattico, di ricerca, o di altro tipo.

Una "variante" di un polipeptide (ad esempio, una proteina legante l'antigene come un anticorpo) comprende una sequenza di amminoacidi in cui uno o più residui di amminoacidi vengono inseriti nella, deleti dalla, e/o sostituiti nella, sequenza di amminoacidi rispetto a

un'altra sequenza di polipeptide. Le varianti includono le proteine di fusione.

Un "derivato" di un polipeptide è un polipeptide (ad esempio, una proteina legante l'antigene come un anticorpo) che è stato modificato chimicamente in un modo diverso dalle varianti di inserzione, delezione o sostituzione, ad esempio tramite coniugazione a un'altra frazione chimica.

Il termine "presente in natura", secondo l'uso fattone in tutta la descrizione in relazione a materiali biologici quali polipeptidi, acidi nucleici, cellule ospiti, e simili, si riferisce a materiali che si trovano in natura.

Secondo l'uso fattone nella presente, "soggetto" o "paziente" può essere qualsiasi mammifero. In una tipica forma di realizzazione, il soggetto o il paziente è un essere umano.

Come divulgato nella presente, un polipeptide di GIPR descritto dalla presente divulgazione può essere ingegnerizzato e/o prodotto usando una metodologia standard di biologia molecolare. In vari esempi, una sequenza di acido nucleico codificante un GIPR, che può comprendere tutto, o una porzione, di SEQ ID NO: 1, 3 o 5, può essere isolata e/o amplificata da DNA genomico o da cDNA usando appropriati primer oligonucleotidici. I primer possono essere progettati sulla base delle sequenze di nucleotidi e di amminoacidi fornite nella presente, secondo le tecniche standard di amplificazione (RT)-PCR. L'acido

nucleico di GIPR amplificato può poi essere clonato in un vettore adatto e caratterizzato mediante analisi della sequenza del DNA.

Gli oligonucleotidi per l'uso come sonde per l'isolamento o l'amplificazione di tutte le, o di una porzione delle, sequenze di GIPR fornite nella presente possono essere progettati e generati usando tecniche di sintesi standard, ad esempio un apparato di sintesi automatizzata del DNA, oppure possono essere isolati da una sequenza di DNA più lunga.

La sequenza di 466 amminoacidi di GIPR umano è (Volz et al., FEBS Lett. 373:23-29 (1995); sequenza di riferimento NCBI: 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)

ed è codificato dalla sequenza di DNA (sequenza di riferimento NCBI: 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
ttttatttt taaaaaatga ggat (SEQ ID NO: 3142).

Una isoforma di 430 amminoacidi di GIPR umano (isoforma X1), prevista mediante analisi computazionale automatizzata, ha la sequenza (sequenza di riferimento NCBI 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)

ed è codificata dalla sequenza di DNA:

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).

Una isoforma di 493 amminoacidi di GIPR umano, prodotta mediante splicing alternativo, ha la sequenza (Gremlich et al., Diabetes 44:1202-8 (1995); identificatore di sequenza UniProtKB: 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)

ed è codificata dalla sequenza di DNA:

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)

La sequenza di 460 amminoacidi di GIPR murino è (sequenza di riferimento NCBI: NP_001074284; uniprotKB/Swiss-Prot Q0P543-1); si veda 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 GFLVSVLYCF INKEVQSEIRQ
GWRHRRLRLS LQEQRPRPHQ ELAPRAVPLS SACREAAVGN ALPSGMLHVP
GDEVLESYC (SEQ ID NO: 3147)

ed è codificato dalla sequenza di DNA (sequenza di riferimento NCBI: 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)

Una isoforma di 230 amminoacidi di GIPR murino, prodotta mediante splicing alternativo, ha la sequenza (Gerhard et al., Genome Res, 14:2121-2127 (2004); sequenza di riferimento NCBI: 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)

ed è codificata dalla sequenza di DNA:

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).

Come affermato nella presente, il termine "polipeptide di GIPR" racchiude sequenze di polipeptide di GIPR presenti in natura, ad esempio sequenze di amminoacidi umane SEQ ID NO: 3141, 3143 o 3145. Il termine "polipeptide di GIPR", tuttavia, racchiude anche polipeptidi comprendenti una sequenza di amminoacidi che differisce dalla sequenza di amminoacidi di una sequenza di polipeptide di GIPR presente in natura, ad esempio SEQ ID NO: 3141, 3143 o 3145, per uno o più amminoacidi, tale per cui la sequenza è almeno al 90% identica a SEQ ID NO: 3141, 3143 o 3145. Polipeptidi di GIPR possono essere generati introducendo una o più sostituzioni di amminoacidi, conservative o non conservative, e usando amminoacidi presenti o meno in natura, in posizioni particolari del polipeptide di GIPR.

Una "sostituzione di amminoacido conservativa" può comportare una sostituzione di un residuo di amminoacido nativo (ossia un residuo trovato in una data posizione della sequenza di polipeptide di GIPR di tipo selvatico) con un residuo non nativo (ossia un residuo che non si trova in una data posizione della sequenza di polipeptide di GIPR di tipo selvatico) in modo che vi sia poco o nessun effetto sulla polarità o sulla carica del residuo di amminoacido in quella posizione. Sostituzioni di amminoacidi conservative racchiudono anche residui di amminoacidi non

presenti in natura che sono tipicamente incorporati mediante sintesi chimica di peptidi piuttosto che mediante sintesi in sistemi biologici. Queste includono peptidomimetici e altre forme invertite o rovesciate di frazioni amminoacido.

I residui presenti in natura possono essere suddivisi in classi in base alle proprietà comuni della catena laterale:

(1) idrofobi: norleucina, Met, Ala, Val, Leu, Ile;

(2) idrofili neutri: Cys, Ser, Thr;

(3) acidi: Asp, Glu;

(4) basici: Asn, Gln, His, Lys, Arg;

(5) residui che influenzano l'orientamento di catena: Gly, Pro; e

(6) aromatici: Trp, Tyr, Phe.

Gruppi aggiuntivi di amminoacidi possono anche essere formulati usando i principi descritti, ad esempio, in Creighton (1984) PROTEINS: STRUCTURE AND MOLECULAR PROPERTIES (2a ed. 1993), W.H. Freeman and Company. In alcune esemplificazioni, può essere utile caratterizzare ulteriormente le sostituzioni in base a due o più di tali peculiarità (ad esempio, la sostituzione con un residuo "piccolo polare", come un residuo di Thr, può rappresentare una sostituzione altamente conservativa in un contesto appropriato).

Le sostituzioni conservative possono comportare lo scambio di un membro di una di queste classi con un altro membro della stessa classe. Le sostituzioni non conservative possono comportare lo scambio di un membro di una di queste classi con un membro di un'altra classe.

I residui di amminoacidi sintetici, rari, o modificati che hanno proprietà fisico-chimiche note simili a quelle di un raggruppamento sopra descritto possono essere usati come sostituti "conservativi" per un particolare residuo di amminoacidi in una sequenza. Ad esempio, un residuo di D-Arg può fungere da sostituito per un tipico residuo di L-Arg. Può anche accadere che una particolare sostituzione possa essere descritta in termini di due o più delle classi sopra descritte (ad esempio, una sostituzione con un residuo piccolo e idrofobo significa sostituire un amminoacido con uno o più residui che si trovano in entrambe le classi sopra descritte o altri residui sintetici, rari, o modificati che sono noti nell'arte per avere proprietà fisico-chimiche simili a tali residui che soddisfano entrambe le definizioni).

Sequenze di acido nucleico codificanti un polipeptide di GIPR fornite nella presente, incluse quelle degenerate in SEQ ID NO: 3141, 3143 o 3145, e quelle codificanti varianti di polipeptide di SEQ ID NO: 3141, 3143 o 3145 formano altri aspetti della presente divulgazione.

Al fine di esprimere le sequenze di acido nucleico di GIPR fornite nella presente, le sequenze codificanti appropriate, ad esempio SEQ ID NO: 3141, 3143 o 3145, possono essere clonate in un vettore adatto e, dopo l'introduzione in un ospite adatto, la sequenza può essere espressa per produrre il polipeptide codificato secondo tecniche standard di clonaggio ed espressione note nell'arte (ad esempio, come descritto in Sambrook, J., Fritsh, E. F., e Maniatis, T. Molecular Cloning: A Laboratory Manual 2a ed., Cold Spring Harbor Laboratory, Cold Spring Harbor

Laboratory Press, Cold Spring Harbor, N.Y., 1989). L'invenzione riguarda anche tali vettori comprendenti una sequenza di acido nucleico secondo l'invenzione.

Un "vettore" si riferisce a un veicolo di erogazione che (a) promuove l'espressione di una sequenza di acido nucleico codificante un polipeptide; (b) promuove la produzione del polipeptide da esso; (c) promuove la trasfezione/trasformazione di cellule bersaglio con esso; (d) promuove la replicazione della sequenza di acido nucleico; (e) promuove la stabilità dell'acido nucleico; (f) promuove il rilevamento dell'acido nucleico e/o delle cellule trasformate/trasfettate; e/o (g) conferisce altrimenti una funzione biologica e/o fisico-chimica vantaggiosa all'acido nucleico codificante un polipeptide. Un vettore può essere qualsiasi vettore adatto, inclusi vettori di acido nucleico cromosomici, non cromosomici e sintetici (una sequenza di acido nucleico comprendente un insieme adatto di elementi di controllo dell'espressione). Esempi di tali vettori includono derivati di SV40, plasmidi batterici, DNA fagico, baculovirus, plasmidi di lievito, vettori derivati da combinazioni di plasmidi e DNA fagico e vettori di acido nucleico virale (RNA o DNA).

Un vettore di espressione ricombinante può essere progettato per l'espressione di una proteina di GIPR in cellule procariotiche (ad esempio, E. coli) o eucariotiche (ad esempio, cellule di insetti, usando vettori di espressione di baculovirus, cellule di lievito, o cellule di mammifero). In una forma di realizzazione, la cellula ospite è una cellula ospite di mammifero non umana. Cellule ospiti rappresentative includono

quegli ospiti tipicamente usati per il clonaggio e l'espressione, inclusi ceppi di Escherichia coli TOP10F', TOP10, DH10B, DH5a, HB101, W3110, BL21(DE3) e BL21 (DE3)pLysS, BLUESCRIPT (Stratagene), linee cellulari di mammifero CHO, CHO-K1, HEK293, vettori 293-EBNA pIN (Van Heeke e Schuster, J. Biol. Chem. 264: 5503-5509 (1989); vettori pET (Novagen, Madison Wis.). In alternativa, il vettore di espressione ricombinante può essere trascritto e tradotto in vitro, ad esempio usando sequenze regolatrici di promotore T7 e la polimerasi T7 e un sistema di traduzione in vitro. Preferibilmente, il vettore contiene un promotore a monte del sito di clonaggio contenente la sequenza di acido nucleico codificante il polipeptide. Esempi di promotori che possono essere attivati e disattivati sono il promotore lac, il promotore T7, il promotore trc, il promotore tac e il promotore trp.

Perciò, nella presente vengono forniti vettori comprendenti una sequenza di acido nucleico codificante GIPR che facilitano l'espressione di GIPR ricombinante. In varie forme di realizzazione, i vettori comprendono una sequenza di nucleotidi collegata funzionalmente che regola l'espressione di GIPR. Un vettore può comprendere, o essere associato a, qualsiasi promotore, potenziatore e altri elementi che facilitano l'espressione. Esempi di tali elementi includono promotori di espressione forti (ad esempio, un promotore/potenziatore CMV IE di essere umano, un promotore RSV, un promotore SV40, un promotore SL3-3, un promotore MMTV o un promotore LTR di HIV, un promotore EF1alfa, un promotore CAG), sequenze di terminazione di poli(A)

efficaci, un'origine di replicazione per il prodotto plasmidico in E. coli, un gene di resistenza agli antibiotici come marcatore selezionabile, e/o un sito di clonaggio conveniente (ad esempio, un poli-linker). I vettori possono anche comprendere un promotore inducibile anziché un promotore costitutivo come CMV IE. In un aspetto, viene fornito un acido nucleico comprendente una sequenza codificante un polipeptide di GIPR che è collegato funzionalmente a un promotore tessuto-specifico che promuove l'espressione della sequenza in un tessuto metabolicamente rilevante, come tessuto epatico o pancreatico.

In un altro aspetto della presente divulgazione, vengono fornite cellule ospiti comprendenti gli acidi nucleici di GIPR e i vettori divulgati nella presente. In varie forme di realizzazione, il vettore o l'acido nucleico è integrato nel genoma della cellula ospite, mentre, in altre forme di realizzazione, il vettore o l'acido nucleico è extracromosomico.

Sono fornite cellule ricombinanti, quali cellule di lievito, batteriche (ad esempio, E. coli) e di mammifero (ad esempio, cellule di mammifero immortalizzate) comprendenti tale acido nucleico, vettore, o combinazioni di uno di essi o entrambi. In varie forme di realizzazione, vengono fornite cellule comprendenti un acido nucleico non integrato, come un plasmide, un cosmide, un fagemide, o un elemento di espressione lineare, che comprende una sequenza codificante l'espressione di un polipeptide di GIPR.

Un vettore comprendente una sequenza di acido nucleico codificante un polipeptide di GIPR fornito nella presente può essere

introdotto in una cellula ospite mediante trasformazione o mediante trasfezione. Sono ben noti metodi per trasformare una cellula con un vettore di espressione.

Un acido nucleico codificante GIPR può essere posizionato in, e/o erogato a, una cellula ospite o a un animale ospite tramite un vettore virale. A tale scopo può essere usato qualsiasi vettore virale adatto. Un vettore virale può comprendere un numero qualsiasi di polinucleotidi virali, da soli o in combinazione con una o più proteine virali, che facilitano l'erogazione, la replicazione e/o l'espressione dell'acido nucleico dell'invenzione in una cellula ospite desiderata. Il vettore virale può essere un polinucleotide comprendente tutto, o parte di, un genoma virale, un coniugato proteina virale/acido nucleico, una particella simile a virus (VLP), o una particella di virus intatta comprendente acidi nucleici virali e un acido nucleico codificante un polipeptide di GIPR. Un vettore virale di particella virale può comprendere una particella virale di tipo selvatico o una particella virale modificata. Il vettore virale può essere un vettore che richiede la presenza di un altro vettore o di un virus di tipo selvatico per la replicazione e/o l'espressione (ad esempio, un vettore virale può essere un virus dipendente da ausiliario), come un amplicone di vettore adenovirale. Tipicamente, tali vettori virali consistono in una particella virale di tipo selvatico, o una particella virale modificata nel suo contenuto di proteine e/o acidi nucleici per aumentare la capacità di transgene o essere di ausilio nella trasfezione e/o nell'espressione dell'acido nucleico (esempi di tali vettori includono gli ampliconi di

herpesvirus/AAV). Tipicamente, un vettore virale è simile a, e/o è derivato da, un virus che normalmente infetta gli esseri umani. Particelle di vettori virali adatte a questo riguardo includono, ad esempio, particelle di vettori adenovirali (incluso qualsiasi virus degli, o derivato da un virus degli, adenoviridae), particelle di vettori virali adeno-associati (particelle di vettori di AAV) o altri parvovirus e particelle di vettori parvovirali, particelle di vettori papillomavirali, vettori flavivirali, vettori alfavirali, vettori herpesvirali, vettori di poxvirus, vettori retrovirali, inclusi vettori lentivirali.

Un polipeptide di GIPR espresso come descritto nella presente può essere isolato usando metodi standard di purificazione delle proteine. Un polipeptide di GIPR può essere isolato da una cellula in cui è naturalmente espresso oppure può essere isolato da una cellula che è stata ingegnerizzata per esprimere GIPR, ad esempio una cellula che non esprime naturalmente GIPR.

Nell'arte sono noti metodi di purificazione delle proteine che possono essere impiegati per isolare un polipeptide di GIPR, nonché materiali e reagenti associati. Metodi di purificazione aggiuntivi che possono essere utili per isolare un polipeptide di GIPR possono essere trovati in riferimenti quali Bootcov MR, 1997, Proc. Natl. Acad. Sci. USA 94:11514-9, Fairlie WD, 2000, Gene 254: 67-76.

Nella presente vengono fornite proteine leganti l'antigene antagonista che si legano a GIPR, incluso GIPR umano (hGIPR). In una forma di realizzazione, il GIPR umano ha la sequenza di fatto esposta in SEQ ID NO: 3141. In un'altra forma di realizzazione, GIPR umano ha la

sequenza di fatto esposta in SEQ ID NO: 3143. In un'altra forma di realizzazione, GIPR umano ha la sequenza di fatto esposta in SEQ ID NO: 3145.

In un aspetto, la presente invenzione è diretta a una composizione comprendente un anticorpo, o suo frammento funzionale, che si lega specificamente a GIPR umano, in cui l'anticorpo, o suo frammento funzionale, comprende una sostituzione di cisteina o di amminoacido non canonico in uno o più siti di coniugazione, e in cui l'anticorpo, o suo frammento funzionale, è un antagonista di GIPR; e un agonista del recettore di GLP-1, in cui l'agonista del recettore di GLP-1 è coniugato all'anticorpo, o suo frammento funzionale, attraverso la catena laterale del residuo di cisteina o del residuo di amminoacido non canonico sostituito negli uno o più siti di coniugazione.

Le proteine leganti l'antigene fornite sono polipeptidi in cui sono incorporate e/o unite una o più regioni determinanti la complementarità (CDR), come descritto nella presente. In alcune proteine leganti l'antigene, le CDR sono incorporate in una regione "cornice" che orienta la/e CDR in modo che vengano conseguite le corrette proprietà di legame all'antigene della/e CDR. Certe proteine leganti l'antigene descritte nella presente sono anticorpi o sono derivate da anticorpi. In altre proteine leganti l'antigene, le sequenze CDR sono incorporate in un differente tipo di impalcatura proteica. Di seguito vengono ulteriormente descritte le varie strutture.

Le proteine leganti l'antigene che sono divulgate nella presente presentano una varietà di utilità. Le proteine leganti l'antigene, ad esempio, sono utili in saggi di legame specifici, nella purificazione per affinità di GIPR e in saggi di screening per identificare altri antagonisti dell'attività di GIPR. Altri usi delle proteine leganti l'antigene includono, ad esempio, la diagnosi di malattie o condizioni associate a GIPR e saggi di screening per determinare la presenza o l'assenza di GIPR. Poiché le proteine leganti l'antigene fornite sono antagonisti, le proteine leganti l'antigene di GIPR hanno valore in metodi terapeutici in cui è utile ridurre l'aumento di peso, anche mantenendo o aumentando l'assunzione di cibo, aumentando la % di massa grassa e aumentando la % di massa magra, migliorando la tolleranza al glucosio, diminuendo i livelli di insulina, diminuendo i livelli di colesterolo e trigliceridi. Di conseguenza, le proteine leganti l'antigene hanno utilità nel trattamento e nella prevenzione di diabete, ad esempio diabete di tipo 2, obesità, dislipidemia, livelli elevati di glucosio o livelli elevati di insulina.

Viene fornita una varietà di agenti di legame selettivi utili per modulare l'attività di GIPR. Questi agenti includono, ad esempio, proteine leganti l'antigene che contengono un dominio legante l'antigene (ad esempio, scFv, anticorpi di dominio e polipeptidi con una regione legante l'antigene) e che si legano specificamente a un polipeptide di GIPR, in particolare GIPR umano. Alcuni degli agenti, ad esempio, sono utili per potenziare l'attività di GIPR, e possono attivare una o più attività associate a GIPR.

In generale, le proteine leganti l'antigene fornite comprendono tipicamente una o più CDR come descritto nella presente (ad esempio, 1, 2, 3, 4, 5 o 6). In alcune esemplificazioni, la proteina legante l'antigene comprende (a) una struttura di polipeptide e (b) una o più CDR che vengono inserite nella, e/o unite alla, struttura di polipeptide. La struttura di polipeptide può assumere una varietà di forme differenti. Ad esempio, può essere, o comprendere, la cornice di un anticorpo presente in natura, o un/una suo/a frammento o variante, oppure può essere di natura completamente sintetica. Di seguito vengono descritti ulteriormente esempi di varie strutture di polipeptide.

La struttura di polipeptide delle proteine leganti l'antigene è un anticorpo o è derivata da un anticorpo. Di conseguenza, esempi di certe proteine leganti l'antigene che vengono fornite includono, ma senza limitarvisi, anticorpi monoclonali, anticorpi bispecifici, minibody, anticorpi di dominio come i Nanobodies®, anticorpi sintetici (a cui nella presente si fa riferimento talvolta come "mimetici di anticorpi"), anticorpi chimerici, anticorpi umanizzati, anticorpi umani, fusioni di anticorpo, e porzioni o frammenti di ciascuno, rispettivamente. In alcune esemplificazioni, la proteina legante l'antigene è un frammento immunologico di un anticorpo completo (ad esempio, un Fab, un Fab', un F(ab')2). In altre esemplificazioni, la proteina legante l'antigene è un scFv che usa CDR di un anticorpo della presente invenzione.

Le proteine leganti l'antigene come fornite nella presente si legano specificamente a un GIPR umano. In una forma di realizzazione

specifica, la proteina legante l'antigene si lega specificamente a GIPR umano comprendente la, o consistente nella, sequenza di amminoacidi di SEQ ID NO: 3141. In una forma di realizzazione specifica, la proteina legante l'antigene si lega specificamente a GIPR umano comprendente la, o consistente nella, sequenza di amminoacidi di SEQ ID NO: 3143. In una forma di realizzazione specifica, la proteina legante l'antigene si lega specificamente a GIPR umano comprendente la, o consistente nella, sequenza di amminoacidi di SEQ ID NO: 3145.

Le proteine leganti l'antigene che sono fornite sono antagoniste e tipicamente hanno una, due, tre, quattro, cinque, sei, sette o tutte e otto le seguenti caratteristiche:

(a) capacità di prevenire o ridurre il legame di GIP a GIPR, dove i livelli possono essere misurati, ad esempio, mediante i metodi quali lo studio del legame a ligando marcato con radioattività o fluorescenza, o mediante i metodi descritti nella presente (ad esempio, saggio di cAMP o altri saggi funzionali). La diminuzione può essere almeno di 10, 25, 50, 100% o più rispetto ai livelli di pretrattamento di SEQ ID NO: 3141, 3143 o 3145 in condizioni comparabili.

(b) capacità di ridurre il glucosio ematico;

(c) capacità di aumentare la tolleranza al glucosio;

(d) capacità di aumentare la sensibilità all'insulina;

(e) capacità di diminuire il peso corporeo o di ridurre l'aumento di peso corporeo;

(f) capacità di diminuire la massa grassa o di diminuire l'infiammazione nel tessuto adiposo;

(g) capacità di ridurre i livelli di insulina a digiuno;

(h) capacità di ridurre i livelli di colesterolo in circolo;

(i) capacità di ridurre i livelli di trigliceridi in circolo;

(j) capacità di diminuire la steatosi epatica o di ridurre il livello di trigliceridi nel fegato;

(k) diminuire i livelli di AST, ALT e/o ALP.

In una forma di realizzazione, una proteina legante l'antigene di GIPR ha una o più delle seguenti attività:

(a) si lega a GIPR umano in modo che KD sia ≤200 nM, sia ≤150 nM, sia ≤100 nM, sia ≤50 nM, sia ≤10 nM, sia ≤5 nM, sia ≤2 nM, oppure sia ≤1 nM, ad esempio, come misurato tramite una tecnica di risonanza plasmonica di superficie o di saggio di esclusione cinetica.

(b) ha un'emivita nel siero umano di almeno 3 giorni;

Alcune proteine leganti l'antigene che sono fornite hanno un on-rate (ka) per GIPR di almeno 10^4/M × secondi, almeno 10^5/M × secondi, o almeno 10^6/M × secondi, misurato, ad esempio, come descritto di seguito. Certe proteine leganti l'antigene che sono fornite hanno un tasso di dissociazione od off-rate lento. Alcune proteine leganti l'antigene, ad esempio, hanno un kd (off-rate) di 1×10^{-2} s^{-1}, o 1×10^{-3} s^{-1}, o 1×10^{-4} s^{-1}, o 1×10^{-5} s^{-1}. In certe forme di realizzazione, la proteina legante l'antigene ha una KD (affinità di legame all'equilibrio) inferiore a 25 pM, 50 pM, 100 pM, 500 pM, 1 nM, 5 nM, 10 nM, 25 nM o 50 nM.

In un altro aspetto, viene fornita una proteina legante l'antigene avente un'emivita di almeno un giorno in vitro o in vivo (ad esempio, quando somministrata a un soggetto umano). In una forma di realizzazione, la proteina legante l'antigene ha un'emivita di almeno tre giorni. In varie altre forme di realizzazione, la proteina legante l'antigene ha un'emivita di 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 40, 50 o 60 giorni o più. In un'altra forma di realizzazione, la proteina legante l'antigene viene derivatizzata o modificata in modo che abbia un'emivita più lunga rispetto all'anticorpo non derivatizzato o non modificato. In un'altra forma di realizzazione, la proteina legante l'antigene contiene mutazioni puntiformi per aumentare l'emivita sierica. Ulteriori dettagli riguardanti tali forme mutanti e derivatizzate sono forniti di seguito.

Alcune delle proteine leganti l'antigene che sono fornite hanno la struttura tipicamente associata ad anticorpi naturali. Le unità strutturali di questi anticorpi comprendono tipicamente uno o più tetrameri, ciascuno composto da due pariglie identiche di catene polipeptidiche, sebbene alcune specie di mammiferi producano anche anticorpi che hanno una singola catena pesante. In un tipico anticorpo, ciascuna coppia o pariglia include una catena "leggera" a lunghezza intera (in certe forme di realizzazione, circa 25 kDa) e una catena "pesante" a lunghezza intera (in certe forme di realizzazione, circa 50-70 kDa). Ciascuna catena di immunoglobulina individuale è composta da svariati "domini di immunoglobulina", ciascuno consistendo all'incirca in 90-110 amminoacidi ed esprimendo un caratteristico schema di ripiegamento.

Questi domini sono le unità di base di cui sono composti i polipeptidi di anticorpo. La porzione ammino-terminale di ciascuna catena include tipicamente un dominio variabile che è responsabile del riconoscimento dell'antigene. La porzione carbossi-terminale è più conservata evolutivamente rispetto all'altra estremità della catena e vi si fa riferimento come "regione costante" o "regione C". Le catene leggere umane sono generalmente classificate come catene leggere kappa e lambda, e ciascuna di queste contiene un dominio variabile e un dominio costante. Le catene pesanti sono tipicamente classificate come catene mu, delta, gamma, alfa o epsilon, e queste definiscono l'isotipo dell'anticorpo come IgM, IgD, IgG, IgA e IgE, rispettivamente. Una IgG ha svariati sottotipi, inclusi, ma senza limitarvisi, IgG1, IgG2, IgG3 e IgG4. I sottotipi di IgM includono IgM e IgM2. I sottotipi di IgA includono IgA1 e IgA2. Nell'essere umano, gli isotipi IgA e IgD contengono quattro catene pesanti e quattro catene leggere; gli isotipi IgG e IgE contengono due catene pesanti e due catene leggere; e l'isotipo IgM contiene cinque catene pesanti e cinque catene leggere. La regione C della catena pesante comprende tipicamente uno o più domini che possono essere responsabili della funzione effettrice. Il numero di domini di regione costante di catena pesante dipenderà dall'isotipo. Ad esempio, le catene pesanti di IgG contengono ciascuna tre domini di regione C, noti come CH1, CH2 e CH3. Gli anticorpi che sono forniti possono avere uno qualsiasi di questi isotipi e sottotipi. In certe forme di realizzazione, l'anticorpo contro GIPR è del sottotipo IgG1, IgG2 o IgG4. I termini

"anticorpo contro GIPR" e "anticorpo anti-GIPR" sono usati in modo intercambiabile in questa applicazione e nelle figure. Entrambi i termini si riferiscono a un anticorpo che si lega a GIPR.

Nelle catene leggere e pesanti a lunghezza intera, le regioni variabili e costanti sono unite da una regione "J" di circa dodici o più amminoacidi, la catena pesante includendo anche una regione "D" di circa altri dieci amminoacidi. Si veda, ad esempio, Fundamental Immunology, 2a ed., cap. 7 (Paul, W., ed.) 1989, New York: Raven Press. Le regioni variabili di ciascuna coppia catena leggera/pesante formano tipicamente il sito legante l'antigene.

Per gli anticorpi forniti nella presente, le regioni variabili di catene di immunoglobulina esibiscono generalmente la stessa struttura complessiva, comprendente regioni cornice (FR) relativamente conservate unite da tre regioni ipervariabili, più spesso chiamate "regioni determinanti la complementarità" o CDR. Le CDR delle due catene di ciascuna coppia catena pesante/catena leggera sopra menzionata sono tipicamente allineate dalle regioni cornice per formare una struttura che si lega specificamente a uno specifico epitopo su GIPR. Da N-terminale a C-terminale, le regioni variabili di catena leggera e pesante presenti in natura sono tipicamente conformi al seguente ordine di questi elementi: FR1, CDR1, FR2, CDR2, FR3, CDR3 e FR4. È stato ideato un sistema di numerazione per assegnare numeri agli amminoacidi che occupano posizioni in ciascuno di questi domini. Questo sistema di numerazione è definito in Kabat Sequences of Proteins of Immunological Interest (1987

e 1991, NIH, Bethesda, Md.), o Chothia e Lesk, 1987, J. Mol. Biol. 196:901-917; Chothia et al., 1989, Nature 342:878-883.

Le informazioni sulla sequenza per anticorpi specifici preparati e identificati come descritto negli Esempi di seguito sono riassunte nella TABELLA 1. Perciò, in una forma di realizzazione, una proteina legante l'antigene è un anticorpo con la CDR, il dominio variabile e le sequenze di catena leggera e pesante come specificati in una delle righe della TABELLA 1.

SEQ ID NO sono state assegnate a sequenze di catena leggera variabile, catena pesante variabile, catena leggera, catena pesante, CDRL1, CDRL2, CDRL3, CDRH1, CDRH2 e CDRH3 degli anticorpi, e loro frammenti, della presente invenzione e sono mostrate nella TABELLA 1. SEQ ID NO sono state assegnate anche a polinucleotidi codificanti le sequenze di catena leggera variabile, catena pesante variabile, catena leggera, catena pesante, CDRL1, CDRL2, CDRL3, CDRH1, CDRH2 e CDRH3 degli anticorpi, e loro frammenti, della presente invenzione e sono mostrate nella TABELLA 2. Le proteine leganti l'antigene della presente invenzione possono essere identificate mediante SEQ ID NO, ma anche mediante il nome del costrutto (ad esempio, 2C2.005) o il numero identificatore (ad esempio, iPS:336175). Le proteine leganti l'antigene identificate nelle Tabelle 1-5 di seguito possono essere raggruppate in famiglie in base al nome del costrutto. Ad esempio, la "famiglia 4B1" include i costrutti 4B1, 4B1.010, 4B1.011, 4B1.012, 4B1.013, 4B1.014, 4B1.015, e 4B1.016.

Le varie regioni variabili di catena leggera e catena pesante fornite nella presente sono raffigurate nella TABELLA 3. Ciascuna di queste regioni variabili può essere attaccata a regioni costanti di catena pesante o leggera per formare una catena pesante e una leggera di anticorpo completa, rispettivamente. Per di più, ciascuna delle sequenze di catena pesante e leggera così generate può essere combinata per formare una struttura di anticorpo completa.

Tabella 1. SEQ ID NO amminoacidi.

Identificatore	**Costrutto**	**VL**	**VH**	**LC**	**HC**	**CDRL1**	**CDRL2**	**CDRL3**	**CDRH1**	**CDRH2**	**CDRH3**
iPS:336175	**2C2.005**	**1**	**158**	**315**	**472**	**629**	**786**	**943**	**1100**	**1257**	**1414**
iPS:335914	**4B1**	**2**	**159**	**316**	**473**	**630**	**787**	**944**	**1101**	**1258**	**1415**
iPS:335938	**6H1**	**3**	**160**	**317**	**474**	**631**	**788**	**945**	**1102**	**1259**	**1416**
iPS:335941	**2F11**	**4**	**161**	**318**	**475**	**632**	**789**	**946**	**1103**	**1260**	**1417**

Identificatore	Costrutto	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
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

Identificatore	Costrutto	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
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

Identificatore	Costrutto	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
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

Identificatore	Costrutto	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
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

Identificatore	Costrutto	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
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

Identificatore	Costrutto	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
iPS:361017	18F2.008	35	192	349	506	663	820	977	1134	1291	1448
iPS:361021	18F2.009	36	193	350	507	664	821	978	1135	1292	1449
iPS:361028	18F2.010	37	194	351	508	665	822	979	1136	1293	1450
iPS:360535	18F2.011	38	195	352	509	666	823	980	1137	1294	1451
iPS:361035	18F2.012	39	196	353	510	667	824	981	1138	1295	1452
iPS:359940	2F11.002	40	197	354	511	668	825	982	1139	1296	1453

Identificatore	Costrutto	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
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

Identificatore	Costrutto	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
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

Identificatore	Costrutto	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
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

Identificatore	Costrutto	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
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

Identificatore	Costrutto	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
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

Identificatore	Costrutto	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
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

Identificatore	Costrutto	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
iPS:361196	2G10_LC1.009	77	234	391	548	705	862	1019	1176	1333	1490
iPS:361202	2G10_LC1.010	78	235	392	549	706	863	1020	1177	1334	1491
iPS:359644	18E3.002	79	236	393	550	707	864	1021	1178	1335	1492
iPS:361206	18E3.003	80	237	394	551	708	865	1022	1179	1336	1493
iPS:359628	18E3.004	81	238	395	552	709	866	1023	1180	1337	1494
iPS:359637	18E3.005	82	239	396	553	710	867	1024	1181	1338	1495

Identificatore	Costrutto	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
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

Identificatore	Costrutto	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
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

Identificatore	Costrutto	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
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

Identificatore	Costrutto	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
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

Identificatore	Costrutto	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
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

Identificatore	Costrutto	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
iPS:361344	12H11.004	113	270	427	584	741	898	1055	1212	1369	1526
iPS:361351	12H11.005	114	271	428	585	742	899	1056	1213	1370	1527
iPS:361358	12H11.006	115	272	429	586	743	900	1057	1214	1371	1528
iPS:361365	12H11.007	116	273	430	587	744	901	1058	1215	1372	1529
iPS:361372	12H11.008	117	274	431	588	745	902	1059	1216	1373	1530
iPS:361379	12H11.009	118	275	432	589	746	903	1060	1217	1374	1531

Identificatore	Costrutto	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
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

Identificatore	Costrutto	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
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

Identificatore	Costrutto	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
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

Identificatore	Costrutto	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
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

Identificatore	Costrutto	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
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

Identificatore	Costrutto	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
iPS:361491	17B11.002.001	149	306	463	620	777	934	1091	1248	1405	1562
iPS:361499	17B11.002.002	150	307	464	621	778	935	1092	1249	1406	1563
iPS:361503	17B11.002.003	151	308	465	622	779	936	1093	1250	1407	1564
iPS:361507	17B11.002.004	152	309	466	623	780	937	1094	1251	1408	1565
iPS:361514	17B11.002.005	153	310	467	624	781	938	1095	1252	1409	1566
iPS:360582	17B11.002.006	154	311	468	625	782	939	1096	1253	1410	1567

Identificatore	Costrutto	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
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

Tabella 2. SEQ ID NO acidi nucleici.

Identificatore	Costrutto	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

Identificatore	Costrutto	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
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

Identificatore	Costrutto	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
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

Identificatore	Costrutto	VL	VH	LC	HC	CD RL1	CD RL2	CD RL3	CD RH1	CD RH2	CD RH3
iPS:360968	4B1.012	1593	1750	1907	2064	2221	2378	2535	2692	2849	3006
iPS:360974	4B1.013	1594	1751	1908	2065	2222	2379	2536	2693	2850	3007
iPS:360978	4B1.014	1595	1752	1909	2066	2223	2380	2537	2694	2851	3008
iPS:359785	4B1.015	1596	1753	1910	2067	2224	2381	2538	2695	2852	3009
iPS:360982	4B1.016	1597	1754	1911	2068	2225	2382	2539	2696	2853	3010
iPS:335922	18F2	1598	1755	1912	2069	2226	2383	2540	2697	2854	3011
iPS:360986	18F2.002	1599	1756	1913	2070	2227	2384	2541	2698	2855	3012
iPS:360995	18F2.003	1600	1757	1914	2071	2228	2385	2542	2699	2856	3013
iPS:360999	18F2.004	1601	1758	1915	2072	2229	2386	2543	2700	2857	3014

Identificatore	Costruttore	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
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

Identificatore	Costrutto	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
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

Identificatore	Costrutto	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
iPS:359869	6H1.003	1620	1777	1934	2091	2248	2405	2562	2719	2876	3033
iPS:359873	6H1.004	1621	1778	1935	2092	2249	2406	2563	2720	2877	3034
iPS:359877	6H1.005	1622	1779	1936	2093	2250	2407	2564	2721	2878	3035
iPS:361067	6H1.006	1623	1780	1937	2094	2251	2408	2565	2722	2879	3036
iPS:361071	6H1.007	1624	1781	1938	2095	2252	2409	2566	2723	2880	3037
iPS:361075	6H1.008	1625	1782	1939	2096	2253	2410	2567	2724	2881	3038
iPS:361079	6A5.004.001	1626	1783	1940	2097	2254	2411	2568	2725	2882	3039
iPS:361085	6A5.004.002	1627	1784	1941	2098	2255	2412	2569	2726	2883	3040
iPS:361091	6A5.004.003	1628	1785	1942	2099	2256	2413	2570	2727	2884	3041

Identificatore	Costruttore	VL	VH	LC	HC	CD RL1	CD RL2	CD RL3	CD RH1	CD RH2	CD RH3
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

Identificatore	Costrutto	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
iPS:335965	2A11.003	1638	1795	1952	2109	2266	2423	2580	2737	2894	3051
iPS:361158	2A11.004	1639	1796	1953	2110	2267	2424	2581	2738	2895	3052
iPS:361165	2A11.005	1640	1797	1954	2111	2268	2425	2582	2739	2896	3053
iPS:361172	2G10_LC1.003	1641	1798	1955	2112	2269	2426	2583	2740	2897	3054
iPS:361178	2G10_LC1.004	1642	1799	1956	2113	2270	2427	2584	2741	2898	3055
iPS:361185	2G10_LC1.005	1643	1800	1957	2114	2271	2428	2585	2742	2899	3056
iPS:361192	2G10_LC1.006	1644	1801	1958	2115	2272	2429	2586	2743	2900	3057
iPS:359609	2G10_LC1.007	1645	1802	1959	2116	2273	2430	2587	2744	2901	3058
iPS:359615	2G10_LC1.008	1646	1803	1960	2117	2274	2431	2588	2745	2902	3059

Identificatore	Costrutto	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
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

Identificatore	Costrutto	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
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

Identificatore	Costrutto	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
iPS:359669	5C2.015	1665	1822	1979	2136	2293	2450	2607	2764	2921	3078
iPS:359678	5C2.016	1666	1823	1980	2137	2294	2451	2608	2765	2922	3079
iPS:361275	11C1.002	1667	1824	1981	2138	2295	2452	2609	2766	2923	3080
iPS:361282	11C1.003	1668	1825	1982	2139	2296	2453	2610	2767	2924	3081
iPS:361289	11C1.004	1669	1826	1983	2140	2297	2454	2611	2768	2925	3082
iPS:359712	11C1.005	1670	1827	1984	2141	2298	2455	2612	2769	2926	3083
iPS:361293	11C1.006	1671	1828	1985	2142	2299	2456	2613	2770	2927	3084
iPS:361297	11C1.007	1672	1829	1986	2143	2300	2457	2614	2771	2928	3085
iPS:361301	11C1.008	1673	1830	1987	2144	2301	2458	2615	2772	2929	3086

Identificatore	Costrutto	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
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

Identificatore	Costrutto	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
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

Identificatore	Costrutto	VL	VH	LC	HC	CD RL1	CD RL2	CD RL3	CD RH1	CD RH2	CD RH3
iPS:361395	12H11.013	1692	1849	2006	2163	2320	2477	2634	2791	2948	3105
iPS:361402	12H11.014	1693	1850	2007	2164	2321	2478	2635	2792	2949	3106
iPS:361406	2C2.005.001	1694	1851	2008	2165	2322	2479	2636	2793	2950	3107
iPS:361412	2C2.005.002	1695	1852	2009	2166	2323	2480	2637	2794	2951	3108
iPS:361418	2C2.005.003	1696	1853	2010	2167	2324	2481	2638	2795	2952	3109
iPS:361424	2C2.005.004	1697	1854	2011	2168	2325	2482	2639	2796	2953	3110
iPS:361430	2C2.005.005	1698	1855	2012	2169	2326	2483	2640	2797	2954	3111
iPS:361436	2C2.005.006	1699	1856	2013	2170	2327	2484	2641	2798	2955	3112
iPS:361442	2C2.005.007	1700	1857	2014	2171	2328	2485	2642	2799	2956	3113

Identificatore	Costrutto	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
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

Identificatore	Costrutto	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
iPS:361855	2C2.005.015	17 10	18 67	20 24	21 81	2338	2495	2652	2809	2966	3123
iPS:336067	5G12.006	17 11	18 68	20 25	21 82	2339	2496	2653	2810	2967	3124
iPS:336169	17B11.002	17 12	18 69	20 26	21 83	2340	2497	2654	2811	2968	3125
iPS:361127	5G12.006.001	17 13	18 70	20 27	21 84	2341	2498	2655	2812	2969	3126
iPS:361136	5G12.006.002	17 14	18 71	20 28	21 85	2342	2499	2656	2813	2970	3127
iPS:361140	5G12.006.003	17 15	18 72	20 29	21 86	2343	2500	2657	2814	2971	3128
iPS:359919	5G12.006.004	17 16	18 73	20 30	21 87	2344	2501	2658	2815	2972	3129
iPS:361144	5G12.006.005	17 17	18 74	20 31	21 88	2345	2502	2659	2816	2973	3130
iPS:361151	5G12.006.006	17 18	18 75	20 32	21 89	2346	2503	2660	2817	2974	3131

Identificatore	Costrutto	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
iPS:361491	17B11.002.001	1719	1876	2033	2190	2347	2504	2661	2818	2975	3132
iPS:361499	17B11.002.002	1720	1877	2034	2191	2348	2505	2662	2819	2976	3133
iPS:361503	17B11.002.003	1721	1878	2035	2192	2349	2506	2663	2820	2977	3134
iPS:361507	17B11.002.004	1722	1879	2036	2193	2350	2507	2664	2821	2978	3135
iPS:361514	17B11.002.005	1723	1880	2037	2194	2351	2508	2665	2822	2979	3136
iPS:360582	17B11.002.006	1724	1881	2038	2195	2352	2509	2666	2823	2980	3137
iPS:361518	17B11.002.007	1725	1882	2039	2196	2353	2510	2667	2824	2981	3138
iPS:360570	17B11.002.008	1726	1883	2040	2197	2354	2511	2668	2825	2982	3139
iPS:362051	5G12.005.001	1727	1884	2041	2198	2355	2512	2669	2826	2983	3140

Tabella 3. Regioni leggere variabili e pesanti variabili esemplificative: sequenze di acido nucleico ("NA") e di amminoacidi ("AA")

iPS n.	Ab	Tipo	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	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNW 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

		AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR
			SEQ ID NO: 2
iPS:335938	6H1	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

		DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW YQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTD FSFTISSLQPEDIATYYCQQYDILLTFGGGTKVEIKR	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGM HWVRQAPGKGLEWVAVIWYDGSNKYYADSVKG RFTISSDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLDYWGQGTLVTVSS
iPS:335970	5C2	AA	SEQ ID NO: 4	SEQ ID NO: 161
		NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAGCAG CAACCAGGACATCCTCCTAAGCTGCTCATTTACT GGGCATCTACCCGGGAATCCGGGTCCCTGACC GATTCAGTGGCAGCGGGTCTGGGACAGATTTCA CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCGGCCAAGGGACCAAGGTGGA AATCAAACGA	CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCGGCTACTAT ATCCACTGGGTGCGACAGGCCCCTGGACAAGGG CTTGAGTGGATGGGGGTGGATCAACCCTGACAGT GGTGGCACAGACTATTCACAGAGGTTTCAGGGC AGGTTCACCATGACCAGGGACACGTCCATCAGC ACAGCCTACATGGAACTGAACAGGCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGAG GCCACGATTTTTGGAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT CCTCA
		AA	SEQ ID NO: 1575	SEQ ID NO: 1732
			DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK NYLAWYQQQPGHPPKLLIYWASTRESGVPDRFSGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKR	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWINPDSGGTDYSQRFQGR FTMTRDTSISTAYMELNRLRSDDTAVYYCAREATI FGMVIVPFDYWGQGTLVTVSS
iPS:335978	13H12	AA	SEQ ID NO: 5	SEQ ID NO: 162
		NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAGCAG AAACCAGGACATCCTCCTAAGCTGCTCATTTACT GGGCATCTACCCGGGAATCCGGGTCCCTGACC GATTCAGTGGCAGCGGGTCTGGGACAGATTTCA CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCGGCCAAGGGACCAAGGTGGA AATCAAACGA	CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCGGCTACTAT ATCCACTGGGTGCGACAGGCCCCTGGACAAGGA CTTGAGTGGATGGGGGTGGATCAACCCTGACAGT GGTGGCACAGACTATTCACAGAGGTTTCAGGGC AGGTTCACCATGACCAGGGACACGTCCATCAGC ACAGCCTACATGGAACTGAGCAGGCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGAG GCCACGATTTTTGGAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT CCTCA
			SEQ ID NO: 1576	SEQ ID NO: 1733

iPS:335986	11C1	AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK NYIAWYQQKPGHPPKLLIYWASTRESGVPDRFSGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKR
		NA	SEQ ID NO: 6 GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC AACAATAAGAACTACTTAGCTTGGTACCAACAG AAACCAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTCAGCAATATTATCGTA CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG AAATCAAACGA
			SEQ ID NO: 1577
		AA	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK NYLAWYQQKPGQPPNLLIYWTSTRDSGVPDRFSG SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR
		NA	SEQ ID NO: 7 GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC AACAATAAGAACTACTTAGCTTGGTACCAGCAG AAACCAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTCAGCAATATTATCGTA CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG AAATCAAACGA
			SEQ ID NO: 1578
iPS:335994	12H11	AA	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWINPDSGGTDYSQRFQGR FTMTRDTSISTAYMELSRLRSDDTAVYYCAREATI FGMVIVPFDYWGQGTLVTVSS
		NA	SEQ ID NO: 163 CAGGTGCCGCTGGTACAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCGGCTACTAT ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG CTTGTGTGGATGGGGGTGGATCAGCCCTAACAGT GGTGACACAAGCTATGCACAGAAGTTTCAGGAC AGGGTCACCATGACCAGGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGACTGAGATCT GACGACACGGCCGTGTATTTCTGTACGAGAGAG GCCACGATTTTTGGAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT CCTCA
			SEQ ID NO: 1734
		AA	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLVWMGWISPNSGDTSYAQKFQDR VTMTRDTSISTAYMELSRLRSDDTAVYFCTREATI FGMLIVPFDYWGQGTLVTVSS
		NA	SEQ ID NO: 164 CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCGGCTACTAT ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG CTTGAGTGGATGGGGGTGGATAAGCCCTAACAAT GGTGACACAAACTATGCACAGAAGTTTCAGGAC AGGGTCACCATGACCAGGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT GACGACACGGCCGTGTATTACTGTACGAGAGAG GCCACGATTTTTGGAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT CCTCA
			SEQ ID NO: 1735

			DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			NYLAWYQQKPGQPPNLLIYWTSTRDSGVPDRFSG	HWVRQAPGQGLEWMGWISPNNGDTNYAQKFQD
			SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF	RVTMTRDTSISTAYMELSRLRSDDTAVYYCTREA
		AA	GQGTKVEIKR	TIFGMLIVPFDYWGQGTLVTVSS
			SEQ ID NO: 8	SEQ ID NO: 165
			GAAATTGTGTTGACGCAGTCTCCAGGCACCCTG	CAGGTGCAGTTGCAGGAGTCGGGCCCAGGACTG
			TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT	GTGAAGCCTTCACAGACCCTGTCCCTCACCTGC
			GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT	ACTGTCTCTGGTGACTCCATCAGCAGTGGTGGTT
			TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC	ACTACTGGAGCTGGATCCGCCAGCACCCAGGGA
			CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG	AGGGCCTGGAGTGGGTACATCTATTACA
			CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG	GTGGGAGCACCTACTACAACCCGTCCCTCAAGA
		NA	GGTCTGGGACAGACTTCACTCTCACCATCAGCA	GTCGAGTTACCATATCAGTAGACACGTCTAAGA
			GACAGGAGCCTGATGATTTTGCAGTGTATTACT	ACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC
			GTCAGCAGTATGGTAGTTCACCGCTCACTTTCGG	CGCGGACACGGCCGTGTATTACTGTGCGAGAGA
			CGGAGGGACCAAGGTGGAGATCAAACGA	TCGTATTACGATTTTTGGAGTGGTTATGGGGGGC
				GGTATGGACGTCTGGGGCCAAGGGACCACGGTC
				ACCGTCTCCTCA
			SEQ ID NO: 1579	SEQ ID NO: 1736
			EIVLTQSPGTLSLSPGERATLSCRASQSISYSYLAW	QVQLQESGPGLVKPSQTLSLTCTVSGDSISSGGYY
			YQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF	WSWIRQHPGKGLEWIGYIYYSGSTYYNPSLKSRVT
		AA	TLTISRQEPDDFAVYYCQQYGSSPLTFGGGTKVEI	ISVDTSKNQFSLKLSSVTAADTAVYYCARDRITIFG
			KR	VVMGGGMDVWGQGTTVTVSS
			SEQ ID NO: 9	SEQ ID NO: 166
iPS:336041	2G10_LC1		GAAATAGTGATGACGCAGTCTCCAGCCACCCTG	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
			TCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCC	GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			TGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTA	GCAGCATCTGGATTCACCTTCAGTAACTATGGC
			GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC	ATGCACTGGGTCCGCCAGGCTCCAGGCGAGGGG
			AGGCTCCTCATCTATGGTGCAGCCACCAGGGCC	CTGGAGTGGGTGGCAGCTATATGGTTTGATGGA
			ACTGGTATCCCAGCCAGGGTCAGTGGCAGTGGG	AGTGATAAATACTATGCAGACTCCGTGAAGGGC
		NA	TCTGGGACAGAGTTCACTCTCACCATCAGCAGC	CGATTCACCATCTCCAGAGACAACTCCAAGAAC
			CTGCAGTCTGAAGATTTTGCAGTTTATTACTGTC	ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC
			AGCAGTATAATAACTGGCCTCTCACTTTCGGCG	GAGGACACGGCTGTGTATTACTGTGCGAGAGAT
			GAGGGACCAAGGTGGAGATCAAACGA	CAGGCGATTTTTGGAGTGGTCCCCGACTACTGG
				GGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1580	SEQ ID NO: 1737

		AA	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGAATRATGIPARVSGSGSGTE FTLTISSLQSEDFAVYYCQQYNNWPLTFGGGTKVE IKR
			SEQ ID NO: 10
iPS:336077	4H9.004	NA	GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGGCATTAGAAATGAGTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACGCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCATCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAGTTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTTGTAACTTATTACTGTCT ACAGCATAAATAGTTACCCATTCACTTTCGGCCCT GGGACCAAAGTGGATGTCAAACGA
			SEQ ID NO: 1581
		AA	DIQMTQSPSSLSASVGDRVTITCRASQGIRNELGW YQQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFVTYYCLQHNSYPFTFGPGTKVDV KR
			SEQ ID NO: 11
iPS:336088	6A5.004	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTACGATGCTTCCAATTTGGAGCC AGGGGTCCCATCAAGGTTCAGTGGAAGTGGATC TGGGACAGATTTTACTTTCACCATCAGCAGCCTG CAGCCTGAAGATATTGCAACATATTACTGTCAA CAGTATGATGATCTAATTCACTTTCGGCCCTGGGA CCAAAGTGGATATCAAACGA
			SEQ ID NO: 1582
		AA	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGSGTD

		AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGM HWVRQAPGEGLEWVAAIWFDGSDKYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGTLVTVSS
			SEQ ID NO: 167
		NA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGGAA GTAATAAATACTATGCAGACTCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTTGGAGTGCTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1738
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAVIWYDGSNKYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGTLVTVSS
			SEQ ID NO: 168
		NA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCTCCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGGCAAGGGGC TGGAGTGGGTGGCAGCTATATGGTATGATGGAA ATAATAAATACTATGCAGACTCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGATATC GGACGATTTTTTGGAGTGGTCCTTGAGTACCTCG GCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1739
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAAIWYDGNNKYYADSVKG

		FTFTISSLQPEDIATYYCQQYDDLFTFGPGTKVDIK R	RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYLGQGTLVTVSS
iPS:336099	17H11.004	SEQ ID NO: 12	SEQ ID NO: 169
	NA	GACATCCAGATGACCCAGTCTCCATCTTCCGTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GTCGGGCGAGTCAGGGTCTTATCATCTGGTTAG CCTGGTATCAGCAGAAACCGGGGAAAGCCCCTA AACTCCTGATCTATGCTGCATCCAGTTTGCAAAG TGGGGTCCCATCAAGGTTCAGCGGCAGTGGCTC TGGGACAGATTTCACTCTCACCATCAGCAGCCT ACAGCCTGAAGATTTTGCAACTTACTATTGTCAA CAGACTAACAGTTTCCCTCCGACGTTCGGCCAA GGGACCAAGGTGGAAATCAAACGA	CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTG GTGAAGCCTTCGGAGACCCTGTCCCTCACCTGC ACTGTCTCTCAGGGCTCCATCAGTAGTTACTACT GGAGCTGGATCCGGCAGCCCCGCCGGGAAGGGA CTAGAGTGGATTGGCCGTATCTATACCAGTGGG AGCACCAACTACAACCCCTCCCTCAAGAGTCGA GTCACCATGTCAATAGACACGTCCAAGAACCAG TTCTCCCTGAAACTGAACTCTGTGACCGCCGCG GACACGGCCGTGTATTACTGTGCGAGAGATGTA GCAGTGGCTGGCTTTGACTACTGGGGCCAGGGA ACCCTGGTCACCGTCTCCTCA
		SEQ ID NO: 1583	SEQ ID NO: 1740
	AA	DIQMTQSPSSVSASVGDRVTITCRASQGLIIWLAW YQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTD FTLTISSLQPEDFATYYCQQTNSFPPTFGQGTKVEI KR	QVQLQESGPGLVKPSETLSLTCTVSQGSISSYYWS WIRQPAGKGLEWIGRIYTSGSTNYNPSLKSRVTMS IDTSKNQFSLKLNSVTAADTAVYYCARDVAVAGF DYWGQGTLVTVSS
		SEQ ID NO: 13	SEQ ID NO: 170
iPS:359621	17H11.004.001	SEQ ID NO: 1584	SEQ ID NO: 1741
	NA	GACATCCAGATGACCCAGTCTCCATCTTCCGTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GTCGGGCGAGTCAGGGTCTTATCATCTGGTTAG CCTGGTATCAGCAGAAACCGGGGAAAGCCCCTA AACTCCTGATCTATGCTGCATCCAGTTTGCAAAG TGGGGTCCCATCAAGGTTCAGCGGCAGTGGCTC TGGGACAGATTTCACTCTCACCATCAGCAGCCT ACAGCCTGAAGATTTTGCAACTTACTATTGTCAA CAGACTAACAGTTTCCCTCCGACGTTCGGCCAA GGGACCAAGGTGGAAATCAAACGA	CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTG GTGAAGCCTTCGGAGACCCTGTCCCTCACCTGC ACTGTCTCTGGGGGCTCCATCAGTAGTTACTACT GGAGCTGGATCCGGCAGCCCCGCCGGGAAGGGA CTAGAGTGGATTGGCCGTATCTATACCAGTGGG AGCACCAACTACAACCCCTCCCTCAAGAGTCGA GTCACCATGTCAATAGACACGTCCAAGAACCAG TTCTCCCTGAAACTGAACTCTGTGACCGCCGCG GACACGGCCGTGTATTACTGTGCGAGAGATGTA GCAGTGGCTGGCTTTGACTACTGGGGCCAGGGA ACCCTGGTCACCGTCTCCTCA
		SEQ ID NO: 1584	SEQ ID NO: 1741
	AA	DIQMTQSPSSVSASVGDRVTITCRASQGLIIWLAW YQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTD	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWS WIRQPAGKGLEWIGRIYTSGSTNYNPSLKSRVTMS

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

SEQ ID NO: 16

SEQ ID NO: 173

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

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

iPS:360955	4B1.010	NA	SEQ ID NO: 20
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTATAGGAGACAGAGTCACCATCACTT
			GCCGGGCAAGTCAGGACATTAGAGATTATTTAG
			GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA
			AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA
			GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT
			CTGGGACAGAATTCACTCTCACAATCAGCAGCC
			TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT
			ACAGCATAATAATTACCCCTTCACTTTCGGCCAA
			GGGACCAAAGTGGATATCAAACGA
			SEQ ID NO: 1591
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY
			QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFT
			LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK
			R
			SEQ ID NO: 21
iPS:360962	4B1.011	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTATAGGAGACAGAGTCACCATCACTT
			GCCGGGCAAGTCAGGACATTAGAGATTATTTAG
			GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA
			AGCGCCTGATCTATGGTGCATCCAGTTTTGCAAA
			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	SEQ ID NO: 179
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
			CTGCATCTATAGGAGACAGAGTCACCATCACTT	GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCCGGGCAAGTCAGGACATTAGAGATTATTTAG	GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA
			GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA	TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC
			AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA	TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
			GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT	GTAATGAAAACTATGCAGACGCCGTGAAGGGCC
			CTGGGACAGAATTCACTCTCACAATCAGCAGCC	GATTCACCATCTCCAGAGACAATTCCAAGAATA
			TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT	CGCTGTATCTGCAAATGAACAGCCTGAGAGTCG
			ACAGCATAATAATTACCCCTTCACTTTCGGCCCT	CGGACACGGCTGTGTATTATTGTGCGCGAGATG
			GGGACCAAAGTGGATATCAAACGA	GGACGATCTTTGGAGTGGTCTTGGGGGACTACT
				GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
		AA	SEQ ID NO: 1593	SEQ ID NO: 1750
			DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM
			QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFT	HWVRQAPGKGLEWVAVIWYDASNENYADAVKG
			LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	RFTISRDNSKNTLYLQMNSLRVADTAVYYCARDG
				TIFGVVLGDYWGQGTLVTVSS
			SEQ ID NO: 23	SEQ ID NO: 180
iPS:360974	4B1.013	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
			CTGCATCTATAGGAGACAGAGTCACCATCACTT	GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCCGGGCAAGTCAGGACATTAGAGATTATTTAG	GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA
			GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA	TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC
			AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA	TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
			GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT	GTAATGAAAACTATGCAGACTCCGTGAAGGGCC
			CTGGGACAGAATTCACTCTCACAATCAGCAGCC	GATTCACCATCTCCAGAGACAATTCCAAGAATA
			TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT	CGCTGTATCTGCACATGAACAGCCTGAGAGTCG
			ACAGCATAATAATTACCCCTTCACTTTCGGCCAA	CGGACACGGCTGTGTATTATTGTGCGCGAGATG
			GGGACCAAAGTGGATATCAAACGA	GGACGATCTTTGGAGTGGTCTTGGGGGACTACT
				GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
		AA	SEQ ID NO: 1594	SEQ ID NO: 1751
			DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM
			QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFT	HWVRQAPGKGLEWVAVIWYDASNENYADSVKG
			LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK	RFTISRDNSKNTLYLHMNSLRVADTAVYYCARDG
			R	TIFGVVLGDYWGQGTLVTVSS

iPS:360978	4B1.014	NA	SEQ ID NO: 24
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTATAGGAGACAGAGTCACCATCACTT
			GCCGGGCAAGTCAGGACATTAGAGATTATTTAG
			GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA
			AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA
			GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT
			CTGGGACAGAATTCACTCTCACAATCAGCAGCC
			TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT
			ACAGCATAATAATTACCCCTTCACTTTCGGCCAA
			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
			ACAGCATAATAATTACCCCTTCACTTTCGGCCAA
			GGGACCAAAGTGGATATCAAACGA
			SEQ ID NO: 1596
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY
			QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFT
			LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK
			R
			SEQ ID NO: 181
			CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
			GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA
			TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC
			TGGAGTGGGTGGCAGTTATATGGTATGATGAA
			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	SEQ ID NO: 183
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCAA GGGACCAAAGTGGATATCAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAATA CGCTGTATCTGCAAATGAACAGCCTGAGAGTCG AGGACACGGCTGTGTATTATTGTGCGCGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
		AA	SEQ ID NO: 1597	SEQ ID NO: 1754
			DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK R	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDASNENYADAVKG RFTISRDNSKNTLYLQMNSLRVEDTAVYYCARDG TIFGVVLGDYWGQGTLVTVSS
			SEQ ID NO: 27	SEQ ID NO: 184
iPS:335922	18F2	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCACCAGAAACCAGGGAAAGCCCCTA AGCGCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCCCCAGGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGGAA GTAATGAAAACTATGCAGACTCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCACATGAACAGCCTGAGAGCCG CGGACACGGCTGTGTATTACTGTGCGAGAGATG GGACGATCTTTGGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1598	SEQ ID NO: 1755
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YHQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI KR	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDGSNENYADSVKG RFTISRDNSKNTLYLHMNSLRAADTAVYYCARDG TIFGVVLGDYWGQGTLVTVSS

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

			SEQ ID NO: 185
			CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
			GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA
			TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC
			TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
			GTAATGAAAACTATGCAGACGCCGTGAAGGGCC
			GATTCACCATCTCCAGAGACAATTCCAAGAACA
			CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
			CGGACACGGCTGTGTATTACTGTGCGAGAGATG
			GGACGATCTTTGGAGTGGTCTTGGGGGACTACT
			GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1756
			QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM
			HWVRQAPGKGLEWVAVIWYDASNENYADAVKG
			RFTISRDNSKNTLYLQMNSLRAADTAVYYCARDG
			TIFGVVLGDYWGQGTLVTVSS
			SEQ ID NO: 186
			CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
			GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA
			TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC
			TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
			GTAATGAAAACTATGCAGACGCCGTGAAGGGCC
			GATTCACCATCTCCAGAGACAATTCCAAGAACA
			CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
			CGGACACGGCTGTGTATTACTGTGCGAGAGATG
			GGACGATCTTTGGAGTGGTCTTGGGGGACTACT
			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
		AA	SEQ ID NO: 1601
			DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YHQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI KR
		NA	SEQ ID NO: 31
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCAACAGAAACCAGGGAAAGCCCCTA AGCGCCTGATCTATGGTGCATCCAGTTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGA
iPS:361005	18F2.005	AA	SEQ ID NO: 1602
			DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YQQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI KR

	SEQ ID NO: 187
NA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG CGGACACGGCTGTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
AA	SEQ ID NO: 1758
	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDASNENYADAVKG RFTISRDNSKNTLYLQMNSLRAADTAVYYCARDG TIFGVVLGDYWGQGTLVTVSS
NA	SEQ ID NO: 188
	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG CGGACACGGCTGTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
AA	SEQ ID NO: 1759
	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDASNENYADAVKG RFTISRDNSKNTLYLQMNSLRAADTAVYYCARDG TIFGVVLGDYWGQGTLVTVSS

iPS:361009	18F2.006	NA	SEQ ID NO: 32	SEQ ID NO: 189
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
			CTGCATCTATAGGAGACAGAGTCACCATCACTT	GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG	GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA
			GCTGGTATCAACAGAAACCAGGGAAAGCCCCTA	TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC
			AGCGCCTGATCTATGGTGCATCCAGTTTGCAAA	TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
			GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT	GTAATGAAAACTATGCAGACGCCGTGAAGGGCC
			CTGGGACAGAATTCACTCTCACAATCAGCAGCC	GATTCACCATCTCCAGAGACAATTCCAAGAACA
			TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT	CGCTGTATCTGCACATGAACAGCCTGAGAGCCG
			ACAGCATAATAATTACCCCTTCACTTTCGGCCCT	CGGACACGGCTGTGTATTACTGTGCGAGAGATG
			GGGACCAAAGTGGATATCAAACGA	GGACGATCTTTGGAGTGGTCTTGGGGGACTACT
				GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
		AA	SEQ ID NO: 1603	SEQ ID NO: 1760
			DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM
			YQQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTE	HWVRQAPGKGLEWVAVIWYDASNENYADAVKG
			FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI	RFTISRDNSKNTLYLHMNSLRAADTAVYYCARDG
			KR	TIFGVVLGDYWGQGTLVTVSS
			SEQ ID NO: 33	SEQ ID NO: 190
iPS:361013	18F2.007	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
			CTGCATCTATAGGAGACAGAGTCACCATCACTT	GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG	GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA
			GCTGGTATCAACAGAAACCAGGGAAAGCCCCTA	TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC
			AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA	TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
			GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT	GTAATGAAAACTATGCAGACGCCGTGAAGGGCC
			CTGGGACAGAATTCACTCTCACAATCAGCAGCC	GATTCACCATCTCCAGAGACAATTCCAAGAACA
			TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT	CGCTGTATCTGCACATGAACAGCCTGAGAGCCG
			ACAGCATAATAATTACCCCTTCACTTTCGGCCCT	CGGACACGGCTGTGTATTACTGTGCGAGAGATG
			GGGACCAAAGTGGATATCAAACGA	GGACGATCTTTGGAGTGGTCTTGGGGGACTACT
				GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
		AA	SEQ ID NO: 1604	SEQ ID NO: 1761
			DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM
			YHQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE	HWVRQAPGKGLEWVAVIWYDASNENYADAVKG
			FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI	RFTISRDNSKNTLYLHMNSLRAADTAVYYCARDG
			KR	TIFGVVLGDYWGQGTLVTVSS

iPS:361017	18F2.008	NA	SEQ ID NO: 34	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCACCAGAAACCAGGGAAAGCCCCTA AGCGCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGA
			SEQ ID NO: 1605	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YHQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI KR
		AA	SEQ ID NO: 35	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCAACAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGA
iPS:361021	18F2.009	NA	SEQ ID NO: 1606	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI KR
		AA	SEQ ID NO: 191	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCCCCAGGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG CGGACACGGCTGTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1762	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDASNENYADAVKG RFTISRDNSKNTLYLQMNSLRAADTAVYYCARDG TIFGVVLGDYWGQGTLVTVSS
		AA	SEQ ID NO: 192	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCCCCAGGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG CGGACACGGCTGTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1763	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDGSNENYADAVKG RFTISRDNSKNTLYLQMNSLRAADTAVYYCARDG TIFGVVLGDYWGQGTLVTVSS

iPS:361028	18F2.010	NA	SEQ ID NO: 36
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTATAGGAGACAGAGTCACCATCACTT
			GCCGGGCAAGTCAGGACCTTAGAAATTATTTTAG
			GCTGGTATCAACAGAAACCAGGGAAAGCCCCTA
			AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA
			GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT
			CTGGGACAGAATTCACTCTCACAATCAGCAGCC
			TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT
			ACAGCATAATAATTACCCCTTCACTTTCGGCCCT
			GGGACCAAAGTGGATATCAAACGA
			SEQ ID NO: 1607
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW
			YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE
			FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI
			KR
			SEQ ID NO: 37
iPS:360535	18F2.011	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTATAGGAGACAGAGTCACCATCACTT
			GCCGGGCAAGTCAGGACCTTAGAAATTATTTTAG
			GCTGGTATCAACAGAAACCAGGGAAAGCCCCTA
			AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA
			GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT
			CTGGGACAGAATTCACTCTCACAATCAGCAGCC
			TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT
			ACAGCATAATAATTACCCCTTCACTTTCGGCCAA
			GGGACCAAAGTGGATATCAAACGA
			SEQ ID NO: 1608
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW
			YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE
			FTLTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDI
			KR
			SEQ ID NO: 193
			CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
			GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA
			TGCACTGGGTCCGCCAGGCCCCAGGGCAAGGGGC
			TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
			GTAATGAAAACTATGCAGACTCCGTGAAGGGCC
			GATTCACCATCTCCAGAGACAATTCCAAGAACA
			CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
			CGGACACGGCTGTGTATTACTGTGCGAGAGATG
			GGACGATCTTTGGAGTGGTCTTGGGGGACTACT
			GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1764
			QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM
			HWVRQAPGKGLEWVAVIWYDASNENYADSVKG
			RFTISRDNSKNTLYLQMNSLRAADTAVYYCARDG
			TIFGVVLGDYWGQGTLVTVSS
			SEQ ID NO: 194
			CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
			GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA
			TGCACTGGGTCCGCCAGGCCCCAGGGCAAGGGGC
			TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
			GTAATGAAAACTATGCAGACGCCGTGAAGGGCC
			GATTCACCATCTCCAGAGACAATTCCAAGAACA
			CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
			AGGACACGGCTGTGTATTACTGTGCGAGAGATA
			GGACGATCTTTGGAGTGGTCTTGGGGGACTACT
			GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			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 GCCAGGCGAGTCAGGACATTAGCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTACGATGCATCCAATTTGGAAA CAGGGGTCCCATCAAGGTTCAGTGGAAGTGGAT CTGGGACAGATTTTAGTCTCACCATCAGCAGCC TGCAGCCTGAAGATTTTGCAACATATTACTGTCA ACAGTATGATATTCTCCTCACTTTCGGCGGAGG GACCCAAGGTGGAGATCAAGCGA
			SEQ ID NO: 1610
		AA	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW YQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTD FSLTISSLQPEDFATYYCQQYDILLTFGGGTKVEIK R

			SEQ ID NO: 195
			CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT 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 TGCAGCCTGAAGATTTTGCAACATATTACTGTCA ACAGTATGATATTCTCCTCACTTTCGGCGGAGG GACCCAAGGTGGAGATCAAGCGA
			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 GGACCAAGGGTGGAGATCAAGCGA
			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
			QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGM HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG RFTISSDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLDYWGQGTLVTVSS
			SEQ ID NO: 198
			CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGTTATATGGTATGATGCA AGTAATAAATACTATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGGGACAATTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT AGGACGATTTTTGGAGTGGTTCTTGACTACTGG GGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1769
			QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGM HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLDYWGQGTLVTVSS

iPS:361049	2F11.005	NA	SEQ ID NO: 42	SEQ ID NO: 199
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT	CAGGTGCAACTGGTGGAGTCTGGGGGCAGGCGTG
			CTGCATCTGTAGGAGACAGAGTCACCATCACTT	GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCCAGGCGAGTCAGGACATTAGCAACTATTTAA	GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC
			ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA	ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG
			AGCTCCTGATCTACGATGCATCCAATTTGGAAA	CTGGAGTGGGTGGCAGTTATATGGTATGATGCA
			CAGGGGTCCCATCAAGGTTCAGTGGAAGTGGAT	AGTAATAAATACTATGCAGACGCCGTGAAGGGC
			CTGGGACAGAGATTTTAGTTTCACCATCAGCAGCCT	CGATTCACCATCTCCAGGGACAATTCCAAGAAC
			GCAGCCTGAAGATTTTGCAACATATTACTGTCA	ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC
			ACAGTATGATATTCTCCTCACTTTCGGCGGAGG	GAGGACACGGCTGTGTATTACTGTGCGAGAGAT
			GACCAAGGTGGAGATCAAGCGA	AGGACGATTTTTGGAGTGGTTCTTGACTACTGG
				GGCCAGGGAACCCTGGTCACCGTCTCCTCA
		AA	SEQ ID NO: 1613	SEQ ID NO: 1770
			DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGM
			YQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTD	HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG
			FSFTISSLQPEDFATYYCQQYDILLTFGGGTKVEIK	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR
			R	TIFGVVLDYWGQGTLVTVSS
iPS:361055	2F11.006	NA	SEQ ID NO: 43	SEQ ID NO: 200
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT	CAGGTGCAACTGGTGGAGTCTGGGGGCAGGCGTG
			CTGCATCTGTAGGAGACAGAGTCACCATCACTT	GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCCAGGCGAGTCAGGACATTAGCAACTATTTAA	GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC
			ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA	ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG
			AGCTCCTGATCTACGATGCATCCAATTTGGAAA	CTGGAGTGGGTGGCAGTTATATGGTATGATGCA
			CAGGGGTCCCATCAAGGTTCAGTGGAAGTGGAT	AGTAATAAATACTATGCAGACGCCGTGAAGGGC
			CTGGGACAGAGATTTTAGTCTCACCATCAGCAGCC	CGATTCACCATCTCCAGCGACAATTCCAAGAAC
			TGCAGCCTGAAGATATTGCAACATATTACTGTC	ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC
			AACAGTATGATATTCTCCTCACTTTCGGCGGAG	GAGGACACGGCTGTGTATTACTGTGCGAGAGAT
			GGACCAAGGTGGAGATCAAGCGA	AGGACGATTTTTGGAGTGGTTCTTGACTACTGG
				GGCCAGGGAACCCTGGTCACCGTCTCCTCA
		AA	SEQ ID NO: 1614	SEQ ID NO: 1771
			DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGM
			YQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTD	HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG
			FSLTISSLQPEDIATYYCQQYDILLTFGGGTKVEIKR	RFTISSDNSKNTLYLQMNSLRAEDTAVYYCARDR
				TIFGVVLDYWGQGTLVTVSS

iPS:361059	2F11.007	NA	SEQ ID NO: 44
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTAGCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTACGATGCATCCAATTTGGAAA CAGGGGTCCCATCAAGGTTCAGTGGAAGTGGAT CTGGGACAGATTTTAGTTTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACATATTACTGTCA ACAGTATGATATTCTCCTCACTTTCGGCGGAGG GACCAAGGTGGAGATCAAGCGA
		AA	SEQ ID NO: 1615
			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
		AA	SEQ ID NO: 1772
			QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGM HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG RFTISSDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLDYWGQGTLVTVSS
			SEQ ID NO: 202
		NA	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGTTATATGGTATGATGCA AGTAATAAATACTATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGGGACAATTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT AGGACGATTTTTTGGAGTGGTTCTTGACTACTGG 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 TGCAGCCTGAAGATTTTGCAACATATTACTGTCA ACAGTATGATATTCTCCTCACTTTCGGCGGAGG GACCAAGGTGGAGATCAAGCGA
		AA	SEQ ID NO: 1617
			DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW YQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTD FSLTISSLQPEDFATYYCQQYDILLTFGGGTKVEIK R
		NA	SEQ ID NO: 47
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTAGCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTACGATGCATCCAATTTGGAAA CAGGGGTCCCATCAAGGTTCAGTGGAAGTGGAT CTGGGACAGATTTTAGTCTCACCATCAGCAGCC TGCAGCCTGAAGATTTTGCAACATATTACTGTCA ACAGTATGATATTCTCCTCACTTTCGGCGGAGG GACCAAGGTGGAGATCAAGCGA
iPS:359956	2F11.010		SEQ ID NO: 1618
		AA	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW YQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTD FSLTISSLQPEDFATYYCQQYDILLTFGGGTKVEIK R

iPS:359949	2F11.009	NA	SEQ ID NO: 203
			CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGTTATATGGTATGATGCA AGTAATAAATACTATGCAGACTCCGTGAAGGGC CGATTCACCATCTCCAGGGACAATTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT AGGACGATTTTTGGAGTGGTTCTTGACTACTGG GGCCAGGGAACCCTGGTCACCGTCTCCTCA
		AA	SEQ ID NO: 1774
			QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGM HWVRQAPGKGLEWVAVIWYDASNKYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLDYWGQGTLVTVSS
		NA	SEQ ID NO: 204
			CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGTTATATGGTATGATGGA AGTAATAAATACTATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGGGACAATTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT AGGACGATTTTTTGGAGTGGTTCTTGACTACTGG GGCCAGGGAACCCTGGTCACCGTCTCCTCA
iPS:359956	2F11.010		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
			ACAGCATAATAATTACCCCTTCACTTTCGGCCCT
			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
			ACAGCATAATAATTACCCCTTCACTTTCGGCCCT
			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	6HI.004	NA	SEQ ID NO: 50
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCAA GGGACCAAAGTGGATATCAAACGA
			SEQ ID NO: 1621
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK R
			SEQ ID NO: 51
iPS:359877	6HI.005	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCAA GGGACCAAAGTGGATATCAAACGA
			SEQ ID NO: 1622
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK R

iPS:359873	6HI.004	NA	SEQ ID NO: 207
			CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTTGGAGTGCTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1778
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGTLVTVSS
			SEQ ID NO: 208
iPS:359877	6HI.005	NA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATA GGACGATTTTTGGAGTGCTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1779
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVLLGDYWGQGTLVTVSS

		SEQ ID NO: 52	SEQ ID NO: 209
iPS:361067	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGGAA GTAATAAATACTATGCAGACTCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTTGGAGTGCTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
		SEQ ID NO: 1623	SEQ ID NO: 1780
	AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAVIWYDGSNKYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGTLVTVSS
		SEQ ID NO: 53	SEQ ID NO: 210
iPS:361071	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGAAA GTAATAAATACTATGCAGACTCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTTGGAGTGCTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
		SEQ ID NO: 1624	SEQ ID NO: 1781
	AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAVIWYDASNKYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGTLVTVSS
		SEQ ID NO: 54	SEQ ID NO: 211

iPS:361075	6H1.008	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTTGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGA
			SEQ ID NO: 1625
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR
			SEQ ID NO: 55
iPS:361079	6A5.004.001	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTACGATGCTTCCAATTTGGAGCC AGGGGTCCCATCAAGGTTCAGTGGAAGTGGATC TGGGACAGATTTTACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACTATTACTGTCA ACAGTATGATGATCTATTCACTTTCGGCCCTGGG ACCAAAGTGGATATCAAACGA
			SEQ ID NO: 1626
		AA	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGSGTD FTLTISSLQPEDFATYYCQQYDDLFTFGPGTKVDIK R

iPS:361075	6H1.008	NA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGGAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTTGGAGTGCTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1782
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAVIWYDGSNKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGTLVTVSS
			SEQ ID NO: 212
iPS:361079	6A5.004.001	NA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCTCCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGCTATATGGTATGATGGAA ATAATAAATACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATC GGACGATTTTTGGAGTGGTCCTTGAGTACTGGG GCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1783
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAAIWYDANNKYYADAVKG RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYWGQGTLVTVSS

iPS:361085	6A5.004.002	NA	SEQ ID NO: 56
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTACGATGCTTCCAATTTGGAGCC AGGGGTCCCATCAAGGTTCAGTGGAAGTGGATC TGGGACAGATTTTACTCTCACCATCAGCAGCCT GCAGCCTGAAGATATTTGCAACATATTACTGTCA ACAGTATGATGATCTATTCACTTTCGGCCCTGGG ACCAAAGTGGATATCAAACGA
			SEQ ID NO: 1627
		AA	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGSGTD FTLTISSLQPEDIATYYCQQYDDLFTFGPGTKVDIK R
			SEQ ID NO: 57
iPS:361091	6A5.004.003	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTACGATGCTTCCAATTTGGAGCC AGGGGTCCCATCAAGGTTCAGTGGAAGTGGATC TGGGACAGATTTTACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACATATTACTGTCA ACAGTATGATGATCTATTCACTTTCGGCCCTGGG ACCAAAGTGGATATCAAACGA
			SEQ ID NO: 1628
		AA	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGSGTD FTLTISSLQPEDFATYYCQQYDDLFTFGPGTKVDIK R

iPS:361085	6A5.004.002	NA	SEQ ID NO: 213
			CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCTCCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGCTATATGGTATGATGCAA ATAATAAATACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATC GGACGATTTTTGGAGTGGTCCTTGAGTACTGGG GCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1784
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAAIWYDANNKYYADAVKG RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYWGQGTLVTVSS
			SEQ ID NO: 214
iPS:361091	6A5.004.003	NA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCTCCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGCTATATGGTATGATGCAA ATAATAAATACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATC GGACGATTTTTGGAGTGGTCCTTGAGTACCTCG GCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1785
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAAIWYDANNKYYADAVKG RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYLGQGTLVTVSS

iPS:361095	6A5.004.004	NA	SEQ ID NO: 58
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTACGATGCTTCCAATTTGGAGCC AGGGGTCCCATCAAGGTTCAGTGGAAGTGGATC TGGGACAGATTTTACTTTCACCATCAGCAGCCTG CAGCCTGAAGATTTTGCAACATATTACTGTCAA CAGTATGATGATCTATTCACTTTCGGCCCTGGGA CCAAAGTGGATATCAAACGA
			SEQ ID NO: 1629
		AA	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGSGTD FTFTISSLQPEDFATYYCQQYDDLFTFGPGTKVDIK R
			SEQ ID NO: 59
iPS:361101	6A5.004.005	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTACGATGCTTCCAATTTGGAGCC AGGGGTCCCATCAAGGTTCAGTGGAAGTGGATC TGGGACAGATTTTACTCTCACCATCAGCAGCCT GCAGCCTGAAGATATTGCAACATATTACTGTCA ACAGTATGATGATCTATTCACTTTCGGCCCTGGG ACCAAAGTGGATATCAAACGA
			SEQ ID NO: 1630
		AA	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGSGTD FTLTISSLQPEDIATYYCQQYDDLFTFGPGTKVDIK R
			SEQ ID NO: 215
			CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCTCCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGCTATATGGTATGATGCAA ATAATAAATACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATC GGACGATTTTTGGAGTGGTCCTTGAGTACTGGG GCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1786
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAAIWYDANNKYYADAVKG RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYWGQGTLVTVSS
			SEQ ID NO: 216
		NA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCTCCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGCTATATGGTATGATGCAA ATAATAAATACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATC GGACGATTTTTTGGAGTGGTCCTTGAGTACCTCG GCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1787
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAAIWYDANNKYYADAVKG RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYLGQGTLVTVSS

iPS:361105	6A5.004.006	NA	SEQ ID NO: 60
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTACGATGCTTCCAATTTGGAGCC AGGGGTCCCATCAAGGTTCAGTGGAAGTGGATC TGGGACAGATTTTTACTTTCACCATCAGCAGCCTG CAGCCTGAAGATTTTGCAACATATTACTGTCAA CAGTATGATGATCTATTCACTTTCGGCCCTGGGA CCAAAGTGGATATCAAACGA
			SEQ ID NO: 1631
		AA	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGSGTD FTFTISSLQPEDFATYYCQQYDDLFTFGPGTKVDIK R
			SEQ ID NO: 61
iPS:361109	6A5.004.007	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTACGATGCTTCCAATTTGGAGCC AGGGGTCCCATCAAGGTTCAGTGGAAGTGGATC TGGGACAGATTTTTACTTTCACCATCAGCAGCCTG CAGCCTGAAGATATTGCAACATATTACTGTCAA CAGTATGATGATCTATTCACTTTCGGCCCTGGGA CCAAAGTGGATATCAAACGA
			SEQ ID NO: 1632
		AA	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGSGTD FTFTISSLQPEDIATYYCQQYDDLFTFGPGTKVDIK R

			SEQ ID NO: 217
		NA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCTCCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGCTATATGGTATGATGCAA ATAATAAATACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATC GGACGATTTTTGGAGTGGTCCTTGAGTACCTCG GCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1788
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAAIWYDANNKYYADAVKG RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYLGQGTLVTVSS
			SEQ ID NO: 218
		NA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCTCCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGCTATATGGTATGATGCAA ATAATAAATACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATC GGACGATTTTTGGAGTGGTCCTTGAGTACTGGG GCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1789
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAAIWYDANNKYYADAVKG RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYWGQGTLVTVSS

		SEQ ID NO: 62	SEQ ID NO: 219
iPS:361113	6A5.004.008	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTACGATGCTTCCAATTTGGAGCC AGGGGTCCCATCAAGGTTCAGTGGAAGTGGATC TGGGACAGATTTTACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACATATTACTGTCA ACAGTATGATGATCTATTCACTTTCGGCCCTGGG ACCAAAGTGGATATCAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCTCCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGCTATATGGTATGATGGAA ATAATAAATACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATC GGACGATTTTTGGAGTGGTCCTTGAGTACTGGG GCCAGGGAACCCTGGTCACCGTCTCCTCA
		SEQ ID NO: 1633	SEQ ID NO: 1790
		AA	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGSGTD FTLTISSLQPEDFATYYCQQYDDLFTFGPGTKVDIK R	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAAIWYDGNNKYYADAVKG RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYWGQGTLVTVSS
		SEQ ID NO: 63	SEQ ID NO: 220
iPS:361120	6A5.004.009	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTACGATGCTTCCAATTTGGAGCC AGGGGTCCCATCAAGGTTCAGTGGAAGTGGATC TGGGACAGATTTTACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACATATTACTGTCA ACAGTATGATGATCTATTCACTTTCGGCCCTGGG ACCAAAGTGGATATCAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCTCCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGCTATATGGTATGATGGAA ATAATAAATACTATGCAGACTCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATC GGACGATTTTTTGGAGTGGTCCTTGAGTACTGGG GCCAGGGAACCCTGGTCACCGTCTCCTCA
		SEQ ID NO: 1634	SEQ ID NO: 1791
		AA	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGSGTD FTLTISSLQPEDFATYYCQQYDDLFTFGPGTKVDIK R	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAAIWYDANNKYYADSVKG RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYWGQGTLVTVSS

		SEQ ID NO: 64	SEQ ID NO: 221
iPS.359896	6AS.004.010	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTACGATGCTTCCAATTTGGAGCC AGGGGTCCCATCAAGGTTCAGTGGAAGTGGATC TGGGACAGATTTTACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACATATTACTGTCA 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.359890	6AS.004.011	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTACGATGCTTCCAATTTGGAGCC AGGGGTCCCATCAAGGTTCAGTGGAAGTGGATC TGGGACAGATTTTACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACATATTACTGTCA 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	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT GCAGGGCCAGTCAGATTTTTACCAGCACCTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCAGGCTCCTCATCTATGGTGCATCCAGCAGGG CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG GGTCTGGGACAGACTTCACTCTCACCATCAGCA GATTGGAGCCTGAAGATTTTGCAGTGTATTACT GTCAGCAGTATGGTAGCTCACCTCGCTTCGGCC AAGGGACACGACTGGAGATTAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCAGTTTCAGTAGCTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGA CTGGAGTGGGTGGCAGTTATATGGTATGATGCA AGTAATAAATACTATGAAGACGCCGTGAAGGGC CGATTCACCATCTCCAGAGACAATTCCAAGAAC ACGCTGTTTCTGCAAGTGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGGG ATTACGATTTTTGGTCATGGGTTTGAATATTGGG GCCAGGGAACCCTGGTCACCGTCTCCTCA
	NA	SEQ ID NO: 1637	SEQ ID NO: 1794
	AA	EIVLTQSPGTLSLSPGERATLSCRASQIFTSTYLAW YQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF TLTISRLEPEDFAVYYCQQYGSSPRFGQGTRLEIKR	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQAPGKGLEWVAVIWYDASNKYYEDAVKG RFTISRDNSKNTLFLQVNSLRAEDTAVYYCARGITI FGHGFEYWGQGTLVTVSS
		SEQ ID NO: 67	SEQ ID NO: 224
iPS:335965	2A11.003	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT GCAGGGCCAGTCAGATTTTTACCAGCACCTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCAGGCTCCTCATCTATGGTGCATCCAGCAGGG CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG GGTCTGGGACAGACTTCACTCTCACCATCAGCA GATTGGAGCCTGAAGATTTTGCAGTGTATTACT GTCAGCAGTATGGTAGCTCACCTCGCTTCGGCC AAGGGACACGACTGGAGATTAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCAGTTTCAGTAGCTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGA CTGGAGTGGGTGGCAGTTATATGGTATGATGGA AGTAATAAATACTATGAAGACTCCGTGAAGGGC CGATTCACCATCTCCAGAGACAATTCCAAGAAC ACGCTGTTTCTGCAAGTGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGGG ATTACGATTTTTGGTCATGGGTTTGAATATTGGG GCCAGGGAACCCTGGTCACCGTCTCCTCA
	NA	SEQ ID NO: 1638	SEQ ID NO: 1795
	AA	EIVLTQSPGTLSLSPGERATLSCRASQIFTSTYLAW YQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF TLTISRLEPEDFAVYYCQQYGSSPRFGQGTRLEIKR	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQAPGKGLEWVAVIWYDGSNKYYEDSVKG RFTISRDNSKNTLFLQVNSLRAEDTAVYYCARGITI FGHGFEYWGQGTLVTVSS

iPS:361158	2A11.004	NA	SEQ ID NO: 68	SEQ ID NO: 225
			GAAATTGTGTTGACGCAGTCTCCAGGCACCCTG	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
			TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT	GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCAGGGCCAGTCAGATTTTTACCAGCACCTACT	GCAGCGTCTGGATTCAGTTTCAGTAGCTATGGC
			TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC	ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGA
			CCAGGCTCCTCATCTATGGTGCATCCAGCAGGG	CTGGAGTGGGTGGCAGTTATATGGTATGATGGA
			CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG	AGTAATAAATACTATGCAGACGCCGTGAAGGGC
			GGTCTGGGACAGACTTCACTCTCACCATCAGCA	CGATTCACCATCTCCAGAGACAATTCCAAGAAC
			GATTGGAGCCTGAAGATTTTGCAGTGTATTACT	ACGCTGTTTCTGCAAGTGAACAGCCTGAGAGCC
			GTCAGCAGTATGGTAGCTCACCTCGCTTCGGCC	GAGGACACGGCTGTGTATTACTGTGCGAGAGGG
			AAGGGACACGACTGGAGATTAAACGA	ATTACGATTTTTGGTCATGGGTTTGAATATTGGG
				GCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1639	SEQ ID NO: 1796
		AA	EIVLTQSPGTLSLSPGERATLSCRASQIFTSTYLAW	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM
			YQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF	HWVRQAPGKGLEWVAVIWYDGSNKYYEDAVKG
			TLTISRLEPEDFAVYYCQQYGSSPRFGQGTRLEIKR	RFTISRDNSKNTLFLQVNSLRAEDTAVYYCARGITI
				FGHGFEYWGQGTLVTVSS
			SEQ ID NO: 69	SEQ ID NO: 226
iPS:361165	2A11.005	NA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTG	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
			TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT	GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCAGGGCCAGTCAGATTTTTACCAGCACCTACT	GCAGCGTCTGGATTCAGTTTCAGTAGCTATGGC
			TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC	ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGA
			CCAGGCTCCTCATCTATGGTGCATCCAGCAGGG	CTGGAGTGGGTGGCAGTTATATGGTATGATGCA
			CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG	AGTAATAAATACTATGCAGACTCCGTGAAGGGC
			GGTCTGGGACAGACTTCACTCTCACCATCAGCA	CGATTCACCATCTCCAGAGACAATTCCAAGAAC
			GATTGGAGCCTGAAGATTTTGCAGTGTATTACT	ACGCTGTTTCTGCAAGTGAACAGCCTGAGAGCC
			GTCAGCAGTATGGTAGCTCACCTCGCTTCGGCC	GAGGACACGGCTGTGTATTACTGTGCGAGAGGG
			AAGGGACACGACTGGAGATTAAACGA	ATTACGATTTTTTGGTCATGGGTTTGAATATTGGG
				GCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1640	SEQ ID NO: 1797
		AA	EIVLTQSPGTLSLSPGERATLSCRASQIFTSTYLAW	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM
			YQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF	HWVRQAPGKGLEWVAVIWYDASNKYYEDSVKG
			TLTISRLEPEDFAVYYCQQYGSSPRFGQGTRLEIKR	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
			CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACCTTCAGTAACTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCGAGGGG CTGGAGTGGGTGGCAGCTATATGGTTTGATGCA AGTGATAAATACTATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGAGACAACTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGGCGATTTTTGGAGTGGTCCCCGACTACTGG GGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1798
			QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGM HWVRQAPGEGLEWVAAIWFDASDKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGTLVTVSS
			SEQ ID NO: 228
			CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACCTTCAGTAACTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCGAGGGG CTGGAGTGGGTGGCAGCTATATGGTTTGATGCA AGTGATAAATACTATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGAGACAACTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGGCGATTTTTGGAGTGGTCCCCGACTACTGG GGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1799
			QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGM HWVRQAPGEGLEWVAAIWFDASDKYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGTLVTVSS

iPS:361185	2G10_LC1.005	NA	SEQ ID NO: 72
			GAAATAGTGATGACGCAGTCTCCAGCCACCCTG TCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCC TGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGCAGCCACCAGGGCC ACTGGTATCCCAGCCAGGTTCAGTGGCAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGCAGTCTGAAGATTTTGCAGTTTATTACTGTC AGCAGTATAATAACTGGCCTCTCACTTTCGGCG GAGGGACCAAGGGTGGAGATCAAACGA
			SEQ ID NO: 1643
		AA	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGAATRATGIPARFSGSGSGTE FTLTISSLQSEDFAVYYCQQYNNWPLTFGGGTKVE IKR
			SEQ ID NO: 73
iPS:361192	2G10_LC1.006	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTG TCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCC TGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGCAGCCACCAGGGCC ACTGGTATCCCAGCCAGGGTCAGTGGCAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGCAGTCTGAAGATTTTGCAGTTTATTACTGTC AGCAGTATAATAACTGGCCTCTCACTTTCGGCG GAGGGACCAAGGGTGGAGATCAAACGA
			SEQ ID NO: 1644
		AA	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGAATRATGIPARVSGSGSGTE FTLTISSLQSEDFAVYYCQQYNNWPLTFGGGTKVE IKR

			SEQ ID NO: 229
		NA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACCTTCAGTAACTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCGAGGGG CTGGAGTGGGTGGCAGCTATATGGTTTGATGGA AGTGATAAATACTATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGAGACAACTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGGCGATTTTTGGAGTGGTCCCCGACTACTGG GGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1800
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGM HWVRQAPGEGLEWVAAIWFDGSDKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGTLVTVSS
			SEQ ID NO: 230
		NA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACCTTCAGTAACTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCGAGGGG CTGGAGTGGGTGGCAGCTATATGGTTTGATGCA AGTGATAAATACTATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGAGACAACTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGGCGATTTTTGGAGTGGTCCCCGACTACTGG GGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1801
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGM HWVRQAPGEGLEWVAAIWFDASDKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGTLVTVSS

		SEQ ID NO: 74	SEQ ID NO: 231
iPS:359609	2G10_LC1.007	GAAATAGTGATGACGCAGTCTCCAGCCACCCTG TCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCC TGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGCAGCCACCAGGGCC ACTGGTATCCCAGCCAGGTTCAGTGGCAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGGAGCCTGAAGATTTTGCAGTTTATTACTGTC AGCAGTATAATAACTTCCCTCTCACTTTCGGCGG AGGGACCAAGGTGGAGATCAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACCTTCAGTAACTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGCTATATGGTTTGATGCA AGTGATAAATACTATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGAGACAACTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGGCGATTTTTGGAGTGGTCCCCGACTACTGG GGCCAGGGAACCCTGGTCACCGTCTCCTCA
		SEQ ID NO: 1645	SEQ ID NO: 1802
	AA	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGAATRATGIPARFSGSGSGTE FTLTISSLEPEDFAVYYCQQYNNFPLTFGGGTKVEI KR	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGM HWVRQAPGKGLEWVAAIWFDASDKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGTLVTVSS
		SEQ ID NO: 75	SEQ ID NO: 232
iPS:359615	2G10_LC1.008	GAAATAGTGATGACGCAGTCTCCAGCCACCCTG TCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCC TGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGCAGCCACCAGGGCC ACTGGTATCCCAGCCAGGTTCAGTGGCAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGGAGCCTGAAGATTTTGCAGTTTATTACTGTC AGCAGTATAATAACTATCCTCTCACTTTCGGCGG AGGGACCAAGGTGGAGATCAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACCTTCAGTAACTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGCTATATGGTTTGATGCA AGTGATAAATACTATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGAGACAACTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGGCGATTTTTGGAGTGGTCCCCGACTACTGG GGCCAGGGAACCCTGGTCACCGTCTCCTCA
		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 CAGGCGATTTTTGGAGTGGTTCCCCGACTACTGG 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

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

iPS:359628	18E3.004	NA	SEQ ID NO: 80	SEQ ID NO: 237
			GAAATTGTGTTGACGCAGTCTCCAGGCACCCTG	CAGGTGCAGTTGCAGGAGTCGGGCCCAGGACTG
			TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT	GTGAAGCCTTCACAGACCCTGTCCCTCACCTGC
			GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT	ACTGTCTCTGGTGACTCCATCAGCAGTGGTGGTT
			TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC	ACTACTGGAGCTGGATCCGCCAGCCCCCAGGGA
			CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG	AGGGCCTGGAGTGGATTGGGTACATCTATTACA
			CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG	GTGGGAGCACCTACTACAACCCGTCCCTCAAGA
			GGTCTGGGACAGACTTCACTCTCACCATCAGCA	GTCGAGTTACCATATCAGTAGACACGTCTAAGA
			GACTGGAGCCTGATGATTTTGCAGTGTATTACTG	ACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC
			TCAGCAGTATGGTAGTTCACCGCTCACTTTCGGC	CGCGGACACGGCCGTGTATTACTGTGCGAGAGA
			GGAGGGACCAAGGTGGAGATCAAACGA	TCGTATTACGATTTTTTGGAGTGGTTATGGGGGGC
				GGTATGGACGTCTGGGGCCAAGGGACCACGGTC
				ACCGTCTCCTCA
			SEQ ID NO: 1651	SEQ ID NO: 1808
		AA	EIVLTQSPGTLSLSPGERATLSCRASQSISYSYLAW	QVQLQESGPGLVKPSQTLSLTCTVSGDSISSGGYY
			YQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF	WSWIRQPPGKGLEWIGYIYYSGSTYYNPSLKSRVT
			TLTISRLEPDDFAVYYCQQYGSSPLTFGGGTKVEIK	ISVDTSKNQFSLKLSSVTAADTAVYYCARDRITIFG
			R	VVMGGGMDVWGQGTTVTVSS
			SEQ ID NO: 81	SEQ ID NO: 238
iPS:359637	18E3.005	NA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTG	CAGGTGCAGTTGCAGGAGTCGGGCCCAGGACTG
			TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT	GTGAAGCCTTCAGAGACCCTGTCCCTCACCTGC
			GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT	ACTGTCTCTGGTGACTCCATCAGCAGTGGTGGTT
			TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC	ACTACTGGAGCTGGATCCGCCAGCACCCAGGGA
			CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG	AGGGCCTGGAGTGGATTGGGTACATCTATTACA
			CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG	GTGGGAGCACCTACTACAACCCGTCCCTCAAGA
			GGTCTGGGACAGACTTCACTCTCACCATCAGCA	GTCGAGTTACCATATCAGTAGACACGTCTAAGA
			GACTGGAGCCTGATGATTTTGCAGTGTATTACTG	ACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC
			TCAGCAGTATGGTAGTTCACCGCTCACTTTCGGC	CGCGGACACGGCCGTGTATTACTGTGCGAGAGA
			GGAGGGACCAAGGTGGAGATCAAACGA	TCGTATTACGATTTTTTGGAGTGGTTATGGGGGGC
				GGTATGGACGTCTGGGGCCAAGGGACCACGGTC
				ACCGTCTCCTCA
			SEQ ID NO: 1652	SEQ ID NO: 1809
		AA	EIVLTQSPGTLSLSPGERATLSCRASQSISYSYLAW	QVQLQESGPGLVKPSETLSLTCTVSGDSISSGGYY
			YQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF	WSWIRQHPGKGLEWIGYIYYSGSTYYNPSLKSRVT
			TLTISRLEPDDFAVYYCQQYGSSPLTFGGGTKVEIK	ISVDTSKNQFSLKLSSVTAADTAVYYCARDRITIFG
			R	VVMGGGMDVWGQGTTVTVSS

iPS:361210	18E3.006	NA	SEQ ID NO: 82	SEQ ID NO: 239
			GAAATTGTGTTGACGCAGTCTCCAGGCACCCTG	CAGGTGCAGTTGCAGGAGTCGGGCCCAGGACTG
			TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT	GTGAAGCCTTCACAGACCCTGTCCCTCACCTGC
			GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT	ACTGTCTCTGGTGACTCCATCAGCAGTGGTGGTT
			TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC	ACTACTGGAGCTGGATCCGCCAGCACCCAGGGA
			CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG	AGGGCCTGGAGTGGATTGGGTACATCTATTACA
			CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG	GTGGGAGCACCTACTACAACCCGTCCCTCAAGA
			GGTCTGGGACAGACTTCACTCTCACCATCAGCA	GTCGAGTTACCATATCAGTAGACACGTCTAAGA
			GACTGGAGCCTGATGATTTTGCAGTGTATTACTG	ACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC
			TCAGCAGTATGGTAGTTCACCGCTCACTTTCGGC	CGCGGACACGGCCGTGTATTACTGTGCGAGAGA
			GGAGGGACCAAGGTGGAGATCAAACGA	TCGTATTACGATTTTTGGAGTGGTTATGGGGGGC
				GGTATGGACGTCTGGGGCCAAGGGACCACGGTC
				ACCGTCTCCTCA
		AA	SEQ ID NO: 1653	SEQ ID NO: 1810
			EIVLTQSPGTLSLSPGERATLSCRASQSISYSYLAW	QVQLQESGPGLVKPSQTLSLTCTVSGDSISSGGYY
			YQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF	WSWIRQHPGKGLEWIGYIYYSGSTYYNPSLKSRVT
			TLTISRLEPDDFAVYYCQQYGSSPLTFGGGTKVEIK	ISVDTSKNQFSLKLSSVTAADTAVYYCARDRITIFG
			R	VVMGGGMDVWGQGTTVTVSS
			SEQ ID NO: 83	SEQ ID NO: 240
iPS:361214	18E3.007	NA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTG	CAGGTGCAGTTGCAGGAGTCGGGCCCAGGACTG
			TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT	GTGAAGCCTTCAGAGACCCTGTCCCTCACCTGC
			GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT	ACTGTCTCTGGTGACTCCATCAGCAGTGGTGGTT
			TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC	ACTACTGGAGCTGGATCCGCCAGCACCCAGGGA
			CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG	AGGGCCTGGAGTGGATTGGGTACATCTATTACA
			CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG	GTGGGAGCACCTACTACAACCCGTCCCTCAAGA
			GGTCTGGGACAGACTTCACTCTCACCATCAGCA	GTCGAGTTACCATATCAGTAGACACGTCTAAGA
			GACAGGAGCCTGATGATTTTGCAGTGTATTACT	ACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC
			GTCAGCAGTATGGTAGTTCACCGCTCACTTTCGG	CGCGGACACGGCCGTGTATTACTGTGCGAGAGA
			CGGAGGGACCAAGGTGGAGATCAAACGA	TCGTATTACGATTTTTGGAGTGGTTATGGGGGGC
				GGTATGGACGTCTGGGGCCAAGGGACCACGGTC
				ACCGTCTCCTCA
		AA	SEQ ID NO: 1654	SEQ ID NO: 1811
			EIVLTQSPGTLSLSPGERATLSCRASQSISYSYLAW	QVQLQESGPGLVKPSETLSLTCTVSGDSISSGGYY
			YQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF	WSWIRQHPGKGLEWIGYIYYSGSTYYNPSLKSRVT
			TLTISRQEPDDFAVYYCQQYGSSPLTFGGGTKVEI	ISVDTSKNQFSLKLSSVTAADTAVYYCARDRITIFG
			KR	VVMGGGMDVWGQGTTVTVSS

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

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

IPS:359685	5C2.009	NA	SEQ ID NO: 88	SEQ ID NO: 245
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG	CAGGTGCCGCCTGGTGCAGTCTGGGGCTGAGGTG
			GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC	AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC	AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			AACAATAAGAACTACATAGCTTGGTACCAGCAG	ATCCACTGGGGTGCGACAGGCCCCTGGACAAGGG
			CAACCAGGACATCCTCCTAAGCTGCTCATTTACT	CTTGAGTGGATGGGGTGGATCAACCCTGACGCT
			GGGCATCTACCCGGGAATCCGGGGTCCCTGACC	GGTGGCACAGACTATTCACAGAGGTTTCAGGGC
			GATTCAGTGGCAGCGGGTCTGGGACAGATTTCA	AGGTTCACCATGACCAGGGACACGTCCATCAGC
			CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG	ACAGCCTACATGGAACTGAACAGGCTGAGATCT
			TGGCAGTTTTTTTACTGTCAACAATATTATAGTAC	GACGACACGGCCGTGTATTACTGTGCGAGAGAG
			TCCGTGGACGTTCGGCCAAGGGACCAAGGTGGA	GCCACGATTTTTGGAATGGTTATTGTACCGTTTG
			AATCAAACGA	ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
				CCTCA
		AA	SEQ ID NO: 1659	SEQ ID NO: 1816
			DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			NYIAWYQQQPGHPPKLLIYWASTRESGVPDRFSGS	HWVRQAPGQGLEWMGWINPDAGGTDYSQRFQG
			GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ	RFTMTRDTSISTAYMELNRLRSDDTAVYYCAREA
			GTKVEIKR	TIFGMVIVPFDYWGQGTLVTVSS
			SEQ ID NO: 89	SEQ ID NO: 246
IPS:361240	5C2.010	NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTG
			GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC	AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC	AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			AACAATAAGAACTACATAGCTTGGTACCAGCAG	ATCCACTGGGGTGCGACAGGCCCCTGGACAAGGG
			CAACCAGGACATCCTCCTAAGCTGCTCATTTACT	CTTGAGTGGATGGGGTGGATCAACCCTGACAGT
			GGGCATCTACCCGGGAATCCGGGGTCCCTGACC	GGTGGCACAGACTATTCACAGAGGTTTCAGGGC
			GATTCAGTGGCAGCGGGTCTGGGACAGATTTCA	AGGGTCACCATGACCAGGGACACGTCCATCAGC
			CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG	ACAGCCTACATGGAACTGAACAGGCTGAGATCT
			TGGCAGTTTTTTTACTGTCAACAATATTATAGTAC	GACGACACGGCCGTGTATTACTGTGCGAGAGAG
			TCCGTGGACGTTCGGCCAAGGGACCAAGGTGGA	GCCACGATTTTTGGAATGGTTATTGTACCGTTTG
			AATCAAACGA	ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
				CCTCA
		AA	SEQ ID NO: 1660	SEQ ID NO: 1817
			DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			NYIAWYQQQPGHPPKLLIYWASTRESGVPDRFSGS	HWVRQAPGQGLEWMGWINPDSGGTDYSQRFQGR
			GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ	VTMTRDTSISTAYMELNRLRSDDTAVYYCAREATI
			GTKVEIKR	FGMVIVPFDYWGQGTLVTVSS

iPS:361247	5C2.011	NA	SEQ ID NO: 90	SEQ ID NO: 247
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTG
			GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC	AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC	AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			AACAATAAGAACTACATAGCTTGGTACCAGCAG	ATCCACTGGGTGCGACAGGCCCCTGGACAAGGG
			CAACCAGGACATCCTCCTAAGCTGCTCATTTACT	CTTGAGTGGATGGGGTGGATCAACCCTGACAGT
			GGGCATCTACCCGGGAATCCGGGGTCCCTGACC	GGTGGCACAGACTATTCACAGAGGTTTCAGGGC
			GATTCAGTGGCAGCGGGTCTGGGACAGATTTCA	AGGTTCACCATGACCAGGGACACGTCCATCAGC
			CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG	ACAGCCTACATGGAACTGAACAGGCTGAGATCT
			TGGCAGTTTTTTTACTGTCAACAATATTATAGTAC	GACGACACGGCCGTGTATTACTGTGCGAGAGAG
			TCCGTGGACGTTCGGCCAAGGGACCAAGGTGGA	GCCACGATTTTTGGAATGGTTATTGTACCGTTTG
			AATCAAACGA	ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
				CCTCA
		AA	SEQ ID NO: 1661	SEQ ID NO: 1818
			DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			NYIAWYQQQPGHPPKLLIYWASTRESGVPDRFSGS	HWVRQAPGQGLEWMGWINPDSGGTDYSQRFQGR
			GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ	FTMTRDTSISTAYMELNRLRSDDTAVYYCAREATI
			GTKVEIKR	FGMVIVPFDYWGQGTLVTVSS
			SEQ ID NO: 91	SEQ ID NO: 248
iPS:361254	5C2.012	NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG	CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG
			GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC	AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC	AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			AACAATAAGAACTACATAGCTTGGTACCAGCAG	ATCCACTGGGTGCGACAGGCCCCTGGACAAGGG
			CAACCAGGACATCCTCCTAAGCTGCTCATTTACT	CTTGAGTGGATGGGGTGGATCAACCCTGACAGT
			GGGCATCTACCCGGGAATCCGGGGTCCCTGACC	GGTGGCACAGACTATTCACAGAGGTTTCAGGGC
			GATTCAGTGGCAGCGGGTCTGGGACAGATTTCA	AGGGTCACCATGACCAGGGACACGTCCATCAGC
			CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG	ACAGCCTACATGGAACTGAACAGGCTGAGATCT
			TGGCAGTTTTTTTACTGTCAACAATATTATAGTAC	GACGACACGGCCGTGTATTACTGTGCGAGAGAG
			TCCGTGGACGTTCGGCCAAGGGACCAAGGTGGA	GCCACGATTTTTGGAATGGTTATTGTACCGTTTG
			AATCAAACGA	ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
				CCTCA
		AA	SEQ ID NO: 1662	SEQ ID NO: 1819
			DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			NYIAWYQQQPGHPPKLLIYWASTRESGVPDRFSGS	HWVRQAPGQGLEWMGWINPDSGGTDYSQRFQGR
			GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ	VTMTRDTSISTAYMELNRLRSDDTAVYYCAREATI
			GTKVEIKR	FGMVIVPFDYWGQGTLVTVSS

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

iPS:359669	5C2.015	NA	SEQ ID NO: 94
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAGCAG AAACCAGGACAACCTCCTAAGCTGCTCATTTAC TGGGCATCTACCCGGGAATCCGGGTCCCTGAC CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGAT GTGGCAGTTTTTTACTGTCAACAATATTATAGTA CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG AAATCAAACGA
		AA	SEQ ID NO: 1665 DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK NYIAWYQQKPGQPPKLLIYWASTRESGVPDRFSGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKR
	5C2.016	NA	SEQ ID NO: 95 GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAGCAG AAACCAGGACAACCTCCTAAGCTGCTCATTTAC TGGGCATCTACCCGGGAATCCGGGTCCCTGAC CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGAT GTGGCAGTTTTTTACTGTCAACAATATTATAGTA CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG AAATCAAACGA
		AA	SEQ ID NO: 1666 DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK NYIAWYQQKPGQPPKLLIYWASTRESGVPDRFSGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKR

iPS:359678	5C2.016	NA	SEQ ID NO: 251 CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCGGCTACTAT ATCCACTGGGTGCGACAGGCCCCTGGACAAGGG CTTGAGTGGATGGGGGTGGATCAACCCTGACGCT GGTGGCACAGACTATTCACAGAGGTTTCAGGGC AGGGTCACCATGACCAGGGACACGTCCATCAGC ACAGCCTACATGGAACTGAACAGCCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGAG GCCACGATTTTTGGAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT CCTCA
		AA	SEQ ID NO: 1822 QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWINPDAGGTDYSQRFQG RVTMTRDTSISTAYMELNSLRSDDTAVYYCAREA TIFGMVIVPFDYWGQGTLVTVSS
	5C2.016	NA	SEQ ID NO: 252 CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCGGCTACTAT ATCCACTGGGTGCGACAGGCCCCTGGACAAGGG CTTGAGTGGATGGGGGTGGATCAACCCTGAAAGT GGTGGCACAGAGGTTTCAGGGC AGGGTCACCATGACCAGGGACACGTCCATCAGC ACAGCCTACATGGAACTGAACAGCCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGAG GCCACGATTTTTGGAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT CCTCA
		AA	SEQ ID NO: 1823 QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWINPESGGTDYSQRFQGR VTMTRDTSISTAYMELNSLRSDDTAVYYCAREATI FGMVIVPFDYWGQGTLVTVSS

rPS:361275	11C1.002	NA	SEQ ID NO: 96	SEQ ID NO: 253
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG	CAGGTGCCGCTGGTACAGTCTGGGGCTGAGGTG
			TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC	AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC	AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			AACAATAAGAACTACTTAGCTTGGTACCAACAG	ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
			AAACCAGGACAGCCTCCTAACCTGCTCATTTAC	CTTGTGTGGATGGGGTGGATCAGCCCTAACAGT
			TGGACTTCTACCCGAGAATCCGGGGTCCCTGAC	GGTGAAACAAGCTATGCACAGAAGTTTCAGGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC	AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT	ACAGCCTATATGGAGCTGAGCAGACTGAGATCT
			GTGGCTGTTTATTACTGTCAGCAATATTATCGTA	GACGACACGGCCGTGTATTTCTGTGCGAGAGAG
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG	GCCACGATTTTTGGAATGCTTATTGTACCATTTG
			AAATCAAACGA	ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
				CCTCA
		AA	SEQ ID NO: 1667	SEQ ID NO: 1824
			DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			NYLAWYQQKPGQPPNLLIYWTSTRESGVPDRFSG	HWVRQAPGQGLVWMGWISPNSGETSYAQKFQDR
			SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF	VTMTRDTSISTAYMELSRLRSDDTAVYFCAREATI
			GQGTKVEIKR	FGMLIVPFDYWGQGTLVTVSS
			SEQ ID NO: 97	SEQ ID NO: 254
rPS:361282	11C1.003	NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG	CAGGTGCCGCTGGTACAGTCTGGGGCTGAGGTG
			TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC	AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC	AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			AACAATAAGAACTACTTAGCTTGGTACCAACAG	ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
			AAACCAGGACAGCCTCCTAACCTGCTCATTTAC	CTTGTGTGGATGGGGTGGATCAGCCCTAACAGT
			TGGACTTCTACCCGAGAATCCGGGGTCCCTGAC	GGTGACACAAGCTATGCACAGAAGTTTCAGGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC	AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT	ACAGCCTATATGGAGCTGAGCAGACTGAGATCT
			GTGGCTGTTTATTACTGTCAGCAATATTATCGTA	GACGACACGGCCGTGTATTTCTGTGCGAGAGAG
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG	GCCACGATTTTTGGAATGCTTATTGTACCATTTG
			AAATCAAACGA	ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
				CCTCA
		AA	SEQ ID NO: 1668	SEQ ID NO: 1825
			DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			NYLAWYQQKPGQPPNLLIYWTSTRESGVPDRFSG	HWVRQAPGQGLVWMGWISPNSGDTSYAQKFQDR
			SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF	VTMTRDTSISTAYMELSRLRSDDTAVYFCAREATI
			GQGTKVEIKR	FGMLIVPFDYWGQGTLVTVSS

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

rs3612931	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
rs3612927	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
			CTTGTGTGGATGGGGGTGGATCAGCCCTAACAGT
			GGTGACACAAGCTATGCACAGAAGTTTCAGGAC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTATATGGAGCTGAGCAGACTGAGATCT
			GACGACACGGCCGTGTATTTCTGTACGAGAGAG
			GCCACGATTTTTGGAATGCTTATTGTACCATTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1828
			QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLVWMGWISPNSGDTSYAQKFQDR
			VTMTRDTSISTAYMELSRLRSDDTAVYFCTREATI
			FGMLIVPFDYWGQGTLVTVSS
			SEQ ID NO: 258
			CAGGTGCCGCTGGTACAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
			CTTGTGTGGATGGGGGTGGATCAGCCCTAACAGT
			GGTGAAACAAGCTATGCACAGAAGTTTCAGGAC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTATATGGAGCTGAGCAGACTGAGATCT
			GACGACACGGCCGTGTATTTCTGTACGAGAGAG
			GCCACGATTTTTGGAATGCTTATTGTACCATTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1829
			QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLVWMGWISPNSGETSYAQKFQDR
			VTMTRDTSISTAYMELSRLRSDDTAVYFCTREATI
			FGMLIVPFDYWGQGTLVTVSS

iPS:361301	11C1.008	NA	SEQ ID NO: 102	SEQ ID NO: 259
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG	CAGGTGCCGCCTGGTACAGTCTGGGGCTGAGGTG
			TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC	AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC	AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			AACAATAAGAACTACTTAGCTTGGTACCAACAG	ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
			AAACCAGGACAGCCTCCTAACCTGCTCATTTAC	CTTGTGTGGATGGGGTGGATCAGCCCTAACAGT
			TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC	GGTGACACAAGCTATGCACAGAAGTTTCAGGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC	AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT	ACAGCCTATATGGAGCTGAGCAGACTGAGATCT
			GTGGCTGTTTATTACTGTCAGCAATATTATCGTA	GACGACACGGCCGTGTATTTCTGTGCGAGAGAG
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG	GCCACGATTTTTGGAATGCTTATTGTACCATTTG
			AAATCAAACGA	ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
				CCTCA
		AA	SEQ ID NO: 1673	SEQ ID NO: 1830
			DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			NYLAWYQQKPGQPPNLLIYWTSTRDSGVPDRFSG	HWVRQAPGQGLVWMGWISPNSGDTSYAQKFQDR
			SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF	VTMTRDTSISTAYMELSRLRSDDTAVYFCAREATI
			GQGTKVEIKR	FGMLIVPFDYWGQGTLVTVSS
			SEQ ID NO: 103	SEQ ID NO: 260
iPS:359703	11C1.009	NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG	CAGGTGCAGCTGGTACAGTCTGGGGCTGAGGTG
			GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC	AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC	AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			AACAATAAGAACTACTTAGCTTGGTACCAACAG	ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
			AAACCAGGACAGCCTCCTAAACTGCTCATTTAC	CTTGAGTGGATGGGGTGGATCAGCCCTAACAGT
			TGGACTTCTACCCGAGAATCCGGGGTCCCTGAC	GGTGAAACAAGCTATGCACAGAAGTTTCAGGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC	AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT	ACAGCCTATATGGAGCTGAGCAGCCTGAGATCT
			GTGGCTGTTTATTACTGTCAGCAATATTATCGTA	GACGACACGGCCGTGTATTTCTGTGCGAGAGAG
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG	GCCACGATTTTTGGAATGCTTATTGTACCATTTG
			AAATCAAACGA	ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
				CCTCA
		AA	SEQ ID NO: 1674	SEQ ID NO: 1831
			DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			NYLAWYQQKPGQPPKLLIYWTSTRESGVPDRFSG	HWVRQAPGQGLEWMGWISPNSGETSYAQKFQDR
			SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF	VTMTRDTSISTAYMELSSLRSDDTAVYFCAREATI
			GQGTKVEIKR	FGMLIVPFDYWGQGTLVTVSS

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

iPS:359744	13H12.003	NA	SEQ ID NO: 106
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACATAGCTTGGTACCAGCAG
			AAACCAGGACATCCTCCTAAGCTGCTCATTTACT
			GGGCATCTACCCGGGAATCCGGGGTCCCTGACC
			GATTCAGTGGCAGCGGGTCTGGGACAGATTTCA
			CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG
			TGGCAGTTTTTTTACTGTCAACAATATTATAGTAC
			TCCGTGGACGTTCGGCCAAGGGACCAAGGTGGA
			AATCAAACGA
			SEQ ID NO: 1677
		AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK
			NYIAWYQQKPGHPPKLLIYWASTRESGVPDRFSGS
			GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ
			GTKVEIKR
			SEQ ID NO: 107
iPS:361319	13H12.004	NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACATAGCTTGGTACCAGCAG
			AAACCAGGACATCCTCCTAAGCTGCTCATTTACT
			GGGCATCTACCCGGGAATCCGGGGTCCCTGACC
			GATTCAGTGGCAGCGGGTCTGGGACAGATTTCA
			CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG
			TGGCAGTTTTTTTACTGTCAACAATATTATAGTAC
			TCCGTGGACGTTCGGCCAAGGGACCAAGGTGGA
			AATCAAACGA
			SEQ ID NO: 1678
		AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK
			NYIAWYQQKPGHPPKLLIYWASTRESGVPDRFSGS
			GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ
			GTKVEIKR
			SEQ ID NO: 263
			CAGGTGCCGCCTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATCCACTGGGTGCGACAGGCCCCTGGACAAGGA
			CTTGAGTGGATGGGGGTGGATCAACCCTGAAAGT
			GGTGGCACAGACTATTCACAGAGGTTTCAGGGC
			AGGTTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTACATGGAACTGAGCAGGCTGAGATCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGAG
			GCCACGATTTTTGGAATGGTTATTGTACCGTTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1834
			QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLEWMGWINPESGGTDYSQRFQGR
			FTMTRDTSISTAYMELSRLRSDDTAVYYCAREATI
			FGMVIVPFDYWGQGTLVTVSS
			SEQ ID NO: 264
			CAGGTGCCGCCTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATCCACTGGGTGCGACAGGCCCCTGGACAAGGA
			CTTGAGTGGATGGGGGTGGATCAACCCTGACAGT
			GGTGGCACAGACTATTCACAGAGGTTTCAGGGC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTACATGGAACTGAGCAGGCTGAGATCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGAG
			GCCACGATTTTTGGAATGGTTATTGTACCGTTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1835
			QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLEWMGWINPDSGGTDYSQRFQGR
			VTMTRDTSISTAYMELSRLRSDDTAVYYCAREATI
			FGMVIVPFDYWGQGTLVTVSS

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

		SEQ ID NO: 110	SEQ ID NO: 267
iPS:361330	12H11.002	GACATCGTGATGACCCAGTCTCCAGACTCCCTG	CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG
		TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC	AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
		TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC	AAGGCTTCTGGATACACCTTCACCGGCTACTAT
		AACAATAAGAACTACTTAGCTTGGTACCAGCAG	ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
		AAACCAGGACAGCCTCCTAACCTGCTCATTTAC	CTTGAGTGGATGGGGGTGGATAAGCCCTAACCAA
		TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC	GGTGAAACAAACTATGCACAGAAGTTTCAGGAC
		CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC	AGGGTCACCATGACCAGGGACACGTCCATCAGC
		ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT	ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT
		GTGGCTGTTTATTACTGTCAGCAATATTATCGTA	GACGACACGGCCGTGTATTACTGTGCGAGAGAG
		CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG	GCCACGATTTTTGGAATGCTTATTGTACCATTTG
		AAATCAAACGA	ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
	NA	SEQ ID NO: 1681	SEQ ID NO: 1838
	AA	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
		NYLAWYQQKPGQPPNLLIYWTSTRDSGVPDRFSG	HWVRQAPGQGLEWMGWISPNQGETNYAQKFQD
		SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF	RVTMTRDTSISTAYMELSRLRSDDTAVYYCAREA
		GQGTKVEIKR	TIFGMLIVPFDYWGQGTLVTVSS
		SEQ ID NO: 111	SEQ ID NO: 268
iPS:361337	12H11.003	GACATCGTGATGACCCAGTCTCCAGACTCCCTG	CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG
		TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC	AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
		TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC	AAGGCTTCTGGATACACCTTCACCGGCTACTAT
		AACAATAAGAACTACTTAGCTTGGTACCAGCAG	ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
		AAACCAGGACAGCCTCCTAACCTGCTCATTTAC	CTTGAGTGGATGGGGGTGGATAAGCCCTAACCAA
		TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC	GGTGACACAAACTATGCACAGAAGTTTCAGGAC
		CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC	AGGGTCACCATGACCAGGGACACGTCCATCAGC
		ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT	ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT
		GTGGCTGTTTATTACTGTCAGCAATATTATCGTA	GACGACACGGCCGTGTATTACTGTGCGAGAGAG
		CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG	GCCACGATTTTTGGAATGCTTATTGTACCATTTG
		AAATCAAACGA	ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
	NA	SEQ ID NO: 1682	SEQ ID NO: 1839
	AA	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
		NYLAWYQQKPGQPPNLLIYWTSTRDSGVPDRFSG	HWVRQAPGQGLEWMGWISPNQGDTNYAQKFQD
		SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF	RVTMTRDTSISTAYMELSRLRSDDTAVYYCAREA
		GQGTKVEIKR	TIFGMLIVPFDYWGQGTLVTVSS

IPS:361344	12H11.004	NA	SEQ ID NO: 112
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACTTAGCTTGGTACCAGCAG
			AAACCAGGACAGCCTCCTAACCTGCTCATTTAC
			TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC
			ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT
			GTGGCTGTTTATTACTGTCAGCAATATTATCGTA
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG
			AAATCAAACGA
			SEQ ID NO: 1683
		AA	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK
			NYLAWYQQKPGQPPNLLIYWTSTRDSGVPDRFSG
			SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF
			GQGTKVEIKR
			SEQ ID NO: 113
IPS:361351	12H11.005	NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACTTAGCTTGGTACCAGCAG
			AAACCAGGACAGCCTCCTAACCTGCTCATTTAC
			TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC
			ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT
			GTGGCTGTTTATTACTGTCAGCAATATTATCGTA
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG
			AAATCAAACGA
			SEQ ID NO: 1684
		AA	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK
			NYLAWYQQKPGQPPNLLIYWTSTRDSGVPDRFSG
			SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF
			GQGTKVEIKR
			SEQ ID NO: 269
			CAGGTGCCGCCTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGGGTGGATAAGCCCTAACCAA
			GGTGAAACAAACTATGCACAGAAGTTTCAGGAC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT
			GACGACACGGCCGTGTATTACTGTACGAGAGAG
			GCCACGATTTTTTGGAATGCTTATTGTACCATTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1840
		AA	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLEWMGWISPNQGETNYAQKFQD
			RVTMTRDTSISTAYMELSRLRSDDTAVYYCTREA
			TIFGMLIVPFDYWGQGTLVTVSS
			SEQ ID NO: 270
		NA	CAGGTGCCGCCTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGGGTGGATAAGCCCTAACAAT
			GGTGAAACAAACTATGCACAGAAGTTTCAGGAC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGAG
			GCCACGATTTTTTGGAATGCTTATTGTACCATTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1841
		AA	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLEWMGWISPNNGETNYAQKFQD
			RVTMTRDTSISTAYMELSRLRSDDTAVYYCAREA
			TIFGMLIVPFDYWGQGTLVTVSS

iPS:361358	12H11.006	NA	SEQ ID NO: 114
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACTTAGCTTGGTACCAGCAG
			AAACCAGGACAGCCTCCTAACCTGCTCATTTAC
			TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC
			ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT
			GTGGCTGTTTATTACTGTCAGCAATATTATCGTA
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG
			AAATCAAACGA
			SEQ ID NO: 1685
		AA	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK
			NYLAWYQQKPGQPPNLLIYWTSTRDSGVPDRFSG
			SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF
			GQGTKVEIKR
			SEQ ID NO: 115
iPS:361365	12H11.007	NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACTTAGCTTGGTACCAGCAG
			AAACCAGGACAGCCTCCTAACCTGCTCATTTAC
			TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC
			ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT
			GTGGCTGTTTATTACTGTCAGCAATATTATCGTA
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG
			AAATCAAACGA
			SEQ ID NO: 1686
		AA	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK
			NYLAWYQQKPGQPPNLLIYWTSTRDSGVPDRFSG
			SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF
			GQGTKVEIKR
			SEQ ID NO: 271
			CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGGGTGGATAAGCCCTAACAAT
			GGTGACACAAACTATGCACAGAAGTTTCAGGAC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGAG
			GCCACGATTTTTGGAATGCTTATTGTACCATTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1842
			QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLEWMGWISPNNGDTNYAQKFQD
			RVTMTRDTSISTAYMELSRLRSDDTAVYYCAREA
			TIFGMLIVPFDYWGQGTLVTVSS
			SEQ ID NO: 272
			CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGGGTGGATAAGCCCTAACCAA
			GGTGACACAAACTATGCACAGAAGTTTCAGGAC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT
			GACGACACGGCCGTGTATTACTGTACGAGAGAG
			GCCACGATTTTTGGAATGCTTATTGTACCATTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1843
			QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLEWMGWISPNQGDTNYAQKFQD
			RVTMTRDTSISTAYMELSRLRSDDTAVYYCTREA
			TIFGMLIVPFDYWGQGTLVTVSS

iPS:361372	12H11.008	NA	SEQ ID NO: 116
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACTTAGCTTGGTACCAGCAG
			AAACCAGGACAGCCTCCTAACCTGCTCATTTAC
			TGGACTTCTACCCGAGAATTCCGGGGTCCCTGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC
			ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT
			GTGGCTGTTTATTACTGTCAGCAATATTATCGTA
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG
			AAATCAAACGA
			SEQ ID NO: 1687
		AA	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK
			NYLAWYQQKPGQPPNLLIYWTSTRDSGVPDRFSG
			SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF
			GQGTKVEIKR
			SEQ ID NO: 117
iPS:361379	12H11.009	NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACTTAGCTTGGTACCAGCAG
			AAACCAGGACAGCCTCCTAACCTGCTCATTTAC
			TGGACTTCTACCCGAGAATCCGGGGTCCCTGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC
			ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT
			GTGGCTGTTTATTACTGTCAGCAATATTATCGTA
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG
			AAATCAAACGA
			SEQ ID NO: 1688
		AA	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK
			NYLAWYQQKPGQPPNLLIYWTSTRESGVPDRFSG
			SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF
			GQGTKVEIKR
			SEQ ID NO: 273
			CAGGTGCCGCCTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGGGTGGATAAGCCCTAACAAT
			GGTGAAACAAACTATGCACAGAAGTTTCAGGAC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT
			GACGACACGGCCGTGTATTACTGTACGAGAGAG
			GCCACGATTTTTGGAATGCTTATTGTACCATTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1844
		AA	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLEWMGWISPNNGETNYAQKFQD
			RVTMTRDTSISTAYMELSRLRSDDTAVYYCTREA
			TIFGMLIVPFDYWGQGTLVTVSS
			SEQ ID NO: 274
		NA	CAGGTGCCGCCTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGGGTGGATAAGCCCTAACCAA
			GGTGAAACAAACTATGCACAGAAGTTTCAGGAC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGAG
			GCCACGATTTTTGGAATGCTTATTGTACCATTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1845
		AA	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLEWMGWISPNQGETNYAQKFQD
			RVTMTRDTSISTAYMELSRLRSDDTAVYYCAREA
			TIFGMLIVPFDYWGQGTLVTVSS

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

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

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

IPS:361412	2C2.005.002	NA	SEQ ID NO: 124
			CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG
			GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT
			CTGGAAGTAGCTCCAACATCGGAAGTCAAACTG
			TAAACTGGTACCAGCACCTCCCAGGAACGGCCC
			CCAAACTCCTCATCTATACTAATAATCAGCGGC
			CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA
			GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG
			CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG
			CAACATTCGATGAAAGCCTGCAAGGTCCGGTAT
			TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT
		AA	SEQ ID NO: 1695
			QSVLTQPPSASGTPGQRVTISCSGSSSNIGSQTVNW
			YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
			ASLAISGLQSEDEADYFCATFDESLQGPVFGGGTK
			LTVLG
IPS:361418	2C2.005.003	NA	SEQ ID NO: 125
			CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG
			GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT
			CTGGAAGTAGCTCCAACATCGGAAGTAATTATG
			TAAACTGGTACCAGCACCTCCCAGGAACGGCCC
			CCAAACTCCTCATCTATACTAATAATCAGCGGC
			CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA
			GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG
			CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG
			CAACATTCGATGAAAGCCTGAGGTCCGGTAT
			TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT
		AA	SEQ ID NO: 1696
			QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNYVNW
			YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
			ASLAISGLQSEDEADYFCATFDESLSGPVFGGGTK
			LTVLG

			SEQ ID NO: 281
			CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCCGGATACACCTTCACCGGCTACTAT
			ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGATGGATCAACCCTAACAGT
			GGTGGCACAAACTATGCACAGAAGTTTCAGGGC
			AGGGTCACCATGACCAGGGACACGTCCATCAGT
			ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGGG
			GGGGATTACGTTTGGGGGACTTATCGGCCTCAC
			TACTACTACGGTATGGACGTCTGGGGCCAAGGG
			ACCACGGTCACCGTCTCCTCA
		AA	SEQ ID NO: 1852
			QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY
			MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ
			GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG
			GDYVWGTYRPHYYYGMDVWGQGTTVTVSS
		NA	SEQ ID NO: 282
			CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCCGGATACACCTTCACCGGCTACTAT
			ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGATGGATCAACCCTAACAGT
			GGTGGCACAAACTATGCACAGAAGTTTCAGGGC
			AGGGTCACCATGACCAGGGACACGTCCATCAGT
			ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGGG
			GGGGATTACGTTTGGGGGACTTATCGGCCTCAC
			TACTACTACGGTATGGACGTCTGGGGCCAAGGG
			ACCACGGTCACCGTCTCCTCA
		AA	SEQ ID NO: 1853
			QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY
			MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ
			GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG
			GDYVWGTYRPHYYYGMDVWGQGTTVTVSS

		SEQ ID NO: 126	SEQ ID NO: 283
2C2.005.004	NA	CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT CTGGAAGTAGCTCCAACATCGGAAGTAATTATG TAAACTGGTACCAGCACCTCCCAGGAACGGCCC CCAAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATGAAAGCCTGCAAGGTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT	CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCCGGATACACCTTCACCGGCTACTAT ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG CTTGAGTGGATGGGATGGATCAACCCTAACAGT GGTGGCACAAACTATGCACAGAAGTTTCAGGGC AGGGTCACCATGACCAGGGACACGTCCATCAGT ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT GACGACACGGCCGTGTATTACTGTGCGAGAGGG GGGGATTACGTTTGGGGGACTTATCGGCCTCAC TACTACTACGGTATGGACGTCTGGGGCCAAGGG ACCACGGTCACCGTCTCCTCA
	AA	SEQ ID NO: 1697 QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNYVNW YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDESLQGPVFGGGTK LTVLG	SEQ ID NO: 1854 QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG GDYVWGTYRPHYYYGMDVWGQGTTVTVSS
		SEQ ID NO: 127	SEQ ID NO: 284
iPS:361430	NA	CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT CTGGAAGTAGCTCCAACATCGGAAGTCAAACTG TAAACTGGTACCAGCACCTCCCAGGAACGGCCC CCAAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATGACAGCCTGAATGGTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT	CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCCGGATACACCTTCACCGGCTACTAT ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG CTTGAGTGGATGGGATGGATCAACCCTAACCCTAACAGT GGTGGCACAAACTATGCACAGAAGTTTCAGGGC AGGGTCACCATGACCAGGGACACGTCCATCAGT ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT GACGACACGGCCGTGTATTACTGTGCGAGAGGG GGGGATTACGTTTGGGGGACTTATCGGCCTCAC TACTACTACGGTATGGACGTCTGGGGCCAAGGG ACCACGGTCACCGTCTCCTCA
	AA	SEQ ID NO: 1698 QSVLTQPPSASGTPGQRVTISCSGSSNIGSQTVNW YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDDSLNGPVFGGGTK LTVLG	SEQ ID NO: 1855 QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG GDYVWGTYRPHYYYGMDVWGQGTTVTVSS

ipS:361436	2C2.005.006	NA	SEQ ID NO: 128
			CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG
			GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT
			CTGGAAGTAGCTCCAACATCGGAAGTAATTATG
			TAAACTGGTACCAGCACCTCCCAGGAACGGCCC
			CCAAACTCCTCATCTATACTAATAATCAGCGGC
			CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA
			GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG
			CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG
			CAACATTCGATGACAGCCTGAATGGTCCGGTAT
			TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT
			SEQ ID NO: 1699
		AA	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNYVNW
			YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
			ASLAISGLQSEDEADYFCATFDDSLNGPVFGGGTK
			LTVLG
			SEQ ID NO: 129
ipS:361442	2C2.005.007	NA	CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG
			GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT
			CTGGAAGTAGCTCCAACATCGGAAGTAATACTG
			TAAACTGGTACCAGCACCTCCCAGGAACGGCCC
			CCAAACTCCTCATCTATACTAATAATCAGCGGC
			CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA
			GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG
			CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG
			CAACATTCGATGAAAGCCTGAATGGTCCGGTAT
			TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT
			SEQ ID NO: 1700
		AA	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNW
			YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
			ASLAISGLQSEDEADYFCATFDESLNGPVFGGGTK
			LTVLG
			SEQ ID NO: 285
			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

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

iPS:361460	2C2.005.010	NA	SEQ ID NO: 132
			CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG
			GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT
			CTGGAAGTAGCTCCAACATCGGAAGTAATACTG
			TAAACTGGTACCAGCACCTCCCAGGAACGGCCC
			CCAAACTCCTCATCTATACTAAATAATCAGCGGC
			CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA
			GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG
			CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG
			CAACATTCGATGACAGCCTGAATGGTCCGGTAT
			TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT
		AA	SEQ ID NO: 1703
			QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNW
			YQILPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
			ASLAISGLQSEDEADYFCATFDDSLNAPVFGGGTK
			LTVLG
iPS:361466	2C2.005.011	NA	SEQ ID NO: 133
			CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG
			GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT
			CTGGAAGTAGCTCCAACATCGGAAGTAATACTG
			TAAACTGGTACCAGCACCTCCCAGGAACGGCCC
			CCAAACTCCTCATCTATACTAATAATCAGCGGC
			CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA
			GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG
			CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG
			CAACATTCGATAGCAGCCTGAATGGTCCGGTAT
			TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT
		AA	SEQ ID NO: 1704
			QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNW
			YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
			ASLAISGLQSEDEADYFCATFDSSLNGPVFGGGTK
			LTVLG

			SEQ ID NO: 289
			CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCCGGATACACCTTCACCGGCTACTAT
			ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGATGGATCAACCCTAACAGT
			GGTGGCACAAACTATGCACAGAAGTTTCAGGGC
			AGGGTCACCATGACCAGGGACACGTCCATCAGT
			ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGGG
			GGGGATTACGTTTGGGGGACTTATCGGCCTCAC
			TACTACTACGGTATGGACGTCTGGGGCCAAGGG
			ACCACGGTCACCGTCTCCTCA
		AA	SEQ ID NO: 1860
			QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY
			MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ
			GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG
			GDYVWGTYRPHYYYGMDVWGQGTTVTVSS
		NA	SEQ ID NO: 290
			CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCCGGATACACCTTCACCGGCTACTAT
			ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGATGGATCAACCCTAACAGT
			GGTGGCACAAACTATGCACAGAAGTTTCAGGGC
			AGGGTCACCATGACCAGGGACACGTCCATCAGT
			ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGGG
			GGGGATTACGTTTGGGGGACTTATCGGCCTCAC
			TACTACTACGGTATGGACGTCTGGGGCCAAGGG
			ACCACGGTCACCGTCTCCTCA
		AA	SEQ ID NO: 1861
			QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY
			MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ
			GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG
			GDYVWGTYRPHYYYGMDVWGQGTTVTVSS

		SEQ ID NO: 134	SEQ ID NO: 291
iPS:361472	2C2.005.012	NA	CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT CTGGAAGTAGCTCCAACATCGGAAGTAATTATG TAAACTGGTACCAGCACCTCCCAGGAACGGCCC CCAAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATAGCAGCCTGAATGCTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT
		AA	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNYVNW YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDSSLNAPVFGGGTK LTVLG
		SEQ ID NO: 1705	SEQ ID NO: 1862
		SEQ ID NO: 135	SEQ ID NO: 292
iPS:361478	2C2.005.013	NA	CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT CTGGAAGTAGCTCCAACATCGGAAGTAATTATG TAAACTGGTACCAGCACCTCCCAGGAACGGCCC CCAAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATAGCAGCCTGAATGCTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT
		AA	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNYVNW YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDSSLNAPVFGGGTK LTVLG
		SEQ ID NO: 1706	SEQ ID NO: 1863

iPS:361485	2C2.005.014	NA	SEQ ID NO: 136	SEQ ID NO: 293
			CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG	CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG
			GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT	AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			CTGGAAGTAGCTCCAACATCGGAAGTCAAACTG	AAGGCTTCCGGATACACCTTCACCGGCTACTAT
			TAAACTGGTACCAGCACCTCCCAGGAACGGCCC	ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG
			CCAAACTCCTCATCTATACTAATAATCAGCGGC	CTTGAGTGGATGGGATGGAACCCTAACCAGT
			CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA	GGTGGCACAAACTATGCACAGAAGTTTCAGGGC
			GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG	AGGGTCACCATGACCGAGGACACGTCCATCAGT
			CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG	ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT
			CAACATTCGATGAAAGCCTGAGTGGTCCGGTAT	GACGACACCGCCGTGTATTACTGTGCGAGAGGG
			TCGGCGGAGGGGACCAAGCTGACCGTCCTAGGT	GGGGATTACGTTTTCGGGACTTATCGGCCTCACT
				ACTACTACGGTATGGACGTCTGGGGCCAAGGGA
				CCACGGTCACCGTCTCCTCA
			SEQ ID NO: 1707	SEQ ID NO: 1864
		AA	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSQTVNW	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY
			YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS	MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ
			ASLAISGLQSEDEADYFCATFDESLSGPVFGGGTK	GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG
			LTVLG	GDYVFGTYRPHYYYGMDVWGQGTTVTVSS
			SEQ ID NO: 137	SEQ ID NO: 294
iPS:361845	18F2.013	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
			CTGCATCTATAGGAGACAGAGTCACCATCACTT	GTCCAGCCTGGGGAGGTCCCTGAGACTCTCCTGT
			GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG	GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA
			GCTGGTATCAACAGAAACCAGGGAAAGCCCCTA	TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC
			AGCGCCTGATCTATGGTGCATCCAGTTTGCAAA	TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
			GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT	GTAATGAAAACTATGCAGACGCCGTGAAGGGCC
			CTGGGACAGAATTCACTCTCACAATCAGCAGCC	GATTCACCATCTCCAGAGACAATTCCAAGAACA
			TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT	CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
			ACAGCATAATAATTACCCCTTCACTTTCGGCCAA	AGGACACGGCTGTGTATTACTGTGCGAGAGATA
			GGGACCAAAGTGGATATCAAACGA	GGACGATCTTTGGAGTGGTCTTGGGGGACTACT
				GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1708	SEQ ID NO: 1865
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM
			YQQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTE	HWVRQAPGKGLEWVAVIWYDASNENYADAVKG
			FTLTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDI	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR
			KR	TIFGVVLGDYWGQGTLVTVSS

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

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

iPS:361127	5G12.006.001	NA	SEQ ID NO: 142	SEQ ID NO: 299
			GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTG
			CTGCATCTGTAGGAGACAGAGTCACTATCACTT	GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCCGGGCAAGTCAGACCATTAGCAGGTTTTTAA	GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC
			ATTGGTATCAGCAGAAACCTGGGAAAGCCCCTG	ATACACTGGGTCCGCCAGGCTCCAGGCAAGGGG
			AGCTCCTGATCTATGTTGCATCCAGTTTGCAAAG	CTGGAGTGGGTGGCAGTTATATGGTATGATGCA
			TGGGGTCCCATCAAGATTCAGTGGCAGTGGTTC	AGTAATAAGTTCCATGCAGACGCCGTGAAGGGC
			TGGGACAGATTTCACTCTCACCATCAGCAGTCT	CGATTCACCATCTCCAGAGACAATTCCAAGAAC
			GCAACCTGAAGATTTTTGCAACTTACTACTGTCA	ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC
			ACAGAGTTACAGTACCCTGATCAGTTTTGGCCA	GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA
			GGGGACCAAGCTGGAGATCAAACGA	AAAGTGGCTGGTATGCCTGAAGCTTTTGAAATC
				TGGGGCCAAGGGACAAAGGTCACCGTCTCTTCA
			SEQ ID NO: 1713	SEQ ID NO: 1870
		AA	DIQLTQSPSSLSASVGDRVTITCRASQTISRFLNWY	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGIH
			QQKPGKAPELLIYVASSLQSGVPSRFSGSGSGTDFT	WVRQAPGKGLEWVAVIWYDASNKFHADAVKGR
			LTISSLQPEDFATYYCQQSYSTLISFGQGTKLEIKR	FTISRDNSKNTLYLQMNSLRAEDSAMYFCARGKV
				AGMPEAFEIWGQGTKVTVSS
			SEQ ID NO: 143	SEQ ID NO: 300
iPS:361136	5G12.006.002	NA	GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTG
			CTGCATCTGTAGGAGACAGAGTCACTATCACTT	GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCCGGGCAAGTCAGACCATTAGCAGGTTTTTAA	ACAGCGTCTGGATTCACCTTCAGTAGCTATGGC
			ATTGGTATCAGCAGAAACCTGGGAAAGCCCCTG	ATACACTGGGTCCGCCAGGCTCCAGGCAAGGGG
			AGCTCCTGATCTATGTTGCATCCAGTTTGCAAAG	CTGGAGTGGGTGGCAGTTATATGGTATGATGCA
			TGGGGTCCCATCAAGATTCAGTGGCAGTGGTTC	AGTAATAAGTTCCATGCAGACGCCGTGAAGGGC
			TGGGACAGATTTCACTCTCACCATCAGCAGTCT	CGATTCACCATCTCCAGAGACAATTCCAAGAAC
			GCAACCTGAAGATTTTTGCAACTTACTACTGTCA	ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC
			ACAGAGTTACAGTACCCTGATCAGTTTTGGCCA	GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA
			GGGGACCAAGCTGGAGATCAAACGA	AAAGTGGCTGGTATGCCTGAAGCTTTTGAAATC
				TGGGGCCAAGGGACAAAGGTCACCGTCTCTTCA
			SEQ ID NO: 1714	SEQ ID NO: 1871
		AA	DIQLTQSPSSLSASVGDRVTITCRASQTISRFLNWY	QVQLVESGGGVVQPGRSLRLSCTASGFTFSSYGIH
			QQKPGKAPELLIYVASSLQSGVPSRFSGSGSGTDFT	WVRQAPGKGLEWVAVIWYDASNKFHADAVKGR
			LTISSLQPEDFATYYCQQSYSTLISFGQGTKLEIKR	FTISRDNSKNTLYLQMNSLRAEDSAMYFCARGKV
				AGMPEAFEIWGQGTKVTVSS

		SEQ ID NO: 144	SEQ ID NO: 301
rs361140	5GI2.006.003	GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACTATCACTT GCCGGGCAAGTCAGACCATTAGCAGGTTTTTAA ATTGGTATCAGCAGAAACCTGGGAAAGCCCCTG AGCTCCTGATCTATGTTGCATCCAGTTTGCAAAG TGGGGTCCCATCAAGATTCAGTGGCAGTGGTTC TGGGACAGATTTCACTCTCACCATCAGCAGTCT GCAACCTGAAGATTTTGCAACTTACTACTGTCA ACAGAGTTACAGTACCCTGATCAGTTTTGGCCA GGGGACCAAGCTGGAGATCACACGA	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC ATACACTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGTTATATGGTATGATGCA AGTAATAAGTTCCATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGAGACAATTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA AAAGTGGCTGGTATGCCTGAAGCTTTTGAAATC TGGGGCCAAGGGACAAAGGTCACCGTCTCTTCA
	AA	SEQ ID NO: 1715 DIQLTQSPSSLSASVGDRVTITCRASQTISRFLNWY QQKPGKAPELLIYVASSLQSGVPSRFSGSGSGTDFT LTISSLQPEDFATYYCQQSYSTLISFGQGTKLEITR	SEQ ID NO: 1872 QVQLVESGGGVVQPGRSLRLSCAAASGFTFSSYGIH WVRQAPGKGLEWVAVIWYDASNKFHADAVKGR FTISRDNSKNTLYLQMNSLRAEDSAMYFCARGKV AGMPEAFEIWGQGTKVTVSS
rs359919	5GI2.006.004	GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACTATCACTT GCCGGGCAAGTCAGACCATTAGCAGGTTTTTAA ATTGGTATCAGCAGAAACCTGGGAAAGCCCCTA AGCTCCTGATCTATGTTGCATCCAGTTTGCAAAG TGGGGTCCCATCAAGATTCAGTGGCAGTGGTTC TGGGACAGATTTCACTCTCACCATCAGCAGTCT GCAACCTGAAGATTTTGCAACTTACTACTGTCA ACAGAGTTACAGTACCCTGATCAGTTTTGGCCA GGGGACCAAGCTGGAGATCAAACGA	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC ATACACTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGTTATATGGTATGATGCA AGTAATAAGTTCCATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGAGACAATTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA AAAGTGGCTGGTATGCCTGAAGCTTTTGAAATC TGGGGCCAAGGGACATTGGTCACCGTCTCTTCA
	AA	SEQ ID NO: 1716 DIQLTQSPSSLSASVGDRVTITCRASQTISRFLNWY QQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDF TLTISSLQPEDFATYYCQQSYSTLISFGQGTKLEIKR	SEQ ID NO: 1873 QVQLVESGGGVVQPGRSLRLSCAAASGFTFSSYGIH WVRQAPGKGLEWVAVIWYDASNKFHADAVKGR FTISRDNSKNTLYLQMNSLRAEDSAMYFCARGKV AGMPEAFEIWGQGTLVTVSS

iPS:361144	NA	SEQ ID NO: 146	SEQ ID NO: 303
		GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTG
		CTGCATCTGTAGGAGACAGAGTCACTATCACTT	GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
		GCCGGGCAAGTCAGACCATTAGCAGGTTTTTAA	GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC
		ATTGGTATCAGCAGAAACCTGGGAAAGCCCCTG	ATACACTGGGTCCGCCAGGCTCCAGGCAAGGGG
		AGCTCCTGATCTATGTTGCATCCAGTTTGCAAAG	CTGGAGTGGGTGGCAGTTATATGGTATGATGCA
		TGGGGTCCCATCAAGATTCAGTGGCAGTGGTTC	AGTAATAAGTTCCATGCAGACTCCGTGAAGGGC
		TGGGACAGATTTCACTCTCACCATCAGCAGTCT	CGATTCACCATCTCCAGAGACAATTCCAAGAAC
		GCAACCTGAAGATTTTGCAACTTACTACTGTCA	ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC
		ACAGAGTTACAGTACCCTGATCAGTTTTGGCCA	GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA
		GGGGACCAAGCTGGAGATCAAACGA	AAAGTGGCTGGTATGCCTGAAGCTTTTGAAATC
			TGGGGCCAAGGGACAAAGGTCACCGTCTCTTCA
	AA	SEQ ID NO: 1717	SEQ ID NO: 1874
		DIQLTQSPSSLSASVGDRVTITCRASQTISRFLNWY	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGIH
		QQKPGKAPELLIYVASSLQSGVPSRFSGSGSGTDFT	WVRQAPGKGLEWVAVIWYDASNKFHADSVKGRF
		LTISSLQPEDFATYYCQQSYSTLISFGQGTKLEIKR	TISRDNSKNTLYLQMNSLRAEDSAMYFCARGKVA
			GMPEAFEIWGQGTKVTVSS
		SEQ ID NO: 147	SEQ ID NO: 304
iPS:361151	NA	GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTG
		CTGCATCTGTAGGAGACAGAGTCACTATCACTT	GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
		GCCGGGCAAGTCAGACCATTAGCAGGTTTTTAA	GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC
		ATTGGTATCAGCAGAAACCTGGGAAAGCCCCTG	ATACACTGGGTCCGCCAGGCTCCAGGCAAGGGG
		AGCTCCTGATCTATGTTGCATCCAGTTTGCAAAG	CTGGAGTGGGTGGCAGTTATATGGTATGATGGA
		TGGGGTCCCATCAAGATTCAGTGGCAGTGGTTC	AGTAATAAGTTCCATGCAGACGCCGTGAAGGGC
		TGGGACAGATTTCACTCTCACCATCAGCAGTCT	CGATTCACCATCTCCAGAGACAATTCCAAGAAC
		GCAACCTGAAGATTTTGCAACTTACTACTGTCA	ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC
		ACAGAGTTACAGTACCCTGATCAGTTTTGGCCA	GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA
		GGGGACCAAGCTGGAGATCAAACGA	AAAGTGGCTGGTATGCCTGAAGCTTTTGAAATC
			TGGGGCCAAGGGACAAAGGTCACCGTCTCTTCA
	AA	SEQ ID NO: 1718	SEQ ID NO: 1875
		DIQLTQSPSSLSASVGDRVTITCRASQTISRFLNWY	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGIH
		QQKPGKAPELLIYVASSLQSGVPSRFSGSGSGTDFT	WVRQAPGKGLEWVAVIWYDGSNKFHADAVKGR
		LTISSLQPEDFATYYCQQSYSTLISFGQGTKLEIKR	FTISRDNSKNTLYLQMNSLRAEDSAMYFCARGKV
			AGMPEAFEIWGQGTKVTVSS

		SEQ ID NO: 148	SEQ ID NO: 305
iPS:361491	17B11.002.001	CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTG CGGCCCCAGGACAGAAGGTCACCATCTCCTGCT CTGGAAGCAGCTCCAACATTGGAAATAATTATG TATCCTGGTATCAGCAGCTCCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCCTGACCGATTCTCTGGCTCCAA GTCTGGCACGTCAGCCACCCTGGGCATCACCGG ACTCCAGACTGGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGCTGTGGT ATTCGGCGGAGGGACCAAACTGACCGTCCTAGG T	CAAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCAGTTATGAT ATCAACTGGGTGCGACAGGCCACTGGACAAGGG CTTGAGTGGATGGGATGGAACCCTAACAGT GGTGGCACAGGCTATGCACAGAAGTTCCAGGGC AGAGTCACCATGACCAGGGACACCTCCATAAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT CAGGACACGGCCGTGTATTACTGTGCGAGAGGG GGTGATTACGTTTGGGGGAGTTATCGTCCCTACT ACTACTACTACGGTATGGACGTCTGGGGCCAAG GGACCACGGTCACCGTCTCCTCA
	AA	SEQ ID NO: 1719	SEQ ID NO: 1876
		QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLGITGLQTGDEADYYCGTWDSSLSAVVFGGG TKLTVLG	QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDI NWVRQATGQGLEWMGWMNPNSGGTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSQDTAVYYCARG GDYVWGSYRPYYYYYGMDVWGQGTTVTVSS
iPS:361499	17B11.002.002	CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTG CGGCCCCAGGACAGAAGGTCACCATCTCCTGCT CTGGAAGCAGCTCCAACATTGGAAATAATTATG TATCCTGGTATCAGCAGCTCCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCCTGACCGATTCTCTGGCTCCAA GTCTGGCACGTCAGCCACCCTGGGCATCACCGG ACTCCAGACTGGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGCTGTGGT ATTCGGCGGAGGGACCAAACTGACCGTCCTAGG T	CAAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCAGTTATGAT ATCAACTGGGTGCGACAGGCCACTGGACAAGGG CTTGAGTGGATGGGATGGAACCCTAACAGT GGTAACACAGGCTATGCACAGAAGTTCCAGGGC AGAGTCACCATGACCAGGGACACCTCCATAAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT CAGGACACGGCCGTGTATTACTGTGCGAGAGGG GGTGATTACGTTTGGGGGAGTTATCGTCCCTACT ACTACTACTACGGTATGGACGTCTGGGGCCAAG GGACCACGGTCACCGTCTCCTCA
	AA	SEQ ID NO: 1720	SEQ ID NO: 1877
		QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLGITGLQTGDEADYYCGTWDSSLSAVVFGGG TKLTVLG	QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDI NWVRQATGQGLEWMGWMNPNSGNTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSQDTAVYYCARG GDYVWGSYRPYYYYYGMDVWGQGTTVTVSS

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

iPS:361514	17B11.002.005	NA	SEQ ID NO: 152	SEQ ID NO: 309
			CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTG CGGCCCCAGGACAGAAGGTCACCATCTCCTGCT CTGGAAGCAGCTCCAACATTGGAAATAATTTATG TATCCTGGTATCAGCAGCTCCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCCTGACCGATTCTCTGGCTCCAA GTCTGGCACGTCAGCCACCCTGGCCATCACCGG ACTCCAGACTGGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGCTGTGGT ATTCGGCGGAGGGACCAAACTGACCGTCCTAGG T	CAAATGCAGCTGGTGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCAGTTATGAT ATCAACTGGGTGCGACAGGCCACTGGACAAGGG CTTGAGTGGATGGGATGGAACCCTAACAGT GGTGGCACAGGCTATGCACAGAAGTTCCAGGGC AGAGTCACCATGACCAGGGACACCTCCATAAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT CAGGACACGGCCGTGTATTACTGTGCGAGAGGG GGTGATTACGTTTGGGGGAGTTTATCGTCCCTACT ACTACTACTACGGTATGGACGTCTGGGGCCAAG GGACCACGGTCACCGTCTCCTCA
		AA	SEQ ID NO: 1723	SEQ ID NO: 1880
			QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLAITGLQTGDEADYYCGTWDSSLSAVVFGGG TKLTVLG	QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDI NWVRQATGQGLEWMGWMNPNSGGTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSQDTAVYYCARG GDYVWGSYRPYYYYYGMDVWGQGTTVTVSS
			SEQ ID NO: 153	SEQ ID NO: 310
iPS:360582	17B11.002.006	NA	CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTG CGGCCCCAGGACAGAAGGTCACCATCTCCTGCT CTGGAAGCAGCTCCAACATTGGAAATAATTTATG TATCCTGGTATCAGCAGCTCCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCCTGACCGATTCTCTGGCTCCAA GTCTGGCACGTCAGCCACCCTGGCCATCACCGG ACTCCAGACTGGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGCTGTGGT ATTCGGCGGAGGGACCAAACTGACCGTCCTAGG T	CAAATGCAGCTGGTGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCAGTTATGAT ATCAACTGGGTGCGACAGGCCCCTGGACAAGGG CTTGAGTGGATGGGATGGAACCCTAACAGT GGTAACACAGGCTATGCACAGAAGTTCCAGGGC AGAGTCACCATGACCAGGGACACCTCCATAAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGGG GGTGATTACGTTTGGGGGAGTTTATCGTCCCTACT ACTACTACTACGGTATGGACGTCTGGGGCCAAG GGACCACGGTCACCGTCTCCTCA
		AA	SEQ ID NO: 1724	SEQ ID NO: 1881
			QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLAITGLQTGDEADYYCGTWDSSLSAVVFGGG TKLTVLG	QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDI NWVRQAPGQGLEWMGWMNPNSGNTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSDDTAVYYYCARG GDYVWGSYRPYYYYYGMDVWGQGTTVTVSS

		SEQ ID NO: 154	SEQ ID NO: 311
iPS:361518	17B11.002.007	CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTG CGGCCCCAGGACAGAAGGTCACCATCTCCTGCT CTGGAAGCAGCTCCAACATTGGAAATAATTATG TATCCTGGTATCAGCAGCTCCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCCTGACCGATTCTCTGGCTCCAA GTCTGGCACGTCAGCCACCCTGGGCATCACCGG ACTCCAGACTGGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGCTGTGGT ATTCGGCGGAGGGACCAAACTGACCGTCCTAGG T	CAAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCAGTTATGAT ATCAACTGGGTGCGACAGGCCACTGGACAAGGG CTTGAGTGGATGGGATGGAACCCTAACAGT GGTGGCACAGGCTATGCACAGAAGTTCCAGGGC AGAGTCACCATGACCAGGGACACCTCCATAAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT CAGGACACGGCCGTGTATTACTGTGCGAGAGGG GGTGATTACGTTTTCGGGAGTTATCGTCCCTACT ACTACTACTACGGTATGGACGTCTGGGGCCAAG GGACCACGGTCACCGTCTCCTCA
	AA	SEQ ID NO: 1725 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLGITGLQTGDEADYYCGTWDSSLSAVVFGGG TKLTVLG	SEQ ID NO: 1882 QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDI NWVRQATGQGLEWMGWMNPNSGGTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSQDTAVYYCARG GDYVFGSYRPYYYYYGMDVWGQGTTVTVSS
iPS:360570	17B11.002.008	SEQ ID NO: 155 CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTG CGGCCCCAGGACAGAAGGTCACCATCTCCTGCT CTGGAAGCAGCTCCAACATTGGAAATAATTATG TATCCTGGTATCAGCAGCTCCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCCTGACCGATTCTCTGGCTCCAA GTCTGGCACGTCAGCCACCCTGGCCATCACCGG ACTCCAGACTGGGGACGAGGCCGATTATTACTG CGGAACATTCGAAAGCAGCCTGAGTGCTGTGGT ATTCGGCGGAGGGACCAAACTGACCGTCCTAGG T	SEQ ID NO: 312 CAAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCAGTTATGAT ATCAACTGGGTGCGACAGGCCCCTGGACAAGGG CTTGAGTGGATGGGATGGAACCCTAACAGT GGTGGCACAGGCTATGCACAGAAGTTCCAGGGC AGAGTCACCATGACCAGGGACACCTCCATAAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGGG GGTGATTACGTTTTCGGGAGTTATCGTCCCTACT ACTACTACTACGGTATGGACGTCTGGGGCCAAG GGACCACGGTCACCGTCTCCTCA
	AA	SEQ ID NO: 1726 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLAITGLQTGDEADYYCGTFESSLSAVVFGGGT KLTVLG	SEQ ID NO: 1883 QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDI NWVRQAPGQGLEWMGWMNPNSGGTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSDDTAVYYCARG GDYVFGSYRPYYYYYGMDVWGQGTTVTVSS

			SEQ ID NO: 156	SEQ ID NO: 313
iPS:362051	5G12.005.001	NA	GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACTATCACTT GCCGGGCAAGTCAGACCATTAGCAGGTTTTTAA ATTGGTATCAGCAGAAACCTGGGAAAGCCCCTA AGCTCCTGATCTATGTTGCATCCAGTTTGCAAAG TGGGGTCCCATCAAGATTCAGTGGCAGTGGTTC TGGGACAGATTTCACTCTCACCATCAGCAGTCT GCAACCTGAAGATTTTGCAACTTACTACTGTCA ACAGAGTTACAGTACCCTGCTCAGTTTTGGCCA GGGGACCAAGCTGGAGATCAAACGA	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC ATACACTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGTTATATGGTATGATGCA AGTAATAAGTTCCATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGAGACAATTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA AAAGTGGCTGGTATGCCTGAAGCTTTTGAAATC TGGGGCCAAGGGACATTGGTCACCGTCTCTTCA
			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

Tabella 4. Sequenze di acido nucleico (“NA”) e di amminoacidi (“AA”) di CDRL1, CDRL2, CDRL3, CDRH1, CDRH2 e CDRH3 esemplificative

Tabella 4A. Sequenze di acido nucleico ("NA") e di amminoacidi ("AA") di CDRL1, CDRL2 e CDRL3 esemplificative

iPS n.	Ab	Tipo	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
			SEQ ID NO: 2201	SEQ ID NO: 2358
		AA	RASQDIRDYLG	GASSLQS
			SEQ ID NO: 631	SEQ ID NO: 788
iPS:335941	2F11	NA	CAGGCGAGTCAGGACATTAGCA ACTATTTAAAT	GATGCATCCAATTTGGAAACA
			SEQ ID NO: 2202	SEQ ID NO: 2359
		AA	QASQDISNYLN	DASNLET
			SEQ ID NO: 632	SEQ ID NO: 789
iPS:335970	5C2	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC
			SEQ ID NO: 2203	SEQ ID NO: 2360
		AA	KSSQSVLSSSNNKNYIA	WASTRES
			SEQ ID NO: 633	SEQ ID NO: 790
iPS:335978	13H12	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC
			SEQ ID NO: 2204	SEQ ID NO: 2361
		AA	KSSQSVLSSSNNKNYIA	WASTRES
			SEQ ID NO: 634	SEQ ID NO: 791
iPS:335986	11C1	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGATTCC
			SEQ ID NO: 2205	SEQ ID NO: 2362
		AA	KSSQSVLSSSNNKNYLA	WTSTRDS
			SEQ ID NO: 635	SEQ ID NO: 792
iPS:3359 94	12H11	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGATTCC
			SEQ ID NO: 2206	SEQ ID NO: 2363

CTACAGCATAATAATTACCCCT TCACT	
SEQ ID NO: 2515	
LQHNNYPFT	
SEQ ID NO: 945	
CAACAGTATGATATTCTCCTCA CT	
SEQ ID NO: 2516	
QQYDILLT	
SEQ ID NO: 946	
CAACAATATTATAGTACTCCGT GGACG	
SEQ ID NO: 2517	
QQYYSTPWT	
SEQ ID NO: 947	
CAACAATATTATAGTACTCCGT GGACG	
SEQ ID NO: 2518	
QQYYSTPWT	
SEQ ID NO: 948	
CAGCAATATTATCGTACTCCGT GGACG	
SEQ ID NO: 2519	
QQYYRTPWT	
SEQ ID NO: 949	
CAGCAATATTATCGTACTCCGT GGACG	
SEQ ID NO: 2520	

		KSSQSVLSSSNNKNYLA	WTSTRDS	QQYYRTPWT
iPS:336024	18E3	AA	SEQ ID NO: 636	SEQ ID NO: 793	SEQ ID NO: 950
		NA	AGGGCCAGTCAGAGTATTAGTTACAGTTACTTAGCC	GGTGCATCCAGCAGGGCCACT	CAGCAGTATGGTAGTTCACCGCTCACT
		AA	SEQ ID NO: 2207	SEQ ID NO: 2364	SEQ ID NO: 2521
			RASQSISYSYLA	GASSRAT	QQYGSSPLT
iPS:336041	2G10_LC1	NA	SEQ ID NO: 637	SEQ ID NO: 794	SEQ ID NO: 951
			AGGGCCAGTCAGAGTGTTAGCAGCAACTTAGCC	GGTGCAGCCACCAGGGCCACT	CAGCAGTATAATAACTGGCCTCTCACT
		AA	SEQ ID NO: 2208	SEQ ID NO: 2365	SEQ ID NO: 2522
			RASQSVSSNLA	GAATRAT	QQYNNWPLT
iPS:336077	4H9.004	NA	SEQ ID NO: 638	SEQ ID NO: 795	SEQ ID NO: 952
			CGGGCAAGTCAGGGCATTAGAAATGAGTTTAGGC	GGTGCATCCAGTTTTGCAAAGT	CTACAGCATAATAGTTACCCATTCACT
		AA	SEQ ID NO: 2209	SEQ ID NO: 2366	SEQ ID NO: 2523
			RASQGIRNELG	GASSLQS	LQHNSYPFT
iPS:336088	6A5.004	NA	SEQ ID NO: 639	SEQ ID NO: 796	SEQ ID NO: 953
			CAGGCGAGTCAGGACATTACCAACTATTTAAAT	GATGCTTCCAATTTGGAGCCA	CAACAGTATGATGATCTATTCACT
		AA	SEQ ID NO: 2210	SEQ ID NO: 2367	SEQ ID NO: 2524
			QASQDITNYLN	DASNLEP	QQYDDLFT
iPS:336099	17H11.004	NA	SEQ ID NO: 640	SEQ ID NO: 797	SEQ ID NO: 954
			CGGGCGAGTCAGGGTCTTATCATCTGGTTAGCC	GCTGCATCCAGTTTGCAAAGT	CAACAGACTAACAGTTTCCCTCCGACG
		AA	SEQ ID NO: 2211	SEQ ID NO: 2368	SEQ ID NO: 2525
			RASQGLIIWLA	AASSLQS	QQTNSFPPT
		NA	SEQ ID NO: 641	SEQ ID NO: 798	SEQ ID NO: 955

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

rPS:359761	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
rPS:360955	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
rPS:360962	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
rPS:360968	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
rPS:360974	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
rPS:360978	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
4H9.004.006		4B1.010	4B1.011	4B1.012	4B1.013	4B1.014

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	CTACAGCATAATAATTACCCCT TCACT
			SEQ ID NO: 2230	SEQ ID NO: 2387	SEQ ID NO: 2344
		AA	RASQDLRNYLG	GASSLQS	LQHNNYPFT
			SEQ ID NO: 660	SEQ ID NO: 817	SEQ ID NO: 974
iPS:361009	18F2.006	NA	CGGGCAAGTCAGGACCTTAGAA ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
			SEQ ID NO: 2231	SEQ ID NO: 2388	SEQ ID NO: 2345
		AA	RASQDLRNYLG	GASSLQS	LQHNNYPFT
			SEQ ID NO: 661	SEQ ID NO: 818	SEQ ID NO: 975
iPS:361013	18F2.007	NA	CGGGCAAGTCAGGACCTTAGAA ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
			SEQ ID NO: 2232	SEQ ID NO: 2389	SEQ ID NO: 2346
		AA	RASQDLRNYLG	GASSLQS	LQHNNYPFT
			SEQ ID NO: 662	SEQ ID NO: 819	SEQ ID NO: 976
iPS:361017	18F2.008	NA	CGGGCAAGTCAGGACCTTAGAA ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
			SEQ ID NO: 2233	SEQ ID NO: 2390	SEQ ID NO: 2347
		AA	RASQDLRNYLG	GASSLQS	LQHNNYPFT
			SEQ ID NO: 663	SEQ ID NO: 820	SEQ ID NO: 977
iPS:361021	18F2.009	NA	CGGGCAAGTCAGGACCTTAGAA ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
			SEQ ID NO: 2234	SEQ ID NO: 2391	SEQ ID NO: 2348
		AA	RASQDLRNYLG	GASSLQS	LQHNNYPFT
			SEQ ID NO: 664	SEQ ID NO: 821	SEQ ID NO: 978
iPS:361028	18F2.010	NA	CGGGCAAGTCAGGACCTTAGAA ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
			SEQ ID NO: 2235	SEQ ID NO: 2392	SEQ ID NO: 2349
		AA	RASQDLRNYLG	GASSLQS	LQHNNYPFT
			SEQ ID NO: 665	SEQ ID NO: 822	SEQ ID NO: 979

iPS:360535	18F2.011	NA	CGGGCAAGTCAGGACCTTAGAA ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
			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
iPS:361035	18F2.012	NA	CGGGCAAGTCAGGACCTTAGAA ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
			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
iPS:359940	2F11.002	NA	CAGGCGAGTCAGGACATTAGCA ACTATTTAAAT	GATGCATCCAATTTGGAAACA	CAACAGTATGATATTCTCCTCA CT
			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
iPS:361039	2F11.003	NA	CAGGCGAGTCAGGACATTAGCA ACTATTTAAAT	GATGCATCCAATTTGGAAACA	CAACAGTATGATATTCTCCTCA CT
			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
iPS:361043	2F11.004	NA	CAGGCGAGTCAGGACATTAGCA ACTATTTAAAT	GATGCATCCAATTTGGAAACA	CAACAGTATGATATTCTCCTCA CT
			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
iPS:361049	2F11.005	NA	CAGGCGAGTCAGGACATTAGCA ACTATTTAAAT	GATGCATCCAATTTGGAAACA	CAACAGTATGATATTCTCCTCA CT
			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

iPS:361055	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
iPS:361059	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
iPS:361063	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
iPS:359949	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
iPS:359956	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
iPS:359865	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

iPS:359869	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
iPS:359873	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
iPS:359877	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
iPS:361067	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
iPS:361071	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
iPS:361075	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	6AS.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	6AS.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	6AS.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	6AS.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	6AS.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	6AS.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

iPS:361109	6AS.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
iPS:361113	6AS.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
iPS:361120	6AS.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
iPS:359896	6AS.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
iPS:359890	6AS.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
iPS:359567	2A11.002	NA	AGGGCCAGTCAGATTTTTTACCA 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

iPS:335965	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
iPS:361158	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
iPS:361165	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
iPS:361172	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
iPS:361178	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
iPS:361185	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

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

rs3612206	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
rs3596428	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
rs3596437	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
rs3612210	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
rs3612214	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
rs3612218	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

iPS:361222	5C2.006	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
			SEQ ID NO: 2284	SEQ ID NO: 2441	SEQ ID NO: 2598
		AA	KSSQSVLSSSNNKNY1A	WASTRES	QQYYSTPWT
			SEQ ID NO: 714	SEQ ID NO: 871	SEQ ID NO: 1028
iPS:361229	5C2.007	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
			SEQ ID NO: 2285	SEQ ID NO: 2442	SEQ ID NO: 2599
		AA	KSSQSVLSSSNNKNY1A	WASTRES	QQYYSTPWT
			SEQ ID NO: 715	SEQ ID NO: 872	SEQ ID NO: 1029
iPS:361236	5C2.008	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
			SEQ ID NO: 2286	SEQ ID NO: 2443	SEQ ID NO: 2600
		AA	KSSQSVLSSSNNKNY1A	WASTRES	QQYYSTPWT
			SEQ ID NO: 716	SEQ ID NO: 873	SEQ ID NO: 1030
iPS:359685	5C2.009	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
			SEQ ID NO: 2287	SEQ ID NO: 2444	SEQ ID NO: 2601
		AA	KSSQSVLSSSNNKNY1A	WASTRES	QQYYSTPWT
			SEQ ID NO: 717	SEQ ID NO: 874	SEQ ID NO: 1031
iPS:361240	5C2.010	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
			SEQ ID NO: 2288	SEQ ID NO: 2445	SEQ ID NO: 2602
		AA	KSSQSVLSSSNNKNY1A	WASTRES	QQYYSTPWT
			SEQ ID NO: 718	SEQ ID NO: 875	SEQ ID NO: 1032

iPS:361247	SC2.011	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
			SEQ ID NO: 2289	SEQ ID NO: 2446	SEQ ID NO: 2603
		AA	KSSQSVLSSSNNKNY1A	WASTRES	QQYYSTPWT
			SEQ ID NO: 719	SEQ ID NO: 876	SEQ ID NO: 1033
iPS:361254	SC2.012	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
			SEQ ID NO: 2290	SEQ ID NO: 2447	SEQ ID NO: 2604
		AA	KSSQSVLSSSNNKNY1A	WASTRES	QQYYSTPWT
			SEQ ID NO: 720	SEQ ID NO: 877	SEQ ID NO: 1034
iPS:361261	SC2.013	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
			SEQ ID NO: 2291	SEQ ID NO: 2448	SEQ ID NO: 2605
		AA	KSSQSVLSSSNNKNY1A	WASTRES	QQYYSTPWT
			SEQ ID NO: 721	SEQ ID NO: 878	SEQ ID NO: 1035
iPS:361268	SC2.014	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
			SEQ ID NO: 2292	SEQ ID NO: 2449	SEQ ID NO: 2606
		AA	KSSQSVLSSSNNKNY1A	WASTRES	QQYYSTPWT
			SEQ ID NO: 722	SEQ ID NO: 879	SEQ ID NO: 1036
iPS:359669	SC2.015	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
			SEQ ID NO: 2293	SEQ ID NO: 2450	SEQ ID NO: 2607
		AA	KSSQSVLSSSNNKNY1A	WASTRES	QQYYSTPWT
			SEQ ID NO: 723	SEQ ID NO: 880	SEQ ID NO: 1037

rs3596778	5C2.016	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
			SEQ ID NO: 2294	SEQ ID NO: 2451	SEQ ID NO: 2608
		AA	KSSQSVLSSSNNKNYIA	WASTRES	QQYYSTPWT
			SEQ ID NO: 724	SEQ ID NO: 881	SEQ ID NO: 1038
rs3612175	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
rs3612289	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
rs3597l2	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

iPS:361293	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
iPS:361297	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
iPS:361301	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
iPS:359703	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
iPS:361305	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

rs361312	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
rs359744	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
rs361319	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
rs359737	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
rs361326	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

iPS:361330	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
iPS:361337	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
iPS:361344	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
iPS:361351	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
iPS:361358	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

rs3613865	12H11.007	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGATTCC	CAGCAATATTATCGTACTCCGT GGACG
			SEQ ID NO: 2314	SEQ ID NO: 2471	SEQ ID NO: 2628
		AA	KSSQSVLSSSNNKNYLA	WTSTRDS	QQYYRTPWT
			SEQ ID NO: 744	SEQ ID NO: 901	SEQ ID NO: 1058
rs3613872	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
rs3613879	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
rs3613883	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
rs3613887	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
			SEQ ID NO: 2319	SEQ ID NO: 2476
		AA	KSSQSVLSSSNNKNYLA	WTSTRES
			SEQ ID NO: 749	SEQ ID NO: 906
iPS:361395	12H11.013	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGATTCC
			SEQ ID NO: 2320	SEQ ID NO: 2477
		AA	KSSQSVLSSSNNKNYLA	WTSTRDS
			SEQ ID NO: 750	SEQ ID NO: 907
iPS:361402	12H11.014	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGAATCC
			SEQ ID NO: 2321	SEQ ID NO: 2478
		AA	KSSQSVLSSSNNKNYLA	WTSTRES
			SEQ ID NO: 751	SEQ ID NO: 908
iPS:361406	2C2.005.001	NA	TCTGGAAGTAGCTCCAACATCG GAAGTCAAACTGTAAAC	ACTAATAATCAGCGGCCCTCA
			SEQ ID NO: 2322	SEQ ID NO: 2479
		AA	SGSSSNIGSQTVN	TNNQRPS
			SEQ ID NO: 752	SEQ ID NO: 909
iPS:361412	2C2.005.002	NA	TCTGGAAGTAGCTCCAACATCG GAAGTCAAACTGTAAAC	ACTAATAATCAGCGGCCCTCA
			SEQ ID NO: 2323	SEQ ID NO: 2480
		AA	SGSSSNIGSQTVN	TNNQRPS
			SEQ ID NO: 753	SEQ ID NO: 910

			CAGCAATATTATCGTACTCCGT GGACG
			SEQ ID NO: 2633
			QQYYRTPWT
			SEQ ID NO: 1063
			CAGCAATATTATCGTACTCCGT GGACG
			SEQ ID NO: 2634
			QQYYRTPWT
			SEQ ID NO: 1064
			CAGCAATATTATCGTACTCCGT GGACG
			SEQ ID NO: 2635
			QQYYRTPWT
			SEQ ID NO: 1065
			GCAACATTCGATGAAAGCCTG AGTGGTCCGGTA
			SEQ ID NO: 2636
			ATFDESLSGPV
			SEQ ID NO: 1066
			GCAACATTCGATGAAAGCCTG CAAGGTCCGGTA
			SEQ ID NO: 2637
			ATFDESLQGPV
			SEQ ID NO: 1067

iPS:361418	2C2.005.003	NA	TCTGGAAGTAGCTCCAACATCG GAAGTAATTATGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATTCGATGAAAGCCTG AGTGGTCCGGTA
			SEQ ID NO: 2324	SEQ ID NO: 2481	SEQ ID NO: 2638
		AA	SGSSSNIGSNYVN	TNNQRPS	ATFDESLSGPV
			SEQ ID NO: 754	SEQ ID NO: 911	SEQ ID NO: 1068
iPS:361424	2C2.005.004	NA	TCTGGAAGTAGCTCCAACATCG GAAGTAATTATGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATTCGATGAAAGCCTG CAAGGTCCGGTA
			SEQ ID NO: 2325	SEQ ID NO: 2482	SEQ ID NO: 2639
		AA	SGSSSNIGSNYVN	TNNQRPS	ATFDESLQGPV
			SEQ ID NO: 755	SEQ ID NO: 912	SEQ ID NO: 1069
iPS:361430	2C2.005.005	NA	TCTGGAAGTAGCTCCAACATCG GAAGTCAAACTGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATTCGATGACAGCCTG AATGGTCCGGTA
			SEQ ID NO: 2326	SEQ ID NO: 2483	SEQ ID NO: 2640
		AA	SGSSSNIGSQTVN	TNNQRPS	ATFDDSLNGPV
			SEQ ID NO: 756	SEQ ID NO: 913	SEQ ID NO: 1070
iPS:361436	2C2.005.006	NA	TCTGGAAGTAGCTCCAACATCG GAAGTAATTATGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATTCGATGACAGCCTG AATGGTCCGGTA
			SEQ ID NO: 2327	SEQ ID NO: 2484	SEQ ID NO: 2641
		AA	SGSSSNIGSNYVN	TNNQRPS	ATFDDSLNGPV
			SEQ ID NO: 757	SEQ ID NO: 914	SEQ ID NO: 1071
iPS:361442	2C2.005.007	NA	TCTGGAAGTAGCTCCAACATCG GAAGTAATACTGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATTCGATGAAAGCCTG AATGGTCCGGTA
			SEQ ID NO: 2328	SEQ ID NO: 2485	SEQ ID NO: 2642
		AA	SGSSSNIGSNTVN	TNNQRPS	ATFDESLNGPV
			SEQ ID NO: 758	SEQ ID NO: 915	SEQ ID NO: 1072
iPS:361448	2C2.005.008	NA	TCTGGAAGTAGCTCCAACATCG GAAGTAATACTGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATTCGATGACAGCCTGC AAGGTCCGGTA
			SEQ ID NO: 2329	SEQ ID NO: 2486	SEQ ID NO: 2643
		AA	SGSSSNIGSNTVN	TNNQRPS	ATFDDSLQGPV
			SEQ ID NO: 759	SEQ ID NO: 916	SEQ ID NO: 1073

iPS:361454	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
iPS:361460	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
iPS:361466	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
iPS:361472	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
iPS:361478	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
iPS:361485	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	CTACAGCATAATAATTACCCCT TCACT
			SEQ ID NO: 2336	SEQ ID NO: 2493	SEQ ID NO: 2650
		AA	RASQDLRNYLG	GASSLQS	LQHNNYPFT
			SEQ ID NO: 766	SEQ ID NO: 923	SEQ ID NO: 1080
rs361851	6H1.009	NA	CGGGCAAGTCAGGACATTAGAG ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
			SEQ ID NO: 2337	SEQ ID NO: 2494	SEQ ID NO: 2651
		AA	RASQDIRDYLG	GASSLQS	LQHNNYPFT
			SEQ ID NO: 767	SEQ ID NO: 924	SEQ ID NO: 1081
rs361855	2C2.005.015	NA	TCTGGAAGTAGCTCCAACATCG GAAGTAATACTGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATTCGATAGCAGCCTG AGTGGTCCGGTA
			SEQ ID NO: 2338	SEQ ID NO: 2495	SEQ ID NO: 2652
		AA	SGSSSNIGSNTVN	TNNQRPS	ATFDSSLSGPV
			SEQ ID NO: 768	SEQ ID NO: 925	SEQ ID NO: 1082
rs336067	5G12.006	NA	CGGGCAAGTCAGACCATTAGCA GGTTTTTAAAT	GTTGCATCCAGTTTGCAAAGT	CAACAGAGTTACAGTACCCTG ATCAGT
			SEQ ID NO: 2339	SEQ ID NO: 2496	SEQ ID NO: 2653
		AA	RASQTISRFLN	VASSLQS	QQSYSTLIS
			SEQ ID NO: 769	SEQ ID NO: 926	SEQ ID NO: 1083
rs333616 9	17B11.002	NA	TCTGGAAGCAGCTCCAACATTG GAAATAATTATGTATCC	GACAATAATAAGCGACCCTCA	GGAACATGGGATAGCAGCCTG AGTGCTGTGGTA
			SEQ ID NO: 2340	SEQ ID NO: 2497	SEQ ID NO: 2654
		AA	SGSSSNIGNNYVS	DNNKRPS	GTWDSSLSAVV
			SEQ ID NO: 770	SEQ ID NO: 927	SEQ ID NO: 1084
rs361127	5G12.006.001	NA	CGGGCAAGTCAGACCATTAGCA GGTTTTTAAAT	GTTGCATCCAGTTTGCAAAGT	CAACAGAGTTACAGTACCCTG ATCAGT
			SEQ ID NO: 2341	SEQ ID NO: 2498	SEQ ID NO: 2655
		AA	RASQTISRFLN	VASSLQS	QQSYSTLIS
			SEQ ID NO: 771	SEQ ID NO: 928	SEQ ID NO: 1085

iPS:361136	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
iPS:361140	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
iPS:359919	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
iPS:361144	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
iPS:361151	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
iPS:361491	17B11.002.00 1	NA	TCTGGAAGCAGCTCCAACATTG GAAATAATTATGTATCC	GACAATAATAAGCGACCCTCA	GGAACATGGGATAGCAGCCTG AGTGCTGTGTGGTA
			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

chr17:36149499	2	NA	TCTGGAAGCAGCTCCAACATTG GAAATAATTATGTATCC	GACAATAATAAGCGACCCTCA	GGAACATGGGATAGCAGCCTG AGTGCTGTGGTA
			SEQ ID NO: 2348	SEQ ID NO: 2505	SEQ ID NO: 2662
		AA	SGSSSNIGNNYVS	DNNKRPS	GTWDSSLSAVV
			SEQ ID NO: 778	SEQ ID NO: 935	SEQ ID NO: 1092
chr17:36150303	3	NA	TCTGGAAGCAGCTCCAACATTG GAAATAATTATGTATCC	GACAATAATAAGCGACCCTCA	GGAACATGGGATAGCAGCCTG AGTGCTGTGGTA
			SEQ ID NO: 2349	SEQ ID NO: 2506	SEQ ID NO: 2663
		AA	SGSSSNIGNNYVS	DNNKRPS	GTWDSSLSAVV
			SEQ ID NO: 779	SEQ ID NO: 936	SEQ ID NO: 1093
chr17:36150507	4	NA	TCTGGAAGCAGCTCCAACATTG GAAATAATTATGTATCC	GACAATAATAAGCGACCCTCA	GGAACATTCGAAAGCAGCCTG AGTGCTGTGGTA
			SEQ ID NO: 2350	SEQ ID NO: 2507	SEQ ID NO: 2664
		AA	SGSSSNIGNNYVS	DNNKRPS	GTFESSLSAVV
			SEQ ID NO: 780	SEQ ID NO: 937	SEQ ID NO: 1094
chr17:36151514	5	NA	TCTGGAAGCAGCTCCAACATTG GAAATAATTATGTATCC	GACAATAATAAGCGACCCTCA	GGAACATGGGATAGCAGCCTG AGTGCTGTGGTA
			SEQ ID NO: 2351	SEQ ID NO: 2508	SEQ ID NO: 2665
		AA	SGSSSNIGNNYVS	DNNKRPS	GTWDSSLSAVV
			SEQ ID NO: 781	SEQ ID NO: 938	SEQ ID NO: 1095
chr17:36058582	6	NA	TCTGGAAGCAGCTCCAACATTG GAAATAATTATGTATCC	GACAATAATAAGCGACCCTCA	GGAACATGGGATAGCAGCCTG AGTGCTGTGGTA
			SEQ ID NO: 2352	SEQ ID NO: 2509	SEQ ID NO: 2666
		AA	SGSSSNIGNNYVS	DNNKRPS	GTWDSSLSAVV
			SEQ ID NO: 782	SEQ ID NO: 939	SEQ ID NO: 1096
chr17:36151518	7	NA	TCTGGAAGCAGCTCCAACATTG GAAATAATTATGTATCC	GACAATAATAAGCGACCCTCA	GGAACATGGGATAGCAGCCTG AGTGCTGTGGTA
			SEQ ID NO: 2353	SEQ ID NO: 2510	SEQ ID NO: 2667
		AA	SGSSSNIGNNYVS	DNNKRPS	GTWDSSLSAVV
			SEQ ID NO: 783	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

Tabella 4B. Sequenze di nucleotidi e di amminoacidi di CDRH1, CDRH2 e CDRH3 esemplificative

iPS n.	Ab	Tipo	CDRH1	CDRH2	CDRH3
iPS:336175	2C2.005	NA	GGCTACTATATGCAT	TGGATCAACCCTAACAGTGGTGGCACAAACTATGCACAGAAGTTTCAGGGC	GGGGGGGATTACGTTTGGGGGACTTATCGGCCTCACTACTACTACGGTATGGACGTC
			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	GTTATATGGTATGATGGAAGTAATGAAAACTATGCAGACTCCGTGAAGGGC	GATGGGACGATCTTTGGAGTGGTCTTGGGGGACTAC
			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

rs3359938	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
rs3359941	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
rs3359970	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
rs3359978	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
rs3359986	11C1	NA	GGCTACTATATACAC	TGGATCAGCCCTAACAGTGGTG ACACAAGCTATGCACACAGAAGT 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

iPS:335994	12H11	NA	GGCTACTATATACAC	TGGATAAGCCCTAACAATGGTG ACACAAACTATGCACAGAAGT TTCAGGAC	GAGGCCACGATTTTTGGAATGC TTATTGTACCATTTGACTAC
			SEQ ID NO: 2677	SEQ ID NO: 2834	SEQ ID NO: 2991
		AA	GYYIH	WISPNNGDTNYAQKFQD	EATIFGMLIVPFDY
			SEQ ID NO: 1107	SEQ ID NO: 1264	SEQ ID NO: 1421
iPS:336024	18E3	NA	AGTGGTGGTTACTACTGGAGC	TACATCTATTACAGTGGGAGCA CCTACTACAACCCGTCCCTCAA GAGT	GATCGTATTACGATTTTTGGAG TGGTTATGGGGGGCGGTATGG ACGTC
			SEQ ID NO: 2678	SEQ ID NO: 2835	SEQ ID NO: 2992
		AA	SGGYYWS	YIYYSGSTYYNPSLKS	DRTIIFGVVMGGGMDV
			SEQ ID NO: 1108	SEQ ID NO: 1265	SEQ ID NO: 1422
iPS:336041	2G10_LC1	NA	AACTATGGCATGCAC	GCTATATGGTTTGATGGAAGTG ATAAATACTATGCAGACTCCGT GAAGGGC	GATCAGGCGATTTTTGGAGTGG TCCCCGACTAC
			SEQ ID NO: 2679	SEQ ID NO: 2836	SEQ ID NO: 2993
		AA	NYGMH	AIWFDGSDKYYADSVKG	DQAIFGVVPDY
			SEQ ID NO: 1109	SEQ ID NO: 1266	SEQ ID NO: 1423
iPS:336077	4H9.004	NA	TACTTTGGCATGCAC	GTTATATGGTATGATGGAAGTA ATAAATACTATGCAGACTCCGT GAAGGGC	GATGGGACGATTTTTGGAGTGC TCTTGGGGGACTAC
			SEQ ID NO: 2680	SEQ ID NO: 2837	SEQ ID NO: 2994
		AA	YFGMH	VIWYDGSNKYYADSVKG	DGTIFGVLLGDY
			SEQ ID NO: 1110	SEQ ID NO: 1267	SEQ ID NO: 1424
iPS:336088	6A5.004	NA	AGCTATGGCATGCAC	GCTATATGGTATGATGGAAATA ATAAATACTATGCAGACTCCGT GAAGGGC	GATCGGACGATTTTTGGAGTGG TCCTTGAGTAC
			SEQ ID NO: 2681	SEQ ID NO: 2838	SEQ ID NO: 2995
		AA	SYGMH	AIWYDGNNKYYADSVKG	DRTIFGVVLEY
			SEQ ID NO: 1111	SEQ ID NO: 1268	SEQ ID NO: 1425

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	GATGGGACGATTTTTGGAGTGC TCTTGGGGGACTAC
			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	SFQ 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

iPS:360943	4H9.004.004	NA	TACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGGC	GATGGGACGATTTTTGGAGTGC TCTTGGGGGGACTAC
			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
iPS:360949	4H9.004.005	NA	TACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGGC	GATGGGACGATTTTTGGAGTGC TCTTGGGGGGACTAC
			SEQ ID NO: 2688	SEQ ID NO: 2845	SEQ ID NO: 3002
		AA	YFGMH	VIWYDASNKYYADAVKG	DGTIFGVLLGDY
			SEQ ID NO: 1118	SEQ ID NO: 1275	SEQ ID NO: 1432
iPS:359761	4H9.004.006	NA	TACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGGC	GATAGGACGATTTTTGGAGTGC TCTTGGGGGGACTAC
			SEQ ID NO: 2689	SEQ ID NO: 2846	SEQ ID NO: 3003
		AA	YFGMH	VIWYDASNKYYADAVKG	DRTIFGVLLGDY
			SEQ ID NO: 1119	SEQ ID NO: 1276	SEQ ID NO: 1433
iPS:360955	4B1.010	NA	AACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACGCCG TGAAGGGGC	GATGGGACGATCTTTGGAGTGG TCTTGGGGGGACTAC
			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
iPS:360962	4B1.011	NA	AACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACGCCG TGAAGGGC	GATGGGACGATCTTTGGAGTGG TCTTGGGGGGACTAC
			SEQ ID NO: 2691	SEQ ID NO: 2848	SEQ ID NO: 3005
		AA	NFGMH	VIWYDASNENYADAVKG	DGTIFGVVLGDY
			SEQ ID NO: 1121	SEQ ID NO: 1278	SEQ ID NO: 1435

iPS:360968	4B1.012	NA	AACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACGCCG TGAAGGGC	GATGGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
			SEQ ID NO: 2692	SEQ ID NO: 2849	SEQ ID NO: 3006
		AA	NFGMH	VTWYDASNENYADAVKG	DGTIFGVVLGDY
			SEQ ID NO: 1122	SEQ ID NO: 1279	SEQ ID NO: 1436
iPS:360974	4B1.013	NA	AACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACTCCGT GAAGGGC	GATGGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
			SEQ ID NO: 2693	SEQ ID NO: 2850	SEQ ID NO: 3007
		AA	NFGMH	VTWYDASNENYADSVKG	DGTIFGVVLGDY
			SEQ ID NO: 1123	SEQ ID NO: 1280	SEQ ID NO: 1437
iPS:360978	4B1.014	NA	AACTTTGGCATGCAC	GTTATATGGTATGATGGAAGTA ATGAAAACTATGCAGACGCCG TGAAGGGC	GATGGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
			SEQ ID NO: 2694	SEQ ID NO: 2851	SEQ ID NO: 3008
		AA	NFGMH	VTWYDGSNENYADAVKG	DGTIFGVVLGDY
			SEQ ID NO: 1124	SEQ ID NO: 1281	SEQ ID NO: 1438
iPS:359785	4B1.015	NA	AACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACGCCG TGAAGGGC	GATAGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
			SEQ ID NO: 2695	SEQ ID NO: 2852	SEQ ID NO: 3009
		AA	NFGMH	VTWYDASNENYADAVKG	DRTIFGVVLGDY
			SEQ ID NO: 1125	SEQ ID NO: 1282	SEQ ID NO: 1439
iPS:360982	4B1.016	NA	AACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACGCCG TGAAGGGC	GATGGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
			SEQ ID NO: 2696	SEQ ID NO: 2853	SEQ ID NO: 3010
		AA	NFGMH	VTWYDASNENYADAVKG	DGTIFGVVLGDY
			SEQ ID NO: 1126	SEQ ID NO: 1283	SEQ ID NO: 1440

iPS:335922	18F2	NA		AACTTTGGCATGCAC	GTTATATGGTATGATGGAAGTA ATGAAAACTATGCAGACTCCGT GAAGGGC	GATGGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
			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 TCTTGGGGGACTAC
			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 TCTTGGGGGACTAC
			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 TCTTGGGGGACTAC
			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 TCTTGGGGGACTAC
			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	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACGCCG TGAAGGGC	GATGGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
			SEQ ID NO: 2702	SEQ ID NO: 2859	SEQ ID NO: 3016
		AA	NFGMH	VIWYDASNENYADAVKG	DGTIFGVVLGDY
			SEQ ID NO: 1132	SEQ ID NO: 1289	SEQ ID NO: 1446
iPS:361013	18F2.007	NA	AACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACGCCG TGAAGGGC	GATGGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
			SEQ ID NO: 2703	SEQ ID NO: 2860	SEQ ID NO: 3017
		AA	NFGMH	VIWYDASNENYADAVKG	DGTIFGVVLGDY
			SEQ ID NO: 1133	SEQ ID NO: 1290	SEQ ID NO: 1447
iPS:361017	18F2.008	NA	AACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACGCCG TGAAGGGC	GATGGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
			SEQ ID NO: 2704	SEQ ID NO: 2861	SEQ ID NO: 3018
		AA	NFGMH	VIWYDASNENYADAVKG	DGTIFGVVLGDY
			SEQ ID NO: 1134	SEQ ID NO: 1291	SEQ ID NO: 1448
iPS:361021	18F2.009	NA	AACTTTGGCATGCAC	GTTATATGGTATGATGGAAGTA ATGAAAACTATGCAGACGCCG TGAAGGGC	GATGGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
			SEQ ID NO: 2705	SEQ ID NO: 2862	SEQ ID NO: 3019
		AA	NFGMH	VIWYDGSNENYADAVKG	DGTIFGVVLGDY
			SEQ ID NO: 1135	SEQ ID NO: 1292	SEQ ID NO: 1449
iPS:361028	18F2.010	NA	AACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACTCCGT GAAGGGC	GATGGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
			SEQ ID NO: 2706	SEQ ID NO: 2863	SEQ ID NO: 3020
		AA	NFGMH	VIWYDASNENYADSVKG	DGTIFGVVLGDY
			SEQ ID NO: 1136	SEQ ID NO: 1293	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

iPS: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
iPS: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
iPS: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
iPS: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
iPS: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:3599877	6H1.005	NA	AGCTATGGCATGCAC	GTTATATGGTATGATGGAAGTA ATAAATACTATGCAGACGCCGT GAAGGGC	GATAGGACGATTTTTTGGAGTGG TTCTTGACTAC
			SEQ ID NO: 2717	SEQ ID NO: 2874	SEQ ID NO: 3031
		AA	SYGMH	VIWYDGSNKYYADAVKG	DRTIFGVVLDY
			SEQ ID NO: 1147	SEQ ID NO: 1304	SEQ ID NO: 1461
		NA	TACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGGC	GATGGGACGATTTTTGGAGTGC TCTTGGGGGACTAC
			SEQ ID NO: 2718	SEQ ID NO: 2875	SEQ ID NO: 3032
		AA	YFGMH	VIWYDASNKYYADAVKG	DGTIFGVLLGDY
			SEQ ID NO: 1148	SEQ ID NO: 1305	SEQ ID NO: 1462
	6H1.003	NA	TACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGGC	GATAGGACGATTTTTGGAGTGC TCTTGGGGGACTAC
			SEQ ID NO: 2719	SEQ ID NO: 2876	SEQ ID NO: 3033
		AA	YFGMH	VIWYDASNKYYADAVKG	DRTIFGVLLGDY
			SEQ ID NO: 1149	SEQ ID NO: 1306	SEQ ID NO: 1463
	6H1.004	NA	TACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGGC	GATGGGACGATTTTTGGAGTGC TCTTGGGGGACTAC
			SEQ ID NO: 2720	SEQ ID NO: 2877	SEQ ID NO: 3034
		AA	YFGMH	VIWYDASNKYYADAVKG	DGTIFGVLLGDY
			SEQ ID NO: 1150	SEQ ID NO: 1307	SEQ ID NO: 1464
	6H1.005	NA	TACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGGC	GATAGGACGATTTTTGGAGTGC TCTTGGGGGACTAC
			SEQ ID NO: 2721	SEQ ID NO: 2878	SEQ ID NO: 3035
		AA	YFGMH	VIWYDASNKYYADAVKG	DRTIFGVLLGDY
			SEQ ID NO: 1151	SEQ ID NO: 1308	SEQ ID NO: 1465

iPS:361067	6H1.006	NA	TACTTTGGCATGCAC	GTTATATGGTATGATGGAAGTA ATAAATACTATGCAGACTCCGT GAAGGGC	GATGGGACGATTTTTGGAGTGC TCTTGGGGGGACTAC
			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
iPS:361071	6H1.007	NA	TACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACTCCGT GAAGGGC	GATGGGACGATTTTTGGAGTGC TCTTGGGGGGACTAC
			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
iPS:361075	6H1.008	NA	TACTTTGGCATGCAC	GTTATATGGTATGATGGAAGTA ATAAATACTATGCAGACGCCGT GAAGGGC	GATGGGACGATTTTTGGAGTGC TCTTGGGGGGACTAC
			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
iPS:361079	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
iPS:361085	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	6AS.004.003	NA	AGCTATGGCATGCAC	GCTATATGGTATGATGCAAATA ATAAATACTATGCAGACGCCGT GAAGGGC	GATCGGACGATTTTTGGAGTGG TCCTTGAGTAC
			SEQ ID NO: 2727	SEQ ID NO: 2884	SEQ ID NO: 3041
		AA	SYGMH	AIWYDANNKYYADAVKG	DRTIFGVVLEY
			SEQ ID NO: 1157	SEQ ID NO: 1314	SEQ ID NO: 1471
iPS:361095	6AS.004.004	NA	AGCTATGGCATGCAC	GCTATATGGTATGATGCAAATA ATAAATACTATGCAGACGCCGT GAAGGGC	GATCGGACGATTTTTGGAGTGG TCCTTGAGTAC
			SEQ ID NO: 2728	SEQ ID NO: 2885	SEQ ID NO: 3042
		AA	SYGMH	AIWYDANNKYYADAVKG	DRTIFGVVLEY
			SEQ ID NO: 1158	SEQ ID NO: 1315	SEQ ID NO: 1472
iPS:361101	6AS.004.005	NA	AGCTATGGCATGCAC	GCTATATGGTATGATGCAAATA ATAAATACTATGCAGACGCCGT GAAGGGC	GATCGGACGATTTTTGGAGTGG TCCTTGAGTAC
			SEQ ID NO: 2729	SEQ ID NO: 2886	SEQ ID NO: 3043
		AA	SYGMH	AIWYDANNKYYADAVKG	DRTIFGVVLEY
			SEQ ID NO: 1159	SEQ ID NO: 1316	SEQ ID NO: 1473
iPS:361105	6AS.004.006	NA	AGCTATGGCATGCAC	GCTATATGGTATGATGCAAATA ATAAATACTATGCAGACGCCGT GAAGGGC	GATCGGACGATTTTTGGAGTGG TCCTTGAGTAC
			SEQ ID NO: 2730	SEQ ID NO: 2887	SEQ ID NO: 3044
		AA	SYGMH	AIWYDANNKYYADAVKG	DRTIFGVVLEY
			SEQ ID NO: 1160	SEQ ID NO: 1317	SEQ ID NO: 1474
iPS:361109	6AS.004.007	NA	AGCTATGGCATGCAC	GCTATATGGTATGATGCAAATA ATAAATACTATGCAGACGCCGT GAAGGGC	GATCGGACGATTTTTGGAGTGG TCCTTGAGTAC
			SEQ ID NO: 2731	SEQ ID NO: 2888	SEQ ID NO: 3045
		AA	SYGMH	AIWYDANNKYYADAVKG	DRTIFGVVLEY
			SEQ ID NO: 1161	SEQ ID NO: 1318	SEQ ID NO: 1475

iPS:361113	6A5.004.008	NA	AGCTATGGCATGCAC	GCTATATGGTATGATGGAAATA ATAAATACTATGCAGACGCCGT GAAGGGC	GATCGGACGATTTTTGGAGTGG TCCTTGAGTAC
			SEQ ID NO: 2732	SEQ ID NO: 2889	SEQ ID NO: 3046
		AA	SYGMH	AIWYDGNNKYYADAVKG	DRTIFGVVLEY
			SEQ ID NO: 1162	SEQ ID NO: 1319	SEQ ID NO: 1476
iPS:361120	6A5.004.009	NA	AGCTATGGCATGCAC	GCTATATGGTATGATGCAAATA ATAAATACTATGCAGACTCCGT GAAGGGC	GATCGGACGATTTTTGGAGTGG TCCTTGAGTAC
			SEQ ID NO: 2733	SEQ ID NO: 2890	SEQ ID NO: 3047
		AA	SYGMH	AIWYDANNKYYADSVKG	DRTIFGVVLEY
			SEQ ID NO: 1163	SEQ ID NO: 1320	SEQ ID NO: 1477
iPS:359896	6A5.004.010	NA	AGCTATGGCATGCAC	GCTATATGGTATGATGCAAATA ATAAATACTATGCAGACGCCGT GAAGGGC	GATCGGACGATTTTTGGAGTGG TCCTTGAGTAC
			SEQ ID NO: 2734	SEQ ID NO: 2891	SEQ ID NO: 3048
		AA	SYGMH	AIWYDANNKYYADAVKG	DRTIFGVVLEY
			SEQ ID NO: 1164	SEQ ID NO: 1321	SEQ ID NO: 1478
iPS:359890	6A5.004.011	NA	AGCTATGGCATGCAC	GCTATATGGTATGATGCAAATA ATAAATACTATGCAGACGCCGT GAAGGGC	GATCGGACGATTTTTGGAGTGG TCCTTGAGTAC
			SEQ ID NO: 2735	SEQ ID NO: 2892	SEQ ID NO: 3049
		AA	SYGMH	AIWYDANNKYYADAVKG	DRTIFGVVLEY
			SEQ ID NO: 1165	SEQ ID NO: 1322	SEQ ID NO: 1479
iPS:359567	2A11.002	NA	AGCTATGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGAAGACGCCGT GAAGGGC	GGGATTACGATTTTTGGTCATG GGTTTGAAATAT
			SEQ ID NO: 2736	SEQ ID NO: 2893	SEQ ID NO: 3050
		AA	SYGMH	VIWYDASNKYYEDAVKG	GITIFGHGFEY
			SEQ ID NO: 1166	SEQ ID NO: 1323	SEQ ID NO: 1480

iPS:335965	2A11.003	NA	AGCTATGGCATGCAC	GTTATATGGTATGATGGAAGTA ATAAATACTATGAAGACTCCGT GAAGGGC	GGGATTACGATTTTTGGTCATG GGTTTGAATAT
			SEQ ID NO: 2737	SEQ ID NO: 2894	SEQ ID NO: 3051
		AA	SYGMH	VIWYDGSNKYYEDSVKG	GITIFGHGFEY
			SEQ ID NO: 1167	SEQ ID NO: 1324	SEQ ID NO: 1481
iPS:361158	2A11.004	NA	AGCTATGGCATGCAC	GTTATATGGTATGATGGAAGTA ATAAATACTATGAAGACGCCGT GAAGGGC	GGGATTACGATTTTTGGTCATG GGTTTGAATAT
			SEQ ID NO: 2738	SEQ ID NO: 2895	SEQ ID NO: 3052
		AA	SYGMH	VIWYDGSNKYYEDAVKG	GITIFGHGFEY
			SEQ ID NO: 1168	SEQ ID NO: 1325	SEQ ID NO: 1482
iPS:361165	2A11.005	NA	AGCTATGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGAAGACTCCGT GAAGGGC	GGGATTACGATTTTTGGTCATG GGTTTGAATAT
			SEQ ID NO: 2739	SEQ ID NO: 2896	SEQ ID NO: 3053
		AA	SYGMH	VIWYDASNKYYEDSVKG	GITIFGHGFEY
			SEQ ID NO: 1169	SEQ ID NO: 1326	SEQ ID NO: 1483
iPS:361172	2G10_LC1.003	NA	AACTATGGCATGCAC	GCTATATGGTTTGATGCAAGTG ATAAATACTATGCAGACGCCGT GAAGGGC	GATCAGGCGATTTTTTGGAGTGG TCCCCGACTAC
			SEQ ID NO: 2740	SEQ ID NO: 2897	SEQ ID NO: 3054
		AA	NYGMH	AIWFDASDKYYADAVKG	DQAIFGVVPDY
			SEQ ID NO: 1170	SEQ ID NO: 1327	SEQ ID NO: 1484
iPS:361178	2G10_LC1.004	NA	AACTATGGCATGCAC	GCTATATGGTTTGATGCAAGTG ATAAATACTATGCAGACTCCGT GAAGGGC	GATCAGGCGATTTTTTGGAGTGG TCCCCGACTAC
			SEQ ID NO: 2741	SEQ ID NO: 2898	SEQ ID NO: 3055
		AA	NYGMH	AIWFDASDKYYADSVKG	DQAIFGVVPDY
			SEQ ID NO: 1171	SEQ ID NO: 1328	SEQ ID NO: 1485

iPS:361185	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
iPS:361192	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
iPS:359609	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
iPS:359615	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
iPS:361196	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		AACTATGGCATGCAC	GCTATATGGTTTGATGCAAGTG ATAAATACTATGCAGACGCCGT GAAGGGC	GATCAGGCGATTTTTGGAGTGG TCCCCGACTAC
		NA	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

iPS:361210	18E3.006	NA	AGTGGTGGTTACTACTGGAGC	TACATCTATTACAGTGGGAGCA CCTACTACAACCCGTCCCTCAA GAGT	GATCGTATTACGATTTTTGGAG TGGTTATGGGGGGCGGTATGG ACGTC
			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
iPS:361214	18E3.007	NA	AGTGGTGGTTACTACTGGAGC	TACATCTATTACAGTGGGAGCA CCTACTACAACCCGTCCCTCAA GAGT	GATCGTATTACGATTTTTGGAG TGGTTATGGGGGGCGGTATGG ACGTC
			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
iPS:361218	18E3.008	NA	AGTGGTGGTTACTACTGGAGC	TACATCTATTACAGTGGGAGCA CCTACTACAACCCGTCCCTCAA GAGT	GATCGTATTACGATTTTTGGAG TGGTTATGGGGGGCGGTATGG ACGTC
			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
iPS:361222	5C2.006	NA	GGCTACTATATCCAC	TGGATCAACCCTGAAAGTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC	GAGGCCACGATTTTTGGAATGG TTATTGTACCGTTTGACTAC
			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
iPS:361229	5C2.007	NA	GGCTACTATATCCAC	TGGATCAACCCTGAAAGTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC	GAGGCCACGATTTTTGGAATGG TTATTGTACCGTTTGACTAC
			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

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

iPS:361261	5C2.013	NA	GGCTACTATATCCAC	TGGATCAACCCTGACGCTGGTG GCACAGACTATTCACACAGAGGTT 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
iPS:361268	5C2.014	NA	GGCTACTATATCCAC	TGGATCAACCCTGACGCTGGTG GCACAGACTATTCACACAGAGGTT 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
iPS:359669	5C2.015	NA	GGCTACTATATCCAC	TGGATCAACCCTGACGCTGGTG GCACAGACTATTCACACAGAGGTT 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
iPS:359678	5C2.016	NA	GGCTACTATATCCAC	TGGATCAACCCTGAAAGTGGTG GCACAGACTATTCACACAGAGGTT 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
iPS:361275	11C1.002	NA	GGCTACTATATACAC	TGGATCAGCCCTAACAGTGGTG AAACAAGCTATGCACACAGAAGT 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

iPS:361282	11C1.003	NA	GGCTACTATATACAC	TGGATCAGCCCTAACAGTGGTG ACACAAGCTATGCACACAGAAGT 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
iPS:361289	11C1.004	NA	GGCTACTATATACAC	TGGATCAGCCCTAACAGTGGTG AAACAAGCTATGCACACAGAAGT 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
iPS:359712	11C1.005	NA	GGCTACTATATACAC	TGGATCAGCCCTAACAGTGGTG AAACAAGCTATGCACACAGAAGT 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
iPS:361293	11C1.006	NA	GGCTACTATATACAC	TGGATCAGCCCTAACAGTGGTG ACACAAGCTATGCACACAGAAGT 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
iPS:361297	11C1.007	NA	GGCTACTATATACAC	TGGATCAGCCCTAACAGTGGTG AAACAAGCTATGCACACAGAAGT 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

iPS:361319	13H12.004	NA	GGCTACTATATCCAC	TGGATCAACCCTGACAGTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC	GAGGCCACGATTTTTGGAATGG 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:359737	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
iPS:361326	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
iPS:361330	12H11.002	NA	GGCTACTATATACAC	TGGATAAGCCCTAACCAAGGT GAAACAAACTATGCACAGAAG TTTCAGGAC	GAGGCCACGATTTTTGGAATGC 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
iPS:361337	12H11.003	NA	GGCTACTATATACAC	TGGATAAGCCCTAACCAAGGT GACACAAACTATGCACAGAAG TTTCAGGAC	GAGGCCACGATTTTTGGAATGC 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

iPS:361344	12H11.004	NA	GGCTACTATATACAC	TGGATAAGCCCTAACCAAGGT GAAACAAACTATGCACAGAAG TTTCAGGAC	GAGGCCACGATTTTTGGAATGC 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 AAACAAACTATGCACAGAAGT TTCAGGAC	GAGGCCACGATTTTTGGAATGC 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 ACACAAACTATGCACAGAAGT TTCAGGAC	GAGGCCACGATTTTTGGAATGC 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 GACACAAACTATGCACAGAAG TTTCAGGAC	GAGGCCACGATTTTTGGAATGC 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 AAACAAACTATGCACAGAAGT TTCAGGAC	GAGGCCACGATTTTTGGAATGC 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

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

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

iPS:361430	2C2.005.005	NA	SEQ ID NO: 2797	GGCTACTATATGCAT	TGGATCAACCCTAACAGTGGTG GCACAAACTATGCACAGAAGT TTCAGGGC	GGGGGGGATTACGTTTGGGGG ACTTATCGGCCTCACTACTACT ACGGTATGGACGTC
			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:361436	2C2.005.006	NA	SEQ ID NO: 2798	GGCTACTATATGCAT	TGGATCAACCCTAACAGTGGTG GCACAAACTATGCACAGAAGT TTCAGGGC	GGGGGGGATTACGTTTGGGGG ACTTATCGGCCTCACTACTACT ACGGTATGGACGTC
			SEQ ID NO: 2955		SEQ ID NO: 3112	
		AA	GYYMH		WINPNSGGTNYAQKFQG	GGDYVWGTYRPHYYYGMDV
			SEQ ID NO: 1228		SEQ ID NO: 1385	SEQ ID NO: 1542
iPS:361442	2C2.005.007	NA	SEQ ID NO: 2799	GGCTACTATATGCAT	TGGATCAACCCTAACAGTGGTG GCACAAACTATGCACAGAAGT TTCAGGGC	GGGGGGGATTACGTTTGGGGG ACTTATCGGCCTCACTACTACT ACGGTATGGACGTC
			SEQ ID NO: 2956		SEQ ID NO: 3113	
		AA	GYYMH		WINPNSGGTNYAQKFQG	GGDYVWGTYRPHYYYGMDV
			SEQ ID NO: 1229		SEQ ID NO: 1386	SEQ ID NO: 1543
iPS:361448	2C2.005.008	NA	SEQ ID NO: 2800	GGCTACTATATGCAT	TGGATCAACCCTAACAGTGGTG GCACAAACTATGCACAGAAGT TTCAGGGC	GGGGGGGATTACGTTTGGGGG ACTTATCGGCCTCACTACTACT ACGGTATGGACGTC
			SEQ ID NO: 2957		SEQ ID NO: 3114	
		AA	GYYMH		WINPNSGGTNYAQKFQG	GGDYVWGTYRPHYYYGMDV
			SEQ ID NO: 1230		SEQ ID NO: 1387	SEQ ID NO: 1544
iPS:361454	2C2.005.009	NA	SEQ ID NO: 2801	GGCTACTATATGCAT	TGGATCAACCCTAACAGTGGTG GCACAAACTATGCACAGAAGT TTCAGGGC	GGGGGGGATTACGTTTGGGGG ACTTATCGGCCTCACTACTACT ACGGTATGGACGTC
			SEQ ID NO: 2958		SEQ ID NO: 3115	
		AA	GYYMH		WINPNSGGTNYAQKFQG	GGDYVWGTYRPHYYYGMDV
			SEQ ID NO: 1231		SEQ ID NO: 1388	SEQ ID NO: 1545

iPS:361460	2C2.005.010	NA	GGCTACTATATGCAT	TGGATCAACCCTAACAGTGGTG GCACAAACTATGCACAGAAGT 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 GCACAAACTATGCACAGAAGT 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 GCACAAACTATGCACAGAAGT 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 GCACAAACTATGCACAGAAGT TTCAGGGC	GGGGGGGATTACGTTTTCGGGA 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 GCACAAACTATGCACAGAAGT TTCAGGGC	GGGGGGGATTACGTTTTCGGGA 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	GATAGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
			SEQ ID NO: 2807	SEQ ID NO: 2964	SEQ ID NO: 3121
		AA	NFGMH	VIWYDASNENYADAVKG	DRTIFGVVLGDY
			SEQ ID NO: 1237	SEQ ID NO: 1394	SEQ ID NO: 1551
iPS:361851	6H1.009	NA	TACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGGC	GATAGGACGATTTTTGGAGTGC TCTTGGGGGACTAC
			SEQ ID NO: 2808	SEQ ID NO: 2965	SEQ ID NO: 3122
		AA	YFGMH	VIWYDASNKYYADAVKG	DRTIFGVLLGDY
			SEQ ID NO: 1238	SEQ ID NO: 1395	SEQ ID NO: 1552
iPS:361855	2C2.005.015	NA	GGCTACTATATGCAT	TGGATCAACCCTAACAGTGGTG GCACAAACTATGCACAGAAGT TTCAGGGC	GGGGGGGATTACGTTTGGGGG ACTTATCGGCCTCACTACTACT ACGGTATGGACGTC
			SEQ ID NO: 2809	SEQ ID NO: 2966	SEQ ID NO: 3123
		AA	GYYMH	WINPNSGGTNYAQKFQG	GGDYVWGTYRPHYYYGMDV
			SEQ ID NO: 1239	SEQ ID NO: 1396	SEQ ID NO: 1553
iPS:336067	5G12.006	NA	AGCTATGGCATACAC	GTTATATGGTATGATGGAAGTA ATAAGTTCCATGCAGACTCCGT GAAGGGC	GGAAAAGTGGCTGGTATGCCT GAAGCTTTTGAAATC
			SEQ ID NO: 2810	SEQ ID NO: 2967	SEQ ID NO: 3124
		AA	SYGIH	VIWYDGSNKFHADSVKG	GKVAGMPEAFEI
			SEQ ID NO: 1240	SEQ ID NO: 1397	SEQ ID NO: 1554
iPS:336169	17B11.002	NA	AGTTATGATATCAAC	TGGATGAACCCTAACAGTGGTA ACACAGGCTATGCACAGAAGT TCCAGGGC	GGGGGTGATTACGTTTGGGGG AGTTATCGTCCCTACTACTACT ACTACGGTATGGACGTC
			SEQ ID NO: 2811	SEQ ID NO: 2968	SEQ ID NO: 3125
		AA	SYDIN	WMNPNSGNTGYAQKFQG	GGDYVWGSYRPYYYYYGMDV
			SEQ ID NO: 1241	SEQ ID NO: 1398	SEQ ID NO: 1555

iPS:361127	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
iPS:361136	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
iPS:361140	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
iPS:359919	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
iPS:361144	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	GTTATATGGTATGATGGAAGTA ATAAGTTCCATGCAGACGCCGT GAAGGGC	GGAAAAGTGGCTGGTATGCCT GAAGCTTTTGAAATC
			SEQ ID NO: 2817	SEQ ID NO: 2974	SEQ ID NO: 3131
		AA	SYGIH	VIWYDGSNKFHADAVKG	GKVAGMPEAFEI
			SEQ ID NO: 1247	SEQ ID NO: 1404	SEQ ID NO: 1561
iPS:361491	17B11.002.001	NA	AGTTATGATATCAAC	TGGATGAACCCTAACAGTGGTG GCACAGGCTATGCACACAGAAGT TCCAGGGC	GGGGGTGATTACGTTTGGGGG AGTTATCGTCCCTACTACTACT ACTACGGTATGGACGTC
			SEQ ID NO: 2818	SEQ ID NO: 2975	SEQ ID NO: 3132
		AA	SYDIN	WMNPNSGGTGYAQKFQG	GGDYVWGSYRPYYYYYGMDV
			SEQ ID NO: 1248	SEQ ID NO: 1405	SEQ ID NO: 1562
iPS:361499	17B11.002.002	NA	AGTTATGATATCAAC	TGGATGAACCCTAACAGTGGTA ACACAGGCTATGCACACAGAAGT TCCAGGGC	GGGGGTGATTACGTTTGGGGG AGTTATCGTCCCTACTACTACT ACTACGGTATGGACGTC
			SEQ ID NO: 2819	SEQ ID NO: 2976	SEQ ID NO: 3133
		AA	SYDIN	WMNPNSGNTGYAQKFQG	GGDYVWGSYRPYYYYYGMDV
			SEQ ID NO: 1249	SEQ ID NO: 1406	SEQ ID NO: 1563
iPS:361503	17B11.002.003	NA	AGTTATGATATCAAC	TGGATGAACCCTAACAGTGGTG GCACAGGCTATGCACACAGAAGT TCCAGGGC	GGGGGTGATTACGTTTGGGGG AGTTATCGTCCCTACTACTACT ACTACGGTATGGACGTC
			SEQ ID NO: 2820	SEQ ID NO: 2977	SEQ ID NO: 3134
		AA	SYDIN	WMNPNSGGTGYAQKFQG	GGDYVWGSYRPYYYYYGMDV
			SEQ ID NO: 1250	SEQ ID NO: 1407	SEQ ID NO: 1564
iPS:361507	17B11.002.004	NA	AGTTATGATATCAAC	TGGATGAACCCTAACAGTGGTG GCACAGGCTATGCACACAGAAGT TCCAGGGC	GGGGGTGATTACGTTTGGGGG AGTTATCGTCCCTACTACTACT ACTACGGTATGGACGTC
			SEQ ID NO: 2821	SEQ ID NO: 2978	SEQ ID NO: 3135
		AA	SYDIN	WMNPNSGGTGYAQKFQG	GGDYVWGSYRPYYYYYGMDV
			SEQ ID NO: 1251	SEQ ID NO: 1408	SEQ ID NO: 1565

iPS:361514	17B11.002.005	NA	AGTTATGATATCAAC	TGGATGAACCCTAACAGTGGTG GCACAGGCTATGCACAGAAGT TCCAGGGC	GGGGGTGATTACGTTTGGGGG AGTTATCGTCCCTACTACTACT ACTACGGTATGGACGTC
			SEQ ID NO: 2822	SEQ ID NO: 2979	SEQ ID NO: 3136
		AA	SYDIN	WMNPNSGGTGYAQKFQG	GGDYVWGSYRPYYYYYGMDV
			SEQ ID NO: 1252	SEQ ID NO: 1409	SEQ ID NO: 1566
iPS:360582	17B11.002.006	NA	AGTTATGATATCAAC	TGGATGAACCCTAACAGTGGTA ACACAGGCTATGCACAGAAGT TCCAGGGC	GGGGGTGATTACGTTTGGGGG AGTTATCGTCCCTACTACTACT ACTACGGTATGGACGTC
			SEQ ID NO: 2823	SEQ ID NO: 2980	SEQ ID NO: 3137
		AA	SYDIN	WMNPNSGNTGYAQKFQG	GGDYVWGSYRPYYYYYGMDV
			SEQ ID NO: 1253	SEQ ID NO: 1410	SEQ ID NO: 1567
iPS:361518	17B11.002.007	NA	AGTTATGATATCAAC	TGGATGAACCCTAACAGTGGTG GCACAGGCTATGCACAGAAGT TCCAGGGC	GGGGGTGATTACGTTTTTCGGGA GTTATCGTCCCTACTACTACTA CTACGGTATGGACGTC
			SEQ ID NO: 2824	SEQ ID NO: 2981	SEQ ID NO: 3138
		AA	SYDIN	WMNPNSGGTGYAQKFQG	GGDYVFGSYRPYYYYYGMDV
			SEQ ID NO: 1254	SEQ ID NO: 1411	SEQ ID NO: 1568
iPS:360570	17B11.002.008	NA	AGTTATGATATCAAC	TGGATGAACCCTAACAGTGGTG GCACAGGCTATGCACAGAAGT TCCAGGGC	GGGGGTGATTACGTTTTTCGGGA GTTATCGTCCCTACTACTACTA CTACGGTATGGACGTC
			SEQ ID NO: 2825	SEQ ID NO: 2982	SEQ ID NO: 3139
		AA	SYDIN	WMNPNSGGTGYAQKFQG	GGDYVFGSYRPYYYYYGMDV
			SEQ ID NO: 1255	SEQ ID NO: 1412	SEQ ID NO: 1569
iPS:362051	SG12.005.001	NA	AGCTATGGCATACAC	GTTATATGGTATGATGCAAGTA ATAAGTTCCATGCAGACGCCGT GAAGGGC	GGAAAAGTGGCTGGTATGCCT GAAGCTTTTGAAATC
			SEQ ID NO: 2826	SEQ ID NO: 2983	SEQ ID NO: 3140
		AA	SYGIH	VIWYDASNKFHADAVKG	GKVAGMPEAFEI
			SEQ ID NO: 1256	SEQ ID NO: 1413	SEQ ID NO: 1570

Tabella 5. Sequenze di acido nucleico ("NA") e di amminoacidi ("AA") di catena leggera e pesante esemplificative

iPS n.	Ab	Tipo	LC	HC
iPS:336175	2C2.005	NA	CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT CTGGAAGTAGCTCCAACATCGGAAGTAATACTG TAAACTGGTACCAGCACCTCCCAGGAACGGCCC CCAAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATGACAGCCTGAATGGTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCCTAGGTC AGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCC GCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGC CACACTGGTGTGTCTCATAAGTGACTTCTACCCG GGAGCCGTGACAGTGGCCTGGAAGGCAGATAG CAGCCCCGTCAAGGCGGGAGTGGAGACCACCAC ACCCTCCAAACAAAGCAACAACAAGTACGCGGC CAGCAGCTATCTGAGCCTGACGCCTGAGCAGTG GAAGTCCCACAGAAGCTACAGCTGCCAGGTCAC GCATGAAGGGAGCACCGTGGAGAAGACAGTGG CCCCTACAGAATGTTCA	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
				GAGGCTCTGCACACAACCACTACACGCAGAAGAGC
				CTCTCCCTGTCTCCGGGTAAA
			SEQ ID NO: 1885	SEQ ID NO: 2042
		AA	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 GTCCAGCCTGGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGGAA GTAATGAAAACTATGCAGACTCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAATA CGCTGTATCTGCACATGAACAGCCTGAGAGTCG CGGACACGGCTGTGTATTATTGTGCGCGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT
		4B1		
		IPS:335914		

	GCACCATCTGTCTTCATCTTCCCGCCATCTGATG	GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
	AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT	CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC
	GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA	ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC
	AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT	GGCCCCTGGGCTGCCTGGTCAAGGACTACTTCCC
	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
		AGCAGGTGGCAGCAGGGAACGTCTTCTCATGC
		TCCGTGATGCATGAGGCTCTGCACAACCACTAC
		ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1886	SEQ ID NO: 2043
AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM
	QQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTEFT	HWVRQAPGKGLEWVAVIWYDGSNENYADSVKG
	LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR	RFTISRDNSKNTLYLHMNSLRVADTAVYYCARDG
	TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA	TIFGVVLGDYWGQGTLVTVSSASTKGPSVFPLAPS

		KVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC	SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
		SEQ ID NO: 316	SEQ ID NO: 473
ipS:33593	6HI	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCGCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGAACGGTGGCT GCACCATCTGTCTTCATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT CGGGTAACTCCCAGGAGAGTGTCACAGAGGAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT	CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTG 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 GTCCAGCCTGGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG
	2FI1		
	iPS:335 941		

		AGCTCCTGATCTACGATGCATCCAATTTGGAAA	CTGGAGTGGGTGGCAGTTATATGGTATGATGGA
		CAGGGGTCCCATCAAGGTTCAGTGGAAGTGGAT	AGTAATAAATACTATGCAGACTCCGTGAAGGGC
		CTGGGACAGATTTTAGTTTCACCATCAGCAGCCT	CGATTCACCATCTCCAGCGACAATTCCAAGAAC
		GCAGCCTGAAGATATTGCAACATATTACTGTCA	ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC
		ACAGTATGATATTCTCCTCACTTTCGGCGGAGG	GAGGACACCGGCTGTGTATTACTGTGCGAGAGAT
		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
			GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA
			GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT
			CCTCACCGTCCTGCACCAGGACTGGCTGAATGG
			CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
			CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
			AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
			ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
			AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
			GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
			AGAGCAATGGGCAGCCGGAGAACAACTACAAG
			ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
			TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
			AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC

			TCCGTGATGCATGAGGCTCTGCACAACCACTAC
			ACGCAGAAGAGGCCTCTCCCTGTCTCCGGGTAAA
		SEQ ID NO: 1888	SEQ ID NO: 2045
	AA	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW YQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTD FSFTISSLQPEDIATYYCQQYDILLTFGGGTKVEIKR TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGM HWVRQAPGKGLEWVAVIWYDGSNKYYADSVKG RFTISSDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLDYWGQGTLVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
		SEQ ID NO: 318	SEQ ID NO: 475
iPS:335970	NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAGCAG CAACCAGGACATCCTCCTAAGCTGCTCATTTACT GGGCATCTACCCGGGAATCCGGGGTCCCTGACC GATTCAGTGGCAGCGGGTCTGGGACAGATTTCA CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCGGCCAAGGGACCAAGGTGGA AATCAAACGAACGGTGGCTGCACCATCTGTCTT CATCTTCCCGCCATCTGATGAGCAGTTGAAATCT GGAACTGCCTCTGTTGTGTGCCTGCTGAATAACT TCTATCCCAGAGAGGCCAAAGTACAGTGGAAGG TGGATAACGCCCTCCAATCGGGTAACTCCCAGG AGAGTGTCACAGAGCAGGACAGCAAGGACAGC ACCTACAGCCTCAGCACCCTGACGCTGAGC AAAGCAGACTACGAGAAACACAAAGTCTACGC	CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCGGCTACTAT ATCCACTGGGTGCGACAGGCCCCTGGACAAGGG CTTGAGTGGATGGGGGTGGATCAACCCTGACAGT GGTGGCACAGACTATTCACAGAGGTTTCAGGGC AGGTTCACCATGACCAGGGACACGTCCATCAGC ACAGCCTACATGGAACTGAACAGGCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGAG GCCACGATTTTTGGAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGG CACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTCGTGGAACTC AGGCGCCCTGACCAGCGGCGTGCACACCTTCCC GGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG

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		AAACCAGGACAGCCTCCTAACCTGCTCATTTAC	CTTGAGTGGATGGGGTGGATAAGCCCTAACAAT
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		GACAGGAGCCTGATGATTTTGCAGTGTATTACT	ACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC
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			GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
			VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV
			LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
			KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP
			SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
			LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS
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		SEQ ID NO: 324	SEQ ID NO: 481
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			AACGCCTGATCTATGGTGCATCCAGTTTGCAAA
			GTGGGGTCCCATCAAGGTTCAGCGGCAGTGGAT
			CTGGGACAGAGTTCACTCTCACAATCAGCAGCC
			TGCAGCCTGAAGATTTTGTAACTTATTACTGTCT
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			GGGACCAAAGTGGATGTCAAACGAACGGTGGCT
			GCACCATCTGTCTTCATCTTCCCGCCATCTGATG
			AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT
			GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA
			AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT
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			CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC
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			GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA
			GGGGAGAGTGT
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			CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC
			ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC
			GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC
			CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC
			CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT
			CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC
			GTGGTGACCGTGCCCTCCAGCACTTGGGCACC
			CAGACCTACATCTGCAACGTGAATCACAAGCCC
			AGCAACACCAAGGTGGACAAGAAAGTTGAGCC
			CAAATCTTGTGACAAAACTCACACATGCCCACC
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			AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC
			CCTCATGATCTCCCGGACCCCTGAGGTCACATG
			CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA
			GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
			GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA
			GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT

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			CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
			CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
			AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
			ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
			AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
			GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
			AGAGCAATGGGCAGCCGGAGAACAACTACAAG
			ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
			TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
			AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
			TCCGTGATGCATGAGGCTCTGCACAACCACTAC
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		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
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	6AS.004		
	iPS:33608		

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	CCAAAGTGGATATCAAACGAACGGTGGCTGCAC	GGACGATTTTTGGAGTGGTCCTTGAGTACCTCG
	CATCTGTCTTCATCTTCCCGCCATCTGATGAGCA	GCCAGGGAACCCTGGTCACCGTCTCCTCAGCCT
	GTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTG	CCACCAAGGGCCCATCGGTCTTCCCCCTGGCAC
	CTGAATAACTTCTATCCCAGAGAGGCCAAAGTA	CCTCCTCCAAGAGCACCTCTGGGGGCACAGCGG
	CAGTGGAAGGTGGATAACGCCCTCCAATCGGGT	CCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG
	AACTCCCAGGAGAGTGTCACAGAGCAGGACAG	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
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		AGCAATGGGCAGCCGGAGAACAACTACAAGAC
		CACGCCTCCCGTGCTGGACTCCGACGGCTCCTTC
		TTCCTCTATAGCAAGCTCACCGTGGACAAGAGC
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		FTFTISSLQPEDIATYYCQQYDDLFTFGPGTKVDIK	RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR
		RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE	TIFGVVLEYLGQGTLVTVSSASTKGPSVFPLAPSSK
		AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS	STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV
		TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR	HTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
		GEC	HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP
			SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
			KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVL
			TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
			GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS
			DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL
			TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL
			SPGK
		SEQ ID NO: 326	SEQ ID NO: 483
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		GTCGGGCGAGTCAGGGTCTTATCATCTGGTTAG	ACTGTCTCTCAGGGCTCCATCAGTAGTTACTACT
		CCTGGTATCAGCAGAAACCGGGGAAAGCCCCTA	GGAGCTGGATCCGGCAGCCCGCCGGGAAGGGA
		AACTCCTGATCTATGCTGCATCCAGTTTGCAAAG	CTAGAGTGGATTGGCCGTATCTATACCAGTGGG
		TGGGGTCCCATCAAGGTTCAGCGGCAGTGGCTC	AGCACCAACTACAACCCCTCCCTCAAGAGTCGA
		TGGGACAGATTTCACTCTCACCATCAGCAGCCT	GTCACCATGTCAATAGACACGTCCAAGAACCAG
		ACAGCCTGAAGATTTTGCAACTTACTATTGTCAA	TTCTCCCTGAAACTGAACTCTGTGACCGCCGCG
		CAGACTAACAGTTTCCCTCCGACGTTCGGCCAA	GACACGGCCGTGTATTACTGTGCGAGAGATGTA
		GGGACCAAGGTGGAAATCAAACGAACGGTGGC	GCAGTGGCTGGCTTTGACTACTGGGGCCAGGGA
		TGCACCATCTGTCTTCATCTTCCCGCCATCTGAT	ACCCTGGTCACCGTCTCCTCAGCCTCCACCAAG
		GAGCAGTTGAAATCTGGAACTGCCTCTGTTGTG	GGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCA
		TGCCTGCTGAATAACTTCTATCCCAGAGAGGCC	AGAGCACCTCTGGGGGCACAGCGGCCCTGGGCT
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		GACAGCAAGGACAGCACCTACAGCCTCAGCAGC	GCGTGCACACCTTCCCGGCTGTCCTACAGTCCTC
		ACCCTGACGCTGAGCAAAGCAGACTACGAGAA	AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT
		ACACAAAGTCTACGCCTGCGAAGTCACCCATCA	GCCCTCCAGCAGCTTGGGCACCCAGACCTACAT
		GGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAA	CTGCAACGTGAATCACAAGCCCAGCAACACCAA
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			CAAAACTCACACATGCCCACCGTGCCCAGCACC

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				CCCCCAAAACCCAAGGACACCCTCATGATCTCC
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				GCGACATCGCCGTGGAGTGGGAGAGCAATGGG
				CAGCCGGAGAACAACTACAAGACCACGCCTCCC
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			YQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTD	WIRQPAGKGLEWIGRIYTSGSTNYNPSLKSRVTMS
			FTLTISSLQPEDFATYYCQQTNSFPPTFGQGTKVEI	IDTSKNQFSLKLNSVTAADTAVYYCARDVAVAGF
			KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR	DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGT
			EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS	AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV
			STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN	LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT
	AA		RGEC	KVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFP
				PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY
				VDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQ
				DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
				QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE
				WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
				RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

	SEQ ID NO: 327	SEQ ID NO: 484
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	CCTGGTATCAGCAGAAACCGGGGAAAGCCCCTA	GGAGCTGGATCCGGCAGCCCGCCGGGAAGGGA
	AACTCCTGATCTATGCTGCATCCAGTTTGCAAAG	CTAGAGTGGATTGGCCGTATCTATACCAGTGGG
	TGGGGTCCCATCAAGGTTCAGCGGCAGTGGCTC	AGCACCAACTACAACCCCTCCCTCAAGAGTCGA
	TGGGACAGATTTCACTCTCACCATCAGCAGCCT	GTCACCATGTCAATAGACACGTCCAAGAACCAG
	ACAGCCTGAAGATTTTGCAACTTACTATTGTCAA	TTCTCCCTGAAACTGAACTCTGTGACCGCCGCG
	CAGACTAACAGTTTCCCTCCGACGTTCGGCCAA	GACACGGCCCGTGTATTACTGTGCGAGAGATGTA
	GGGACCAAGGTGGAAATCAAACGAACGGTGGC	GCAGTGGCTGGCTTTGACTACTGGGGCCAGGGA
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	GAGCAGTTGAAATCTGGAACTGCCTCTGTTGTG	GGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCA
	TGCCTGCTGAATAACTTCTATCCCAGAGAGGCC	AGAGCACCTCTGGGGGCACAGCGGCCCTGGGCT
	AAAGTACAGTGGAAGGTGGATAACGCCCTCCAA	GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA
	TCGGGTAACTCCCAGGAGAGTGTCACAGAGCAG	CGGTGTCGTGGAACTCAGGCGCCCTGACCAGCG
	GACAGCAAGGACAGCACCTACAGCCTCAGCAGC	GCGTGCACACCTTCCCGGCTGTCCTACAGTCCTC
	ACCCTGACGCTGAGCAAAGCAGACTACGAGAA	AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT
	ACACAAAGTCTACGCCTGCGAAGTCACCCATCA	GCCCTCCAGCAGCTTGGGCACCCAGACCTACAT
	GGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAA	CTGCAACGTGAATCACAAGCCCAGCAACACCAA
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		YQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTD	WIRQPAGKGLEWIGRIYTSGSTNYNPSLKSRVTMS
		FTLTISSLQPEDFATYYCQQTNSFPPTFGQGTKVEI	IDTSKNQFSLKLNSVTAADTAVYYCARDVAVAGF
		KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR	DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGT
		EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS	AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV
		STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN	LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT
		RGEC	KVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFP
			PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY
			VDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQ
			DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
			QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE
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		TGCAGCCTGAAGATTTTGTAACTTATTACTGTCT	CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
		ACAGCATAATAGTTACCCATTCACTTTCGGCCA	AGGACACGGCTGTGTATTACTGTGCGCGAGATG
		AGGGACCAAAGTGGATGTCAAACGAACGGTGG	GGACGATTTTTGGAGTGCTCTTGGGGGACTACT
		CTGCACCATCTGTCTTCATCTTCCCGCCATCTGA	GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
		TGAGCAGTTGAAATCTGGAACTGCCTCTGTTGT	CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC
		GTGCCTGCTGAATAACTTCTATCCCAGAGAGGC	ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC
		CAAAGTACAGTGGAAGGTGGATAACGCCCTCCA	GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC
		ATCGGGTAACTCCCAGGAGAGTGTCACAGAGCA	CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC

		GGACAGCAAGGACAGCACCTACAGCCTCAGCA GCACCCTGACGCTGAGCAAAGCAGACTACGAGA AACACAAAGTCTACGCCTGCGAAGTCACCCATC AGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCA ACAGGGGAGAGTGT	CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCCACC GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC AGTCTTCCTCTTCCCCCCAAAACCCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATG CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTGTGTCAGCGT CCTCACCGTCCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT ACACCCTGCCCCCATCCCGGGAGGAGATGACCA AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGAACAACTACAAG ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
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			AACTCCTGATCTATGGTGCATCCAGTTTGCAAA TGGAGTGGGTGGCAGTTATATGGTGATGCAA
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			TGCAGCCTGAAGATTTTGTAACTTATTACTGTCT CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
			ACAGCATAATAGTTACCCATTCACTTTCGGCCA AGGACACGGCTGTGTATTACTGTGCGCGAGATG
			AGGGACCAAAGTGGATGTCAAACGAACGGTGG GGACGATTTTTGGAGTGCTCTTGGGGGACTACT
			CTGCACCATCTGTCTTCATCTTCCCGCCATCTGA GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
			TGAGCAGTTGAAATCTGGAACTGCCTCTGTTGT CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC
			GTGCCTGCTGAATAACTTCTATCCCAGAGAGGC ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC
			CAAAGTACAGTGGAAGGTGGATAACGCCCTCCA GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC
			ATCGGGTAACTCCCAGGAGAGTGTCACAGAGCA CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC
			GGACAGCAAGGACAGCACCTACAGCCTCAGCA CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT
			GCACCCTGACGCTGAGCAAAGCAGACTACGAGA CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC
			AACACAAAGTCTACGCCTGCGAAGTCACCCATC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
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			ACAGGGGAGAGTGT AGCAACACCAAGGTGGACAAGAAAGTTGAGCC
			CAAATCTTGTGACAAAACTCACACATGCCCACC
			GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC
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			CCTCATGATCTCCCGGACCCCTGAGGTCACATG
			CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA
			GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
			GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA
			GCAGTACGGCAGCACCGTACCGTTGTGTCAGCGT
			CCTCACCGTCCTGCACCAGGACTGGCTGAATGG
			CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC

			CCTCCCAGCCCCCCATCGAGAAAACCATCTCCAA
			AGCCAAAGGGCAGCCCCCGAGAACCACAGGTGT
			ACACCCTGCCCCCCATCCCGGGAGGAGATGACCA
			AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
			GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
			AGAGCAATGGGCAGCCGGAGAACAACTACAAG
			ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
			TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
			AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
			TCCGTGATGCATGAGGCTCTGCACAACCACTAC
			ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
		SEQ ID NO: 1900	SEQ ID NO: 2057
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	NA	SEQ ID NO: 330	SEQ ID NO: 487
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	4H9.004.003		
	iPS:360936		

		AGGGACCAAAGTGGATGTCAAACGAACGGTGG	GGACGATTTTTGGAGTGCTCTTGGGGGACTACT
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		TGAGCAGTTGAAATCTGGAACTGCCTCTGTTGT	CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC
		GTGCCTGCTGAATAACTTCTATCCCAGAGAGGC	ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC
		CAAAGTACAGTGGAAGGTGGATAACGCCCTCCA	GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC
		ATCGGGTAACTCCCAGGAGAGTGTCACAGAGCA	CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC
		GGACAGCAAGGACAGCACCTACAGCCTCAGCA	CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT
		GCACCCTGACGCTGAGCAAAGCAGACTACGAGA	CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC
		AACACAAAGTCTACGCCTGCGAAGTCACCCATC	GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
		AGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCA	CAGACCTACATCTGCAACGTGAATCACAAGCCC
		ACAGGGGAGAGTGT	AGCAACACCAAGGTGGACAAGAAAGTTGAGCC
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			GTGCCCAGCACCTGAACTCCTGGGGGGGACCGTC
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			CCTCACCGTCCTGCACCAGGACTGGCTGAATGG
			CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
			CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
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		SEQ ID NO: 1901	SEQ ID NO: 2058
AA		DIQMTQSPSSLSASVGDRVTITCRASQGIRNELGW	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM
		YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE	HWVRQAPGKGLEWVAVIWYDGSNKYYADAVKG
		FTLTISSLQPEDFVTYYCLQHNSYPFTFGQGTKVD	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG

		VKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF NRGEC	TIFGVLLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
		SEQ ID NO: 331	SEQ ID NO: 488
iPS:360943	**4H9.004.004**	NA	GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGGCATTAGAAATGAGTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCATCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAGTTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTTGTAACTTATTACTGTCT ACAGCATAATAGTTACCCATTCACTTTCGGCCCT GGGACCAAAGTGGATGTCAAACGAACGGTGGCT 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 GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT CCTCACCGTCCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT ACACCCTGCCCCCATCCCGGGAGGAGATGACCA AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGAACAACTACAAG ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
			SEQ ID NO: 1902	SEQ ID NO: 2059
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		SEQ ID NO: 332	SEQ ID NO: 489
iPS:360949	4H9.004.005	NA	GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGGCATTAGAAATGAGTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACGCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCATCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAGTTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTTGTAACTTATTACTGTCT ACAGCATAATAGTTACCCATTTCACTTTCGGCCA AGGGACCAAAGTGGATGTGTCAAACGAACGGTGG CTGCACCATCTGTCTTCATCTTCCCGCCATCTGA TGAGCAGTTGAAATCTGGAACTGCCTCTGTTGT GTGCCTGCTGAATAACTTCTATCCCAGAGAGGC CAAAGTACAGTGGAAGGTGGGATAACGCCCTCCA ATCGGGTAACTCCCAGGAGAGTGTCACAGAGCA GGACAGCAAGGACAGCACCTACAGCCTCAGCA GCACCCTGACGCTGAGCAAAGCAGACTACGAGA AACACAAAGTCTACGCCTGCGAAGTCACCCATC AGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCA ACAGGGGAGAGTGT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGGAGGTCCCTGAGACTCTCCTGT 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
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			TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
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		SEQ ID NO: 1903	SEQ ID NO: 2060
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		SEQ ID NO: 333	SEQ ID NO: 490
4H9.004.006	NA	GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGGCATTAGAAATGAGTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCATCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAGTTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTTGTAACTTATTACTGTCT ACAGCATAATAGTTACCCATTCACTTTCGGCCA AGGGACCAAAGTGGATGTCAAACGAACGGTGG CTGCACCATCTGTCTTCATCTTCCCGCCATCTGA TGAGCAGTTGAAATCTGGAACTGCCTCTTGTTGT GTGCCTGCTGAATAACTTCTATCCCAGAGAGGC CAAAGTACAGTGGAAGGTGGATAACGCCCTCCA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATA GGACGATTTTTGGAGTGCTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC

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			PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
iPS:360955	4BL.010	NA	SEQ ID NO: 334 GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCAA GGGACCAAAGTGGATATCAAACGAACGGTGGCT GCACCATCTGTCTTCATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT	SEQ ID NO: 491 CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAATA CGCTGTATCTGCAAATGAACAGCCTGAGAGTCG CGGACACGGCTGTGTATTATTGTGCGCGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCCACC GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATG CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT CCTCACCGTCCTGCACCAGGACTGGCTGAATGG

			CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
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			ACACCCTGCCCCCCATCCCGGGAGGAGATGACCA
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			AGAGCAATGGGCAGCCGGAGAACAACTACAAG
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			TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
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		LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK	RFTISRDNSKNTLYLQMNSLRVADTAVYYCARDG
		RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE	TIFGVVLGDYWGQGTLVTVSSASTKGPSVFPLAPS
		AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS	SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS
		TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR	GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN
		GEC	VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL
			GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED
			PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV
			SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK
			AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF
			YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
			SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS
			LSLSPGK
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		GACATCCAGATGACCCAGTCTCCATCCTCCCTGT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
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		GCCGGGCAAGTCAGGACATTAGAGATTATTTAG	GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA
		GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA	TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC
		AGCGCCTGATCTATGGTGCATCCAGTTTGCAAA	TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
		GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT	GTAATGAAAACTATGCAGACGCCGTGAAGGGCC
		CTGGGACAGAATTCACTCTCACAATCAGCAGCC	GATTCACCATCTCCAGAGACAATTCCAAGAATA
		TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT	CGCTGTATCTGCAAATGAACAGCCTGAGAGGTCG

			ACAGCATAATAATTACCCCTTCACTTTCGGCCAA GGGACCAAAGTGGATATCAAACGAACGGTGGCT GCACCATCTGTCTTCATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT	CGGACACGGCTGTGTATTATTGTGCGCGAGATG 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 AGAGCAATGGGCAGCCGGAGAACAACTACAAG ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
			SEQ ID NO: 1906	SEQ ID NO: 2063
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTEFT	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDASNENYADAVKG

		LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR GEC	RFTISRDNSKNTLYLQMNSLRVADTAVYYCARDG TIFGVVLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
		SEQ ID NO: 336	SEQ ID NO: 493
iPS:360968	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGAACGGTGGCT GCACCATCTGTCTTCATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAATA CGCTGTATCTGCAAATGAACAGCCTGAGAGTCG CGGACACGGCTGTGTATTATTGTGCGCGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCCACC GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC
4BL.012			

			CCTCATGATCTCCCGGACCCCTGAGGTCACATG
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			GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT
			CCTCACCGTCCTGCACCAGGACTGGCTGAATGG
			CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
			CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
			AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
			ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
			AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
			GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
			AGAGCAATGGGCAGCCGGAGAACAACTACAAG
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			TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
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iPS:360974	4B1.013	NA	SEQ ID NO: 337	SEQ ID NO: 494
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			GCCGGGCAAGTCAGGACATTAGAGATTATTTAG	GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA
			GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA	TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC
			AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA	TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
			GTGGGGTCCCTTCAGGTTCAGCGGCAGTGGGAT	GTAATGAAAACTATGCAGACTCCGTGAAGGGCC
			CTGGGACAGAATTCACTCTCACAATCAGCAGCC	GATTCACCATCTCCAGAGACAATTCCAAGAATA
			TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT	CGCTGTATCTGCACATGAACAGCCTGAGAGTCG
			ACAGCATAATAATTACCCCTTCACTTTCGGCCAA	CGGACACGGCTGTGTATTATTGTGCGCGAGATG
			GGGACCAAAGTGGATATCAAACGAACGGTGGCT	GGACGATCTTTGGAGTGGTCTTGGGGGACTACT
			GCACCATCTGTCTTCATCTTCCCGCCATCTGATG	GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
			AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT	CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC
			GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA	ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC
			AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT	GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC
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			CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC	CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC
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			GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA	CAGACCTACATCTGCAACGTGAATCACAAGCCC
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				AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC
				CCTCATGATCTCCCGGACCCCTGAGGTCACATG
				CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA
				GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
				GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA
				GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT
				CCTCACCGTCCTGCACCAGGACTGGCTGAATGG
				CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
				CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
				AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
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				AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
				GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG

			AGAGCAATGGGCAGCCGGAGAACAACTACAAG
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		AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS	SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS
		TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR	GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN
		GEC	VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL
			GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED
			PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV
			SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK
			AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF
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		GCCGGGCAAGTCAGGACATTAGAGATTATTTAG	GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA
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		AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA	TGGAGTGGGTGGCAGTTATATGGTATGATGGAA
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		GGGACCAAAGTGGATATCAAACGAACGGTGGCT	GGACGATCTTTTGGAGTGGTCTTGGGGGACTACT
		GCACCATCTGTCTTCATCTTCCCGCCATCTGATG	GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
		AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT	CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC
		GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA	ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC
		AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT	GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC

		CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG	CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC
		ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA	CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT
		CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC	CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC
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		GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA	CAGACCTACATCTGCAACGTGAATCACAAGCCC
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			GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC
			AGTCTTCCTCTTCCCCCCAAAACCCAAGGACAC
			CCTCATGATCTCCCGGACCCCTGAGGTCACATG
			CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA
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			CCTCACCGTCCTGCACCAGGACTGGCTGAATGG
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			TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
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		LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK	RFTISRDNSKNTLYLHMNSLRVADTAVYYCARDG
		RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE	TIFGVVLGDYWGQGTLVTVSSASTKGPSVFPLAPS
		AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS	SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS
		TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR	GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN
		GEC	VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL
			GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED

			PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV
			SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK
			AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF
			YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
			SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS
			LSLSPGK
iPS:359785	4BI.015		SEQ ID NO: 496
		SEQ ID NO: 339	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
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		GCCGGGCAAGTCAGGACATTAGAGATTATTTAG	TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC
		GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA	TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
		AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA	GTAATGAAAACTATGCAGACGCCGTGAAGGGCC
		GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT	GATTCACCATCTCCAGAGACAATTCCAAGAATA
		CTGGGACAGAATTCACTCTCACAATCAGCAGCC	CGCTGTATCTGCAAATGAACAGCCTGAGAGTCG
		TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT	AGGACACGGCTGTGTATTATTGTGCGCGAGATA
		ACAGCATAATAATTACCCCTTCACTTTCGGCCAA	GGACGATCTTTGGAGTGGTCTTGGGGGACTACT
		GGGACCAAAGTGGATATCAAACGAACGGTGGCT	GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
		GCACCATCTGTCTTCATCTTCCCGCCATCTGATG	CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC
		AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT	ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC
		GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA	GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC
		AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT	CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC
		CGGGTAACTCCCAGGAGAGTGTCACAGAGGACAGG	CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT
		ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA	CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC
		CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC	GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
		ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG	CAGACCTACATCTGCAACGTGAATCACAAGCCC
		GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA	AGCAACACCAAGGTGGACAAGAAAGTTGAGCC
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			CCTCATGATCTCCCGGACCCCTGAGGTCACATG
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	AA	TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR	GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN
		GEC	VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL
			GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED
			PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV
			SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK
			AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF
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			LSLSPGK
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		GCCGGGCAAGTCAGGACATTAGAGATTATTTAG	GCAGCGTCTGGAATTCACTTTCAGTAACTTTGGCA
	NA	GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA	TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC
		AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA	TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
		GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT	GTAATGAAAACTATGCAGACGCCGTGAAGGGCC
		CTGGGACAGAATTCACTCTCACAATCAGCAGCC	GATTCACCATCTCCAGAGACAATTCCAAGAATA
		TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT	CGCTGTATCTGCAAATGAACAGCCTGAGAGTCG
iPS:360982	4BI.016		

		ACAGCATAATAATTACCCCTTCACTTTCGGCCAA	AGGACACGGCTGTGTATTATTGTGCGCGAGATG
		GGGACCAAAGTGGATATCAAACGAACGGTGGCT	GGACGATCTTTGGAGTGGTCTTGGGGGACTACT
		GCACCATCTGTCTTCATCTTCCCGCCATCTGATG	GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
		AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT	CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC
		GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA	ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC
		AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT	GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC
		CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG	CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC
		ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA	CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT
		CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC	CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC
		ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG	GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
		GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA	CAGACCTACATCTGCAACGTGAATCACAAGCCC
		GGGGAGAGTGT	AGCAACACCAAGGTGGACAAGAAAGTTGAGCC
			CAAATCTTGTGACAAAACTCACACATGCCCACC
			GTGCCCAGCACCTGAACTCCTGGGGGGGACCGTC
			AGTCTTCCTCTTCCCCCCAAAACCCAAGGACAC
			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

		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
iPS:33592	18F2	NA	
		GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCACCAGAAACCAGGGAAAGCCCCTA AGCGCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAAATAACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGAACGGTGGCT GCACCATCTGTCTTCATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGGAA GTAATGAAAACTATGCAGACTCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCACATGAACAGCCTGAGAGCCG CGGACACGGCTGTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCCACC GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC AGTCTTCCTCTTCCCCCCAAAACCCAAGGACAC

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

iPS:360986	18F2.002	NA	SEQ ID NO: 342	SEQ ID NO: 499
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
			CTGCATCTATAGGAGACAGAGTCACCATCACTT	GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG	GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA
			GCTGGTATCAACAGAAACCAGGGAAAGCCCCTA	TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC
			AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA	TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
			GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT	GTAATGAAAACTATGCAGACGCCGTGAAGGGCC
			CTGGGACAGAATTCACTCTCACAATCAGCAGCC	GATTCACCATCTCCAGAGACAATTCCAAGAACA
			TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT	CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
			ACAGCATAATAATTACCCCTTCACTTTCGGCCCT	CGGACACGGCTGTGTATTACTGTGCGAGAGATG
			GGGACCAAAGTGGATATCAAACGAACGGTGGCT	GGACGATCTTTGGAGTGGTCTTGGGGGACTACT
			GCACCATCTGTCTTCATCTTCCCGCCATCTGATG	GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
			AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT	CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC
			GCCTGCTGAATAACTTTCTATCCCAGAGAGGCCA	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
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			TCCGTGATGCATGAGGCTCTGCACAACCACTAC
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		SEQ ID NO: 1913	SEQ ID NO: 2070
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		SEQ ID NO: 343	SEQ ID NO: 500
iPS:360995	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCAACAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTATGGTGCATCCAGTTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTTCGGCCCT GGGACCAAAGTGGATATCAAACGAACGGTGGCT GCACCATCTGTCTTCATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCACATGAACAGCCTGAGAGCCG CGGACACGGCTGTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC

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

			PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV
			SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK
			AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF
			YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
			SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS
			LSLSPGK
iPS:360999	18F2.004	NA	SEQ ID NO: 501
			CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
			GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA
			TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC
			TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
			GTAATGAAAACTATGCAGACGCCGTGAAGGGCC
			GATTCACCATCTCCAGAGACAATTCCAAGAACA
			CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
			CGGACACGGCTGTGTATTACTGTGCGAGAGATG
			GGACGATCTTTGGAGTGGTCTTGGGGACTACT
			GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
			CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC
			ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC
			GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC
			CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC
			CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT
			CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC
			GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
			CAGACCTACATCTGCAACGTGAATCACAAGCCC
			AGCAACACCAAGGTGGACAAGAAAGTTGAGCC
			CAAATCTTGTGACAAAACTCACACATGCCCACC
			GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC
			AGTCTTCCTCTTCCCCCCAAAACCCAAGGACAC
			CCTCATGATCTCCCGGACCCCTGAGGTCACATG
			CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA
			GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
			GGTGCATAATGCCAAGACAAAGCCGCGTGTGAGGA
			GCAGTACGGCAGCACGTACCGTGTGGTCAGCGT
			CCTCACCGTCCTGCACCAGGACTGGCTGAATGG

			CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
			CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
			AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
			ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
			AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
			GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
			AGAGCAATGGGCAGCCGGAGAACAACTACAAG
			ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
			TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
			AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
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		SEQ ID NO: 1915	SEQ ID NO: 2072
	AA	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YHQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDASNENYADAVKG RFTISRDNSKNTLYLQMNSLRAADTAVYYCARDG TIFGVVLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
	NA	SEQ ID NO: 345	SEQ ID NO: 502
		GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCAACAGAAACCAGGGAAAGCCCCTA AGCGCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG

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

			FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC	RFTISRDNSKNTLYLQMNSLRAADTAVYYCARDG TIFGVVLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
		SEQ ID NO: 346	SEQ ID NO: 503
iPS:361009	**18F2.006**	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCAACAGAAACCAGGGAAAGCCCCTA AGCGCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGAACGGTGGCT GCACCATCTGTCTTCATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAAACTATGCAGACGCCGTGAAGGGCC 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 AGAGCAATGGGCAGCCGGAGAACAACTACAAG ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
			SEQ ID NO: 1917	SEQ ID NO: 2074
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YQQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDASNENYADAVKG RFTISRDNSKNTLYLHMNSLRAADTAVYYCARDG TIFGVVLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK

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

			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 GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGAACGGTGGCT GCACCATCTGTCTTCATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG CGGACACGGCTGTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC

CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAGCAGACTACGAGAAAAC 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
AA	SEQ ID NO: 1919 DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YHQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC	SEQ ID NO: 2076 QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDASNENYADAVKG RFTISRDNSKNTLYLQMNSLRAADTAVYYCARDG TIFGVVLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED

			PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
iPS:361021	18F2.009	NA	SEQ ID NO: 349 GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCAACAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGAACGGTGGCT GCACCATCTGTCTTCATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT	SEQ ID NO: 506 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 GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT CCTCACCGTCCTGCACCAGGACTGGCTGAATGG

			CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
			CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
			AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
			ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
			AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
			GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
			AGAGCAATGGGCAGCCGGAGAACAACTACAAG
			ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
			TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
			AGCAGGTGGCAGCAGGGAACGTCTTCTCATGC
			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
	NA	SEQ ID NO: 350	SEQ ID NO: 507
		GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCAACAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACTATGCAGACTCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
	18F2.010		
	iPS:361028		

			ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGAACGGTGGCT GCACCATCTGTCTTCATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT	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 AGAGCAATGGGCAGCCGGAGAACAACTACAAG ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
			SEQ ID NO: 1921	SEQ ID NO: 2078
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDASNENYADSVKG

		FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC	RFTISRDNSKNTLYLQMNSLRAADTAVYYCARDG TIFGVVLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
		SEQ ID NO: 351	SEQ ID NO: 508
iPS:360535	18F2.011	NA	
		GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCAACAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATATAATTAATTACCCCTTCACTTTCGGCCAA GGGACCAAAGTGGATATCAAACGAACGGTGGCT GCACCATCTGTCTTCATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATA GGACGATCTTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCCACC GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC

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

	SEQ ID NO: 352			SEQ ID NO: 509	
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	GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG			GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA	
	GCTGGTATCAACAGAAACCAGGGAAAGCCCCTA			TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC	
	AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA			TGGAGTGGGTGGCAGTTATATGGTATGATGCAA	
	GTGGGGTCCCTTCAGGTTCAGCGGCAGTGGAT			GTAATGAAAACTATGCAGACGCCGTGAAGGGCC	
	CTGGGACAGAATTCACTCTCACAATCAGCAGCC			GATTCACCATCTCCAGAGACAATTCCAAGAACA	
	TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT			CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG	
	ACAGCATAATAATTACCCCTTCACTTTCGGCCCT			AGGACACGGCTGTGTATTACTGTGCGAGAGATG	
	GGGACCAAAGTGGATATCAAACGAACGGTGGCT			GGACGATCTTTGGAGTGGTCTTGGGGGACTACT	
	GCACCATCTGTCTTCATCTTCCCGCCATCTGATG			GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG	
	AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT			CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC	
	GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA			ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC	
	AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT			GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC	
	CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG			CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC	
	ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA			CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT	
	CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC			CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC	
NA	ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG			GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC	
	GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA			CAGACCTACATCTGCAACGTGAATCACAAGCCC	
	GGGGAGAGTGT			AGCAACACCAAGGTGGACAAGAAAGTTGAGCC	
				CAAATCTTGTGACAAAACTCACACATGCCCACC	
				GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC	
				AGTCTTCCTCTTCCCCCCAAAACCCAAGGACAC	
				CCTCATGATCTCCCGGACCCCTGAGGTCACATG	
				CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA	
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				GGTGCATAATGCCAAGACAAAGCCGCGTGTGAGGA	
				GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT	
				CCTCACCGTCCTGCACCAGGACTGGCTGAATGG	
				CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC	
				CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA	
				AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT	
				ACACCCTGCCCCCATCCCGGGAGGAGATGACCA	
				AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG	
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			AGAGCAATGGGCAGCCGGAGAACAACTACAAG
			ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
			TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
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		SEQ ID NO: 1923	SEQ ID NO: 2080
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		SEQ ID NO: 353	SEQ ID NO: 510
	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTAGCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTACGATGCATCCAATTTGGAAA CAGGGGTCCCATCAAGGTTCAGTGGAAGTGGAT CTGGGACAGATTTTAGTCTCACCATCAGCAGCC TGCAGCCTGAAGATTTTGCAACATATTACTGTCA ACAGTATGATAATCTCCTCACTTTCGGCGGAGG GACCAAGGTGGAGATCAAGCGAACGGTGGCTG CACCATCTGTCTTCATCTTCCCGCCATCTGATGA GCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGC CTGCTGAATAACTTCTATCCCAGAGAGGCCAAA GTACAGTGGAAGGTGGATAACGCCCTCCAATCG	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGTTATATGGTATGATGCA AGTAATAAATACTATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGGGACAATTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT AGGACGATTTTTGGAGTGGTTCTTGACTACTGG GGCCAGGGAACCCTGGTCACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC
		iPS:359940	2F11.002

	GGTAACTCCCAGGAGAGTGTCACAGAGCAGGAC AGCAAGGACAGCACCTACAGCCTCAGCAGCACC CTGACGCTGAGCAAAGCAGACTACGAGAAACA CAAAGTCTACGCCTGCGAAGTCACCCATCAGGG CCTGAGCTCGCCCGTCACAAAGAGCTTCAACAG GGGAGAGTGT		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: 1924	SEQ ID NO: 2081	
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			VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV
			LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
			KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP
			SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
			LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS
			LSPGK
iPS:361039	2F11.003		SEQ ID NO: 511
		NA	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG
			GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC
			ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG
			CTGGAGTGGGTGGCAGTTATATGGTATGATGCA
			AGTAATAAATACTATGCAGACGCCGTGAAGGGC
			CGATTCACCATCTCCAGCGACAATTCCAAGAAC
			ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC
			GAGGACACGGCTGTGTATTACTGTGCGAGAGAT
			AGGACGATTTTTGGAGTGGTTCTTGACTACTGG
			GGCCAGGGAACCCTGGTCACCGTCTCCTCAGCC
			TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA
			CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG
			GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC
			GAACCGGTGACGGTGTCGTGGAACTCAGGCGCC
			CTGACCAGCCGGCGTGCACACCTTCCCGGCTGTC
			CTACAGTCCTCAGGACTCTACTCCCTCAGCAGC
			GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
			CAGACCTACATCTGCAACGTGAATCACAAGCCC
			AGCAACACCAAGGTGGACAAGAAAGTTGAGCC
			CAAATCTTGTGACAAAACTCACACATGCCCACC
			GTGCCCAGCACCTGAACTCCTGGGGGGGACCGTC
			AGTCTTCCTCTTCCCCCCAAAACCCAAGGACAC
			CCTCATGATCTCCCGGACCCCTGAGGTCACATG
			CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA
			GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
			GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA
			GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT
			CCTCACCGTCCTGCACCAGGACTGGCTGAATGG

			CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
			CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
			AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
			ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
			AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
			GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
			AGAGCAATGGGCAGCCGGAGAACAACTACAAG
			ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
			TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
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			ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
		SEQ ID NO: 1925	SEQ ID NO: 2082
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		AACAGTATGATATTCTCCTCACTTTCGGCGGAG	GAGGACACGGCTGTGTATTACTGTGCGAGAGAT
		GGACCAAGGTGGAGATCAAGCGAACGGTGGCT	AGGACGATTTTTGGAGTGGTTCTTGACTACTGG
		GCACCATCTGTCTTCATCTTCCCGCCATCTGATG	GGCCAGGGAACCCCTGGTCACCGTCTCCTCAGCC
		AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT	TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA
		GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA	CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG
		AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT	GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC
		CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG	GAACCGGTGACGGTGTCGTGGAACTCAGGCGCC
		ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA	CTGACCAGCGGCGTGCACACCTTCCCGGCTGTC
		CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC	CTACAGTCCTCAGGACTCTACTCCCTCAGCAGC
		ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG	GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
		GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA	CAGACCTACATCTGCAACGTGAATCACAAGCCC
		GGGGAGAGTGT	AGCAACACCAAGGTGGACAAGAAAGTTGAGCC
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			GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
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			GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT
			CCTCACCGTCCTGCACCAGGACTGGCTGAATGG
			CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
			CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
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			AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
			GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
			AGAGCAATGGGCAGCCGGAGAACAACTACAAG
			ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
			TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
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		SEQ ID NO: 1926	SEQ ID NO: 2083
	AA	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGM
		YQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTD	HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG

			FSLTISSLQPEDIATYYCQQYDILLTFGGGTKVEIKR TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC
		SEQ ID NO: 356	SEQ ID NO: 513
iPS:361049	2F11.005	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTAGCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTACGATGCATCCAATTTGGAAA CAGGGGTCCCATCAAGGTTCAGTGGAAGTGGAT CTGGGACAGATTTTAGTTTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACATATTACTGTCA ACAGTATGATATTCTCCTCACTTTCGGCGGAGG GACCAAGGTGGAGATCAAGCGAACGGTGGCTG CACCATCTGTCTTCATCTTCCCGCCATCTGATGA GCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGC CTGCTGAATAACTTCTATCCCAGAGAGGCCAAA GTACAGTGGAAGGTGGATAACGCCCTCCAATCG GGTAACTCCCAGGAGAGTGTCACAGAGCAGGAC AGCAAGGACAGCACCTACAGCCTCAGCAGCACC CTGACGCTGAGCAAAGCAGACTACGAGAAACA CAAAGTCTACGCCTGCGAAGTCACCCATCAGGG CCTGAGCTCGCCCGTCACAAAGAGCTTCAACAG GGGAGAGTGT	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGTTATATGGTATGATGCA AGTAATAAATACTATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGGGACAATTCCAAGAAC 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: 1927	SEQ ID NO: 2084
		AA	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW YQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTD FSFTISSLQPEDFATYYCQQYDILLTFGGGTKVEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR GEC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGM HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLDYWGQGTLVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK

		SEQ ID NO: 357	SEQ ID NO: 514
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		GCCAGGCGAGTCAGGACATTAGCAACTATTTAA	GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC
		ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA	ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG
		AGCTCCTGATCTACGATGCATCCAATTTGGAAA	CTGGAGTGGGTGGCAGTTATATGGTATGATGCA
		CAGGGGTCCCATCAAGGTTCAGTGGAAGTGGAT	AGTAATAAATACTATGCAGACGCCGTGAAGGGC
		CTGGGACAGATTTTAGTCTCACCATCAGCAGCC	CGATTCACCATCTCCAGCGACAATTCCAAGAAC
		TGCAGCCTGAAGATATTGCAACATATTACTGTC	ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC
		AACAGTATGATATTCTCCTCACTTTCGGCGGAG	GAGGACACGGCTGTGTATTACTGTGCGAGAGAT
		GGACCAAGGTGGAGATCAAGCGAACGGTGGCT	AGGACGATTTTTGGAGTGGTTCTTGACTACTGG
		GCACCATCTGTCTTCATCTTCCCGCCATCTGATG	GGCCAGGGAACCCTGGTCACCGTCTCCTCAGCC
		AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT	TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA
		GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA	CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG
		AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT	GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC
		CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG	GAACCGGTGACGGTGTCGTGGAACTCAGGCGCC
		ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA	CTGACCAGCGGCGTGCACACCTTCCCGGCTGTC
		CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC	CTACAGTCCTCAGGACTCTACTCCCTCAGCAGC
		ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG	GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
		GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA	CAGACCTACATCTGCAACGTGAATCACAAGCCC
		GGGGAGAGTGT	AGCAACACCAAGGTGGACAAGAAAGTTGAGCC
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			GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC
			AGTCTTCCTCTTCCCCCCAAAACCCAAGGACAC
			CCTCATGATCTCCCGGACCCCTGAGGTCACATG
			CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA
			GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
			GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA
			GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT
			CCTCACCGTCCTGCACCAGGACTGGCTGAATGG
			CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
			CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
			AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
			ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
			AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
			GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG

			AGAGCAATGGGCAGCCGGAGAACAACTACAAG
			ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
			TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
			AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
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		SEQ ID NO: 1928	SEQ ID NO: 2085
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		SEQ ID NO: 358	SEQ ID NO: 515
	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTAGCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTACGATGCATCCAATTTGGAAA CAGGGGTCCCATCAAGGTTCAGTGGAAGTGGAT CTGGGACAGATTTTAGTTTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACATATTACTGTCA ACAGTATGATAATCTCCTCACTTTCGGCGGAGG GACCAAGGTGGAGATCAAGCGAACGGTGGCTG CACCATCTGTCTTCATCTTCCCGCCATCTGATGA GCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGC CTGCTGAATAACTTCTATCCCAGAGAGGCCAAA GTACAGTGGAAGGTGGATAACGCCCTCCAATCG	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGTTATATGGTATGATGCA AGTAATAAATACTATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGCGACAATTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT AGGACGATTTTTGGAGTGGTTCTTGACTACTGG GGCCAGGGAACCCTGGTCACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC
		iPS:361059	
		2F11.007	

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

			CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
			CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
			AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
			ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
			AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
			GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
			AGAGCAATGGGCAGCCGGAGAACAACTACAAG
			ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
			TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
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		FSFTISSLQPEDIATYYCQQYDILLTFGGGTKVEIKR	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR
		TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA	TIFGVVLDYWGQGTLVTVSSASTKGPSVFPLAPSS
		KVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST	KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG
		LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG	VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV
		EC	NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG
			GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
			VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV
			LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
			KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP
			SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
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			LSPGK
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		GCCAGGCGAGTCAGGACATTAGCAACTATTTAA	GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC
		ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA	ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG
		AGCTCCTGATCTACGATGCATCCAATTTGGAAA	CTGGAGTGGGTGGCAGTTATATGGTATGATGCA
		CAGGGGTCCCATCAAGGTTCAGTGGAAGTGGAT	AGTAATAAATACTATGCAGACTCCGTGAAGGGC
		CTGGGACAGATTTTAGTCTCACCATCAGCAGCC	CGATTCACCATCTCCAGGGACAATTCCAAGAAC
		TGCAGCCTGAAGATTTTGCAACATATTACTGTCA	ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC

		ACAGTATGATATTCTCCTCACTTTCGGCGGAGG	GAGGACACGGCTGTGTATTACTGTGCGAGAGAT
		GACCAAGGTGGAGATCAAGCGAACGGTGGCTG	AGGACGATTTTTGGAGTGGTTCTTGACTACTGG
		CACCATCTGTCTTCATCTTCCCGCCATCTGATGA	GGCCAGGGAACCCTGGTCACCGTCTCCTCAGCC
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		CTGCTGAATAACTTCTATCCCAGAGAGGCCAAA	CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG
		GTACAGTGGAAGGTGGATAACGCCCTCCAATCG	GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC
		GGTAACTCCCAGGAGAGTGTCACAGAGCAGGAC	GAACCGGTGACGGTGTCGTGGAACTCAGGCGCC
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		CTGACGCTGAGCAAAGCAGACTACGAAAACA	CTACAGTCCTCAGGACTCTACTCCCTCAGCAGC
		CAAAGTCTACGCCTGCGAAGTCACCCATCAGGG	GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
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			CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
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			TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
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		SEQ ID NO: 1931	SEQ ID NO: 2088
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		FSLITSSLQPEDFATYYCQQYDILLTFGGGTKVEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR GEC	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLDYWGQGTLVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
		SEQ ID NO: 361	SEQ ID NO: 518
iPS:359956	2F11.010	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTAGCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTACGATGCATCCAATTTGGAAA CAGGGGTCCCATCAAGGTTCAGTGGAAGTGGAT CTGGGACAGATTTTAGTCTCACCATCAGCAGCC TGCAGCCTGAAGATTTTGCAACATATTACTGTCA ACAGTATGATATTCTCCTCACTTTCGGCGGAGG GACCAAGGTGGAGATCAAGCGAACGGTGGCTG CACCATCTGTCTTCATCTTCCCGCCATCTGATGA GCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGC CTGCTGAATAACTTCTATCCCAGAGAGGCCAAA GTACAGTGGAAGGTGGATAACGCCCTCCAATCG GGTAACTCCCAGGAGAGTGTCACAGAGCAGGAC AGCAAGGACAGCACCTACAGCCTCAGCAGCACC CTGACGCTGAGCAAAGCAGACTACGAGAAACA CAAAGTCTACGCCTGCGAAGTCACCCATCAGGG CCTGAGCTCGCCCGTCACAAAGAGCTTCAACAG GGGAGAGTGT
			CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGTTATATGGTATGATGGA AGTAATAAATACTATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGGGACAATTCCAAGAAC 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: 1932	SEQ ID NO: 2089
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		GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA	TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC
		AGCGCCTGATCTATGGTGCATCCAGTTTGCAAA	TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
		GTGGGGTCCCTTCAGGTTCAGCGGCAGTGGAT	GTAATAAATACTATGCAGACGCCGTGAAGGGCC
		CTGGGACAGAAATTCACTCTCACAATCAGCAGCC	GCTTCACCATCTCCAGAGACAATTCCAAGAACA
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		ACAGCATAATAATTACCCCTTCACTTTCGGCCCT	AGGACACGGCTGTGTATTACTGTGCGCGAGATG
		GGGACCAAAGTGGATATCAAACGAACGGTGGCT	GGACGATTTTTGGAGTGCTCTTGGGGGACTACT
		GCACCATCTGTCTTCATCTTCCCGCCATCTGATG	GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
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		GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA	ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC
		AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT	GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC
		CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG	CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC
		ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA	CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT
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			GTGCCCAGCACCTGAACTCCTGGGGGGGACCGTC
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			CCTCATGATCTCCCGGACCCCTGAGGTCACATG
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			GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA
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			CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
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		SEQ ID NO: 1933	SEQ ID NO: 2090
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		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
		6HI.003	
		JPS:359869	

		CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAGCAGACTACGAGAAAAC ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT	CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC 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: 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
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			GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
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			TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC
			TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
			GTAATAAATACTATGCAGACGCCGTGAAGGGCC
			GCTTCACCATCTCCAGAGACAATTCCAAGAACA
			CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
			AGGACACGGCTGTGTATTACTGTGCGCGAGATG
			GGACGATTTTTGGAGTGCTCTTGGGGGACTACT
			GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
			CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC
			ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC
			GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC
			CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC
			CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT
			CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC
			GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
			CAGACCTACATCTGCAACGTGAATCACAAGCCC
			AGCAACACCAAGGTGGACAAGAAAGTTGAGCC
			CAAATCTTGTGACAAAACTCACACATGCCCACC
			GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC
			AGTCTTCCTCTTCCCCCCAAAACCCAAGGACAC
			CCTCATGATCTCCCGGACCCCTGAGGTCACATG
			CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA
			GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
			GGTGCATAATGCCAAGACAAAGCCGCGTGTGAGGA
			GCAGTACGGCAGCACGTACCGTGTGGTCAGCGT
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			CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
			CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
			AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
			ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
			AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
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			ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
			TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
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		SEQ ID NO: 1935	SEQ ID NO: 2092
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	NA	SEQ ID NO: 365	SEQ ID NO: 522
		GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG

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

			LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR GEC	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVLLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
		SEQ ID NO: 366	SEQ ID NO: 523
iPS:361067	6H1.006	NA		
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGAACGGTGGCT GCACCATCTGTCTTCATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT	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: 1937	SEQ ID NO: 2094
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAVIWYDGSNKYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK

iPS:361071	6HI.007	NA	SEQ ID NO: 367	SEQ ID NO: 524
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
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			GCCGGGCAAGTCAGGACATTAGAGATTATTTAG	GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA
			GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA	TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC
			AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA	TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
			GTGGGGTCCCTTCAGGTTCAGCGGCAGTGGGAT	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	CAGACCTACATCTGCAACGTGAATCACAAGCCCC
			GGGGAGAGTGT	AGCAACACCAAGGTGGACAAGAAAGTTGAGCC
				CAAATCTTGTGACAAAACTCACACATGCCCACC
				GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC
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				CCTCATGATCTCCCGGACCCCTGAGGTCACATG
				CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA
				GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
				GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA
				GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT
				CCTCACCGTCCTGCACCAGGACTGGCTGAATGG
				CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
				CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
				AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
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				AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
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			AGAGCAATGGGCAGCCGGAGAACAACTACAAG
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			TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
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			TCCGTGATGCATGAGGCTCTGCACAACCACTAC
			ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
		SEQ ID NO: 1938	SEQ ID NO: 2095
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	NA	SEQ ID NO: 368	SEQ ID NO: 525
		GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGAATTATTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGAACGGTGGCT GCACCATCTGTCTTCATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGGAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTTGGAGTGCTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC

		CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAGCAGACTACGAGAAAAC ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT	CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCCACC GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATG CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTGTGTCAGCGT CCTCACCGTCCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT ACACCCTGCCCCCATCCCGGGAGGAGATGACCA AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGAACAACTACAAG ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
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			PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV
			SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK
			AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF
			YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
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			AACTCCTGATCTACGATGCTTCCAATTTGGAGCC TGGAGTGGGTGGCAGCTATATGGTATGATGCAA
			AGGGGTCCCATCAAGGTTCAGTGGAAGTGGATC ATAATAAATACTATGCAGACGCCGTGAAGGGCC
			TGGGACAGATTTTACTCTCACCATCAGCAGCCT GATTCACCATCTCCAGAGACAGTTCCAAGAACA
			GCAGCCTGAAGATTTTGCAACATATTACTGTCA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
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			ACCAAAGTGGATATCAACGAACGGTGGCTGCA GGACGATTTTTGGAGTGGTTCCTTGAGTACTGGG
			CCATCTGTCTTCATCTTCCCGCCATCTGATGAGC GCCAGGGAACCCTGGTCACCGTCTCCTCAGCCT
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			GCTGAATAACTTCTATCCCAGAGAGGCCAAAGT CCTCCTCCAAGAGCACCTCTGGGGGCACAGCGG
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			TAACTCCCAGGAGAGTGTCACAGAGCAGGACAG AACCGGTGACGGTGTCGTGGAACTCAGGCGCCC
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			GAGAGTGT CAACACCAAGGTGGACAAGAAAGTTGAGCCCA
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			CCAAAGGGCAGCCCCGAGAACCACAGGTGTAC
			ACCCTGCCCCCATCCCGGGAGGAGATGACCAAG
			AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC
			TTCTATCCCAGCGACATCGCCGTGGAGTGGGAG
			AGCAATGGGCAGCCGGAGAACAACTACAAGAC
			CACGCCTCCCGTGCTGGACTCCGACGGCTCCTTC
			TTCCTCTATAGCAAGCTCACCGTGGACAAGAGC
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		FTLTISSLQPEDFATYYCQQYDDLFTFGPGTKVDIK	RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR
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		AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS	KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG
		TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR	VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV
		GEC	NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG
			GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
			VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV
			LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
			KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP
			SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
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			LSPGK
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		AACTCCTGATCTACGATGCTTCCAATTTGGAGCC	TGGAGTGGGTGGCAGCTATATGGTATGATGCAA
		AGGGGTCCCATCAAGGTTCAGTGGAAGTGGATC	ATAATAAATACTATGCAGACGCCGTGAAGGGCC
		TGGGACAGATTTTACTCTCACCATCAGCAGCCT	GATTCACCATCTCCAGAGACAGTTCCAAGAACA
		GCAGCCTGAAGATATTGCAACATATTACTGTCA	CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG

		ACAGTATGATGATCTATTCACTTTCGGCCCTGGG	AGGACACGGCTGTGTATTACTGTGCGAGAGATC
		ACCAAAGTGGATATCAAACGAACGGTGGCTGCA	GGACGATTTTTGGAGTGGTCCTTGAGTACTGGG
		CCATCTGTCTTCATCTTCCCGCCATCTGATGAGC	GCCAGGGAACCCTGGTCACCGTCTCCTCAGCCT
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		GCTGAATAACTTCTATCCCAGAGAGGCCAAAGT	CCTCCTCCAAGAGCACCTCTGGGGGCACAGCGG
		ACAGTGGAAGGTGGATAACGCCCTCCAATCGGG	CCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG
		TAACTCCCAGGAGAGTGTCACAGAGCAGGACAG	AACCGGTGACGGTGTCGTGGAACTCAGGCGCCC
		CAAGGACAGCACCTACAGCCTCAGCAGCACCCT	TGACCAGCGGCGTGCACACCTTCCCCGGCTGTCC
		GACGCTGAGCAAAGCAGACTACGAGAAACACA	TACAGTCCTCAGGACTCTACTCCCTCAGCAGCGT
		AAGTCTACGCCTGCGAAGTCACCCATCAGGGCC	GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCA
		TGAGCTCGCCCGTCACAAAGAGCTTCAACAGGG	GACCTACATCTGCAACGTGAATCACAAGCCCAG
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			NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG
			GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
			VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV
			LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
			KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP
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			LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS
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		AACTCCTGATCTACGATGCTTCCAATTTGGAGCC	TGGAGTGGGTGGCAGCTATATGGTATGATGCAA
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		CAAGGACAGCACCTACAGCCTCAGCAGCACCCT	TGACCAGCGGCGTGCACACCTTCCCGGCTGTCC
		GACGCTGAGCAAAGCAGACTACGAGAAACACA	TACAGTCCTCAGGACTCTACTCCCTCAGCAGCGT
		AAGTCTACGCCTGCGAAGTCACCCATCAGGGCC	GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCA
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				CATGATCTCCCGGACCCCTGAGGTCACATGCGT GGTGGTGGACGTGAGCCACGAAGACCCTGAGGT CAAGTTCAACTGGTACGTGGACGGCGTGGAGGT GCATAATGCCAAGACAAAGCCGTGTGAGGAGC AGTACGGCAGCACGTACCGTTGTGTCAGCGTCC TCACCGTCCTGCACCAGGACTGGCTGAATGGCA AGGAGTACAAGTGCAAGGTCTCCAACAAAGCCC TCCCAGCCCCCATCGAGAAAACCATCTCCAAAG CCAAAGGGCAGCCCCGAGAACCACAGGTGTAC ACCCTGCCCCCATCCCGGGAGGAGATGACCAAG AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC TTCTATCCCAGCGACATCGCCGTGGAGTGGGAG AGCAATGGGCAGCCGGAGAACAACTACAAGAC CACGCCTCCCGTGCTGGACTCCGACGGCTCCTTC TTCCTCTATAGCAAGCTCACCGTGGACAAGAGC AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC GTGATGCATGAGGCTCTGCACAACCACTACACG CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
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		GACGCTGAGCAAAGCAGACTACGAGAAACACA	TACAGTCCTCAGGACTCTACTCCCTCAGCAGCGT
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		iPS.361101	

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	AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS		STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV

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		SEQ ID NO: 374	SEQ ID NO: 531
iPS:36110 5	6AS.004.006	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTACGATGCTTCCAATTTGGAGCC AGGGGTCCCATCAAGGTTCAGTGGAAGTGGATC TGGGACAGATTTTACTTTCACCATCAGCAGCCTG CAGCCTGAAGATTTTGCAACATATTACTGTCAA CAGTATGATGATCTATTCACTTTCGGCCCTGGGA CCAAAGTGGATATCAAACGAACGGTGGCTGCAC CATCTGTCTTCATCTTCCCGCCATCTGATGAGCA GTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTG CTGAATAACTTCTATCCCAGAGAGGCCAAAGTA CAGTGGAAGGTGGATAACGCCCTCCAATCGGGT AACTCCCAGGAGAGTGTCACAGAGCAGGACAG CAAGGACAGCACCTACAGCCTCAGCAGCACCCT GACGCTGAGCAAAGCAGACTACGAGAAACACA AAGTCTACGCCTGCGAAGTCACCCATCAGGGCC TGAGCTCGCCCGTCACAAAGAGCTTCAACAGGG GAGAGTGT	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

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6AS.004.00 7			

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		GEC	NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG
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	NA	SEQ ID NO: 378	SEQ ID NO: 535
		GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTACGATGCTTCCAATTTGGAGCC AGGGGTCCCATCAAGGTTCAGTGGAAGTGGATC TGGGACAGATTTTACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACATATTACTGTCA ACAGTATGATGATCTATTCACTTTCGGCCAAGG GACCAAAGTGGATATCAAACGAACGGTGGCTGC ACCATCTGTCTTCATCTTCCCGCCATCTGATGAG CAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCC TGCTGAATAACTTCTATCCCAGAGAGGCCAAAG TACAGTGGAAGGTGGATAACGCCCTCCAATCGG	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCTCCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGCCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGCTATATGGTATGATGCAA ATAATAAATACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATC GGACGATTTTTGGAGTGGTCCTTGAGTACTGGG GCCAGGGAACCCTGGTCACCGTCTCCTCAGCCT CCACCAAGGGCCCATCGGTCTTCCCCCTGGCAC CCTCCTCCAAGAGCACCTCTGGGGGCACAGCGG CCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG

	GTAACTCCCAGGAGAGTGTCACAGAGCAGGACA	AACCGGTGACGGTGTCGTGGAACTCAGGCGCCC
	GCAAGGACAGCACCTACAGCCTCAGCAGCACCC	TGACCAGCGGCGTGCACACCTTCCCGGCTGTCC
	TGACGCTGAGCAAAGCAGACTACGAGAAACAC	TACAGTCCTCAGGACTCTACTCCCTCAGCAGCGT
	AAAGTCTACGCCTGCGAAGTCACCCATCAGGGC	GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCA
	CTGAGCTCGCCCGTCACAAAGAGCTTCAACAGG	GACCTACATCTGCAACGTGAATCACAAGCCCAG
	GGAGAGTGT	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: 1949	SEQ ID NO: 2106
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	YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGSGTD	HWVRQPPGKGLEWVAAIWYDANNKYYADAVKG
	FTLTISSLQPEDFATYYCQQYDDLFTFGQGTKVDI	RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR
	KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR	TIFGVVLEYWGQGTLVTVSSASTKGPSVFPLAPSS
	EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS	KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG
	STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN	VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV
	RGEC	NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG
		GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE

		SEQ ID NO: 379	SEQ ID NO: 536
iPS:359890	6A5.004.011	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTACGATGCTTCCAATTTGGAGCC AGGGGTCCCATCAAGGTTCAGTGGAAGTGGATC TGGGACAGATTTTACTCTCACCATCAGCCT GCAGCCTGAAGATTTTGCAACATATTACTGTCA ACAGTATGATGATCTATTCACTTTCGGCCAAGG GACCAAAGTGGATATCAAACGAACGGTGGCTGC ACCATCTGTCTTCATCTTCCCGCCATCTGATGAG CAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCC TGCTGAATAACTTCTATCCCAGAGAGGCCAAAG TACAGTGGAAGGTGGATAACGCCCTCCAATCGG GTAACTCCCAGGAGAGTGTCACAGAGCAGGACA GCAAGGACAGCACCTACAGCCTCAGCAGCACCC TGACGCTGAGCAAAGCAGACTACGAGAAACAC AAAGTCTACGCCTGCGAAGTCACCCATCAGGGC CTGAGCTCGCCCGTCACAAAGAGCTTCAACAGG GGAGAGTGT	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 GCATAATGCCAAGACAAAGCCGTGTGAGGAGC AGTACGGCAGCACGTACCGTTGTGTCAGCGTCC TCACCGTCCTGCACCAGGACTGGCTGAATGGCA

VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP
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LSPGK

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			TCCCAGCCCCCATCGAGAAAACCATCTCCAAAG
			CCAAAGGGCAGCCCCGAGAACCACAGGTGTAC
			ACCCTGCCCCCATCCCGGGAGGAGATGACCAAG
			AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC
			TTCTATCCCAGCGACATCGCCGTGGAGTGGGAG
			AGCAATGGGCAGCCGGAGAACAACTACAAGAC
			CACGCCTCCCGTGCTGGACTCCGACGGCTCCTTC
			TTCCTCTATAGCAAGCTCACCGTGGACAAGAGC
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	AA	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM
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		FTLTISSLQPEDFATYYCQQYDDLFTFGQGTKVDI	RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR
		KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR	TIFGVVLEYLGQGTLVTVSSASTKGPSVFPLAPSSK
		EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS	STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV
		STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN	HTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
		RGEC	HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP
			SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
			KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVL
			TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
			GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS
			DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL
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			SPGK
	NA	SEQ ID NO: 380	SEQ ID NO: 537
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		GCAGGGCCAGTCAGATTTTTACCAGCACCTACT	GCAGCGTCTGGATTCAGTTTCAGTAGCTATGGC
		TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC	ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGA
		CCAGGCTCCTCATCTATGGTGCATCCAGCAGGG	CTGGAGTGGGTGGCAGTTATATGGTATGATGCA
		CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG	AGTAATAAATACTATGCAGACGCCGTGAAGGGC
		GGTCTGGGACAGACTTCACTCTCACCATCAGCA	CGATTCACCATCTCCAGAGACAATTCCAAGAAC
		GATTGGAGCCTGAAGATTTTGCAGTGTATTACT	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
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			GCCCAGCACCTGAACTCCTGGGGGGGACCGTCAG
			TCTTCCTCTTCCCCCCAAAACCCAAGGACACCCT
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			CAAGTTCAACTGGTACGTGGACGGCGTGGAGGT
			GCATAATGCCAAGACAAAGCCGTGTGTGAGGAGC
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			AGCAATGGGCAGCCGGAGAACAACTACAAGAC
			CACGCCTCCCCGTGCTGGACTCCGACGGCTCCTTC
			TTCCTCTATAGCAAGCTCACCGTGGACAAGAGC
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	SEQ ID NO: 1951		SEQ ID NO: 2108
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	YQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF		HWVRQAPGKGLEWVAVIWYDASNKYYEDAVKG

			TLTISRLEPEDFAVYYCQQYGSSPRFGQGTRLEIKR TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC	RFTISRDNSKNTLFLQVNSLRAEDTAVYYCARGITI FGHGFEYWGQGTLVTVSSASTKGPSVFPLAPSSKS TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP GK
iPS:333965	2A11.003	NA	SEQ ID NO: 381	SEQ ID NO: 538
			GAAATTGTGTTGACGCAGTCTCCAGGCACCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT GCAGGGCCAGTCAGATTTTTACCAGCACCTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCAGGCTCCTCATCTATGGTGCATCCAGCAGGG CCACTGGCATCCCCAGACAGGTTCAGTGGCAGTG 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

				CATGATCTCCCGGACCCCTGAGGTCACATGCGT GGTGGTGGACGTGAGCCACGAAGACCCTGAGGT CAAGTTCAACTGGTACGTGGACGGCGTGGAGGT GCATAATGCCAAGACAAAGCCGTGTGAGGAGC AGTACGGCAGCACGTACCGTTGTGTCAGCGTCC TCACCGTCCTGCACCAGGACTGGCTGAATGGCA AGGAGTACAAGTGCAAGGTCTCCAACAAAGCCC TCCCAGCCCCCATCGAGAAAACCATCTCCAAAG CCAAAGGGCAGCCCCGAGAACCACAGGTGTAC ACCCTGCCCCCATCCCGGGAGGAGATGACCAAG AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC TTCTATCCCAGCGACATCGCCGTGGAGTGGGAG AGCAATGGGCAGCCGGAGAACAACTACAAGAC CACGCCTCCCGTGCTGGACTCCGACGGCTCCTTC TTCCTCTATAGCAAGCTCACCGTGGACAAGAGC AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC GTGATGCATGAGGCTCTGCACAACCACTACACG CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
			SEQ ID NO: 1952	SEQ ID NO: 2109
		AA	EIVLTQSPGTLSLSPGERATLSCRASQIFTSTYLAW YQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF TLTISRLEPEDFAVYYCQQYGSSPRFGQGTRLEIKR TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQAPGKGLEWVAVIWYDGSNKYYEDSVKG RFTISRDNSKNTLFLQVNSLRAEDTAVYYCARGITI FGHGFEYWGQGTLVTVSSASTKGPSVFPLAPSSKS TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP GK

		SEQ ID NO: 382	SEQ ID NO: 539
iPS:361158	2A11.004	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTG	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
		TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT	GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
		GCAGGGCCAGTCAGATTTTTACCAGCACCTACT	GCAGCGTCTGGATTCAGTTTCAGTAGCTATGGC
		TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC	ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGA
		CCAGGCTCCTCATCTATGGTGCATCCAGCAGGG	CTGGAGTGGGTGGCAGTTATATGGTATGATGGA
		CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG	AGTAATAAATACTATGCAGACGCCGTGAAGGGC
		GGTCTGGGACAGACTTCACTCTCACCATCAGCA	CGATTCACCATCTCCAGAGACAATTCCAAGAAC
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		AAGGGACACGACTGGAGATTAAACGAACGGTG	ATTACGATTTTTGGTCATGGGTTTGAATATTGGG
		GCTGCACCATCTGTCTTCATCTTCCCGCCATCTG	GCCAGGGAACCCTGGTCACCGTCTCCTCAGCCT
		ATGAGCAGTTGAAATCTGGAACTGCCTCTGTTG	CCACCAAGGGCCCATCGGTCTTCCCCCTGGCAC
		TGTGCCTGCTGAATAACTTCTATCCCAGAGAGG	CCTCCTCCAAGAGCACCTCTGGGGGCACAGCGG
		CCAAAGTACAGTGGAAGGTGGATAACGCCCTCC	CCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG
		AATCGGGTAACTCCCAGGAGAGTGTCACAGAGC	AACCGGTGACGGTGTCGTGGAACTCAGGCGCCC
		AGGACAGCAAGGACAGCACCTACAGCCTCAGC	TGACCAGCGGCGTGCACACCTTCCCGGCTGTCC
		AGCACCCTGACGCTGAGCAAAGCAGACTACGAG	TACAGTCCTCAGGACTCTACTCCCTCAGCAGCGT
		AAACACAAAGTCTACGCCTGCGAAGTCACCCAT	GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCA
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		AACAGGGGAGAGTGT	CAACACCAAGGTGGACAAGAAAGTTGAGCCCA
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			GCCCAGCACCTGAACTCCTGGGGGGACCGTCAG
			TCTTCCTCTTCCCCCAAAACCCAAGGACACCCT
			CATGATCTCCCGGACCCCTGAGGTCACATGCGT
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			CAAGTTCAACTGGTACGTGGACGGCGTGGAGGT
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			TCCCAGCCCCCATCGAGAAAACCATCTCCAAAG
			CCAAAGGGCAGCCCCGAGAACCACAGGTGTAC
			ACCCTGCCCCCATCCCGGGAGGATGACCAAG
			AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC
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			CACGCCTCCCGTGCTGGACTCCGACGGCTCCTTC
			TTCCTCTATAGCAAGCTCACCGTGGACAAGAGC
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		SEQ ID NO: 1953	SEQ ID NO: 2110
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		YQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF	HWVRQAPGKGLEWVAVIWYDGSNKYYEDAVKG
		TLTISRLEPEDFAVYYCQQYGSSPRFGQGTRLEIKR	RFTISRDNSKNTLFLQVNSLRAEDTAVYYCARGITI
		TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA	FGHGFEYWGQGTLVTVSSASTKGPSVFPLAPSSKS
		KVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST	TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH
		LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG	TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH
		EC	KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPS
			VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK
			FNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLT
			VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
			QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSD
			IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT
			VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
			GK
		SEQ ID NO: 383	SEQ ID NO: 540
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		GCAGGGCCAGTCAGATTTTTACCAGCACCTACT	GCAGCGTCTGGATTCAGTTTCAGTAGCTATGGC
		TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC	ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGA
		CCAGGCTCCTCATCTATGGTGCATCCAGCAGGG	CTGGAGTGGGTGGCAGTTATATGGTATGATGCA
		CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG	AGTAATAAATACTATGCAGACTCCGTGAAGGGC
		GGTCTGGGACAGACTTCACTCTCACCATCAGCA	CGATTCACCATCTCCAGAGACAATTCCAAGAAC
		GATTGGAGCCTGAAGATTTTGCAGTGTATTACT	ACGCTGTTTCTGCAAGTGAACAGCCTGAGAGCC
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	SEQ ID NO: 1964	SEQ ID NO: 2121
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	YQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF	WSWIRQPPGKGLEWIGYIYYSGSTYYNPSLKSRVT
	TLTISRQEPDDFAVYYCQQYGSSPLTFGGGTKVEI	ISVDTSKNQFSLKLSSVTAADTAVYYCARDRITIFG
	KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR	VVMGGGMDVWGQGTTVTVSSASTKGPSVFPLAP
	EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS	SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS
		GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN

iPS:359628			
18E3.004			
NA	STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC	SEQ ID NO: 394	VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
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		GAAATTGTGTTGACGCAGTCTCCAGGCACCCTG	CAGGTGCAGTTGCAGGAGTCGGGCCCAGGACTG
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		GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT	ACTGTCTCTGGTGACTCCATCAGCAGTGGTGGTT
		TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC	ACTACTGGAGCTGGATCCGCCAGCCCCCAGGGA
		CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG	AGGGCCTGGAGTGGATTGGGTACATCTATTACA
		CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG	GTGGGAGCACCTACTACAACCCGTCCCTCAAGA
		GGTCTGGGACAGACTTCACTCTCACCATCAGCA	GTCGAGTTACCATATCAGTAGACACGTCTAAGA
		GACTGGAGCCTGATGATTTTGCAGTGTATTACTG	ACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC
		TCAGCAGTATGGTAGTTCACCGCTCACTTTCGGC	CGCGGACACGGCCGTGTATTACTGTGCGAGAGA
		GGAGGGACCAAGGTGGAGATCAAACGAACGGT	TCGTATTACGATTTTTGGAGTGGTTATGGGGGGC
		GGCTGCACCATCTGTCTTCATCTTCCCGCCATCT	GGTATGGACGTCTGGGGCCAAGGGACCACGGTC
		GATGAGCAGTTGAAATCTGGAACTGCCTCTGTT	ACCGTCTCCTCAGCCTCCACCAAGGGCCCATCG
		GTGTGCCTGCTGAATAACTTCTATCCCAGAGAG	GTCTTCCCCCCTGGCACCCTCCTCCAAGAGCACCT
		GCCAAAGTACAGTGGAAGGTGGATAACGCCCTC	CTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCA
		CAATCGGGTAACTCCCAGGAGAGTGTCACAGAG	AGGACTACTTCCCCGAACCGGTGACGGTGTCGT
		CAGGACAGCAAGGACAGCACCTACAGCCTCAGC	GGAACTCAGGCGCCCTGACCAGCGGCGTGCACA
		AGCACCCTGACGCTGAGCAAAGCAGACTACGAG	CCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTA
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			AGAACAACTACAAGACCACGCCTCCCGTGCTGG
			ACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCT
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			CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG	GTGGGAGCACCTACTACAACCCGTCCCTCAAGA
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			GACTGGAGCCTGATGATTTTGCAGTGTATTACTG	ACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC
			TCAGCAGTATGGTAGTTCACCGCTCACTTTCGGC	CGCGGACACGGCCGTGTATTACTGTGCGAGAGA
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			CAATCGGGTAACTCCCAGGAGAGTGTCACAGAG	AGGACTACTTCCCCCGAACCGGTGACGGTGTCGT
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			AGCACCCTGACGCTGAGCAAAGCAGACTACGAG	CCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTA
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			CAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTC	CAGCTTGGGCACCCAGACCTACATCTGCAACGT
			AACAGGGGAGAGTGT	GAATCACAAGGACACCCTCATGATCTCCCGGACCCC
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				AGAACAACTACAAGACCACGCCTCCCGTGCTGG
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		SEQ ID NO: 396	SEQ ID NO: 553
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			YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
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		GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT	ACTGTCTCTGGTGACTCCATCAGCAGTGGTGGTT
		TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC	ACTACTGGAGCTGGATCCGCCAGCACCCAGGGA
		CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG	AGGGCCTGGAGTGGATTGGGTACATCTATTACA
		CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG	GTGGGAGCACCTACTACAACCCGTCCCTCAAGA
		GGTCTGGGACAGACTTCACTCTCACCATCAGCA	GTCGAGTTACCATATCAGTAGACACGTCTAAGA
		GACAGGAGCCTGATGATTTTGCAGTGTATTACT	ACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC
		GTCAGCAGTATGGTAGTTCACCGCTCACTTTCGG	CGCGGACACGGCCGTGTATTACTGTGCGAGAGA
		CGGAGGGACCAAGGTGGAGATCAAACGAACGG	TCGTATTACGATTTTTGGAGTGGTTATGGGGGGC
		TGGCTGCACCATCTGTCTTCATCTTCCCGCCATC	GGTATGGACGTCTGGGGCCAAGGGACCACGGTC
		TGATGAGCAGTTGAAATCTGGAACTGCCTCTGT	ACCGTCTCCTCAGCCTCCACCAAGGGCCCATCG
		TGTGTGCCTGCTGAATAACTTCTATCCCAGAGA	GTCTTCCCCCCTGGCACCCTCCTCCAAGAGCACCT
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		CCAATCGGGTAACTCCCAGGAGAGTGTCACAGA	AGGACTACTTCCCCGAACCGGTGACGGTGTCGT
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		GATTCAGTGGCAGCGGGTCTGGGACAGATTTCA	AGGGTCACCATGACCAGGGACACGTCCATCAGC
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		AATCAAACGAACGGTGGCTGCACCATCTGTCTT	ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
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		GGAACTGCCTCTGTTGTGTGCCTGCTGAATAACT	CCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGG
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		AGAGTGTCACAGAGCAGGACAGCAAGGACAGC	AGGCGCCCTGACCAGCGGCGTGCACACCTTCCC
		ACCTACAGCCTCAGCAGCACCCTGACGCTGAGC	GGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC
		AAAGCAGACTACGAGAAAACACAAAGTCTACGC	AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG
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		CGTCACAAAGAGCTTCAACAGGGGAGAGTGT	AAGCCCAGCAACACCAAGGTGGACAAGAAAGT
			TGAGCCCAAATCTTGTGACAAAACTCACACATG
			CCCACCCGTGCCCAGCACCTGAACTCCTGGGGGG
			ACCGTCAGTCTTCCTCTTCCCCCAAAACCCAAG
			GACACCCTCATGATCTCCCGGACCCCTGAGGTC

				ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC AGCGTCCTCACCGTCCTGCACCAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCCAGCCCCCATCGAGAAAACCATC TCCAAAGCCAAAGGGCAGCCCCGAGAACCACA GGTGTACACCCTGCCCCCATCCCGGGAGGAGAT GACCAAGAACCAGGTCAGCCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGCAGCCGGAGAACAACT ACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG TAAA
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			CAACCAGGACATCCTCCTAAGCTGCTCATTTACT	CTTGAGTGGATGGGGGTGGATCAACCCTGAAAGT
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		NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK	SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS
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		VTKSFNRGEC	VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL
			GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED
			PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV
			SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK
			AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF
			YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
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		TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC	AAGGCTTCTGGATACACCTTCACCGGCTACTAT
		AACAATAAGAACTACATAGCTTGGTACCAGCAG	ATCCACTGGGTGCGACAGGCCCCTGGACAAGGG
		CAACCAGGACATCCTCCTAAGCTGCTCATTTACT	CTTGAGTGGATGGGGTGGATCAACCCTGACGCT
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		TCCGTGGACGTTCGGCCAAGGGACCAAGGTGGA	GCCACGATTTTTGGAATGGTTATTGTACCGTTTG
		AATCAAACGAACGGTGGCTGCACCATCTGTCTT	ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
		CATCTTCCCGCCATCTGATGAGCAGTTGAAATCT	CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC
		GGAACTGCCTCTGTTGTGTGCCTGCTGAATAACT	CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGG
		TCTATCCCAGAGAGGCCAAAGTACAGTGGAAGG	CACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA

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AA	SEQ ID NO: 1972 DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK NYLAWYQQQPGHPPKLLIYWASTRESGVPDRFSGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC	SEQ ID NO: 2129 QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWINPDAGGTDYSQRFQG RVTMTRDTSISTAYMELNRLRSDDTAVYYCAREA TIFGMVIVPFDYWGQGTLVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL

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		KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG
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	AACAATAAGAACTACATAGCTTGGTACCAGCAG	ATCCACTGGGTGCGACAGGCCCCTGGACAAGGG
	CAACCAGGACATCCTCCTAAGCTGCTCATTTACT	CTTGAGTGGATGGGGGTGGATCAACCCTGACGCT
	GGGCATCTACCCGGGAATCCGGGGTCCCTGACC	GGTGGCACAGACTATTCACAGAGGTTTCAGGGC
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	CATCTTCCCGCCATCTGATGAGCAGTTGAAATCT	CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC
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			CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG	ACAGCCTACATGGAACTGAACAGGCTGAGATCT
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		SEQ ID NO: 1975	SEQ ID NO: 2132
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		NYIAWYQQQPGHPPKLLIYWASTRESGVPDRFSGS	HWVRQAPGQGLEWMGWINPDSGGTDYSQRFQGR
		GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ	FTMTRDTSISTAYMELNRLRSDDTAVYYCAREATI
		GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL	FGMVIVPFDYWGQGTLVTVSSASTKGPSVFPLAPS
		NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK	SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS
		DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSP	GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN
		VTKSFNRGEC	VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL
			GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED
			PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV
			SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK
			AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF
			YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY

			SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
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			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			AACAATAAGAACTACATAGCTTGGTACCAGCAG ATCCACTGGGTGCGACAGGCCCCTGGACAAGGG
			CAACCAGGACATCCTCCTCTAAGCTGCTCATTTACT CTTGAGTGGATGGGGGTGGATCAACCCTGACAGT
			GGGCATCTACCCGGGAATCCGGGGTCCCTGACC GGTGGCACAGACTATTCACAGAGGTTTCAGGGC
			GATTCAGTGGCAGCGGGTCTGGGACAGATTTCA AGGGTCACCATGACCAGGGACACGTCCATCAGC
			CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG ACAGCCTACATGGAACTGAACAGGCTGAGATCT
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			CCCACCGTGCCCAGCACCTGAACTCCTGGGGGG
			ACCGTCAGTCTTCCTCTTCCCCCAAAACCCAAG
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			AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC
			AAAGCCCTCCCAGCCCCCATCGAGAAAACCATC
			TCCAAAGCCAAAGGGCAGCCCCGAGAACCACA
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			CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA
			GTGGGAGAGCAATGGGCAGCCGGAGAACAACT
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		NYIAWYQQQPGHPPKLLIYWASTRESGVPDRFSGS	HWVRQAPGQGLEWMGWINPDSGGTDYSQRFQGR
		GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ	VTMTRDTSISTAYMELNRLRSDDTAVYYCAREATI
		GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL	FGMVIVPFDYWGQGTLVTVSSASTKGPSVFPLAPS
		NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK	SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS
		DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSP	GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN
		VTKSFNRGEC	VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL
			GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED
			PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV
			SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK
			AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF
			YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
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		TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC	AAGGCTTCTGGATACACCTTCACCGGCTACTAT
		AACAATAAGAACTACATAGCTTGGTACCAGCAG	ATCCACTGGGTGCGACAGGCCCCTGGACAAGGG
		CAACCAGGACATCCTCCTAAGCTGCTCATTTACT	CTTGAGTGGATGGGGGTGGATCAACCCTGACGCT
		GGGCATCTACCCGGGAATCCGGGTCCCTGACC	GGTGGCACAGACTATTCACAGAGGTTTCAGGGC
		GATTCAGTGGCAGCGGGTCTGGGACAGATTTCA	AGGTTCACCATGACCAGGGACACGTCCATCAGC
		CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG	ACAGCCTACATGGAACTGAACAGGCTGAGATCT
		TGGCAGTTTTTTACTGTCAACAATATTATAGTAC	GACGACACGGCCGTGTATTACTGTGCGAGAGAG
		TCCGTGGACGTTCGGCCAAGGGACCAAGGTGGA	GCCACGATTTTTGGAATGGTTATTGTACCGTTTG
		AATCAAACGAACGGTGGCTGCACCATCTGTCTT	ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT

		CATCTTCCCGCCATCTGATGAGCAGTTGAAATCT	CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC
		GGAACTGCCTCTGTTGTGTGCCTGCTGAATAACT	CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGG
		TCTATCCCAGAGAGGCCAAAGTACAGTGGAAGG	CACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA
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		AGAGTGTCACAGAGCAGGACAGCAAGGACAGC	AGGCGCCCTGACCAGCGGCGTGCACACCTTCCC
		ACCTACAGCCTCAGCAGCACCCTGACGCTGAGC	GGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC
		AAAGCAGACTACGAGAAACACAAAGTCTACGC	AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG
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		CGTCACAAAGAGCTTCAACAGGGGAGAGTGT	AAGCCCAGCAACACCAAGGTGGACAAGAAAGT
			TGAGCCCAAATCTTGTGACAAAACTCACACATG
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			GACACCCTCATGATCTCCCGGACCCCTGAGGTC
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			CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC
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			GAGGAGCAGTACGGCAGCACGTACCGTGTGTC
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			AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC
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			GACCAAGAACCAGGTCAGCCTGACCTGCCTGGT
			CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA
			GTGGGAGAGCAATGGGCAGCCGGAGAACAACT
			ACAAGACCACGCCTCCCGTGCTGGACTCCGACG
			GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA
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		NYIAWYQQQPGHPPKLLIYWASTRESGVPDRFSGS	HWVRQAPGQGLEWMGWINPDAGGTDYSQRFQG
		GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ	RFTMTRDTSISTAYMELNRLRSDDTAVYYCAREA
		GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL	TIFGMVIVPFFDYWGQGTLVTVSSASTKGPSVFPLA

		NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC	PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK SLSLSPGK
		SEQ ID NO: 407	SEQ ID NO: 564
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			GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC
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			GTGGGAGAGCAATGGGCAGCCGGAGAACAACT
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			GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA
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		GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ	RVTMTRDTSISTAYMELNRLRSDDTAVYYCAREA
		GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL	TIFGMVIVPFDYWGQGTLVTVSSASTKGPSVFPLA
		NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK	PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT
		DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSP	SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC
		VTKSFNRGEC	NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL
	AA		LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
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			VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
			KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG
			FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL
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			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC	AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			AACAATAAGAACTACATAGCTTGGTACCAGCAG	ATCCACTGGGTGCGACAGGCCCCTGGACAAGGG
			AAACCAGGACAACCTCCTAAGCTGCTCATTTAC	CTTGAGTGGATGGGGGTGGATCAACCCTGACGCT
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			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC	AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACTCTCACCATCAGCAGCCTGCAGGCTGAAGAT	ACAGCCTACATGGAACTGAACAGCCTGAGATCT
			GTGGCAGTTTTTTTACTGTCAACAATATTATAGTA	GACGACACGGCCGTGTATTACTGTGCGAGAGAG
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG	GCCACGATTTTTGGAATGGTTATTGTACCGTTTG
			AAATCAAACGAACGGTGGCTGCACCATCTGTCT	ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC	CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC
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				GACCAAGAACCAGGTCAGCCTGACCTGCCTGGT
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			GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA
			CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC
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		GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ	RVTMTRDTSISTAYMELNSLRSDDTAVYYCAREA
		GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL	TIFGMVTVPFDYWGQGTLVTVSSASTKGPSVFPLA
		NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK	PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT
		DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSP	SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC
		VTKSFNRGEC	NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL
			LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
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			KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG
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		AAACCAGGACAACCTCCTAAGCTGCTCATTTAC	CTTGAGTGGATGGGGTGGATCAACCCTGAAAGT
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		GTGGCAGTTTTTTACTGTCAACAATATTATAGTA	GACGACACGGCCGTGTATTACTGTGCGAGAGAG
		CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG	GCCACGATTTTTGGAATGGTTATTGTACCGTTTG
		AAATCAAACGAACGGTGGCTGCACCATCTGTCT	ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
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		TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAAC	CCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGG

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		CAAAGCAGACTACGAGAAACACAAAGTCTACG	AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG
		CCTGCGAAGTCACCCATCAGGGCCTGAGCTCGC	GGCACCCAGACCTACATCTGCAACGTGAATCAC
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			GACACCCTCATGATCTCCCGGACCCCTGAGGTC
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			GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA
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	NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK		SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS
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11C1.003			
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		ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT	ACAGCCTATATGGAGCTGAGCAGACTGAGATCT
		GTGGCTGTTTATTACTGTCAGCAATATTATCGTA	GACGACACGGCCGTGTATTTCTGTGCGAGAGAG
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		AAATCAAACGAACGGTGGCTGCACCATCTGTCT	ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
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		TTCTATCCCAGAGAGGCCAAAGTACAGTGGAAG	CACAGCGGCCCTGGCTGCCTGGTCAAGGACTA
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			ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC
			CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC
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			GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC
			AGCGTCCTCACCGTCCTGCACCAGGACTGGCTG
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			GACCAAGAACCAGGTCAGCCTGACCTGCCTGGT
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			GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA
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		CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC	ACAGCCTATATGGAGCTGAGCAGACTGAGATCT
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		SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF	VTMTRDTSISTAYMELSRLRSDDTAVYFCTREATI

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	11C1.007		
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			SEQ ID NO: 416	SEQ ID NO: 573

iPS:361301	11C1.008	NA		
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			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC	AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			AACAATAAGAACTACTTAGCTTGGTACCAACAG	ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
			AAACCAGGACAGCCTCCTAACCTGCTCATTTAC	CTTGTGTGGATGGGGTGGATCAGCCCTAACAGT
			TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC	GGTGACACAAGCTATGCACAGAAGTTTCAGGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC	AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT	ACAGCCTATATGGAGCTGAGCAGACTGAGATCT
			GTGGCTGTTTATTACTGTCAGCAATATTATCGTA	GACGACACGGCCGTGTATTTCTGTGCGAGAGAG
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG	GCCACGATTTTTGGAATGCTTATTGTACCATTTG
			AAATCAAACGAACGGTGGCTGCACCATCTGTCT	ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC	CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC
			TGGAACTGCCTCTGTTGTGCCTGCTGAATAAC	CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGG
			TTCTATCCCAGAGAGGCCAAAGTACAGTGGAAG	CACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA
			GTGGATAACGCCCTCCAATCGGGTAACTCCCAG	CTTCCCCGAACCGGTGACGGTGTCGTGGAACTC
			GAGAGTGTCACAGAGCAGGACAGCAAGGACAG	AGGCGCCCTGACCAGCGGCGTGCACACCTTCCC
			CACCTACAGCCTCAGCACCCTGACGCTGAG	GGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC
			CAAAGCAGACTACGAGAAACACAAAGTCTACG	AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG
			CCTGCGAAGTCACCCATCAGGGCCTGAGCTCGC	GGCACCCAGACCTACATCTGCAACGTGAATCAC
			CCGTCACAAAGAGCTTCAACAGGGGAGAGTGT	AAGCCCAGCAACACCAAGGTGGACAAGAAAGT
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				AAAGCCCTCCCAGCCCCCATCGAGAAAACCATC
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				GGTGTACACCCTGCCCCCATCCCGGGAGGAGAT
				GACCAAGAACCAGGTCAGCCTGACCTGCCTGGT
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				GTGGGAGAGCAATGGGCAGCCGGAGAACAACT

			ACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG TAAA
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		SEQ ID NO: 417	SEQ ID NO: 574
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	CCTGCGAAGTCACCCATCAGGGCCTGAGCTCGC		GGCACCCAGACCTACATCTGCAACGTGAATCAC
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			GTGGGAGAGCAATGGGCAGCCGGAGAACAACT
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		SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF	VTMTRDTSISTAYMELSSLRSDDTAVYFCAREATI
		GQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVC	FGMLIVPFDYWGQGTLVTVSSASTKGPSVFPLAPS
		LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS	SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS
		KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSS	GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN
		PVTKSFNRGEC	VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL

			GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
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		TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC	AAGGCTTCTGGATACACCTTCACCGGCTACTAT
		AACAATAAGAACTACTTAGCTTGGTACCAACAG	ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
		AAACCAGGACAGCCTCCTAACCTGCTCATTTAC	CTTGAGTGGATGGGGGTGGATCAGCCCTAACAGT
		TGGACTTCTACCCGAGAATCCGGGTCTCCCTGAC	GGTGAAACAAGCTATGCACAGAAGTTTCAGGAC
		CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC	AGGGTCACCATGACCAGGGACACGTCCATCAGC
		ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT	ACAGCCTATATGGAGCTGAGCAGACTGAGATCT
		GTGGCTGTTTATTACTGTCAGCAATATTATCGTA	GACGACACGGCCGTGTATTTCTGTGCGAGAGAG
		CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG	GCCACGATTTTTGGAATGCTTATTGTACCATTTG
		AAATCAAACGAACGGTGGCTGCACCATCTGTCT	ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
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		TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAAC	CCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGG
		TTCTATCCCAGAGAGGCCAAAGTACAGTGGAAG	CACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA
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		CCGTCACAAAGAGCTTCAACAGGGGAGAGTGT	AAGCCCAGCAACACCAAGGTGGACAAGAAAGT
			TGAGCCCAAATCTTGTGACAAAACTCACACATG
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			GGTGTACACCCTGCCCCCATCCCGGGAGGAGAT
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			GTGGGAGAGCAATGGGCAGCCGGAGAACAACT
			ACAAGACCACGCCTCCCGTGCTGGACTCCGACG
			GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA
			CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC
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		SEQ ID NO: 419	SEQ ID NO: 576
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jPS:361312			

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		TAAA

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			GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ	VTMTRDTSISTAYMELSRLRSDDTAVYYCAREATI
			GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL	FGMVIVPFDYWGQGTLVTVSSASTKGPSVFPLAPS
			NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK	SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS
			DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSP	GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN
			VTKSFNRGEC	VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL
				GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED
				PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV
				SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK
				AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF
				YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
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			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC	AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			AACAATAAGAACTACATAGCTTGGTACCAGCAG	ATCCACTGGGTGCGACAGGCCCCTGGACAAGGA
			AAACCAGGACATCCTCCTAAGCTGCTCATTTACT	CTTGAGTGGATGGGGTGGATCAACCCTGAAAGT
			GGGCATCTACCCGGGAATCCGGGGTCCCTGACC	GGTGGCACAGACTATTCACAGAGGTTTCAGGGC
			GATTCAGTGGCAGCGGGTCTGGGACAGATTTCA	AGGTTCACCATGACCAGGGACACGTCCATCAGC
			CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG	ACAGCCTACATGGAACTGAGCAGGCTGAGATCT
			TGGCAGTTTTTTACTGTCAACAATATTATAGTAC	GACGACACGGCCGTGTATTACTGTGCGAGAGAG
			TCCGTGGACGTTCGGCCAAGGGACCAAGGTGGA	GCCACGATTTTTGGAATGGTTATTGTACCGTTTG
			AATCAAACGAACGGTGGCTGCACCATCTGTCTT	ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
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			GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA
			CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC
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		GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL	FGMVIVPFDYWGQGTLVTVSSASTKGPSVFPLAPS
		NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK	SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS
		DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSP	GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN
		VTKSFNRGEC	VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL
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			SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK
			AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF
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		GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL	FGMVTVPFDYWGQGTLVTVSSASTKGPSVFPLAPS
		NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK	SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS
		DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSP	GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN
		VTKSFNRGEC	VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL
			GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED
			PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV
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			AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF
			YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
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		AAACCAGGACAACCTCCTAAGCTGCTCATTTAC	CTTGAGTGGATGGGGGTGGATCAACCCTGAAAGT
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		CGATTCAGTGGCAGCGGGTCTGGGACAGATTTTC	AGGGTCACCATGACCAGGGACACGTCCATCAGC
		ACTCTCACCATCAGCAGCCTGCAGGCTGAAGAT	ACAGCCTACATGGAACTGAGCAGCCTGAGATCT
		GTGGCAGTTTTTTACTGTCAACAATATTATAGTA	GACGACACGGCCGTGTATTACTGTGCGAGAGAG
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	GTGGATAACGCCCTCCAATCGGGTAACTCCCAG	CTTCCCCCGAACCCGGTGACGGTGTCGTGGAACTC
	GAGAGTGTCACAGAGCAGGACAGCAAGGACAG	AGGCGCCCTGACCAGCGGCGTGCACACCTTCCC
	CACCTACAGCCTCAGCAGCACCCTGACGCTGAG	GGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC
	CAAAGCAGACTACGAGAAACACAAAGTCTACG	AGCAGCGTGGGTGACCGTGCCCTCCAGCAGCTTG
	CCTGCGAAGTCACCCATCAGGGCCTGAGCTCGC	GGCACCCAGACCTACATCTGCAACGTGAATCAC
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		TGAGCCCAAATCTTGTGACAAAACTCACACATG
		CCCACCGTGCCCAGCACCTGAACTCCTGGGGGG
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		SEQ ID NO: 423	SEQ ID NO: 580
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			AAACCAGGACAGCCTCCTAACCTGCTCATTTAC	CTTGAGTGGATGGGGTGGATAAGCCCTAACCAA
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			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC	AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT	ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT
			GTGGCTGTTTATTACTGTCAGCAATATTATCGTA	GACGACACGGCCGTGTATTACTGTGCGAGAGAG
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG	GCCACGATTTTTGGAATGCTTATTGTACCATTTG
			AAATCAAACGAACGGTGGCTGCACCATCTGTCT	ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC	CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC
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		GQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVC	TIFGMLIVPFDYWGQGTLVTVSSASTKGPSVFPLA
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		PVTKSFNRGEC	NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL
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	AAATCAAACGAACGGTGGCTGCACCATCTGTCT	ACTACTGGGGGCCAGGGAACCCTGGTCACCGTCT	
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		GTGGGAGAGCAATGGGCAGCCGGAGAACAACT	
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			GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA
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		SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF	RVTMTRDTSISTAYMELSRLRSDDTAVYYCAREA
		GQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVC	TIFGMLIVPFDYWGQGTLVTVSSASTKGPSVFPLA
		LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS	PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT
		KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSS	SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC
		PVTKSFNRGEC	NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL
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			VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
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		GQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVC	TIFGMLJVPFDYWGQGTLVTVSSASTKGPSVFPLA
		LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS	PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT
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			DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC
			VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
			KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG
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		ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT	ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT
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		SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF	RVTMTRDTSISTAYMELSRLRSDDTAVYYCTREA
		GQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVC	TIFGMLIVPFDYWGQGTLVTVSSASTKGPSVFPLA

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	12H11.009		SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC
		LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS	NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL
		KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSS	LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
		PVTKSFNRGEC	DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC
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			KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG
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		AAACCAGGACAGCCTCCTAACCTGCTCATTTAC	CTTGAGTGGATGGGGGTGGATAAGCCCTAACCAA
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iPS:361383	12H11.010	NA		
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			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC	AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			AACAATAAGAACTACTTAGCTTGGTACCAGCAG	ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
			AAACCAGGACAGCCTCCTAACCTGCTCATTTAC	CTTGAGTGGATGGGGGTGGATAAGCCCTAACAAT
			TGGACTTCTACCCGAGAATCCGGGGTCCCTGAC	GGTGACACAAACTATGCACAGAAGTTTCAGGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC	AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT	ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT
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			AAATCAAACGAACGGTGGCTGCACCATCTGTCT	ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
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				AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC
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	SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF	RVTMTRDTSISTAYMELSRLRSDDTAVYYCAREA
	GQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVC	TIFGMLIVPFDYWGQGTLVTVSSASTKGPSVFPLA
	LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS	PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT
	KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSS	SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC
	PVTKSFNRGEC	NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL

		LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
		DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC
		VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
		KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG
		FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL
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	TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC	AAGGCTTCTGGATACACCTTCACCGGCTACTAT
	AACAATAAGAACTACTTAGCTTGGTACCAGCAG	ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
	AAACCAGGACAGCCTCCTAACCTGCTCATTTAC	CTTGAGTGGATGGGGGTGGATAAGCCCTAACAAT
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	CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC	AGGGTCACCATGACCAGGGACACGTCCATCAGC
	ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT	ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT
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		SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF	RVTMTRDTSISTAYMELSSLRSDDTAVYYCAREA
		GQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVC	TIFGMLIVPFDYWGQGTLVTVSSASTKGPSVFPLA
		LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS	PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT
		KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSS	SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC
		PVTKSFNRGEC	NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL
			LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
			DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC
			VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
			KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG
			FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL

			YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK SLSLSPGK
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		CTGGAAGTAGCTCCAACATCGGAAGTCAAACTG	AAGGCTTCCGGATACACCTTCACCGGCTACTAT
		TAAACTGGTACCAGCACCTCCCAGGAACGGCCC	ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG
		CCAAACTCCTCATCTATACTAATAATCAGCGGC	CTTGAGTGGATGGGATGGATCAACCCTAACAGT
		CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA	GGTGGCACAAACTATGCACAGAAGTTTCAGGGC
		GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG	AGGGTCACCATGACCAGGGACACGTCCATCAGT
		CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG	ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT
		CAACATTCGATGAAAGCCTGAGTGGTCCGGTAT	GACGACACGGCCGTGTATTACTGTGCGAGAGGG
		TCGGCGGAGGGACCAAGCTGACCGTCCTAGGTC	GGGGATTACGTTTGGGGGACTTATCGGCCTCAC
		AGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCC	TACTACTACGGTATGGACGTCTGGGGCCAAGGG
		GCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGC	ACCACGGTCACCGTCTCCTCAGCCTCCACCAAG
		CACACTGGTGTGTCTCATAAGTGACTTCTACCCG	GGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCA
		GGAGCCGTGACAGTGGCCTGGAAGGCAGATAG	AGAGCACCTCTGGGGGCACAGCGGCCCTGGGCT
		CAGCCCCGTCAAGGCGGGAGTGGGAGACCACCAC	GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA
		ACCCTCCAAACAAAGCAACAACAAGTACGCGGC	CGGTGTCGTGGAACTCAGGCGCCCTGACCAGCG
		CAGCAGCTATCTGAGCCTGACGCCTGAGCAGTG	GCGTGCACACCTTCCCGGCTGTCCTACAGTCCTC
		GAAGTCCCACAGAAGCTACAGCTGCCAGGTCAC	AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT
		GCATGAAGGGAGCACCGTGGAGAAGACAGTGG	GCCCTCCAGCAGCTTGGGCACCCAGACCTACAT
		CCCCTACAGAATGTTCA	CTGCAACGTGAATCACAAGCCCAGCAACACCAA
			GGTGGACAAGAAAGTTGAGCCCAAATCTTGTGA
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			TGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTC
			CCCCAAAACCCAAGGACACCCTCATGATCTCCC
			CGGACCCCTGAGGTCACATGCGTGGTGGTGGAC
			GTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC
			TGGTACGTGGACGGCGTGGAGGTGCATAATGCC
			AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG
			CACGTACCGTTGTGTCAGCGTCCTCACCGTCCTG
			CACCAGGACTGGCTGAATGGCAAGGAGTACAA
			GTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCC
			CATCGAGAAAACCATCTCCAAAGCCAAAGGGCA
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			GCGACATCGCCGTGGAGTGGGAGAGCAATGGG
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		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
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2C2.005.002			

		GCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGC	ACCACGGTCACCGTCTCCTCAGCCTCCACCAAG
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		GGAGCCGTGACAGTGGCCTGGAAGGCAGATAG	AGAGCACCTCTGGGGGCACAGCGGCCCTGGGCT
		CAGCCCCGTCAAGGCGGGAGTGGAGACCACCAC	GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA
		ACCCTCCAAACAAAGCAACAACAAGTACGCGGC	CGGTGTCGTGGAACTCAGGCGCCCTGACCAGCG
		CAGCAGCTATCTGAGCCTGACGCCTGAGCAGTG	GCGTGCACACCTTCCCGGCTGTCCTACAGTCCTC
		GAAGTCCCACAGAAGCTACAGCTGCCAGGTCAC	AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT
		GCATGAAGGGAGCACCGTGGAGAAGACAGTGG	GCCCTCCAGCAGCTTGGGCACCCAGACCTACAT
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			GGTGGACAAGAAAGTTGAGCCCAAATCTTGTGA
			CAAAACTCACACATGCCCACCGTGCCCAGCACC
			TGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTC
			CCCCCAAAACCCAAGGACACCCTCATGATCTCC
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			GTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC
			TGGTACGTGGACGGCGTGGAGGTGCATAATGCC
			AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG
			CACGTACCGTTGTGTCAGCGTCCTCACCGTCCTG
			CACCAGGACTGGCTGAATGGCAAGGAGTACAA
			GTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCC
			CATCGAGAAAACCATCTCCAAAGCCAAAGGGCA
			GCCCCGAGAACCACAGGTGTACACCCTGCCCCC
			ATCCCGGGAGGAGATGACCAAGAACCAGGTCA
			GCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA
			GCGACATCGCCGTGGAGTGGGAGAGCAATGGG
			CAGCCGGAGAACAACTACAAGACCACGCCTCCC
			GTGCTGGACTCCGACGGCTCCTTCTTCCTCTATA
			GCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
			CAGGGGAACGTCTTCTCATGCTCCGTGATGCAT
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		SEQ ID NO: 2009	SEQ ID NO: 2166
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		ASLAISGLQSEDEADYFCATFDESLQGPVFGGGTK	GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG
		LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD	GDYVWGTYRPHYYYGMDVWGQGTTVTVSSAST

		FYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKY AASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV APTECS	KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK
		SEQ ID NO: 439	SEQ ID NO: 596
iPS:361418	2C2.005.003	NA	CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT CTGGAAGTAGCTCCAACATCGGAAGTAATTATG TAAACTGGTACCAGCACCTCCCAGGAACGGCCC CCAAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATGAAAGCCTGAGTGGTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCCTAGGTC AGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCC GCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGC CACACTGGTGTGTCTCATAAGTGACTTCTACCCG GGAGCCGTGACAGTGGCCTGGAAGGCAGATAG CAGCCCCGTCAAGGCGGGAGTGGAGACCACCAC ACCCTCCAAACAAAGCAACAACAAGTACGGCGGC CAGCAGCTATCTGAGCCTGACGCCTGAGCAGTG GAAGTCCCACAGAAGCTACAGCTGCCAGGTCAC GCATGAAGGGAGCACCGTGGAGAAGACAGTGG CCCCTACAGAATGTTCA

				GTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC TGGTACGTGGACGGCGTGGAGGTGCATAATGCC AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG CACGTACCGTTGTGTCAGCGTCCTCACCGTCCTG CACCAGGACTGGCTGAATGGCAAGGAGTACAA GTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCC CATCGAGAAAACCATCTCCAAAGCCAAAGGGCA GCCCCGAGAACCACAGGTGTACACCCTGCCCCC ATCCCGGGAGGAGATGACCAAGAACCAGGTCA GCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA GCGACATCGCCGTGGAGTGGGAGAGCAATGGG CAGCCGGAGAACAACTACAAGACCACGCCTCCC GTGCTGGACTCCGACGGCTCCTTCTTCCTCTATA GCAAGCTCACCGTGGACAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAACCACTACACGCAGAAGAGC CTCTCCCTGTCTCCGGGTAAA
			SEQ ID NO: 2010	SEQ ID NO: 2167
		AA	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNYVNW YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDESLSGPVFGGGTK LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD FYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKY AASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV APTECS	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG GDYVWGTYRPHYYYGMDVWGQGTTVTVSSAST KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK
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iPS;361424	2C2.005.004	NA		
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			CTGGAAGTAGCTCCAACATCGGAAGTAATTATG	AAGGCTTCCGGATACACCTTCACCGGCTACTAT
			TAAACTGGTACCAGCACCTCCCAGGAACGGCCC	ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG
			CCAAACTCCTCATCTATACTAATAATCAGCGGC	CTTGAGTGGATGGGATGGATCAACCCTAACAGT
			CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA	GGTGGCACAAACTATGCACAGAAGTTTCAGGGC
			GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG	AGGGTCACCATGACCAGGGACACGTCCATCAGT
			CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG	ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT
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			AGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCC	TACTACTACGGTATGGACGTCTGGGGCCAAGGG
			GCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGC	ACCACGGTCACCGTCTCCTCAGCCTCCACCAAG
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			ACCCTCCAAACAAAGCAACAACAAGTACGCGGC	CGGTGTCGTGGAACTCAGGCGCCCTGACCAGCG
			CAGCAGCTATCTGAGCCTGACGCCTGAGCAGTG	GCGTGCACACCTTCCCGGCTGTCCTACAGTCCTC
			GAAGTCCCACAGAAGCTACAGCTGCCAGGTCAC	AGGGACTCTACTCCCTCAGCAGCGTGGTGACCGT
			GCATGAAGGGAGCACCGTGGAGAAGACAGTGG	GCCCTCCAGCAGCTTGGGCACCCAGACCTACAT
			CCCCTACAGAATGTTCA	CTGCAACGTGAATCACAAGCCCAGCAACACCAA
				GGTGGACAAGAAAGTTGAGCCCAAATCTTGTGA
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				GTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC
				TGGTACGTGGACGGCGTGGAGGTGCATAATGCC
				AAGACAAAGCCGCGTGTGAGGAGCAGTACGGCAG
				CACGTACCGTTGTGTCAGCGTCCTCACCGTCCTG
				CACCAGGACTGGCTGAATGGCAAGGAGTACAA
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				GCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA
				GCGACATCGCCGTGGAGTGGGAGAGCAATGGG

			CAGCCGGAGAACAACTACAAGACCACGCCTCCC
			GTGCTGGACTCCGACGGCTCCTTCTTCCTCTATA
			GCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
			CAGGGGAACGTCTTCTCATGCTCCGTGATGCAT
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		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
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		CAGCCCCGTCAAGGCGGGAGTGGAGACCACCAC	GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA
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		CAGCAGCTATCTGAGCCTGACGCCTGAGCAGTG	GCGTGCACACCTTCCCGGCTGTCCTACAGTCCTC
		GAAGTCCCACAGAAGCTACAGCTGCCAGGTCAC	AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT
		GCATGAAGGGAGCACCGTGGAAGAACAGTGG	GCCCTCCAGCAGCTTGGGCACCCAGACCTACAT
		CCCCTACAGAATGTTCA	CTGCAACGTGAATCACAAGCCCAGCAACACCAA
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			CAAAACTCACACATGCCCACCGTGCCCAGCACC
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			GTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC
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			AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG
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			CACCAGGACTGGCTGAATGGCAAGGAGTACAA
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			GCGACATCGCCGTGGAGTGGGAGAGCAATGGG
			CAGCCGGAGAACAACTACAAGACCACGCCTCCC
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			GCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
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		SEQ ID NO: 2012	SEQ ID NO: 2169
AA		QSVLTQPPSASGTPGQRVTISCSGSSSNIGSQTVNW	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY
		YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS	MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ
		ASLAISGLQSEDEADYFCATFDDSLNGPVFGGGTK	GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG
		LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD	GDYVWGTYRPHYYYGMDVWGQGTTVTVSSAST
		FYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKY	KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT
		AASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV	VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPS
		APTECS	SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH

iPS:361436		TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT
		CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE
		EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK
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		VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
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2C2.005.006	SEQ ID NO: 442	SEQ ID NO: 599
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	GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG	AGGGTCACCATGACCAGGGACACGTCCATCAGT
	CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG	ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT
	CAACATTCGATGACAGCCTGAATGGTCCGGTAT	GACGACACGGCCGTGTATTACTGTGCGAGAGGG
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	AGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCC	TACTACTACGGTATGGACGTCTGGGGCCAAGGG
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	CACACTGGTGTGTCTCATAAGTGACTTCTACCCG	GGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCA
	GGAGCCGTGACAGTGGCCTGGAAGGCAGATAG	AGAGCACCTCTGGGGGCACAGCGGCCCTGGGCT
	CAGCCCCGTCAAGGCGGGAGTGGAGACCACCAC	GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA
	ACCCTCCAAACAAAGCAACAACAAGTACGCGGC	CGGTGTCGTGGAACTCAGGCGCCCTGACCAGCG
	CAGCAGCTATCTGAGCCTGACGCCTGAGCAGTG	GCGTGCACACCTTCCCGGCTGTCCTACAGTCCTC
	GAAGTCCCACAGAAGCTACAGCTGCCAGGTCAC	AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT
	GCATGAAGGGAGCACCGTGGAGAAGACAGTGG	GCCCTCCAGCAGCTTGGGCACCCAGACCTACAT
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		TGGTACGTGGACGGCGTGGAGGTGCATAATGCC
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			GTGCTGGACTCCGACGGCTCCTTCTTCCTCTATA
			GCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
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		SEQ ID NO: 2013	SEQ ID NO: 2170
	AA	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNYVNW YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDDSLNGPVFGGGTK LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD FYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKY AASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV APTECS	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG GDYVWGTYRPHYYYGMDVWGQGTTVTVSSAST KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK
		SEQ ID NO: 443	SEQ ID NO: 600
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	2C2.005.007		
	iPS:361442		

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	CACACTGGTGTGTCTCATAAGTGACTTCTACCCG	GGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCA
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	ACCCTCCAAACAAAGCAACAACAAGTACGCGGC	CGGTGTCGTGGAACTCAGGCGCCCTGACCAGCG
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	GAAGTCCCACAGAAGCTACAGCTGCCAGGTCAC	AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT
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			SEQ ID NO: 2014	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: 444	SEQ ID NO: 601
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		TGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTC
		CCCCCAAAACCCAAGGACACCCTCATGATCTCC
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		GTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC
		TGGTACGTGGACGGCGTGGAGGTGCATAATGCC
		AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG
		CACGTACCGTTGTGTCAGCGTCCTCACCGTCCTG
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		ATCCCGGGAGGAGATGACCAAGAACCAGGTCA
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		GCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
		CAGGGGAACGTCTTCTCATGCTCCGTGATGCAT
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			LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK
		SEQ ID NO: 445	SEQ ID NO: 602
iPS:361454	NA	CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT CTGGAAGTAGCTCCAACATCGGAAGTAATACTG TAAACTGGTACCAGCACCTCCCAGGAACGGCCC CCAAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATGACAGCCTGAGTGGTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCCTAGGTC AGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCC GCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGC CACACTGGTGTGTCTCATAAGTGACTTCTACCCG GGAGCCGTGACAGTGGCCTGGAAGGCAGATAG CAGCCCCGTCAAGGCGGGAGTGGAGACCACCAC ACCCTCCAAACAAAGCAACAACAAGTACGCGGC CAGCAGCTATCTGAGCCTGACGCCTGAGCAGTG GAAGTCCCACAGAAGCTACAGCTGCCAGGTCAC GCATGAAGGGAGCACCGTGGAGAAGACAGTGG CCCCTACAGAATGTTCA	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
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	AA	QSVLTQPPSASGTPGQRVTISCSGSSNIGSNTVNW YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDDSLSGPVFGGGTK LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD FYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKY AASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV APTECS	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG GDYVWGTYRPHYYYGMDVWGQGTTVTVSSAST KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK
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2C2.005.010			

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		CAGCCCCGTCAAGGCGGGAGTGGAGACCACCAC	GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA
		ACCCTCCAAACAAAGCAACAACAAGTACGCGGC	CGGTGTCGTGGAACTCAGGCGCCCTGACCAGCG
		CAGCAGCTATCTGAGCCTGACGCCTGAGCAGTG	GCGTGCACACCTTCCCGGCTGTCCTACAGTCCTC
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		ASLAISGLQSEDEADYFCATFDDSLNAPVFGGGTK	GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG
		LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD	GDYVWGTYRPHYYYGMDVWGQGTTVTVSSAST

		FYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKY AASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV APTECS	KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK
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2C2.005.011	NA	CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT CTGGAAGTAGCTCCAACATCGGAAGTAATACTG TAAACTGGTACCAGCACCTCCCAGGAACGGCCC CCAAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATAGCAGCCTGAATGGTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCCTAGGTC AGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCC GCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGC CACACTGGTGTGTCTCATAAGTGACTTCTACCCG GGAGCCGTGACAGTGGCCTGGAAGGCAGATAG CAGCCCCGTCAAGGCGGGAGTGGAGACCACCAC ACCCTCCAAACAAAGCAACAACAAGTACGCGGC CAGCAGCTATCTGAGCCTGACGCCTGAGCAGTG GAAGTCCCACAGAAGCTACAGCTGCCAGGTCAC GCATGAAGGGAGCACCGTGGAGAAGACAGTGG CCCCTACAGAATGTTCA	CAGATGCCAGGTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCCGGATACACCTTCACCGGCTACTAT ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG CTTGAGTGGATGGGATGGATCAACCCTAACAGT GGTGGCACAAACTATGCACAGAAGTTTCAGGGC AGGGTCACCATGACCAGGGACACGTCCATCAGT ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT GACGACACGGCCGTGTATTACTGTGCGAGAGGG GGGGATTACGTTTGGGGGACTTATCGGCCTCAC TACTACTACGGTATGGACGTCTGGGGCCAAGGG ACCACGGTCACCGTCTCCTCAGCCTCCACCAAG GGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCA AGAGCACCTCTGGGGGCACAGCGGCCCTGGGCT GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA CGGTGTCGTGGAACTCAGGCGCCCTGACCAGCG GCGTGCACACCTTCCCGGCTGTCCTACAGTCCTC AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT GCCCTCCAGCAGCTTGGGCACCCAGACCTACAT CTGCAACGTGAATCACAAGCCCAGCAACACCAA GGTGGACAAGAAAGTTGAGCCCAAATCTTGTGA CAAAACTCACACATGCCCACCGTGCCCAGCACC TGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTC CCCCCAAAACCCAAGGACACCCTCATGATCTCCC CGGACCCCTGAGGTCACATGCGTGGTGGTGGAC

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	AASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV	VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPS
	APTECS	SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH
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		CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE
		EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK
		ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ
		VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
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		LHNHYTQKSLSLSPGK
	SEQ ID NO: 448	SEQ ID NO: 605
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	GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT	AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
	CTGGAAGTAGCTCCAACATCGGAAGTAATTATG	AAGGCTTCCGGATACACCTTCACCGGCTACTAT

	TAAACTGGTACCAGCACCTCCCAGGAACGGCCC	ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG
	CCAAACTCCTCATCTATACTAATAATCAGCGGC	CTTGAGTGGGATGGGATGGATCAACCCTAACAGT
	CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA	GGTGGCACAAACTATGCACAGAAGTTTCAGGGC
	GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG	AGGGTCACCATGACCAGGGACACGTCCATCAGT
	CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG	ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT
	CAACATTCGATAGCAGCCTGAATGCTCCGGTAT	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
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		TGGTACGTGGACGGCGTGGAGGTGCATAATGCC
		AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG
		CACGTACCGTTGTGTCAGCGTCCTCACCGTCCTG
		CACCAGGACTGGCTGAATGGCAAGGAGTACAA
		GTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCC
		CATCGAGAAAACCATCTCCAAAGCCAAAGGGCA
		GCCCCGAGAACCACAGGTGTACACCCTGCCCCC
		ATCCCGGGAGGAGATGACCAAGAACCAGGTCA
		GCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA
		GCGACATCGCCGTGGAGTGGGAGAGCAATGGG
		CAGCCGGAGAACAACTACAAGACCACGCCTCCC
		GTGCTGGACTCCGACGGCTCCTTCTTCCTCTATA
		GCAAGCTCACCGTGGACAAGAGCAGGTGGCAG

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		SEQ ID NO: 449	SEQ ID NO: 606
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2C2.005.013			

		GAAGTCCCACAGAAGCTACAGCTGCCAGGTCAC GCATGAAGGGAGCACCGTGGAGAAAGACAGTGG 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
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		LPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQV
		SLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL
		DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL
		HNHYTQKSLSLSPGK
	SEQ ID NO: 450	SEQ ID NO: 607
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	CTGGAAGTAGCTCCAACATCGGAAGTCAAACTG	AAGGCTTCCGGATACACCTTCACCGGCTACTAT
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	CCAAACTCCTCATCTATACTAATAATCAGCGGC	CTTGAGTGGATGGGATGGATCAACCCTAACAGT
	CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA	GGTGGCACAAACTATGCACAGAAGTTTCAGGGC
	GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG	AGGGTCACCATGACCAGGGACACGTCCATCAGT
	CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG	ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT
	CAACATTCGATGAAAGCCTGAGTGGTCCGGTAT	GACGACACGGCCGTGTATTACTGTGCGAGAGGG
	TCGGCGGAGGGACCAAGCTGACCGTCCTAGGTC	GGGGATTACGTTTTCGGACTTATCGGCCTCACT
	AGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCC	ACTACTACGGTATGGACGTCTGGGGCCAAGGGA
	GCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGC	CCACGGTCACCGTCTCCTCAGCCTCCACCAAGG
	CACACTGGTGTGTCTCATAAGTGACTTCTACCCG	GCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAA
	GGAGCCGTGACAGTGGCCTGGAAGGCAGATAG	GAGCACCTCTGGGGGCACAGCGGCCCTGGGCTG
	CAGCCCCGTCAAGGCGGGAGTGGAGACCACCAC	CCTGGTCAAGGACTACTTCCCCGAACCGGTGAC
NA	ACCCTCCAAACAAAGCAACAACAAGTACGCGGC	GGTGTCGTGGAACTCAGGCGCCCTGACCAGCGG
	CAGCAGCTATCTGAGCCTGACGCCTGAGCAGTG	CGTGCACACCTTCCCGGCTGTCCTACAGTCCTCA
	GAAGTCCCACAGAAGCTACAGCTGCCAGGTCAC	GGACTCTACTCCCTCAGCAGCGTGGTGACCGTG
	GCATGAAGGGAGCACCGTGGAGAAGACAGTGG	CCCTCCAGCAGCTTGGGCACCCAGACCTACATC
	CCCCTACAGAATGTTCA	TGCAACGTGAATCACAAGCCCAGCAACACCAAG
		GTGGACAAGAAAGTTGAGCCCAAATCTTGTGAC
		AAAACTCACACATGCCCACCGTGCCCAGCACCT
		GAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCC
		CCCCAAAACCCAAGGACACCCTCATGATCTCCC
		GGACCCCTGAGGTCACATGCGTGGTGGTGGACG
		TGAGCCACGAAGACCCTGAGGTCAAGTTCAACT
		GGTACGTGGACGGCGTGGAGGTGCATAATGCCA
		AGACAAAGCCGTGTGAGGAGCAGTACGGCAGC
		ACGTACCGTTGTGTCAGCGTCCTCACCGTCCTGC
		ACCAGGACTGGCTGAATGGCAAGGAGTACAAGT
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			CCCGGGAGGAGATGACCAAGAACCAGGTCAGC
			CTGACCTGCCTGGTCAAAGGCTTCTATCCCAGC
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			GCTGGACTCCGACGGCTCCTTCTTCCTCTATAGC
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		ASLAISGLQSEDEADYFCATFDESLSGPVFGGGTK	GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG
		LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD	GDYYVFGTYRPHYYYGMDVWGQGTTVTVSSASTK
		FYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKY	GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV
		AASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV	SWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSS
	AA	APTECS	SLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT
			CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC
			VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEE
			QYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKA
			LPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQV
			SLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL
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		GACATCCAGATGACCCAGTCTCCATCCTCCCTGT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
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		GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG	GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA
		GCTGGTATCAACAGAAACCAGGGAAAGCCCCTA	TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC
	NA	AGCGCCTGATCTATGGTGCATCCAGTTTGCAAA	TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
		GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT	GTAATGAAAACTATGCAGACGCCGTGAAGGGCC
		CTGGGACAGAATTCACTCTCACAATCAGCCAGCC	GATTCACCATCTCCAGAGACAATTCCAAGAACA
		TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT	CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
		ACAGCATAATAATTACCCCTTCACTTTCGGCCAA	AGGACACGGCTGTGTATTACTGTGCGAGAGATA

		GGGACCAAAGTGGATATCAAACGAACGGTGGCT	GGACGATCTTTGGAGTGGTCTTGGGGGGACTACT
		GCACCATCTGTCTTCATCTTCCCGCCATCTGATG	GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
		AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT	CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC
		GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA	ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC
		AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT	GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC
		CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG	CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC
		ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA	CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT
		CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC	CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC
		ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG	GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
		GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA	CAGACCTACATCTGCAACGTGAATCACAAGCCC
		GGGGAGAGTGT	AGCAACACCAAGGTGGACAAGAAAGTTGAGCC
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			GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC
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			CCTCATGATCTCCCGGACCCCTGAGGTCACATG
			CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA
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		SEQ ID NO: 2022	SEQ ID NO: 2179
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		YQQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTE	HWVRQAPGKGLEWVAVIWYDASNENYADAVKG
		FTLTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDI	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR

		KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC	TIFGVVLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
		SEQ ID NO: 452	SEQ ID NO: 609
iPS:361851	6HL.009	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCGCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCAA GGGACCAAAGTGGATATCAAACGAACGGTGGCT GCACCATCTGTCTTTCATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATA GGACGATTTTTGGAGTGCTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCCACC GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATG

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			SEQ ID NO: 2023	SEQ ID NO: 2180
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iPS.361855	2C2.005.015	NA		
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			CTGGAAGTAGCTCCAACATCGGAAGTAATACTG	AAGGCTTCCGGATACACCTTCACCGGCTACTAT
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			CCAAACTCCTCATCTATACTAATAATCAGCGGC	CTTGAGTGGATGGGATGGATCAACCCTAACAGT
			CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA	GGTGGCACAAACTATGCACAGAAGTTTCAGGGC
			GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG	AGGGTCACCATGACCAGGGACACGTCCATCAGT
			CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG	ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT
			CAACATTCGATAGCAGCCTGAGTGGTCCGGTAT	GACGACACGGCCGTGTATTACTGTGCGAGAGGG
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			CACACTGGTGTGTCTCATAAGTGACTTCTACCCG	GGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCA
			GGAGCCGTGACAGTGGCCTGGAAGGCAGATAG	AGAGCACCTCTGGGGGCACAGCGGCCCTGGGCT
			CAGCCCCGTCAAGGCGGGAGTGGAGACCACCAC	GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA
			ACCCTCCAAACAAAGCAACAACAAGTACGCGGC	CGGTGTCGTGGAACTCAGGCGCCCTGACCAGCG
			CAGCAGCTATCTGAGCCTGACGCCTGAGCAGTG	GCGTGCACACCTTCCCGGCTGTCCTACAGTCCTC
			GAAGTCCCACAGAAGCTACAGCTGCCAGGTCAC	AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT
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				CCCCCAAAACCCAAGGACACCCTCATGATCTCC
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	AA	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNW YQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS ASLAISGLQSEDEADYYCATFDSSLSGPVFGGGTK LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD FYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKY AASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV APTECS	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG GDYVWGTYRPHYYYGMDVWGQGTTVTVSSAST KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK
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		iPS:336067	
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AA	SEQ ID NO: 2025 DIQLTQSPSSLSASVGDRVTITCRASQTISRFLNWY QQKPGKAPELLIYVASSLQSGVPSRFSGSGSGTDFT LTISSLQPEDFATYYCQQSYSTLISFGQGTKLEITRT VAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC	SEQ ID NO: 2182 QVQLVESGGGVVQPGRSLRLSCTASGFTFSSYGIH WVRQAPGKGLEWVAVIWYDGSNKFHADSVKGRF TISRDNSKNTLYLQMNSLRAEDSAMYFCARGKVA GMPEAFEIWGQGTKVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP	

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			GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS
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	TATCCTGGTATGAGCAGTTCCCAGGAACAGCCC		ATCAACTGGGTGCGACAGGCCACTGGACAAGGG
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		SEQ ID NO: 2027	SEQ ID NO: 2184
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		VAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA	AGMPEAFEIWGQGTKVTVSSASTKGPSVFPLAPSS
		KVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST	KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG
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		SEQ ID NO: 459	SEQ ID NO: 616
	NA	GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTG
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		GCCGGGCAAGTCAGACCATTAGCAGGTTTTTAA	GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC
		ATTGGTATCAGCAGAAACCTGGGAAAGCCCCTA	ATACACTGGGTCCGCCAGGCTCCAGGCAAGGGG
		AGCTCCTGATCTATGTTGCATCCAGTTTGCAAAG	CTGGAGTGGGTGGCAGTTATATGGTATGATGCA
		TGGGGTCCCATCAAGATTCAGTGGCAGTGGTTC	AGTAATAAGTTCCATGCAGACCGCCGTGAAGGGC
		TGGGACAGATTTCACTCTCACCATCAGCAGTCT	CGATTCACCATCTCCAGAGACAATTCCAAGAAC
		GCAACCTGAAGATTTTGCAACTTACTACTGTCA	ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC
		ACAGAGTTACAGTACCCTGATCAGTTTTGGCCA	GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA

			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: 2030	SEQ ID NO: 2187
		AA	DIQLTQSPSSLSASVGDRVTITCRASQTISRFLNWY QQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDF	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGIH WVRQAPGKGLEWVAVIWYDASNKFHADAVKGR

		TLTISSLQPEDFATYYCQQSYSTLISFGQGTKLEIKR TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC	FTISRDNSKNTLYLQMNSLRAEDSAMYFCARGKV AGMPEAFEIWGQGTLVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
		SEQ ID NO: 460	SEQ ID NO: 617
iPS:361144	5G12.006.005	NA	GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACTATCACTT GCCGGGCAAGTCAGACCATTAGCAGGTTTTTTAA ATTGGTATCAGCAGAAACCTGGGAAAGCCCCCTG AGCTCCTGATCTATGTTGCATCCAGTTTGCAAAG TGGGGTCCCATCAAGATTCAGTGGCAGTGGTTC TGGGACAGATTTCACTCTCACCATCAGCAGTCT GCAACCTGAAGATTTTGCAACTTACTACTGTCA ACAGAGTTACAGTACCCTGATCAGTTTTGGCCA GGGGACCAAGCTGGAGATCAAACGAACGGTGG CTGCACCATCTGTCTTCATCTTCCCGCCATCTGA TGAGCAGTTGAAATCTGGAACTGCCTCTGTTGT GTGCCTGCTGAATAACTTCTATCCCAGAGAGGC CAAAGTACAGTGGAAGGTGGATAACGCCCTCCA ATCGGGTAACTCCCAGGAGAGTGTCACAGAGCA GGACAGCAAGGACAGCACCTACAGCCTCAGCA GCACCCTGACGCTGAGCAAAGCAGACTACGAGA AACACAAAGTCTACGCCTGCGAAGTCACCCATC AGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCA ACAGGGGAGAGTGT

			CCCTCATGATCTCCCGGACCCCCTGAGGTCACAT
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			AGGTCAAGTTCAACTGGTACGTGGACGGCGTGG
			AGGTGCATAATGCCAAGACAAAGCCGTGTGAGG
			AGCAGTACGGCAGCACGTACCGTTGTGTCAGCG
			TCCTCACCGTCCTGCACCAGGACTGGCTGAATG
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			GCCCTCCCAGCCCCCATCGAGAAAACCATCTCC
			AAAGCCAAAGGGCAGCCCCGAGAACCACAGGT
			GTACACCCTGCCCCCATCCCGGGAGGAGATGAC
			CAAGAACCAGGTCAGCCTGACCTGCCTGGTCAA
			AGGCTTCTATCCCAGCGACATCGCCGTGGAGTG
			GGAGAGCAATGGGCAGCCGGAGAACAACTACA
			AGACCACGCCTCCCGTGCTGGACTCCGACGGCT
			CCTTCTTCCTCTATAGCAAGCTCACCGTGGACAA
			GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATG
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iPS:361151	5G12.006.006	NA		
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			GCCGGGCAAGTCAGACCATTAGCAGGTTTTTAA	GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC
			ATTGGTATCAGCAGAAACCTGGGAAAGCCCCTG	ATACACTGGGTCCGCCAGGCTCCAGGCAAGGGG
			AGCTCCTGATCTATGTTGCATCCAGTTTGCAAAG	CTGGAGTGGGTGGCAGTTATATGGTATGATGGA
			TGGGGTCCCATCAAGATTCAGTGGCAGTGGTTC	AGTAATAAGTTCCATGCAGACGCCGTGAAGGGC
			TGGGACAGATTTCACTCTCACCATCAGCAGTCT	CGATTCACCATCTCCAGAGACAATTCCAAGAAC
			GCAACCTGAAGATTTTTGCAACTTACTACTGTCA	ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC
			ACAGAGTTACAGTACCCTGATCAGTTTTGGCCA	GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA
			GGGGACCAAGCTGGAGATCAAACGAACGGTGG	AAAGTGGCTGGTATGCCTGAAGCTTTTGAAATC
			CTGCACCATCTGTCTTCATCTTCCCGCCATCTGA	TGGGGCCAAGGGACAAAGGTCACCGTCTCTTCA
			TGAGCAGTTGAAATCTGGAACTGCCTCTGTTGT	GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTG
			GTGCCTGCTGAATAACTTCTATCCCAGAGAGGC	GCACCCTCCTCCAAGAGCACCTCTGGGGGCACA
			CAAAGTACAGTGGAAGGTGGATAACGCCCTCCA	GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTC
			ATCGGGTAACTCCCAGGAGAGTGTCACAGAGCA	CCCGAACCGGTGACGGTGTCGTGGAACTCAGGC
			GGACAGCAAGGACAGCACCTACAGCCTCAGCA	GCCCTGACCAGCGGCGTGCACACCTTCCCGGCT
			GCACCCTGACGCTGAGCAAAGCAGACTACGAGA	GTCCTACAGTCCTCAGGACTCTACTCCCTCAGCA
			AACACAAAGTCTACGCCTGCGAAGTCACCCATC	GCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCA
			AGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCA	CCCAGACCTACATCTGCAACGTGAATCACAAGC
			ACAGGGGAGAGTGT	CCAGCAACACCAAGGTGGACAAGAAAGTTGAG
				CCCAAATCTTGTGACAAAACTCACACATGCCCA
				CCGTGCCCAGCACCTGAACTCCTGGGGGGACCG
				TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACA
				CCCTCATGATCTCCCGGACCCCTGAGGTCACAT
				GCGTGGTGGTGGACGTGAGCCACGAAGACCCTG
				AGGTCAAGTTCAACTGGTACGTGGACGGCGTGG
				AGGTGCATAATGCCAAGACAAAGCCGTGTGAGG
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				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	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGIH WVRQAPGKGLEWVAVIWYDGSNKFHADAVKGR FTISRDNSKNTLYLQMNSLRAEDSAMYFCARGKV AGMPEAFEIWGQGTKVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
	NA	SEQ ID NO: 462	SEQ ID NO: 619
iPS:361491	17B11.002.001	CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTG CGGCCCCAGGACAGAAGGTCACCATCTCCTGCT CTGGAAGCAGCTCCAACATTGGAAATAATTATG TATCCTGGTATCAGCAGCTCCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAAAGCGAC CCTCAGGGATTCCTGACCGATTCTCTGGCTCCAA GTCTGGCACGTCAGCCACCCTGGGCATCACCGG ACTCCAGACTGGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGCTGTGGT ATTCGGCGGAGGGACCAAACTGACCGTCCTAGG TCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTC CCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAG GCCACACTGGTGTGTCTCATAAGTGACTTCTACC CGGGAGCCGTGACAGTGGCCTGGAAGGCAGAT	CAAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCAGTTATGAT ATCAACTGGGTGCGACAGGCCACTGGACAAGGG CTTGAGTGGATGGGATGGAACCCTAACAGT GGTGGCACAGGCTATGCACAGAAGTTCCAGGGC AGAGTCACCATGACCAGGGACACCTCCATAAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT CAGGACACGGCCGTGTATTACTGTGCGAGAGGG GGTGATTACGTTTGGGGGAGTTATCGTCCCTACT ACTACTACTACGGTATGGACGTCTGGGGCCAAG GGACCACGGTCACCGTCTCCTCAGCCTCCACCA AGGGCCCATCGGTCTTCCCCCTGGCACCCTCTC CAAGAGCACCTCTGGGGGCACAGCGGCCCTGGG

	AGCAGCCCCGTCAAGGCGGGAGTGGAGACCAC CACACCCTCCAAACAAAGCAACAACAAGTACGC GGCCAGCAGCTATCTGAGCCTGACGCCTGAGCA GTGGAAGTCCCACAGAAGCTACAGCTGCCAGGT CACGCATGAAGGGAGCACCGTGGAGAAGACAG TGGCCCCTACAGAATGTTCA	CTGCCTGGTCAAGGACTACTTCCCCGAACCGGT GACGGTGTCGTGGAACTCAGGCGCCCTGACCAG CGGCGTGCACACCTTCCCGGCTGTCCTACAGTCC TCAGGACTCTACTCCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCACCCAGACCTAC ATCTGCAACGTGAATCACAAGCCCAGCAACACC AAGGTGGACAAGAAAGTTGAGCCCAAATCTTGT GACAAAACTCACACATGCCCACCGTGCCCAGCA CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCT TCCCCCCAAAACCCAAGGACACCCTCATGATCT CCCGGACCCCTGAGGTCACATGCGTGGTGGTGG ACGTGAGCCACGAAGACCCTGAGGTCAAGTTCA ACTGGTACGTGGACGGCGTGGAGGTGCATAATG CCAAGACAAAGCCGTGTGAGGAGCAGTACGGC AGCACGTACCGTTGTGTCAGCGTCCTCACCGTCC TGCACCAGGACTGGCTGAATGGCAAGGAGTACA AGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCC CCATCGAGAAAACCATCTCCAAAGCCAAAGGGC AGCCCCGAGAACCACAGGTGTACACCCTGCCCCC CATCCCGGGAGGAGATGACCAAGAACCAGGTC AGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC AGCGACATCGCCGTGGAGTGGGAGAGCAATGG GCAGCCGGAGAACAACTACAAGACCACGCCTCC CGTGCTGGACTCCGACGGCTCCTTCTTCCTCTAT AGCAAGCTCACCGTGGACAAGAGCAGGTGGCA GCAGGGGAACGTCTTCTCATGCTCCGTGATGCA TGAGGCTCTGCACAACCACTACACGCAGAAGAG CCTCTCCCTGTCTCCGGGTAAA
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AA	QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLGITGLQTGDEADYYCGTWDSSLSAVVFGGG TKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNN KYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK TVAPTECS	QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDI NWVRQATGQGLEWMGWMNPNSGGTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSQDTAVYYCARG GDYVWGSYRPYYYYYGMDVWGQGTTVTVSSAS TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP SSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH

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

			AGCACGTACCGTTGTGTCAGCGTCCTCACCGTCC
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			AGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCC
			CCATCGAGAAAACCATCTCCAAAGCCAAAGGGC
			AGCCCCGAGAACCACAGGTGTACACCCTGCCCC
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			AGCGACATCGCCGTGGAGTGGGAGAGCAATGG
			GCAGCCGGAGAACAACTACAAGACCACGCCTCC
			CGTGCTGGACTCCGACGGCTCCTTCTTCCTCTAT
			AGCAAGCTCACCGTGGACAAGAGCAGGTGGCA
			GCAGGGGAACGTCTTCTCATGCTCCGTGATGCA
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		SEQ ID NO: 2034	SEQ ID NO: 2191
	AA	QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLGITGLQTGDEADYYCGTWDSSLSAVVFGGG TKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNN KYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK TVAPTECS	QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDI NWVRQATGQGLEWMGWMNPNSGNTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSQDTAVYYCARG GDYVWGSYRPYYYYYGMDVWGQGTTVTVSSAS TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP SSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK
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17B11.002.00 3			

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		CGGAACATGGGATAGCAGCCTGAGTGCTGTGGT	CAGGACACGGCCGTGTATTACTGTGCGAGAGGG
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		TCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTC	ACTACTACTACGGTATGGACGTCTGGGGCCAAG
		CCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAG	GGACCACGGTCACCGTCTCCTCAGCCTCCACCA
		GCCACACTGGTGTGTCTCATAAGTGACTTCTACC	AGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTC
		CGGGAGCCGTGACAGTGGCCTGGAAGGCAGAT	CAAGAGCACCCTCTGGGGGCACAGCGGCCCTGGG
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			AGCAAGCTCACCGTGGACAAGAGCAGGTGGCA
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			CCTCTCCCTGTCTCCGGGTAAA

			SEQ ID NO: 2035	SEQ ID NO: 2192
		AA	QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVS WYEQFPGTAPKLLIYDNNKRPSGIPDRFSGSKSGTS ATLGITGLQTGDEADYYCGTWDSSLSAVVFGGGT KLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLIS DFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNK YAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKT VAPTECS	QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDI NWVRQATGQGLEWMGWMNPNSGGTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSQDTAVYYCARG GDYVWGSYRPYYYYYGMDVWGQGTTVTVSSAS TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP SSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK
			SEQ ID NO: 465	SEQ ID NO: 622
iPS:361507	17BI1.002.004	NA	CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTG CGGCCCCAGGACAGAAGGTCACCATCTCCTGCT CTGGAAGCAGCTCCAACATTGGAAATAATTATG TATCCTGGTATCAGCAGCTCCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC 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
			TCCCCCCAAAACCCAAGGACACCCTCATGATCT
			CCCGGACCCCTGAGGTCACATGCGTGGTGGTGG
			ACGTGAGCCACGAAGACCCTGAGGTCAAGTTCA
			ACTGGTACGTGGACGGCGTGGAGGTGCATAATG
			CCAAGACAAAGCCGTGTGAGGAGCAGTACGGC
			AGCACGTACCGTTGTGTCAGCGTCCTCACCGTCC
			TGCACCAGGACTGGCTGAATGGCAAGGAGTACA
			AGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCC
			CCATCGAGAAAACCATCTCCAAAGCCAAAGGGC
			AGCCCCGAGAACCACAGGTGTACACCCTGCCCC
			CATCCCGGGAGGAGATGACCAAGAACCAGGTC
			AGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC
			AGCGACATCGCCGTGGAGTGGGAGAGCAATGG
			GCAGCCGGAGAACAACTACAAGACCACGCCTCC
			CGTGCTGGACTCCGACGGCTCCTTCTTCCTCTAT
			AGCAAGCTCACCGTGGACAAGAGCAGGTGGCA
			GCAGGGGAACGTCTTCTCATGCTCCGTGATGCA
			TGAGGCTCTGCACAACCACTACACGCAGAAGAG
			CCTCTCCCTGTCTCCGGGTAAA
		SEQ ID NO: 2036	SEQ ID NO: 2193
	AA	QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLAITGLQTGDEADYYCGTFESSLSAVVFGGGT KLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLIS DFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNK YAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKT VAPTECS	QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDI NWVRQAPGQGLEWMGWMNPNSGGTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSDDTAVYYCARG GDYYWGSYRPYYYYYGMDVWGQGTTVTVSSAS TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP SSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV

				LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA
				LHNHYTQKSLSLSPGK
			SEQ ID NO: 466	SEQ ID NO: 623
iPS:361514	17B11.002.005	NA	CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTG	CAAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG
			CGGCCCCAGGACAGAAGGTCACCATCTCCTGCT	AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			CTGGAAGCAGCTCCAACATTGGAAATAATTATG	AAGGCTTCTGGATACACCTTCACCAGTTATGAT
			TATCCTGGTATCAGCAGCTCCCAGGAACAGCCC	ATCAACTGGGTGCGACAGGCCACTGGACAAGGG
			CCAAACTCCTCATTTATGACAATAATAAGCGAC	CTTGAGTGGATGGGATGGAATGAACCCTAACAGT
			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
				CCAAGACAAAGCCCGTGTGAGGAGCAGTACGGC
				AGCACGTACCGTTGTGTCAGCGTCCTCACCGTCC
				TGCACCAGGACTGGCTGAATGGCAAGGAGTACA
				AGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCC
				CCATCGAGAAAACCATCTCCAAAGCCAAAGGGC
				AGCCCCGAGAACCACAGGTGTACACCCTGCCCC

			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 GDYVWGSYRPVYYYYGMDVWGQGTTVTVSSAS TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP SSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK
		SEQ ID NO: 467	SEQ ID NO: 624
iPS:360582	NA	CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTG CGGCCCCAGGACAGAAGGTCACCATCTCCTGCT CTGGAAGCAGCTCCAACATTGGAAATAATTATG TATCCTGGTATCAGCAGCTCCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCCTGACCGATTCTCTGGCTCCAA GTCTGGCACGTCAGCCACCCTGGCCATCACCGG ACTCCAGACTGGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGCTGTGGT ATTCGGCGGAGGGACCAAACTGACCGTCCTAGG TCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTC	CAAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCAGTTATGAT ATCAACTGGGTGCGACAGGCCCCTGGACAAGGG CTTGAGTGGATGGGATGGAACCCTAACAGT GGTAACACAGGCTATGCACAGAAGTTCCAGGGC AGAGTCACCATGACCAGGGACACCTCCATAAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGGG GGTGATTACGTTTGGGGGAGTTATCGTCCCTACT ACTACTACTACGGTATGGACGTCTGGGGCCAAG

		CCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAG	GGACCACGGTCACCGTCTCCTCAGCCTCCACCA
		GCCACACTGGTGTGTCTCATAAGTGACTTCTACC	AGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTC
		CGGGAGCCGTGACAGTGGCCTGGAAGGCAGAT	CAAGAGCACCTCTGGGGGCACAGCGGCCCTGGG
		AGCAGCCCCGTCAAGGCGGGAGTGGAGACCAC	CTGCCTGGTCAAGGACTACTTCCCCGAACCGGT
		CACACCCTCCAAACAAAGCAACAACAAGTACGC	GACGGTGTCGTGGAACTCAGGCGCCCTGACCAG
		GGCCAGCAGCTATCTGAGCCTGACGCCTGAGCA	CGGCGTGCACACCTTCCCGGCTGTCCTACAGTCC
		GTGGAAGTCCCACAGAAGCTACAGCTGCCAGGT	TCAGGACTCTACTCCCTCAGCAGCGTGGTGACC
		CACGCATGAAGGGAGCACCGTGGAGAAGACAG	GTGCCCTCCAGCAGCTTGGGCACCCAGACCTAC
		TGGCCCCTACAGAATGTTCA	ATCTGCAACGTGAATCACAAGCCCAGCAACACC
			AAGGTGGACAAGAAAGTTGAGCCCAAATCTTGT
			GACAAAACTCACACATGCCCACCGTGCCCAGCA
			CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCT
			TCCCCCAAAACCCAAGGACACCCTCATGATCT
			CCCGGACCCCTGAGGTCACATGCGTGGTGGTGG
			ACGTGAGGCCACGAAGACCCTGAGGTCAAGTTCA
			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

	iPS:361518		
	17B11.002.007		
	NA	SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNN KYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK TVAPTECS	TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP SSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK
		SEQ ID NO: 468	SEQ ID NO: 625
		CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTG CGGCCCCAGGACAGAAGGTCACCATCTCCTGCT CTGGAAGCAGCTCCAACATTGGAAATAATTATG TATCCTGGTATCAGCAGCTCCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAAGCGAC CCTCAGGGATTCCTGACCGATTCTCTGGCTCCAA GTCTGGCACGTCAGCCACCCTGGGCATCACCGG ACTCCAGACTGGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGCTGTGGT ATTCGGCGGAGGGACCAAACTGACCGTCCTAGG TCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTC CCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAG GCCACACTGGTGTGTCTCATAAGTGACTTCTACC CGGGAGCCGTGACAGTGGCCTGGAAGGCAGAT AGCAGCCCCGTCAAGGCGGGAGTGGAGACCAC CACACCCTCCAAACAAAGCAACAACAAGTACGC GGCCAGCAGCTATCTGAGCCTGACGCCTGAGCA GTGGAAGTCCCACAGAAGCTACAGCTGCCAGGT CACGCATGAAGGGAGCACCGTGGAGAAGACAG TGGCCCCTACAGAATGTTCA	CAAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCAGTTATGAT ATCAACTGGGTGCGACAGGCCACTGGACAAGGG CTTGAGTGGATGGGATGGATGAACCCTAACAGT 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
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			CCATCGAGAAAACCATCTCCAAAGCCAAAGGGC
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			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 KGPSVFPLAPSSKSTSGGTAALGCLVKDYTPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK
		SEQ ID NO: 469	SEQ ID NO: 626

iPS:360570	17B11.002.008	NA		
			CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTG	CAAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG
			CGGCCCCAGGACAGAAGGTCACCATCTCCTGCT	AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			CTGGAAGCAGCTCCAACATTGGAAATAATTATG	AAGGCTTCTGGATACACCTTCACCAGTTATGAT
			TATCCTGGTATCAGCAGCTCCCAGGAACAGCCC	ATCAACTGGGTGCGACAGGCCCCTGGACAAGGG
			CCAAACTCCTCATTTATGACAATAATAAGCGAC	CTTGAGTGGATGGGATGGAATGAACCCTAACAGT
			CCTCAGGGATTCCTGACCGATTCTCTGGCTCCAA	GGTGGCACAGGCTATGCACAGAAGTTCCAGGGC
			GTCTGGCACGTCAGCCACCCTGGCCATCACCGG	AGAGTCACCATGACCAGGGACACCTCCATAAGC
			ACTCCAGACTGGGGACGAGGCCGATTATTACTG	ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT
			CGGAACATTCGAAAGCAGCCTGAGTGCTGTGGT	GACGACACGGCCGTGTATTACTGTGCGAGAGGG
			ATTCGGCGGAGGGACCAAACTGACCGTCCTAGG	GGTGATTACGTTTTCGGGAGTTATCGTCCCTACT
			TCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTC	ACTACTACTACGGTATGGACGTCTGGGGCCAAG
			CCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAG	GGACCACGGTCACCGTCTCCTCAGCCTCCACCA
			GCCACACTGGTGTGTCTCATAAGTGACTTCTACC	AGGGCCCATCGGTCTTTCCCCCTGGCACCCTCCTC
			CGGGAGCCGTGACAGTGGCCTGGAAGGCAGAT	CAAGAGCACCCTCTGGGGGCACAGCGGCCCTGGG
			AGCAGCCCCGTCAAGGCGGGAGTGGAGACCAC	CTGCCTGGTCAAGGACTACTTCCCCGAACCGGT
			CACACCCTCCAAACAAAGCAACAACAAGTACGC	GACGGTGTCGTGGAACTCAGGCGCCCTGACCAG
			GGCCAGCAGCTATCTGAGCCTGACGCCTGAGCA	CGGCGTGCACACCTTCCCGGCTGTCCTACAGTCC
			GTGGAAGTCCCACAGAAGCTACAGCTGCCAGGT	TCAGGACTCTACTCCCTCAGCAGCGTGGTGACC
			CACGCATGAAGGGGAGCACCGTGGAGAAGACAG	GTGCCCTCCAGCAGCTTGGGCACCCAGACCTAC
			TGGCCCCTACAGAATGTTCA	ATCTGCAACGTGAATCACAAGCCCAGCAACACC
				AAGGTGGACAAGAAAGTTGAGCCCAAATCTTGT
				GACAAAACTCACACATGCCCACCGTGCCCAGCA
				CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCT
				TCCCCCCAAAACCCAAGGACACCCTCATGATCT
				CCCGGACCCCTGAGGTCACATGCGTGGTGGTGG
				ACGTGAGCCACGAAGACCCTGAGGTCAAGTTCA
				ACTGGTACGTGGACGGCGTGGAGGTGCATAATG
				CCAAGACAAAGCCGTGTGAGGAGGAGCAGTACGGC
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				CATCCCGGGAGGAGATGACCAAGAACCAGGTC
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			GCAGCCGGAGAACAACTACAAGACCACGCCTCC
			CGTGCTGGACTCCGACGGCTCCTTCTTCCTCTAT
			AGCAAGCTCACCGTGGACAAGAGCAGGTGGCA
			GCAGGGGAACGTCTTCTCATGCTCCGTGATGCA
			TGAGGCTCTGCACAACCACTACACGCAGAAGAG
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		SEQ ID NO: 2040	SEQ ID NO: 2197
	AA	QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVS	QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDI
		WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT	NWVRQAPGQGLEWMGWMNPNSGGTGYAQKFQ
		SATLAITGLQTGDEADYYCGTFESSLSAVVFGGGT	GRVTMTRDTSISTAYMELSSLRSDDTAVYYCARG
		KLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLIS	GDYVFGSYRPYYYYYGMDVWGQGTTVTVSSAST
		DFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNK	KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT
		YAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKT	VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPS
		VAPTECS	SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH
			TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT
			CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE
			EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK
			ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ
			VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
			LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA
			LHNHYTQKSLSLSPGK
		SEQ ID NO: 470	SEQ ID NO: 627
	NA	GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTG
		CTGCATCTGTAGGAGACAGAGTCACTATCACTT	GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
		GCCGGGCAAGTCAGACCATTAGCAGGTTTTTAA	GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC
		ATTGGTATCAGCAGAAACCTGGGAAAGCCCCTA	ATACACTGGGTCCGCCAGGCTCCAGGCAAGGGG
		AGCTCCTGATCTATGTTGCATCCAGTTTGCAAAG	CTGGAGTGGGTGGCAGTTATATGGTATGATGCA
		TGGGGTCCCATCAAGATTCAGTGGCAGTGGTTC	AGTAATAAGTTCCATGCAGACGCCGTGAAGGGC
		TGGGACAGATTTCACTCTCACCATCAGCAGTCT	CGATTCACCATCTCCAGAGACAATTCCAAGAAC
		GCAACCTGAAGATTTTGCAACTTACTACTGTCA	ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC
		ACAGAGTTACAGTACCCTGCTCAGTTTTGGCCA	GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA
		GGGGACCAAGCTGGAGATCAAACGAACGGTGG	AAAGTGGCTGGTATGCCTGAAGCTTTTGAAATC
		CTGCACCATCTGTCTTCATCTTCCCGCCATCTGA	TGGGGCCAAGGGACATTGGTCACCGTCTCTTCA
		TGAGCAGTTGAAATCTGGAACTGCCTCTGTTGT	GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTG
		GTGCCTGCTGAATAACTTCTATCCCAGAGAGGC	GCACCCTCCTCCAAGAGCACCTCTGGGGGCACA
		CAAAGTACAGTGGAAGGTGGATAACGCCCTCCA	GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTC

	ATCGGGTAACTCCCAGGAGAGTGTCACAGAGCA GGACAGCAAGGACAGCACCTACAGCCTCAGCA GCACCCTGACGCTGAGCAAAGCAGACTACGAGA AACACAAAGTCTACGCCTGCGAAGTCACCCATC AGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCA ACAGGGGAGAGTGT		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 CACGCAGAAGAGCCTCTCCCTGTCTCCGGTAA A
	SEQ ID NO: 2041	SEQ ID NO: 2198	
AA	DIQLTQSPSSLSASVGDRVTITCRASQTISRFLNWY QQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDF TLTISSLQPEDFATYYCQQSYSTLLSFGQGTKLEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR GEC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGIH WVRQAPGKGLEWVAVIWYDASNKFHADAVKGR FTISRDNSKNTLYLQMNSLRAEDSAMYFCARGKV AGMPEAFEIWGQGTLVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG	

GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK	SEQ ID NO: 628	
	SEQ ID NO: 471	

In una forma di realizzazione, l'anticorpo, o suo frammento, comprende una regione variabile di catena leggera comprendente una

sequenza selezionata dal gruppo consistente in SEQ ID NO: 1-157 e una regione variabile di catena pesante comprendente una sequenza selezionata dal gruppo consistente in SEQ ID NO: 158-314, in cui l'anticorpo, o suo frammento funzionale, comprende una sostituzione di cisteina o di amminoacido non canonico in uno o più siti di coniugazione selezionati dal gruppo consistente in D70 della catena leggera di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 455, E276 della catena pesante di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 612, e T363 della catena pesante di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 612.

In una forma di realizzazione, l'anticorpo, o suo frammento, comprende una combinazione di regione variabile di catena leggera e una regione variabile di catena pesante selezionata dal gruppo consistente in una regione variabile di catena leggera comprendente SEQ ID NO: 1 e una regione variabile di catena pesante comprendente SEQ ID NO: 158; una regione variabile di catena leggera comprendente SEQ ID NO: 2 e una regione variabile di catena pesante comprendente SEQ ID NO: 159; una regione variabile di catena leggera comprendente SEQ ID NO: 3 e una regione variabile di catena pesante comprendente SEQ ID NO: 160; una regione variabile di catena leggera comprendente SEQ ID NO: 4 e una regione variabile di catena pesante comprendente SEQ ID NO: 161; una regione variabile di catena leggera comprendente SEQ ID NO: 5 e una regione variabile di catena pesante comprendente SEQ ID NO: 162; una regione variabile di catena leggera comprendente

SEQ ID NO: 6 e una regione variabile di catena pesante comprendente SEQ ID NO: 163; una regione variabile di catena leggera comprendente SEQ ID NO: 7 e una regione variabile di catena pesante comprendente SEQ ID NO: 164; una regione variabile di catena leggera comprendente SEQ ID NO: 8 e una regione variabile di catena pesante comprendente SEQ ID NO: 165; una regione variabile di catena leggera comprendente SEQ ID NO: 9 e una regione variabile di catena pesante comprendente SEQ ID NO: 166; una regione variabile di catena leggera comprendente SEQ ID NO: 10 e una regione variabile di catena pesante comprendente SEQ ID NO: 167; una regione variabile di catena leggera comprendente SEQ ID NO: 11 e una regione variabile di catena pesante comprendente SEQ ID NO: 168; una regione variabile di catena leggera comprendente SEQ ID NO: 12 e una regione variabile di catena pesante comprendente SEQ ID NO: 169; una regione variabile di catena leggera comprendente SEQ ID NO: 13 e una regione variabile di catena pesante comprendente SEQ ID NO: 170; una regione variabile di catena leggera comprendente SEQ ID NO: 14 e una regione variabile di catena pesante comprendente SEQ ID NO: 171; una regione variabile di catena leggera comprendente SEQ ID NO: 15 e una regione variabile di catena pesante comprendente SEQ ID NO: 172; una regione variabile di catena leggera comprendente SEQ ID NO: 16 e una regione variabile di catena pesante comprendente SEQ ID NO: 173; una regione variabile di catena leggera comprendente SEQ ID NO: 17 e una regione variabile di catena pesante comprendente SEQ ID NO: 174; una regione variabile di catena leggera comprendente

SEQ ID NO: 18 e una regione variabile di catena pesante comprendente SEQ ID NO: 175; una regione variabile di catena leggera comprendente SEQ ID NO: 19 e una regione variabile di catena pesante comprendente SEQ ID NO: 176; una regione variabile di catena leggera comprendente SEQ ID NO: 20 e una regione variabile di catena pesante comprendente SEQ ID NO: 177; una regione variabile di catena leggera comprendente SEQ ID NO: 21 e una regione variabile di catena pesante comprendente SEQ ID NO: 178; una regione variabile di catena leggera comprendente SEQ ID NO: 22 e una regione variabile di catena pesante comprendente SEQ ID NO: 179; una regione variabile di catena leggera comprendente SEQ ID NO: 23 e una regione variabile di catena pesante comprendente SEQ ID NO: 180; una regione variabile di catena leggera comprendente SEQ ID NO: 24 e una regione variabile di catena pesante comprendente SEQ ID NO: 181; una regione variabile di catena leggera comprendente SEQ ID NO: 25 e una regione variabile di catena pesante comprendente SEQ ID NO: 182; una regione variabile di catena leggera comprendente SEQ ID NO: 26 e una regione variabile di catena pesante comprendente SEQ ID NO: 183; una regione variabile di catena leggera comprendente SEQ ID NO: 27 e una regione variabile di catena pesante comprendente SEQ ID NO: 184; una regione variabile di catena leggera comprendente SEQ ID NO: 28 e una regione variabile di catena pesante comprendente SEQ ID NO: 185; una regione variabile di catena leggera comprendente SEQ ID NO: 29 e una regione variabile di catena pesante comprendente SEQ ID NO: 186; una regione variabile di catena leggera comprendente

SEQ ID NO: 30 e una regione variabile di catena pesante comprendente SEQ ID NO: 187; una regione variabile di catena leggera comprendente SEQ ID NO: 31 e una regione variabile di catena pesante comprendente SEQ ID NO: 188; una regione variabile di catena leggera comprendente SEQ ID NO: 32 e una regione variabile di catena pesante comprendente SEQ ID NO: 189; una regione variabile di catena leggera comprendente SEQ ID NO: 33 e una regione variabile di catena pesante comprendente SEQ ID NO: 190; una regione variabile di catena leggera comprendente SEQ ID NO: 34 e una regione variabile di catena pesante comprendente SEQ ID NO: 191; una regione variabile di catena leggera comprendente SEQ ID NO: 35 e una regione variabile di catena pesante comprendente SEQ ID NO: 192; una regione variabile di catena leggera comprendente SEQ ID NO: 36 e una regione variabile di catena pesante comprendente SEQ ID NO: 193; una regione variabile di catena leggera comprendente SEQ ID NO: 37 e una regione variabile di catena pesante comprendente SEQ ID NO: 194; una regione variabile di catena leggera comprendente SEQ ID NO: 38 e una regione variabile di catena pesante comprendente SEQ ID NO: 195; una regione variabile di catena leggera comprendente SEQ ID NO: 39 e una regione variabile di catena pesante comprendente SEQ ID NO: 196; una regione variabile di catena leggera comprendente SEQ ID NO: 40 e una regione variabile di catena pesante comprendente SEQ ID NO: 197; una regione variabile di catena leggera comprendente SEQ ID NO: 41 e una regione variabile di catena pesante comprendente SEQ ID NO: 198; una regione variabile di catena leggera comprendente

SEQ ID NO: 42 e una regione variabile di catena pesante comprendente SEQ ID NO: 199; una regione variabile di catena leggera comprendente SEQ ID NO: 43 e una regione variabile di catena pesante comprendente SEQ ID NO: 200; una regione variabile di catena leggera comprendente SEQ ID NO: 44 e una regione variabile di catena pesante comprendente SEQ ID NO: 201; una regione variabile di catena leggera comprendente SEQ ID NO: 45 e una regione variabile di catena pesante comprendente SEQ ID NO: 202; una regione variabile di catena leggera comprendente SEQ ID NO: 46 e una regione variabile di catena pesante comprendente SEQ ID NO: 203; una regione variabile di catena leggera comprendente SEQ ID NO: 47 e una regione variabile di catena pesante comprendente SEQ ID NO: 204; una regione variabile di catena leggera comprendente SEQ ID NO: 48 e una regione variabile di catena pesante comprendente SEQ ID NO: 205; una regione variabile di catena leggera comprendente SEQ ID NO: 49 e una regione variabile di catena pesante comprendente SEQ ID NO: 206; una regione variabile di catena leggera comprendente SEQ ID NO: 50 e una regione variabile di catena pesante comprendente SEQ ID NO: 207; una regione variabile di catena leggera comprendente SEQ ID NO: 51 e una regione variabile di catena pesante comprendente SEQ ID NO: 208; una regione variabile di catena leggera comprendente SEQ ID NO: 52 e una regione variabile di catena pesante comprendente SEQ ID NO: 209; una regione variabile di catena leggera comprendente SEQ ID NO: 53 e una regione variabile di catena pesante comprendente SEQ ID NO: 210; una regione variabile di catena leggera comprendente

SEQ ID NO: 54 e una regione variabile di catena pesante comprendente SEQ ID NO: 211; una regione variabile di catena leggera comprendente SEQ ID NO: 55 e una regione variabile di catena pesante comprendente SEQ ID NO: 212; una regione variabile di catena leggera comprendente SEQ ID NO: 56 e una regione variabile di catena pesante comprendente SEQ ID NO: 213; una regione variabile di catena leggera comprendente SEQ ID NO: 57 e una regione variabile di catena pesante comprendente SEQ ID NO: 214; una regione variabile di catena leggera comprendente SEQ ID NO: 58 e una regione variabile di catena pesante comprendente SEQ ID NO: 215; una regione variabile di catena leggera comprendente SEQ ID NO: 59 e una regione variabile di catena pesante comprendente SEQ ID NO: 216; una regione variabile di catena leggera comprendente SEQ ID NO: 60 e una regione variabile di catena pesante comprendente SEQ ID NO: 217; una regione variabile di catena leggera comprendente SEQ ID NO: 61 e una regione variabile di catena pesante comprendente SEQ ID NO: 218; una regione variabile di catena leggera comprendente SEQ ID NO: 62 e una regione variabile di catena pesante comprendente SEQ ID NO: 219; una regione variabile di catena leggera comprendente SEQ ID NO: 63 e una regione variabile di catena pesante comprendente SEQ ID NO: 220; una regione variabile di catena leggera comprendente SEQ ID NO: 64 e una regione variabile di catena pesante comprendente SEQ ID NO: 221; una regione variabile di catena leggera comprendente SEQ ID NO: 65 e una regione variabile di catena pesante comprendente SEQ ID NO: 222; una regione variabile di catena leggera comprendente

SEQ ID NO: 66 e una regione variabile di catena pesante comprendente SEQ ID NO: 223; una regione variabile di catena leggera comprendente SEQ ID NO: 67 e una regione variabile di catena pesante comprendente SEQ ID NO: 224; una regione variabile di catena leggera comprendente SEQ ID NO: 68 e una regione variabile di catena pesante comprendente SEQ ID NO: 225; una regione variabile di catena leggera comprendente SEQ ID NO: 69 e una regione variabile di catena pesante comprendente SEQ ID NO: 226; una regione variabile di catena leggera comprendente SEQ ID NO: 70 e una regione variabile di catena pesante comprendente SEQ ID NO: 227; una regione variabile di catena leggera comprendente SEQ ID NO: 71 e una regione variabile di catena pesante comprendente SEQ ID NO: 228; una regione variabile di catena leggera comprendente SEQ ID NO: 72 e una regione variabile di catena pesante comprendente SEQ ID NO: 229; una regione variabile di catena leggera comprendente SEQ ID NO: 73 e una regione variabile di catena pesante comprendente SEQ ID NO: 230; una regione variabile di catena leggera comprendente SEQ ID NO: 74 e una regione variabile di catena pesante comprendente SEQ ID NO: 231; una regione variabile di catena leggera comprendente SEQ ID NO: 75 e una regione variabile di catena pesante comprendente SEQ ID NO: 232; una regione variabile di catena leggera comprendente SEQ ID NO: 76 e una regione variabile di catena pesante comprendente SEQ ID NO: 233; una regione variabile di catena leggera comprendente SEQ ID NO: 77 e una regione variabile di catena pesante comprendente SEQ ID NO: 234; una regione variabile di catena leggera comprendente

SEQ ID NO: 78 e una regione variabile di catena pesante comprendente SEQ ID NO: 235; una regione variabile di catena leggera comprendente SEQ ID NO: 79 e una regione variabile di catena pesante comprendente SEQ ID NO: 236; una regione variabile di catena leggera comprendente SEQ ID NO: 80 e una regione variabile di catena pesante comprendente SEQ ID NO: 237; una regione variabile di catena leggera comprendente SEQ ID NO: 81 e una regione variabile di catena pesante comprendente SEQ ID NO: 238; una regione variabile di catena leggera comprendente SEQ ID NO: 82 e una regione variabile di catena pesante comprendente SEQ ID NO: 239; una regione variabile di catena leggera comprendente SEQ ID NO: 83 e una regione variabile di catena pesante comprendente SEQ ID NO: 240; una regione variabile di catena leggera comprendente SEQ ID NO: 84 e una regione variabile di catena pesante comprendente SEQ ID NO: 241; una regione variabile di catena leggera comprendente SEQ ID NO: 85 e una regione variabile di catena pesante comprendente SEQ ID NO: 242; una regione variabile di catena leggera comprendente SEQ ID NO: 86 e una regione variabile di catena pesante comprendente SEQ ID NO: 243; una regione variabile di catena leggera comprendente SEQ ID NO: 87 e una regione variabile di catena pesante comprendente SEQ ID NO: 244; una regione variabile di catena leggera comprendente SEQ ID NO: 88 e una regione variabile di catena pesante comprendente SEQ ID NO: 245; una regione variabile di catena leggera comprendente SEQ ID NO: 89 e una regione variabile di catena pesante comprendente SEQ ID NO: 246; una regione variabile di catena leggera comprendente

SEQ ID NO: 90 e una regione variabile di catena pesante comprendente SEQ ID NO: 247; una regione variabile di catena leggera comprendente SEQ ID NO: 91 e una regione variabile di catena pesante comprendente SEQ ID NO: 248; una regione variabile di catena leggera comprendente SEQ ID NO: 92 e una regione variabile di catena pesante comprendente SEQ ID NO: 249; una regione variabile di catena leggera comprendente SEQ ID NO: 93 e una regione variabile di catena pesante comprendente SEQ ID NO: 250; una regione variabile di catena leggera comprendente SEQ ID NO: 94 e una regione variabile di catena pesante comprendente SEQ ID NO: 251; una regione variabile di catena leggera comprendente SEQ ID NO: 95 e una regione variabile di catena pesante comprendente SEQ ID NO: 252; una regione variabile di catena leggera comprendente SEQ ID NO: 96 e una regione variabile di catena pesante comprendente SEQ ID NO: 253; una regione variabile di catena leggera comprendente SEQ ID NO: 97 e una regione variabile di catena pesante comprendente SEQ ID NO: 254; una regione variabile di catena leggera comprendente SEQ ID NO: 98 e una regione variabile di catena pesante comprendente SEQ ID NO: 255; una regione variabile di catena leggera comprendente SEQ ID NO: 99 e una regione variabile di catena pesante comprendente SEQ ID NO: 256; una regione variabile di catena leggera comprendente SEQ ID NO: 100 e una regione variabile di catena pesante comprendente SEQ ID NO: 257; una regione variabile di catena leggera comprendente SEQ ID NO: 101 e una regione variabile di catena pesante comprendente SEQ ID NO: 258; una regione variabile di catena leggera comprendente

SEQ ID NO: 102 e una regione variabile di catena pesante comprendente SEQ ID NO: 259; una regione variabile di catena leggera comprendente SEQ ID NO: 103 e una regione variabile di catena pesante comprendente SEQ ID NO: 260; una regione variabile di catena leggera comprendente SEQ ID NO: 104 e una regione variabile di catena pesante comprendente SEQ ID NO: 261; una regione variabile di catena leggera comprendente SEQ ID NO: 105 e una regione variabile di catena pesante comprendente SEQ ID NO: 262; una regione variabile di catena leggera comprendente SEQ ID NO: 106 e una regione variabile di catena pesante comprendente SEQ ID NO: 263; una regione variabile di catena leggera comprendente SEQ ID NO: 107 e una regione variabile di catena pesante comprendente SEQ ID NO: 264; una regione variabile di catena leggera comprendente SEQ ID NO: 108 e una regione variabile di catena pesante comprendente SEQ ID NO: 265; una regione variabile di catena leggera comprendente SEQ ID NO: 109 e una regione variabile di catena pesante comprendente SEQ ID NO: 266; una regione variabile di catena leggera comprendente SEQ ID NO: 110 e una regione variabile di catena pesante comprendente SEQ ID NO: 267; una regione variabile di catena leggera comprendente SEQ ID NO: 111 e una regione variabile di catena pesante comprendente SEQ ID NO: 268; una regione variabile di catena leggera comprendente SEQ ID NO: 112 e una regione variabile di catena pesante comprendente SEQ ID NO: 269; una regione variabile di catena leggera comprendente SEQ ID NO: 113 e una regione variabile di catena pesante comprendente SEQ ID NO: 270; una regione variabile di catena leggera comprendente

SEQ ID NO: 114 e una regione variabile di catena pesante comprendente SEQ ID NO: 271; una regione variabile di catena leggera comprendente SEQ ID NO: 115 e una regione variabile di catena pesante comprendente SEQ ID NO: 272; una regione variabile di catena leggera comprendente SEQ ID NO: 116 e una regione variabile di catena pesante comprendente SEQ ID NO: 273; una regione variabile di catena leggera comprendente SEQ ID NO: 117 e una regione variabile di catena pesante comprendente SEQ ID NO: 274; una regione variabile di catena leggera comprendente SEQ ID NO: 118 e una regione variabile di catena pesante comprendente SEQ ID NO: 275; una regione variabile di catena leggera comprendente SEQ ID NO: 119 e una regione variabile di catena pesante comprendente SEQ ID NO: 276; una regione variabile di catena leggera comprendente SEQ ID NO: 120 e una regione variabile di catena pesante comprendente SEQ ID NO: 277; una regione variabile di catena leggera comprendente SEQ ID NO: 121 e una regione variabile di catena pesante comprendente SEQ ID NO: 278; una regione variabile di catena leggera comprendente SEQ ID NO: 122 e una regione variabile di catena pesante comprendente SEQ ID NO: 279; una regione variabile di catena leggera comprendente SEQ ID NO: 123 e una regione variabile di catena pesante comprendente SEQ ID NO: 280; una regione variabile di catena leggera comprendente SEQ ID NO: 124 e una regione variabile di catena pesante comprendente SEQ ID NO: 281; una regione variabile di catena leggera comprendente SEQ ID NO: 125 e una regione variabile di catena pesante comprendente SEQ ID NO: 282; una regione variabile di catena leggera comprendente

SEQ ID NO: 126 e una regione variabile di catena pesante comprendente SEQ ID NO: 283; una regione variabile di catena leggera comprendente SEQ ID NO: 127 e una regione variabile di catena pesante comprendente SEQ ID NO: 284; una regione variabile di catena leggera comprendente SEQ ID NO: 128 e una regione variabile di catena pesante comprendente SEQ ID NO: 285; una regione variabile di catena leggera comprendente SEQ ID NO: 129 e una regione variabile di catena pesante comprendente SEQ ID NO: 286; una regione variabile di catena leggera comprendente SEQ ID NO: 130 e una regione variabile di catena pesante comprendente SEQ ID NO: 287; una regione variabile di catena leggera comprendente SEQ ID NO: 131 e una regione variabile di catena pesante comprendente SEQ ID NO: 288; una regione variabile di catena leggera comprendente SEQ ID NO: 132 e una regione variabile di catena pesante comprendente SEQ ID NO: 289; una regione variabile di catena leggera comprendente SEQ ID NO: 133 e una regione variabile di catena pesante comprendente SEQ ID NO: 290; una regione variabile di catena leggera comprendente SEQ ID NO: 134 e una regione variabile di catena pesante comprendente SEQ ID NO: 291; una regione variabile di catena leggera comprendente SEQ ID NO: 135 e una regione variabile di catena pesante comprendente SEQ ID NO: 292; una regione variabile di catena leggera comprendente SEQ ID NO: 136 e una regione variabile di catena pesante comprendente SEQ ID NO: 293; una regione variabile di catena leggera comprendente SEQ ID NO: 137 e una regione variabile di catena pesante comprendente SEQ ID NO: 294; una regione variabile di catena leggera comprendente

SEQ ID NO: 138 e una regione variabile di catena pesante comprendente SEQ ID NO: 295; una regione variabile di catena leggera comprendente SEQ ID NO: 139 e una regione variabile di catena pesante comprendente SEQ ID NO: 296; una regione variabile di catena leggera comprendente SEQ ID NO: 140 e una regione variabile di catena pesante comprendente SEQ ID NO: 297; una regione variabile di catena leggera comprendente SEQ ID NO: 141 e una regione variabile di catena pesante comprendente SEQ ID NO: 298; una regione variabile di catena leggera comprendente SEQ ID NO: 142 e una regione variabile di catena pesante comprendente SEQ ID NO: 299; una regione variabile di catena leggera comprendente SEQ ID NO: 143 e una regione variabile di catena pesante comprendente SEQ ID NO: 300; una regione variabile di catena leggera comprendente SEQ ID NO: 144 e una regione variabile di catena pesante comprendente SEQ ID NO: 301; una regione variabile di catena leggera comprendente SEQ ID NO: 145 e una regione variabile di catena pesante comprendente SEQ ID NO: 302; una regione variabile di catena leggera comprendente SEQ ID NO: 146 e una regione variabile di catena pesante comprendente SEQ ID NO: 303; una regione variabile di catena leggera comprendente SEQ ID NO: 147 e una regione variabile di catena pesante comprendente SEQ ID NO: 304; una regione variabile di catena leggera comprendente SEQ ID NO: 148 e una regione variabile di catena pesante comprendente SEQ ID NO: 305; una regione variabile di catena leggera comprendente SEQ ID NO: 149 e una regione variabile di catena pesante comprendente SEQ ID NO: 306; una regione variabile di catena leggera comprendente

SEQ ID NO: 150 e una regione variabile di catena pesante comprendente SEQ ID NO: 307; una regione variabile di catena leggera comprendente SEQ ID NO: 151 e una regione variabile di catena pesante comprendente SEQ ID NO: 308; una regione variabile di catena leggera comprendente SEQ ID NO: 152 e una regione variabile di catena pesante comprendente SEQ ID NO: 309; una regione variabile di catena leggera comprendente SEQ ID NO: 153 e una regione variabile di catena pesante comprendente SEQ ID NO: 310; una regione variabile di catena leggera comprendente SEQ ID NO: 154 e una regione variabile di catena pesante comprendente SEQ ID NO: 311; una regione variabile di catena leggera comprendente SEQ ID NO: 155 e una regione variabile di catena pesante comprendente SEQ ID NO: 312; una regione variabile di catena leggera comprendente SEQ ID NO: 156 e una regione variabile di catena pesante comprendente SEQ ID NO: 313; e una regione variabile di catena leggera comprendente SEQ ID NO: 157 e una regione variabile di catena pesante comprendente SEQ ID NO: 314, in cui l'anticorpo, o suo frammento funzionale, comprende una sostituzione di cisteina o di amminoacido non canonico in uno o più siti di coniugazione selezionati dal gruppo consistente in D70 della catena leggera di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 455, E276 della catena pesante di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 612, e T363 della catena pesante di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 612.

In una forma di realizzazione, l'anticorpo, o suo frammento, comprende una regione variabile di catena leggera codificata da una sequenza polinucleotidica selezionata dal gruppo consistente in SEQ ID NO: 1571-1727 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica selezionata dal gruppo consistente in SEQ ID NO: 1728-1884, in cui l'anticorpo, o suo frammento funzionale, comprende una sostituzione di cisteina o di amminoacido non canonico in uno o più siti di coniugazione selezionati dal gruppo consistente in D70 della catena leggera di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 455, E276 della catena pesante di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 612, e T363 della catena pesante di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 612.

In una forma di realizzazione, l'anticorpo, o suo frammento, comprende una combinazione di regione variabile di catena leggera e una regione variabile di catena pesante selezionata dal gruppo consistente in una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1571 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1728; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1572 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1729; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1573 e una

regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1730; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1574 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1731; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1575 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1732; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1576 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1733; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1577 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1734; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1578 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1735; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1579 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1736; una regione variabile di catena leggera codificata da una sequenza polinucleotidica

comprendente SEQ ID NO: 1580 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1737; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1581 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1738; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1582 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1739; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1583 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1740; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1584 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1741; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1585 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1742; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1586 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1743; una regione variabile di catena leggera codificata da una

sequenza polinucleotidica comprendente SEQ ID NO: 1587 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1744; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1588 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1745; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1589 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1746; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1590 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1747; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1591 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1748; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1592 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1749; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1593 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1750; una regione variabile

di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1594 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1751; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1595 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1752; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1596 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1753; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1597 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1754; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1598 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1755; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1599 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1756; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1600 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ

ID NO: 1757; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1601 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1758; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1602 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1759; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1603 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1760; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1604 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1761; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1605 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1762; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1606 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1763; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1607 e una regione variabile di catena pesante codificata da una sequenza

polinucleotidica comprendente SEQ ID NO: 1764; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1608 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1765; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1609 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1766; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1610 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1767; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1611 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1768; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1612 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1769; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1613 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1770; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1614 e una regione variabile di catena

pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1771; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1615 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1772; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1616 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1773; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1617 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1774; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1618 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1775; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1619 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1776; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1620 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1777; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1621 e una

regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1778; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1622 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1779; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1623 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1780; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1624 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1781; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1625 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1782; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1626 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1783; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1627 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1784; una regione variabile di catena leggera codificata da una sequenza polinucleotidica

comprendente SEQ ID NO: 1628 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1785; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1629 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1786; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1630 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1787; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1631 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1788; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1632 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1789; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1633 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1790; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1634 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1791; una regione variabile di catena leggera codificata da una

sequenza polinucleotidica comprendente SEQ ID NO: 1635 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1792; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1636 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1793; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1637 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1794; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1638 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1795; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1639 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1796; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1640 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1797; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1641 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1798; una regione variabile

di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1642 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1799; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1643 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1800; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1644 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1801; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1645 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1802; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1646 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1803; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1647 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1804; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1648 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ

ID NO: 1805; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1649 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1806; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1650 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1807; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1651 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1808; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1652 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1809; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1653 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1810; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1654 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1811; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1655 e una regione variabile di catena pesante codificata da una sequenza

polinucleotidica comprendente SEQ ID NO: 1812; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1656 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1813; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1657 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1814; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1658 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1815; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1659 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1816; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1660 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1817; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1661 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1818; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1662 e una regione variabile di catena

pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1819; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1663 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1820; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1664 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1821; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1665 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1822; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1666 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1823; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1667 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1824; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1668 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1825; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1669 e una

regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1826; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1670 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1827; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1671 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1828; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1672 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1829; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1673 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1830; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1674 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1831; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1675 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1832; una regione variabile di catena leggera codificata da una sequenza polinucleotidica

comprendente SEQ ID NO: 1676 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1833; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1677 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1834; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1678 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1835; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1679 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1836; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1680 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1837; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1681 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1838; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1682 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1839; una regione variabile di catena leggera codificata da una

sequenza polinucleotidica comprendente SEQ ID NO: 1683 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1840; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1684 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1841; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1685 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1842; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1686 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1843; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1687 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1844; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1688 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1845; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1689 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1846; una regione variabile

di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1690 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1847; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1691 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1848; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1692 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1849; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1693 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1850; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1694 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1851; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1695 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1852; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1696 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ

ID NO: 1853; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1697 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1854; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1698 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1855; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1699 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1856; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1700 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1857; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1701 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1858; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1702 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1859; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1703 e una regione variabile di catena pesante codificata da una sequenza

polinucleotidica comprendente SEQ ID NO: 1860; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1704 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1861; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1705 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1862; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1706 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1863; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1707 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1864; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1708 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1865; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1709 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1866; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1710 e una regione variabile di catena

pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1867; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1711 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1868; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1712 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1869; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1713 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1870; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1714 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1871; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1715 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1872; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1716 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1873; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1717 e una

regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1874; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1718 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1875; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1719 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1876; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1720 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1877; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1721 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1878; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1722 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1879; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1723 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1880; una regione variabile di catena leggera codificata da una sequenza polinucleotidica

comprendente SEQ ID NO: 1724 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1881; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1725 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1882; una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1726 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1883; e una regione variabile di catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1727 e una regione variabile di catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1884, in cui l'anticorpo, o suo frammento funzionale, comprende una sostituzione di cisteina o di amminoacido non canonico in uno o più siti di coniugazione selezionati dal gruppo consistente in D70 della catena leggera di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 455, E276 della catena pesante di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 612, e T363 della catena pesante di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 612.

La presente invenzione riguarda una composizione comprendente una proteina legante l'antigene anti-GIPR avente almeno un sito di coniugazione. Il sito di coniugazione deve essere idoneo alla coniugazione di una frazione funzionale aggiuntiva (ad esempio, un

agonista del recettore di GLP-1) mediante una chimica di coniugazione definita attraverso la catena laterale di un residuo di amminoacido nel sito di coniugazione. Conseguire una coniugazione altamente selettiva e sito-specifica alla proteina legante l'antigene anti-GIPR, in conformità alla presente invenzione, richiede prendere in considerazione una vasta gamma di criteri di progettazione. Innanzitutto, deve essere definita o predeterminata una chimica di coniugazione o di accoppiamento preferita. Frazioni funzionali, come agonisti del recettore di GLP-1, possono essere coniugate o accoppiate al sito di coniugazione selezionato della proteina legante l'antigene anti-GIPR attraverso una serie di differenti chimiche di coniugazione note nell'arte. Ad esempio, un partner di coniugazione attivato da maleimide avente come bersaglio un tiolo di cisteina accessibile sulla proteina legante l'antigene anti-GIPR è una forma di realizzazione, ma numerose chimiche di coniugazione o accoppiamento aventi come bersaglio le catene laterali di amminoacidi canonici o non canonici, ad esempio non naturali, nella sequenza della proteina legante l'antigene anti-GIPR, possono essere impiegate in conformità alla presente invenzione.

Chimiche per la coniugazione chemoselettiva includono: cicloaddizioni dipolari azoturo-alchino catalizzate da rame(I) [3+2], legatura di Staudinger, altri processi di trasferimento di acile (S→N; X→N), ossimazioni, formazione di legami idrazonici e altre reazioni chimiche organiche adatte come accoppiamenti incrociati usando catalizzatori di palladio solubili in acqua. (Ad esempio 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 e Bertozzi CR, Chemistry in living system, Nature Chemical Biology 1(1); 13-21 (2005)).

Come menzionato sopra, la coniugazione (o legame covalente) alla proteina legante l'antigene anti-GIPR avviene attraverso la catena laterale di un residuo di amminoacido nel sito di coniugazione, ad esempio, ma senza limitarvisi, un residuo di cisteinile. Il residuo di amminoacido, ad esempio un residuo di cisteinile nel sito di coniugazione interno che è selezionato, può essere uno che occupa la stessa posizione del residuo di amminoacido in una sequenza nativa di dominio Fc, oppure il residuo di amminoacido può essere ingegnerizzato nella sequenza di dominio Fc mediante sostituzione o inserzione.

Altri esempi di residui di amminoacidi non naturali che possono essere particolarmente utili come sito di coniugazione in alcune forme di realizzazione dei processi e delle composizioni di sostanze dell'invenzione includono: residui di amminoacidi contenenti azoturo, ad esempio azoturo-omoalanina, p-azoturo-fenilalanina; residui di amminoacidi contenenti cheto, ad esempio p-acetil-fenilalanina; residui

di amminoacidi contenenti alchino, ad esempio p-etinilfenilalanina, omopropargilglicina, p-(prop-2-inil)-tirosina; residui di amminoacidi contenenti alchene, ad esempio omoallilglicina; residui di amminoacidi contenenti alogenuro arilico, ad esempio p-iodofenilalanina, p-bromofenilalanina; e residui di amminoacidi contenenti 1,2-amminotiolo.

I residui di amminoacidi non canonici possono essere incorporati mediante sostituzione o inserzione di amminoacidi. Residui di amminoacidi non canonici possono essere incorporati nel peptide mediante sintesi peptidica chimica anziché mediante sintesi in sistemi biologici, come cellule esprimenti in modo ricombinante; in alternativa, il tecnico del ramo può impiegare tecniche note di ingegneria proteica che usano cellule esprimenti in modo ricombinante. (Si veda, ad esempio, 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, brevetto statunitense n. 7,045,337).

Un altro aspetto importante della selezione di un sito di coniugazione interno in conformità alla presente invenzione è la selezione del posizionamento del sito di coniugazione nella proteina legante l'antigene anti-GIPR complessiva. Qualsiasi dei residui di amminoacidi esposti sulla proteina legante l'antigene anti-GIPR può essere un sito di coniugazione potenzialmente utile e può essere mutato in cisteina o in qualche altro amminoacido reattivo per l'accoppiamento sito-selettivo, se non sono già presente nel sito di coniugazione

selezionato della sequenza della proteina legante l'antigene anti-GIPR. Tuttavia, questo approccio non tiene conto dei potenziali vincoli sterici che potrebbero perturbare l'attività del partner coniugato o limitare la reattività della mutazione ingegnerizzata.

La proteina legante l'antigene anti-GIPR dell'invenzione è un anticorpo o un suo frammento funzionale. L'anticorpo anti-GIPR, o suo frammento funzionale, comprende una sostituzione di cisteina o di amminoacido non canonico in uno o più siti di coniugazione. Il/i sito/i di coniugazione può/possono essere essenzialmente su qualsiasi residuo della proteina legante l'antigene. In certe forme di realizzazione, il sito di coniugazione è situato all'interno della regione CL, CH1, CH2 o CH3 di un anticorpo, o suo frammento funzionale. In certe forme di realizzazione, il/i sito/i di coniugazione è/sono selezionato/i dal gruppo consistente in D70 della catena leggera di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 455; E276 della catena pesante di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 612; e T363 della catena pesante di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 612. Per chiarezza, "D70 della catena leggera di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 455" è lo stesso sito di sostituzione della posizione AHo D88 della catena leggera dell'anticorpo 5G12.006 e della posizione Kabat D70 della catena leggera dell'anticorpo 5G12.006; "E276 della catena pesante di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 612" è lo stesso sito di sostituzione della posizione E384 di AHo della catena pesante

dell'anticorpo 5G12.006 e della posizione E285 di Kabat della catena pesante dell'anticorpo 5G12.006; e "T363 della catena pesante di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 612" è lo stesso sito di sostituzione della posizione AHo T487 della catena pesante dell'anticorpo 5G12.006 e della posizione Kabat T382 della catena pesante di anticorpo 5G12.006.

Alcune proteine leganti l'antigene comprendono un dominio leggero variabile e un dominio pesante variabile, come elencato in una delle righe per uno degli anticorpi elencati nella TABELLA 3. In alcune esemplificazioni, la proteina legante l'antigene è composta da due domini leggeri variabili identici e due domini pesanti variabili identici da uno degli anticorpi elencati nella TABELLA 3. Alcune proteine leganti l'antigene che sono fornite comprendono un dominio leggero variabile e un dominio pesante variabile come elencato in una delle righe per uno degli anticorpi elencati nella TABELLA 3, eccetto per il fatto che uno o entrambi i domini differiscono dalla sequenza specificata nella tabella solo in 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 o 15 residui di amminoacidi, in cui ciascuna tale differenza di sequenza è indipendentemente una singolo delezione, inserzione o sostituzione di amminoacidi, le delezioni, inserzioni e/o sostituzioni risultando in non più di 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 o 15 cambiamenti di amminoacidi rispetto alle sequenze di dominio variabile specificate nella TABELLA 3. In una forma di realizzazione, la proteina legante l'antigene comprende una sequenza di regione variabile della Tabella 3, ma con la metionina N-terminale deleta. Anche altre

proteine leganti l'antigene comprendono un dominio leggero variabile e un dominio pesante variabile come elencato in una delle righe per uno degli anticorpi elencati nella TABELLA 3, eccetto per il fatto che uno o entrambi i domini differiscono dalla sequenza specificata nella tabella in quanto il dominio variabile di catena pesante e/o il dominio variabile di catena leggera comprende, o consiste in, una sequenza di amminoacidi che ha almeno 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98% o 99% di identità di sequenza con le sequenze di amminoacidi delle sequenze di dominio variabile di catena pesante o di dominio variabile di catena leggera come specificate nella TABELLA 3.

In un altro aspetto, la proteina legante l'antigene consiste solo in un dominio leggero variabile o in un dominio pesante variabile di un anticorpo elencato nella TABELLA 3. In un altro aspetto ancora, la proteina legante l'antigene comprende due o più degli stessi domini pesanti variabili o due o più degli stessi domini leggeri variabili tra quelli elencati nella TABELLA 3. Tali anticorpi di dominio possono essere fusi insieme o uniti tramite un linker, come descritto più dettagliatamente di seguito. Gli anticorpi di dominio possono anche essere fusi o collegati a una o più molecole per prolungarne l'emivita (ad esempio, PEG o albumina).

Altre proteine leganti l'antigene che sono fornite sono varianti di anticorpi formate mediante combinazione delle catene pesanti e leggere mostrate nella TABELLA 3 e comprendono catene leggere e/o pesanti che hanno ciascuna almeno 70%, 75%, 80%, 85%, 90%, 95%, 96%,

97%, 98% o 99% di identità con le sequenze di amminoacidi di queste catene. In alcune esemplificazioni, tali anticorpi includono almeno una catena pesante e una catena leggera, mentre, in altre esemplificazioni, le forme varianti contengono due catene leggere identiche e due catene pesanti identiche.

Le varie combinazioni di regioni variabili di catena pesante possono essere combinate con qualsiasi delle varie combinazioni di regioni variabili di catena leggera.

In un'ulteriore forma di realizzazione, la proteina legante l'antigene isolata fornita nella presente è un anticorpo umano comprendente una sequenza esposta nella TABELLA 3 ed è del tipo IgG_1, IgG_2, IgG_3 o IgG_4.

Le proteine leganti l'antigene divulgate nella presente sono polipeptidi in cui una o più CDR sono innestate, inserite e/o unite. Una proteina legante l'antigene può avere 1, 2, 3, 4, 5 o 6 CDR. Una proteina legante l'antigene può perciò avere, ad esempio, una CDR1 di catena pesante ("CDRH1"), e/o una CDR2 di catena pesante ("CDRH2"), e/o una CDR3 di catena pesante ("CDRH3"), e/o una CDR1 di catena leggera ("CDRL1"), e/o una CDR2 di catena leggera ("CDRL2"), e/o una CDR3 di catena leggera ("CDRL3"). Alcune proteine leganti l'antigene includono sia una CDRH3 che una CDRL3. CDR di catena leggera e pesante specifiche sono identificate nelle TABELLE 4A e 4B, rispettivamente.

Le regioni determinanti la complementarità (CDR) e le regioni cornice (FR) di un dato anticorpo possono essere identificate usando il sistema descritto da Kabat et al. in Sequences of Proteins of Immunological Interest, 5a ed., US Dept. of Health and Human Services, PHS, NIH, pubblicazione NIH n. 91-3242, 1991. Certi anticorpi che sono divulgati nella presente comprendono una o più sequenze di amminoacidi che sono identiche o che hanno un'identità di sequenza sostanziale alle sequenze di amminoacidi di una o più delle CDR presentate nelle TABELLE 4A e 4B. Queste CDR usano il sistema descritto da Kabat et al. come sopra indicato.

La struttura e le proprietà delle CDR all'interno di un anticorpo naturale sono state descritte sopra. In breve, in un anticorpo tradizionale, le CDR sono incorporate all'interno di una cornice nella regione variabile di catena pesante e leggera dove costituiscono le regioni responsabili del legame e del riconoscimento dell'antigene. Una regione variabile comprende almeno tre CDR di catena pesante o leggera, *si veda* sopra (Kabat et al., 1991, Sequences of Proteins of Immunological Interest, Public Health Service N.I.H., Bethesda, MD; *si veda* anche Chothia e Lesk, 1987, J. Mol. Biol. 196:901-917; Chothia et al., 1989, Nature 342: 877-883), all'interno di una regione cornice (regioni cornice 1-4 designate, FR1, FR2, FR3 e FR4, da Kabat *et al.*, 1991, sopra, *si veda* anche Chothia e Lesk, 1987, *supra*). Tuttavia, le CDR fornite nella presente possono non solo essere usate per definire il dominio legante l'antigene di una struttura di anticorpale tradizionale, ma possono essere

incorporate in una varietà di altre strutture di polipeptide, come descritto nella presente.

In una forma di realizzazione, l'anticorpo, o suo frammento, comprende una CDRL1, una CDRL2, una CDRL3, una CDRH1, una CDRH2 e una CDRH3, in cui l'anticorpo, o suo frammento funzionale, comprende una sostituzione di cisteina o di amminoacido non canonico in uno o più siti di coniugazione selezionati dal gruppo consistente in D70 della catena leggera di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 455, E276 della catena pesante di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 612, e T363 della catena pesante di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 612. In una forma di realizzazione, l'anticorpo, o suo frammento, comprende una CDRL1, una CDRL2, una CDRL3, una CDRH1, una CDRH2 e una CDRH3, in cui ciascuna CDRL1, CDRL2, CDRL3, CDRH1, CDRH2 e CDRH3, rispettivamente, comprende una sequenza selezionata dal gruppo consistente in SEQ ID NO: 629, SEQ ID NO: 786, SEQ ID NO: 943, SEQ ID NO: 1100, SEQ ID NO: 1257, e SEQ ID NO: 1414; SEQ ID NO: 630, SEQ ID NO: 787, SEQ ID NO: 944, SEQ ID NO: 1101, SEQ ID NO: 1258, e SEQ ID NO: 1415; SEQ ID NO: 631, SEQ ID NO: 788, SEQ ID NO: 945, SEQ ID NO: 1102, SEQ ID NO: 1259, e SEQ ID NO: 1416; SEQ ID NO: 632, SEQ ID NO: 789, SEQ ID NO: 946, SEQ ID NO: 1103, SEQ ID NO: 1260, e SEQ ID NO: 1417; SEQ ID NO: 633, SEQ ID NO: 790, SEQ ID NO: 947, SEQ ID NO: 1104, SEQ ID NO: 1261, e SEQ ID NO: 1418; SEQ ID NO: 634, SEQ ID NO: 791, SEQ ID NO: 948, SEQ ID

NO: 1105, SEQ ID NO: 1262, e SEQ ID NO: 1419; SEQ ID NO: 635, SEQ ID NO: 792, SEQ ID NO: 949, SEQ ID NO: 1106, SEQ ID NO: 1263, e SEQ ID NO: 1420; SEQ ID NO: 636, SEQ ID NO: 793, SEQ ID NO: 950, SEQ ID NO: 1107, SEQ ID NO: 1264, e SEQ ID NO: 1421; SEQ ID NO: 637, SEQ ID NO: 794, SEQ ID NO: 951, SEQ ID NO: 1108, SEQ ID NO: 1265, e SEQ ID NO: 1422; SEQ ID NO: 638, SEQ ID NO: 795, SEQ ID NO: 952, SEQ ID NO: 1109, SEQ ID NO: 1266, e SEQ ID NO: 1423; SEQ ID NO: 639, SEQ ID NO: 796, SEQ ID NO: 953, SEQ ID NO: 1110, SEQ ID NO: 1267, e SEQ ID NO: 1424; SEQ ID NO: 640, SEQ ID NO: 797, SEQ ID NO: 954, SEQ ID NO: 1111, SEQ ID NO: 1268, e SEQ ID NO: 1425; SEQ ID NO: 641, SEQ ID NO: 798, SEQ ID NO: 955, SEQ ID NO: 1112, SEQ ID NO: 1269, e SEQ ID NO: 1426; SEQ ID NO: 642, SEQ ID NO: 799, SEQ ID NO: 956, SEQ ID NO: 1113, SEQ ID NO: 1270, e SEQ ID NO: 1427; SEQ ID NO: 643, SEQ ID NO: 800, SEQ ID NO: 957, SEQ ID NO: 1114, SEQ ID NO: 1271, e SEQ ID NO: 1428; SEQ ID NO: 644, SEQ ID NO: 801, SEQ ID NO: 958, SEQ ID NO: 1115, SEQ ID NO: 1272, e SEQ ID NO: 1429; SEQ ID NO: 645, SEQ ID NO: 802, SEQ ID NO: 959, SEQ ID NO: 1116, SEQ ID NO: 1273, e SEQ ID NO: 1430; SEQ ID NO: 646, SEQ ID NO: 803, SEQ ID NO: 960, SEQ ID NO: 1117, SEQ ID NO: 1274, e SEQ ID NO: 1431; SEQ ID NO: 647, SEQ ID NO: 804, SEQ ID NO: 961, SEQ ID NO: 1118, SEQ ID NO: 1275, e SEQ ID NO: 1432; SEQ ID NO: 648, SEQ ID NO: 805, SEQ ID NO: 962, SEQ ID NO: 1119, SEQ ID NO: 1276, e SEQ ID NO: 1433; SEQ ID NO: 649, SEQ ID NO: 806, SEQ ID NO: 963, SEQ ID NO: 1120, SEQ ID NO: 1277, e SEQ ID

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1413, e SEQ ID NO: 1570, in cui l'anticorpo, o suo frammento funzionale, comprende una sostituzione di cisteina o di amminoacido non canonico in uno o più siti di coniugazione selezionati dal gruppo consistente in D70 della catena leggera di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 455, E276 della catena pesante di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 612, e T363 della catena pesante di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 612.

In una forma di realizzazione, l'anticorpo, o suo frammento, comprende una CDRL1, una CDRL2, una CDRL3, una CDRH1, una CDRH2 e una CDRH3, in cui l'anticorpo, o suo frammento funzionale, comprende una sostituzione di cisteina o di amminoacido non canonico in uno o più siti di coniugazione selezionati dal gruppo consistente in D70 della catena leggera di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 455, E276 della catena pesante di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 612, e T363 della catena pesante di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 612, codificata da un polinucleotide. In una forma di realizzazione, l'anticorpo, o suo frammento, comprende una CDRL1, una CDRL2, una CDRL3, una CDRH1, una CDRH2 e una CDRH3, in cui l'anticorpo, o suo frammento funzionale, comprende una sostituzione di cisteina o di amminoacido non canonico in uno o più siti di coniugazione selezionati dal gruppo consistente in D70 della catena leggera di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 455, E276 della catena pesante di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 612, e T363

della catena pesante di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 612, in cui ciascuna CDRL1, CDRL2, CDRL3, CDRH1, CDRH2 e CDRH3, rispettivamente, è codificata da una sequenza selezionata dal gruppo consistente in SEQ ID NO: 2199, SEQ ID NO: 2356, SEQ ID NO: 2513, SEQ ID NO: 2670, SEQ ID NO: 2827, e SEQ ID NO: 2984; SEQ ID NO: 2200, SEQ ID NO: 2357, SEQ ID NO: 2514, SEQ ID NO: 2671, SEQ ID NO: 2828, e SEQ ID NO: 2985; SEQ ID NO: 2201, SEQ ID NO: 2358, SEQ ID NO: 2515, SEQ ID NO: 2672, SEQ ID NO: 2829, e SEQ ID NO: 2986; SEQ ID NO: 2202, SEQ ID NO: 2359, SEQ ID NO: 2516, SEQ ID NO: 2673, SEQ ID NO: 2830, e SEQ ID NO: 2987; SEQ ID NO: 2203, SEQ ID NO: 2360, SEQ ID NO: 2517, SEQ ID NO: 2674, SEQ ID NO: 2831, e SEQ ID NO: 2988; SEQ ID NO: 2204, SEQ ID NO: 2361, SEQ ID NO: 2518, SEQ ID NO: 2675, SEQ ID NO: 2832, e SEQ ID NO: 2989; SEQ ID NO: 2205, SEQ ID NO: 2362, SEQ ID NO: 2519, SEQ ID NO: 2676, SEQ ID NO: 2833, e SEQ ID NO: 2990; SEQ ID NO: 2206, SEQ ID NO: 2363, SEQ ID NO: 2520, SEQ ID NO: 2677, SEQ ID NO: 2834, e SEQ ID NO: 2991; SEQ ID NO: 2207, SEQ ID NO: 2364, SEQ ID NO: 2521, SEQ ID NO: 2678, SEQ ID NO: 2835, e SEQ ID NO: 2992; SEQ ID NO: 2208, SEQ ID NO: 2365, SEQ ID NO: 2522, SEQ ID NO: 2679, SEQ ID NO: 2836, e SEQ ID NO: 2993; SEQ ID NO: 2209, SEQ ID NO: 2366, SEQ ID NO: 2523, SEQ ID NO: 2680, SEQ ID NO: 2837, e SEQ ID NO: 2994; SEQ ID NO: 2210, SEQ ID NO: 2367, SEQ ID NO: 2524, SEQ ID NO: 2681, SEQ ID NO: 2838, e SEQ ID NO: 2995; SEQ ID NO: 2211, SEQ ID NO: 2368, SEQ ID NO: 2525,

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SEQ ID NO: 2427, SEQ ID NO: 2584, SEQ ID NO: 2741, SEQ ID NO: 2898, e SEQ ID NO: 3055; SEQ ID NO: 2271, SEQ ID NO: 2428, SEQ ID NO: 2585, SEQ ID NO: 2742, SEQ ID NO: 2899, e SEQ ID NO: 3056; SEQ ID NO: 2272, SEQ ID NO: 2429, SEQ ID NO: 2586, SEQ ID NO: 2743, SEQ ID NO: 2900, e SEQ ID NO: 3057; SEQ ID NO: 2273, SEQ ID NO: 2430, SEQ ID NO: 2587, SEQ ID NO: 2744, SEQ ID NO: 2901, e SEQ ID NO: 3058; SEQ ID NO: 2274, SEQ ID NO: 2431, SEQ ID NO: 2588, SEQ ID NO: 2745, SEQ ID NO: 2902, e SEQ ID NO: 3059; SEQ ID NO: 2275, SEQ ID NO: 2432, SEQ ID NO: 2589, SEQ ID NO: 2746, SEQ ID NO: 2903, e SEQ ID NO: 3060; SEQ ID NO: 2276, SEQ ID NO: 2433, SEQ ID NO: 2590, SEQ ID NO: 2747, SEQ ID NO: 2904, e SEQ ID NO: 3061; SEQ ID NO: 2277, SEQ ID NO: 2434, SEQ ID NO: 2591, SEQ ID NO: 2748, SEQ ID NO: 2905, e SEQ ID NO: 3062; SEQ ID NO: 2278, SEQ ID NO: 2435, SEQ ID NO: 2592, SEQ ID NO: 2749, SEQ ID NO: 2906, e SEQ ID NO: 3063; SEQ ID NO: 2279, SEQ ID NO: 2436, SEQ ID NO: 2593, SEQ ID NO: 2750, SEQ ID NO: 2907, e SEQ ID NO: 3064; SEQ ID NO: 2280, SEQ ID NO: 2437, SEQ ID NO: 2594, SEQ ID NO: 2751, SEQ ID NO: 2908, e SEQ ID NO: 3065; SEQ ID NO: 2281, SEQ ID NO: 2438, SEQ ID NO: 2595, SEQ ID NO: 2752, SEQ ID NO: 2909, e SEQ ID NO: 3066; SEQ ID NO: 2282, SEQ ID NO: 2439, SEQ ID NO: 2596, SEQ ID NO: 2753, SEQ ID NO: 2910, e SEQ ID NO: 3067; SEQ ID NO: 2283, SEQ ID NO: 2440, SEQ ID NO: 2597, SEQ ID NO: 2754, SEQ ID NO: 2911, e SEQ ID NO: 3068; SEQ ID NO: 2284, SEQ ID NO: 2441, SEQ ID NO: 2598, SEQ ID NO: 2755, SEQ ID NO: 2912, e

SEQ ID NO: 3069; SEQ ID NO: 2285, SEQ ID NO: 2442, SEQ ID NO: 2599, SEQ ID NO: 2756, SEQ ID NO: 2913, e SEQ ID NO: 3070; SEQ ID NO: 2286, SEQ ID NO: 2443, SEQ ID NO: 2600, SEQ ID NO: 2757, SEQ ID NO: 2914, e SEQ ID NO: 3071; SEQ ID NO: 2287, SEQ ID NO: 2444, SEQ ID NO: 2601, SEQ ID NO: 2758, SEQ ID NO: 2915, e SEQ ID NO: 3072; SEQ ID NO: 2288, SEQ ID NO: 2445, SEQ ID NO: 2602, SEQ ID NO: 2759, SEQ ID NO: 2916, e SEQ ID NO: 3073; SEQ ID NO: 2289, SEQ ID NO: 2446, SEQ ID NO: 2603, SEQ ID NO: 2760, SEQ ID NO: 2917, e SEQ ID NO: 3074; SEQ ID NO: 2290, SEQ ID NO: 2447, SEQ ID NO: 2604, SEQ ID NO: 2761, SEQ ID NO: 2918, e SEQ ID NO: 3075; SEQ ID NO: 2291, SEQ ID NO: 2448, SEQ ID NO: 2605, SEQ ID NO: 2762, SEQ ID NO: 2919, e SEQ ID NO: 3076; SEQ ID NO: 2292, SEQ ID NO: 2449, SEQ ID NO: 2606, SEQ ID NO: 2763, SEQ ID NO: 2920, e SEQ ID NO: 3077; SEQ ID NO: 2293, SEQ ID NO: 2450, SEQ ID NO: 2607, SEQ ID NO: 2764, SEQ ID NO: 2921, e SEQ ID NO: 3078; SEQ ID NO: 2294, SEQ ID NO: 2451, SEQ ID NO: 2608, SEQ ID NO: 2765, SEQ ID NO: 2922, e SEQ ID NO: 3079; SEQ ID NO: 2295, SEQ ID NO: 2452, SEQ ID NO: 2609, SEQ ID NO: 2766, SEQ ID NO: 2923, e SEQ ID NO: 3080; SEQ ID NO: 2296, SEQ ID NO: 2453, SEQ ID NO: 2610, SEQ ID NO: 2767, SEQ ID NO: 2924, e SEQ ID NO: 3081; SEQ ID NO: 2297, SEQ ID NO: 2454, SEQ ID NO: 2611, SEQ ID NO: 2768, SEQ ID NO: 2925, e SEQ ID NO: 3082; SEQ ID NO: 2298, SEQ ID NO: 2455, SEQ ID NO: 2612, SEQ ID NO: 2769, SEQ ID NO: 2926, e SEQ ID NO: 3083; SEQ ID NO: 2299, SEQ ID NO: 2456, SEQ ID NO: 2613,

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SEQ ID NO: 3113; SEQ ID NO: 2329, SEQ ID NO: 2486, SEQ ID NO: 2643, SEQ ID NO: 2800, SEQ ID NO: 2957, e SEQ ID NO: 3114; SEQ ID NO: 2330, SEQ ID NO: 2487, SEQ ID NO: 2644, SEQ ID NO: 2801, SEQ ID NO: 2958, e SEQ ID NO: 3115; SEQ ID NO: 2331, SEQ ID NO: 2488, SEQ ID NO: 2645, SEQ ID NO: 2802, SEQ ID NO: 2959, e SEQ ID NO: 3116; SEQ ID NO: 2332, SEQ ID NO: 2489, SEQ ID NO: 2646, SEQ ID NO: 2803, SEQ ID NO: 2960, e SEQ ID NO: 3117; SEQ ID NO: 2333, SEQ ID NO: 2490, SEQ ID NO: 2647, SEQ ID NO: 2804, SEQ ID NO: 2961, e SEQ ID NO: 3118; SEQ ID NO: 2334, SEQ ID NO: 2491, SEQ ID NO: 2648, SEQ ID NO: 2805, SEQ ID NO: 2962, e SEQ ID NO: 3119; SEQ ID NO: 2335, SEQ ID NO: 2492, SEQ ID NO: 2649, SEQ ID NO: 2806, SEQ ID NO: 2963, e SEQ ID NO: 3120; SEQ ID NO: 2336, SEQ ID NO: 2493, SEQ ID NO: 2650, SEQ ID NO: 2807, SEQ ID NO: 2964, e SEQ ID NO: 3121; SEQ ID NO: 2337, SEQ ID NO: 2494, SEQ ID NO: 2651, SEQ ID NO: 2808, SEQ ID NO: 2965, e SEQ ID NO: 3122; SEQ ID NO: 2338, SEQ ID NO: 2495, SEQ ID NO: 2652, SEQ ID NO: 2809, SEQ ID NO: 2966, e SEQ ID NO: 3123; SEQ ID NO: 2339, SEQ ID NO: 2496, SEQ ID NO: 2653, SEQ ID NO: 2810, SEQ ID NO: 2967, e SEQ ID NO: 3124; SEQ ID NO: 2340, SEQ ID NO: 2497, SEQ ID NO: 2654, SEQ ID NO: 2811, SEQ ID NO: 2968, e SEQ ID NO: 3125; SEQ ID NO: 2341, SEQ ID NO: 2498, SEQ ID NO: 2655, SEQ ID NO: 2812, SEQ ID NO: 2969, e SEQ ID NO: 3126; SEQ ID NO: 2342, SEQ ID NO: 2499, SEQ ID NO: 2656, SEQ ID NO: 2813, SEQ ID NO: 2970, e SEQ ID NO: 3127; SEQ ID NO: 2343, SEQ ID NO: 2500, SEQ ID NO: 2657,

SEQ ID NO: 2814, SEQ ID NO: 2971, e SEQ ID NO: 3128; SEQ ID NO: 2344, SEQ ID NO: 2501, SEQ ID NO: 2658, SEQ ID NO: 2815, SEQ ID NO: 2972, e SEQ ID NO: 3129; SEQ ID NO: 2345, SEQ ID NO: 2502, SEQ ID NO: 2659, SEQ ID NO: 2816, SEQ ID NO: 2973, e SEQ ID NO: 3130; SEQ ID NO: 2346, SEQ ID NO: 2503, SEQ ID NO: 2660, SEQ ID NO: 2817, SEQ ID NO: 2974, e SEQ ID NO: 3131; SEQ ID NO: 2347, SEQ ID NO: 2504, SEQ ID NO: 2661, SEQ ID NO: 2818, SEQ ID NO: 2975, e SEQ ID NO: 3132; SEQ ID NO: 2348, SEQ ID NO: 2505, SEQ ID NO: 2662, SEQ ID NO: 2819, SEQ ID NO: 2976, e SEQ ID NO: 3133; SEQ ID NO: 2349, SEQ ID NO: 2506, SEQ ID NO: 2663, SEQ ID NO: 2820, SEQ ID NO: 2977, e SEQ ID NO: 3134; SEQ ID NO: 2350, SEQ ID NO: 2507, SEQ ID NO: 2664, SEQ ID NO: 2821, SEQ ID NO: 2978, e SEQ ID NO: 3135; SEQ ID NO: 2351, SEQ ID NO: 2508, SEQ ID NO: 2665, SEQ ID NO: 2822, SEQ ID NO: 2979, e SEQ ID NO: 3136; SEQ ID NO: 2352, SEQ ID NO: 2509, SEQ ID NO: 2666, SEQ ID NO: 2823, SEQ ID NO: 2980, e SEQ ID NO: 3137; SEQ ID NO: 2353, SEQ ID NO: 2510, SEQ ID NO: 2667, SEQ ID NO: 2824, SEQ ID NO: 2981, e SEQ ID NO: 3138; SEQ ID NO: 2354, SEQ ID NO: 2511, SEQ ID NO: 2668, SEQ ID NO: 2825, SEQ ID NO: 2982, e SEQ ID NO: 3139; e SEQ ID NO: 2355, SEQ ID NO: 2512, SEQ ID NO: 2669, SEQ ID NO: 2826, SEQ ID NO: 2983, e SEQ ID NO: 3140.

In un altro aspetto, una proteina legante l'antigene include 1, 2, 3, 4, 5 o 6 forme varianti delle CDR elencate nelle TABELLE 4A e 4B, ciascuna avendo almeno 80%, 85%, 90%, 95%, 96%, 97%, 98% o 99%

di identità di sequenza con una sequenza di CDR elencata nelle TABELLE 4A e 4B. Alcune proteine leganti l'antigene includono 1, 2, 3, 4, 5 o 6 delle CDR elencate nelle TABELLE 4A e 4B, ciascuna, o collettivamente, differendo per non più di 1, 2, 3, 4 o 5 amminoacidi dalle CDR elencate in questa tabella.

In varie altre forme di realizzazione, la proteina legante l'antigene è derivata da tali anticorpi. Ad esempio, in un aspetto, la proteina legante l'antigene comprende 1, 2, 3, 4, 5 o tutti e 6 delle CDR elencate in una delle righe per qualsiasi anticorpo specifico elencato nelle TABELLE 4A e 4B. In un altro aspetto, una proteina legante l'antigene include 1, 2, 3, 4, 5 o 6 forme varianti delle CDR elencate in una delle righe per un anticorpo nelle TABELLE 4A e 4B, ciascuna CDR avendo almeno 80%, 85%, 90%, 95%, 96%, 97%, 98% o 99% di identità di sequenza con una sequenza di CDR elencata nelle TABELLE 4A e 4B. Alcune proteine leganti l'antigene includono 1, 2, 3, 4, 5 o 6 delle CDR elencate in una delle righe nelle TABELLE 4A e 4B, ciascuna differendo per non più di 1, 2, 3, 4 o 5 amminoacidi dalle CDR elencate in queste tabelle. In un altro aspetto, la proteina legante l'antigene comprende tutti e 6 le CDR elencate in una riga delle TABELLE 4A e 4B, e il numero totale di cambiamenti di amminoacidi nelle CDR, collettivamente, non è superiore a 1, 2, 3, 4 o 5 amminoacidi.

In una forma di realizzazione, l'anticorpo, o suo frammento, comprende una catena leggera comprendente una sequenza selezionata dal gruppo consistente in SEQ ID NO: 472-628 e una catena

pesante comprendente una sequenza selezionata dal gruppo consistente in SEQ ID NO: 472-628, in cui l'anticorpo, o suo frammento funzionale, comprende una sostituzione di cisteina o di amminoacido non canonico in uno o più siti di coniugazione selezionati dal gruppo consistente in D70 della catena leggera di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 455, E276 della catena pesante di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 612, e T363 della catena pesante di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 612. In una forma di realizzazione, l'anticorpo, o suo frammento, comprende una combinazione di una catena leggera e una catena pesante selezionata dal gruppo consistente in una catena leggera comprendente SEQ ID NO: 315 e una catena pesante comprendente SEQ ID NO: 472; una catena leggera comprendente SEQ ID NO: 316 e una catena pesante comprendente SEQ ID NO: 473; una catena leggera comprendente SEQ ID NO: 317 e una catena pesante comprendente SEQ ID NO: 474; una catena leggera comprendente SEQ ID NO: 318 e una catena pesante comprendente SEQ ID NO: 475; una catena leggera comprendente SEQ ID NO: 319 e una catena pesante comprendente SEQ ID NO: 476; una catena leggera comprendente SEQ ID NO: 320 e una catena pesante comprendente SEQ ID NO: 477; una catena leggera comprendente SEQ ID NO: 321 e una catena pesante comprendente SEQ ID NO: 478; una catena leggera comprendente SEQ ID NO: 322 e una catena pesante comprendente SEQ ID NO: 479; una catena leggera comprendente SEQ ID NO: 323 e una catena pesante comprendente

SEQ ID NO: 480; una catena leggera comprendente SEQ ID NO: 324 e una catena pesante comprendente SEQ ID NO: 481; una catena leggera comprendente SEQ ID NO: 325 e una catena pesante comprendente SEQ ID NO: 482; una catena leggera comprendente SEQ ID NO: 326 e una catena pesante comprendente SEQ ID NO: 483; una catena leggera comprendente SEQ ID NO: 327 e una catena pesante comprendente SEQ ID NO: 484; una catena leggera comprendente SEQ ID NO: 328 e una catena pesante comprendente SEQ ID NO: 485; una catena leggera comprendente SEQ ID NO: 329 e una catena pesante comprendente SEQ ID NO: 486; una catena leggera comprendente SEQ ID NO: 330 e una catena pesante comprendente SEQ ID NO: 487; una catena leggera comprendente SEQ ID NO: 331 e una catena pesante comprendente SEQ ID NO: 488; una catena leggera comprendente SEQ ID NO: 332 e una catena pesante comprendente SEQ ID NO: 489; una catena leggera comprendente SEQ ID NO: 333 e una catena pesante comprendente SEQ ID NO: 490; una catena leggera comprendente SEQ ID NO: 334 e una catena pesante comprendente SEQ ID NO: 491; una catena leggera comprendente SEQ ID NO: 335 e una catena pesante comprendente SEQ ID NO: 492; una catena leggera comprendente SEQ ID NO: 336 e una catena pesante comprendente SEQ ID NO: 493; una catena leggera comprendente SEQ ID NO: 337 e una catena pesante comprendente SEQ ID NO: 494; una catena leggera comprendente SEQ ID NO: 338 e una catena pesante comprendente SEQ ID NO: 495; una catena leggera comprendente SEQ ID NO: 339 e una catena pesante comprendente

SEQ ID NO: 496; una catena leggera comprendente SEQ ID NO: 340 e una catena pesante comprendente SEQ ID NO: 497; una catena leggera comprendente SEQ ID NO: 341 e una catena pesante comprendente SEQ ID NO: 498; una catena leggera comprendente SEQ ID NO: 342 e una catena pesante comprendente SEQ ID NO: 499; una catena leggera comprendente SEQ ID NO: 343 e una catena pesante comprendente SEQ ID NO: 500; una catena leggera comprendente SEQ ID NO: 344 e una catena pesante comprendente SEQ ID NO: 501; una catena leggera comprendente SEQ ID NO: 345 e una catena pesante comprendente SEQ ID NO: 502; una catena leggera comprendente SEQ ID NO: 346 e una catena pesante comprendente SEQ ID NO: 503; una catena leggera comprendente SEQ ID NO: 347 e una catena pesante comprendente SEQ ID NO: 504; una catena leggera comprendente SEQ ID NO: 348 e una catena pesante comprendente SEQ ID NO: 505; una catena leggera comprendente SEQ ID NO: 349 e una catena pesante comprendente SEQ ID NO: 506; una catena leggera comprendente SEQ ID NO: 350 e una catena pesante comprendente SEQ ID NO: 507; una catena leggera comprendente SEQ ID NO: 351 e una catena pesante comprendente SEQ ID NO: 508; una catena leggera comprendente SEQ ID NO: 352 e una catena pesante comprendente SEQ ID NO: 509; una catena leggera comprendente SEQ ID NO: 353 e una catena pesante comprendente SEQ ID NO: 510; una catena leggera comprendente SEQ ID NO: 354 e una catena pesante comprendente SEQ ID NO: 511; una catena leggera comprendente SEQ ID NO: 355 e una catena pesante comprendente

SEQ ID NO: 512; una catena leggera comprendente SEQ ID NO: 356 e una catena pesante comprendente SEQ ID NO: 513; una catena leggera comprendente SEQ ID NO: 357 e una catena pesante comprendente SEQ ID NO: 514; una catena leggera comprendente SEQ ID NO: 358 e una catena pesante comprendente SEQ ID NO: 515; una catena leggera comprendente SEQ ID NO: 359 e una catena pesante comprendente SEQ ID NO: 516; una catena leggera comprendente SEQ ID NO: 360 e una catena pesante comprendente SEQ ID NO: 517; una catena leggera comprendente SEQ ID NO: 361 e una catena pesante comprendente SEQ ID NO: 518; una catena leggera comprendente SEQ ID NO: 362 e una catena pesante comprendente SEQ ID NO: 519; una catena leggera comprendente SEQ ID NO: 363 e una catena pesante comprendente SEQ ID NO: 520; una catena leggera comprendente SEQ ID NO: 364 e una catena pesante comprendente SEQ ID NO: 521; una catena leggera comprendente SEQ ID NO: 365 e una catena pesante comprendente SEQ ID NO: 522; una catena leggera comprendente SEQ ID NO: 366 e una catena pesante comprendente SEQ ID NO: 523; una catena leggera comprendente SEQ ID NO: 367 e una catena pesante comprendente SEQ ID NO: 524; una catena leggera comprendente SEQ ID NO: 368 e una catena pesante comprendente SEQ ID NO: 525; una catena leggera comprendente SEQ ID NO: 369 e una catena pesante comprendente SEQ ID NO: 526; una catena leggera comprendente SEQ ID NO: 370 e una catena pesante comprendente SEQ ID NO: 527; una catena leggera comprendente SEQ ID NO: 371 e una catena pesante comprendente

SEQ ID NO: 528; una catena leggera comprendente SEQ ID NO: 372 e una catena pesante comprendente SEQ ID NO: 529; una catena leggera comprendente SEQ ID NO: 373 e una catena pesante comprendente SEQ ID NO: 530; una catena leggera comprendente SEQ ID NO: 374 e una catena pesante comprendente SEQ ID NO: 531; una catena leggera comprendente SEQ ID NO: 375 e una catena pesante comprendente SEQ ID NO: 532; una catena leggera comprendente SEQ ID NO: 376 e una catena pesante comprendente SEQ ID NO: 533; una catena leggera comprendente SEQ ID NO: 377 e una catena pesante comprendente SEQ ID NO: 534; una catena leggera comprendente SEQ ID NO: 378 e una catena pesante comprendente SEQ ID NO: 535; una catena leggera comprendente SEQ ID NO: 379 e una catena pesante comprendente SEQ ID NO: 536; una catena leggera comprendente SEQ ID NO: 380 e una catena pesante comprendente SEQ ID NO: 537; una catena leggera comprendente SEQ ID NO: 381 e una catena pesante comprendente SEQ ID NO: 538; una catena leggera comprendente SEQ ID NO: 382 e una catena pesante comprendente SEQ ID NO: 539; una catena leggera comprendente SEQ ID NO: 383 e una catena pesante comprendente SEQ ID NO: 540; una catena leggera comprendente SEQ ID NO: 384 e una catena pesante comprendente SEQ ID NO: 541; una catena leggera comprendente SEQ ID NO: 385 e una catena pesante comprendente SEQ ID NO: 542; una catena leggera comprendente SEQ ID NO: 386 e una catena pesante comprendente SEQ ID NO: 543; una catena leggera comprendente SEQ ID NO: 387 e una catena pesante comprendente

SEQ ID NO: 544; una catena leggera comprendente SEQ ID NO: 388 e una catena pesante comprendente SEQ ID NO: 545; una catena leggera comprendente SEQ ID NO: 389 e una catena pesante comprendente SEQ ID NO: 546; una catena leggera comprendente SEQ ID NO: 390 e una catena pesante comprendente SEQ ID NO: 547; una catena leggera comprendente SEQ ID NO: 391 e una catena pesante comprendente SEQ ID NO: 548; una catena leggera comprendente SEQ ID NO: 392 e una catena pesante comprendente SEQ ID NO: 549; una catena leggera comprendente SEQ ID NO: 393 e una catena pesante comprendente SEQ ID NO: 550; una catena leggera comprendente SEQ ID NO: 394 e una catena pesante comprendente SEQ ID NO: 551; una catena leggera comprendente SEQ ID NO: 395 e una catena pesante comprendente SEQ ID NO: 552; una catena leggera comprendente SEQ ID NO: 396 e una catena pesante comprendente SEQ ID NO: 553; una catena leggera comprendente SEQ ID NO: 397 e una catena pesante comprendente SEQ ID NO: 554; una catena leggera comprendente SEQ ID NO: 398 e una catena pesante comprendente SEQ ID NO: 555; una catena leggera comprendente SEQ ID NO: 399 e una catena pesante comprendente SEQ ID NO: 556; una catena leggera comprendente SEQ ID NO: 400 e una catena pesante comprendente SEQ ID NO: 557; una catena leggera comprendente SEQ ID NO: 401 e una catena pesante comprendente SEQ ID NO: 558; una catena leggera comprendente SEQ ID NO: 402 e una catena pesante comprendente SEQ ID NO: 559; una catena leggera comprendente SEQ ID NO: 403 e una catena pesante comprendente

SEQ ID NO: 560; una catena leggera comprendente SEQ ID NO: 404 e una catena pesante comprendente SEQ ID NO: 561; una catena leggera comprendente SEQ ID NO: 405 e una catena pesante comprendente SEQ ID NO: 562; una catena leggera comprendente SEQ ID NO: 406 e una catena pesante comprendente SEQ ID NO: 563; una catena leggera comprendente SEQ ID NO: 407 e una catena pesante comprendente SEQ ID NO: 564; una catena leggera comprendente SEQ ID NO: 408 e una catena pesante comprendente SEQ ID NO: 565; una catena leggera comprendente SEQ ID NO: 409 e una catena pesante comprendente SEQ ID NO: 566; una catena leggera comprendente SEQ ID NO: 410 e una catena pesante comprendente SEQ ID NO: 567; una catena leggera comprendente SEQ ID NO: 411 e una catena pesante comprendente SEQ ID NO: 568; una catena leggera comprendente SEQ ID NO: 412 e una catena pesante comprendente SEQ ID NO: 569; una catena leggera comprendente SEQ ID NO: 413 e una catena pesante comprendente SEQ ID NO: 570; una catena leggera comprendente SEQ ID NO: 414 e una catena pesante comprendente SEQ ID NO: 571; una catena leggera comprendente SEQ ID NO: 415 e una catena pesante comprendente SEQ ID NO: 572; una catena leggera comprendente SEQ ID NO: 416 e una catena pesante comprendente SEQ ID NO: 573; una catena leggera comprendente SEQ ID NO: 417 e una catena pesante comprendente SEQ ID NO: 574; una catena leggera comprendente SEQ ID NO: 418 e una catena pesante comprendente SEQ ID NO: 575; una catena leggera comprendente SEQ ID NO: 419 e una catena pesante comprendente

SEQ ID NO: 576; una catena leggera comprendente SEQ ID NO: 420 e una catena pesante comprendente SEQ ID NO: 577; una catena leggera comprendente SEQ ID NO: 421 e una catena pesante comprendente SEQ ID NO: 578; una catena leggera comprendente SEQ ID NO: 422 e una catena pesante comprendente SEQ ID NO: 579; una catena leggera comprendente SEQ ID NO: 423 e una catena pesante comprendente SEQ ID NO: 580; una catena leggera comprendente SEQ ID NO: 424 e una catena pesante comprendente SEQ ID NO: 581; una catena leggera comprendente SEQ ID NO: 425 e una catena pesante comprendente SEQ ID NO: 582; una catena leggera comprendente SEQ ID NO: 426 e una catena pesante comprendente SEQ ID NO: 583; una catena leggera comprendente SEQ ID NO: 427 e una catena pesante comprendente SEQ ID NO: 584; una catena leggera comprendente SEQ ID NO: 428 e una catena pesante comprendente SEQ ID NO: 585; una catena leggera comprendente SEQ ID NO: 429 e una catena pesante comprendente SEQ ID NO: 586; una catena leggera comprendente SEQ ID NO: 430 e una catena pesante comprendente SEQ ID NO: 587; una catena leggera comprendente SEQ ID NO: 431 e una catena pesante comprendente SEQ ID NO: 588; una catena leggera comprendente SEQ ID NO: 432 e una catena pesante comprendente SEQ ID NO: 589; una catena leggera comprendente SEQ ID NO: 433 e una catena pesante comprendente SEQ ID NO: 590; una catena leggera comprendente SEQ ID NO: 434 e una catena pesante comprendente SEQ ID NO: 591; una catena leggera comprendente SEQ ID NO: 435 e una catena pesante comprendente

SEQ ID NO: 592; una catena leggera comprendente SEQ ID NO: 436 e una catena pesante comprendente SEQ ID NO: 593; una catena leggera comprendente SEQ ID NO: 437 e una catena pesante comprendente SEQ ID NO: 594; una catena leggera comprendente SEQ ID NO: 438 e una catena pesante comprendente SEQ ID NO: 595; una catena leggera comprendente SEQ ID NO: 439 e una catena pesante comprendente SEQ ID NO: 596; una catena leggera comprendente SEQ ID NO: 440 e una catena pesante comprendente SEQ ID NO: 597; una catena leggera comprendente SEQ ID NO: 441 e una catena pesante comprendente SEQ ID NO: 598; una catena leggera comprendente SEQ ID NO: 442 e una catena pesante comprendente SEQ ID NO: 599; una catena leggera comprendente SEQ ID NO: 443 e una catena pesante comprendente SEQ ID NO: 600; una catena leggera comprendente SEQ ID NO: 444 e una catena pesante comprendente SEQ ID NO: 601; una catena leggera comprendente SEQ ID NO: 445 e una catena pesante comprendente SEQ ID NO: 602; una catena leggera comprendente SEQ ID NO: 446 e una catena pesante comprendente SEQ ID NO: 603; una catena leggera comprendente SEQ ID NO: 447 e una catena pesante comprendente SEQ ID NO: 604; una catena leggera comprendente SEQ ID NO: 448 e una catena pesante comprendente SEQ ID NO: 605; una catena leggera comprendente SEQ ID NO: 449 e una catena pesante comprendente SEQ ID NO: 606; una catena leggera comprendente SEQ ID NO: 450 e una catena pesante comprendente SEQ ID NO: 607; una catena leggera comprendente SEQ ID NO: 451 e una catena pesante comprendente

SEQ ID NO: 608; una catena leggera comprendente SEQ ID NO: 452 e una catena pesante comprendente SEQ ID NO: 609; una catena leggera comprendente SEQ ID NO: 453 e una catena pesante comprendente SEQ ID NO: 610; una catena leggera comprendente SEQ ID NO: 454 e una catena pesante comprendente SEQ ID NO: 611; una catena leggera comprendente SEQ ID NO: 455 e una catena pesante comprendente SEQ ID NO: 612; una catena leggera comprendente SEQ ID NO: 456 e una catena pesante comprendente SEQ ID NO: 613; una catena leggera comprendente SEQ ID NO: 457 e una catena pesante comprendente SEQ ID NO: 614; una catena leggera comprendente SEQ ID NO: 458 e una catena pesante comprendente SEQ ID NO: 615; una catena leggera comprendente SEQ ID NO: 459 e una catena pesante comprendente SEQ ID NO: 616; una catena leggera comprendente SEQ ID NO: 460 e una catena pesante comprendente SEQ ID NO: 617; una catena leggera comprendente SEQ ID NO: 461 e una catena pesante comprendente SEQ ID NO: 618; una catena leggera comprendente SEQ ID NO: 462 e una catena pesante comprendente SEQ ID NO: 619; una catena leggera comprendente SEQ ID NO: 463 e una catena pesante comprendente SEQ ID NO: 620; una catena leggera comprendente SEQ ID NO: 464 e una catena pesante comprendente SEQ ID NO: 621; una catena leggera comprendente SEQ ID NO: 465 e una catena pesante comprendente SEQ ID NO: 622; una catena leggera comprendente SEQ ID NO: 466 e una catena pesante comprendente SEQ ID NO: 623; una catena leggera comprendente SEQ ID NO: 467 e una catena pesante comprendente

SEQ ID NO: 624; una catena leggera comprendente SEQ ID NO: 468 e una catena pesante comprendente SEQ ID NO: 625; una catena leggera comprendente SEQ ID NO: 469 e una catena pesante comprendente SEQ ID NO: 626; una catena leggera comprendente SEQ ID NO: 470 e una catena pesante comprendente SEQ ID NO: 627; e una catena leggera comprendente SEQ ID NO: 471 e una catena pesante comprendente SEQ ID NO: 628, in cui l'anticorpo, o suo frammento funzionale, comprende una sostituzione di cisteina o di amminoacido non canonico in uno o più siti di coniugazione selezionati dal gruppo consistente in D70 della catena leggera di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 455, E276 della catena pesante di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 612, e T363 della catena pesante di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 612.

In una forma di realizzazione, l'anticorpo, o suo frammento, comprende una catena leggera codificata da una sequenza polinucleotidica selezionata dal gruppo consistente in SEQ ID NO: 1885-2014 e una catena pesante comprendente una sequenza selezionata dal gruppo consistente in SEQ ID NO: 2042-2198, in cui l'anticorpo, o suo frammento funzionale, comprende una sostituzione di cisteina o di amminoacido non canonico in uno o più siti di coniugazione selezionati dal gruppo consistente in D70 della catena leggera di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 455, E276 della catena pesante di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 612, e T363

della catena pesante di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 612. In una forma di realizzazione, l'anticorpo, o suo frammento, comprende una combinazione di una catena leggera e una catena pesante, in cui l'anticorpo, o suo frammento funzionale, comprende una sostituzione di cisteina o di amminoacido non canonico in uno o più siti di coniugazione selezionati dal gruppo consistente in D70 della catena leggera di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 455, E276 della catena pesante di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 612, e T363 della catena pesante di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 612, selezionata dal gruppo consistente in una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1885 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2042; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1886 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2043; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1887 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2044; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1888 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2045; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1889 e una catena pesante codificata da una sequenza

polinucleotidica comprendente SEQ ID NO: 2046; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1890 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2047; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1891 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2048; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1892 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2049; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1893 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2050; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1894 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2051; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1895 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2052; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1896 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2053; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1897 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2054; una catena leggera codificata da una sequenza polinucleotidica

comprendente SEQ ID NO: 1898 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2055; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1899 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2056; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1900 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2057; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1901 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2058; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1902 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2059; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1903 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2060; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1904 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2061; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1905 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2062; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1906 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ

ID NO: 2063; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1907 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2064; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1908 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2065; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1909 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2066; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1910 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2067; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1911 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2068; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1912 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2069; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1913 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2070; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1914 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2071; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO:

1915 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2072; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1916 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2073; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1917 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2074; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1918 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2075; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1919 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2076; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1920 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2077; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1921 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2078; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1922 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2079; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1923 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2080; una catena

leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1924 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2081; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1925 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2082; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1926 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2083; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1927 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2084; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1928 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2085; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1929 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2086; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1930 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2087; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1931 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2088; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1932 e una catena pesante

codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2089; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1933 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2090; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1934 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2091; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1935 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2092; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1936 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2093; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1937 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2094; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1938 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2095; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1939 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2096; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1940 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2097; una catena leggera codificata da una

sequenza polinucleotidica comprendente SEQ ID NO: 1941 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2098; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1942 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2099; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1943 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2100; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1944 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2101; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1945 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2102; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1946 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2103; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1947 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2104; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1948 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2105; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1949 e una catena pesante codificata da una sequenza

polinucleotidica comprendente SEQ ID NO: 2106; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1950 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2107; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1951 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2108; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1952 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2109; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1953 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2110; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1954 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2111; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1955 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2112; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1956 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2113; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1957 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2114; una catena leggera codificata da una sequenza polinucleotidica

comprendente SEQ ID NO: 1958 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2115; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1959 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2116; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1960 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2117; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1961 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2118; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1962 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2119; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1963 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2120; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1964 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2121; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1965 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2122; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1966 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ

ID NO: 2123; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1967 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2124; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1968 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2125; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1969 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2126; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1970 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2127; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1971 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2128; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1972 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2129; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1973 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2130; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1974 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2131; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO:

1975 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2132; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1976 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2133; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1977 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2134; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1978 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2135; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1979 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2136; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1980 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2137; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1981 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2138; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1982 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2139; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1983 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2140; una catena

leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1984 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2141; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1985 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2142; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1986 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2143; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1987 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2144; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1988 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2145; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1989 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2146; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1990 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2147; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1991 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2148; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1992 e una catena pesante

codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2149; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1993 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2150; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1994 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2151; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1995 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2152; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1996 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2153; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1997 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2154; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1998 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2155; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 1999 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2156; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2000 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2157; una catena leggera codificata da una

sequenza polinucleotidica comprendente SEQ ID NO: 2001 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2158; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2002 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2159; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2003 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2160; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2004 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2161; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2005 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2162; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2006 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2163; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2007 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2164; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2008 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2165; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2009 e una catena pesante codificata da una sequenza

polinucleotidica comprendente SEQ ID NO: 2166; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2010 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2167; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2011 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2168; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2012 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2169; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2013 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2170; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2014 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2171; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2015 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2172; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2016 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2173; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2017 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2174; una catena leggera codificata da una sequenza polinucleotidica

comprendente SEQ ID NO: 2018 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2175; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2019 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2176; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2020 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2177; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2021 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2178; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2022 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2179; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2023 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2180; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2024 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2181; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2025 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2182; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2026 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ

ID NO: 2183; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2027 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2184; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2028 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2185; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2029 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2186; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2030 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2187; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2031 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2188; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2032 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2189; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2033 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2190; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2034 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2191; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO:

2035 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2192; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2036 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2193; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2037 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2194; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2038 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2195; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2039 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2196; una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2040 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2197; e una catena leggera codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2041 e una catena pesante codificata da una sequenza polinucleotidica comprendente SEQ ID NO: 2198.

In un altro aspetto, la proteina legante l'antigene comprende una catena leggera a lunghezza intera e una catena pesante a lunghezza intera, come elencato in una delle righe per uno degli anticorpi elencati nella TABELLA 5. Alcune proteine leganti l'antigene che sono fornite comprendono una catena leggera a lunghezza intera e una catena

pesante a lunghezza intera come elencato in una delle righe per uno degli anticorpi elencati nella TABELLA 5, eccetto per il fatto che una o entrambe le catene differiscono dalla sequenza specificata nella tabella solo in 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 o 15 residui di amminoacidi, in cui ciascuna tale differenza di sequenza è indipendentemente una singolo delezione, inserzione o sostituzione di amminoacidi, le delezioni, inserzioni e/o sostituzioni risultando in non più di 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 o 15 cambiamenti di amminoacidi rispetto alle sequenze a lunghezza intera specificate nella TABELLA 5. In una forma di realizzazione, la proteina legante l'antigene comprende una catena leggera a lunghezza intera e/o una catena pesante a lunghezza intera della Tabella 5 con la metionina N-terminale deleta. In una forma di realizzazione, la proteina legante l'antigene comprende una catena leggera a lunghezza intera e/o una catena pesante a lunghezza intera della Tabella 5 con la lisina C-terminale deleta. Anche altre proteine leganti l'antigene comprendono una catena leggera a lunghezza intera e una catena pesante a lunghezza intera come elencate in una delle righe per uno degli anticorpi elencati nella TABELLA 5, eccetto per il fatto che una o entrambe le catene differiscono dalla sequenza specificata nella tabella in quanto la catena leggera e/o la catena pesante comprende, o consiste in, una sequenza di amminoacidi che ha almeno 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98% o 99% di identità di sequenza con le sequenze di amminoacidi

delle sequenze di catena leggera o catena pesante come specificate nella TABELLA 5.

In un'altra forma di realizzazione, la proteina legante l'antigene consiste solo in un polipeptide di catena leggera o pesante, come esposto nella TABELLA 5.

In un altro aspetto ancora, le proteine leganti l'antigene contenenti le CDR, i domini variabili e/o le sequenze a lunghezza intera elencati nelle TABELLE 3, 4A, 4B e 5 sono un anticorpo monoclonale, un anticorpo chimerico, un anticorpo umanizzato, un anticorpo umano, un anticorpo multispecifico, o un frammento di anticorpo di quanto sopra. In un'altra forma di realizzazione, il frammento di anticorpo delle proteine leganti l'antigene isolate fornite nella presente è un frammento Fab, un frammento Fab', un frammento $F(ab')_2$, un frammento Fv, un diabody, o un scFv basato su un anticorpo con le sequenze come elencate nella TABELLA 5.

In un altro aspetto ancora, la proteina legante l'antigene isolata fornita nella TABELLA 5 può essere accoppiata a un gruppo di marcatura e può competere per il legame a GIPR con una proteina legante l'antigene di una delle proteine leganti l'antigene isolate fornite nella presente.

In un'altra forma di realizzazione, vengono fornite proteine leganti l'antigene che competono con uno degli anticorpi o frammenti funzionali esemplificati descritti sopra per il legame specifico a un GIPR umano (ad esempio, SEQ ID NO: 3141). Tali proteine leganti l'antigene

possono legarsi allo stesso epitopo di una delle proteine leganti l'antigene descritte nella presente, oppure a un epitopo sovrapposto. Si prevede che proteine e frammenti leganti l'antigene che competono con le proteine leganti l'antigene esemplificate mostrino proprietà funzionali simili. Le proteine e i frammenti leganti l'antigene esemplificati includono quelli descritti sopra, inclusi quelli con catene pesanti e leggere, domini di regione variabile e CDR inclusi nelle TABELLE 3, 4A, 4B e 5. Perciò, come esempio specifico, le proteine leganti l'antigene che sono fornite includono quelle che competono con un anticorpo avente:

tutti e 6 le CDR elencate per qualsiasi anticorpo elencato nelle TABELLE 4A e 4B;

una VH e una VL elencate per qualsiasi anticorpo elencato nella TABELLA 3; o

due catene leggere e due catene pesanti come specificato per qualsiasi anticorpo elencato nella TABELLA 5.

Le proteine leganti l'antigene che sono fornite includono anticorpi monoclonali che si legano a GIPR. Gli anticorpi monoclonali possono essere prodotti usando qualsiasi tecnica nota nell'arte, ad esempio rendendo immortali cellule della milza raccolte dall'animale transgenico dopo il completamento del programma di immunizzazione. Le cellule della milza possono essere rese immortali usando qualsiasi tecnica nota nell'arte, ad esempio fondendole con cellule di mieloma per produrre ibridomi. Le cellule di mieloma per uso nelle procedure di fusione per la produzione di ibridomi preferibilmente non producono anticorpi, hanno

un'alta efficienza di fusione e carenze enzimatiche che le rendono incapaci di crescere in certi terreni selettivi che supportano la crescita solo delle cellule fuse desiderate (ibridomi). Esempi di linee cellulari adatte per uso nelle fusioni di topi includono 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 e S194/5XXO Bul; esempi di linee cellulari usate nelle fusioni di ratto includono R210.RCY3, Y3-Ag 1.2.3, IR983F e 4B210. Altre linee cellulari utili per le fusioni cellulari sono U-266, GM1500-GRG2, LICR-LON-HMy2 e UC729-6.

In alcune esemplificazioni, una linea cellulare di ibridoma viene prodotta immunizzando un animale (ad esempio, un animale transgenico avente sequenze di immunoglobuline umane) con un immunogeno di GIPR; prelevando cellule della milza dall'animale immunizzato; fondendo le cellule della milza prelevate con una linea cellulare di mieloma, generando così cellule di ibridoma; consolidando linee cellulari di ibridoma dalle cellule di ibridoma, e identificando una linea cellulare di ibridoma che produce un anticorpo che si lega a un polipeptide di GIPR. Tali linee cellulari di ibridoma, e gli anticorpi monoclonali anti-GIPR da esse prodotti sono aspetti della presente domanda.

Gli anticorpi monoclonali secreti da una linea cellulare di ibridoma possono essere purificati usando qualsiasi tecnica nota nell'arte. Ibridomi o mAb possono essere ulteriormente sottoposti a screening per identificare mAb con proprietà particolari, come la capacità di aumentare l'attività di GIPR.

Vengono inoltre forniti anticorpi chimerici e umanizzati basati sulle sequenze di cui sopra. Gli anticorpi monoclonali per uso come agenti terapeutici possono essere modificati in vari modi prima dell'uso. Un esempio è un anticorpo chimerico, che è un anticorpo composto da segmenti di proteina di anticorpi differenti uniti in modo covalente per produrre catene leggere o pesanti di immunoglobulina funzionali o loro porzioni immunologicamente funzionali. Generalmente, una porzione della catena pesante e/o della catena leggera è identica o omologa a una sequenza corrispondente in anticorpi derivati da una particolare specie o appartenenti a una particolare classe o sottoclasse di anticorpi, mentre il resto della/e catena/e è identico o omologo a una sequenza corrispondente in anticorpi derivati da un'altra specie o appartenenti a un'altra classe o sottoclasse di anticorpi. Per i metodi relativi agli anticorpi chimerici, *si veda*, ad esempio, il brevetto statunitense n. 4,816,567; e Morrison et al., 1985, Proc. Natl. Acad. Sci. USA 81:6851-6855. L'innesto di CDR è descritto, ad esempio, nei brevetti statunitensi n. 6,180,370, n. 5,693,762, n. 5,693,761, n. 5,585,089, e n. 5,530,101.

Generalmente, l'obiettivo del realizzare un anticorpo chimerico è creare una chimera in cui il numero di amminoacidi della specie del paziente interessato sia massimizzato. Un esempio è l'anticorpo "con innesto di CDR", in cui l'anticorpo comprende una o più regioni determinanti la complementarità (CDR) di una specie particolare o appartenenti a una classe o sottoclasse di anticorpi particolare, mentre il resto della/e catena/e dell'anticorpo è identico o omologo a una sequenza

corrispondente in anticorpi derivati da un'altra specie o appartenenti a un'altra classe o sottoclasse di anticorpi. Per l'uso negli esseri umani, la regione variabile o le CDR selezionate di un anticorpo di roditore vengono spesso innestate in un anticorpo umano, sostituendo le regioni variabili o le CDR presenti in natura dell'anticorpo umano.

Un tipo utile di anticorpo chimerico è un anticorpo "umanizzato". Generalmente, un anticorpo umanizzato viene prodotto da un anticorpo monoclonale inizialmente sviluppato in un animale non umano. Certi residui di amminoacidi in questo anticorpo monoclonale, tipicamente da porzioni dell'anticorpo che non riconoscono l'antigene, vengono modificati per essere omologhi a residui corrispondenti in un anticorpo umano dell'isotipo corrispondente. L'umanizzazione può essere eseguita, ad esempio, usando vari metodi sostituendo almeno una porzione di una regione variabile di roditore con le regioni corrispondenti di un anticorpo umano (*si vedano*, ad esempio, i brevetti statunitensi n. 5,585,089, e n. 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).

In un aspetto, le CDR delle regioni variabili di catena leggera e pesante degli anticorpi forniti nella presente vengono innestate in regioni cornice (FR) di anticorpi della stessa specie filogenetica o di una differente. Ad esempio, le CDR delle regioni variabili di catena pesante e leggera V_H1, V_H2, V_H3, V_H4, V_H5, V_H6, V_H7, V_H8, V_H9, V_H10, V_H11, V_H12 e/o V_L1, e V_L2 possono essere innestate su FR umane consenso. Per

creare FR umane consenso, FR da svariate sequenze di amminoacidi di catena pesante o catena leggera umane possono essere allineate per identificare una sequenza di amminoacidi consenso. In altre forme di realizzazione, gli FR di una catena pesante o di una catena leggera divulgata nella presente vengono sostituiti con gli FR di una catena pesante o di una catena leggera differente. In un aspetto, amminoacidi rari negli FR delle catene pesanti e leggere di anticorpi contro GIPR non vengono sostituiti, mentre il resto degli amminoacidi di FR viene sostituito. Un "amminoacido raro" è un amminoacido specifico che è in una posizione in cui questo particolare amminoacido non viene solitamente trovato in un FR. In alternativa, le regioni variabili innestate dall'una catena pesante o leggera possono essere usate con una regione costante che è differente rispetto alla regione costante di quella particolare catena pesante o leggera, come divulgato nella presente. In altre forme di realizzazione, le regioni variabili innestate fanno parte di un anticorpo Fv a catena singola.

In alcune forme di realizzazione, regioni costanti di specie diverse dall'essere umano possono essere usate insieme alla/e regione/i variabile/i umana/e per produrre anticorpi ibridi.

Sono forniti anche anticorpi contro GIPR completamente umani. Sono disponibili metodi per realizzare anticorpi completamente umani specifici per un dato antigene senza esporre esseri umani all'antigene ("anticorpi completamente umani"). Un mezzo specifico fornito per implementare la produzione di anticorpi completamente umani è

l'"umanizzazione" del sistema immunitario umorale di topo. L'introduzione di loci di immunoglobulina (Ig) umani nei topi in cui i geni Ig endogeni sono stati inattivati è un mezzo per produrre anticorpi monoclonali (mAb) completamente umani nel topo, un animale che può essere immunizzato con qualsiasi antigene desiderabile. Usare anticorpi completamente umani può ridurre al minimo le risposte immunogene e allergiche che possono talvolta essere causate dalla somministrazione di mAb di topo o derivati da topo agli esseri umani come agenti terapeutici.

Anticorpi completamente umani possono essere prodotti immunizzando animali transgenici (solitamente topi) che sono in grado di produrre un repertorio di anticorpi umani in assenza di produzione di immunoglobuline endogene. Gli antigeni per questo scopo hanno tipicamente sei o più amminoacidi contigui e, facoltativamente, sono coniugati a un trasportatore, come un aptene. *Si veda*, ad esempio, Jakobovits et al., 1993, Proc. Natl. Acad. Sci. USA 90:2551-2555; Jakobovits et al., 1993, Nature 362:255-258; e Bruggermann et al., 1993, Year in Immunol. 7:33. In un esempio di tale metodo, animali transgenici vengono prodotti inabilitando i loci di immunoglobulina di topo endogeni codificanti le catene di immunoglobulina pesanti e leggere di topo in essi presenti, e inserendo nel genoma di topo grandi frammenti di DNA di genoma umano contenenti loci che codificano le proteine di catena pesante e leggera umane. Animali parzialmente modificati, che hanno meno della gamma completa di loci di immunoglobulina umani, vengono poi incrociati per ottenere un animale avente tutte le modifiche desiderate

del sistema immunitario. Quando viene somministrato un immunogeno, questi animali transgenici producono anticorpi immunospecifici per l'immunogeno, ma hanno sequenze di amminoacidi umane anziché di topo, incluse le regioni variabili. Per ulteriori dettagli su tali metodi, *si veda*, ad esempio, WO96/33735 e WO94/02602. Metodi aggiuntivi relativi ai topi transgenici per realizzare anticorpi umani sono descritti nei brevetti statunitensi n. 5,545,807; n. 6,713,610; n. 6,673,986; n. 6,162,963; n. 5,545,807; n. 6,300,129; n. 6,255,458; n. 5,877,397; n. 5,874,299 e n. 5,545,806; nelle pubblicazioni PCT WO91/10741, WO90/04036, e in EP 546073B1 e EP 546073A1.

I topi transgenici descritti sopra, cui nella presente si fa riferimento come topi "HuMab", contengono un minilocus di gene di immunoglobulina umano che codifica sequenze di immunoglobuline di catena pesante ([mu] e [gamma]) e leggera [kappa] umane non riarrangiate, insieme a mutazioni mirate che inattivano i loci di catena [mu] e [kappa] endogeni (Lonberg et al., 1994, Nature 368:856-859). Di conseguenza, i topi esibiscono un'espressione ridotta di IgM o [kappa] di topo e in risposta all'immunizzazione, e i transgeni di catena pesante e leggera umana introdotti subiscono un cambio di classe e una mutazione somatica per generare anticorpi monoclonali IgG [kappa] umani ad alta affinità (Lonberg *et al.*, sopra; Lonberg e Huszar, 1995, Intern. Rev. Immunol. 13: 65-93; Harding e Lonberg, 1995, Ann. N.Y. Acad. Sci. 764:536-546). La preparazione di topi HuMab è descritta in dettaglio 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 e Huszar, 1995, Intern. Rev. Immunol. 13:65-93; Harding e Lonberg, 1995, Ann. N.Y. Acad. Sci. 764:536-546; Fishwild et al., 1996, Nature Biotechnology 14:845-851. *Si vedano* inoltre i brevetti statunitensi n. 5,545,806; n. 5,569,825; n. 5,625,126; n. 5,633,425; n. 5,789,650; n. 5,877,397; n. 5,661,016; n. 5,814,318; n. 5,874,299; e n. 5,770,429; nonché il brevetto statunitense n. 5,545,807; le domande internazionali n. WO 93/1227; WO 92/22646; e WO 92/03918. Le tecnologie utilizzate per produrre anticorpi umani in questi topi transgenici sono divulgate anche in WO 98/24893 e Mendez et al., 1997, Nature Genetics 15:146-156. Ad esempio, i ceppi di topi transgenici HCo7 e HCo12 possono essere usati per generare anticorpi monoclonali umani contro GIPR. Di seguito vengono forniti ulteriori dettagli riguardanti la produzione di anticorpi umani usando topi transgenici.

Usando la tecnologia degli ibridomi, mAb umani specifici per l'antigene con la specificità desiderata possono essere prodotti e selezionati dai topi transgenici come quelli descritti sopra. Tali anticorpi possono essere clonati ed espressi usando un vettore e una cellula ospite adatti, oppure gli anticorpi possono essere raccolti da cellule di ibridoma coltivate.

Anticorpi completamente umani possono anche essere derivati da librerie di esposizione su fagi (come descritto in Hoogenboom et al., 1991, J. Mol. Biol. 227:381; e Marks et al., 1991, J. Mol. Biol. 222:581). Le tecniche di esposizione su fagi imitano la selezione immunitaria attraverso l'esposizione di repertori di anticorpi sulla superficie di un batteriofago filamentoso, e la successiva selezione di un fago mediante il suo legame con un antigene di scelta. Una di queste tecniche è descritta nella pubblicazione PCT n. WO 99/10494.

La proteina legante GIPR può anche essere una variante, un mimetico, un derivato o un oligomero basata/o sulla struttura di proteine leganti l'antigene di GIPR aventi le CDR, le regioni variabili e/o le catene a lunghezza intera come descritti sopra.

In una forma di realizzazione, ad esempio, una proteina legante l'antigene è una forma variante delle proteine leganti l'antigene divulgate sopra. Ad esempio, alcune delle proteine leganti l'antigene hanno una o più sostituzioni di amminoacidi conservative in una o più tra le catene pesanti o leggere, le regioni variabili o le CDR.

Gli amminoacidi presenti in natura possono essere suddivisi in classi in base alle proprietà comuni della catena laterale:

1) idrofobi: norleucina, Met, Ala, Val, Leu, Ile;

2) idrofili neutri: Cys, Ser, Thr, Asn, Gln;

3) acidi: Asp, Glu;

4) basici: His, Lys, Arg;

5) residui che influenzano l'orientamento di catena: Gly, Pro; e

6) aromatici: Trp, Tyr, Phe.

Sostituzioni di amminoacidi conservative possono includere lo scambio di un membro di una di queste classi con un altro membro della stessa classe. Sostituzioni di amminoacidi conservative possono includere residui di amminoacidi non presenti in natura che sono tipicamente incorporati mediante sintesi chimica di peptidi piuttosto che mediante sintesi in sistemi biologici. Queste includono peptidomimetici e altre forme invertite o rovesciate di frazioni amminoacido.

Le sostituzioni non conservative possono comportare lo scambio di un membro di una delle classi sopra menzionate con un membro di un'altra classe. Tali residui sostituiti possono essere introdotti in regioni dell'anticorpo che sono omologhe ad anticorpi umani, oppure nelle regioni non omologhe della molecola.

Nel realizzare tali cambiamenti, secondo certe forme di realizzazione, può essere preso in considerazione l'indice idropatico degli amminoacidi. Il profilo idropatico di una proteina viene calcolato assegnando a ciascun amminoacido un valore numerico ("indice idropatico") e poi calcolando ripetutamente la media di questi valori lungo la catena di peptide. A ciascun amminoacido è stato assegnato un indice idropatico sulla base della sua idrofobicità e delle sue caratteristiche di carica. Essi sono: isoleucina (+4,5); valina (+4,2); leucina (+3,8); fenilalanina (+2,8); cisteina/cistina (+2,5); metionina (+1,9); alanina (+1,8); glicina (-0,4); treonina (-0,7); serina (-0,8); triptofano (-0,9); tirosina (-1,3); prolina (-1,6); istidina (-3,2); glutammato (-3,5);

glutammina (-3,5); aspartato (-3,5); asparagina (-3,5); lisina (-3,9); e arginina (-4,5).

L'importanza del profilo idropatico nel conferire una funzione biologica interattiva a una proteina è compresa nell'arte (*si veda*, ad esempio, Kyte et al., 1982, J. Mol. Biol. 157: 105-131). È noto che certi amminoacidi possono sostituire altri amminoacidi aventi un indice o punteggio idropatico simile e mantenere comunque un'attività biologica simile. Nel realizzare cambiamenti in base all'indice idropatico, in certe forme di realizzazione, è inclusa la sostituzione di amminoacidi i cui indici idropatici sono entro ±2. In alcuni aspetti sono inclusi quelli compresi tra ±1, e, in altri aspetti, sono inclusi quelli compresi tra ±0,5.

È inoltre noto nell'arte che la sostituzione di amminoacidi simili può essere realizzata efficacemente sulla base dell'idrofilia, particolarmente quando la proteina o il peptide biologicamente funzionale così creato è destinato all'uso in forme di realizzazione immunologiche, come nel caso presente. In certe forme di realizzazione, la massima idrofilia media locale di una proteina, regolata dall'idrofilia dei suoi amminoacidi adiacenti, è correlata alla sua immunogenicità e al legame con l'antigene o all'immunogenicità, vale a dire a una proprietà biologica della proteina.

Ai residui di amminoacidi sono stati assegnati i seguenti valori di idrofilia: arginina (+ 3,0); lisina (+ 3,0); aspartato (+ 3,0±1); glutammato (+ 3,0±1); serina (+ 0,3); asparagina (+ 0,2); glutammina (+ 0,2); glicina (+0); treonina (-0,4); prolina (-0,5±1); alanina (-0,5); istidina (-0,5);

cisteina (-1,0); metionina (-1,3); valina (-1,5); leucina (-1,8); isoleucina (-1,8); tirosina (-2,3); fenilalanina (-2,5) e triptofano (-3,4). Nel realizzare cambiamenti in base a valori di idrofilia simili, in certe forme di realizzazione è inclusa la sostituzione di amminoacidi i cui valori di idrofilia sono compresi tra ±2, in altre forme di realizzazione sono inclusi quelli che sono compresi tra ±1 e, in altre forme di realizzazione ancora, sono inclusi quelli che sono compresi tra ±0,5. In alcune esemplificazioni, è anche possibile identificare epitopi di sequenze di amminoacidi primarie sulla base dell'idrofilia. A queste regioni di fa riferimento ance come "regioni nucleo epitopiche".

Nella Tabella 6 sono esposte alcune sostituzioni di amminoacidi conservative.

Tabella 8: sostituzioni di amminoacidi conservative

Residuo originale	**Sostituzioni esemplificative**
Ala	Ser
Arg	Lys
Asn	Gln, His
Asp	Glu
Cys	Ser
Gln	Asn
Glu	Asp
Gly	Pro

Residuo originale	Sostituzioni esemplificative
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

Un tecnico del ramo sarà in grado di determinare varianti adatte di polipeptidi come esposto nella presente usando tecniche ben note. Un tecnico del ramo può identificare aree adatte della molecola che possono essere cambiate senza distruggere l'attività prendendo come bersaglio regioni che non si ritiene siano importanti per l'attività. Il tecnico del ramo sarà anche in grado di identificare residui e porzioni delle molecole che sono conservate tra polipeptidi simili. In ulteriori forme di realizzazione, anche aree che possono essere importanti per l'attività biologica o per la

struttura possono essere soggette a sostituzioni di amminoacidi conservative senza distruggere l'attività biologica o senza influenzare negativamente la struttura del polipeptide.

In aggiunta, un tecnico del ramo può esaminare gli studi struttura-funzione identificando residui in polipeptidi simili che sono importanti per l'attività o la struttura. Alla luce di tale confronto, è possibile prevedere l'importanza di residui di amminoacidi in una proteina che corrispondono a residui di amminoacidi importanti per l'attività o la struttura in proteine simili. Un tecnico del ramo può optare per sostituzioni con amminoacidi chimicamente simili di tali residui di amminoacidi importanti previsti.

Un tecnico del ramo può anche analizzare la struttura tridimensionale e la sequenza di amminoacidi in relazione a tale struttura in polipeptidi simili. Alla luce di tali informazioni, un tecnico del ramo può prevedere l'allineamento dii residui di amminoacidi di un anticorpo rispetto alla sua struttura tridimensionale. Un tecnico del ramo potrebbe scegliere di non apportare cambiamenti radicali ai residui di amminoacidi che si prevede siano sulla superficie della proteina, poiché tali residui potrebbero essere coinvolti in interazioni importanti con altre molecole. Oltretutto, un tecnico del ramo può generare varianti di test contenenti una singola sostituzione di amminoacidi in ciascun residuo di amminoacido desiderato. Queste varianti possono poi essere sottoposte a screening usando saggi per l'attività di GIPR, a rendere così informazioni su quali amminoacidi possono essere cambiati e quali non

devono essere cambiati. In altre parole, sulla base delle informazioni raccolte da tali esperimenti di routine, un tecnico del ramo può facilmente determinare le posizioni di amminoacidi in cui ulteriori sostituzioni dovrebbero essere evitate, da sole o in combinazione con altre mutazioni.

Numerose pubblicazioni scientifiche sono state dedicate alla previsione della struttura secondaria. *Si veda*, 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; e Chou et al., 1979, Biophys. J. 26:367-384. Oltretutto, attualmente sono disponibili programmi per computer che aiutano a prevedere la struttura secondaria. Un metodo per prevedere la struttura secondaria si basa sulla modellizzazione dell'omologia. Ad esempio, due polipeptidi o proteine che hanno un'identità di sequenza superiore al 30% o una similarità superiore al 40% possono avere topologie strutturali simili. La recente crescita del database delle strutture delle proteine (PDB) ha migliorato la prevedibilità della struttura secondaria, incluso il numero potenziale di ripiegamenti all'interno della struttura di un polipeptide o di una proteina. *Si veda*, Holm et al., 1999, Nucl. Acid. Res. 27:244-247. È stato suggerito (Brenner et al., 1997, Curr. Op. Struct. Biol. 7:369-376) che vi è un numero limitato di ripiegamenti in un dato polipeptide o una data proteina e che, una volta risolto un numero critico

di strutture, la previsione della struttura diventerà notevolmente più accurata.

Metodi aggiuntivi per prevedere la struttura secondaria includono il "riconoscimento dei ripiegamenti" (Jones, 1997, Curr. Opin. Struct. Biol. 7:377-387; Sippl et al., 1996, Structure 4: 15-19), l'"analisi del profilo" (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), e il "collegamento evolutivo" (*si veda* Holm, 1999, sopra; e Brenner, 1997, sopra).

In alcune forme di realizzazione, vengono realizzate sostituzioni di amminoacidi che: (1) riducono la suscettibilità alla proteolisi, (2) riducono la suscettibilità all'ossidazione, (3) alterano l'affinità di legame per formare complessi proteici, (4) alterano le affinità di legame a ligando o ad antigene e/o (4) conferiscono o modificano altre proprietà fisico-chimiche o funzionali su tali polipeptidi. Ad esempio, possono essere realizzate sostituzioni di amminoacidi singole o multiple (in certe forme di realizzazione, sostituzioni di amminoacidi conservative) nella sequenza presente in natura. Le sostituzioni possono essere realizzate in quella porzione dell'anticorpo che si trova all'esterno del/dei dominio/domini che forma/formano i contatti intermolecolari. In tali forme di realizzazione, possono essere usate sostituzioni di amminoacidi conservative che non cambiano sostanzialmente le caratteristiche strutturali della sequenza parentale (ad esempio, uno o più amminoacidi sostitutivi che non interrompono la struttura secondaria che caratterizza la proteina legante

l'antigene parentale o nativa). Esempi di strutture secondarie e terziarie di polipeptidi riconosciute nell'arte sono descritti in Proteins, Structures and Molecular Principles (Creighton, Ed.), 1984, W. H. New York: Freeman and Company; Introduction to Protein Structure (Branden e Tooze, curatori), 1991, New York: Garland Publishing; e Thornton et al., 1991, Nature 354:105.

Varianti di anticorpi preferite aggiuntive includono varianti di cisteina in cui uno o più residui di cisteina nella sequenza di amminoacidi parentale o nativa vengono deleti o sostituiti con un altro amminoacido (ad esempio serina). Le varianti di cisteina sono utili, tra l'altro, quando gli anticorpi devono essere nuovamente ripiegati in una conformazione biologicamente attiva. Le varianti di cisteina possono avere meno residui di cisteina rispetto all'anticorpo nativo e tipicamente ne hanno un numero pari per ridurre al minimo le interazioni risultanti da cisteine spaiate.

Le catene pesanti e leggere, i domini di regioni variabili e le CDR che sono divulgati possono essere usati per preparare polipeptidi che contengono una regione legante l'antigene che può legarsi specificamente a GIPR. Ad esempio, una o più CDR possono essere incorporate in una molecola (ad esempio un polipeptide) in modo covalente o in modo non covalente per realizzare un'immunoadesione. Un'immunoadesione può incorporare la/e CDR come parte di una catena di polipeptide più grande, può collegare in modo covalente la/e CDR a un'altra catena di polipeptide oppure può incorporare la/e CDR in modo non covalente. La/e CDR consente/consentono all'immunoadesione di

legarsi specificamente a un particolare antigene di interesse (ad esempio un polipeptide di GIPR o un suo epitopo).

Vengono anche forniti mimetici (ad esempio "mimetici peptidici" o "peptidomimetici") basati sui domini di regione variabile e sulle CDR che sono descritti nella presente. Questi analoghi possono essere peptidi, non peptidi o combinazioni di regioni di peptide e di non peptide. Fauchere, 1986, Adv. Drug Res. 15:29; Veber e Freidinger, 1985, TINS p. 392; ed Evans et al., 1987, J. Med. Chem. 30:1229. I mimetici peptidici che sono strutturalmente simili a peptidi terapeuticamente utili possono essere usati per produrre un effetto terapeutico o profilattico simile. Tali composti vengono spesso sviluppati con l'ausilio della modellizzazione molecolare computerizzata. Generalmente, i peptidomimetici sono proteine che sono strutturalmente simili a un anticorpo che mostra un'attività biologica desiderata, qui, di fatto, la capacità di legarsi specificamente a GIPR, ma che hanno uno o più collegamenti peptidici facoltativamente sostituiti da un collegamento selezionato tra: $-CH_2NH-$, $-CH_2S-$, $-CH_2-CH_2-$, -CH-CH-(cis e trans), $-COCH_2-$, $-CH(OH)CH_2-$, e $-CH_2SO-$, mediante metodi ben noti nell'arte. La sostituzione sistematica di uno o più amminoacidi di una sequenza consenso con un D-amminoacido dello stesso tipo (ad esempio D-lisina al posto di L-lisina) può essere usata in certe forme di realizzazione per generare proteine più stabili. In aggiunta, peptidi vincolati comprendenti una sequenza consenso o una variazione di sequenza consenso sostanzialmente identica possono essere generati mediante metodi noti nell'arte (Rizo e

Gierasch, 1992, Ann. Rev. Biochem. 61:387)), ad esempio aggiungendo residui di cisteina interni in grado di formare ponti disolfuro intramolecolari che ciclizzano il peptide.

Vengono inoltre forniti derivati delle proteine leganti l'antigene che sono descritte nella presente. Le proteine leganti l'antigene derivatizzate possono comprendere qualsiasi molecola o sostanza che conferisca una proprietà desiderata all'anticorpo o al frammento, come, ad esempio, un'emivita aumentata in un uso particolare. La proteina legante l'antigene derivatizzata può comprendere, ad esempio, una frazione rilevabile (o di marcatura) (ad esempio una molecola radioattiva, colorimetrica, antigenica o enzimatica, una biglia rilevabile (come una biglia magnetica o elettrondensa (ad esempio d'oro)), o una molecola che si lega ad un'altra molecola (ad esempio biotina o streptavidina)), una frazione terapeutica o diagnostica (ad esempio una frazione radioattiva, citotossica o farmaceuticamente attiva), o una molecola che aumenta l'idoneità della proteina legante l'antigene per un uso particolare (ad esempio somministrazione a un soggetto, come un soggetto umano, o altri usi *in vivo* o *in vitro*). Esempi di molecole che possono essere usate per derivatizzare una proteina legante l'antigene includono albumina (ad esempio albumina sierica umana) e glicole di polietilene (PEG). Derivati collegati ad albumina e PEGilati di proteine leganti l'antigene possono essere preparati usando tecniche ben note nell'arte. Certe proteine leganti l'antigene includono un polipeptide a catena singola PEGilato come descritto nella presente. In una forma di realizzazione, la proteina

legante l'antigene è coniugata o altrimenti collegata a transtiretina (TTR) o a una variante di TTR. La TTR o la variante di TTR può essere modificata chimicamente, ad esempio, con una sostanza chimica selezionata dal gruppo consistente in destrano, poli(n-vinilpirrolidone), glicoli di polietilene, omopolimeri di glicole di propropilene, copolimeri di ossido di polipropilene/ossido di etilene, polioli poliossietilati e alcoli polivinilici.

Altri derivati includono coniugati covalenti o aggregativi di proteine leganti l'antigene di GIPR con altre proteine o polipeptidi, come mediante l'espressione di proteine di fusione ricombinanti comprendenti polipeptidi eterologhi fusi all'N-terminale o al C-terminale di una proteina legante l'antigene di GIPR. Ad esempio, il peptide coniugato può essere un polipeptide segnale (o leader) eterologo, ad esempio il leader di fattore alfa di lievito o un peptide come un tag epitopico. Proteine di fusione contenenti proteine leganti l'antigene di GIPR possono comprendere peptidi aggiunti per facilitare la purificazione o l'identificazione della proteina legante l'antigene di GIPR (ad esempio poli-His). Una proteina legante l'antigene di GIPR può anche essere collegata al peptide FLAG come descritto in Hopp et al., 1988, Bio/Technology 6:1204; e nel brevetto statunitense n. 5,011,912. Il peptide FLAG è altamente antigenico e fornisce un epitopo legato in modo reversibile da uno specifico anticorpo monoclonale (mAb), consentendo un rapido saggio e una facile purificazione della proteina ricombinante espressa. Reagenti utili per la preparazione di proteine di

fusione in cui il peptide FLAG è fuso a un dato polipeptide sono disponibili in commercio (Sigma, St. Louis, MO).

In alcune forme di realizzazione, la proteina legante l'antigene comprende una o più marcature. Il termine "gruppo di marcatura" o "marcatura" significa qualsiasi marcatura rilevabile. Esempi di gruppi di marcatura adatti includono, ma senza limitarvisi, quanto segue: radioisotopi o radionuclidi (ad esempio ^{3}H, ^{14}C, ^{15}N, ^{35}S, ^{90}Y, ^{99}Tc, ^{111}In, ^{125}I, ^{131}I), gruppi fluorescenti (ad esempio FITC, rodamina, fosfori lantanidi), gruppi enzimatici (ad esempio perossidasi di rafano, β-galattosidasi, luciferasi, fosfatasi alcalina), gruppi chemiluminescenti, gruppi biotinile, o epitopi di polipeptidi predeterminati riconosciuti da un reporter secondario (ad esempio sequenze di coppie di cerniera di leucine, siti di legame per anticorpi secondari, domini di legame a metalli, tag epitopici). In alcune forme di realizzazione, il gruppo di marcatura è accoppiato alla proteina legante l'antigene tramite bracci di distanziatore di varie lunghezze per ridurre il potenziale ingombro sterico. Nell'arte sono noti vari metodi per marcare le proteine che possono essere usati a seconda delle esigenze.

Il termine "gruppo effettore" significa qualsiasi gruppo accoppiato a una proteina legante l'antigene che agisce come agente citotossico. Esempi di gruppi effettori adatti sono radioisotopi o radionuclidi (ad esempio ^{3}H, ^{14}C, ^{15}N, ^{35}S, ^{90}Y, ^{99}Tc, ^{111}In, ^{125}I, ^{131}I). Altri gruppi adatti includono tossine, gruppi terapeutici, o gruppi chemioterapici. Esempi di gruppi adatti includono calicheamicina, auristatine, geldanamicina e

maitansina. In alcune forme di realizzazione, il gruppo effettore è accoppiato alla proteina legante l'antigene tramite bracci di distanziatore di varie lunghezze per ridurre il potenziale ingombro sterico.

In generale, le marcature rientrano in una varietà di classi, a seconda del saggio in cui devono essere rilevate: a) marcature isotopiche, che possono essere isotopi radioattivi o pesanti; b) marcature magnetiche (ad esempio particelle magnetiche); c) frazioni redox attive; d) coloranti ottici; gruppi enzimatici (ad esempio perossidasi di rafano, β-galattosidasi, luciferasi, fosfatasi alcalina); e) gruppi biotinilati; e f) epitopi di polipeptidi predeterminati riconosciuti da un reporter secondario (ad esempio sequenze di coppie di cerniera di leucine, siti di legame per anticorpi secondari, domini di legame a metalli, tag epitopici, eccetera). In alcune forme di realizzazione, il gruppo di marcatura è accoppiato alla proteina legante l'antigene tramite bracci di distanziatore di varie lunghezze per ridurre il potenziale ingombro sterico. Nell'arte sono noti vari metodi per la marcatura delle proteine.

Marcature specifiche includono coloranti ottici, inclusi, ma senza limitarvisi, cromofori, fosfori e fluorofori, questi ultimi essendo specifici in molte esemplificazioni. I fluorofori possono essere fluori "a piccola molecola" o fluori proteici.

Per "marcatura fluorescente" si intende qualsiasi molecola che può essere rilevata tramite le sue proprietà fluorescenti intrinseche. Marcature fluorescenti adatte includono, ma senza limitarvisi, fluoresceina, rodamina, tetrametilrodamina, eosina, eritrosina, cumarina,

metil-cumarine, pirene, verde malachite, stilbene, giallo Lucifero, Cascade BlueJ, rosso Texas, IAEDANS, EDANS, BODIPY FL, LC Red 640, Cy 5, Cy 5.5, LC Red 705, verde Oregon, i coloranti Alexa-Fluor (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), blu Cascade, giallo Cascade e R-ficoeritrina (PE) (Molecular Probes, Eugene, OR), FITC, rodamina, e Texas Red (Pierce, Rockford, IL), Cy5, Cy5.5, Cy7 (Amersham Life Science, Pittsburgh, PA). Coloranti ottici adatti, inclusi fluorofori, sono descritti in Molecular Probes Handbook di Richard P. Haugland.

Marcature fluorescenti proteiche adatte includono anche, ma senza limitarvisi, proteine fluorescenti verdi, inclusa una specie di GFP di Renilla, Ptilosarcus o Aequorea (Chalfie et al., 1994, Science 263:802-805), EGFP (Clontech Labs., Inc., numero di accesso Genbank U55762), proteina fluorescente blu (BFP, Quantum Biotechnologies, Inc., Quebec, Canada; Stauber, 1998, Biotechniques 24:462-471; Heim et al., 1996, Curr. Biol. 6:178-182), proteina fluorescente gialla potenziata (EYFP, Clontech Labs., Inc.), luciferasi (Ichiki et al., 1993, J. Immunol. 150:5408-5417), β-galattosidasi (Nolan *et al.*, 1988, Proc. Natl. Acad. Sci. U.S.A. 85:2603-2607) e Renilla (WO92/15673, WO95/07463, WO98/14605, WO98/26277, WO99/49019, brevetti statunitensi n. 5292658, n. 5418155, n. 5683888, n. 5741668, n. 5777079, n. 5804387, n. 5874304, n. 5876995, n. 5925558).

Sono inoltre forniti acidi nucleici che codificano le proteine leganti l'antigene descritte nella presente, o loro porzioni, inclusi acidi nucleici codificanti una o entrambe le catene di un anticorpo, o un/una suo/a frammento, derivato, muteina o variante, polinucleotidi codificanti regioni variabili di catena pesante o solo CDR, polinucleotidi sufficienti per l'uso come sonde di ibridazione, primer per PCR o primer di sequenziamento per identificare, analizzare, mutare o amplificare un polinucleotide codificante un polipeptide, acidi nucleici antisenso per inibire l'espressione di un polinucleotide, e sequenze complementari di quanto sopra. Gli acidi nucleici possono avere qualsiasi lunghezza. Possono avere, ad esempio, una lunghezza di 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 o più nucleotidi e/o possono comprendere una o più sequenze aggiuntive, ad esempio sequenze regolatrici, e/o far parte di un acido nucleico più grande, ad esempio un vettore. Gli acidi nucleici possono essere a singolo filamento o a doppio filamento e possono comprendere nucleotidi di RNA e/o DNA e loro varianti artificiali (ad esempio, acidi peptidonucleici). Qualsiasi regione variabile fornita nella presente può essere attaccata a queste regioni costanti per formare sequenze di catene pesanti e leggere complete. Tuttavia, resta inteso che queste sequenze di regioni costanti sono fornite solo come esempi specifici. In alcune forme di realizzazione, le sequenze di regione variabile vengono unite ad altre sequenze di regione costante che sono note nell'arte.

Acidi nucleici codificanti certe proteine leganti l'antigene, o loro porzioni (ad esempio anticorpo a lunghezza intera, catena pesante o leggera, dominio variabile, o CDRH1, CDRH2, CDRH3, CDRL1, CDRL2 o CDRL3), possono essere isolati da cellule B di topi che sono stati immunizzati con GIPR o un suo frammento immunogeno. L'acido nucleico può essere isolato mediante procedure convenzionali come la reazione a catena della polimerasi (PCR). L'esposizione su fagi è un altro esempio di tecnica nota con cui possono essere preparati derivati di anticorpi e altre proteine leganti l'antigene. In un approccio, polipeptidi che sono componenti di una proteina legante l'antigene di interesse vengono espressi in qualsiasi sistema di espressione ricombinante adatto, e ai polipeptidi espressi viene consentito di assemblarsi per formare proteine leganti l'antigene.

Un ulteriore aspetto fornisce acidi nucleici che si ibridano con altri acidi nucleici in particolari condizioni di ibridazione. Metodi per l'ibridazione di acidi nucleici sono ben noti nell'arte. *Si veda*, ad esempio, Current Protocols in Molecular Biology, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. Come definito nella presente, una condizione di ibridazione moderatamente stringente usa una soluzione di prelavaggio contenente 5x cloruro di sodio/citrato di sodio (SSC), 0,5% di SDS, EDTA 1,0 mM (pH 8,0), tampone di ibridazione di circa il 50% di formammide, 6x SSC, e una temperatura di ibridazione di 55 °C (o altre soluzioni di ibridazione simili, come una contenente circa il 50% di formammide, con una temperatura di ibridazione di 42 °C) e condizioni di lavaggio di 60 °C, in

0,5x SSC, 0,1% di SDS. Una condizione di ibridazione stringente ibrida in 6x SSC a 45 °C, cui fanno seguito uno o più lavaggi in 0,1x SSC, 0,2% di SDS a 68 °C. Per di più, un tecnico del ramo può manipolare le condizioni di ibridazione e/o lavaggio per aumentare o diminuire la stringenza di ibridazione in modo che gli acidi nucleici comprendenti sequenze di nucleotidi che sono almeno al 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% o 99% identiche tra loro rimangano tipicamente ibridati tra loro.

I parametri di base che influenzano la scelta delle condizioni di ibridazione e le linee guida per l'elaborazione di condizioni adatte sono esposti, ad esempio, da Sambrook, Fritsch e Maniatis (2001, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., sopra; e Current Protocols in Molecular Biology, 1995, Ausubel et al., curatori, John Wiley & Sons, Inc., sezioni 2.10 e 6.3-6.4), e possono essere facilmente determinati dai tecnici del ramo di ordinarie competenze in base, ad esempio, alla lunghezza e/o alla composizione in basi dell'acido nucleico.

Cambiamenti possono essere introdotti tramite mutazione in un acido nucleico, portando così a cambiamenti nella sequenza di amminoacidi di un polipeptide (ad esempio un anticorpo o un derivato di anticorpo) che codifica. Le mutazioni possono essere introdotte usando qualsiasi tecnica nota nell'arte. In una forma di realizzazione, uno o più residui di amminoacidi particolari vengono cambiati usando, ad esempio, un protocollo di mutagenesi sito-diretta. In un'altra forma di realizzazione,

uno o più residui selezionati casualmente vengono cambiati usando, ad esempio, un protocollo di mutagenesi casuale. Comunque venga realizzato, un polipeptide mutante può essere espresso e sottoposto a screening per una proprietà desiderata.

Le mutazioni possono essere introdotte in un acido nucleico senza alterare significativamente l'attività biologica del polipeptide che codifica. Ad esempio, è possibile realizzare sostituzioni di nucleotidi che portano a sostituzioni di amminoacidi in residui di amminoacidi non essenziali. In alternativa, in un acido nucleico possono essere introdotte una o più mutazioni che cambiano selettivamente l'attività biologica di un polipeptide che codifica. Ad esempio, la mutazione può cambiare quantitativamente o qualitativamente l'attività biologica. Esempi di cambiamenti quantitativi includono aumentare, ridurre o eliminare l'attività. Esempi di cambiamenti qualitativi includono cambiare la specificità per l'antigene di un anticorpo. In una forma di realizzazione, un acido nucleico codificante qualsiasi proteina legante l'antigene descritta nella presente può essere mutato per alterare la sequenza di amminoacidi usando tecniche di biologia molecolare ben consolidate nell'arte.

Un altro aspetto fornisce molecole di acido nucleico che sono adatte per l'uso come primer o sonde di ibridazione per il rilevamento di sequenze di acido nucleico. Una molecola di acido nucleico può comprendere solo una porzione di una sequenza di acido nucleico codificante un polipeptide a lunghezza intera, ad esempio un frammento

che può essere usato come sonda o primer oppure un frammento codificante una porzione attiva di un polipeptide.

Le sonde basate sulla sequenza di un acido nucleico possono essere usate per rilevare l'acido nucleico o acidi nucleici simili, ad esempio trascritti codificanti un polipeptide. La sonda può comprendere un gruppo di marcatura, ad esempio un radioisotopo, un composto fluorescente, un enzima, o un cofattore enzimatico. Tali sonde possono essere usate per identificare una cellula che esprime il polipeptide.

Un altro aspetto fornisce vettori comprendenti un acido nucleico codificante un polipeptide o una sua porzione (ad esempio un frammento contenente una o più CDR o uno o più domini di regione variabile). Esempi di vettori includono, ma senza limitarvisi, plasmidi, vettori virali, vettori di mammifero non episomali e vettori di espressione, ad esempio vettori di espressione ricombinante. I vettori di espressione ricombinante possono comprendere un acido nucleico in una forma adatta all'espressione dell'acido nucleico in una cellula ospite. I vettori di espressione ricombinante includono una o più sequenze regolatrici, selezionate sulla base delle cellule ospiti da usare per l'espressione, che sono collegate funzionalmente alla sequenza di acido nucleico da esprimere. Le sequenze regolatrici includono quelle che dirigono l'espressione costitutiva di una sequenza di nucleotidi in molti tipi di cellule ospiti (ad esempio il potenziatore del gene precoce SV40, il promotore di virus del sarcoma di Rous e il promotore di citomegalovirus), quelli che dirigono l'espressione della sequenza di

nucleotidi solo in certe cellule ospiti (ad esempio sequenze regolatrici tessuto-specifiche, *si veda* Voss et al., 1986, Trends Biochem. Sci. 11:287, Maniatis et al., 1987, Science 236: 1237, incorporati nella presente per riferimento nella loro interezza), e quelle che dirigono l'espressione inducibile di una sequenza di nucleotidi in risposta a un trattamento o a una condizione particolare (ad esempio il promotore di metallotioneina in cellule di mammifero e il promotore che risponde a tet e/o che risponde alla streptomicina in sistemi sia procariotici che eucariotici (*si veda, id.*). I tecnici del ramo comprenderanno che la progettazione del vettore di espressione può dipendere da fattori quali la scelta della cellula ospite da trasformare, il livello di espressione della proteina desiderata, eccetera. I vettori di espressione possono essere introdotti nelle cellule ospiti per produrre in tal modo proteine o peptidi, incluse proteine di fusione o peptidi, codificati da acidi nucleici come descritto nella presente.

Un altro aspetto fornisce cellule ospiti nelle quali è stato introdotto un vettore di espressione ricombinante. Una cellula ospite può essere qualsiasi cellula procariotica (ad esempio, *E. coli)* o cellula eucariotica (ad esempio, cellule di lievito, di insetto o di mammifero (ad esempio cellule CHO)). DNA vettoriale può essere introdotto in cellule procariotiche o eucariotiche tramite tecniche convenzionali di trasformazione o trasfezione. Per la trasfezione stabile di cellule di mammifero, è noto che, a seconda del vettore di espressione e della tecnica di trasfezione usati, solo una piccola quota di cellule può integrare

il DNA estraneo nel proprio genoma. Al fine di identificare e selezionare questi integranti, un gene che codifica un marcatore selezionabile (ad esempio per la resistenza agli antibiotici) viene generalmente introdotto nelle cellule ospiti insieme al gene di interesse. Marcatori selezionabili preferiti includono quelli che conferiscono resistenza ai farmaci, come G418, igromicina e metotrexato. Le cellule trasfettate stabilmente con l'acido nucleico introdotto possono essere identificate mediante la selezione con farmaci (ad esempio le cellule che hanno incorporato il gene di marcatore selezionabile sopravviveranno, mentre le altre cellule muoiono), tra gli altri metodi.

Nella presente vengono inoltre forniti sistemi e costrutti di espressione sotto forma di plasmidi, vettori di espressione, cassette di trascrizione o espressione che comprendono almeno un polinucleotide come descritto sopra, nonché cellule ospiti comprendenti tali sistemi o costrutti di espressione.

Le proteine leganti l'antigene fornite nella presente possono essere preparate mediante qualsiasi di numerose tecniche convenzionali. Ad esempio, proteine leganti l'antigene di GIPR possono essere prodotte mediante sistemi di espressione ricombinante, usando qualsiasi tecnica nota nell'arte. *Si veda*, ad esempio, Monoclonal Antibodies, Hybridomas: A New Dimension in Biological Analyses, Kennet et al. (curatore) Plenum Press, New York (1980); e Antibodies: A Laboratory Manual, Harlow e Lane (curatore), Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1988).

Le proteine leganti l'antigene possono essere espresse in linee cellulari di ibridoma (ad esempio, in particolare, gli anticorpi possono essere espressi in ibridomi) o in linee cellulari diverse dagli ibridomi. I costrutti di espressione codificanti gli anticorpi possono essere usati per trasformare una cellula ospite di mammifero, insetto o microbo. La trasformazione può essere eseguita usando qualsiasi metodo noto per introdurre polinucleotidi in una cellula ospite, incluso, ad esempio, l'impacchettamento del polinucleotide in un virus o in un batteriofago e la trasduzione di una cellula ospite con il costrutto mediante procedure di trasfezione note nell'arte, come esemplificato dai brevetti statunitensi n. 4,399,216; n. 4,912,040; n. 4,740,461; n. 4,959,455. La procedura di trasformazione ottimale usata dipenderà dal tipo di cellula ospite che si sta trasformando. I metodi per l'introduzione di polinucleotidi eterologhi in cellule di mammifero sono ben noti nell'arte e includono, ma senza limitarvisi, la trasfezione mediata da destrano, la precipitazione con fosfato di calcio, la trasfezione mediata da polibrene, la fusione di protoplasti, l'elettroporazione, l'incapsulamento del/dei polinucleotide/i in liposomi, la miscelazione di acido nucleico con lipidi caricati positivamente, e la microiniezione diretta del DNA nei nuclei.

I costrutti di espressione ricombinante comprendono tipicamente una molecola di acido nucleico codificante un polipeptide comprendente uno o più dei seguenti: una o più CDR fornite nella presente; una regione costante di catena leggera; una regione variabile di catena leggera; una regione costante di catena pesante (ad esempio C_H1, C_H2 e/o C_H3); e/o

un'altra porzione di impalcatura di una proteina legante l'antigene di GIPR. Queste sequenze di acido nucleico vengono inserite in un vettore di espressione appropriato usando tecniche di ligazione standard. La regione costante di catena pesante o leggera può essere apposta al C-terminale della regione variabile di catena pesante o leggera specifica anti-GIPR e viene legata in un vettore di espressione. Il vettore viene tipicamente selezionato per essere funzionale nella particolare cellula ospite impiegata (ossia il vettore è compatibile con il macchinario della cellula ospite, permettendo il verificarsi dell'amplificazione e/o dell'espressione del gene). Possono essere usati vettori che impiegano saggi di complementazione proteina-frammento usando proteine reporter, come la diidrofolato reduttasi (*si veda*, ad esempio, il brevetto statunitense n. 6,270,964). Vettori di espressione adatti possono essere acquistati, ad esempio, da Invitrogen Life Technologies o BD Biosciences (in precedenza "Clontech"). Altri vettori utili per il clonaggio e l'espressione di anticorpi e frammenti includono quelli descritti in Bianchi e McGrew, 2003, Biotech. Biotechnol. Bioeng. 84:439-44. Altri vettori di espressione adatti sono discussi, ad esempio, in Methods Enzymol., vol. 185 (D. V. Goeddel, ed.), 1990, New York: Academic Press.

Tipicamente, i vettori di espressione usati in qualsiasi delle cellule ospiti conterranno sequenze per il mantenimento del plasmide e per il clonaggio e l'espressione di sequenze di nucleotidi esogene. Tali sequenze, cui si fa riferimento collettivamente come "sequenze fiancheggianti" in certe forme di realizzazione, includeranno tipicamente

una o più delle seguenti sequenze di nucleotidi: un promotore, una o più sequenze di potenziatore, un'origine di replicazione, una sequenza di terminazione trascrizionale, una sequenza intronica completa contenente un sito di splicing donatore e accettore, una sequenza codificante una sequenza leader per la secrezione di polipeptidi, un sito di legame al ribosoma, una sequenza di poliadenilazione, una regione poli-linker per l'inserimento dell'acido nucleico codificante il polipeptide da esprimere, e un elemento marcatore selezionabile. Di seguito viene discussa ciascuna di queste sequenze.

Facoltativamente, il vettore può contenere una sequenza codificante un "tag", ossia una molecola oligonucleotidica situata all'estremità 5' o 3' della sequenza codificante la proteina legante l'antigene di GIPR; la sequenza oligonucleotidica codifica poli-His (come esa-His) o un altro "tag" come FLAG®, HA (emoagglutinina di virus influenzale) o myc, per il quale esistono anticorpi disponibili in commercio. Questo tag viene tipicamente fuso al polipeptide in seguito all'espressione del polipeptide e può servire come mezzo per la purificazione per affinità o il rilevamento della proteina legante l'antigene di GIPR dalla cellula ospite. La purificazione per affinità può essere assolta, ad esempio, mediante cromatografia su colonna usando anticorpi contro il tag come matrice di affinità. Facoltativamente, il tag può essere successivamente rimosso dalla proteina legante l'antigene di GIPR purificata mediante vari mezzi, ad esempio usando certe peptidasi per il clivaggio.

Le sequenze fiancheggianti possono essere omologhe (ossia della/o stessa/o specie e/o ceppo della cellula ospite), eterologhe (ossia da una specie diversa dalla specie o dal ceppo della cellula ospite), ibride (ossia una combinazione di sequenze fiancheggianti da più di una fonte), sintetiche o native. Di fatto, la fonte di una sequenza fiancheggiante può essere qualsiasi organismo procariotico o eucariotico, qualsiasi organismo vertebrato o invertebrato, oppure qualsiasi pianta, a condizione che la sequenza fiancheggiante sia funzionale nel, e possa essere attivata dal, macchinario della cellula ospite.

Sequenze fiancheggianti utili nei vettori possono essere ottenute mediante qualsiasi di svariati metodi ben noti nell'arte. Tipicamente, sequenze fiancheggianti utili nella presente saranno state precedentemente identificate mediante mappatura e/o digestione con endonucleasi di restrizione e potranno perciò essere isolate dalla fonte tessutale appropriata usando le endonucleasi di restrizione appropriate. In alcuni casi, può essere nota la sequenza di nucleotidi completa di una sequenza fiancheggiante. Qui, la sequenza fiancheggiante può essere sintetizzata usando i metodi descritti nella presente per la sintesi o il clonaggio di acidi nucleici.

Che sia nota tutta o solo una porzione della sequenza fiancheggiante, essa può essere ottenuta mediante reazione a catena della polimerasi (PCR) e/o mediante lo screening di una libreria genomica con una sonda adatta, come un oligonucleotide e/o un frammento di sequenza fiancheggiante della stessa specie o di un'altra.

Quando la sequenza fiancheggiante non è nota, un frammento di DNA contenente una sequenza fiancheggiante può essere isolato da un pezzo di DNA più grande che può contenere, ad esempio, una sequenza codificante o persino un altro gene o altri geni. L'isolamento può essere assolto mediante digestione con endonucleasi di restrizione per produrre il frammento di DNA corretto, cui fa seguito isolamento usando la purificazione su gel di agarosio, la cromatografia su colonna Qiagen® (Chatsworth, CA) o altri metodi noti al tecnico del ramo. La selezione di enzimi adatti per assolvere questo scopo sarà immediatamente evidente a un tecnico del ramo.

Un'origine di replicazione è tipicamente una parte di quei vettori di espressione procariotici acquistati in commercio e l'origine è di ausilio nell'amplificazione del vettore in una cellula ospite. Se il vettore scelto non contiene un sito di origine di replicazione, è possibile sintetizzarne uno chimicamente sulla base di una sequenza nota e legarlo al vettore. Ad esempio, l'origine di replicazione del plasmide pBR322 (New England Biolabs, Beverly, MA) è adatta alla maggior parte dei batteri Gram-negativi e varie origini virali (ad esempio, SV40, polyoma, adenovirus, virus della stomatite vescicolare (VSV) o papillomavirus come HPV o BPV) sono utili per il clonaggio di vettori nelle cellule di mammifero. Generalmente, il componente di origine di replicazione non è necessario per i vettori di espressione di mammifero (ad esempio, l'origine di SV40 è spesso usata solo perché contiene anche il promotore precoce del virus).

Una sequenza di terminazione della trascrizione è tipicamente situata 3' rispetto all'estremità di una regione codificante polipeptidi e serve per terminare la trascrizione. Solitamente, una sequenza di terminazione della trascrizione nelle cellule procariotiche è un frammento ricco di G-C seguito da una sequenza di poli-T. Sebbene la sequenza possa essere facilmente clonata da una libreria o addirittura acquistata in commercio come parte di un vettore, può anche essere prontamente sintetizzata usando metodi per la sintesi di acidi nucleici come quelli descritti nella presente.

Un gene di marcatore selezionabile codifica una proteina necessaria per la sopravvivenza e la crescita di una cellula ospite fatta crescere in un terreno di coltura selettivo. I geni di marcatori di selezione tipici codificano proteine che (a) conferiscono resistenza ad antibiotici o ad altre tossine, ad esempio ampicillina, tetraciclina o kanamicina per le cellule ospiti procariotiche; (b) sopperiscono alle carenze auxotrofiche della cellula; o (c) forniscono nutrienti critici non disponibili in terreni complessi o definiti. I marcatori selezionabili specifici sono il gene di resistenza alla kanamicina, il gene di resistenza all'ampicillina e il gene di resistenza alla tetraciclina. Vantaggiosamente, un gene di resistenza alla neomicina può anche essere usato per la selezione sia in cellule ospiti procariotiche che eucariotiche.

Altri geni selezionabili possono essere usati per amplificare il gene che verrà espresso. L'amplificazione è il processo in cui i geni necessari per la produzione di una proteina critica per la crescita o la

sopravvivenza cellulare vengono ripetuti in tandem all'interno dei cromosomi di generazioni successive di cellule ricombinanti. Esempi di marcatori selezionabili adatti per le cellule di mammifero includono i geni della diidrofolato reduttasi (DHFR) e della timidina chinasi senza promotore. I trasformanti delle cellule di mammifero vengono sottoposti a pressione di selezione in cui solo i trasformanti sono adattati in modo univoco a sopravvivere in virtù del gene selezionabile presente nel vettore. La pressione di selezione viene imposta coltivando le cellule trasformate in condizioni in cui la concentrazione dell'agente di selezione nel terreno viene aumentata progressivamente, portando così all'amplificazione sia del gene selezionabile sia del DNA che codifica un altro gene, come una proteina legante l'antigene che si lega al polipeptide di GIPR. Conseguentemente, dal DNA amplificato vengono sintetizzati quantitativi maggiori di un polipeptide, come una proteina legante l'antigene.

Un sito di legame al ribosoma è solitamente necessario per l'inizio della traduzione dell'mRNA ed è caratterizzato da una sequenza di Shine-Dalgarno (procarioti) o una sequenza di Kozak (eucarioti). L'elemento è tipicamente situato 3' rispetto al promotore e 5' rispetto alla sequenza codificante del polipeptide da esprimere.

In alcuni casi, come quando si desidera la glicosilazione in un sistema di espressione di cellule ospiti eucariotiche, si possono alterare le varie pre- o pro-sequenze per migliorare la glicosilazione o la resa. Ad esempio, si può alterare il sito di clivaggio della peptidasi di un particolare

peptide segnale, o aggiungere pro-sequenze, che possono anche influenzare la glicosilazione. Il prodotto proteico finale può avere, nella posizione -1 (relativamente al primo amminoacido della proteina matura), uno o più amminoacidi aggiuntivi incidenti all'espressione, che potrebbero non essere stati completamente rimossi. Ad esempio, il prodotto proteico finale può avere uno o due residui di amminoacidi trovati nel sito di clivaggio della peptidasi, attaccati all'ammino-terminale. In alternativa, l'uso di alcuni siti di clivaggio enzimatico può risultare in una forma leggermente tronca del polipeptide desiderato, se l'enzima taglia in tale area all'interno del polipeptide maturo.

L'espressione e il clonaggio conterranno tipicamente un promotore che è riconosciuto dall'organismo ospite e collegato funzionalmente alla molecola codificante la proteina legante l'antigene di GIPR. I promotori sono sequenze non trascritte situate a monte (ossia 5') del codone di avvio di un gene strutturale (generalmente entro circa 100-1000 bp) che controlla la trascrizione del gene strutturale. I promotori sono convenzionalmente raggruppati in una delle due classi: promotori inducibili e promotori costitutivi. I promotori inducibili avviano livelli aumentati di trascrizione dal DNA sotto il loro controllo in risposta a qualche cambiamento nelle condizioni di coltura, come la presenza o l'assenza di un nutriente o un cambiamento di temperatura. I promotori costitutivi, d'altra parte, trascrivono uniformemente un gene a cui sono funzionalmente collegati, vale a dire con poco o nessun controllo sull'espressione genica. Un gran numero di promotori, riconosciuti da

una varietà di potenziali cellule ospiti, è ben noto. Un promotore adatto viene collegato funzionalmente al DNA codificante la catena pesante o la catena leggera comprendente una proteina legante l'antigene di GIPR rimuovendo il promotore dal DNA sorgente mediante digestione con enzimi di restrizione e inserendo la sequenza di promotore desiderata nel vettore.

Promotori adatti per l'uso con ospiti di lievito sono anche ben noti nell'arte. I potenziatori di lievito sono vantaggiosamente usati con promotori di lievito. Promotori adatti per l'uso con cellule ospiti di mammifero sono ben noti e includono, ma senza limitarvisi, quelli ottenuti dai genomi di virus come polyomavirus, virus del vaiolo aviario, adenovirus (come Adenovirus 2), papillomavirus bovino, virus del sarcoma aviario, citomegalovirus, retrovirus, virus dell'epatite B, e virus delle scimmie 40 (SV40). Altri promotori di mammifero adatti includono promotori di mammifero eterologhi, ad esempio promotori di shock termico e promotore di actina.

Una sequenza di potenziatore può essere inserita nel vettore per aumentare la trascrizione di DNA codificante la catena leggera o la catena pesante comprendente una proteina legante l'antigene di GIPR da parte di eucarioti superiori. I potenziatori sono elementi agenti in cis del DNA, solitamente lunghi circa 10-300 bp, che agiscono sul promotore per aumentare la trascrizione. I potenziatori sono relativamente indipendenti dall'orientamento e dalla posizione, essendo stati trovati sia in posizione 5' che 3' rispetto all'unità di trascrizione. Sono note svariate

sequenze di potenziatore disponibili da geni di mammifero (ad esempio globina, elastasi, albumina, alfa-feto-proteina e insulina). Tipicamente, tuttavia, viene utilizzato un potenziatore da un virus. Il potenziatore di SV40, il potenziatore del promotore precoce del citomegalovirus, il potenziatore di polyoma e i potenziatori di adenovirus noti nell'arte sono elementi potenziatori esemplificativi per l'attivazione dei promotori eucariotici. Sebbene un potenziatore possa essere posizionato nel vettore 5' o 3' rispetto ad una sequenza codificante, tipicamente è sito in un sito 5' dal promotore. Una sequenza codificante una sequenza segnale nativa o eterologa appropriata (sequenza leader o peptide segnale) può essere incorporata in un vettore di espressione per promuovere la secrezione extracellulare dell'anticorpo. La scelta del peptide segnale o del leader dipende dal tipo di cellule ospiti in cui l'anticorpo deve essere prodotto; e una sequenza segnale eterologa può sostituire la sequenza segnale nativa. Esempi di peptidi segnale che sono funzionali in cellule ospiti di mammifero includono quanto segue: la sequenza segnale per l'interleuchina-7 (IL-7) descritta nel brevetto statunitense n. 4,965,195; la sequenza segnale per il recettore dell'interleuchina-2 descritta in Cosman et al., 1984, Nature 312:768; il peptide segnale del recettore dell'interleuchina-4 descritto nel brevetto EP n. 0367 566; il peptide segnale del recettore dell'interleuchina-1 di tipo I descritto nel brevetto statunitense n. 4,968,607; il peptide segnale del recettore dell'interleuchina-1 di tipo II descritto nel brevetto EP n. 0 460 846.

In una forma di realizzazione la sequenza leader comprende SEQ ID NO: 3157 (MDMRVPAQLL GLLLLWLRGA RC) che è codificata da SEQ ID NO: 3158 (atggacatga gagtgcctgc acagctgctg ggcctgctgc tgctgtggct gagaggcgcc agatgc). In un'altra forma di realizzazione, la sequenza leader comprende SEQ ID NO: 3159 (MAWALLLLTL LTQGTGSWA) che è codificata da SEQ ID NO: 3160 (atggcctggg ctctgctgct cctcaccctc ctcactcagg gcacagggtc ctgggcc).

I vettori di espressione che sono forniti possono essere costruiti da un vettore di partenza, ad esempio un vettore disponibile in commercio. Tali vettori possono contenere o meno tutte le sequenze fiancheggianti desiderate. Qualora una o più sequenze fiancheggianti descritte nella presente non siano già presenti nel vettore, possono essere ottenute individualmente e legate al vettore. I metodi usati per ottenere ciascuna delle sequenze fiancheggianti sono ben noti a un tecnico del ramo.

Dopo che il vettore è stato costruito e una molecola di acido nucleico codificante una catena leggera, una catena pesante, o una catena leggera e una catena pesante comprendenti una sequenza legante l'antigene di GIPR è stata inserita nel sito corretto del vettore, il vettore completato può essere inserito in una cellula ospite adatta per l'amplificazione e/o l'espressione del polipeptide. La trasformazione di un vettore di espressione per una proteina legante l'antigene in una cellula ospite selezionata può essere assolta mediante metodi noti, tra cui trasfezione, infezione, co-precipitazione con fosfato di calcio,

elettroporazione, microiniezione, lipofezione, trasfezione mediata da DEAE-destrano, o altre tecniche note. Il metodo selezionato sarà in parte una funzione del tipo di cellula ospite da utilizzare. Questi metodi e altri metodi adatti sono ben noti al tecnico del ramo e sono esposti, ad esempio, in Sambrook *et al.*, 2001, sopra.

Una cellula ospite, quando coltivata in condizioni appropriate, sintetizza una proteina legante l'antigene che può essere successivamente raccolta dal terreno di coltura (se la cellula ospite la secerne nel terreno) o direttamente dalla cellula ospite che la produce (se non viene secreta). La selezione di una cellula ospite appropriata dipenderà da vari fattori, come i livelli di espressione desiderati, le modifiche al polipeptide che sono desiderabili o necessarie per l'attività (come glicosilazione o fosforilazione) e la facilità di ripiegamento in una molecola biologicamente attiva.

Le linee cellulari di mammifero disponibili come ospiti per l'espressione sono ben note nell'arte e includono, ma senza limitarvisi, linee cellulari immortalizzate disponibili dall'American Type Culture Collection (ATCC), incluse, ma senza limitarvisi, cellule ovariche di criceto cinese (CHO), cellule HeLa, cellule renali di criceto neonato (BHK), cellule renali di scimmia (COS), cellule di carcinoma epatocellulare umano (ad esempio Hep G2) e numerose altre linee cellulari. In certe forme di realizzazione, le linee cellulari possono essere selezionate determinando quali linee cellulari hanno livelli di espressione alti e producono in modo costitutivo proteine leganti l'antigene con

proprietà di legame a GIPR. In un'altra forma di realizzazione, può essere selezionata una linea cellulare del lignaggio delle cellule B che non produce il proprio anticorpo ma che ha la capacità di produrre e secernere un anticorpo eterologo.

In una forma di realizzazione, la presente invenzione è diretta a una proteina legante l'antigene prodotta da una cellula esprimente uno o più polinucleotidi identificati nelle Tabelle 2, 3, 4 e 5.

Sono inoltre fornite composizioni farmaceutiche che comprendono una proteina legante l'antigene di GIPR, le quali possono essere utilizzate in qualsiasi dei metodi preventivi e terapeutici divulgati nella presente. In una forma di realizzazione, vengono inoltre forniti una quantità terapeuticamente efficace di una o più delle proteine leganti l'antigene e un diluente, un trasportatore, un solubilizzante, un emulsionante, un conservante e/o un coadiuvante farmaceuticamente accettabili. I materiali di formulazione accettabili sono atossici per i riceventi ai dosaggi e alle concentrazioni impiegati.

In certe forme di realizzazione, la composizione farmaceutica può contenere materiali di formulazione per modificare, mantenere o preservare, ad esempio, il pH, l'osmolarità, la viscosità, la limpidezza, il colore, l'isotonicità, l'odore, la sterilità, la stabilità, il tasso di dissoluzione o rilascio, l'adsorbimento o la penetrazione della composizione. In tali forme di realizzazione, i materiali di formulazione adatti includono, ma senza limitarvisi, amminoacidi (come glicina, glutammina, asparagina, arginina o lisina); antimicrobici; antiossidanti (come acido ascorbico,

solfito di sodio o idrogenosolfito di sodio); tamponi (come borato, bicarbonato, Tris-HCl, citrati, fosfati o altri acidi organici); agenti di carica (come mannitolo o glicina); agenti chelanti (come acido etilendiamminotetraacetico (EDTA)); agenti complessanti (come caffeina, polivinilpirrolidone, beta-ciclodestrina o idrossipropil-beta-ciclodestrina); cariche; monosaccaridi; disaccaridi; e altri carboidrati (come glucosio, mannosio o destrine); proteine (come albumina sierica, gelatina o immunoglobuline); agenti coloranti, aromatizzanti e diluenti; agenti emulsionanti; polimeri idrofili (come polivinilpirrolidone); polipeptidi a basso peso molecolare; controioni formanti sale (come sodio); conservanti (come cloruro di benzalconio, acido benzoico, acido salicilico, tiomersale, alcol fenetilico, metilparabene, propilparabene, clorexidina, acido sorbico o perossido di idrogeno); solventi (come glicerina, glicole di propilene o glicole di polietilene); alditoli (come mannitolo o sorbitolo); agenti di sospensione; tensioattivi o agenti bagnanti (come Pluronic, PEG, esteri di sorbitano, polisorbati come polisorbato 20, polisorbato, triton, trometamina, lecitina, colesterolo, tiloxapolo); agenti che potenziano la stabilità (come saccarosio o sorbitolo); agenti che potenziano la tonicità (come alogenuri di metalli alcalini, preferibilmente cloruro di sodio o potassio, mannitolo, sorbitolo); veicoli di erogare; diluenti; eccipienti e/o coadiuvanti farmaceutici. REMINGTON'S PHARMACEUTICAL SCIENCES, 18a edizione, (a cura di A.R. Genrmo), 1990, Mack Publishing Company fornisce ulteriori

dettagli e opzioni per agenti adatti che possono essere incorporati nelle composizioni farmaceutiche.

In certe forme di realizzazione, la composizione farmaceutica ottimale sarà determinata da un tecnico del ramo a seconda, ad esempio, della via di somministrazione prevista, del formato di erogazione e del dosaggio desiderato. *Si veda*, ad esempio, REMINGTON'S PHARMACEUTICAL SCIENCES, sopra. In certe forme di realizzazione, tali composizioni possono influenzare lo stato fisico, la stabilità, il tasso di rilascio *in vivo* e il tasso di clearance *in vivo* delle proteine leganti l'antigene divulgate. In certe forme di realizzazione, il veicolo o trasportatore primario in una composizione farmaceutica può essere di natura acquosa o non acquosa. Ad esempio, un veicolo o trasportatore adatto può essere acqua per preparazioni iniettabili o soluzione fisiologica salina. In certe forme di realizzazione, le composizioni di proteine leganti l'antigene di GIPR possono essere preparate per la conservazione miscelando la composizione selezionata avente il grado di purezza desiderato con agenti di formulazione facoltativi (REMINGTON'S PHARMACEUTICAL SCIENCES, sopra) sotto forma di un panello liofilizzato o di una soluzione acquosa. Inoltre, in certe forme di realizzazione, la proteina legante l'antigene di GIPR può essere formulata come un liofilizzato usando eccipienti appropriati come il saccarosio.

Le composizioni farmaceutiche possono essere selezionate per l'erogazione parenterale. In alternativa, le composizioni possono essere

selezionate per l'inalazione o per l'erogazione attraverso il tratto digerente, ad esempio per via orale. La preparazione di tali composizioni farmaceuticamente accettabili rientra nelle competenze dell'arte.

I componenti di formulazione sono presenti preferibilmente in concentrazioni che sono accettabili per il sito di somministrazione. In certe forme di realizzazione, vengono usati tamponi per mantenere la composizione a un pH fisiologico o a un pH leggermente inferiore, tipicamente entro un intervallo di pH da circa 5 a circa 8.

Quando è contemplata la somministrazione parenterale, le composizioni terapeutiche possono essere fornite sotto forma di una soluzione acquosa apirogena accettabile per via parenterale comprendente la proteina legante l'antigene di GIPR umano desiderata in un veicolo farmaceuticamente accettabile. Un veicolo particolarmente adatto per l'iniezione parenterale è acqua distillata sterile in cui la proteina legante l'antigene di GIPR è formulata come soluzione sterile e isotonica, opportunamente conservata. In certe forme di realizzazione, la preparazione può comportare la formulazione della molecola desiderata con un agente, come microsfere iniettabili, particelle bioerodibili, composti polimerici (come acido polilattico o acido poliglicolico), biglie o liposomi, che possono fornire un rilascio controllato o prolungato del prodotto che può essere erogato tramite iniezione di deposito. In certe forme di realizzazione può anche essere usato acido ialuronico, avente l'effetto di promuovere una durata prolungata nella circolazione. In certe forme di realizzazione, possono essere usati dispositivi di erogazione di

farmaci impiantabili per introdurre la proteina legante l'antigene desiderata.

Certe composizioni farmaceutiche sono formulate per l'inalazione. In alcune forme di realizzazione, le proteine leganti l'antigene di GIPR sono formulate come polvere inalabile secca. In forme di realizzazione specifiche, le soluzioni per inalazione di proteine leganti l'antigene di GIPR possono anche essere formulate con un propellente per l'erogazione tramite aerosol. In certe forme di realizzazione, le soluzioni possono essere nebulizzate. Pertanto, metodi di somministrazione e formulazione polmonare sono ulteriormente descritti nella domanda di brevetto internazionale n. PCT/US94/001875, che descrive l'erogazione polmonare di proteine modificate chimicamente. Alcune formulazioni possono essere somministrate per via orale. Le proteine leganti l'antigene di GIPR che sono somministrate in questo modo possono essere formulate con o senza trasportatori comunemente usati nella preparazione di forme di dosaggio solide, quali compresse e capsule. In certe forme di realizzazione, una capsula può essere progettata per rilasciare la porzione attiva della formulazione nel punto del tratto gastrointestinale in cui la biodisponibilità è massimizzata e la degradazione pre-sistemica è ridotta al minimo. Agenti aggiuntivi possono essere inclusi per facilitare l'assorbimento della proteina legante l'antigene di GIPR. Possono essere impiegati anche diluenti, aromi, cere a basso punto di fusione, oli vegetali, lubrificanti, agenti di sospensione, agenti disintegranti per compresse, e leganti.

Alcune composizioni farmaceutiche comprendono un quantitativo efficace di una o di una pluralità di proteina/e legante/i l'antigene di GIPR in una miscela con eccipienti atossici che sono adatti alla produzione di compresse. Sciogliendo le compresse in acqua sterile o in un altro veicolo appropriato, possono essere preparate soluzioni in forma di dose unitaria. Eccipienti adatti includono, ma senza limitarvisi, diluenti inerti, quali carbonato di calcio, carbonato o bicarbonato di sodio, lattosio, o fosfato di calcio; o agenti leganti, quali amido, gelatina o acacia; o agenti lubrificanti quali stearato di magnesio, acido stearico, o talco.

Composizioni farmaceutiche aggiuntive saranno evidenti ai tecnici del ramo, incluse formulazioni che coinvolgono proteine leganti GIPR in formulazioni ad erogazione prolungata o controllata. Sono anche note ai tecnici del ramo tecniche per formulare una varietà di altri mezzi di erogazione prolungata o controllata, come trasportatori liposomici, microparticelle bioerodibili o biglie porose e iniezioni depot. *Si veda*, ad esempio, la domanda di brevetto internazionale n. PCT/US93/00829, che descrive il rilascio controllato di microparticelle polimeriche porose per l'erogazione di composizioni farmaceutiche. Le preparazioni a rilascio prolungato possono includere matrici polimeriche semipermeabili sotto forma di articoli sagomati, ad esempio pellicole o microcapsule. Le matrici a rilascio prolungato possono includere poliesteri, idrogel, polilattidi (come divulgato nel brevetto statunitense n. 3,773,919 e nella pubblicazione della domanda di brevetto europeo n. EP 058481),

copolimeri di acido L-glutammico e gamma etil-L-glutammato (Sidman et al., 1983, Biopolymers 2:547-556), poli(2-idrossietil-metacrilato) (Langer et al., 1981, J. Biomed. Mater. Res. 15:167-277 e Langer, 1982, Chem. Tech. 12:98-105), etilene vinil acetato (Langer *et al.*, 1981, sopra) o acido poli-D(-)-3-idrossibutirrico (pubblicazione di domanda di brevetto europeo n. EP 133.988). Composizioni a rilascio prolungato possono anche includere liposomi che possono essere preparati mediante uno qualsiasi degli svariati metodi noti nell'arte. *Si veda*, ad esempio, Eppstein et al., 1985, Proc. Natl. Acad. Sci. U.S.A. 82:3688-3692; la pubblicazione della domanda di brevetto europeo n. EP 036,676; EP 088,046 e EP 143,949.

Composizioni farmaceutiche usate per la somministrazione *in vivo* vengono tipicamente fornite sotto forma di preparazioni sterili. La sterilizzazione può essere assolta mediante filtrazione attraverso membrane di filtrazione sterili. Quando la composizione è liofilizzata, la sterilizzazione che usa questo metodo può essere condotta prima o dopo la liofilizzazione e la ricostituzione. Le composizioni per somministrazione parenterale possono essere conservate in forma liofilizzata o in soluzione. Le composizioni parenterali vengono generalmente poste in un contenitore avente una porta di accesso sterile, ad esempio una sacca o una fiala per soluzione endovenosa avente un tappo perforabile da un ago per iniezione ipodermica.

In certe formulazioni, una proteina legante l'antigene ha una concentrazione di almeno 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 o 150 mg/ml. In una forma di realizzazione, una composizione farmaceutica comprende la proteina legante l'antigene, un tampone e polisorbato. In altre forme di realizzazione, la composizione farmaceutica comprende una proteina legante l'antigene, un tampone, saccarosio e polisorbato. Un esempio di una composizione farmaceutica è una contenente 50-100 mg/ml di proteina legante l'antigene, acetato di sodio 5-20 mM, 5-10% p/v di saccarosio e 0,002-0,008% p/v di polisorbato. Ad esempio, certe composizioni contengono 65-75 mg/ml di una proteina legante l'antigene in tampone acetato di sodio 9-11 mM, 8-10% p/v di saccarosio e 0,005-0,006% p/v di polisorbato. Il pH di certe di tali formulazioni è nell'intervallo da 4,5 a 6. Altre formulazioni hanno un pH da 5,0 a 5,5 (ad esempio, pH 5,0, 5,2 o 5,4).

Una volta che la composizione farmaceutica è stata formulata, può essere stoccata in fiale sterili come una soluzione, una sospensione, un gel, un'emulsione, un solido, un cristallo, o come una polvere disidratata o liofilizzata. Tali formulazioni possono essere conservate sia in una forma pronta all'uso sia in una forma (ad esempio liofilizzata) che viene ricostituita prima della somministrazione. Vengono forniti anche kit per la produzione di un'unità di somministrazione a dose singola. Certi kit contengono un primo contenitore avente una proteina essiccata e un secondo contenitore avente una formulazione acquosa. In certe forme di realizzazione, sono forniti kit contenenti siringhe preriempite a camera singola e multicamera (ad esempio siringhe per liquidi e siringhe per

liofilizzati). La quantità terapeuticamente efficace di una composizione farmaceutica contenente una proteina legante l'antigene di GIPR da impiegare dipenderà, ad esempio, dal contesto e dagli obiettivi terapeutici. Un tecnico del ramo comprenderà che i livelli di dosaggio appropriati per il trattamento varieranno a seconda, in parte, della molecola erogata, dell'indicazione per la quale viene usata la proteina legante l'antigene di GIPR, della via di somministrazione e delle dimensioni (peso corporeo, superficie corporea o dimensioni degli organi) e/o delle condizioni (età e salute generale) del paziente. In certe forme di realizzazione, il medico può titolare il dosaggio e modificare la via di somministrazione per ottenere l'effetto terapeutico ottimale.

La frequenza di dosaggio dipenderà dai parametri farmacocinetici della particolare proteina legante l'antigene di GIPR nella formulazione usata. Tipicamente, un medico somministra la composizione fino al raggiungimento del dosaggio che consegue l'effetto desiderato. La composizione può pertanto essere somministrata come dose singola, o come due o più dosi (che possono o meno contenere la stessa quantità della molecola desiderata) nel tempo, o come infusione continua tramite un dispositivo di impianto o un catetere. I dosaggi appropriati possono essere accertati attraverso l'uso di dati dose-risposta appropriati. In certe forme di realizzazione, le proteine leganti l'antigene possono essere somministrate ai pazienti per un periodo di tempo prolungato. In certe forme di realizzazione, la proteina legante l'antigene

viene dosata ogni due settimane, ogni mese, ogni due mesi, ogni tre mesi, ogni quattro mesi, ogni cinque mesi, o ogni sei mesi.

La via di somministrazione della composizione farmaceutica è conforme ai metodi noti, ad esempio per via orale, tramite iniezione per via endovenosa, intraperitoneale, intracerebrale (intraparenchimale), intracerebroventricolare, intramuscolare, intraoculare, endoarteriosa, intraportale, o intralesionale; mediante sistemi a rilascio prolungato o mediante dispositivi di impianto. In certe forme di realizzazione, le composizioni possono essere somministrate mediante iniezione in bolo o in modo continuo mediante infusione, oppure mediante dispositivo di impianto.

La composizione può anche essere somministrata localmente tramite impianto di una membrana, una spugna o altro materiale appropriato su cui è stata assorbita o incapsulata la molecola desiderata. In certe forme di realizzazione, in cui viene usato un dispositivo di impianto, il dispositivo può essere impiantato in qualsiasi tessuto o organo adatto, e l'erogazione della molecola desiderata può avvenire tramite diffusione, bolo a rilascio temporizzato, o somministrazione continua.

Potrebbe anche essere desiderabile usare composizioni farmaceutiche di proteine leganti l'antigene di GIPR secondo quanto divulgato *ex vivo*. In tali esemplificazioni, cellule, tessuti od organi che sono stati organi rimossi dal paziente vengono esposti a composizioni farmaceutiche di proteine leganti l'antigene di GIPR, dopodiché le cellule,

i tessuti e/o gli organi vengono successivamente nuovamente impiantati nel paziente.

Un medico sarà in grado di selezionare un'indicazione di trattamento appropriata e livelli di lipidi bersaglio in base al profilo individuale di un determinato paziente. Uno standard ampiamente accettato per guidare il trattamento dell'iperlipidemia è il 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, pubblicazione NIH n. 02-5215 (2002).

L'efficacia di una particolare dose può essere giudicata facendo riferimento a biomarcatori o al miglioramento di certi parametri fisiologici. Esempi di biomarcatori adatti includono il rapporto tra colesterolo libero e lipidi plasmatici, colesterolo libero e proteine di membrana, fosfatidilcolina e sfingomielina o i livelli di HDL-C.

Nella presente vengono inoltre fornite composizioni comprendenti una proteina legante l'antigene di GIPR e uno o più agenti terapeutici aggiuntivi, nonché metodi in cui tali agenti vengono somministrati contemporaneamente a, o in sequenza con, una proteina legante l'antigene di GIPR per uso nei metodi preventivi e terapeutici divulgati nella presente. L'uno o più agenti aggiuntivi possono essere co-formulati con una proteina legante l'antigene di GIPR o possono essere co-somministrati con una proteina legante l'antigene di GIPR. In generale, i metodi terapeutici, le composizioni e i composti possono

essere impiegati anche in combinazione con altri agenti terapeutici nel trattamento di vari stati di malattia, gli agenti aggiuntivi essendo somministrati contemporaneamente.

In un aspetto, la presente invenzione è diretta a una composizione come rivendicata per l'uso in un metodo per trattare un soggetto con un disturbo metabolico, il metodo comprendendo somministrare al soggetto la composizione come rivendicata. In una forma di realizzazione, l'antagonista di GIPR inibisce il legame di GIP a GIPR.

In un aspetto, la presente invenzione è diretta ad una composizione come rivendicata per l'uso in un metodo per trattare un soggetto con un disturbo metabolico, il metodo comprendendo somministrare al soggetto una composizione comprendente l'anticorpo, o suo frammento funzionale, e l'agonista del recettore di GLP-1.

In un aspetto, la presente invenzione è diretta a un metodo per promuovere l'internalizzazione di GIPR e GLP-1R nella cellula su cui sono co-espressi, somministrando alla cellula un antagonista di GIPR coniugato a un agonista del recettore di GLP-1. In una forma di realizzazione, il GIPR e il GLP-1R sono co-localizzati mentre vengono internalizzati.

In un aspetto, la presente invenzione è diretta a un metodo per stimolare il flusso di calcio in una cellula somministrando alla cellula un antagonista di GIPR coniugato a un agonista del recettore di GLP-1.

In un aspetto, la presente invenzione è diretta a un metodo per promuovere il reclutamento della beta-arrestina in una cellula somministrando alla cellula un antagonista di GIPR coniugato a un agonista del recettore di GLP-1.

In un aspetto, la presente invenzione è diretta a un metodo per stimolare la secrezione di insulina da una cellula somministrando alla cellula un antagonista di GIPR coniugato a un agonista del recettore di GLP-1. In una forma di realizzazione, la cellula è una micro-isola pancreatica umana.

Un "agonista del recettore di GLP-1" si riferisce a composti avente attività di recettore di GLP-1. Tali composti esemplificativi includono exendine, analoghi di exendina, agonisti di exendina, GLP-1(7-37), analoghi di GLP-1(7-37), agonisti di GLP-1(7-37), e simili. I composti agonisti del recettore di GLP-1 possono essere facoltativamente ammidati. I termini "agonista del recettore di GLP-1" e "composto agonista del recettore di GLP-1" hanno lo stesso significato.

Il termine "exendina" include peptidi di exendina presenti in natura (o versioni sintetiche di peptidi presenti in natura) trovati nelle secrezioni salivari del mostro di Gila. Tra le exendine di particolare interesse ci sono l'exendina-3 e l'exendina-4. Le exendine, gli analoghi delle exendine e gli agonisti delle exendine per uso nei metodi descritti nella presente possono essere facoltativamente ammidati e possono anche essere in forma di acido, in forma di sale farmaceuticamente

accettabile, o in qualsiasi altra forma fisiologicamente attiva della molecola.

In una forma di realizzazione, l'agonista del recettore di GLP-1 è GLP-1(7-37) o un analogo di GLP-1(7-37).

In una forma di realizzazione, l'agonista del recettore di GLP-1 è selezionato dal gruppo consistente in exenatide, liraglutide, lixisenatide, albiglutide, dulaglutide, semaglutide, e taspoglutide.

In un aspetto, la presente invenzione è diretta a una composizione comprendente a) un anticorpo, o suo frammento funzionale, che si lega specificamente a GIPR umano, in cui l'anticorpo, o suo frammento funzionale, comprende una sostituzione di cisteina o di amminoacido non canonico in uno o più siti di coniugazione, e in cui l'anticorpo, o suo frammento funzionale, è un antagonista di GIPR; e un agonista del recettore di GLP-1, in cui l'agonista del recettore di GLP-1 è coniugato all'anticorpo, o suo frammento funzionale, attraverso la catena laterale del residuo di cisteina o del residuo di amminoacido non canonico sostituito negli uno o più siti di coniugazione, per uso in un metodo di trattamento comprendente somministrare a un soggetto una quantità terapeuticamente efficace di almeno un agonista del recettore di GLP-1 in combinazione con la somministrazione di almeno un antagonista di GIPR, in cui l'antagonista di GIPR è coniugato all'agonista del recettore di GLP-1, che, in seguito alla somministrazione a un soggetto con sintomi di un disturbo metabolico, fornisce effetti benefici prolungati.

In una forma di realizzazione, la somministrazione di almeno un agonista del recettore di GLP-1 in combinazione con la somministrazione di almeno un antagonista di GIPR fornisce effetti benefici prolungati su almeno un sintomo di un disturbo metabolico.

In una forma di realizzazione, le quantità terapeuticamente efficaci dell'agonista del recettore di GLP-1 e dell'antagonista di GIPR vengono combinate prima della somministrazione al soggetto.

In una forma di realizzazione, le quantità terapeuticamente efficaci dell'agonista del recettore di GLP-1 e dell'antagonista di GIPR vengono somministrate al soggetto in sequenza.

In una forma di realizzazione, le quantità terapeuticamente efficaci di un agonista del recettore di GLP-1 e di un antagonista di GIPR sono quantità sinergicamente efficaci.

Exendina-4 (HGEGTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGAPPPS-NH_2 (SEQ ID NO: 3163)) è un peptide trovato nella saliva del mostro di Gila, *Heloderma suspectum*; ed exendina-3 (HSDGTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGAPPPS-NH_2(SEQ ID NO: 3164)) è un peptide trovato nella saliva della lucertola perlinata, *Eloderma horridum.* Le exendine hanno una certa somiglianza nella sequenza di amminoacidi con alcuni membri della famiglia del peptide simile al glucagone (GLP). Ad esempio, l'exendina-4 ha circa il 53% di identità di sequenza con il peptide-1 simile al glucagone (GLP-1) (7-37) (HAEGTFTSDVSSYLEGQAAKEFIAWLVKGRG (SEQ ID NO: 3184)).

Tuttavia, l'exendina-4 viene trascritta da un gene distinto e non dall'omologo del mostro di Gila del gene proglucagone dei mammiferi da cui viene espresso il GLP-1. In aggiunta, l'exendina-4 non è un analogo di GLP-1(7-37) perché la struttura del peptide di exendina-4 sintetica non è stata creata mediante modifica sequenziale della struttura di GLP-1. Nielsen et al., Current Opinion in Investigational Drugs, 4(4):401-405 (2003).

L'exendina-4 sintetica, nota anche come exenatide, è disponibile in commercio come BYETTA® (Amylin Pharmaceuticals, Inc. e Eli Lilly and Company). Una formulazione di exenatide da assumere una volta alla settimana è descritta in WO 2005/102293.

"Analogo di exendina" si riferisce a peptidi che suscitano un'attività biologica di un peptide di riferimento di exendina, preferibilmente aventi una potenza uguale o migliore rispetto al peptide di riferimento di exendina (ad esempio, exendina-4), o entro cinque ordini di grandezza (più o meno) di potenza rispetto al peptide di riferimento di exendina, quando valutati mediante misure note nell'arte quali studi di legame e/o competizione per il recettore, come descritto, ad esempio, da Hargrove et al., Regulatory Peptides, 141:113-119 (2007). Preferibilmente, gli analoghi di exendina si legheranno in tali saggi con un'affinità inferiore a 1 μM e, più preferibilmente, con un'affinità inferiore a 3 nM, inferiore a 1 nM o inferiore a 0,1 nM. Al termine "analogo di exendina" si può fare riferimento anche come "agonista di exendina". In

una forma di realizzazione preferita, l'analogo di exendina è un analogo di exendina-4.

Gli analoghi di exendina includono anche i peptidi descritti nella presente che sono stati derivatizzati o alterati chimicamente, ad esempio peptidi con residui di amminoacidi non naturali (ad esempio taurina, residui di β amminoacidi, residui di γ amminoacidi e residui di D amminoacidi), modifiche del gruppo funzionale C-terminale, come ammidi, esteri e modifiche del chetone C-terminale e modifiche del gruppo funzionale N-terminale, come ammine acilate, basi di Schiff, o ciclizzazione, come trovato, ad esempio, nell'amminoacido acido piroglutammico. Gli analoghi di exendina possono contenere anche altre frazioni chimiche, come mimetici dei peptidi.

Exendine e analoghi di exendina esemplificativi, exendina-4 (SEQ ID NO: 3163); exendina-3 (SEQ ID NO: 3164); Leu^{14}-exendina-4 (SEQ ID NO: 3165); Leu^{14},Phe^{25}-exendina-4 (SEQ ID NO: 3166); Leu^{14},Ala^{19},Phe^{25}-exendina-4 (SEQ ID NO: 3167); exendina-4(1~30) (SEQ ID NO: 3168); Leu^{14}-exendina-4(1-30) (SEQ ID NO: 3169); Leu^{14},Phe^{25}-exendina-4(1-30) (SEQ ID NO: 3170); Leu^{14},Ala^{19},Phe^{25}-exendina-4(1-30) (SEQ ID NO: 3171), exendina-4(1-28) (SEQ ID NO: 3172); Leu^{14}-exendina-4(1-28) (SEQ ID NO: 3173); Leu^{14},Phe^{25}-exendina-4(1-28) (SEQ ID NO: 3174); Leu^{14},Ala^{19},Phe^{25}-exendina-4 (1-28) (SEQ ID NO: 3175); Leu^{14},$Lys^{17,20}$,Ala^{19},Glu^{21},Phe^{25},Gln^{28}-exendina-4 (SEQ ID NO: 3176); Leu^{14},$Lys^{17,20}$,Ala^{19},Glu^{21},Gln^{28}-exendina-4 (SEQ ID NO: 3177); ottilGly^{14},Gln^{28}-exendina-4 (SEQ ID NO: 3178),

Leu^{14},Gln^{28},ottilGly^{34}-exendina-4 (SEQ ID NO: 3179), Phe^{4},Leu^{14},Gln^{28},Lys^{33},Glu^{34}, Ile,^{11,36}, Ser^{37}-exendina-4(1-37) (SEQ ID NO: 3180); Phe^{4},Leu^{14},Lys^{17,20},Ala^{19},Glu^{21},Gln^{28}-exendina-4 (SEQ ID NO: 3181); Val^{11},Ile^{13},Leu^{14}Ala^{16},Lys^{21},Phe^{25}-exendina-4 (SEQ ID NO: 3182); exendina-4-Lys^{40} (SEQ ID NO: 3183); lixisenatide (Sanofi-Aventis/Zealand Pharma); CJC-1134 (ConjuChem, Inc.), [N^{e}-(acido 17-carbossieptadecanoico)Lys^{20}]exendina-4-NH_2 (SEQ ID NO: 3208); [N^{e}-(17-carbossiepta-decanoil)Lys^{32}]exendina-4-NH_2 (SEQ ID NO: 3209); [desammino-His^{1},N^{e}-(17-carbossieptadecanoil)Lys^{20}]exendina-4-NH_2 (SEQ ID NO: 3210), [Arg^{12,27},NLe^{14},N^{e}-(17-carbossi-eptadecanoil)Lys^{32}]exendina-4-NH_2 (SEQ ID NO: 32(1); [N^{e}-(19-carbossi-nonadecanoilammino)Lys^{20}]-exendina-4-NH_2 (SEQ ID NO: 32(2); [N^{e}-(15-carbossipentadecanoilammino)Lys^{20}]-exendina-4-NH_2(SEQ ID NO: 3213); [N^{e}-(13-carbossitridecanoilammino)Lys^{20}]exendina-4-NH_2 (SEQ ID NO: 3214); [N^{e}-(11-carbossi-undecanoil-ammino)Lys^{20}]exendina-4-NH_2 (SEQ ID NO: 3215); exendina-4-Lys^{40}(e-MPA)-NH_2 (SEQ ID NO: 3216); exendina-4-Lys^{40}(e-AEEA-AEEA-MPA)-NH_2 (SEQ ID NO: 3217); exendina-4-Lys^{40}(e-AEEA-MPA)-NH_2 (SEQ ID NO: 3218); exendina-4-Lys^{40}(e-MPA)-albumina (SEQ ID NO: 3219); exendina-4-Lys^{40}(e-AEEA-AEEA-MPA)-albumina (SEQ ID NO: 3220); exendina-4-Lys^{40}(e-AEEA-MPA)-albumina (SEQ ID NO: 3221); e simili. AEEA si riferisce ad acido [2-(2-ammino)etossi)]acetico. EDA si riferisce ad etilendiammina. MPA si

riferisce ad acido maleimidopropionico. Le exendine e gli analoghi di exendina possono essere facoltativamente ammidati.

In una forma di realizzazione, il composto agonista del recettore di GLP-1 è un analogo di exendina-4 che ha almeno 80% di identità di sequenza con exendina-4 (SEQ ID NO: 3163); almeno 85% di identità di sequenza con exendina-4 (SEQ ID NO: 3163); almeno 90% di identità di sequenza con exendina-4 (SEQ ID NO: 3163); o almeno 95% di identità di sequenza con exendina-4 (SEQ ID NO: 3163).

Altre exendine e analoghi di exendina utili nei metodi descritti nella presente includono quelli descritti 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; nel brevetto statunitense n. 6,956,026; brevetto statunitense n. 6,506,724; brevetto statunitense n. 6,703,359; brevetto statunitense n. 6,858,576; brevetto statunitense n. 6,872,700; brevetto statunitense n. 6,902,744; brevetto statunitense n. 7,157,555; brevetto statunitense n. 7,223,725; brevetto statunitense n. 7,220,721; nella pubblicazione statunitense n. 2003/0036504; e nella pubblicazione statunitense n. 2006/0094652.

"Analoghi di GLP-1(7-37)" si riferisce ai peptidi che suscitano un'attività biologica simile a quella di GLP-1(7-37), quando valutata mediante misure note nell'arte quali saggi di legame al recettore o saggi del glucosio ematico in vivo, come descritto, ad esempio, da Hargrove et al., Regulatory Peptides, 141:113-119 (2007). In una forma di realizzazione, il termine "analogo di GLP-1(7-37)" si riferisce a un peptide

che ha una sequenza di amminoacidi con 1, 2, 3, 4, 5, 6, 7 o 8 sostituzioni, inserzioni, delezioni di amminoacidi, o una combinazione di due o più di loro, rispetto alla sequenza di amminoacidi di GLP-1(7-37). In una forma di realizzazione, l'analogo di GLP-1(7-37) è GLP-1(7-36)-NH_2. Gli analoghi di GLP-1(7-37) includono le forme ammidate, la forma di acido, la forma di sale farmaceuticamente accettabile, e qualsiasi altra forma fisiologicamente attiva della molecola. In alcune forme di realizzazione viene usata una nomenclatura semplice per descrivere l'agonista del recettore di GLP-1, ad esempio, [Aib8] GLP-1(7-37) designa un analogo di GLP-1(7-37) in cui l'Ala presente in natura in posizione 8 è stata sostituita con Aib.

GLP-1(7-37) e analoghi di GLP-1(7-37) esemplificativi includono GLP-1(7-37) (SEQ ID NO: 3184); GLP-1(7-36)-NH_2 (SEQ ID NO: 3185); liraglutide (VICTOZA® di Novo Nordisk); albiglutide (SYNCRIA® di GlaxoSmithKline), taspoglutide (Hoffman La-Roche); dulaglutide (nota come LY2189265; Eli Lilly and Company); LY2428757 (Eli Lilly and Company), desammino-His^{7},Arg^{26},Lys^{34}(N^{ε}-(γ-Glu(N-α-edadecanoil)))-GLP-1(7-37) (peptide nucleo divulgato come SEQ ID NO: 3222); desammino-His^{7},Arg^{26},Lys^{34}(N^{ε}-ottanoil)-GLP-1(7-37) (SEQ ID NO: 3223); $Arg^{26,34}$,Lys^{38}(N^{ε}-((ω-carbossipentadecanoil))-GLP-1(7-38) (SEQ ID NO: 3224); $Arg^{26,34}$,Lys^{36}(N^{ε}-(γ-Glu(N-α-esadecanoil)))-GLP-1(7-36) (peptide nucleo divulgato come SEQ ID NO: 3225); $Aib^{8,35}$,$Arg^{26,34}$,Phe^{31}-GLP-1(7-36) (SEQ ID NO: 3186); $HXaa_8EGTFTSDVSSYLEXaa_{22}Xaa_{23}AAKEFIXaa_{30}WLXaa_{33}Xaa_{34}G$

$Xaa_{36}Xaa_{37}$; in cui Xaa_3 è A, V, o G; Xaa_{22} è G, K, o E; Xaa_{23} è Q o K; Xaa_{30} è A o E; Xaa_{33} è V o K; Xaa_{34} è K, N, o R; Xaa_{36} è R o G; e Xaa_{37} è G, H, P, o assente (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},$Glu^{22}Lys^{33}$,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). Ciascuno tra GLP-1(7-37) e analoghi di GLP-1(7-37) può essere facoltativamente ammidato.

Gli agonisti del recettore di GLP-1 della composizione di sostanze dell'invenzione possono anche essere derivatizzati chimicamente in uno o più residui di amminoacidi mediante tecniche di chimica organica note. "Derivato chimico" o "derivatizzato chimicamente" si riferisce a un peptide in oggetto avente uno o più residui derivatizzati chimicamente mediante la reazione di un gruppo funzionale laterale. Tali molecole derivatizzate includono, ad esempio, molecole in cui gruppi

ammino liberi sono stati derivatizzati per formare ammina cloridrato, gruppi p-toluen solfonile, gruppi carbobenzossi, gruppi t-butilossicarbonile, gruppi cloroacetile o gruppi formile. Gruppi carbossile liberi possono essere derivatizzati per formare sali, esteri di metile ed etile o altri tipi di esteri o idrazidi. Gruppi idrossile liberi possono essere derivatizzati per formare derivati di O-acile o O-alchile. L'azoto imidazolico di istidina può essere derivatizzato per formare N-im-benzilistidina. Sono inclusi anche come derivati chimici quei peptidi che contengono uno o più derivati di amminoacidi presenti in natura dei venti amminoacidi canonici, sia in forma L che D. Ad esempio, 4-idrossiprolina può essere sostituita a prolina; 5-idrossilisina può essere sostituita a lisina; 3-metilistidina può essere sostituita a istidina; omoserina può essere sostituita a serina; e ornitina può essere sostituita a lisina.

Derivatizzazioni utili includono, in alcune forme di realizzazione, quelle in cui il terminale ammino del peptide è bloccato chimicamente in modo che sia impedito che una coniugazione con il veicolo abbia luogo in corrispondenza di un gruppo ammino libero N-terminale. Potrebbe esserci anche altri effetti benefici di tale modifica, ad esempio una riduzione della suscettibilità dell'analogo di peptide di tossina alla proteolisi enzimatica. L'N-terminale può essere acilato o modificato in un'ammina sostituita, o derivatizzato con un altro gruppo funzionale, come una frazione aromatica (ad esempio, un acido indolico, benzile (Bzl o Bn), dibenzile (DiBzl o Bn_2), o benzilossicarbonile (Cbz o Z)), *N-N.*-dimetilglicina o creatina. Ad esempio, in alcune forme di realizzazione,

una frazione acile, come, ma senza limitarvisi, formile, acetile (Ac), propanoile, butanile, eptanile, esanoile, ottanoile o nonanoile, può essere collegata in modo covalente all'estremità N terminale del peptide, il che può impedire reazioni secondarie indesiderate durante la coniugazione del veicolo al peptide. Altri gruppi derivati N terminali esemplificativi includono -NRR^1 (diverso da -NH$_2$), -NRC(O)R^1, - NRC(O)OR^1, -NRS(O)$_2$R^1, -NHC(O)NHR^1, succinimmide o benzilossicarbonile-NH- (Cbz-NH-), in cui R e R^1 sono ciascuno indipendentemente idrogeno o alchile inferiore e in cui l'anello fenilico può essere sostituito con 1-3 sostituenti selezionati tra C$_1$-C$_4$ alchile, C$_1$-C$_4$ alcossi, cloro e bromo.

In alcune forme di realizzazione, uno o più collegamenti (legami) peptidilici [-C(O)NR-] tra residui di amminoacidi possono essere sostituiti da un collegamento non peptidilico. Collegamenti non peptidilici esemplificativi sono -CH$_2$-carbammato [-CH$_2$-OC(O)NR-], fosfonato, -CH$_2$-solfonammide [-CH$_2$-S(O)$_2$NR-], urea [-NHC(O)NH-], -CH$_2$-ammina secondaria e peptide alchilato [-C(O)NR^6- in cui R^6 è un alchile inferiore].

In alcune forme di realizzazione, uno o più residui di amminoacidi individuali possono essere derivatizzati. Sono noti vari agenti di derivatizzazione che reagiscono specificamente con catene laterali o residui terminali selezionati, come descritto nel dettaglio di seguito a titolo esemplificativo.

Residui di lisinile e residui di terminale ammino possono essere fatti reagire con anidridi succiniche o di altri acidi carbossilici, che invertono la carica dei residui di lisinile. Altri reagenti adatti per

derivatizzare residui contenenti alfa-ammino includono immidoesteri come metil picolinimidato; piridossal fosfato; piridossale; cloroboroidruro; acido trinitrobenzensolfonico; O-metilisourea; 2,4 pentandione; e reazione catalizzata da transaminasi con gliossilato.

I residui di arginile possono essere modificati mediante reazione con uno qualsiasi o una combinazione di svariati reagenti convenzionali, inclusi fenilgliossale, 2,3-butandione, 1,2-cicloesandione e ninidrina. La derivatizzazione di residui di arginile richiede che la reazione sia eseguita a condizioni alcaline a causa dell'elevata pKa del gruppo funzionale guanidina. Per di più, questi reagenti possono reagire con i gruppi di lisina nonché con il gruppo epsilon-ammino di arginina.

La modifica specifica dei residui di tirosile è stata ampiamente studiata, con particolare interesse nell'introduzione di marcature spettrali nei residui di tirosile mediante reazione con composti aromatici di diazonio o tetranitrometano. Più comunemente, N-acetilimidizolo e tetranitrometano sono usati per formare specie di O-acetil tirosile e derivati di 3-nitro, rispettivamente.

Gruppi di catene laterali carbossile (aspartile o glutammile) possono essere selettivamente modificati mediante la reazione con carbodiimmidi (R'-N=C=N-R') come 1-cicloesile-3-(2-morfolinil-(4-etil) carbodiimmide o 1-etil-3-(4-azonia-4,4-dimetilpentil) carbodiimmide. Per di più, residui di aspartile e glutammile possono essere convertiti in residui di asparaginile e glutamminile mediante reazione con ioni di ammonio.

Residui di glutamminile e asparaginile possono essere sottoposti a deammidazione nei corrispondenti residui di glutammile e aspartile. In alternativa, questi residui sono sottoposti a deammidazione in condizioni leggermente acide. Entrambe le forme di questi residui rientrano entro la portata di questa invenzione.

Residui di cisteinile possono essere sostituiti da residui di amminoacidi o altre frazioni per eliminare il legame disolfuro o, al contrario, per stabilizzare la reticolazione. (Si veda, ad esempio, Bhatnagar et al., J. Med. Chem., 39:3814-3819 (1996)).

Altre possibili modifiche includono idrossilazione di prolina e lisina, fosforilazione di gruppi idrossile di residui di serile o treonile, ossidazione dell'atomo di zolfo in Cys, metilazione dei gruppi alfa-amminici di catene laterali di lisina, arginina e istidina. Creighton, Proteins: Structure and Molecule Properties (W. H. Freeman & Co., San Francisco), 79-86 (1983).

Gli esempi di derivatizzazioni di cui sopra non intendono costituire un trattamento esaustivo, ma semplicemente illustrativo.

In una forma di realizzazione, il GLP-1(7-37) o gli analoghi di GLP-1(7-37) sono collegati in modo covalente (direttamente o tramite un gruppo di collegamento) a una porzione Fc di un'immunoglobulina (ad esempio, IgG, IgE, IgG e simili). Ad esempio, una qualsiasi tra SEQ ID NO:25-40 può essere collegata in modo covalente alla porzione Fc di un'immunoglobulina comprendente la sequenza di:

AESKYGPPCPPCPAPXaa$_{16}$Xaa$_{17}$Xaa$_{18}$GGPSWLFPPKPKDTL MISRTPEVTCVVVDVSQ EDPEVQFNWYVOGVEVHNAKTKPREEQFXaa$_{80}$STYRVVSVLTVLHQD WLNGKEYK CKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCL VKGFYPSDIA VEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFS CSVMEALHN HYTQKSLSLSLGXaa$_{230}$; in cui Xaa$_{16}$ è P o E; Xaa$_{17}$ è F, V o A; Xaa$_{18}$ è L, E o A; Xaa$_{80}$ è N o A, e Xaa$_{230}$ è K o assente (SEQ ID NO: 3203). Il gruppo di collegamento può essere qualsiasi frazione chimica (ad esempio, amminoacidi e/o gruppi chimici). In una forma di realizzazione, il gruppo di collegamento è (-GGGGS-)$_x$(SEQ ID NO: 3204) dove x è 1, 2, 3, 4, 5 o 6; preferibilmente 2, 3 o 4; più preferibilmente 3. In una forma di realizzazione, l'analogo di GLP-1(7-37) collegato in modo covalente alla porzione Fc di un'immunoglobulina comprende la sequenza di amminoacidi:

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

In un'altra forma di realizzazione, il GLP-1(7-37) o l'analogo di GLP-1(7-37) può essere collegato in modo covalente (direttamente o attraverso un gruppo di collegamento) a una o due molecole di glicole di polietilene. Ad esempio, un analogo di GLP-1(7-37) può comprendere la sequenza di amminoacidi: HXaa$_{8E}$GTFTSDVS

SYLEXaa$_{22}$QAAKEFIAWLXaa$_{33}$KGGPSSGAPPPC$_{45}$C$_{46}$-Z, in cui Xaa$_8$ è: D-Ala, G, V, L, I, S o T; Xaa$_{22}$ è G, E, D o K; Xaa$_{33}$ è: V o I; e Z è OH o NH_2, (SEQ ID NO: 3206), e, facoltativamente, in cui (i) una frazione glicole di polietilene è attaccata in modo covalente a C$_{45}$, (ii) una frazione glicole di polietilene è attaccata in modo covalente a C$_{46}$, o (iii) una frazione glicole di polietilene è attaccata a C$_{45}$ e una frazione glicole di polietilene è attaccata a C$_{46}$. In una forma di realizzazione, l'analogo di GLP-1(7-37) è HVEGTFTSDVSSYLEEQAAKEFI AWLIKGGPSSGAPPPC$_{45}$C$_{46}$-NH_2 (SEQ ID NO: 3207) e, facoltativamente, in cui (i) una frazione glicole di polietilene è attaccata in modo covalente a C$_4$, (ii) una frazione glicole di polietilene è attaccata in modo covalente a C$_{46}$, o (iii) una frazione glicole di polietilene è attaccata a C$_{45}$ e una frazione glicole di polietilene è attaccata a C$_{46}$.

I residui di amminoacidi agonisti di recettore di GLP-1 che possono fornire una frazione ammina primaria per la coniugazione includono residui di lisina, omolisina, ornitina, acido α, β-diamminopropionico (Dap), acido α, β-diamminopropionoico (Dpr) e acido α, γ-diamminobutirrico (Dab), acido amminobutirrico (Abu) e acido α-amminoisobutirrico (Aib). L'N-terminale di polipeptide fornisce anche un utile gruppo α-ammino per la coniugazione, così come un C-terminale di polipeptide ammidato. In certe forme di realizzazione, il GLP-1(7-37) o l'analogo di GLP-1(7-37) è coniugato all'anticorpo, o suo frammento, in un residuo che corrisponde a K26 (posizione 20 di SEQ ID NO: 3184), K34 (posizione 28 di SEQ ID NO: 3184), K36 (posizione 30 di SEQ ID

NO: 3184; ad esempio tramite una mutazione R36K), K37 (posizione 31 di SEQ ID NO: 3184; ad esempio tramite una mutazione G37K), K39 (ad esempio tramite aggiunta di due amminoacidi al GLP-1(7-37) o all'analogo di GLP-1(7-37) con lisina in posizione 39) o un gruppo ammina C-terminale di detto analogo. Residui di amminoacidi che possono fornire una frazione ammina secondaria includono ε-N-alchil lisina, α-N-alchil lisina, δ-N-alchil ornitina, α-N-alchil ornitina o una prolina terminale N, in cui l'alchile è da C_1 a C_6.

Una "frazione linker", secondo l'uso fattone nella presente, si riferisce a un gruppo organico peptidile o non peptidile biologicamente accettabile che è legato in modo covalente a un residuo di amminoacido di un analogo di peptide di tossina o altra catena di polipeptide (ad esempio, un dominio HC o LC di immunoglobulina o uno Fc di immunoglobulina) contenuto nella composizione dell'invenzione, la quale frazione linker unisce o coniuga in modo covalente l'analogo di peptide di tossina o l'altra catena di polipeptide a un'altra catena di peptide o polipeptide nella composizione, o a una frazione estendente l'emivita. In alcune forme di realizzazione della composizione, una frazione estendente l'emivita, come descritto nella presente, è coniugata, ossia legata in modo covalente, direttamente a un residuo di amminoacido dell'analogo di peptide di tossina stesso, o, facoltativamente, a una frazione linker peptidilico o non peptidilico (inclusi, ma senza limitarvisi, linker aromatici o arilici) che è legata in modo covalente a un residuo di amminoacido dell'analogo di peptide di tossina. La presenza di qualsiasi

frazione linker è facoltativa. Quando presente, la sua struttura chimica non è critica, poiché serve principalmente come distanziatore per posizionare, unire, connettere, o ottimizzare la presentazione o la posizione di una frazione funzionale in relazione a una o più altre frazioni funzionali di una molecola della composizione dell'invenzione. La presenza di una frazione linker può essere utile per ottimizzare l'attività farmacologica di alcune forme di realizzazione della composizione dell'invenzione. Il linker, se presente, può essere costituito da amminoacidi collegati tra loro mediante legami peptidici. La frazione linker, se presente, può essere indipendentemente uguale a, o differente da, qualsiasi altro linker, o più linker, che può essere presente nella composizione dell'invenzione. In alcune forme di realizzazione, il linker può essere un linker multivalente che facilita l'esposizione multivalente di analoghi di peptide di tossina della presente invenzione; l'esposizione multivalente di tali composti biologicamente attivi può aumentare l'affinità di legame e/o la potenza attraverso l'avidità. Le proprietà in vivo di un agente terapeutico possono essere modificate (ossia, bersagliamento specifico, estensione dell'emivita, profilo di distribuzione, eccetera) attraverso la coniugazione a un polimero o a una proteina.

Linker peptidilici. Come dichiarato in precedenza, la frazione linker, se presente (che sia all'interno della sequenza di amminoacidi primaria dell'analogo di peptide di tossina o come linker per l'attacco di una frazione estendente l'emivita all'analogo di peptide di tossina), può essere "peptidilica" per natura (ossia costituita da amminoacidi collegati

tra loro mediante legami peptidici) e costituita con una lunghezza, preferibilmente, da 1 fino a circa 40 residui di amminoacidi, più preferibilmente da 1 fino a circa 20 residui di amminoacidi, e, in modo massimamente preferito, da 1 fino a circa 10 residui di amminoacidi. Preferibilmente, ma non necessariamente, i residui di amminoacidi nel linker sono tra i venti amminoacidi canonici, più preferibilmente cisteina, glicina, alanina, prolina, asparagina, glutammina, e/o serina. Ancora più preferibilmente, un linker peptidilico è costituito dalla maggior parte di amminoacidi stericamente non ostacolati, come glicina, serina e alanina collegati mediante un legame peptidico. È anche desiderabile che, se presente, venga selezionato un linker peptidico che eviti un rapido turnover proteolitico nella circolazione. *in vivo.* Alcuni di questi amminoacidi possono essere glicosilati, come è ben noto nell'arte. Ad esempio, una sequenza linker utile che costituisce un sito di sialilazione è $X_1X_2NX_4X_5G$ (SEQ ID NO: 3250), in cui X_1, X_2, X_4 e X_5 sono, ciascuno indipendentemente, un qualsiasi residuo di amminoacido.

In altre forme di realizzazione, gli amminoacidi da 1 a 40 della frazione linker peptidilico sono selezionati tra glicina, alanina, prolina, asparagina, glutammina e lisina. Preferibilmente, un linker è costituito per la maggior parte da amminoacidi stericamente non ostacolati, come glicina e alanina. Perciò, linker preferiti includono poliglicine, poliserine, e polialanine, o combinazioni di qualsiasi di questi. Alcuni esempi di linker peptidilici sono poli$(Gly)_{1-8}$, particolarmente $(Gly)_3$ (SEQ ID NO:3251), $(Gly)_4$(SEQ ID NO:480), $(Gly)_5$ (SEQ ID NO:3251) e $(Gly)_7$ (SEQ ID

NO:3252), nonché GlySer e poli$(Gly)_4$Ser, come "L15" (GGGGSGGGGSGGGGS; SEQ ID NO:3253), poli$(Gly\text{-}Ala)_{2\text{-}4}$ e poli$(Ala)_{1\text{-}8}$. Altri esempi specifici di linker peptidilici includono $(Gly)_5$Lys (SEQ ID NO:3254), e $(Gly)_5$LysArg (SEQ ID NO:3255). Altri esempi di linker peptidilico utili sono: Altri esempi di linker peptidilico utili sono:

$(Gly)_3Lys(Gly)_4$ (SEQ ID NO:3256);

$(Gly)_3AsnGlySer(Gly)_2$ (SEQ ID NO:3257);

$(Gly)_3Cys(Gly)_4$ (SEQ ID NO:3258); e

GlyProAsnGlyGly (SEQ ID NO:3259).

Per spiegare la nomenclatura di cui sopra, ad esempio, $(Gly)_3Lys(Gly)_4$ significa Gly-Gly-Gly-Lys-Gly-Gly-Gly-Gly (SEQ ID NO:3260). Sono utili anche altre combinazioni di Gly e Ala.

Altri linker preferiti sono quelli identificati nella presente come "L5" (GGGGS; o "G_4S"; SEQ ID NO:3261), "L10" (GGGGSGGGGS; SEQ ID NO:3262); "L20" (GGGGSGGGGSGGGGSGGGGS; SEQ ID NO:3263); "L25" (GGGGSGGGGSGGGGSGGGGSGGGGS; SEQ ID NO:3264) e qualsiasi linker usato negli esempi di lavoro di seguito.

In alcune forme di realizzazione delle composizioni di questa invenzione, che comprendono una frazione linker peptidico, i residui acidi, ad esempio residui di glutammato o aspartato, sono posti nella sequenza di amminoacidi della frazione linker. Esempi includono le seguenti sequenze linker peptidiche:

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); o

FFEEEFF (SEQ ID NO:3279).

In altre forme di realizzazione, il linker costituisce un sito di fosforilazione, ad esempio $X_1X_2YX_4X_5G$ (SEQ ID NO:3280), in cui X_1, X_2, X_4, e X_5 sono, ciascuno indipendentemente, qualsiasi residuo di amminoacido; $X_1X_2SX_4X_5G$ (SEQ ID NO:3281), in cui X_1, X_2, X_4 e X_5 sono, ciascuno indipendentemente, qualsiasi residuo di amminoacido; o $X_1X_2TX_4X_5G$ (SEQ ID NO:3282), in cui X_1, X_2, X_4 e X_5 sono, ciascuno indipendentemente, qualsiasi residuo di amminoacido.

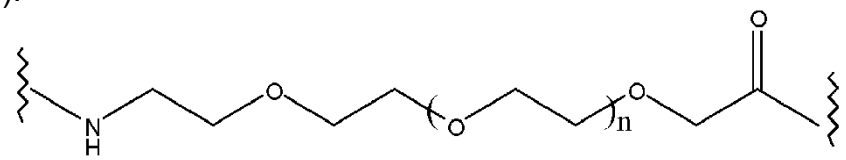
I linker qui mostrati sono esemplificativi; linker peptidilici rientranti nella portata di questa invenzione possono essere molto più lunghi e possono includere altri residui. Un linker peptidilico può contenere, ad esempio, una cisteina, un altro tiolo o nucleofilo per la coniugazione con

una frazione estendente l'emivita. In un'altra forma di realizzazione, il linker contiene un residuo di cisteina o omocisteina, o un'altra frazione 2-ammino-etantiolo o 3-ammino-propantiolo per la coniugazione a una frazione estendente l'emivita funzionalizzata con maleimide, iodoacetammide o tioestere.

Un altro linker peptidilico utile è un linker grande flessibile comprendente una sequenza Gly/Ser/Thr casuale, per esempio: GSGSATGGSGSTASSGSGSATH (SEQ ID NO:3283) o HGSGSATGGSGSTASSGSGSAT (SEQ ID NO:3284) che si stima abbia all'incirca le dimensioni di una molecola di PEG da 1 kDa. In alternativa, un linker peptidilico utile può essere costituito da sequenze di amminoacidi note nell'arte in quanto formano strutture elicoidali rigide (ad esempio, linker rigido: - AEAAAKEAAAKEAAAKAGG-// SEQ ID NO:3285). In aggiunta, un linker peptidilico può anche comprendere un segmento non peptidilico come una molecola alifatica a 6 atomi di carbonio di formula $-CH_2-CH_2-CH_2-CH_2-CH_2-CH_2-$. I linker peptidilici possono essere alterati per formare derivati come descritto nella presente.

Linker non peptidilici. Facoltativamente, una frazione linker non peptidilico è utile anche per coniugare la frazione estendente l'emivita alla porzione peptidica dell'analogo di peptide di tossina coniugata alla frazione estendente l'emivita. Ad esempio, possono essere usati linker alchile come $-NH-(CH_2)_s-C(O)-$, in cui s = 2-20. Questi linker alchile possono ulteriormente essere sostituiti da qualsiasi gruppo non

stericamente ostacolato come alchile inferiore (ad esempio, C_1-C_6) acile inferiore, alogeno (ad esempio, Cl, Br), CN, NH_2, fenile, eccetera. Linker non peptidilici esemplificativi sono linker di PEG (ad esempio, mostrati di seguito):



dove n è tale che il linker ha un peso molecolare da circa 100 a circa 5000 Dalton (Da), preferibilmente da circa 100 a circa 500 Da.

In una forma di realizzazione, il linker non peptidilico è arile. I linker possono essere alterati per formare derivati alla stessa maniera descritta nella presente. "Arile" è fenile o fenile fuso in prossimità con un ponte di carbonio a 3, 4 o 5 elementi saturo, parzialmente saturo o insaturo, il fenile o il ponte essendo sostituito da 0, 1, 2 o 3 sostituenti selezionati tra C_{1-8} alchile, C_{1-4} aloalchile o alo. "Eteroarile" è un anello monociclico insaturo a 5, 6 o 7 elementi o biciclico parzialmente saturo o insaturo a 6, 7, 8, 9, 10 o 11 elementi, in cui almeno un anello è insaturo, gli anelli monociclico e biciclico contengono 1, 2, 3 o 4 atomi selezionati tra N, O e S, in cui l'anello è sostituito da 0, 1, 2 o 3 sostituenti selezionati tra C_{1-8} alchile, C_{1-4} aloalchile e alo.

Le porzioni non peptidiche della composizione di sostanze dell'invenzione, quali linker non peptidilici o le frazioni estendenti l'emivita non peptidiche, possono essere sintetizzate mediante reazioni di chimica organica convenzionali.

Altre forme di realizzazione del linker multivalente comprendono un nucleo polieterociclico rigido di lunghezza controllata. I linker sono differenziati chimicamente su entrambe su una o l'altra estremità per adattarsi alle chimiche di accoppiamento ortogonale (ad esempio "click" di azoturo, accoppiamento ammidico, formazione di tioetere mediante alchilazione con maleimide o aloacetammide, formazione di ossima, amminazione riduttiva, eccetera).

Quanto sopra è meramente illustrativo e non un trattamento esaustivo dei tipi di linker che possono essere facoltativamente impiegati in conformità alla presente invenzione.

In una forma di realizzazione, il composto agonista del recettore di GLP-1 è un peptide che ha almeno 80% di identità di sequenza con GLP-1(7-37) (SEQ ID NO: 3184); almeno 85% di identità di sequenza con GLP-1(7-37) (SEQ ID NO: 3184); almeno 90% di identità di sequenza con GLP-1(7-37) (SEQ ID NO: 3184); o almeno 95% di identità di sequenza con GLP-1(7-37) (SEQ ID NO: 3184).

Composti agonisti del recettore di GLP-1 possono essere preparati mediante processi ben noti nell'arte, ad esempio la purificazione di peptidi come descritta in Eng et al., *J. Biol. Chem.,* 265:20259-62 (1990); tecniche standard di sintesi peptidica in fase solida come descritte in Raufman et al., *J. Biol. Chem.,* 267:21432-37 (1992); tecniche di DNA ricombinante come descritte in Sambrook et al., *Molecular Cloning: A Laboratory Manual, 2a ed., Cold Spring Harbor* (1989); e simili.

Tabella 7. Esempi di sequenze di agonisti del recettore di GLP-1

SEQ ID NO:	Sequenza	Descrizione
3163	HGEGTFTSDLSKQMEEEAVRLFIEGGPSSGAPPPS	Exendina-4
3164	HSDGTFTSDLSKQMEEEAVRLFIEGGPSSGAPPPS	Exendina-3
3165	HGEGTFTSDLSKQLEEEAVRLFIEGGPSSGAPPPS	Leu^{14}-exendina-4
3166	HGEGTFTSDLSKQLEEEAVRLFIEGGPSSGAPPPS	Leu^{14},Phe^{25}-exendina-4

SEQ ID NO:	Sequenza	Descrizione
3167	HGEGTFTSDLSKQLEEEAARLFIEWLKGGPSSGAPPPS	Leu^{14},Ala,^{19},Phe^{25}-exendina-4
3168	HGEGTFTSDLSKQMEEEAVRLFIEWLKGG	exendina-4(1-30)
3169	HGEGTFTSDLSKQLEEEAVRLFIEWLKGG	Leu^{14}-exendina-4(1-30)
3170	HGEGTFTSDLSKQLEEEAVRLFIEFLKGG	Leu^{14},Phe^{25}-exendina-4(1-30)
3171	HGEGTFTSDLSKQLEEEAARLFIEFLKGG	Leu^{14},Ala^{19},Phe^{25}-exendina-4(1-30)
3172	HGEGTFTSDLSKQMEEEAVRLFIEWLKN	exendina-4(1-28)

SEQ ID NO:	Sequenza	Descrizione
3173	HGEGTFTSDLSKQLEEEAVRLFIEWLKN	Leu^{14}-exendina-4(1-28)
3174	HGEGTFTSDLSKQLEEEAVRLFIEFLKN	Leu^{14},Phe^{25}-exendina-4(1-28)
3175	HGEGTFTSDLSKQLEEEAARLFIEFLKN	Leu^{14},Ala^{19},Phe^{25}-exendina-4 (1-28)
3176	HGEGTFTSDLSKQLEEKAAKEFIEGGPSSGAPPPS	Leu^{14},Lys^{17,20},Ala^{19},Glu^{21},Phe^{25},Gln^{28}-exendina-4
3177	HGEGTFTSDLSKQLEEKAAKEFIEGGPSSGAPPPS	Leu^{14},Lys^{17,20},Ala^{19},Glu^{21},Gln^{28}-exendina-4
3178	HGEGTFTSDLSKQ(octylG)EEEFIEWLKQGGPSSGAPPPS	ottilGly^{14},Gln^{28}-exendina-4
3179	HGEGTFTSDLSKQLEEEAVRLFIEGGPSS(octylG)APPPS	Leu^{14},Gln^{28},ottilGly^{34}-exendina-4

SEQ ID NO:	Sequenza	Descrizione
3180	HGEFTFTSDLSKQLEEEAVRLFIEGGPSKEIIS	Phe[4],Leu[14],Gln[28],Lys[33],Glu[34], Ile[35,36], Ser[37]/-exendina-4(1-37)
3181	HGEFTFTSDLSKQLEEKAAKEFIEGGPSSGAPPPS	Phe[4],Leu[14],Lys[17,20],Ala[19],Glu[21],Gln[28]-exendina-4
3182	HGEGTFTSDLVKILEAEAVRKFIEGGPSSGAPPPS	Val[11],Ile[13],Leu[14],Ala[16],Lys[21],Phe[25]-exendina-4
3183	HGEGTFTSDLSKQMEEEAVRLFIEGGPSSGAPPPSK	exendina-4-Lys[40]
3184	HAEGTFTSDVSSYLEGQAAKEFIAGRG	GLP-1(7-37)

SEQ ID NO:	Sequenza	Descrizione
3185	HAEGTFTSDVSSYLEGQAAKEFIAGR	GLP-1(7-36)-NH_2
3186	H(Aib)EGTFTSDVSSYLEGQAAKEFLVR(Aib)R	$Alb^{8,35}$,$Arg^{26,34}$,Phe^{31}-GLP-1(7-36))
3187	$HXaa_8$EGTFTSDVSSYLE$Xaa_{22}Xaa_{23}$AAKEFIXaa_{30}WL$Xaa_{33}Xaa_{34}$G$Xaa_{36}Xaa_{37}$	$HXaa_8$EGTFTSDVSSYLE$Xaa_{22}Xaa_{23}$AAKEFIXaa_{30}WL$Xaa_{33}Xaa_{34}$G$Xaa_{36}Xaa_{37}$ in cui Xaa_8 è A, V, o G
	Xaa_{30}WL$Xaa_{33}Xaa_{34}$G$Xaa_{36}Xaa_{37}$ in cui Xaa_8 è A, V, o G	
	Xaa_{22} è G, K, o E	Xaa_{22} è G, K, o E
	Xaa_{23} è Q o K	Xaa_{23} è Q o K
	Xaa_{30} è A o E	Xaa_{30} è A o E
	Xaa_{33} è V o K	Xaa_{33} è V o K
	Xaa_{34} è K, N, o R	Xaa_{34} è K, N, o R

SEQ ID NO:	Sequenza	Descrizione
	Xaa_{36} è R o G	Xaa_{36} è R o G
	e Xaa_{37} è G, H, P, o assente	e Xaa_{37} è G, H, P, o assente
3188	HAEGTFTSDVSSYLEGQAAKEFIAGRG	Arg^{34}-GLP-1 (7-37)
3189	HAEGTFTSDVSSYLEGQAAKEFIEGRG	Glu^{30}-GLP-1(7-37)
3190	HAEGTFTSDVSSYLEKQAAKEFIAGRG	Lys^{22}-GLP-1(7-37)
3191	HGEGTFTSDVSSYLEEQAAKEFIAGGG	$Gly^{8,36,}Glu^{22}$-GLP-1(7-37)
3192	HVEGTFTSDVSSYLEEQAAKEFIAGGG	Val^{8},Glu^{22},Gly^{36}-GLP-1(7-37)

SEQ ID NO:	Sequenza	Descrizione
3193	HGEGTFTSDVSSYLEEQAAKEFIAGGG	Gly[8,36],Glu[22],Lys[33],Asn[34]-GLP-1(7-37)
3194	HVEGTFTSDVSSYLEEQAAKEFIAGGG	Val[8],Glu[22],Lys[33],Asn[34],Gly[36]-GLP-1(7-37)
3195	HGEGTFTSDVSSYLEEQAAKEFIAGGP	Gly[8,36],Glu[22],Pro[37]-GLP-1(7-37)
3196	HVEGTFTSDVSSYLEEQAAKEFIAGGP	Val[8],Glu[22],Gly[36],Pro[37]-GLP-1(7-37)
3197	HGEGTFTSDVSSYLEEQAAKEFIAGGP	Gly[8,36],Glu[22],Lys[33], Asn[34],Pro[37]-GLP-1(7-37)
3198	HVEGTFTSDVSSYLEEQAAKEFIAGGP	Val[8],Glu[22],Lys[33],Asn[34],Gly[36],Pro[37] -GLP-1(7-37)

SEQ ID NO:	Sequenza	Descrizione
3199	HGEGTFTSDVSSYLEEQAAKEFIAGG	Gly^{8,36},Glu^{22}-GLP-1(7-36)
3200	HVEGTFTSDVSSYLEEQAAKEFIAGG	Val^{8},Glu^{22},Gly^{36}-GLP-1(7-36)
3201	HVEGTFTSDVSSYLEEQAAKEFIAGG	Val^{8},Glu^{22},Asn^{34},Gly^{36}-GLP-1(7-36)
3202	HGEGTFTSDVSSYLEEQAAKEFIAGG	Gly^{8,36},Glu^{22},Asn^{34}-GLP-1(7-36)
3203		Porzione Fc di un'immunoglobulina

SEQ ID NO:	Sequenza	Descrizione
	AESKYGPPCPPCPAPXaa$_{16}$Xaa$_{17}$ GGPSVFLFPPKPKDTLMISRTPE VDVSQEDPEVQFNWYVDGVEVHN REEQFXaa$_{80}$STYRVVSVLTVLHQ KEYKCKVSNKGLPSSIEKTISKA EPQVYTLPPSQEEMTKNQVSLTC YPSDIAVEWESNGQPENNYKTTP DGSFFLYSRLTVDKSRWQEGNVF HEALHNHYTQKSLSLSLGXaa$_{230}$	
	in cui Xaa$_{16}$ è P o E	
	Xaa$_{17}$ è F, V o A.	
	Xaa$_{18}$ è L, E o A	
	Xaa$_{80}$ è N o A	
	e Xaa$_{230}$ è K o assente	
3204	(-GGGGS-)$_x$ in cui x è 1, 2, 3, 4, 5 o 6	Linker
3205		Porzione Fc di un'immunoglobulina

SEQ ID NO:	Sequenza	Descrizione
	HGEGTFTSDVSSYLEEQAAKEFI GGGGGGGSGGGGSGGGGSAESKY PCPAPEAAGGPSVFLFPPKPKDT TPEVTCVVVDVSQEDPEVQFNWY VHNAKTKPREEQFNSTYRVVSVL DWLNGKEYKCKVSNKGLPSSIEK KGQPREPQVYTLPPSQEEMTKNQ LVKGFYPSDIAVEWESNGQPENN PVLDSDGSFFLYSR LTVDKSRWQEGNVFSCSVMHEAL QKSLSLSLG	
3206	HXaa$_8$EGTFTSDVS	Analogo di GLP-1
	SYLEXaa$_{22}$QAAKEFIAWL Xaa$_{33}$KGGPSS GAPPPC$_{45}$C$_{46}$-Z, in cui	
	Xaa$_8$ è: D-Ala, G, V, L, I, S o T	
	Xaa$_{22}$ è G, E, D o K	
	Xaa$_{33}$ è: V o I	
	e Z è OH o NH_2, e, facoltativamente, in cui (i)	

SEQ ID NO:	Sequenza	Descrizione
	una frazione glicole di polietilene è attaccata in modo covalente a C_{45}, (ii) una frazione glicole di polietilene è attaccata in modo covalente a C_{46}, o (iii) una frazione glicole di polietilene è attaccata a C_{45} e una frazione glicole di polietilene è attaccata a C_{46}.	
3207	HVEGTFTSDVSSYLEEQAAKEFIAWLIK GGPSSGAPP$C_{45}C_{46}$-NH_2, e, facoltativamente, in cui (i) una frazione glicole di polietilene è attaccata in modo covalente a C_4, (ii)	Analogo di GLP-1

SEQ ID NO:	Sequenza	Descrizione
	una frazione glicole di polietilene è attaccata in modo covalente a C_{46}, o (iii) un polietilene a C_{46}, o (iii) una frazione glicole di polietilene è attaccata a C_{45} e una frazione glicole di polietilene è attaccata a C_{46}.	
3208	HGEGTFTSDLSKQMEEEAVKLFIE GGPSSGAPPPS	[N^e-(acido 17-carbossieptadecanoico)Lys^{20}]exendina-4-NH_2
3209	HGEGTFTSDLSKQMEEEAVRLFIE GGPKSGAPPPS	[N^e-(17-carbossiepta-decanoil)Lys^{32}]exendina-4-NH_2
3210	GEGTFTSDLSKQMEEEAVKLFIEV GPSSGAPPPS	[desammino-His^1,N^e-(17-carbossieptadecanoil)Lys^{20}]exendina-4-NH_2

SEQ ID NO:	Sequenza	Descrizione
3211	HGEGTFTSDLSRQNorLeEEEAVRWLRNGGPKSGAPPPS	[Arg^{12,27},NLe^{14},N^{e}-(17-carbossi-eptadecanoil)Lys^{32}]exendina-4-NH_2
3212	HGEGTFTSDLSKQMEEEAVKLFIEGGPSSGAPPPS	[N^{e}-(19-carbossi-nonadecanoilammino)Lys^{20}]-exendina-4-NH_2
3213	HGEGTFTSDLSKQMEEEAVKLFIEGGPSSGAPPPS	[N^{e}-(15-carbossipentadecanoilammino)Lys^{20}]-exendina-4-NH_2
3214	HGEGTFTSDLSKQMEEEAVKLFIEGGPSSGAPPPS	[N^{e}-(13-carbossitridecanoilammino)Lys^{20}]exendina-4-NH_2
3215	HGEGTFTSDLSKQMEEEAVKLFIEGGPSSGAPPPS	[N^{e}-(11-carbossi-undecanoil-ammino)Lys^{20}]exendina-4-NH_2
3216	HGEGTFTSDLSKQMEEEAVRLFIEGGPSSGAPPPSK	exendina-4-Lys^{40}(e-MPA)-NH_2

SEQ ID NO:	Sequenza	Descrizione
3217	HGEGTFTSDLSKQMEEEAVRLFIEGGPSSGAPPPSK	exendina-4-Lys^{40}(e-AEEA-AEEA-MPA)-NH_2
3218	HGEGTFTSDLSKQMEEEAVRLFIEGGPSSGAPPPSK	exendina-4-Lys^{40}(e-AEEA-MPA)-NH_2
3219	HGEGTFTSDLSKQMEEEAVRLFIEGGPSSGAPPPSK	exendina-4-Lys^{40}(e-MPA)-albumina
3220	HGEGTFTSDLSKQMEEEAVRLFIEGGPSSGAPPPSK	exendina-4-Lys^{40}(e-AEEA-AEEA-MPA)-albumina
3221	HGEGTFTSDLSKQMEEEAVRLFIEGGPSSGAPPPSK	exendina-4-Lys^{40}(e-AEEA-MPA)-albumina

SEQ ID NO:	Sequenza	Descrizione
3222	AEGTFTSDVSSYLEGQAAREFIAWRG	desammino-His^{7},Arg^{26},Lys^{34}N$^{\varepsilon}$-(γ-Glu(N-α-esadecanoil)))-GLP-1(7-37) (peptide nucleo divulgato come SEQ ID NO: 3222)
3223	AEGTFTSDVSSYLEGQAAREFIAWRG	desammino-His^{7},Arg^{26},Lys^{34}(N$^{\varepsilon}$-ottanoil)-GLP-1(7-37)
3224	HAEGTFTSDVSSYLEGQAAREFIAGRGK	Arg^{26,34},Lys^{38}(N$^{\varepsilon}$-(ω carbossipentadecanoil))-GLP-1(7-38)
3225	HAEGTFTSDVSSYLEGQAAREFIAGRGK	Arg^{26,34},Lys^{36}(N$^{\varepsilon}$-(γ-Glu(N-α-esadecanoil)))-GLP-1 (7-3 6) (peptide nucleo divulgato come SEQ ID NO: 3225)
3226	H[Aib]EGTFTSDVSSYLEGQAAWLVKGRK	[Aib^{8};Lys^{37}]GLP-1-(7-37)

SEQ ID NO:	Sequenza	Descrizione
3227	H[Aib]EGTFTSDVSSYLEGQAA WLVKGKG	[Aib^{8}, Lys^{36}]GLP-1-(7-37)
3228	H[Aib]EGTFTSDVSSYLE[Aib] EFIAWLVKGK	[Aib^{8,22};Lys^{36}]GLP-1(7-36)-ammide
3229	H[Aib]EGTFTSDVSSYLE[Aib] EFIAW[BLeu]VKGK	[Aib^{8,22};BLeu^{32};Lys^{36}]GLP-1(7-36)-ammide
3230	H[Aib]EGTFTSDVSSYLE[Aib] EFIAWLVKGRK	[Aib^{8,22};Lys^{37}]GLP-1(7-37)-ammide
3231	H[Aib]EGTFTSDVSSYLE[Aib] EFIAW[BLeu]VKGRK	[Aib^{8,22};BLeu^{32};Lys^{37}]GLP-1(7-37)-ammide
3232	H[Aib]EGTFTSDVSSYLE[Aib] EFIAW[aMeLeu]VKGRK	[Aib^{8,22},aMeLeu^{32};Lys^{37}]GLP-1(7-37)-ammide

SEQ ID NO:	Sequenza	Descrizione
3233	H[Aib]EGT[AMEF]TSDVSSYLE]QAAKEFIAWLVKGRK	[Aib^{8,22};AMEF^{12};Lys^{37}]GLP-1(7-37)-ammide
3234	H[Aib]EGTFTSD[BLeu]SSYLE]QAAKEFIAWLVKGRK	[Aib^{8,22};BLeu^{16};Lys^{37}]GLP-1(7-37)-ammide
3235	H[Aib]EGTFTSDVSSYLE[Aib]EFIAWLVKGGK	[Aib^{8,22};Gly^{36};Lys^{37}]GLP-1(7-37)-ammide
3236	H[Aib]EGTFTSDVSSYLE[Aib]EFIAWLKNGGK	[Aib^{8,22};Lys^{33,37};Asn^{34};Gly^{36}]GLP-1(7-37)-ammide
3237	H[Aib]EGTFTSDVSSYLE[Aib]EFIAWLKNGG[Aeea]	[Aib^{8,22};Lys^{33};Asn^{34};Gly^{36};Aeea^{37}] GLP-1(7-37)-Aeea-Lys-ammide

SEQ ID NO:	Sequenza	Descrizione
3238	H[Aib]EGTFTSDVSSYLE[Aib]EFIAWLVKGGG	Gly^{36}]GLP-1(7-37)
3239	H[Aib]EGTFTSDVSSYLEGEAAWLVKGGG	ciclo[E^{23}-K^{27}][Aib^{8};Gly^{36}]GLP-1(7-37)
3240	H[Aib]EGTFTSDVSSYLEEQAAAWLVKGGK	ciclo[E^{22}-K^{26}][Aib^{8};Gly^{36};Lys^{37}]GLP-1(7-37)-ammide
3241	H[Aib]EGTFTSDVSSYLE[Aib]LFIEWLKNGGPSSGAPPPS	[Aib^{8,22}]-GLP-1(7-22)-Ex4(17-39)
3242	HGEGTFTSDVSSYLEEQAAKEFIAGGG	[Gly^{8,36};Glu^{22}]GLP-1(7-37)
3243	H[Aib]EGTFTSDVSSYLEEQAAWLVKGGG	[Aib^{8};Glu^{22};Gly^{36}]GLP-1(7-37)-ammide

SEQ ID NO:	Sequenza	Descrizione
3244	H[Aib]EGTFTSDYSSYLEEQAA WLVKGGG	[Aib[8];Tyr[16];(Glu[22];Gly[36]]GLP-1(7-37)
3245	H[Aib]EGTFTSDVSKYLEEEAV 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]EGTFTSDVSKYLEEEAA WLKNGGG	[Aib[8];Lys[18,33];Glu[22,23,30]Leu[27];Asn[34];Gly[36]]GLP-1(7-37)
3247	H[Aib]EGTFTSDVSKYLEEEAA WLVKGGG	[Aib[8];Lys[18];Glu[22,23,30];Leu[27];Gly[36]]GLP-1(7-37)
3248	H[Aib]IGTFTSDVSSYLE[Aib] EFIAWLVKGG	[Aib[8,22];Ile[9];Gly[36]]GLP-1_(7-36)

SEQ ID NO:	Sequenza	Descrizione
3249	H[Aib]EGTFTSEVSSYLE[Aib]EFIAWLVKGG	[Aib^{8,22};Glu^{15};Gly^{36}]GLP-1_(7-36)
3286	{H2}H[Aib]EGTFTSDVSSYLE[QAAKEFIAWLKNGG[Aeea][AeeCONH2}	
3287	{H2}H[Aib]EGTFTSDVSSYLEQAAKEFIAWLVKGGG	
3288	{H2}H[Aib]EGTFTSDVSSYLECKFIAWLVKGGG	
3289	{H2}H[Aib]EGTFTSDVSSYLEFEFIAWLVKGGK{CONH2}	

SEQ ID NO:	Sequenza	Descrizione
3290	{H2}H[Aib]EGTFTSDVSSYLEEAVRLFIEWLKNGGPSSGAPPPS	
3291	{H2}HGEGTFTSDVSSYLEEQAAWLVKGGG	
3292	{H2}H[Aib]EGTFTSDVSSYLEEFIAWLVKGGG	
3293	{H2}H[Aib]EGTFTSDYSSYLEEFIAWLVKGGG	
3294	{H2}H[Aib]EGTFTSDVSKYLEELFIEWLKNGGG	

SEQ ID NO:	Sequenza	Descrizione
3295	{H2}H[Aib]EGTFTSDVSKYLEELFIEWLKNGGG	
3296	{H2}H[Aib]EGTFTSDVSKYLEELFIEWLVKGGG	
3297	{H2}H[Aib]IGTFTSDVSSYLEQAAKEFIAWLVKGG	
3298	{H2}H[Aib]EGTFTSEVSSYLEQAAKEFIAWLVKGG	
3299	{H2}H[Aib]AGTFTSDVSSYLEQAAKEFIAWLVKGG	
3300	{H2}H[Aib]EGTFTSDVSSYLEQAAKEFAAWLVKGG	

SEQ ID NO:	Sequenza	Descrizione
3301	{H2}H[Aib]EGTFTSDVSSYLEQAAKEFIAALVKGG	
3302	{H2}H[Aib]TGTFTSDVSSYLEQAAKEFIAWLVKGGG	
3303	{H2}H[Aib]EGTFTSEVSSYLEQAAKEFIAALVKGGG	
3304	{H2}H[Aib]EGTFTSDVSSYLEQAAKEFIAALVKGGG	
3305	{H2}H[Aib]EGTFTSDVSSYLEILFIEWLKNGGPSSGAPPPS	

SEQ ID NO:	Sequenza	Descrizione
3306	{H2}H[Aib]EGTFTSDYSSYLE|QAAKEFIAWLVKGGG	
3307	{H2}H[Aib]EGTFTSDVSSYLE|QAAKEFIAWLVKGGG{CONH2}	
3308	{Dmia}SQGTFTSDYSKYLDERR/QWLMNT	
3309	{H2}HGEGTFTSDLSKQMEEEAVF|WLKNGGPSSGAPPPS	

AEEA si riferisce ad acido [2-(2-ammino)etossi)]acetico

EDA si riferisce ad etilendiammina.

MPA si riferisce ad acido maleimidopropionico.

La divulgazione fornisce anche composizioni farmaceutiche comprendenti i composti agonisti del recettore di GLP-1 descritti nella

presente e un trasportatore farmaceuticamente accettabile. I composti agonisti del recettore di GLP-1 possono essere presenti nella composizione farmaceutica in una quantità terapeuticamente efficace e possono essere presenti in una quantità tale da fornire un livello plasmatico nel sangue minimo del composto agonista del recettore di GLP-1 necessario per l'efficacia terapeutica. Tali composizioni farmaceutiche sono note nell'arte e descritte, ad esempio, nel brevetto statunitense. n. 7,521,423; brevetto statunitense n. 7,456,254; WO 2000/037098; WO 2005/021022; WO 2005/102293; WO 2006/068910; WO 2006/125763; WO 2009/068910; nella pubblicazione statunitense n. 2004/0106547; e simili.

Composizioni farmaceutiche contenenti i composti agonisti del recettore di GLP-1 descritti nella presente possono essere fornite per la somministrazione periferica, come somministrazione parenterale (ad esempio sottocutanea, endovenosa, intramuscolare), un'infusione continua (ad esempio flebo, bolo endovenoso, infusione endovenosa), topica, nasale, o orale. Trasportatori farmaceuticamente accettabili adatti e la loro formulazione sono descritti nei trattati di formulazione standard, come Remington's Pharmaceutical Sciences di Martin; e Wang et al., *Journal of Parenteral Science and Technology,* Technical Report n. 10, supp. 42:2S (1988). I composti agonisti del recettore di GLP-1 descritti nella presente possono essere forniti in composizioni parenterali per iniezione o infusione. Possono, ad esempio, essere sospesi in acqua; in un olio inerte, come un olio vegetale (ad esempio, olio di sesamo, di

arachidi, di oliva, e simili); o in un altro trasportatore farmaceuticamente accettabile. In una forma di realizzazione, i composti sono sospesi in un trasportatore acquoso, ad esempio in una soluzione tampone isotonica a un pH da circa 3,0 a 8,0, o da circa 3,0 a 5,0. Le composizioni possono essere sterilizzate mediante tecniche di sterilizzazione convenzionali oppure possono essere sterilizzate per filtrazione. Le composizioni possono contenere sostanze ausiliarie farmaceuticamente accettabili, se necessario, per imitare le condizioni fisiologiche, come agenti tamponanti il pH.

Tamponi utili includono, ad esempio, i tamponi di acido acetico. Una forma di preparazione a lento rilascio in deposito o "depot" può essere usata in modo che quantità terapeuticamente efficaci della preparazione vengano erogate nel flusso sanguigno nell'arco di molte ore o giorni dopo un'iniezione sottocutanea, un'iniezione transdermica o altro metodo di erogazione. L'isotonicità desiderata può essere ottenuta usando cloruro di sodio o altri agenti farmaceuticamente accettabili come destrosio, acido borico, tartrato di sodio, glicole di propilene, polioli (come mannitolo e sorbitolo), o altri soluti inorganici o organici. In una forma di realizzazione per infusione endovenosa, la formulazione può comprendere (i) il composto agonista del recettore di GLP-1, (2) acqua sterile e, facoltativamente, (3) cloruro di sodio, destrosio, o una loro combinazione.

Possono essere usati anche trasportatori o eccipienti per facilitare la somministrazione dei composti agonisti del recettore di GLP-

1. Esempi di trasportatori ed eccipienti includono carbonato di calcio, fosfato di calcio, vari zuccheri come lattosio, glucosio o saccarosio, o tipi di amido, derivati della cellulosa, gelatina, oli vegetali, glicoli di polietilene e solventi fisiologicamente compatibili.

I composti agonisti del recettore di GLP-1 possono anche essere formulati come sali farmaceuticamente accettabili (ad esempio sali di addizione di acidi) e/o loro complessi. I sali farmaceuticamente accettabili sono sali atossici alla concentrazione alla quale vengono somministrati. I sali farmaceuticamente accettabili includono sali di addizione di acidi, come quelli contenenti solfato, cloridrato, fosfato, solfammato, acetato, citrato, lattato, tartrato, metansolfonato, etansolfonato, benzensolfonato, p-toluensolfonato, cicloesilsolfammato, e chinato. Sali farmaceuticamente accettabili possono essere ottenuti da acidi quali acido cloridrico, acido solforico, acido fosforico, acido solfammico, acido acetico, acido citrico, acido lattico, acido tartarico, acido malonico, acido metansolfonico, acido etansolfonico, acido benzensolfonico, acido p-toluensolfonico, acido cicloesilsolfammico, e acido chinico. Tali sali possono essere preparati, ad esempio, facendo reagire le forme di acido o base libere del prodotto con uno o più equivalenti della base o dell'acido appropriati in un solvente o mezzo in cui il sale è insolubile, o in un solvente come l'acqua che viene poi rimosso sotto vuoto o mediante liofilizzazione o scambiando gli ioni di un sale esistente con un altro ione su una resina a scambio ionico adatta.

Formulazioni farmaceutiche esemplificative di composti agonisti del recettore di GLP-1 sono descritte nel brevetto statunitense n. 7,521,423, nel brevetto statunitense n. 7,456,254; nella pubblicazione statunitense n. 2004/0106547, WO 2006/068910, WO 2006/125763, e simili.

La quantità terapeuticamente efficace dei composti agonisti del recettore di GLP-1 descritti nella presente per uso nei metodi descritti nella presente sarà tipicamente da circa 0,01 µg a circa 5 mg; da circa 0,1 µg a circa 2,5 mg; da circa 1 µg a circa 1 mg; da circa 1 µg a circa 50 µg; o da circa 1 µg a circa 25 µg. In alternativa, la quantità terapeuticamente efficace dei composti agonisti del recettore di GLP-1 può essere da circa 0,001 µg a circa 100 µg in base al peso di un paziente di 70 kg; o da circa 0,01 µg a circa 50 µg in base al peso di un paziente di 70 kg. Queste dosi terapeuticamente efficaci possono essere somministrate una volta al giorno, due volte al giorno, tre volte al giorno, una volta alla settimana, due volte a settimana, o una volta al mese, a seconda della formulazione. La dose esatta da somministrare è determinata, ad esempio, dalla formulazione, come una formulazione a rilascio immediato o una formulazione a rilascio prolungato. Per le forme di dosaggio transdermiche, nasali o orali, il dosaggio può essere aumentato da circa 5 volte a circa 10 volte.

Le proteine leganti l'antigene di GIPR che sono fornite nella presente sono utili per rilevare GIPR in campioni biologici. Ad esempio, le proteine leganti l'antigene di GIPR possono essere usate in saggi

diagnostici, ad esempio saggi di legame per rilevare e/o quantificare GIPR espresso nel siero.

Le proteine leganti l'antigene descritte possono essere usate a fini diagnostici per rilevare, diagnosticare o monitorare malattie e/o condizioni associate a GIPR. Le proteine leganti l'antigene divulgate forniscono un mezzo per il rilevamento della presenza di GIPR in un campione usando metodi immunoistologici classici noti ai tecnici del ramo (ad esempio Tijssen, 1993, Practice and Theory of Enzyme Immunoassays, vol. 15 (curatori R.H. Burdon e P.H. van Knippenberg, Elsevier, Amsterdam); Zola, 1987, Monoclonal Antibodies: A Manual of Techniques, pagine 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). Il rilevamento di GIPR può essere eseguito *in vivo* o *in vitro.*

Le applicazioni diagnostiche fornite nella presente includono l'uso delle proteine leganti l'antigene per rilevare l'espressione di GIPR. Esempi di metodi utili nel rilevamento della presenza di GIPR includono i saggi immunologici, come il saggio di immunoassorbimento enzimatico (ELISA) e il saggio radioimmunologico (RIA).

Per applicazioni diagnostiche, la proteina legante l'antigene verrà tipicamente marcata con un gruppo di marcatura rilevabile. Gruppi di marcatura adatti includono, ma senza limitarvisi, quanto segue: radioisotopi o radionuclidi (ad esempio ^{3}H, ^{14}C, ^{15}N, ^{35}S, ^{90}Y, ^{99}Tc, ^{111}In, ^{125}I, ^{131}I), gruppi fluorescenti (ad esempio FITC, rodamina, fosfori lantanidi), gruppi enzimatici (ad esempio perossidasi di rafano, β-

galattosidasi, luciferasi, fosfatasi alcalina), gruppi chemiluminescenti, gruppi biotinile, o epitopi di polipeptidi predeterminati riconosciuti da un reporter secondario (ad esempio sequenze di coppie di cerniera di leucine, siti di legame per anticorpi secondari, domini di legame a metalli, tag epitopici). In alcune forme di realizzazione, il gruppo di marcatura è accoppiato alla proteina legante l'antigene tramite bracci di distanziatore di varie lunghezze per ridurre il potenziale ingombro sterico. Nell'arte sono noti vari metodi per marcare le proteine che possono essere usati.

In alcune forme di realizzazione, la proteina legante l'antigene di GIPR viene isolata e misurata usando tecniche note nell'arte. *Si veda*, ad esempio, Harlow e Lane, 1988, Antibodies: A Laboratory Manual, New York: Cold Spring Harbor (ed. 1991 e supplementi periodici); John E. Coligan, ed., 1993, Current Protocols In Immunology New York: John Wiley & Sons.

Un altro aspetto di quanto divulgato fornisce un rilevamento della presenza di una molecola di test che compete per il legame a GIPR con le proteine leganti l'antigene fornite. Un esempio di un tale saggio potrebbe comportare rilevare la quantità di proteina legante l'antigene libera in una soluzione contenente una quantità di GIPR in presenza o in assenza della molecola di test. Un aumento della quantità di proteina legante l'antigene libera (ossia la proteina legante l'antigene non legata a GIPR) indicherebbe che la molecola di test è in grado di competere per il legame a GIPR con la proteina legante l'antigene. In una forma di realizzazione, la proteina legante l'antigene è marcata con un gruppo di

marcatura. In alternativa, la molecola di test viene marcata e la quantità di molecola di test libera viene monitorata in presenza e in assenza di una proteina legante l'antigene.

Le proteine leganti GIPR possono essere utilizzate per trattare, diagnosticare o migliorare una condizione o un disturbo metabolica/o. In una forma di realizzazione, il disturbo metabolico da trattare è il diabete, ad esempio diabete di tipo 2. In un'altra forma di realizzazione, la condizione o il disturbo metabolica/o è l'obesità. In altre forme di realizzazione, la condizione o il disturbo metabolica/o è dislipidemia, livelli elevati di glucosio, livelli elevati di insulina o nefropatia diabetica. Ad esempio, una condizione o un disturbo metabolica/o che può essere trattata/o o migliorata/o usando un peptide legante GIPR include uno stato in cui un soggetto umano ha un livello di glucosio ematico a digiuno pari o superiore a 125 mg/dl, ad esempio 130, 135, 140, 145, 150, 155, 160, 165, 170, 175, 180, 185, 190, 195, 200 o superiore a 200 mg/dl. I livelli di glucosio ematico possono essere determinati a stomaco pieno o a digiuno, oppure in modo casuale. La condizione o il disturbo metabolica/o può anche comprendere una condizione in cui un soggetto è esposto a un rischio aumentato di sviluppare una condizione metabolica. Per un soggetto umano, tali condizioni includono un livello di glucosio ematico a digiuno di 100 mg/dl. Condizioni che possono essere trattate usando una composizione farmaceutica comprendente una proteina legante GIPR possono anche essere trovate in American Diabetes Association Standards of Medical Care in Diabetes Care-2011,

American Diabetes Association, Diabetes Care, vol. 34, n. supplemento 1, S11-S61, 2010, incorporati nella presente per riferimento.

In pratica, un disturbo o una condizione metabolico/a, come diabete di tipo 2, livelli elevati di glucosio, livelli elevati di insulina, dislipidemia, obesità o nefropatia diabetica, può essere trattato/a somministrando una dose terapeuticamente efficace di una proteina legante GIPR a un paziente che ne ha bisogno. La somministrazione può essere eseguita come descritto nella presente, ad esempio tramite iniezione endovenosa, iniezione intraperitoneale (IP), iniezione sottocutanea, iniezione intramuscolare, o per via orale sotto forma di una compressa o una formazione liquida. In alcune situazioni, una dose terapeuticamente efficace o preferita di una proteina legante GIPR può essere determinata da un medico. Una dose terapeuticamente efficace di proteina legante GIPR dipenderà, tra l'altro, dal programma di somministrazione, dalla dose unitaria di agente somministrata, dal fatto che la proteina legante GIPR venga somministrata in combinazione con altri agenti terapeutici, dallo stato immunitario e dalla salute del ricevente. Il termine "dose terapeuticamente efficace", secondo l'uso fattone nella presente, significano una quantità di proteina legante GIPR che suscita una risposta biologica o medica in un sistema tessutale, un animale o un essere umano ricercata da un ricercatore, un medico, o altro clinico, che include alleviamento o miglioramento dei sintomi della malattia o del disturbo che viene trattata/o, ossia una quantità di una proteina legante GIPR che supporta un livello osservabile di una o più risposte biologiche

o mediche desiderate, ad esempio abbassando i livelli ematici di glucosio, insulina, trigliceridi o colesterolo; riducendo il peso corporeo; o migliorando la tolleranza al glucosio, il dispendio energetico, o la sensibilità all'insulina.

Si noti che una dose terapeuticamente efficace di una proteina legante GIPR può variare anche a seconda del risultato desiderato. Perciò, ad esempio, in situazioni in cui è indicato un livello più basso di glucosio ematico, una dose di proteina legante GIPR sarà corrispondentemente più alta di una dose in situazioni in cui è desiderato un livello relativamente più basso di glucosio ematico. Al contrario, in situazioni in cui è indicato un livello più alto di glucosio ematico, una dose di proteina legante GIPR sarà corrispondentemente più bassa di una dose in situazioni in cui è desiderato un livello relativamente più alto di glucosio ematico.

In varie forme di realizzazione, un soggetto è un essere umano avente un livello di glucosio ematico pari o superiore a 100 mg/dl che può essere trattato con una proteina legante GIPR.

In una forma di realizzazione, un metodo della presente divulgazione comprende innanzitutto misurare un livello basale di uno o più composti metabolicamente rilevanti quali glucosio, insulina, colesterolo, lipidi in un soggetto. Una composizione farmaceutica comprendente una proteina legante GIPR viene poi somministrata al soggetto. Dopo un periodo di tempo desiderato, viene nuovamente misurato il livello di uno o più composti metabolicamente rilevanti (ad

esempio glucosio ematico, insulina, colesterolo, lipidi) nel soggetto. I due livelli possono quindi essere confrontati al fine di determinare il cambiamento relativo del composto metabolicamente rilevante nel soggetto. A seconda dell'esito di tale confronto, un'altra dose della composizione farmaceutica comprendente una proteina legante GIPR può essere somministrata per conseguire il livello desiderato di uno o più composti metabolicamente rilevanti.

Si noti che una composizione farmaceutica comprendente una proteina legante GIPR può essere co-somministrata con un altro composto. L'identità e le proprietà di un composto co-somministrato insieme alla proteina legante GIPR dipenderanno dalla natura della condizione da trattare o migliorare. Un elenco non limitativo di esempi di composti che possono essere somministrati in combinazione con una composizione farmaceutica comprendente una proteina legante GIPR include rosiglitazone, pioglitazone, repaglinide, nateglinide, metformina, exenatide, sitagliptin, pramlintide, glipizide, glimepiride, acarbosio, e miglitol.

Esempio 1

Generazione di mAb anti-GIPR cys con cappuccio di bis-cisteamina (scala 2 g)

Lo schema di reazione per la generazione di coniugati di peptidi anti-GIPR/GLP-1 è mostrato nella Figura 1. Anticorpi monoclonali anti-GIPR con mutazione specifica della cisteina (mAb anti-GIPR cys, 2 g) sono stati incubati con 800 ml di soluzione di cistamina 2,5 mM e

cisteamina 2,5 mM in tampone HEPES 40 mM, pH 7,5-8,5, per 15-20 ore. La miscela di reazione è stata filtrata usando un filtro da 0,22 µm e diluita in 1200 ml di tampone acetato di sodio 100 mM, pH 5. La cromatografia a scambio cationico è stata usata per purificare il mAb anti-GIPR cys con cappuccio di bis-cisteamina dalla miscela di reazione. Innanzitutto, 2 L di miscela di reazione diluita in tampone acetato di sodio 100 mM, pH 5, sono stati caricati su una colonna SP HP da 240 ml a 20 ml/min. La colonna è stata lavata con 2 volumi di colonna di acetato di sodio 100 mM, pH 5, seguiti da un gradiente di 0-20% di acetato di sodio 100 mM con NaCl 1,2 M, pH 5. Il picco principale contenente il mAb anti-GIPR cys con cappuccio di bis-cisteamina è stato raccolto e sottoposto a scambio di tampone con acetato di sodio 10 mM con 9% di saccarosio, pH 5,2, usando una filtrazione a flusso tangenziale.

Esempio 2

Generazione di coniugati di peptidi anti-GIPR/GLP-1

Il mAb anti-GIPR cys con cappuccio di bis-cisteamina (6 mg/ml in acetato di sodio 10 mM con 9% di saccarosio) è stato parzialmente ridotto usando 3-4 equivalenti di tris(2-carbossietil)fosfina (TCEP) a temperatura ambiente per 60-90 minuti. Il TCEP è stato rimosso e il mAb cys parzialmente ridotto è stato sottoposto a scambio di tampone con tampone fosfato di sodio 50 mM contenente acido etilendiamminotetraacetico (EDTA) 2 mM, pH 7,5. Al mAb cys parzialmente ridotto sono stati aggiunti 6-10 equivalenti di acido deidroascorbico (DHAA) e l'ossidazione è stata effettuata a temperatura

ambiente fino a quando non sono state osservate solo tracce di specie di mAb parzialmente ridotte (30-120 minuti). Senza rimuovere dhAA, 3-8 equivalenti di peptidi bromoacetil-GLP-1 sono stati aggiunti alla miscela di reazione e incubati a temperatura ambiente per 15-20 ore. Tutti i reagenti sono stati rimossi e il prodotto di coniugato di peptidi anti-GIPR/GLP-1 è stato sottoposto a scambio di tampone secondo la formulazione finale usando una concentrazione per centrifugazione o una filtrazione a flusso tangenziale.

Tabella 9. Costrutti di coniugati bispecifici antagonista anti-GIPR/agonista del recettore di GLP-1.

Coniugato n.	Descrizione	Informazioni sui peptidi	Sito/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-	[Aib8,Lys26(SGGAcBr)]GLP-1 (7-37)	Lys26/SGG	0,059	101,6

Coniugato n.	Descrizione	Informazioni sui peptidi	Sito/linker	hGLP-1 IC_{50}(nM)	hGIPR IC50 (nM)
	3156820				
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-	[Aib8,Lys26(SGGAcBr)]GLP-1 (7-37)	Lys26/SGG	0,065	50,6

Coniugato n.	Descrizione	Informazioni sui peptidi	Sito/linker	hGLP-1 IC_{50}(nM)	hGIPR IC50 (nM)
	3156820				
1143-1	5G12-E384C-3161655	[Aib8,22;Gly36;Lys37(PEG11AcBr)]GLP-1(7-37)-ammide	Lys37/PEG11	0,047	37,0
1144-1	5G12-E384C-3161021	[Aib8,22;Lys36(SGGACBr)]GLP-1(7-36)-ammide	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-	[Aib8,22;Gly36]GLP-1(7-37)[GGGGSGGGGSGGGGSK(BrAc)]	C-term/(GGGGS)3	0,171	43,5

Coniugato n.	Descrizione	Informazioni sui peptidi	Sito/linker	hGLP-1 IC_{50}(nM)	hGIPR IC50 (nM)
	3166119				
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

Coniugato n.	Descrizione	Informazioni sui peptidi	Sito/linker	hGLP-1 IC_{50}(nM)	hGIPR IC50 (nM)
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	ciclo[E22-K26][Aib8;Lys(NPeg11-BrAc)37]GLP-1(7-37)-ammide	Lys37/PEG11	0,044	50
1198-1	5G12-E384C-3169018	[Aib8,22;Gly36;Lys(NPeg27-BrAc)37]GLP-1(7-37)-ammide	Lys37/PEG27	0,0329	98,5
1199-1	5G12-T487C-3169018	[Aib8,22;Gly36;Lys(NPeg27-BrAc)37]GLP-1(7-37)-ammide	Lys37/PEG27	0,006	84

Coniugato n.	Descrizione	Informazioni sui peptidi	Sito/linker	hGLP-1 IC_{50}(nM)	hGIPR IC50 (nM)
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-316773	[Aib8;Glu22-Lys26;Gly36]GLP-1(7-	C-term/(GGGGS)3	0,0072	45,4

Coniugato n.	Descrizione	Informazioni sui peptidi	Sito/linker	hGLP-1 IC_{50}(nM)	hGIPR IC50 (nM)
	6-DAR1	37)[GGGGSGGGGSGGGGSK(BrAc)]			
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	Exendina-4(1-39)[GGGGSGGGGSGGGGSK(BrAc)]	C-term/(GGGGS)3	0,013	84,9
1230-1	5G12-E384C-	[Gly8,36;Glu22]GLP-1(7-37)[GGGGSGGGGSGGGGSK(BrAc)]	C-term/(GGGGS)3	0,0376	92,2

Coniugato n.	Descrizione	Informazioni sui peptidi	Sito/linker	hGLP-1 IC_{50}(nM)	hGIPR IC50 (nM)
	3340577				
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)-ammide	C-term/(GGGGS)3	0,118	121
1234-1	aGIPR 5G12 E384C Ab-	[Aib8,22;Gly36]GLP-1(7-37)-(G4S)2K(BrAc)-ammide	Lys37(C-term)/(GGGGS)2	0,0446	108

Coniugato n.	Descrizione	Informazioni sui peptidi	Sito/linker	hGLP-1 IC_{50}(nM)	hGIPR IC50 (nM)
	3341281				
1235-1	aGIPR 5G12 E384C Ab-3341282	[Aib8,22;Gly36]GLP-1(7-37)-AS(AP)5GSK(BrAc)-ammide	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	[Aib8;Tyr16;Glu22;Gly36]GLP-1_(7-37)-(G4S)3-K(AcBr)	C-term/(GGGGS)3	0,0046	82,8

Coniugato n.	Descrizione	Informazioni sui peptidi	Sito/linker	hGLP-1 IC_{50}(nM)	hGIPR IC50 (nM)
	E384C-3341285				
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

Coniugato n.	Descrizione	Informazioni sui peptidi	Sito/linker	hGLP-1 IC_{50}(nM)	hGIPR 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-	[Aib8,22;Ala31;Gly36]GLP-1_(7-36)-(G4S)3-K(AcBr)	C-term/(GGGGS)3	1,147	75,9

Coniugato n.	Descrizione	Informazioni sui peptidi	Sito/linker	hGLP-1 IC_{50}(nM)	hGIPR IC50 (nM)
	3342051				
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	[Aib8,22;Glu15;Ala31;Gly36]GLP-1_(7-37)-(G4S)3-K(AcBr)	C-term/(GGGGS)3	0,32	85

Coniugato n.	Descrizione	Informazioni sui peptidi	Sito/linker	hGLP-1 IC_{50}(nM)	hGIPR IC50 (nM)
	E384C-3343109				
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	[Aib8,22;LysG4S3G(AcBr)26;Gly36]GLP-1_(7-37)	Lys26/(GGGGS)3	0,0084	51,4

Coniugato n.	Descrizione	Informazioni sui peptidi	Sito/linker	hGLP-1 IC_{50}(nM)	hGIPR IC50 (nM)
	SEFL2E384C-3343906				
1254-1	aGIPR5G12 SEFL2E384C-3343905	[Aib8,22;Tyr16;Gly36]GLP-1_(7-37)-(G4S)3-K(AcBr)	C-term/(GGGGS)3	0,0058	73,8
1255-1	aGIPR2G10 SEFL2E384C-3341281	[Aib8,22;Gly36]GLP-1(7-37)-G4S2K(BrAc)	C-term/(GGGGS)2	0,026	56,4

Coniugato n.	Descrizione	Informazioni sui peptidi	Sito/linker	hGLP-1 IC_{50}(nM)	hGIPR IC50 (nM)
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

Coniugato n.	Descrizione	Informazioni sui peptidi	Sito/linker	hGLP-1 IC_{50}(nM)	hGIPR IC50 (nM)
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
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

Coniugato n.	Descrizione	Informazioni sui peptidi	Sito/linker	hGLP-1 IC_{50}(nM)	hGIPR IC50 (nM)
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

Coniugato n.	Descrizione	Informazioni sui peptidi	Sito/linker	hGLP-1 IC_{50}(nM)	hGIPR IC50 (nM)
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	ciclo[E22-K26][Aib8;(NPeg11-BrAc)37]GLP-1(7-37)-ammide	Lys37/PEG11	0,0049	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

Coniugato n.	Descrizione	Informazioni sui peptidi	Sito/linker	hGLP-1 IC_{50}(nM)	hGIPR IC50 (nM)
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-	[Aib8;Tyr16;Glu22;Gly36]GLP-1_(7-37)-(GGGGSGG)-K(AcBr)	C-term/(GGGGS)3	0,061	42,3

Coniugato n.	Descrizione	Informazioni sui peptidi	Sito/linker	hGLP-1 IC_{50}(nM)	hGIPR IC50 (nM)
	3341285				
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-	[Aib8,22]-GLP-1(7-22)-Ex4(17-39)-(G4S)3K-BrAc	C-term/(GGGGS)3	0,094	43,9

Coniugato n.	Descrizione	Informazioni sui peptidi	Sito/linker	hGLP-1 IC_{50}(nM)	hGIPR IC50 (nM)
	E384C-3173043				
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

Esempio 3

Metodi per saggi in vitro e in vivo

Attività di agonista del recettore di GLP-1

Cellule CHOK1 esprimenti stabilmente il GLP-1R umano da solo o sia GLP-1R sia GIPR (M1) sono state usate per misurare la produzione di cAMP indotta da peptide/coniugato in un saggio di fluorescenza omogenea a tempo risolto (HTRF) (CISBIO, n. di cat. 62AM4PEJ). Peptidi/coniugati diluiti in serie (3×10^{-7} M - 3×10^{-14} M) sono stati incubati con 40.000 cellule nel tampone di saggio (0,1% BSA, IBMX 500 µM in terreno F12) per 15 minuti a 37 °C. Le cellule sono state poi lisate con tampone di lisi contenente cAMP-d2 e criptato di cAMP (CISBIO) e incubate per 1 ora a temperatura ambiente prima di essere misurate nel lettore per piastre EnVision (PerkinElmer). I livelli di cAMP sono espressi come rapporto di fluorescenza di 665/620 nm e sono mostrati nelle Figure 2A-2E e nella Figura 3.

Esempio 4

Attività di antagonista di GIPR

Cellule HEK 293T esprimenti stabilmente il GIPR umano sono state usate per misurare la generazione di cAMP indotta da peptide/coniugato nel saggio HTRF (Cisbio, n. di cat. 62AM4PEJ). Coniugati diluiti in serie o anticorpo contro GIPR (3×10^{-6} M - 1×10^{-11} M) sono stati incubati con 30.000 cellule in tampone di saggio (0,1% BSA, IBMX 500 µM in terreno F12) per 30 minuti a 37 °C prima di essere trattati con GIP alla concentrazione finale di 0,05 nM. Le cellule sono state incubate per 30 minuti a 37 °C e poi lisate in tampone di lisi contenente

cAMP-d2 e criptato di cAMP (CISBIO) per 1 ora a temperatura ambiente. La fluorescenza è stata misurata nel lettore per piastre EnVision (PerkinElmer) e i livelli di cAMP sono espressi come un rapporto di 665/620 nm e sono mostrati nelle Figure 2A-2E e nella Figura.

Esempio 5

Materiali e metodi per topo bispecifico *in vivo*

Topi diabetici sono stati selezionati principalmente per lo screening dell'attività di GLP-1 delle molecole bispecifiche. Le molecole sono state selezionate in base alla loro capacità di ridurre i livelli plasmatici di glucosio in differenti punti temporali successivi all'iniezione. In aggiunta, è stata misurata anche la perdita di peso corporeo o l'inibizione dell'aumento di peso corporeo indicative di attività di GLP-1, inibizione di GIPR o, una combinazione di entrambe, sia per la co-somministrazione di ciascuno che della molecola bispecifica, come mostrato nelle Figure 4A-4I. Topi maschi db/db (#642) sono stati ottenuti dai Jackson Laboratories (Bar Harbor, ME) e consegnati all'età di 8-9 settimane. All'arrivo, i topi sono stati alloggiati in gruppi, in numero di quattro per gabbia, e mantenuti in condizioni ambientali controllate, con cicli di 12 ore di luce (dalle 6:30 alle 18:30) e di buio (dalle 18:30 alle 6:30). Ai topi è stata somministrata una dieta standard per roditori (2020x Harlan Teklad) con libero accesso all'acqua potabile.

In altri studi, il test di tolleranza al glucosio è stato usato per classificare la potenza degli analoghi di GLP-1 (Figure 5A-5C). I topi C57Bl6 sono stati fatti acclimatare alle condizioni ambientali per una o

due settimane. Prima del dosaggio, i topi sono stati maneggiati e ne è stato misurato il peso corporeo. Un giorno prima del dosaggio, in topi coscienti è stato effettuato un prelievo dal seno retro-orbitale per la misurazione del glucosio plasmatico mediante un glucometro portatile progettato per il plasma dei roditori. Il giorno del dosaggio, sono stati effettuate misurazioni del glucosio plasmatico e del peso corporeo al basale. Per stratificare le gabbie in gruppi di trattamento è stata usata la media di gabbia del glucosio plasmatico e del peso corporeo. I topi sono stati tenuti nelle loro gabbie. Dopo la somministrazione dell'articolo di test, il glucosio plasmatico è stato misurato in vari punti temporali a (1, 3 e 6 ore) o (4 ore) e le misurazioni del glucosio plasmatico e del peso corporeo sono state effettuate ogni 24 ore successive. Sono stati misurati i livelli di glucosio plasmatico fino a quando i livelli non sono tornati a livelli prossimi a quelli del basale e sono state effettuate misurazioni del peso corporeo fino a quando il tasso di aumento del peso corporeo è stato simile a quello del gruppo di controllo trattato con veicolo.

Topi con obesità indotta dalla dieta (DIO) sono stati usati anche come modello per misurare gli effetti della perdita di peso derivanti dal trattamento con differenti molecole, come mostrato nella Figura 6.

Topi c57bl6 maschi sono stati ottenuti dagli Harlan Laboratories e consegnati all'età di 26 giorni. I topi sono stati alloggiati in gruppi con esemplari della stessa cucciolata consistenti in due-quattro topi per gabbia. Dopo una settimana di acclimatazione, ai topi è stato somministrato un regime alimentare ricco di grassi (HFD: D12492,

Research Diets, New Brunswick, NJ) o si è continuato a somministrare la dieta standard per roditori (2020x, Harlan Laboratories). Dopo 12 settimane di alimentazione, i topi alloggiati singolarmente sono stati abituati alla manipolazione di routine, alla misurazione dell'assunzione di cibo e alle iniezioni giornaliere di soluzione salina (IP). Il sangue è stato prelevato dal seno retro-orbitale di topi DIO coscienti. Un piccolo volume di sangue è stato immediatamente posto su un glucometro portatile progettato per il plasma dei roditori e il sangue rimanente è stato posto in provette di raccolta con EDTA con un cocktail di inibitori della proteasi (Roche Diagnostics, Indianapolis, IN). Dopo la centrifugazione, il plasma è stato conservato a -80 °C. I topi sono stati stratificati in gruppi di trattamento in base alle misurazioni di peso corporeo e glucosio plasmatico. I topi sono stati trattati con veicolo (Q3D), Ab contro GIPR (2,5 o 10 mg/kg, Q3D), peptide di GLP-1 (0,06 mg/kg, QD), dulaglutide (1 mg/kg, Q3D) o coniugato bispecifico (2,5 o 10 mg/kg, Q3D). Altri 2 gruppi di topi hanno ricevuto un trattamento di combinazione con GLP-1 e Ab contro GIPR al dosaggio e alla frequenza di dose di cui sopra (GIPR 2,5 mg/kg + peptide di GLP-1 e GIPR 2,5 mg/kg + dulaglutide). A parte i gruppi trattati con il peptide di GLP-1, a tutti gli altri topi è stata iniettata soluzione salina quando non ricevevano il rispettivo articolo di test. Il peso corporeo è stato misurato quotidianamente e l'assunzione di cibo cumulativa nell'arco di tre giorni è stata mediata in base a un valore di assunzione di cibo giornaliera. L'assunzione di cibo è stata misurata tra i giorni 0-3 e i giorni 6-9 dello studio. Un prelievo di sangue è stato

effettuato il giorno 9 dello studio, 1 ora dopo l'iniezione, mentre un prelievo di sangue al sacrificio è stato effettuato il giorno 12 dello studio, 1 o 3 giorni dopo l'iniezione precedente dell'articolo di test.

L'insulina plasmatica è stata misurata con un kit ELISA per topi seguendo le istruzioni del produttore (ALPCO, Salem, NH). Glucosio, colesterolo, trigliceridi, acidi grassi non esterificati, AST e ALT nel plasma sono stati misurati usando un Olympus AU400e Chemistry Analyzer (Olympus America, Center Valley, PA).

Esempio 6

Materiali e metodi per cino bispecifico *in vivo*

Macachi cinomolgo maschi spontaneamente obesi (età 9-14 anni) sono stati fatti acclimatare/addestrati alle procedure sperimentali prima dell'inizio dello studio e sono stati suddivisi in 7 gruppi di trattamento con n=10 scimmie, ciascuno con distribuzione equa tra i gruppi per tutti i parametri di suddivisione (peso corporeo e analisi del sangue). Alle scimmie è stato poi iniettato una volta alla settimana per 6 settimane veicolo o coniugati GLP-1R-GIPR (1264, 1273, 1248 o 1257). Dopo il periodo di trattamento di 6 settimane, le scimmie sono state sottoposte a una fase di washout di 4 settimane. Durante le fasi di addestramento/trattamento/washout dello studio, l'apporto di energia totale è stato monitorato quotidianamente; il peso corporeo, le analisi del sangue e l'esposizione al farmaco sono stati monitorati settimanalmente o ogni due settimane, come mostrato nelle Figure 7-21.

Esempio 7

Materiali e metodi per un saggio di legame di competizione di radioligandi GIP e GLP-1

Le membrane sono state preparate da linee cellulari di mammifero che sovraesprimono hu GIPR e hu GLP-1R e sono state tipicamente conservate a -80 °C in tampone di saggio: 50 mM HEPES (7,4), 5 mM $MgCl_2$, 1 mM $CaCl_2$, 0,2% BSA, e compresse di inibitore della proteasi "senza EDTA". Peptidi di GIP e GLP-1 non marcati sono stati ottenuti da Phoenix Pharmaceuticals e ^{125}I-GIP e ^{125}I-GLP-1 radiomarcati sono stati ordinati da Perkin Elmer. Le reazioni primarie sono state condotte per 2 ore a temperatura ambiente sotto agitazione in piastre per coltura cellulare a fondo rotondo da 96 pozzetti (Costar). La concentrazione della membrana cellulare è stata fissata a 0,6 mg/ml e i radioligandi sono stati usati a una concentrazione di 0,1 nM. Gli articoli di test sono stati titolati a sei concentrazioni in duplicato. La piastra primaria è stata raccolta dopo due ore con TRIS 50 mM ghiacciato (pH 7,4) usando un Filtermate Harvester (Perkin Elmer) e le membrane cellulari sono state catturate su piastre GF/C UniFilter trattate con PEI (Perkin Elmer). Le piastre sono state asciugate per 15 minuti usando un forno a vuoto e Microscint 20 è stato aggiunto a ciascun pozzetto prima del conteggio in uno strumento Perkin Elmer TopCount NXT HTS. Il legame specifico è stato determinato prendendo la differenza tra i conteggi totali e quelli aspecifici. I pozzetti aspecifici contenevano ligando freddo 1 µM. I dati sono stati analizzati e rappresentati graficamente usando GraphPad Prism 7, come mostrato nella Figura 22.

Esempio 8

Saggio di internalizzazione

L'internalizzazione di GLP-1R e GIPR è stata giudicata in cellule CHOK1 esprimenti sia GLP-1R sia GIPR umano. Le cellule sono state piastrate a una densità di 25.000 cellule/pozzetto in piastre da 96 pozzetti e coltivate durante la notte a 37 °C, 5% di CO_2. Le cellule sono state deprivate di siero in un terreno F12 (Thermo Fisher) con 0,1% di BSA per 4 ore prima del trattamento. Le cellule sono state trattate con 20 nM o titolazioni di dose di GLP-1, GIP o coniugati bispecifici per 30 minuti o per il tempo specificato nelle rispettive figure. Le cellule sono state lavate e fissate con 4% di formaldeide e permeabilizzate con 0,1% di Triton-X 100. Per rilevare GIPR o GLP-1R, le cellule sono state prima bloccate con tampone di blocco Odyssey (LiCor) per 1 ora a temperatura ambiente e incubate con 2 µg/ml di anticorpo anti-GLP-1R umano (R&D Systems) o 5 µg/ml di anticorpo anti-GIPR umano (R&D Systems) di topo a 4 °C durante la notte, seguito da anticorpo secondario anti-topo coniugato con AlexaFluor-555 o Alexa-Fluor 647 (Thermo Fisher) per il rilevamento di GLP-1R o GIPR, rispettivamente. Le immagini (Figura 23) sono state acquisite usando il sistema di immaginografia ad alto contenuto Operetta (Perkin Elmer) e analizzate usando il software Harmony (Perkin Elmer) per quantificare il contenuto intracellulare di GLP-1R (area totale del punto) come parametro di lettura per il grado di internalizzazione (Figura 24).

Esempio 9

GLP-1R, GIPR e coniugato bispecifico si co-localizzano dopo l'internalizzazione

Cellule U2OS esprimenti GIPR e SNAP-GLP-1R sono state piastrate a una densità di 15.000 cellule per pozzetto in una piastra da 96 pozzetti e coltivate durante la notte a 37 °C con il 5% di CO_2. Prima del trattamento, le cellule sono state deprivate per 3,5 ore in terreno McCoy's 5A (Thermo Fisher) con lo 0,1% di BSA. Prima del trattamento, il GLP-1R sulla superficie delle cellule U2OS è stato marcato con Alexa-Fluor 564 incubando con il substrato SNAP-Surface Alexa-Fluor 564 (New England Biolabs) per 30 minuti. Le cellule sono state poi lavate per rimuovere l'eccesso di marcatura e trattate con coniugati bispecifici 5 nM per 30 minuti. Dopo 3 lavaggi, le cellule sono state fissate con 4% di formaldeide e permeabilizzate con 0,1% di Triton-X 100 in cellule in PBS. Per il rilevamento di GIPR, le cellule sono state prima bloccate con il tampone di blocco Odyssey (LiCor) per 1 ora a temperatura ambiente e poi incubate con 5 µg/ml di anticorpo di topo anti-GIPR umano (R&D Systems) a 4 °C durante la notte, cui ha fatto seguito incubazione con anticorpo secondario anti-topo coniugato con Alexa-Fluor 647 (Thermo Fisher) per 1 ora a temperatura ambiente. Il coniugato bispecifico è stato rilevato usando anticorpo anti-Fc umano marcato con Alexa-Fluor. Per il rilevamento dei nuclei è stato usato Hoechst 33342 (Thermo Fisher). Le immagini sono state acquisite usando il sistema di immaginografia ad alto contenuto Operetta CLS (Perkin Elmer) come mostrato nella Figura 25.

Esempio 10

Saggio GloSensor cAMP

Il saggio GloSensor cAMP è stato condotto secondo il protocollo del produttore (Promega). In breve, cellule umane ChoK1 esprimenti GLP-1R/GIPR sono state seminate a 15.000 cellule per pozzetto in una piastra da 96 pozzetti e incubate per 16 ore in un incubatore umidificato a 37 °C al 5% di CO_2. Le cellule sono state trasfettate transitoriamente con 100 ng di plasmide pGloSensor-22F cAMP usando FuGENE HD per 24 ore. Le cellule sono state poi equilibrate con 0,1% di BSA, 2% di reagente GloSensor cAMP in terreno indipendente da CO_2 (Invitrogen) per 2 ore a temperatura ambiente. Le cellule sono state pre-incubate per 15 minuti con o senza saccarosio 0,43 M (Sigma). Le misurazioni della luminescenza al basale sono state effettuate per 10 minuti prima dell'aggiunta di 1248 in condizioni con o senza saccarosio. Subito dopo l'aggiunta di 1248, la luminescenza cinetica è stata misurata usando un tempo di integrazione di 0,1-1 secondi ogni 60 secondi. I dati sono stati analizzati usando il software GraphPad Prism e sono presentati nella Figura 26.

Esempio 11

Analisi FACS

Cellule CHOK1-GLP-1R H20, 293T-GIPR clone 10 e CHOK1-GLP-1R/GIPR sono state sospese a una densità di 1×10^6 cellule in 100 µl di terreno di coltura F12 contenente 1% di FBS, 0,05% di azoturo di sodio e incubate con 10 µg/ml di anticorpi indicati o coniugati bispecifici anti-GIPR/GLP-1R per 1 ora a 4 °C. Le cellule sono state lavate una volta

con tampone di saggio e poi incubate con 10 µg/ml di Alexa Fluor 647-anti-Fc umano di capra (Jackson) per 30 minuti a 4 °C. La fluorescenza è stata misurata usando il citometro a flusso BD LSR II (BD Biosciences) ed è mostrata nella Figura 27.

Esempio 12

Saggio del flusso di calcio

Cellule CHOK1 esprimenti GIPR e GLP-1-R sono state piastrate a una densità di 30.000 cellule per pozzetto in una piastra da 96 pozzetti a fondo trasparente nero e coltivate durante la notte a 37 °C con il 5% di CO_2. Le cellule sono state deprivate di siero in un terreno F12 (Thermo Fisher) con HEPES 20 mM per 2 ore. Le cellule sono state poi caricate con tampone contenente il colorante sensibile al calcio (BD Biosciences) e incubate per 1 ora a temperatura ambiente prima di essere trattate con titolazioni di dose di GLP-1 o coniugati bispecifici. I cambiamenti del contenuto di calcio intracellulare sono stati monitorati usando un FLIPR (Molecular Devices). L'altezza massima del picco in ciascun pozzetto è stata registrata come rappresentante l'afflusso di calcio, come mostrato nella Figura 28.

Esempio 13

Saggio della beta-arrestina

Cellule CHOK1 PathHunter esprimenti GLP-1R e GIPR con tag ProLink™ di DiscoverX sono state trasfettate con GIPR o GLP-1R senza tag, rispettivamente. Le cellule sono state piastrate a una densità di 20.000 cellule per pozzetto in terreno di saggio (F12/0,1% BSA) e

incubate a 37 °C durante la notte. Le cellule sono state trattate con titolazioni di dose di GLP-1, GIP o coniugati bispecifici per 90 minuti. La soluzione di rilevamento di lavoro (DiscoverX) è stata poi aggiunta alle cellule e incubata per 60 minuti a temperatura ambiente e al buio. Il segnale chemiluminescente rappresentante il reclutamento della beta-arrestina è stato misurato usando EnVision ed è mostrato nella Figura 29.

Esempio 14

Saggio sulla secrezione di insulina stimolata dal glucosio (GSIS) in microtessuto di isole pancreatiche umane

Microtessuti di isole pancreatiche umane sono stati acquistati da InSphero nel formato a 96 pozzetti. I microtessuti sono stati incubati per 16 ore in terreno di saggio InSphero. Sono stati poi trattati per 1 ora con tampone KREBS fresco (NaCl 129 mM, KCl 4,8 mM, KH_2PO_4 1,2 mM, $MgSO_4$-$7H_2O$ 1,2 mM, HEPES 10 mM, $CaCl_2$ 1,3 mM, 0,5% BSA, pH 7,4) con glucosio 2,8 mM. Dopo 2 lavaggi con tampone KREBS, sono stati poi incubati con tampone KREBS da solo, glucosio 2,8 mM o 11 mM in tampone KREBS con o senza GLP-1 (Phoenix Pharmaceuticals) e una risposta alla dose di 1248 per 16 ore. Il surnatante è stato raccolto e analizzato per la secrezione di insulina secondo il protocollo del produttore (Mercodia). La densità ottica è stata letta a 450 nm su un lettore per micropiastre TECAN ed è mostrata nella Figura 30.

RIVENDICAZIONI

1. Composizione comprendente

a) un anticorpo, o suo frammento funzionale, che si lega specificamente a GIPR umano, in cui l'anticorpo, o suo frammento funzionale, comprende una sostituzione di cisteina o di amminoacido non canonico in uno o più siti di coniugazione; e

b) un agonista del recettore di GLP-1, in cui l'agonista del recettore di GLP-1 è coniugato all'anticorpo, o suo frammento funzionale, attraverso la catena laterale del residuo di cisteina o del residuo di amminoacido non canonico sostituito negli uno o più siti di coniugazione,

in cui l'anticorpo, o suo frammento funzionale, è un antagonista di GIPR.

2. Composizione della rivendicazione 1, in cui detto GIPR umano ha una sequenza comprendente una sequenza selezionata dal gruppo consistente in SEQ ID NO: 3141, SEQ ID NO: 3143, e SEQ ID NO: 3145.

3. Composizione della rivendicazione 1 o 2, in cui detto anticorpo è un anticorpo monoclonale, un anticorpo ricombinante, un anticorpo umano, un anticorpo umanizzato, un anticorpo chimerico, o un anticorpo multispecifico, o in cui detto frammento funzionale è un frammento funzionale di un anticorpo monoclonale, un anticorpo ricombinante, un anticorpo umano, un anticorpo umanizzato, un anticorpo chimerico, o un anticorpo multispecifico.

4. Composizione della rivendicazione 3, in cui detto frammento di anticorpo è un frammento Fab, un frammento Fab' o un frammento F(ab')2,

in cui detto anticorpo, o suo frammento funzionale, è un anticorpo umano,

in cui detto anticorpo, o suo frammento funzionale, è un anticorpo monoclonale,

in cui detto anticorpo, o suo frammento funzionale, è del tipo IgG1, IgG2, IgG3, o IgG4,

in cui, preferibilmente, detto anticorpo, o suo frammento funzionale, è del tipo IgG1 o IgG2, o

in cui detto anticorpo, o suo frammento funzionale, inibisce il legame di GIP alla porzione extracellulare di GIPR umano.

5. Composizione della rivendicazione 3, in cui detto anticorpo comprende una CDRL1, una CDRL2, una CDRL3, una CDRH1, una CDRH2 e una CDRH3, in cui detta CDRL1 comprende una sequenza selezionata dal gruppo consistente in SEQ ID NO: 629-785; detta CDRL2 comprende una sequenza selezionata dal gruppo consistente in SEQ ID NO: 786-942; detta CDRL3 comprende una sequenza selezionata dal gruppo consistente in SEQ ID NO: 943-1099; detta CDRH1 comprende una sequenza selezionata dal gruppo consistente in SEQ ID NO: 1100-1256; detta CDRH2 comprende una sequenza selezionata dal gruppo consistente in SEQ ID NO: 1257-1413; e detta CDRH3 comprende una

sequenza selezionata dal gruppo consistente in SEQ ID NO: 1414-1570, in cui

l'anticorpo, o suo frammento funzionale, comprende una sostituzione di cisteina o di amminoacido non canonico in uno o più siti di coniugazione selezionati dal gruppo consistente in

D70 della catena leggera di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 455,

E276 della catena pesante di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 612, e

T363 della catena pesante di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 612.

6. Composizione della rivendicazione 3, in cui detto anticorpo comprende una CDRL1, una CDRL2, una CDRL3, una CDRH1, una CDRH2 e una CDRH3, e in cui la combinazione della CDRL1, della CDRL2, della CDRL3, della CDRH1, della CDRH2 e della CDRH3 è selezionata dal gruppo di combinazioni consistente in:

Combinazione	**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

Combinazione	CDRL1 (SEQ ID NO)	CDRL2 (SEQ ID NO)	CDRL3 (SEQ ID NO)	CDRH1 (SEQ ID NO)	CDRH2 (SEQ ID NO)	CDRH3 (SEQ ID NO)
5C2	633	790	947	1104	1261	1418
13H12	634	791	948	1105	1262	1419
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

Combinazione	CDRL1 (SEQ ID NO)	CDRL2 (SEQ ID NO)	CDRL3 (SEQ ID NO)	CDRH1 (SEQ ID NO)	CDRH2 (SEQ ID NO)	CDRH3 (SEQ ID NO)
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
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

Combinazione	CDRL1 (SEQ ID NO)	CDRL2 (SEQ ID NO)	CDRL3 (SEQ ID NO)	CDRH1 (SEQ ID NO)	CDRH2 (SEQ ID NO)	CDRH3 (SEQ ID NO)
18F2.012	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

Combinazione	CDRL1 (SEQ ID NO)	CDRL2 (SEQ ID NO)	CDRL3 (SEQ ID NO)	CDRH1 (SEQ ID NO)	CDRH2 (SEQ ID NO)	CDRH3 (SEQ ID NO)
6A5.004.001	684	841	998	1155	1312	1469
6A5.004.002	685	842	999	1156	1313	1470
6A5.004.003	686	843	1000	1157	1314	1471
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

Combinazione	CDRL1 (SEQ ID NO)	CDRL2 (SEQ ID NO)	CDRL3 (SEQ ID NO)	CDRH1 (SEQ ID NO)	CDRH2 (SEQ ID NO)	CDRH3 (SEQ ID NO)
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
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

Combinazione	CDRL1 (SEQ ID NO)	CDRL2 (SEQ ID NO)	CDRL3 (SEQ ID NO)	CDRH1 (SEQ ID NO)	CDRH2 (SEQ ID NO)	CDRH3 (SEQ ID NO)
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

Combinazione	CDRL1 (SEQ ID NO)	CDRL2 (SEQ ID NO)	CDRL3 (SEQ ID NO)	CDRH1 (SEQ ID NO)	CDRH2 (SEQ ID NO)	CDRH3 (SEQ ID NO)
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
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

Combinazione	CDRL1 (SEQ ID NO)	CDRL2 (SEQ ID NO)	CDRL3 (SEQ ID NO)	CDRH1 (SEQ ID NO)	CDRH2 (SEQ ID NO)	CDRH3 (SEQ ID NO)
2C2.005.001	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
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

Combinazione	CDRL1 (SEQ ID NO)	CDRL2 (SEQ ID NO)	CDRL3 (SEQ ID NO)	CDRH1 (SEQ ID NO)	CDRH2 (SEQ ID NO)	CDRH3 (SEQ ID NO)
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

in cui

l'anticorpo, o suo frammento funzionale, comprende una sostituzione di cisteina o di amminoacido non canonico in uno o più siti di coniugazione selezionati dal gruppo consistente in

D70 della catena leggera di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 455,

E276 della catena pesante di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 612, e

T363 della catena pesante di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 612.

7. Composizione della rivendicazione 3, in cui detto anticorpo, o suo frammento, comprende una regione variabile di catena leggera comprendente una sequenza selezionata dal gruppo consistente in SEQ ID NO: 1-157 e una regione variabile di catena pesante comprendente una sequenza selezionata dal gruppo consistente in SEQ ID NO: 158-314, in cui

l'anticorpo, o suo frammento funzionale, comprende una sostituzione di cisteina o di amminoacido non canonico in uno o più siti di coniugazione selezionati dal gruppo consistente in

D70 della catena leggera di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 455,

E276 della catena pesante di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 612, e

T363 della catena pesante di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 612.

8. Composizione della rivendicazione 3, in cui detto anticorpo, o suo frammento, comprende una combinazione di una regione variabile di catena leggera e di una regione variabile di catena pesante selezionata dal gruppo consistente in una regione variabile di catena leggera comprendente SEQ ID NO: 1 e una regione variabile di catena pesante comprendente SEQ ID NO: 158; una regione variabile di catena leggera comprendente SEQ ID NO: 2 e una regione variabile di catena pesante comprendente SEQ ID NO: 159; una regione variabile di catena leggera comprendente SEQ ID NO: 3 e una regione variabile di catena pesante comprendente SEQ ID NO: 160; una regione variabile di catena leggera comprendente SEQ ID NO: 4 e una regione variabile di catena pesante comprendente SEQ ID NO: 161; una regione variabile di catena leggera comprendente SEQ ID NO: 5 e una regione variabile di catena pesante comprendente SEQ ID NO: 162; una regione variabile di catena leggera comprendente SEQ ID NO: 6 e una regione variabile di catena pesante comprendente SEQ ID NO: 163; una regione variabile di catena leggera comprendente SEQ ID NO: 7 e una regione variabile di catena pesante comprendente SEQ ID NO: 164; una regione variabile di catena leggera comprendente SEQ ID NO: 8 e una regione variabile di catena pesante comprendente SEQ ID NO: 165; una regione variabile di catena leggera comprendente SEQ ID NO: 9 e una regione variabile di catena pesante comprendente SEQ ID NO: 166; una regione variabile di catena leggera

comprendente SEQ ID NO: 10 e una regione variabile di catena pesante comprendente SEQ ID NO: 167; una regione variabile di catena leggera comprendente SEQ ID NO: 11 e una regione variabile di catena pesante comprendente SEQ ID NO: 168; una regione variabile di catena leggera comprendente SEQ ID NO: 12 e una regione variabile di catena pesante comprendente SEQ ID NO: 169; una regione variabile di catena leggera comprendente SEQ ID NO: 13 e una regione variabile di catena pesante comprendente SEQ ID NO: 170; una regione variabile di catena leggera comprendente SEQ ID NO: 14 e una regione variabile di catena pesante comprendente SEQ ID NO: 171; una regione variabile di catena leggera comprendente SEQ ID NO: 15 e una regione variabile di catena pesante comprendente SEQ ID NO: 172; una regione variabile di catena leggera comprendente SEQ ID NO: 16 e una regione variabile di catena pesante comprendente SEQ ID NO: 173; una regione variabile di catena leggera comprendente SEQ ID NO: 17 e una regione variabile di catena pesante comprendente SEQ ID NO: 174; una regione variabile di catena leggera comprendente SEQ ID NO: 18 e una regione variabile di catena pesante comprendente SEQ ID NO: 175; una regione variabile di catena leggera comprendente SEQ ID NO: 19 e una regione variabile di catena pesante comprendente SEQ ID NO: 176; una regione variabile di catena leggera comprendente SEQ ID NO: 20 e una regione variabile di catena pesante comprendente SEQ ID NO: 177; una regione variabile di catena leggera comprendente SEQ ID NO: 21 e una regione variabile di catena pesante comprendente SEQ ID NO: 178; una regione variabile di catena leggera

comprendente SEQ ID NO: 22 e una regione variabile di catena pesante comprendente SEQ ID NO: 179; una regione variabile di catena leggera comprendente SEQ ID NO: 23 e una regione variabile di catena pesante comprendente SEQ ID NO: 180; una regione variabile di catena leggera comprendente SEQ ID NO: 24 e una regione variabile di catena pesante comprendente SEQ ID NO: 181; una regione variabile di catena leggera comprendente SEQ ID NO: 25 e una regione variabile di catena pesante comprendente SEQ ID NO: 182; una regione variabile di catena leggera comprendente SEQ ID NO: 26 e una regione variabile di catena pesante comprendente SEQ ID NO: 183; una regione variabile di catena leggera comprendente SEQ ID NO: 27 e una regione variabile di catena pesante comprendente SEQ ID NO: 184; una regione variabile di catena leggera comprendente SEQ ID NO: 28 e una regione variabile di catena pesante comprendente SEQ ID NO: 185; una regione variabile di catena leggera comprendente SEQ ID NO: 29 e una regione variabile di catena pesante comprendente SEQ ID NO: 186; una regione variabile di catena leggera comprendente SEQ ID NO: 30 e una regione variabile di catena pesante comprendente SEQ ID NO: 187; una regione variabile di catena leggera comprendente SEQ ID NO: 31 e una regione variabile di catena pesante comprendente SEQ ID NO: 188; una regione variabile di catena leggera comprendente SEQ ID NO: 32 e una regione variabile di catena pesante comprendente SEQ ID NO: 189; una regione variabile di catena leggera comprendente SEQ ID NO: 33 e una regione variabile di catena pesante comprendente SEQ ID NO: 190; una regione variabile di catena leggera

comprendente SEQ ID NO: 34 e una regione variabile di catena pesante comprendente SEQ ID NO: 191; una regione variabile di catena leggera comprendente SEQ ID NO: 35 e una regione variabile di catena pesante comprendente SEQ ID NO: 192; una regione variabile di catena leggera comprendente SEQ ID NO: 36 e una regione variabile di catena pesante comprendente SEQ ID NO: 193; una regione variabile di catena leggera comprendente SEQ ID NO: 37 e una regione variabile di catena pesante comprendente SEQ ID NO: 194; una regione variabile di catena leggera comprendente SEQ ID NO: 38 e una regione variabile di catena pesante comprendente SEQ ID NO: 195; una regione variabile di catena leggera comprendente SEQ ID NO: 39 e una regione variabile di catena pesante comprendente SEQ ID NO: 196; una regione variabile di catena leggera comprendente SEQ ID NO: 40 e una regione variabile di catena pesante comprendente SEQ ID NO: 197; una regione variabile di catena leggera comprendente SEQ ID NO: 41 e una regione variabile di catena pesante comprendente SEQ ID NO: 198; una regione variabile di catena leggera comprendente SEQ ID NO: 42 e una regione variabile di catena pesante comprendente SEQ ID NO: 199; una regione variabile di catena leggera comprendente SEQ ID NO: 43 e una regione variabile di catena pesante comprendente SEQ ID NO: 200; una regione variabile di catena leggera comprendente SEQ ID NO: 44 e una regione variabile di catena pesante comprendente SEQ ID NO: 201; una regione variabile di catena leggera comprendente SEQ ID NO: 45 e una regione variabile di catena pesante comprendente SEQ ID NO: 202; una regione variabile di catena leggera

comprendente SEQ ID NO: 46 e una regione variabile di catena pesante comprendente SEQ ID NO: 203; una regione variabile di catena leggera comprendente SEQ ID NO: 47 e una regione variabile di catena pesante comprendente SEQ ID NO: 204; una regione variabile di catena leggera comprendente SEQ ID NO: 48 e una regione variabile di catena pesante comprendente SEQ ID NO: 205; una regione variabile di catena leggera comprendente SEQ ID NO: 49 e una regione variabile di catena pesante comprendente SEQ ID NO: 206; una regione variabile di catena leggera comprendente SEQ ID NO: 50 e una regione variabile di catena pesante comprendente SEQ ID NO: 207; una regione variabile di catena leggera comprendente SEQ ID NO: 51 e una regione variabile di catena pesante comprendente SEQ ID NO: 208; una regione variabile di catena leggera comprendente SEQ ID NO: 52 e una regione variabile di catena pesante comprendente SEQ ID NO: 209; una regione variabile di catena leggera comprendente SEQ ID NO: 53 e una regione variabile di catena pesante comprendente SEQ ID NO: 210; una regione variabile di catena leggera comprendente SEQ ID NO: 54 e una regione variabile di catena pesante comprendente SEQ ID NO: 211; una regione variabile di catena leggera comprendente SEQ ID NO: 55 e una regione variabile di catena pesante comprendente SEQ ID NO: 212; una regione variabile di catena leggera comprendente SEQ ID NO: 56 e una regione variabile di catena pesante comprendente SEQ ID NO: 213; una regione variabile di catena leggera comprendente SEQ ID NO: 57 e una regione variabile di catena pesante comprendente SEQ ID NO: 214; una regione variabile di catena leggera

comprendente SEQ ID NO: 58 e una regione variabile di catena pesante comprendente SEQ ID NO: 215; una regione variabile di catena leggera comprendente SEQ ID NO: 59 e una regione variabile di catena pesante comprendente SEQ ID NO: 216; una regione variabile di catena leggera comprendente SEQ ID NO: 60 e una regione variabile di catena pesante comprendente SEQ ID NO: 217; una regione variabile di catena leggera comprendente SEQ ID NO: 61 e una regione variabile di catena pesante comprendente SEQ ID NO: 218; una regione variabile di catena leggera comprendente SEQ ID NO: 62 e una regione variabile di catena pesante comprendente SEQ ID NO: 219; una regione variabile di catena leggera comprendente SEQ ID NO: 63 e una regione variabile di catena pesante comprendente SEQ ID NO: 220; una regione variabile di catena leggera comprendente SEQ ID NO: 64 e una regione variabile di catena pesante comprendente SEQ ID NO: 221; una regione variabile di catena leggera comprendente SEQ ID NO: 65 e una regione variabile di catena pesante comprendente SEQ ID NO: 222; una regione variabile di catena leggera comprendente SEQ ID NO: 66 e una regione variabile di catena pesante comprendente SEQ ID NO: 223; una regione variabile di catena leggera comprendente SEQ ID NO: 67 e una regione variabile di catena pesante comprendente SEQ ID NO: 224; una regione variabile di catena leggera comprendente SEQ ID NO: 68 e una regione variabile di catena pesante comprendente SEQ ID NO: 225; una regione variabile di catena leggera comprendente SEQ ID NO: 69 e una regione variabile di catena pesante comprendente SEQ ID NO: 226; una regione variabile di catena leggera

comprendente SEQ ID NO: 70 e una regione variabile di catena pesante comprendente SEQ ID NO: 227; una regione variabile di catena leggera comprendente SEQ ID NO: 71 e una regione variabile di catena pesante comprendente SEQ ID NO: 228; una regione variabile di catena leggera comprendente SEQ ID NO: 72 e una regione variabile di catena pesante comprendente SEQ ID NO: 229; una regione variabile di catena leggera comprendente SEQ ID NO: 73 e una regione variabile di catena pesante comprendente SEQ ID NO: 230; una regione variabile di catena leggera comprendente SEQ ID NO: 74 e una regione variabile di catena pesante comprendente SEQ ID NO: 231; una regione variabile di catena leggera comprendente SEQ ID NO: 75 e una regione variabile di catena pesante comprendente SEQ ID NO: 232; una regione variabile di catena leggera comprendente SEQ ID NO: 76 e una regione variabile di catena pesante comprendente SEQ ID NO: 233; una regione variabile di catena leggera comprendente SEQ ID NO: 77 e una regione variabile di catena pesante comprendente SEQ ID NO: 234; una regione variabile di catena leggera comprendente SEQ ID NO: 78 e una regione variabile di catena pesante comprendente SEQ ID NO: 235; una regione variabile di catena leggera comprendente SEQ ID NO: 79 e una regione variabile di catena pesante comprendente SEQ ID NO: 236; una regione variabile di catena leggera comprendente SEQ ID NO: 80 e una regione variabile di catena pesante comprendente SEQ ID NO: 237; una regione variabile di catena leggera comprendente SEQ ID NO: 81 e una regione variabile di catena pesante comprendente SEQ ID NO: 238; una regione variabile di catena leggera

comprendente SEQ ID NO: 82 e una regione variabile di catena pesante comprendente SEQ ID NO: 239; una regione variabile di catena leggera comprendente SEQ ID NO: 83 e una regione variabile di catena pesante comprendente SEQ ID NO: 240; una regione variabile di catena leggera comprendente SEQ ID NO: 84 e una regione variabile di catena pesante comprendente SEQ ID NO: 241; una regione variabile di catena leggera comprendente SEQ ID NO: 85 e una regione variabile di catena pesante comprendente SEQ ID NO: 242; una regione variabile di catena leggera comprendente SEQ ID NO: 86 e una regione variabile di catena pesante comprendente SEQ ID NO: 243; una regione variabile di catena leggera comprendente SEQ ID NO: 87 e una regione variabile di catena pesante comprendente SEQ ID NO: 244; una regione variabile di catena leggera comprendente SEQ ID NO: 88 e una regione variabile di catena pesante comprendente SEQ ID NO: 245; una regione variabile di catena leggera comprendente SEQ ID NO: 89 e una regione variabile di catena pesante comprendente SEQ ID NO: 246; una regione variabile di catena leggera comprendente SEQ ID NO: 90 e una regione variabile di catena pesante comprendente SEQ ID NO: 247; una regione variabile di catena leggera comprendente SEQ ID NO: 91 e una regione variabile di catena pesante comprendente SEQ ID NO: 248; una regione variabile di catena leggera comprendente SEQ ID NO: 92 e una regione variabile di catena pesante comprendente SEQ ID NO: 249; una regione variabile di catena leggera comprendente SEQ ID NO: 93 e una regione variabile di catena pesante comprendente SEQ ID NO: 250; una regione variabile di catena leggera

comprendente SEQ ID NO: 94 e una regione variabile di catena pesante comprendente SEQ ID NO: 251; una regione variabile di catena leggera comprendente SEQ ID NO: 95 e una regione variabile di catena pesante comprendente SEQ ID NO: 252; una regione variabile di catena leggera comprendente SEQ ID NO: 96 e una regione variabile di catena pesante comprendente SEQ ID NO: 253; una regione variabile di catena leggera comprendente SEQ ID NO: 97 e una regione variabile di catena pesante comprendente SEQ ID NO: 254; una regione variabile di catena leggera comprendente SEQ ID NO: 98 e una regione variabile di catena pesante comprendente SEQ ID NO: 255; una regione variabile di catena leggera comprendente SEQ ID NO: 99 e una regione variabile di catena pesante comprendente SEQ ID NO: 256; una regione variabile di catena leggera comprendente SEQ ID NO: 100 e una regione variabile di catena pesante comprendente SEQ ID NO: 257; una regione variabile di catena leggera comprendente SEQ ID NO: 101 e una regione variabile di catena pesante comprendente SEQ ID NO: 258; una regione variabile di catena leggera comprendente SEQ ID NO: 102 e una regione variabile di catena pesante comprendente SEQ ID NO: 259; una regione variabile di catena leggera comprendente SEQ ID NO: 103 e una regione variabile di catena pesante comprendente SEQ ID NO: 260; una regione variabile di catena leggera comprendente SEQ ID NO: 104 e una regione variabile di catena pesante comprendente SEQ ID NO: 261; una regione variabile di catena leggera comprendente SEQ ID NO: 105 e una regione variabile di catena pesante comprendente SEQ ID NO: 262; una regione variabile di catena leggera

comprendente SEQ ID NO: 106 e una regione variabile di catena pesante comprendente SEQ ID NO: 263; una regione variabile di catena leggera comprendente SEQ ID NO: 107 e una regione variabile di catena pesante comprendente SEQ ID NO: 264; una regione variabile di catena leggera comprendente SEQ ID NO: 108 e una regione variabile di catena pesante comprendente SEQ ID NO: 265; una regione variabile di catena leggera comprendente SEQ ID NO: 109 e una regione variabile di catena pesante comprendente SEQ ID NO: 266; una regione variabile di catena leggera comprendente SEQ ID NO: 110 e una regione variabile di catena pesante comprendente SEQ ID NO: 267; una regione variabile di catena leggera comprendente SEQ ID NO: 111 e una regione variabile di catena pesante comprendente SEQ ID NO: 268; una regione variabile di catena leggera comprendente SEQ ID NO: 112 e una regione variabile di catena pesante comprendente SEQ ID NO: 269; una regione variabile di catena leggera comprendente SEQ ID NO: 113 e una regione variabile di catena pesante comprendente SEQ ID NO: 270; una regione variabile di catena leggera comprendente SEQ ID NO: 114 e una regione variabile di catena pesante comprendente SEQ ID NO: 271; una regione variabile di catena leggera comprendente SEQ ID NO: 115 e una regione variabile di catena pesante comprendente SEQ ID NO: 272; una regione variabile di catena leggera comprendente SEQ ID NO: 116 e una regione variabile di catena pesante comprendente SEQ ID NO: 273; una regione variabile di catena leggera comprendente SEQ ID NO: 117 e una regione variabile di catena pesante comprendente SEQ ID NO: 274; una regione variabile di catena leggera

comprendente SEQ ID NO: 118 e una regione variabile di catena pesante comprendente SEQ ID NO: 275; una regione variabile di catena leggera comprendente SEQ ID NO: 119 e una regione variabile di catena pesante comprendente SEQ ID NO: 276; una regione variabile di catena leggera comprendente SEQ ID NO: 120 e una regione variabile di catena pesante comprendente SEQ ID NO: 277; una regione variabile di catena leggera comprendente SEQ ID NO: 121 e una regione variabile di catena pesante comprendente SEQ ID NO: 278; una regione variabile di catena leggera comprendente SEQ ID NO: 122 e una regione variabile di catena pesante comprendente SEQ ID NO: 279; una regione variabile di catena leggera comprendente SEQ ID NO: 123 e una regione variabile di catena pesante comprendente SEQ ID NO: 280; una regione variabile di catena leggera comprendente SEQ ID NO: 124 e una regione variabile di catena pesante comprendente SEQ ID NO: 281; una regione variabile di catena leggera comprendente SEQ ID NO: 125 e una regione variabile di catena pesante comprendente SEQ ID NO: 282; una regione variabile di catena leggera comprendente SEQ ID NO: 126 e una regione variabile di catena pesante comprendente SEQ ID NO: 283; una regione variabile di catena leggera comprendente SEQ ID NO: 127 e una regione variabile di catena pesante comprendente SEQ ID NO: 284; una regione variabile di catena leggera comprendente SEQ ID NO: 128 e una regione variabile di catena pesante comprendente SEQ ID NO: 285; una regione variabile di catena leggera comprendente SEQ ID NO: 129 e una regione variabile di catena pesante comprendente SEQ ID NO: 286; una regione variabile di catena leggera

comprendente SEQ ID NO: 130 e una regione variabile di catena pesante comprendente SEQ ID NO: 287; una regione variabile di catena leggera comprendente SEQ ID NO: 131 e una regione variabile di catena pesante comprendente SEQ ID NO: 288; una regione variabile di catena leggera comprendente SEQ ID NO: 132 e una regione variabile di catena pesante comprendente SEQ ID NO: 289; una regione variabile di catena leggera comprendente SEQ ID NO: 133 e una regione variabile di catena pesante comprendente SEQ ID NO: 290; una regione variabile di catena leggera comprendente SEQ ID NO: 134 e una regione variabile di catena pesante comprendente SEQ ID NO: 291; una regione variabile di catena leggera comprendente SEQ ID NO: 135 e una regione variabile di catena pesante comprendente SEQ ID NO: 292; una regione variabile di catena leggera comprendente SEQ ID NO: 136 e una regione variabile di catena pesante comprendente SEQ ID NO: 293; una regione variabile di catena leggera comprendente SEQ ID NO: 137 e una regione variabile di catena pesante comprendente SEQ ID NO: 294; una regione variabile di catena leggera comprendente SEQ ID NO: 138 e una regione variabile di catena pesante comprendente SEQ ID NO: 295; una regione variabile di catena leggera comprendente SEQ ID NO: 139 e una regione variabile di catena pesante comprendente SEQ ID NO: 296; una regione variabile di catena leggera comprendente SEQ ID NO: 140 e una regione variabile di catena pesante comprendente SEQ ID NO: 297; una regione variabile di catena leggera comprendente SEQ ID NO: 141 e una regione variabile di catena pesante comprendente SEQ ID NO: 298; una regione variabile di catena leggera

comprendente SEQ ID NO: 142 e una regione variabile di catena pesante comprendente SEQ ID NO: 299; una regione variabile di catena leggera comprendente SEQ ID NO: 143 e una regione variabile di catena pesante comprendente SEQ ID NO: 300; una regione variabile di catena leggera comprendente SEQ ID NO: 144 e una regione variabile di catena pesante comprendente SEQ ID NO: 301; una regione variabile di catena leggera comprendente SEQ ID NO: 145 e una regione variabile di catena pesante comprendente SEQ ID NO: 302; una regione variabile di catena leggera comprendente SEQ ID NO: 146 e una regione variabile di catena pesante comprendente SEQ ID NO: 303; una regione variabile di catena leggera comprendente SEQ ID NO: 147 e una regione variabile di catena pesante comprendente SEQ ID NO: 304; una regione variabile di catena leggera comprendente SEQ ID NO: 148 e una regione variabile di catena pesante comprendente SEQ ID NO: 305; una regione variabile di catena leggera comprendente SEQ ID NO: 149 e una regione variabile di catena pesante comprendente SEQ ID NO: 306; una regione variabile di catena leggera comprendente SEQ ID NO: 150 e una regione variabile di catena pesante comprendente SEQ ID NO: 307; una regione variabile di catena leggera comprendente SEQ ID NO: 151 e una regione variabile di catena pesante comprendente SEQ ID NO: 308; una regione variabile di catena leggera comprendente SEQ ID NO: 152 e una regione variabile di catena pesante comprendente SEQ ID NO: 309; una regione variabile di catena leggera comprendente SEQ ID NO: 153 e una regione variabile di catena pesante comprendente SEQ ID NO: 310; una regione variabile di catena leggera

comprendente SEQ ID NO: 154 e una regione variabile di catena pesante comprendente SEQ ID NO: 311; una regione variabile di catena leggera comprendente SEQ ID NO: 155 e una regione variabile di catena pesante comprendente SEQ ID NO: 312; una regione variabile di catena leggera comprendente SEQ ID NO: 156 e una regione variabile di catena pesante comprendente SEQ ID NO: 313; e una regione variabile di catena leggera comprendente SEQ ID NO: 157 e una regione variabile di catena pesante comprendente SEQ ID NO: 314, in cui

l'anticorpo, o suo frammento funzionale, comprende una sostituzione di cisteina o di amminoacido non canonico in uno o più siti di coniugazione selezionati dal gruppo consistente in

D70 della catena leggera di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 455,

E276 della catena pesante di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 612, e

T363 della catena pesante di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 612.

9. Composizione della rivendicazione 3, in cui detto anticorpo, o suo frammento funzionale, è un anticorpo, e in cui detto anticorpo comprende una catena leggera comprendente una sequenza selezionata dal gruppo consistente in SEQ ID NO: 315-471 e una catena pesante comprendente una sequenza selezionata dal gruppo consistente in SEQ ID NO: 472-628, in cui

l'anticorpo, o suo frammento funzionale, comprende una sostituzione di cisteina o di amminoacido non canonico in uno o più siti di coniugazione selezionati dal gruppo consistente in

D70 della catena leggera di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 455,

E276 della catena pesante di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 612, e

T363 della catena pesante di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 612.

10. Composizione della rivendicazione 3, in cui detto anticorpo, o suo frammento funzionale, è un anticorpo, e in cui detto anticorpo comprende una combinazione di una catena leggera e di una catena pesante selezionata dal gruppo consistente in una catena leggera comprendente SEQ ID NO: 315 e una catena pesante comprendente SEQ ID NO: 472; una catena leggera comprendente SEQ ID NO: 316 e una catena pesante comprendente SEQ ID NO: 473; una catena leggera comprendente SEQ ID NO: 317 e una catena pesante comprendente SEQ ID NO: 474; una catena leggera comprendente SEQ ID NO: 318 e una catena pesante comprendente SEQ ID NO: 475; una catena leggera comprendente SEQ ID NO: 319 e una catena pesante comprendente SEQ ID NO: 476; una catena leggera comprendente SEQ ID NO: 320 e una catena pesante comprendente SEQ ID NO: 477; una catena leggera comprendente SEQ ID NO: 321 e una catena pesante comprendente SEQ ID NO: 478; una catena leggera comprendente SEQ ID NO: 322 e

una catena pesante comprendente SEQ ID NO: 479; una catena leggera comprendente SEQ ID NO: 323 e una catena pesante comprendente SEQ ID NO: 480; una catena leggera comprendente SEQ ID NO: 324 e una catena pesante comprendente SEQ ID NO: 481; una catena leggera comprendente SEQ ID NO: 325 e una catena pesante comprendente SEQ ID NO: 482; una catena leggera comprendente SEQ ID NO: 326 e una catena pesante comprendente SEQ ID NO: 483; una catena leggera comprendente SEQ ID NO: 327 e una catena pesante comprendente SEQ ID NO: 484; una catena leggera comprendente SEQ ID NO: 328 e una catena pesante comprendente SEQ ID NO: 485; una catena leggera comprendente SEQ ID NO: 329 e una catena pesante comprendente SEQ ID NO: 486; una catena leggera comprendente SEQ ID NO: 330 e una catena pesante comprendente SEQ ID NO: 487; una catena leggera comprendente SEQ ID NO: 331 e una catena pesante comprendente SEQ ID NO: 488; una catena leggera comprendente SEQ ID NO: 332 e una catena pesante comprendente SEQ ID NO: 489; una catena leggera comprendente SEQ ID NO: 333 e una catena pesante comprendente SEQ ID NO: 490; una catena leggera comprendente SEQ ID NO: 334 e una catena pesante comprendente SEQ ID NO: 491; una catena leggera comprendente SEQ ID NO: 335 e una catena pesante comprendente SEQ ID NO: 492; una catena leggera comprendente SEQ ID NO: 336 e una catena pesante comprendente SEQ ID NO: 493; una catena leggera comprendente SEQ ID NO: 337 e una catena pesante comprendente SEQ ID NO: 494; una catena leggera comprendente SEQ ID NO: 338 e

una catena pesante comprendente SEQ ID NO: 495; una catena leggera comprendente SEQ ID NO: 339 e una catena pesante comprendente SEQ ID NO: 496; una catena leggera comprendente SEQ ID NO: 340 e una catena pesante comprendente SEQ ID NO: 497; una catena leggera comprendente SEQ ID NO: 341 e una catena pesante comprendente SEQ ID NO: 498; una catena leggera comprendente SEQ ID NO: 342 e una catena pesante comprendente SEQ ID NO: 499; una catena leggera comprendente SEQ ID NO: 343 e una catena pesante comprendente SEQ ID NO: 500; una catena leggera comprendente SEQ ID NO: 344 e una catena pesante comprendente SEQ ID NO: 501; una catena leggera comprendente SEQ ID NO: 345 e una catena pesante comprendente SEQ ID NO: 502; una catena leggera comprendente SEQ ID NO: 346 e una catena pesante comprendente SEQ ID NO: 503; una catena leggera comprendente SEQ ID NO: 347 e una catena pesante comprendente SEQ ID NO: 504; una catena leggera comprendente SEQ ID NO: 348 e una catena pesante comprendente SEQ ID NO: 505; una catena leggera comprendente SEQ ID NO: 349 e una catena pesante comprendente SEQ ID NO: 506; una catena leggera comprendente SEQ ID NO: 350 e una catena pesante comprendente SEQ ID NO: 507; una catena leggera comprendente SEQ ID NO: 351 e una catena pesante comprendente SEQ ID NO: 508; una catena leggera comprendente SEQ ID NO: 352 e una catena pesante comprendente SEQ ID NO: 509; una catena leggera comprendente SEQ ID NO: 353 e una catena pesante comprendente SEQ ID NO: 510; una catena leggera comprendente SEQ ID NO: 354 e

una catena pesante comprendente SEQ ID NO: 511; una catena leggera comprendente SEQ ID NO: 355 e una catena pesante comprendente SEQ ID NO: 512; una catena leggera comprendente SEQ ID NO: 356 e una catena pesante comprendente SEQ ID NO: 513; una catena leggera comprendente SEQ ID NO: 357 e una catena pesante comprendente SEQ ID NO: 514; una catena leggera comprendente SEQ ID NO: 358 e una catena pesante comprendente SEQ ID NO: 515; una catena leggera comprendente SEQ ID NO: 359 e una catena pesante comprendente SEQ ID NO: 516; una catena leggera comprendente SEQ ID NO: 360 e una catena pesante comprendente SEQ ID NO: 517; una catena leggera comprendente SEQ ID NO: 361 e una catena pesante comprendente SEQ ID NO: 518; una catena leggera comprendente SEQ ID NO: 362 e una catena pesante comprendente SEQ ID NO: 519; una catena leggera comprendente SEQ ID NO: 363 e una catena pesante comprendente SEQ ID NO: 520; una catena leggera comprendente SEQ ID NO: 364 e una catena pesante comprendente SEQ ID NO: 521; una catena leggera comprendente SEQ ID NO: 365 e una catena pesante comprendente SEQ ID NO: 522; una catena leggera comprendente SEQ ID NO: 366 e una catena pesante comprendente SEQ ID NO: 523; una catena leggera comprendente SEQ ID NO: 367 e una catena pesante comprendente SEQ ID NO: 524; una catena leggera comprendente SEQ ID NO: 368 e una catena pesante comprendente SEQ ID NO: 525; una catena leggera comprendente SEQ ID NO: 369 e una catena pesante comprendente SEQ ID NO: 526; una catena leggera comprendente SEQ ID NO: 370 e

una catena pesante comprendente SEQ ID NO: 527; una catena leggera comprendente SEQ ID NO: 371 e una catena pesante comprendente SEQ ID NO: 528; una catena leggera comprendente SEQ ID NO: 372 e una catena pesante comprendente SEQ ID NO: 529; una catena leggera comprendente SEQ ID NO: 373 e una catena pesante comprendente SEQ ID NO: 530; una catena leggera comprendente SEQ ID NO: 374 e una catena pesante comprendente SEQ ID NO: 531; una catena leggera comprendente SEQ ID NO: 375 e una catena pesante comprendente SEQ ID NO: 532; una catena leggera comprendente SEQ ID NO: 376 e una catena pesante comprendente SEQ ID NO: 533; una catena leggera comprendente SEQ ID NO: 377 e una catena pesante comprendente SEQ ID NO: 534; una catena leggera comprendente SEQ ID NO: 378 e una catena pesante comprendente SEQ ID NO: 535; una catena leggera comprendente SEQ ID NO: 379 e una catena pesante comprendente SEQ ID NO: 536; una catena leggera comprendente SEQ ID NO: 380 e una catena pesante comprendente SEQ ID NO: 537; una catena leggera comprendente SEQ ID NO: 381 e una catena pesante comprendente SEQ ID NO: 538; una catena leggera comprendente SEQ ID NO: 382 e una catena pesante comprendente SEQ ID NO: 539; una catena leggera comprendente SEQ ID NO: 383 e una catena pesante comprendente SEQ ID NO: 540; una catena leggera comprendente SEQ ID NO: 384 e una catena pesante comprendente SEQ ID NO: 541; una catena leggera comprendente SEQ ID NO: 385 e una catena pesante comprendente SEQ ID NO: 542; una catena leggera comprendente SEQ ID NO: 386 e

una catena pesante comprendente SEQ ID NO: 543; una catena leggera comprendente SEQ ID NO: 387 e una catena pesante comprendente SEQ ID NO: 544; una catena leggera comprendente SEQ ID NO: 388 e una catena pesante comprendente SEQ ID NO: 545; una catena leggera comprendente SEQ ID NO: 389 e una catena pesante comprendente SEQ ID NO: 546; una catena leggera comprendente SEQ ID NO: 390 e una catena pesante comprendente SEQ ID NO: 547; una catena leggera comprendente SEQ ID NO: 391 e una catena pesante comprendente SEQ ID NO: 548; una catena leggera comprendente SEQ ID NO: 392 e una catena pesante comprendente SEQ ID NO: 549; una catena leggera comprendente SEQ ID NO: 393 e una catena pesante comprendente SEQ ID NO: 550; una catena leggera comprendente SEQ ID NO: 394 e una catena pesante comprendente SEQ ID NO: 551; una catena leggera comprendente SEQ ID NO: 395 e una catena pesante comprendente SEQ ID NO: 552; una catena leggera comprendente SEQ ID NO: 396 e una catena pesante comprendente SEQ ID NO: 553; una catena leggera comprendente SEQ ID NO: 397 e una catena pesante comprendente SEQ ID NO: 554; una catena leggera comprendente SEQ ID NO: 398 e una catena pesante comprendente SEQ ID NO: 555; una catena leggera comprendente SEQ ID NO: 399 e una catena pesante comprendente SEQ ID NO: 556; una catena leggera comprendente SEQ ID NO: 400 e una catena pesante comprendente SEQ ID NO: 557; una catena leggera comprendente SEQ ID NO: 401 e una catena pesante comprendente SEQ ID NO: 558; una catena leggera comprendente SEQ ID NO: 402 e

una catena pesante comprendente SEQ ID NO: 559; una catena leggera comprendente SEQ ID NO: 403 e una catena pesante comprendente SEQ ID NO: 560; una catena leggera comprendente SEQ ID NO: 404 e una catena pesante comprendente SEQ ID NO: 561; una catena leggera comprendente SEQ ID NO: 405 e una catena pesante comprendente SEQ ID NO: 562; una catena leggera comprendente SEQ ID NO: 406 e una catena pesante comprendente SEQ ID NO: 563; una catena leggera comprendente SEQ ID NO: 407 e una catena pesante comprendente SEQ ID NO: 564; una catena leggera comprendente SEQ ID NO: 408 e una catena pesante comprendente SEQ ID NO: 565; una catena leggera comprendente SEQ ID NO: 409 e una catena pesante comprendente SEQ ID NO: 566; una catena leggera comprendente SEQ ID NO: 410 e una catena pesante comprendente SEQ ID NO: 567; una catena leggera comprendente SEQ ID NO: 411 e una catena pesante comprendente SEQ ID NO: 568; una catena leggera comprendente SEQ ID NO: 412 e una catena pesante comprendente SEQ ID NO: 569; una catena leggera comprendente SEQ ID NO: 413 e una catena pesante comprendente SEQ ID NO: 570; una catena leggera comprendente SEQ ID NO: 414 e una catena pesante comprendente SEQ ID NO: 571; una catena leggera comprendente SEQ ID NO: 415 e una catena pesante comprendente SEQ ID NO: 572; una catena leggera comprendente SEQ ID NO: 416 e una catena pesante comprendente SEQ ID NO: 573; una catena leggera comprendente SEQ ID NO: 417 e una catena pesante comprendente SEQ ID NO: 574; una catena leggera comprendente SEQ ID NO: 418 e

una catena pesante comprendente SEQ ID NO: 575; una catena leggera comprendente SEQ ID NO: 419 e una catena pesante comprendente SEQ ID NO: 576; una catena leggera comprendente SEQ ID NO: 420 e una catena pesante comprendente SEQ ID NO: 577; una catena leggera comprendente SEQ ID NO: 421 e una catena pesante comprendente SEQ ID NO: 578; una catena leggera comprendente SEQ ID NO: 422 e una catena pesante comprendente SEQ ID NO: 579; una catena leggera comprendente SEQ ID NO: 423 e una catena pesante comprendente SEQ ID NO: 580; una catena leggera comprendente SEQ ID NO: 424 e una catena pesante comprendente SEQ ID NO: 581; una catena leggera comprendente SEQ ID NO: 425 e una catena pesante comprendente SEQ ID NO: 582; una catena leggera comprendente SEQ ID NO: 426 e una catena pesante comprendente SEQ ID NO: 583; una catena leggera comprendente SEQ ID NO: 427 e una catena pesante comprendente SEQ ID NO: 584; una catena leggera comprendente SEQ ID NO: 428 e una catena pesante comprendente SEQ ID NO: 585; una catena leggera comprendente SEQ ID NO: 429 e una catena pesante comprendente SEQ ID NO: 586; una catena leggera comprendente SEQ ID NO: 430 e una catena pesante comprendente SEQ ID NO: 587; una catena leggera comprendente SEQ ID NO: 431 e una catena pesante comprendente SEQ ID NO: 588; una catena leggera comprendente SEQ ID NO: 432 e una catena pesante comprendente SEQ ID NO: 589; una catena leggera comprendente SEQ ID NO: 433 e una catena pesante comprendente SEQ ID NO: 590; una catena leggera comprendente SEQ ID NO: 434 e

una catena pesante comprendente SEQ ID NO: 591; una catena leggera comprendente SEQ ID NO: 435 e una catena pesante comprendente SEQ ID NO: 592; una catena leggera comprendente SEQ ID NO: 436 e una catena pesante comprendente SEQ ID NO: 593; una catena leggera comprendente SEQ ID NO: 437 e una catena pesante comprendente SEQ ID NO: 594; una catena leggera comprendente SEQ ID NO: 438 e una catena pesante comprendente SEQ ID NO: 595; una catena leggera comprendente SEQ ID NO: 439 e una catena pesante comprendente SEQ ID NO: 596; una catena leggera comprendente SEQ ID NO: 440 e una catena pesante comprendente SEQ ID NO: 597; una catena leggera comprendente SEQ ID NO: 441 e una catena pesante comprendente SEQ ID NO: 598; una catena leggera comprendente SEQ ID NO: 442 e una catena pesante comprendente SEQ ID NO: 599; una catena leggera comprendente SEQ ID NO: 443 e una catena pesante comprendente SEQ ID NO: 600; una catena leggera comprendente SEQ ID NO: 444 e una catena pesante comprendente SEQ ID NO: 601; una catena leggera comprendente SEQ ID NO: 445 e una catena pesante comprendente SEQ ID NO: 602; una catena leggera comprendente SEQ ID NO: 446 e una catena pesante comprendente SEQ ID NO: 603; una catena leggera comprendente SEQ ID NO: 447 e una catena pesante comprendente SEQ ID NO: 604; una catena leggera comprendente SEQ ID NO: 448 e una catena pesante comprendente SEQ ID NO: 605; una catena leggera comprendente SEQ ID NO: 449 e una catena pesante comprendente SEQ ID NO: 606; una catena leggera comprendente SEQ ID NO: 450 e

una catena pesante comprendente SEQ ID NO: 607; una catena leggera comprendente SEQ ID NO: 451 e una catena pesante comprendente SEQ ID NO: 608; una catena leggera comprendente SEQ ID NO: 452 e una catena pesante comprendente SEQ ID NO: 609; una catena leggera comprendente SEQ ID NO: 453 e una catena pesante comprendente SEQ ID NO: 610; una catena leggera comprendente SEQ ID NO: 454 e una catena pesante comprendente SEQ ID NO: 611; una catena leggera comprendente SEQ ID NO: 455 e una catena pesante comprendente SEQ ID NO: 612; una catena leggera comprendente SEQ ID NO: 456 e una catena pesante comprendente SEQ ID NO: 613; una catena leggera comprendente SEQ ID NO: 457 e una catena pesante comprendente SEQ ID NO: 614; una catena leggera comprendente SEQ ID NO: 458 e una catena pesante comprendente SEQ ID NO: 615; una catena leggera comprendente SEQ ID NO: 459 e una catena pesante comprendente SEQ ID NO: 616; una catena leggera comprendente SEQ ID NO: 460 e una catena pesante comprendente SEQ ID NO: 617; una catena leggera comprendente SEQ ID NO: 461 e una catena pesante comprendente SEQ ID NO: 618; una catena leggera comprendente SEQ ID NO: 462 e una catena pesante comprendente SEQ ID NO: 619; una catena leggera comprendente SEQ ID NO: 463 e una catena pesante comprendente SEQ ID NO: 620; una catena leggera comprendente SEQ ID NO: 464 e una catena pesante comprendente SEQ ID NO: 621; una catena leggera comprendente SEQ ID NO: 465 e una catena pesante comprendente SEQ ID NO: 622; una catena leggera comprendente SEQ ID NO: 466 e

una catena pesante comprendente SEQ ID NO: 623; una catena leggera comprendente SEQ ID NO: 467 e una catena pesante comprendente SEQ ID NO: 624; una catena leggera comprendente SEQ ID NO: 468 e una catena pesante comprendente SEQ ID NO: 625; una catena leggera comprendente SEQ ID NO: 469 e una catena pesante comprendente SEQ ID NO: 626; una catena leggera comprendente SEQ ID NO: 470 e una catena pesante comprendente SEQ ID NO: 627; e una catena leggera comprendente SEQ ID NO: 471 e una catena pesante comprendente SEQ ID NO: 628, in cui

l'anticorpo, o suo frammento funzionale, comprende una sostituzione di cisteina o di amminoacido non canonico in uno o più siti di coniugazione selezionati dal gruppo consistente in

D70 della catena leggera di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 455,

E276 della catena pesante di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 612, e

T363 della catena pesante di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 612.

11. Composizione di una qualsiasi delle rivendicazioni 1-10, in cui l'agonista del recettore di GLP-1 è selezionato dal gruppo consistente in SEQ ID NO: 3184; SEQ ID NO: 3185; liraglutide; albiglutide; taspoglutide; dulaglutide; semaglutide; 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; e SEQ ID NO: 3249, preferibilmente l'agonista del recettore di GLP-1 è coniugato all'anticorpo, o suo frammento, in un residuo che corrisponde a K26, K36, K37, K39 o un gruppo ammina C-terminale di detto analogo.

12. Composizione di una qualsiasi delle rivendicazioni 1-10, in cui l'agonista del recettore di GLP-1 è selezionato dal gruppo consistente in exenatide, liraglutide, lixisenatide, albiglutide, dulaglutide, semaglutide, e taspoglutide.

13. Composizione della rivendicazione 1, in cui l'agonista del recettore di GLP-1 è coniugato all'anticorpo, o suo frammento, tramite un linker peptidico che comprende una sequenza selezionata dal gruppo consistente in $(Gly_3Ser)_2$, $(Gly_4Ser)_2$, $(Gly_3Ser)_3$, $(Gly_4Ser)_3$, $(Gly_3Ser)_4$, $(Gly_4Ser)_4$, $(Gly_3Ser)_5$, $(Gly_4Ser)_5$, $(Gly_3Ser)_6$, e $(Gly_4Ser)_6$.

14. Composizione della rivendicazione 3,

(i) in cui detto anticorpo comprende una combinazione di una regione variabile di catena leggera e di una regione variabile di catena pesante in cui la regione variabile di catena leggera comprende SEQ ID NO: 74 e la regione variabile di catena pesante comprende SEQ ID NO: 231, e in cui detto anticorpo comprende una combinazione di una catena leggera e di una catena pesante in cui la catena leggera comprende SEQ ID NO: 388 e la catena pesante comprende SEQ ID NO: 545, e

(ii) in cui detto agonista del recettore di GLP-1 comprende SEQ ID NO: 3244,

in cui detto anticorpo comprende una cisteina in E276 della catena pesante di anticorpo rispetto alla sequenza di riferimento SEQ ID NO: 612.

15. Composizione di una qualsiasi delle rivendicazioni 1-14 per uso in un metodo per trattare un disturbo metabolico.

Si attesta la perfetta conformità della traduzione che precede.

LEGENDA DELLE TAVOLE DEI DISEGNI

TAVOLA 1/40

Figura 1

“Bromoacetyl-peptide” = Bromoacetil-peptide

TAVOLA 2/40

Figura 2A

“GLP1 cAMP assay in ChoK1 hGLP1R clone H20” = Saggio di cAMP di GLP1 in ChoK1 hGLP1R clone H20

“Log [conjugates]” = Log [coniugati]

Figura 2B

“GIPR antagonist cAMP assay in 293T/huGIPR clone10” = Saggio di cAMP di antagonista di GIPR in 293T/huGIPR clone10

“Log [conjugates]” = Log [coniugati]

Figura 2C

“GLP1 cAMP assay in ChoK1 hGLP1R clone H20” = Saggio di cAMP di GLP1 in ChoK1 hGLP1R clone H20

“Log [conjugates]” = Log [coniugati]

Figura 2D

“GIPR cAMP assay in 293T/huGIPR clone10” = Saggio di cAMP di GIPR in 293T/huGIPR clone10

“Log [conjugates]” = Log [coniugati]

TAVOLA 3/40

Figura 2E

“cAMP assay (GLP-1 agonist mode} in CHOK1 hGLP1R H20” = Saggio di cAMP (modalità agonista di GLP-1) in CHOK1 hGLP1R H20

“Log [conjugates]” = Log [coniugati]

Figura 2F

“cAMP assay (GIPR antagonist mode) in 293T/hGIPR #10” = Saggio di cAMP (modalità agonista di GIPR) in 293T/hGIPR #10

“Log [conjugates]” = Log [coniugati]

Figura 2G

“cAMP assay (GLP-1 agonist mode) in CHOK1 hGLP1R H20” = Saggio di cAMP (modalità agonista di GLP-1) in CHOK1 hGLP1R H20

“Log [conjugates]” = Log [coniugati]

Figura 2H

“cAMP assay (GIPR antagonist mode} in 293T/hGIPR #10” = Saggio di cAMP (modalità agonista di GIPR) in 293T/hGIPR #10

“Log [conjugates]” = Log [coniugati]

TAVOLA 4/40

Figura 2I

“cAMP assay (GLP-1 agonist mode) in CHOK1 hGLP1R H20” = Saggio di cAMP (modalità agonista di GLP-1) in CHOK1 hGLP1R H20

“Log [conjugates]” = Log [coniugati]

Figura 2J

“cAMP assay (GIPR antagonist mode) in 293T/hGIPR #10” = Saggio di cAMP (modalità agonista di GIPR) in 293T/hGIPR #10

“Log [conjugates]” = Log [coniugati]

Figura 2K

“cAMP assay (GLP-1 agonist mode) in CHOK1 hGLP1R H20” = Saggio di cAMP (modalità agonista di GLP-1) in CHOK1 hGLP1R H20

“Log [conjugates]” = Log [coniugati]

Figura 2L

“cAMP assay (GIPR antagonist mode) in 293T/hGIPR #10” = Saggio di cAMP (modalità agonista di GIPR) in 293T/hGIPR #10

“Log [conjugates]” = Log [coniugati]

TAVOLA 5/40

Figura 2M

“cAMP assay (GLP-1 agonist mode) in CHOK1 hGLP1R H20: Chemical Conjugates on 5G12” = Saggio di cAMP (modalità agonista di GLP-1) in CHOK1 hGLP1R H20: coniugati chimici su 5G12

“Log [conjugates]” = Log [coniugati]

“Exendin-4” = Exendina-4

Figura 2N

“cAMP assay (GIPR antagonist mode) in 293T/hGIPR #10” = Saggio di cAMP (modalità agonista di GIPR) in 293T/hGIPR #10

“Chemical Conjugates on 5G12” = Coniugati chimici su 5G12

TAVOLA 6/40

Figura 2O

“cAMP assay (GLP-1 agonist mode) in CHOK1 hGLP1R H20: Chemical Conjugates on 5G12” = Saggio di cAMP (modalità agonista di GLP-1) in CHOK1 hGLP1R H20: coniugati chimici su 5G12

“Log [conjugates]” = Log [coniugati]

“Exendin-4” = Exendina-4

Figura 2P

“cAMP assay (GIPR antagonist mode) in 293T/hGIPR #10” = Saggio di cAMP (modalità antgonista di GIPR) in 293T/hGIPR #10

“Chemical Conjugates on 5G12” = Coniugati chimici su 5G12

TAVOLA 7/40

Figura 2Q

“cAMP assay (GLP-1 agonist mode) in CHOK1 hGLP1R H20: Chemical Conjugates on 2G10” = Saggio di cAMP (modalità agonista di GLP-1) in CHOK1 hGLP1R H20: coniugati chimici su 2G10

“Log [conjugates]” = Log [coniugati]

“Exendin-4” = Exendina-4

Figura 2R

“cAMP assay (GIPR antagonist mode) in 293T/hGIPR #10 Chemical Conjugates on 2G10” = saggi di cAMP (modalità antagonista di GIPR) in 293T/hGIPR #10 Coniugati chimici su 2G10

“Log [conjugates]” = Log [coniugati]

Figura 2S

“cAMP assay (GLP-1 agonist mode) in CHOK1 hGLP1R H20: Chemical Conjugates on 2G10” = Saggio di cAMP (modalità agonista di GLP-1) in CHOK1 hGLP1R H20: coniugati chimici su 2G10

“Log [conjugates]” = Log [coniugati]

“Exendin-4” = Exendina-4

Figura 2T

“cAMP assay (GIPR antagonist mode) in 293T/hGIPR #10 Chemical Conjugates on 2G10” = saggi di cAMP (modalità antagonista di GIPR) in 293T/hGIPR #10 Coniugati chimici su 2G10

“Log [conjugates]” = Log [coniugati]

TAVOLA 8/40

Figura 3A

“Reg #” = N. reg.

“Description” = Descrizione

“Peptide information” = Informazioni sui peptidi

Figura 3B

“cAMP assay (GLP-1 agonist mode) in CHOK1 hGLP1R H20” = Saggio di cAMP (modalità agonista di GLP-1) in CHOK1 hGLP1R H20

“Log [conjugates]” = Log [coniugati]

TAVOLA 9/40

Figura 3C

“cAMP assay (GLP-1 agonist mode) in CHOK1 hGLP1R/hGIPR M1” = Saggio di cAMP (modalità agonista di GLP-1) in CHOK1 hGLP1R/hGIPR M1

“Log [conjugates]” = Log [coniugati]

TAVOLA 10/40

Figura 4A

“% Change in Plasma Glucose” = % di cambiamento del glucosio plasmatico

“Hours post Inj” = Ore dopo l'iniezione

“Vehicle” = Veicolo

Figura 4B

“Change in Body Weight” = Cambiamento di peso corporeo

“Day *” = Giorno*

“Days Post Inj” = Giorni dopo l'iniezione

“Vehicle” = Veicolo

TAVOLA 11/40

Figura 4C

“%ch in Plasma Glucose” = % di cambiamento del glucosio plasmatico

“Hours post Inj” = Ore dopo l'iniezione

“Vehicle” = Veicolo

“GIPR5G12-E384C capped” = GIPR5G12-E384C incappucciato

“Dulaglutide” = Dulaglutide

“Combo Dula” = Combinazione dulag.

Figura 4D

“Change in Body Weight” = Cambiamento di peso corporeo

“Day *” = Giorno*

“Days Post Inj” = Giorni dopo l'iniezione

“Vehicle” = Veicolo

“GIPR5G12-E384C capped” = GIPR5G12-E384C incappucciato

“Dulaglutide” = Dulaglutide

“Combo Dula” = Combinazione dulag.

TAVOLA 12/40

Figura 4E

“% Change in Plasma Glucose” = % di cambiamento del glucosio plasmatico

“Hours post Inj” = Ore dopo l'iniezione

“Vehicle” = Veicolo

“cyclo” = ciclo

“Combo Dula” = Combinazione dulag.

Figura 4F

“Change in Body Weight” = Cambiamento di peso corporeo

“Day *” = Giorno*

“Days Post Inj” = Giorni dopo l'iniezione

“Vehicle” = Veicolo

“cyclo” = ciclo

“Combo Dula” = Combinazione dulag.

TAVOLA 13/40

Figura 4G

“% Change in Plasma Glucose” = % di cambiamento del glucosio plasmatico

“Study Day” = Giorno dello studio

“Vehicle” = Veicolo

Figura 4H

“Change in Body Weight” = Cambiamento di peso corporeo

“Study Day” = Giorno dello studio

“Vehicle” = Veicolo

TAVOLA 14/40

Figura 4I

“% Change in Plasma Glucose” = % di cambiamento del glucosio plasmatico

“Hours post Inj” = Ore dopo l'iniezione

“Vehicle” = Veicolo

Figura 4J

“Change in Body Weight” = Cambiamento di peso corporeo

“Day *” = Giorno*

“Days Post Inj” = Giorni dopo l'iniezione

“Vehicle” = Veicolo

TAVOLA 15/40

Figura 4K

“% Change in Plasma Glucose” = % di cambiamento del glucosio plasmatico

“Hours post Inj” = Ore dopo l'iniezione

“Vehicle” = Veicolo

Figura 4L

“Change in Body Weight” = Cambiamento di peso corporeo

“Day *” = Giorno*

“Days Post Inj” = Giorni dopo l'iniezione

“Vehicle” = Veicolo

TAVOLA 16/40

Figura 4M

“% Change in Plasma Glucose” = % di cambiamento del glucosio plasmatico

“Time (hours)” = Tempo (ore)

“Cntrl Vehicle” = Controllo veicolo

Figura 4N

“Change in Body Weight” = Cambiamento di peso corporeo

“Time (hours)” = Tempo (ore)

“Cntrl Vehicle” = Controllo veicolo

TAVOLA 17/40

Figura 4O

“% Change in Plasma Glucose” = % di cambiamento del glucosio plasmatico

“Hours post Inj” = Ore dopo l'iniezione

“Vehicle” = Veicolo

Figura 4P

“Change in Body Weight” = Cambiamento di peso corporeo

“Day *” = Giorno*

“Days Post Inj” = Giorni dopo l'iniezione

“Vehicle” = Veicolo

TAVOLA 18/40

Figura 4Q

“% Change in Plasma Glucose” = % di cambiamento del glucosio plasmatico

“Hours post Inj” = Ore dopo l'iniezione

“Vehicle” = Veicolo

Figura 4R

“Change in Body Weight” = Cambiamento di peso corporeo

“Day *” = Giorno*

“Days Post Inj” = Giorni dopo l'iniezione

“Vehicle” = Veicolo

TAVOLA 19/40

Figura 5A

“Plasma Glucose” = Glucosio plasmatico

“Glucose Inj” = Iniez. glucosio

“Veh Inj” = Iniez. veicolo

“4hr lapse” = periodo di 4 ore

“Vehicle” = Veicolo

Figura 5B

“Change in Body Weight” = Cambiamento di peso corporeo

“Days Post Inj” = Giorni dopo l'iniezione

“Vehicle” = Veicolo

TAVOLA 20/40

Figura 5C

“Plasma Glucose” = Glucosio plasmatico

“Glucose Inj” = Iniez. glucosio

“Veh Inj” = Iniez. veicolo

“4hr lapse” = periodo di 4 ore

“Vehicle” = Veicolo

Figura 5D

“Change in Body Weight” = Cambiamento di peso corporeo

“Days Post Inj” = Giorni dopo l'iniezione

“Vehicle” = Veicolo

TAVOLA 21/40

Figura 6A

“Change in Body Weight” = Cambiamento di peso corporeo

“Study Day” = Giorno dello studio

“Dulaglutide” = Dulaglutide

“Combo” = Combinazione

“Conjugate” = Coniugato

Figura 6B

“Food Intake (g/day)” = Assunzione di cibo (g/giorno)

“Vehicle” = Veicolo

“Dulaglutide” = Dulaglutide

“Combo” = Combinazione

“Conjugate” = Coniugato

TAVOLA 22/40

Figura 7

“Body weight (% change)” = Peso corporeo (% di cambiamento)

“TREATMENT” = TRATTAMENTO

“WASHOUT” = WASHOUT

“Time (days)” = Tempo (giorni)

“Vehicle” = Veicolo

“ANCOVA; ***p<0.001 vs vehicle for 0.25 mg/kg; ^^^p<0.001 vs vehicle for 0.75 mg/kg” = ANCOVA; ***p<0,001 rispetto al veicolo per 0,25 mg/kg; ^^^p<0,001 rispetto al veicolo per 0,75 mg/kg

“Data represented as group mean ± SEM; n=8-9/group” = Dati rappresentati come media del gruppo ± SEM; n=8-9/gruppo

TAVOLA 23/40

Figura 8

“total energy intake (% change)” = “apporto energetico totale (% di cambiamento)

“TREATMENT” = TRATTAMENTO

“WASHOUT” = WASHOUT

“Time (day)” = Tempo (giorno)

“Vehicle” = Veicolo

“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 for 0.75 mg/kg” = ANCOVA; **p<0,01, ***p<0,001 rispetto al veicolo per 0,25 mg/kg; ^p<0,05, ^^p<0,01, ^^^p<0,001 rispetto al veicolo per 0,75 mg/kg

“Data represented as group mean ± SEM; n=8-9/group” = Dati rappresentati come media del gruppo ± SEM; n=8-9/gruppo

Figura 9

“Cholesterol (% change)” = Colesterolo (% di cambiamento)

“TREATMENT” = TRATTAMENTO

“WASHOUT” = WASHOUT

“Time (days)” = Tempo (giorni)

“Vehicle” = Veicolo

“ANCOVA; **p<0.01 vs vehicle for 0.25 mg/kg; ^p<0.05, ^^p<0.01 vs vehicle for 0.75 mg/kg” = ANCOVA; **p<0,01 rispetto al veicolo per 0,25 mg/kg; ^p<0,05, ^^p<0,01 rispetto al veicolo per 0,75 mg/kg

“Data represented as group mean ± SEM; n=8-9/group” = Dati rappresentati come media del gruppo ± SEM; n=8-9/gruppo

TAVOLA 24/40

Figura 10

“Triglyceride (% change)” = Trigliceridi (% di cambiamento)

“TREATMENT” = TRATTAMENTO

“WASHOUT” = WASHOUT

“Time (days)” = Tempo (giorni)

“Vehicle” = Veicolo

“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 for 0.75 mg/kg” = ANCOVA; **p<0,01, ***p<0,001 rispetto al veicolo per 0,25 mg/kg; ^p<0,05, ^^p<0,01, ^^^p<0,001 rispetto al veicolo per 0,75 mg/kg

“Data represented as group mean ± SEM; n=8-9/group” = Dati rappresentati come media del gruppo ± SEM; n=8-9/gruppo

Figura 11

“Cholesterol (% change)” = Colesterolo (% di cambiamento)

“TREATMENT” = TRATTAMENTO

“WASHOUT” = WASHOUT

“Time (days)” = Tempo (giorni)

“Vehicle” = Veicolo

“ANCOVA; **p<0.01 vs vehicle for 0.25 mg/kg; ^p<0.05, ^^p<0.01 vs vehicle for 0.75 mg/kg” = ANCOVA; **p<0,01 rispetto al veicolo per 0,25 mg/kg; ^p<0,05, ^^p<0,01 rispetto al veicolo per 0,75 mg/kg

“Data represented as group mean ± SEM; n=8-9/group” = Dati rappresentati come media del gruppo ± SEM; n=8-9/gruppo

TAVOLA 25/40

Figura 12

“Body weight (% change)” = Peso corporeo (% di cambiamento)

“TREATMENT” = TRATTAMENTO

“WASHOUT” = WASHOUT

“Time (days)” = Tempo (giorni)

“Vehicle” = Veicolo

“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” = ANCOVA; *p<0,05, **p<0,01, ***p<0,001 rispetto al veicolo per 0,75 mg/kg; ^p<0,05, ^^p<0,01, ^^^p<0,001 rispetto al veicolo per 2,5 mg/kg

“Data represented as group mean ± SEM; n=9/group” = Dati rappresentati come media del gruppo ± SEM; n=9/gruppo

Figura 13

“total energy intake (% change)” = “apporto energetico totale (% di cambiamento)

“TREATMENT” = TRATTAMENTO

“WASHOUT” = WASHOUT

“Time (day)” = Tempo (giorno)

“Vehicle” = Veicolo

“Statistical analysis not performed on total energy intake; error bars not shown; data represented as group mean; n=9/group” = Analisi statistica non eseguita sull'apporto di energia totale; barre di errore non mostrate; dati rappresentati come media del gruppo; n=9/gruppo

TAVOLA 26/40

Figura 14

“Insulin (% change)” = Insulina (% di cambiamento)

“TREATMENT” = TRATTAMENTO

“WASHOUT” = WASHOUT

“Time (days)” = Tempo (giorni)

“Vehicle” = Veicolo

“ANCOVA; *p<0.05, **p<0.01 vs vehicle for 0.75 mg/kg; ^p<0.05 vs vehicle for 2.5 mg/kg” = ANCOVA; *p<0,05, **p<0,01 rispetto al veicolo per 0,75 mg/kg; ^p<0,05 rispetto al veicolo per 2,5 mg/kg

“Data represented as group mean ± SEM; n=9/group” = Dati rappresentati come media del gruppo ± SEM; n=9/gruppo

Figura 15

“Triglyceride (% change)” = Trigliceridi (% di cambiamento)

“TREATMENT” = TRATTAMENTO

“WASHOUT” = WASHOUT

“Time (days)” = Tempo (giorni)

“Vehicle” = Veicolo

“ANCOVA; *p<0.05 vs vehicle for 0.75 mg/kg; ^p<0.05 vs vehicle for 2.5 mg/kg” = ANCOVA; *p<0,05 rispetto al veicolo per 0,75 mg/kg; ^p<0,05 rispetto al veicolo per 2,5 mg/kg

“Data represented as group mean ± SEM; n=9/group” = Dati rappresentati come media del gruppo ± SEM; n=9/gruppo

TAVOLA 27/40

Figura 16

“Cholesterol (% change)” = Colesterolo (% di cambiamento)

“TREATMENT” = TRATTAMENTO

“WASHOUT” = WASHOUT

“Time (days)” = Tempo (giorni)

“Vehicle” = Veicolo

“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” = ANCOVA; *p<0,05, **p<0,01 rispetto al veicolo per 0,75 mg/kg; ^p<0,05, ^^p<0,01 rispetto al veicolo per 2,5 mg/kg

“Data represented as group mean ± SEM; n=9/group” = Dati rappresentati come media del gruppo ± SEM; n=9/gruppo

Figura 17

“Body weight (% change)” = Peso corporeo (% di cambiamento)

“TREATMENT” = TRATTAMENTO

“WASHOUT” = WASHOUT

“Time (days)” = Tempo (giorni)

“Vehicle” = Veicolo

“ANCOVA; ***p<0.001 vs vehicle for 1248 0.75 mg/kg; ^^^p<0.001 vs vehicle for 1257 0.75 mg/kg” = ANCOVA; ***p<0,001 rispetto al veicolo per 1248 0,75 mg/kg; ^^^p<0,001 rispetto al veicolo per 1257 0,75 mg/kg

“Data represented as group mean ± SEM; n=7-10/group” = Dati rappresentati come media del gruppo ± SEM; n=7-10/gruppo

TAVOLA 28/40

Figura 18

“total energy intake (% change)” = “apporto energetico totale (% di cambiamento)

“TREATMENT” = TRATTAMENTO

“WASHOUT” = WASHOUT

“Time (day)” = Tempo (giorno)

“Vehicle” = Veicolo

“ANCOVA; ***p<0.001 vs vehicle for 1248 0.75 mg/kg; ^^^p<0.001 vs vehicle for 1257 0.75 mg/kg” = ANCOVA; ***p<0,001 rispetto al veicolo per 1248 0,75 mg/kg; ^^^p<0,001 rispetto al veicolo per 1257 0,75 mg/kg

“Data represented as group mean ± SEM; n=7-10/group” = Dati rappresentati come media del gruppo ± SEM; n=7-10/gruppo

Figura 19

“Insulin (% change)” = Insulina (% di cambiamento)

“TREATMENT” = TRATTAMENTO

“WASHOUT” = WASHOUT

“Time (days)” = Tempo (giorni)

“Vehicle” = Veicolo

“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” = ANCOVA; *p<0,05, **p<0,01, ***p<0,001 rispetto al veicolo per 1248 0,75 mg/kg; ^^p<0,01 rispetto al veicolo per 1257 0,75 mg/kg

“Data represented as group mean ± SEM; n=7-10/group” = Dati rappresentati come media del gruppo ± SEM; n=7-10/gruppo

TAVOLA 29/40

Figura 20

“Triglyceride (% change)” = Trigliceridi (% di cambiamento)

“TREATMENT” = TRATTAMENTO

“WASHOUT” = WASHOUT

“Time (days)” = Tempo (giorni)

“Vehicle” = Veicolo

“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” = ANCOVA; *p<0,05, **p<0,01, ***p<0,001 rispetto al veicolo per 1248 0,75 mg/kg; ^^p<0,01 rispetto al veicolo per 1257 0,75 mg/kg

“Data represented as group mean ± SEM; n=7-10/group” = Dati rappresentati come media del gruppo ± SEM; n=7-10/gruppo

Figura 21

“Cholesterol (% change)” = Colesterolo (% di cambiamento)

“TREATMENT” = TRATTAMENTO

“WASHOUT” = WASHOUT

“Time (days)” = Tempo (giorni)

“Vehicle” = Veicolo

“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” = ANCOVA; *p<0,05, **p<0,01, ***p<0,001 rispetto al veicolo per 1248 0,75 mg/kg; ^p<0,05, ^^p<0,01 rispetto al veicolo per 1257 0,75 mg/kg

“Data represented as group mean ± SEM; n=7-10/group” = Dati rappresentati come media del gruppo ± SEM; n=7-10/gruppo

TAVOLA 30/40

Figura 22A

“^{125}I huGIP Radioligand Binding Assay” = Saggio di legame di radioligando ^{125}I huGIP

“% ^{125}I huGIP Bound” = % di ^{125}I huGIP legato

“log [inhibitor] M” = log [inibitore] M

Figura 22B

“^{125}I huGLP-1 Radioligand Binding Assay” = Saggio di legame di radioligando ^{125}I huGLP-1

“% ^{125}I huGLP-1 Bound” = % di ^{125}I huGLP-1 legato

“log [inhibitor] M” = log [inibitore] M

TAVOLA 32/40

Figura 24A

“GLP1 R Internalization in CHOK1 GIPR/GLP-1R M1 cells” = Internalizzazione di GLP1 R in cellule CHOK1 GIPR/GLP-1R M1

“total spot area” = area totale del punto

“Time (min)” = Tempo (min)

Figura 24B

“GLP-1 R Internalization in CHOK1 GIPR/GLP-1R M1 cells” = Internalizzazione di GLP1 R in cellule CHOK1 GIPR/GLP-1R M1

“total spot area” = area totale del punto

“log[compound],” = log [composto],

TAVOLA 33/40

Figura 25D

“merge” = unione

TAVOLA 34/40

Figura 26A

“Effects of inhibition of receptor internalization on 1248 induced cAMP activity” = Effetti dell’inibizione dell’internalizzazione del recettore

“Luminescence (RLU)” = Luminescenza (RLU)

“control” = controllo

“sucrose” = saccarosio

Figura 26B

“GloSensor cAMP assay” = Saggio GloSensor cAMP

“Luminescence (RLU)” = Luminescenza (RLU)

“time (seconds)” = tempo (secondi)

“control” = controllo

“sucrose” = saccarosio

TAVOLE 35-37/40

Figure 27A-27C

“Count” = Conteggio

“2nd (AlexaFluor 647 goat-anti-huFc Ab) only” = Solo secondario (Ab anti-huFc di capra AlexaFluor 647)

“huIgG1 control” = controllo huIgG1

“Delaglutide” = Delaglutide

TAVOLA 38/40

Figura 28

“Calcium Flux assay in ChoK1 GLP1 R/GIPR M1 cells” = Saggio del flusso di calcio in cellule ChoK1 GLP1 R/GIPR M1

“Peak Signal/Baseline” = Segnale di picco/basale

“Log [GLP1 or conjugates]” = Log [GLP1 o coniugati]

TAVOLA 39/40

Figura 29A

“GLP-1R PathHunter/GIPR β-arrestin assay” = Saggio della β-arrestina GLP-1R PathHunter/GIPR

Figura 29B

“GIPR PathHunter/GLP-1R β-arrestin assay” = Saggio della β-arrestina GIPR PathHunter/GLP-1R

TAVOLA 40/40

Figura 30

“Glucose-stimulated insulin secretion assay: low and high glucose conditions in human pancreatic microislets” = Saggio di secrezione di insulina stimolata dal glucosio: condizioni a basso e ad alto glucosio in micro-isole pancreatiche umane

“Insulin” = insulina

“glucose” = glucosio

FIG. 1

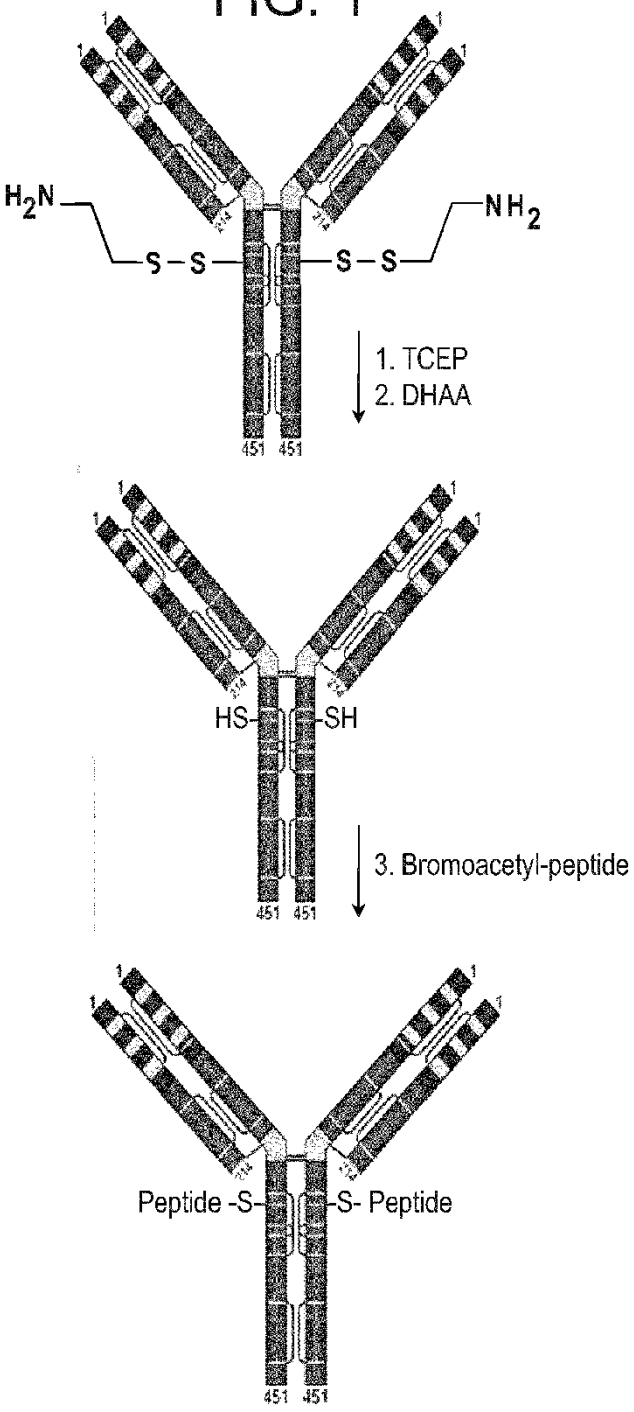

H2N
NH2
S–S
S–S
1. TCEP
2. DHAA
451 451
HS-
-SH
3. Bromoacetyl-peptide
451 451
Peptide -S-
-S- Peptide
451 451

FIG. 2A

GLP1 cAMP assay in ChoK1 hGLP1R clone H20

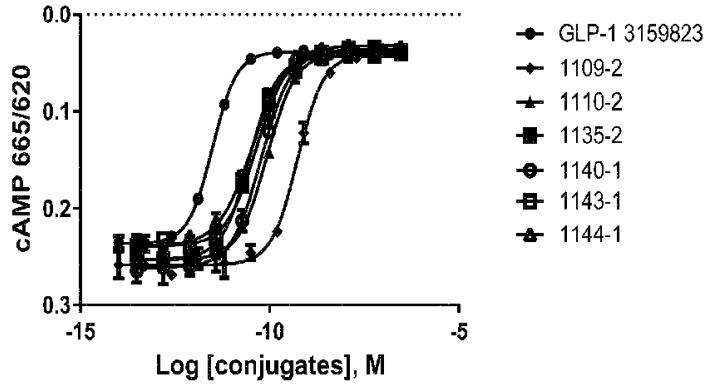


FIG. 2B

GIPR antagonist cAMP assay in 293T/huGIPR clone10

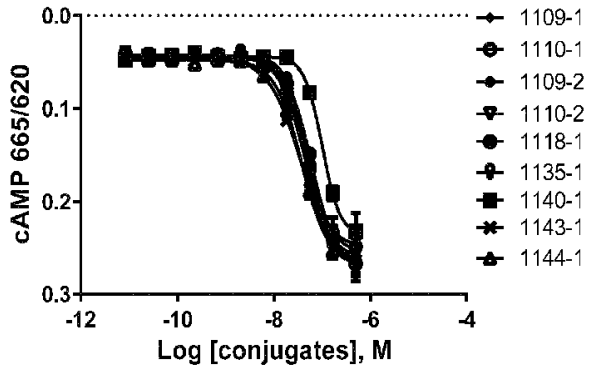


FIG. 2C

GLP1 cAMP assay in ChoK1 hGLP1R clone H20

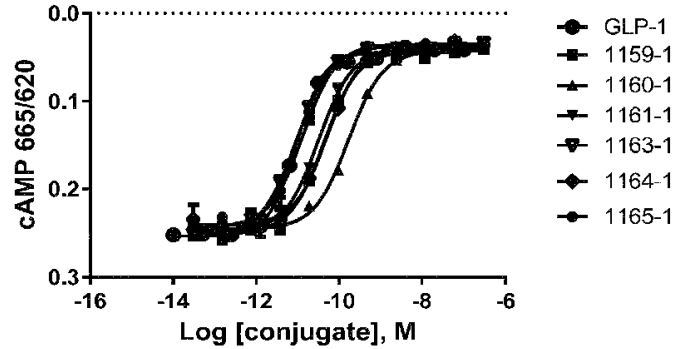


FIG. 2D

GIPR cAMP assay in 293T/huGIPR clone10

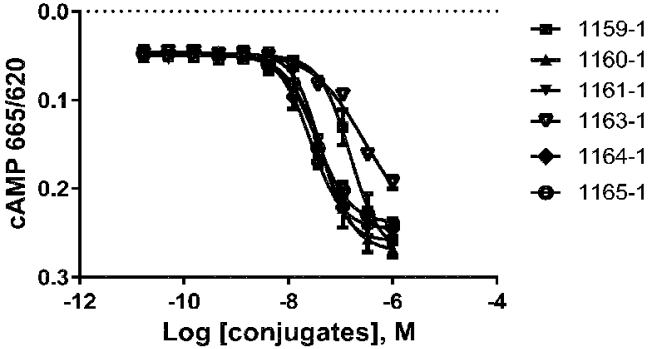


FIG. 2E

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

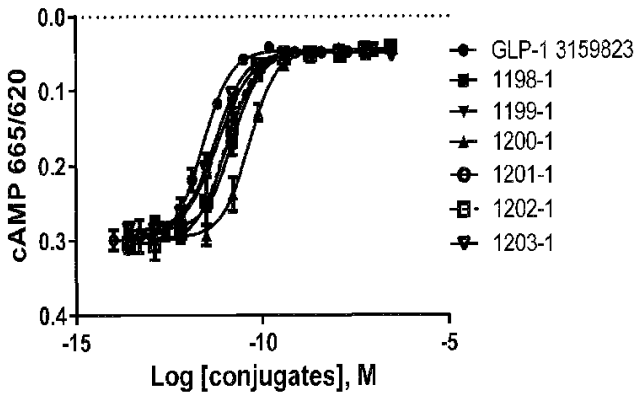


FIG. 2F

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

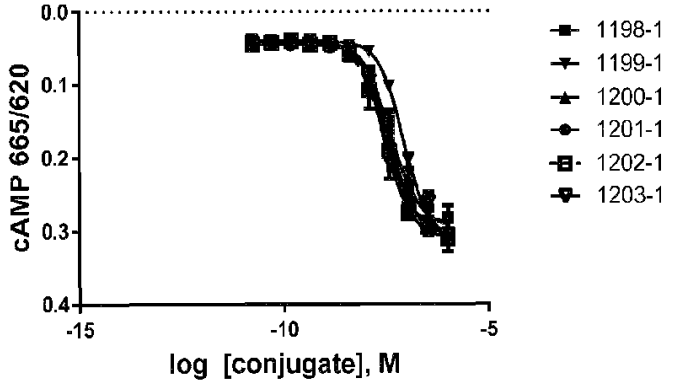


FIG. 2G

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

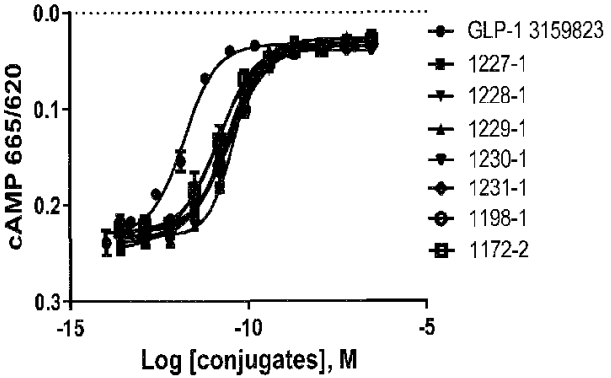


FIG. 2H

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

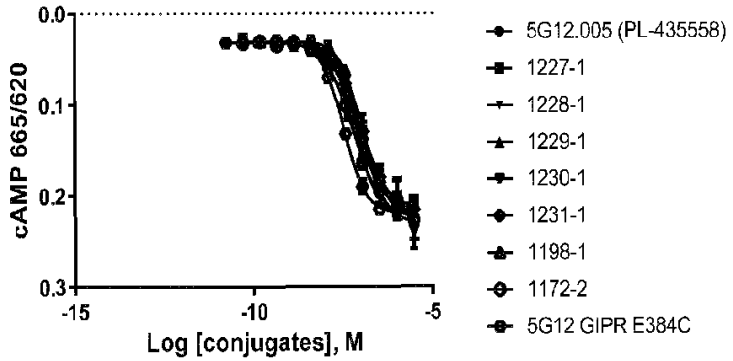


FIG. 2I

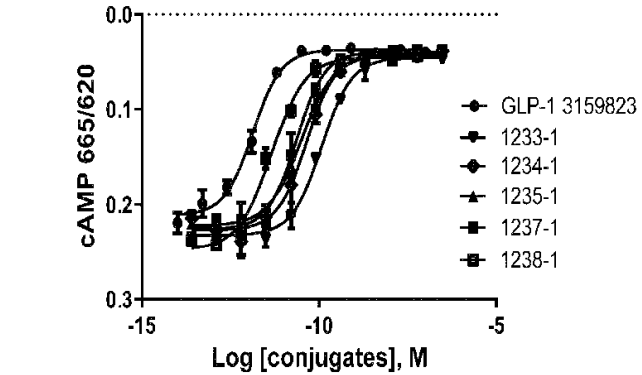


FIG. 2J

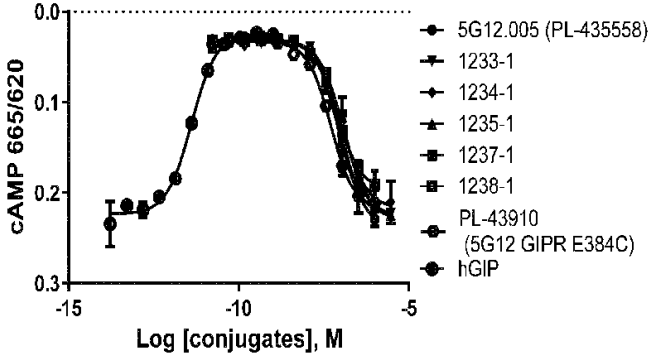


FIG. 2K

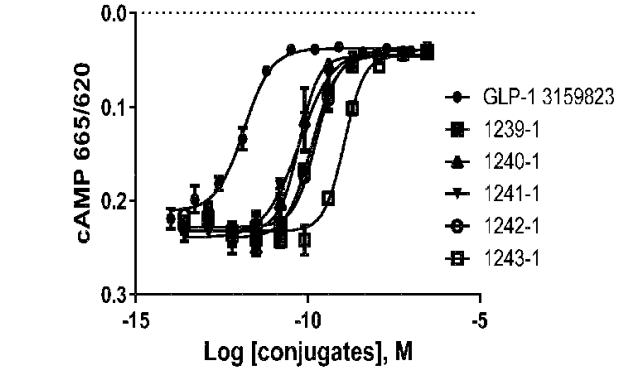


FIG. 2L

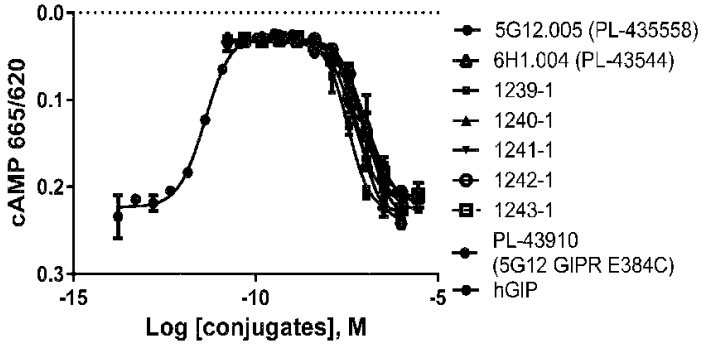


FIG. 2M

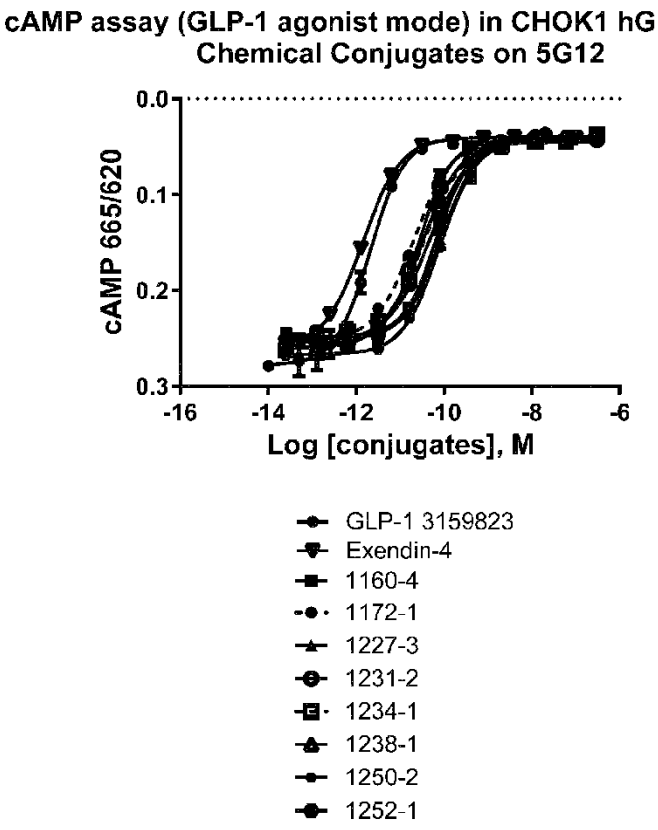

cAMP assay (GLP-1 agonist mode) in CHOK1 hGLP1R H20:
Chemical Conjugates on 5G12
cAMP 665/620
0.0
0.1
0.2
0.3
-16
-14
-12
-10
-8
-6
Log [conjugates], M
GLP-1 3159823
Exendin-4
1160-4
1172-1
1227-3
1231-2
1234-1
1238-1
1250-2
1252-1

FIG. 2N

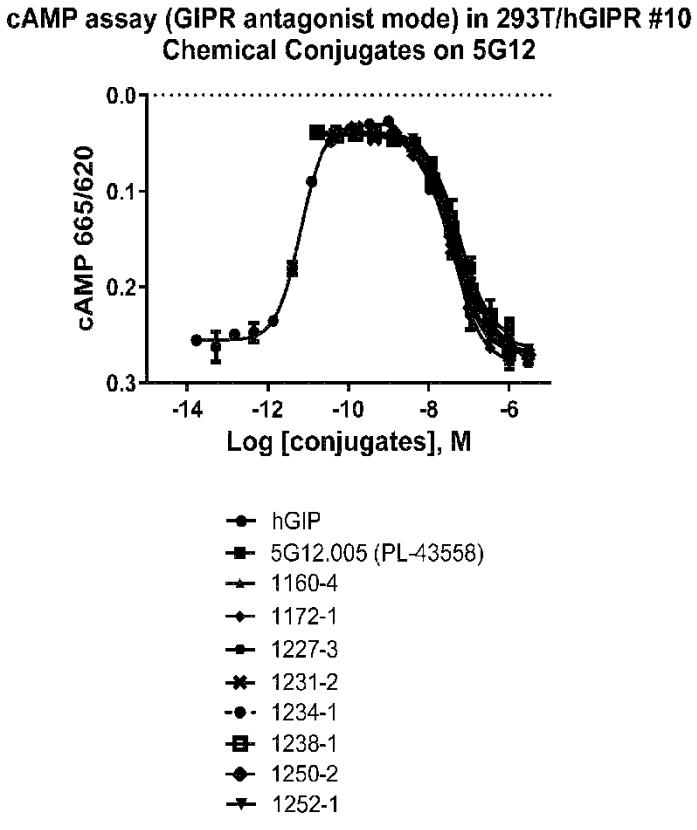

cAMP assay (GIPR antagonist mode) in 293T/hGIPR #10
Chemical Conjugates on 5G12
cAMP 665/620
0.0
0.1
0.2
0.3
-14
-12
-10
-8
-6
Log [conjugates], M
hGIP
5G12.005 (PL-43558)
1160-4
1172-1
1227-3
1231-2
1234-1
1238-1
1250-2
1252-1

FIG. 2O

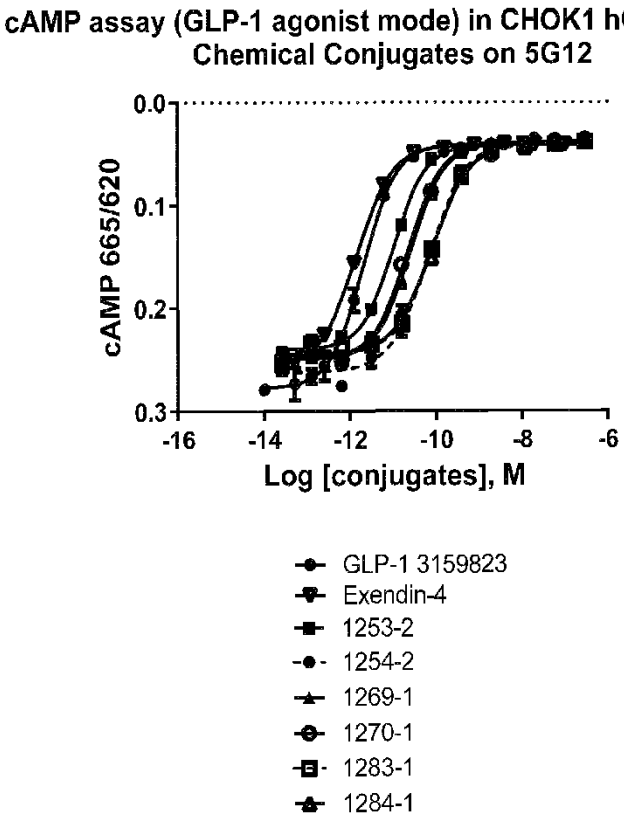

cAMP assay (GLP-1 agonist mode) in CHOK1 hGLP1R H20:
Chemical Conjugates on 5G12
cAMP 665/620
0.0
0.1
0.2
0.3
-16
-14
-12
-10
-8
-6
Log [conjugates], M
GLP-1 3159823
Exendin-4
1253-2
1254-2
1269-1
1270-1
1283-1
1284-1

FIG. 2P

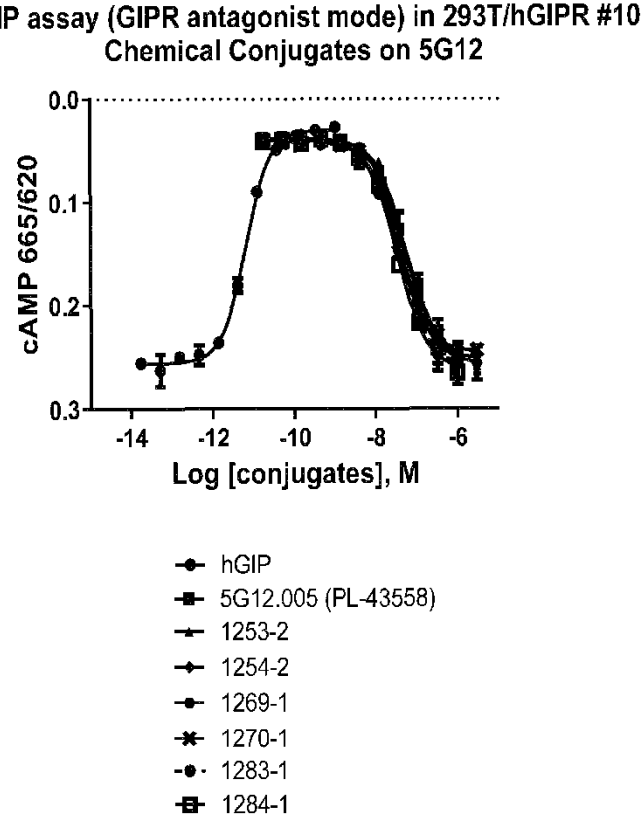

cAMP assay (GIPR antagonist mode) in 293T/hGIPR #10
Chemical Conjugates on 5G12
cAMP 665/620
0.0
0.1
0.2
0.3
-14
-12
-10
-8
-6
Log [conjugates], M
hGIP
5G12.005 (PL-43558)
1253-2
1254-2
1269-1
1270-1
1283-1
1284-1

FIG. 2Q

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

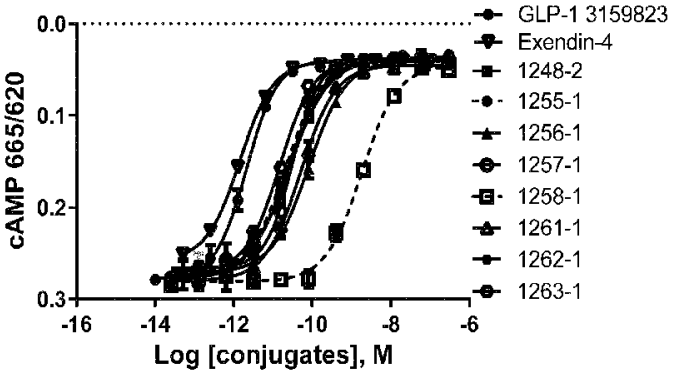


FIG. 2R

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

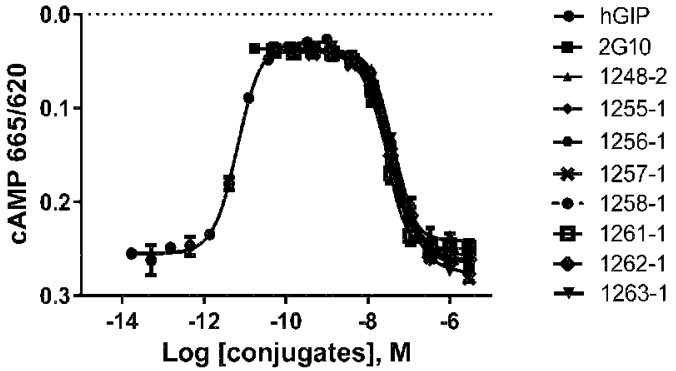


FIG. 2S

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

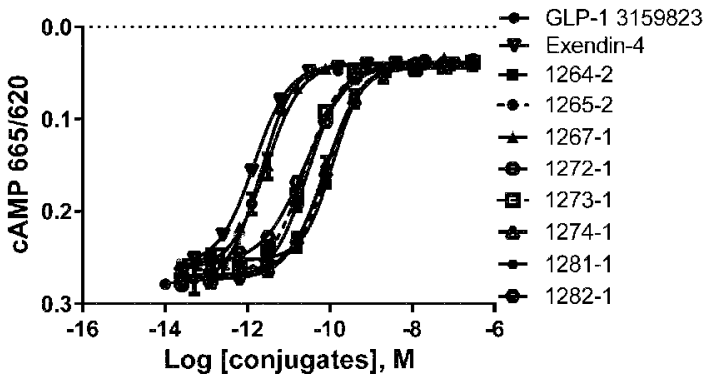


FIG. 2T

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

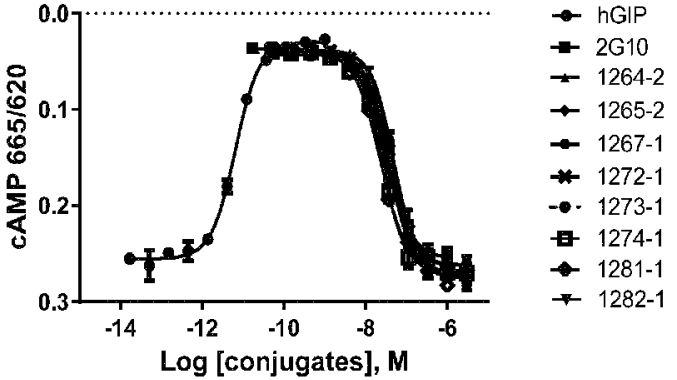
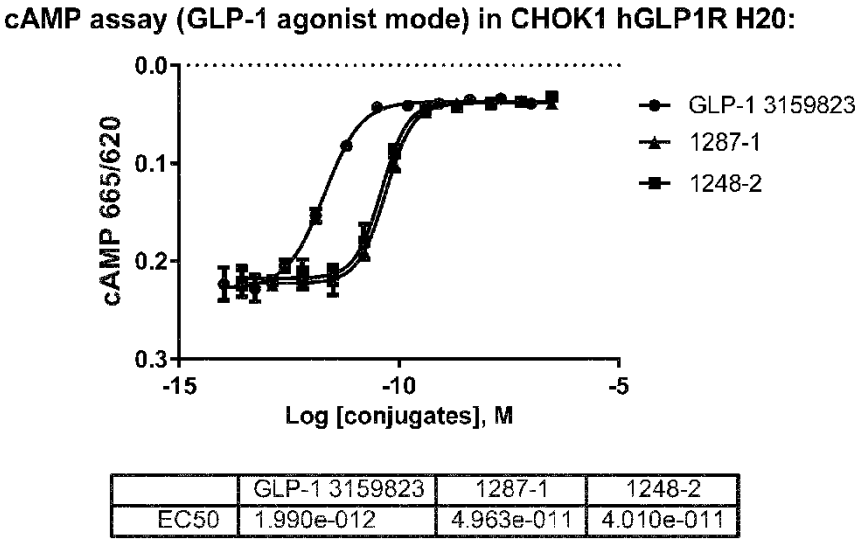


FIG. 3A

Reg #	Description	Peptide information	CHOK1 hGLP-1R	CHOK1 hGLP-1R/GIPR
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

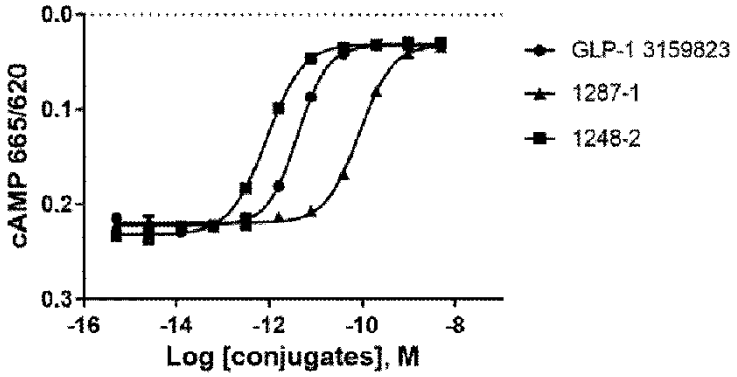
FIG. 3B



	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

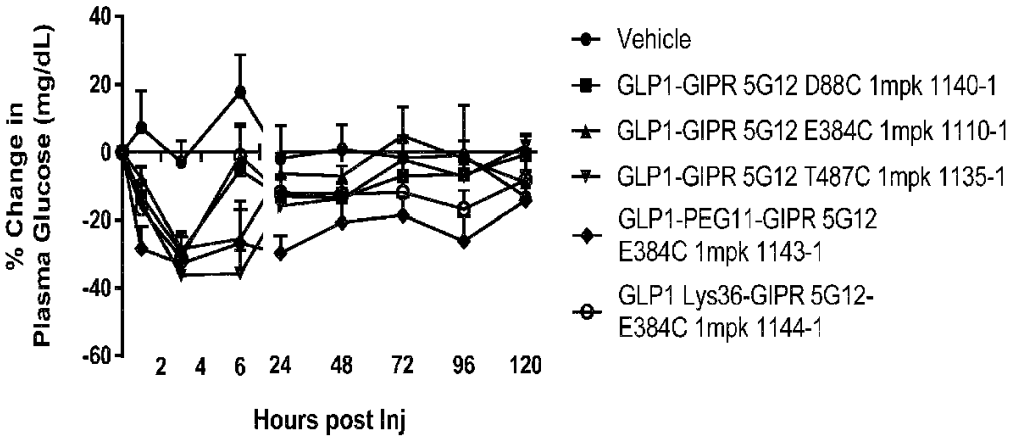

% Change in Plasma Glucose (mg/dL)
40
20
0
-20
-40
-60
2
4
6
24
48
72
96
120
Hours post Inj
Vehicle
GLP1-GIPR 5G12 D88C 1mpk 1140-1
GLP1-GIPR 5G12 E384C 1mpk 1110-1
GLP1-GIPR 5G12 T487C 1mpk 1135-1
GLP1-PEG11-GIPR 5G12 E384C 1mpk 1143-1
GLP1 Lys36-GIPR 5G12-E384C 1mpk 1144-1

FIG. 4B

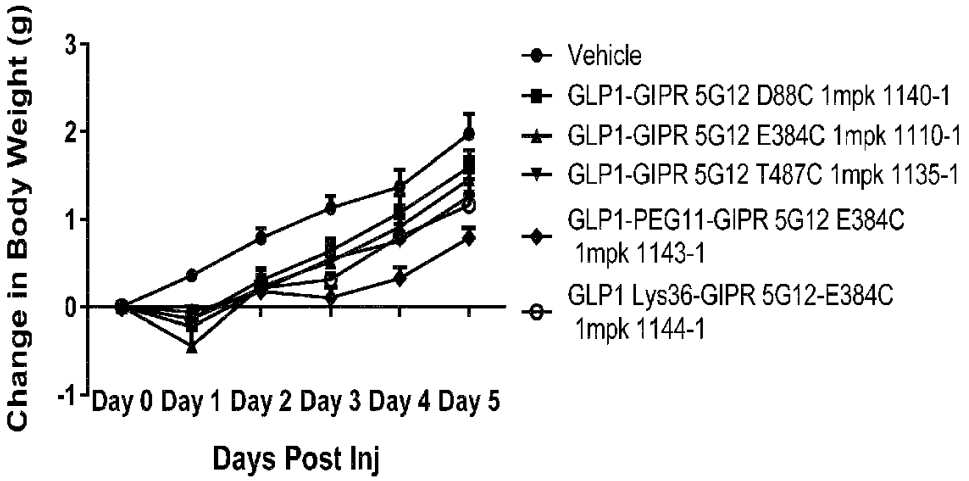

Change in Body Weight (g)
3
2
1
0
-1
Day 0
Day 1
Day 2
Day 3
Day 4
Day 5
Days Post Inj
Vehicle
GLP1-GIPR 5G12 D88C 1mpk 1140-1
GLP1-GIPR 5G12 E384C 1mpk 1110-1
GLP1-GIPR 5G12 T487C 1mpk 1135-1
GLP1-PEG11-GIPR 5G12 E384C 1mpk 1143-1
GLP1 Lys36-GIPR 5G12-E384C 1mpk 1144-1

FIG. 4C

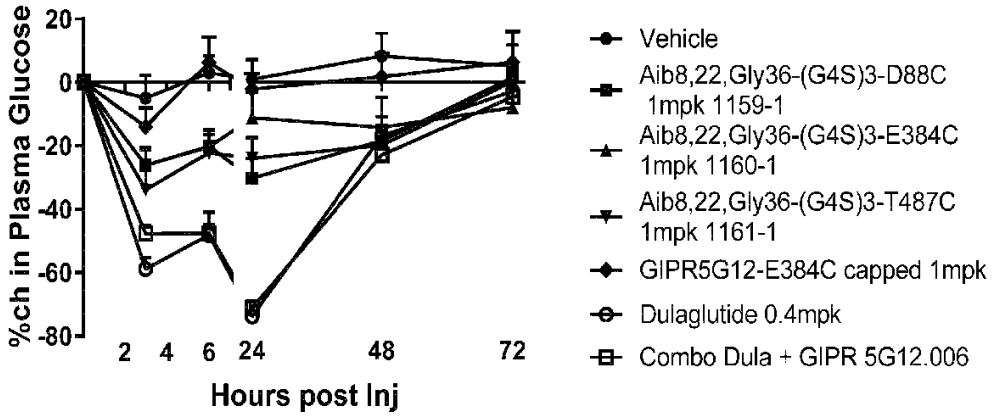

%ch in Plasma Glucose
20
0
-20
-40
-60
-80
2
4
6
24
48
72
Hours post Inj
Vehicle
Aib8,22,Gly36-(G4S)3-D88C 1mpk 1159-1
Aib8,22,Gly36-(G4S)3-E384C 1mpk 1160-1
Aib8,22,Gly36-(G4S)3-T487C 1mpk 1161-1
GIPR5G12-E384C capped 1mpk
Dulaglutide 0.4mpk
Combo Dula + GIPR 5G12.006

FIG. 4D

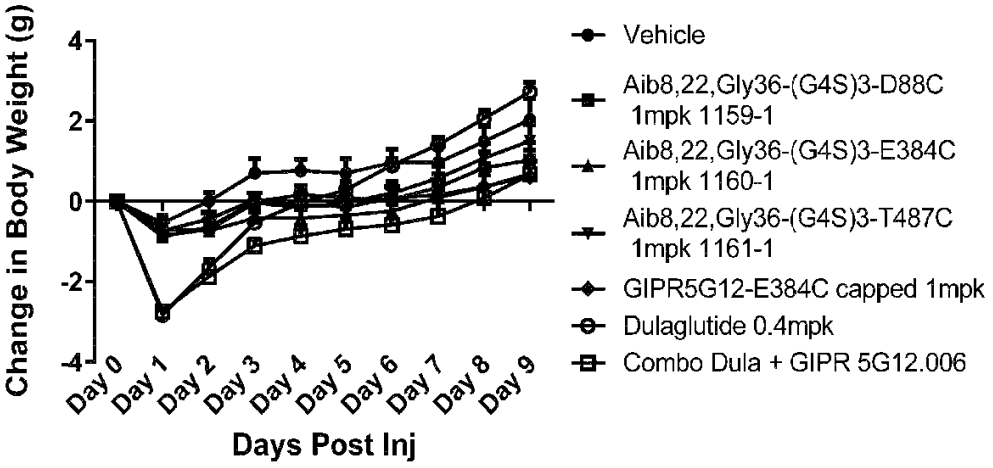

Change in Body Weight (g)
4
2
0
-2
-4
Day 0
Day 1
Day 2
Day 3
Day 4
Day 5
Day 6
Day 7
Day 8
Day 9
Days Post Inj
Vehicle
Aib8,22,Gly36-(G4S)3-D88C 1mpk 1159-1
Aib8,22,Gly36-(G4S)3-E384C 1mpk 1160-1
Aib8,22,Gly36-(G4S)3-T487C 1mpk 1161-1
GIPR5G12-E384C capped 1mpk
Dulaglutide 0.4mpk
Combo Dula + GIPR 5G12.006

FIG. 4E

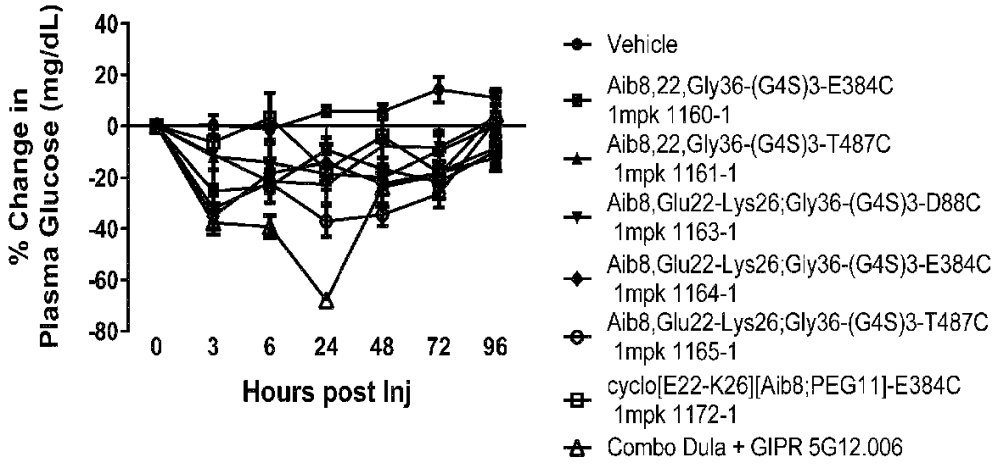

% Change in Plasma Glucose (mg/dL)
40
20
0
-20
-40
-60
-80
0
3
6
24
48
72
96
Hours post Inj
Vehicle
Aib8,22,Gly36-(G4S)3-E384C 1mpk 1160-1
Aib8,22,Gly36-(G4S)3-T487C 1mpk 1161-1
Aib8,Glu22-Lys26;Gly36-(G4S)3-D88C 1mpk 1163-1
Aib8,Glu22-Lys26;Gly36-(G4S)3-E384C 1mpk 1164-1
Aib8,Glu22-Lys26;Gly36-(G4S)3-T487C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

FIG. 4F

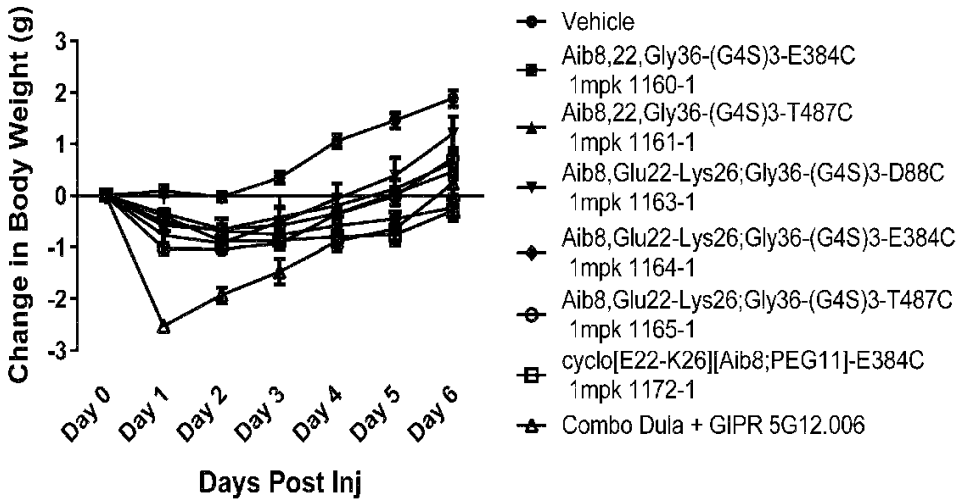

Change in Body Weight (g)
3
2
1
0
-1
-2
-3
Day 0
Day 1
Day 2
Day 3
Day 4
Day 5
Day 6
Days Post Inj
Vehicle
Aib8,22,Gly36-(G4S)3-E384C 1mpk 1160-1
Aib8,22,Gly36-(G4S)3-T487C 1mpk 1161-1
Aib8,Glu22-Lys26;Gly36-(G4S)3-D88C 1mpk 1163-1
Aib8,Glu22-Lys26;Gly36-(G4S)3-E384C 1mpk 1164-1
Aib8,Glu22-Lys26;Gly36-(G4S)3-T487C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

FIG. 4G

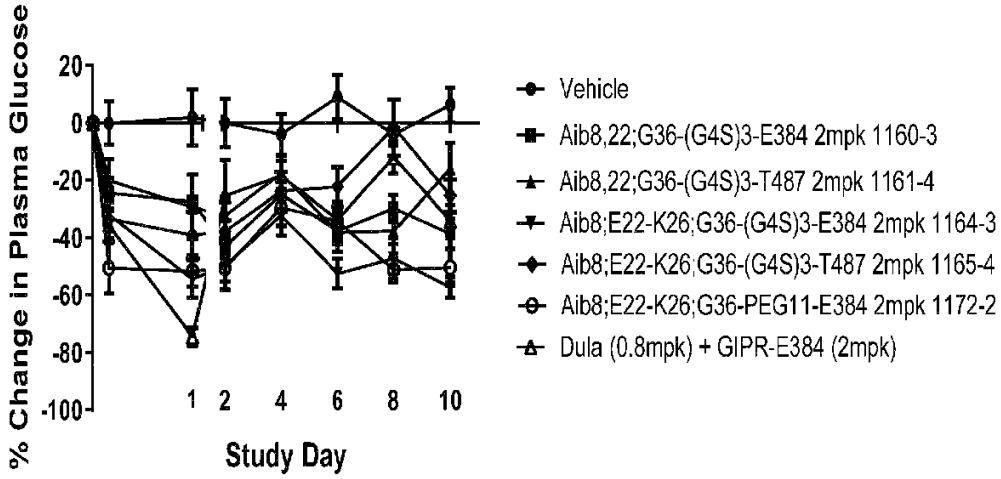

% Change in Plasma Glucose
20
0
-20
-40
-60
-80
-100
1
2
4
6
8
10
Study Day
Vehicle
Aib8,22;G36-(G4S)3-E384 2mpk 1160-3
Aib8,22;G36-(G4S)3-T487 2mpk 1161-4
Aib8;E22-K26;G36-(G4S)3-E384 2mpk 1164-3
Aib8;E22-K26;G36-(G4S)3-T487 2mpk 1165-4
Aib8;E22-K26;G36-PEG11-E384 2mpk 1172-2
Dula (0.8mpk) + GIPR-E384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

FIG. 4H

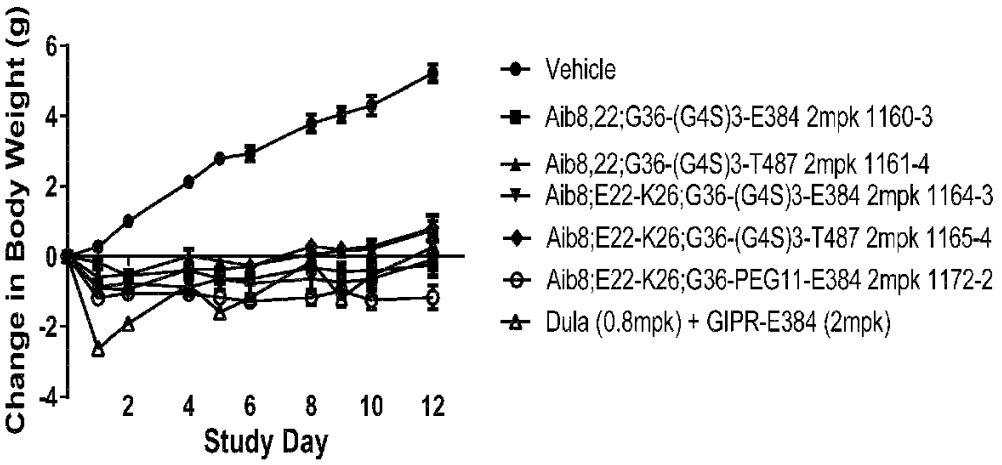

Change in Body Weight (g)
6
4
2
0
-2
-4
2
4
6
8
10
12
Study Day
Vehicle
Aib8,22;G36-(G4S)3-E384 2mpk 1160-3
Aib8,22;G36-(G4S)3-T487 2mpk 1161-4
Aib8;E22-K26;G36-(G4S)3-E384 2mpk 1164-3
Aib8;E22-K26;G36-(G4S)3-T487 2mpk 1165-4
Aib8;E22-K26;G36-PEG11-E384 2mpk 1172-2
Dula (0.8mpk) + GIPR-E384 (2mpk)

FIG. 4I

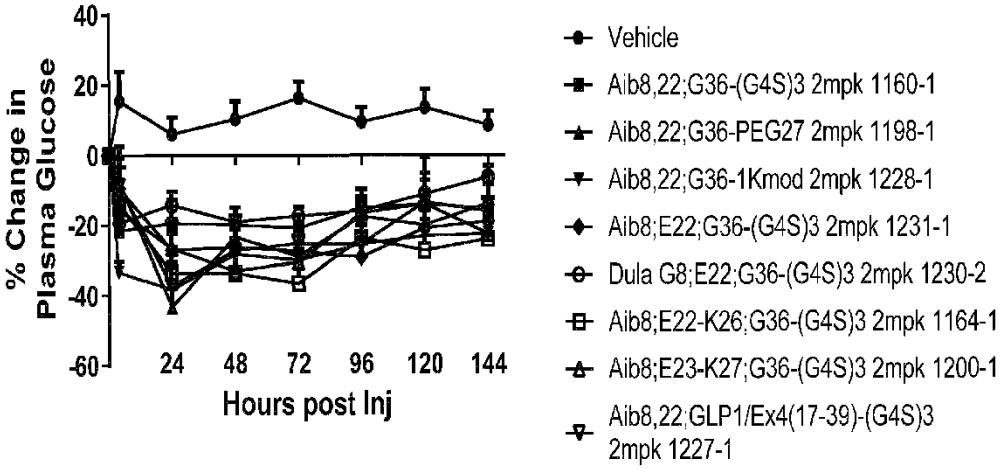

% Change in Plasma Glucose
40
20
0
-20
-40
-60
24
48
72
96
120
144
Hours post Inj
Vehicle
Aib8,22;G36-(G4S)3 2mpk 1160-1
Aib8,22;G36-PEG27 2mpk 1198-1
Aib8,22;G36-1Kmod 2mpk 1228-1
Aib8;E22;G36-(G4S)3 2mpk 1231-1
Dula G8;E22;G36-(G4S)3 2mpk 1230-2
Aib8;E22-K26;G36-(G4S)3 2mpk 1164-1
Aib8;E23-K27;G36-(G4S)3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

FIG. 4J

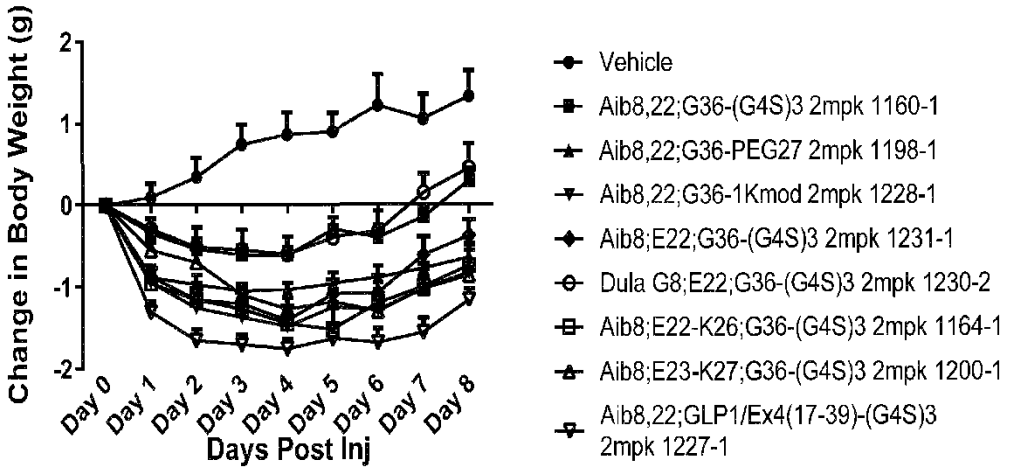

Change in Body Weight (g)
2
1
0
-1
-2
Day 0
Day 1
Day 2
Day 3
Day 4
Day 5
Day 6
Day 7
Day 8
Days Post Inj
Vehicle
Aib8,22;G36-(G4S)3 2mpk 1160-1
Aib8,22;G36-PEG27 2mpk 1198-1
Aib8,22;G36-1Kmod 2mpk 1228-1
Aib8;E22;G36-(G4S)3 2mpk 1231-1
Dula G8;E22;G36-(G4S)3 2mpk 1230-2
Aib8;E22-K26;G36-(G4S)3 2mpk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

FIG. 4K

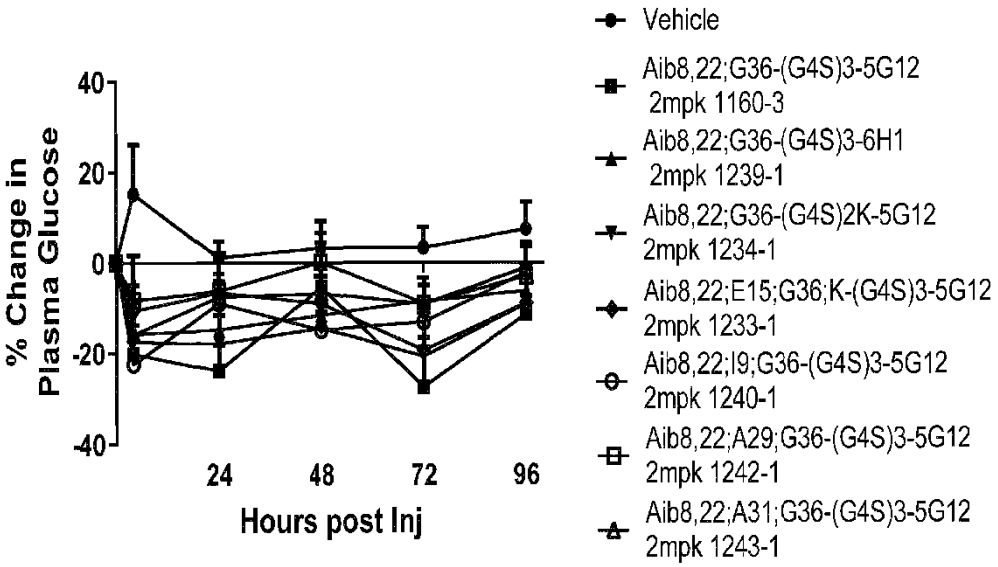

% Change in Plasma Glucose
40
20
0
-20
-40
24
48
72
96
Hours post Inj
Vehicle
Aib8,22;G36-(G4S)3-5G12 2mpk 1160-3
Aib8,22;G36-(G4S)3-6H1 2mpk 1239-1
Aib8,22;G36-(G4S)2K-5G12 2mpk 1234-1
Aib8,22;E15;G36;K-(G4S)3-5G12 2mpk 1233-1
Aib8,22;I9;G36-(G4S)3-5G12 2mpk 1240-1
Aib8,22;A29;G36-(G4S)3-5G12 2mpk 1242-1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

FIG. 4L

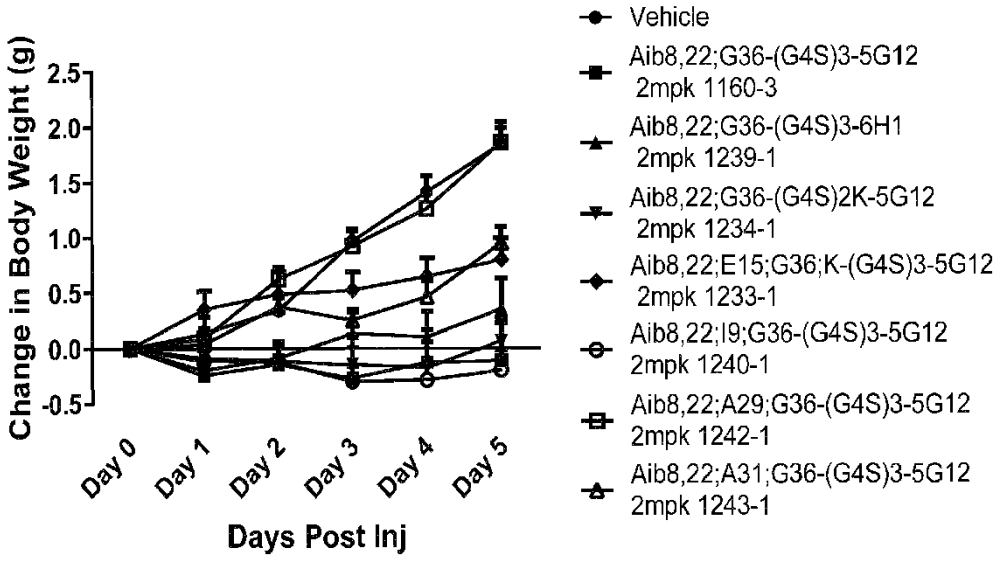

Change in Body Weight (g)
2.5
2.0
1.5
1.0
0.5
0.0
-0.5
Day 0
Day 1
Day 2
Day 3
Day 4
Day 5
Days Post Inj
Vehicle
Aib8,22;G36-(G4S)3-5G12 2mpk 1160-3
Aib8,22;G36-(G4S)3-6H1 2mpk 1239-1
Aib8,22;G36-(G4S)2K-5G12 2mpk 1234-1
Aib8,22;E15;G36;K-(G4S)3-5G12 2mpk 1233-1
Aib8,22;I9;G36-(G4S)3-5G12 2mpk 1240-1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

FIG. 4M

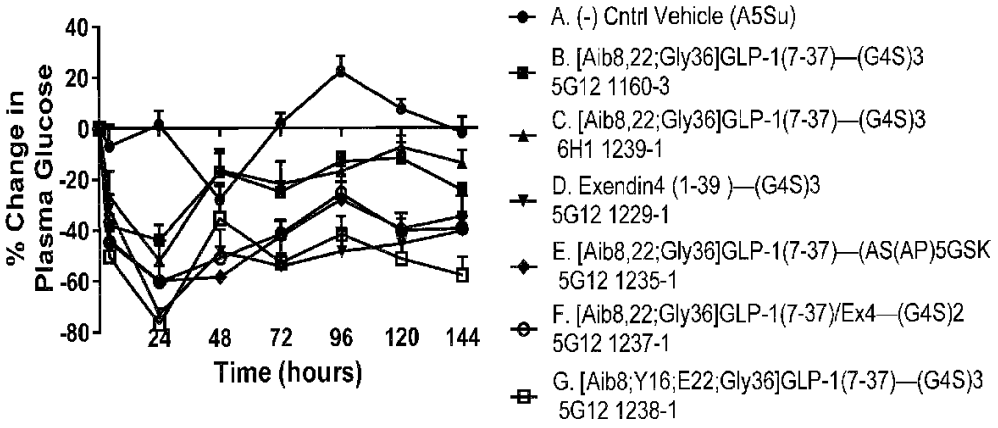

% Change in Plasma Glucose
40
20
0
-20
-40
-60
-80
24
48
72
96
120
144
Time (hours)
A. (-) Cntrl Vehicle (A5Su)
B. [Aib8,22;Gly36]GLP-1(7-37)—(G4S)3 5G12 1160-3
C. [Aib8,22;Gly36]GLP-1(7-37)—(G4S)3 6H1 1239-1
D. Exendin4 (1-39)—(G4S)3 5G12 1229-1
E. [Aib8,22;Gly36]GLP-1(7-37)—(AS(AP)5GSK 5G12 1235-1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

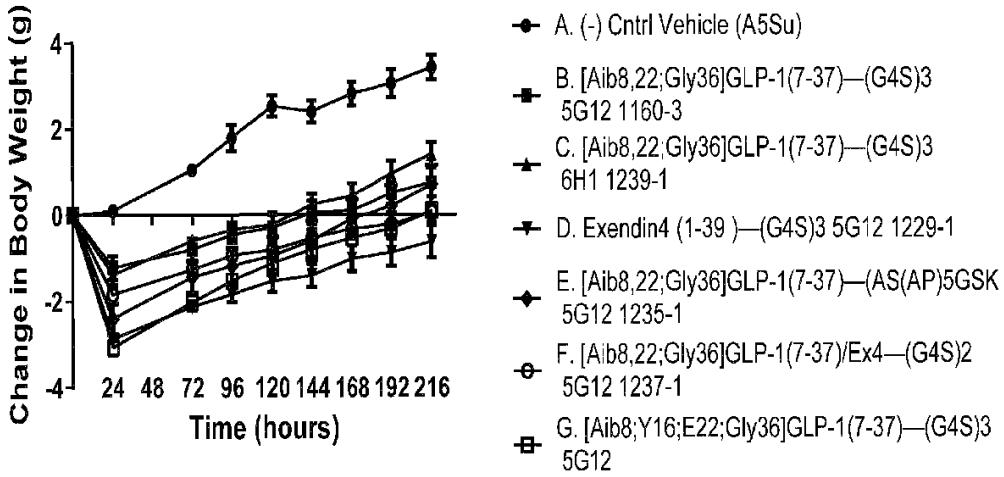

Change in Body Weight (g)
4
2
0
-2
-4
24
48
72
96
120
144
168
192
216
Time (hours)
A. (-) Cntrl Vehicle (A5Su)
B. [Aib8,22;Gly36]GLP-1(7-37)—(G4S)3 5G12 1160-3
C. [Aib8,22;Gly36]GLP-1(7-37)—(G4S)3 6H1 1239-1
D. Exendin4 (1-39)—(G4S)3 5G12 1229-1
E. [Aib8,22;Gly36]GLP-1(7-37)—(AS(AP)5GSK 5G12 1235-1
F.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

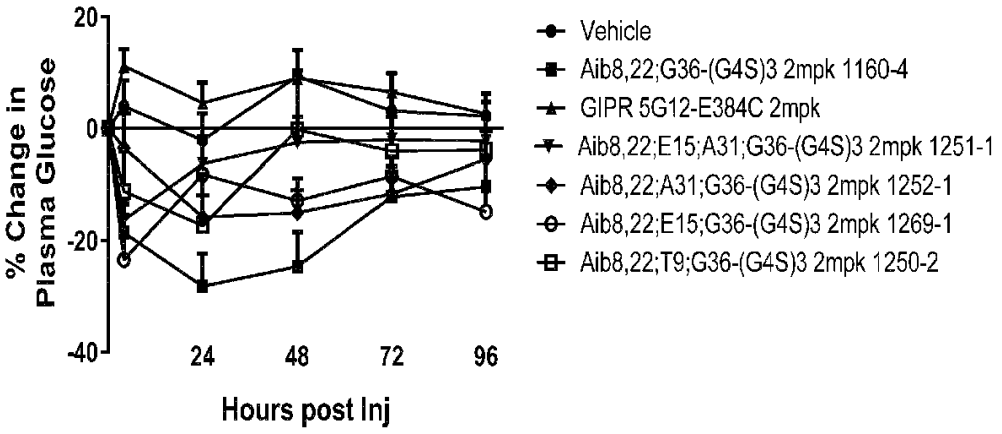

20
0
-20
-40
% Change in Plasma Glucose
24
48
72
96
Hours post Inj
Vehicle
Aib8,22;G36-(G4S)3 2mpk 1160-4
GIPR 5G12-E384C 2mpk
Aib8,22;E15;A31;G36-(G4S)3 2mpk 1251-1
Aib8,22;A31;G36-(G4S)3 2mpk 1252-1
Aib8,22;E15;G36-(G4S)3 2mpk 1269-1
Aib8,22;T9;G36-(G4S)3 2mpk 1250-2

FIG. 4P

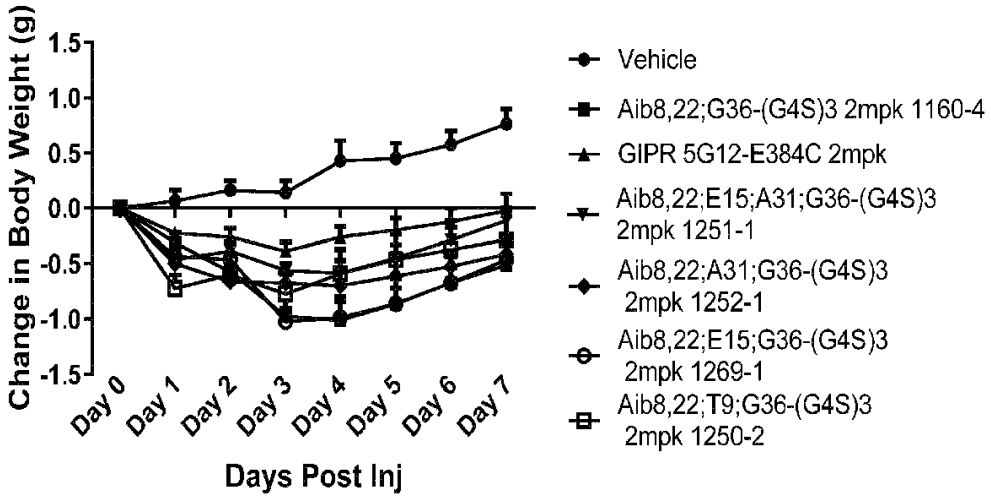

1.5
1.0
0.5
0.0
-0.5
-1.0
-1.5
Change in Body Weight (g)
Day 0
Day 1
Day 2
Day 3
Day 4
Day 5
Day 6
Day 7
Days Post Inj
Vehicle
Aib8,22;G36-(G4S)3 2mpk 1160-4
GIPR 5G12-E384C 2mpk
Aib8,22;E15;A31;G36-(G4S)3 2mpk 1251-1
Aib8,22;A31;G36-(G4S)3 2mpk 1252-1
Aib8,22;E15;G36-(G4S)3 2mpk 1269-1
Aib8,22;T9;G36-(G4S)3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

FIG. 4Q

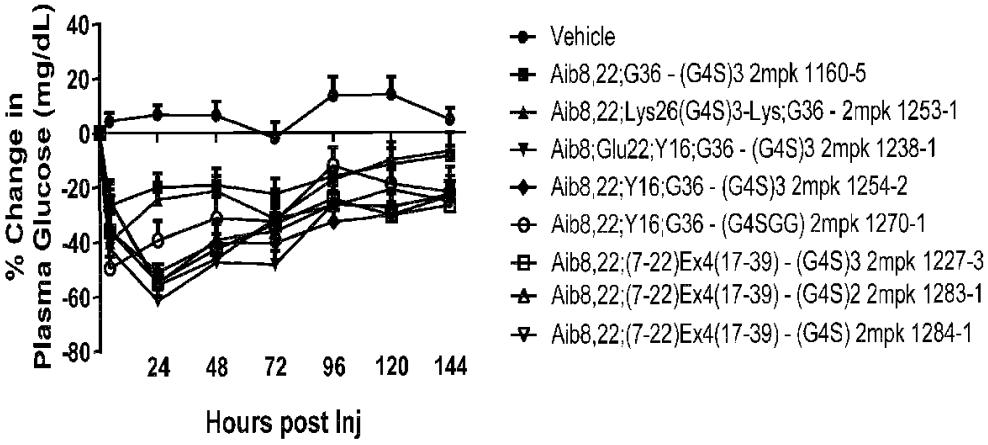

% Change in Plasma Glucose (mg/dL)
40
20
0
-20
-40
-60
-80
24
48
72
96
120
144
Hours post Inj
Vehicle
Aib8,22;G36 - (G4S)3 2mpk 1160-5
Aib8,22;Lys26(G4S)3-Lys;G36 - 2mpk 1253-1
Aib8;Glu22;Y16;G36 - (G4S)3 2mpk 1238-1
Aib8,22;Y16;G36 - (G4S)3 2mpk 1254-2
Aib8,22;Y16;G36 - (G4SGG) 2mpk 1270-1
Aib8,22;(7-22)Ex4(17-39)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

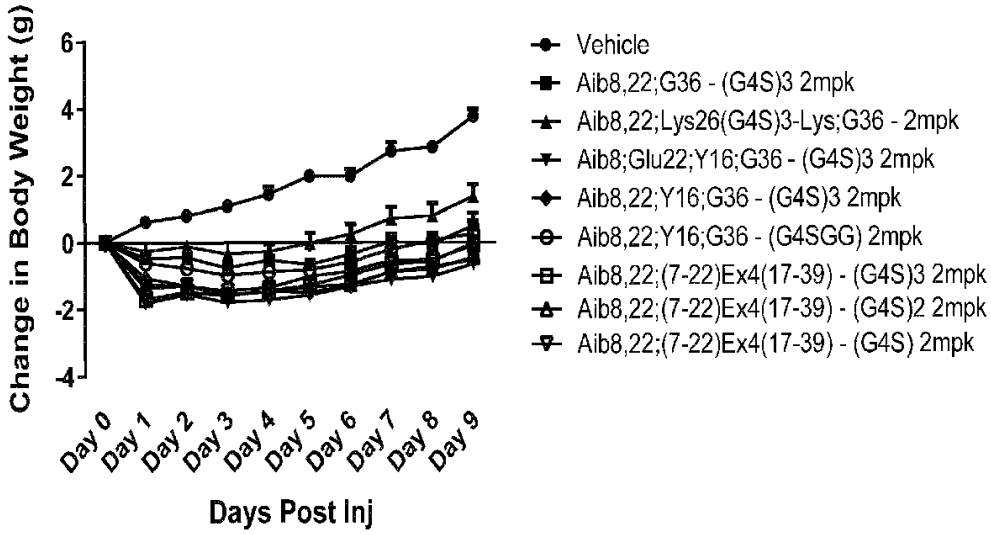

Change in Body Weight (g)
6
4
2
0
-2
-4
Day 0
Day 1
Day 2
Day 3
Day 4
Day 5
Day 6
Day 7
Day 8
Day 9
Days Post Inj
Vehicle
Aib8,22;G36 - (G4S)3 2mpk
Aib8,22;Lys26(G4S)3-Lys;G36 - 2mpk
Aib8;Glu22;Y16;G36 - (G4S)3 2mpk
Aib8,22;Y16;G36 - (G4S)3 2mpk
Aib8,22;Y16;G36 - (G4SGG) 2mpk
Aib8,22;(7-22)Ex4(17-39)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

FIG. 5A

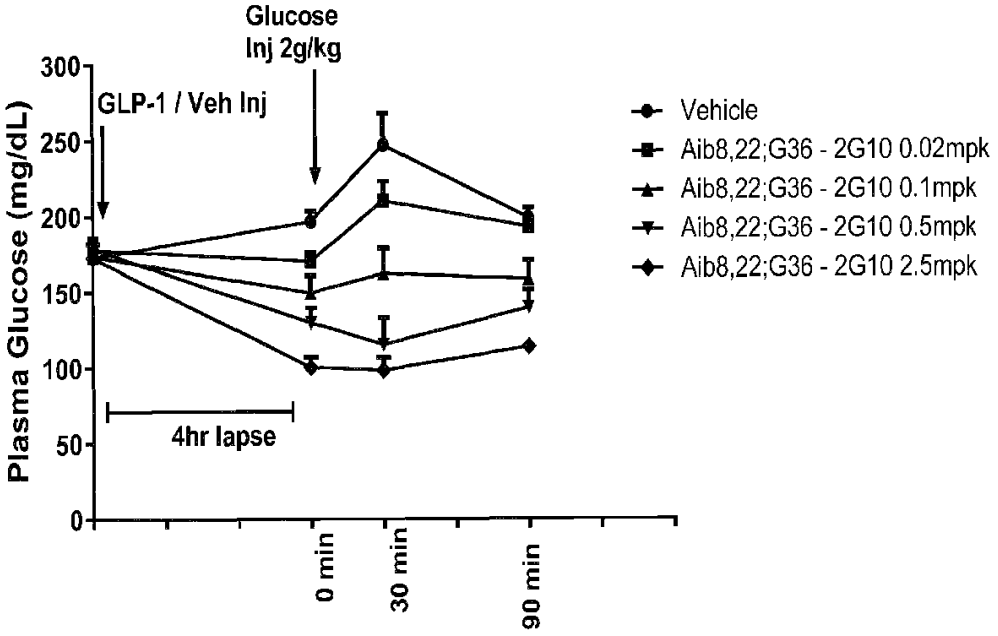

Glucose
Inj 2g/kg
GLP-1 / Veh Inj
Plasma Glucose (mg/dL)
300
250
200
150
100
50
0
4hr lapse
0 min
30 min
90 min
Vehicle
Aib8,22;G36 - 2G10 0.02mpk
Aib8,22;G36 - 2G10 0.1mpk
Aib8,22;G36 - 2G10 0.5mpk
Aib8,22;G36 - 2G10 2.5mpk

FIG. 5B

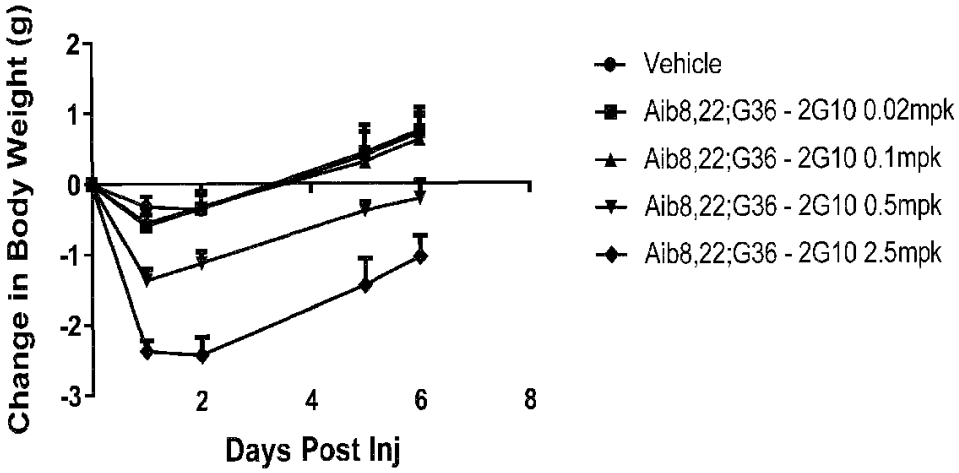

Change in Body Weight (g)
2
1
0
-1
-2
-3
2
4
6
8
Days Post Inj
Vehicle
Aib8,22;G36 - 2G10 0.02mpk
Aib8,22;G36 - 2G10 0.1mpk
Aib8,22;G36 - 2G10 0.5mpk
Aib8,22;G36 - 2G10 2.5mpk

FIG. 5C

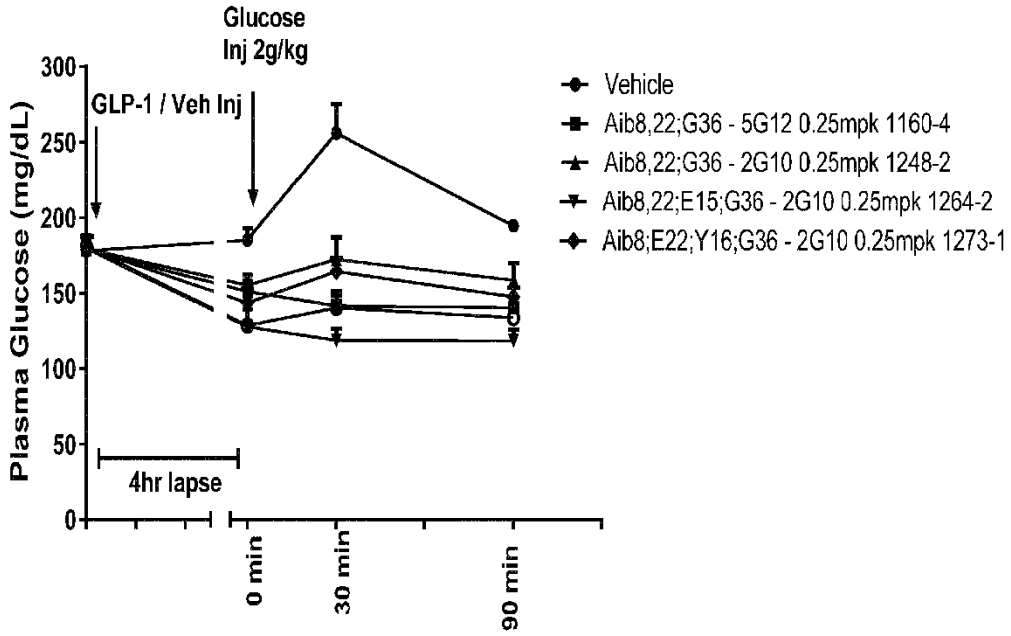

Glucose
Inj 2g/kg
GLP-1 / Veh Inj
Plasma Glucose (mg/dL)
300
250
200
150
100
50
0
4hr lapse
0 min
30 min
90 min
Vehicle
Aib8,22;G36 - 5G12 0.25mpk 1160-4
Aib8,22;G36 - 2G10 0.25mpk 1248-2
Aib8,22;E15;G36 - 2G10 0.25mpk 1264-2
Aib8;E22;Y16;G36 - 2G10 0.25mpk 1273-1

FIG. 5D

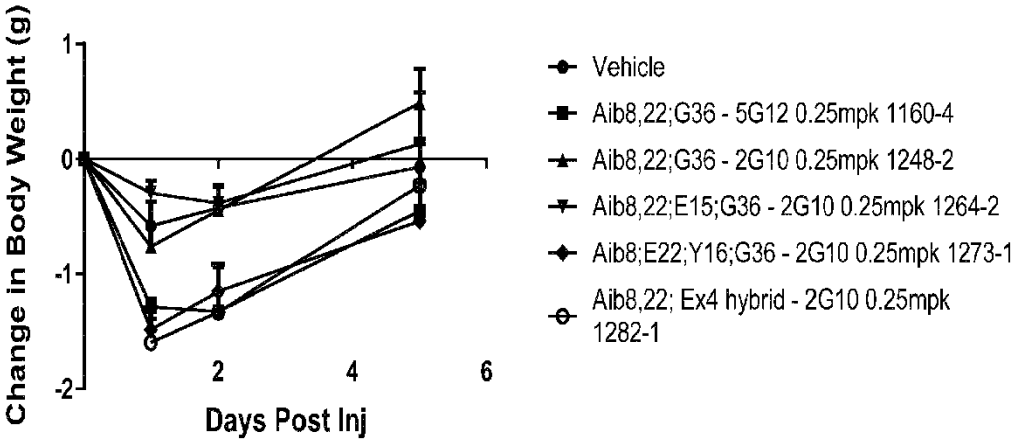

Change in Body Weight (g)
1
0
-1
-2
2
4
6
Days Post Inj
Vehicle
Aib8,22;G36 - 5G12 0.25mpk 1160-4
Aib8,22;G36 - 2G10 0.25mpk 1248-2
Aib8,22;E15;G36 - 2G10 0.25mpk 1264-2
Aib8;E22;Y16;G36 - 2G10 0.25mpk 1273-1
Aib8,22; Ex4 hybrid - 2G10 0.25mpk 1282-1

FIG. 6A

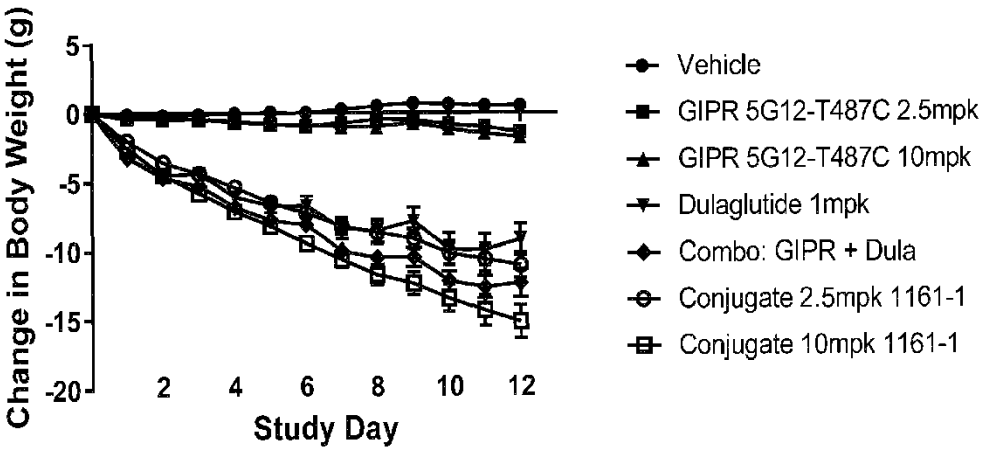

Change in Body Weight (g)
5
0
-5
-10
-15
-20
2
4
6
8
10
12
Study Day
Vehicle
GIPR 5G12-T487C 2.5mpk
GIPR 5G12-T487C 10mpk
Dulaglutide 1mpk
Combo: GIPR + Dula
Conjugate 2.5mpk 1161-1
Conjugate 10mpk 1161-1

FIG. 6B

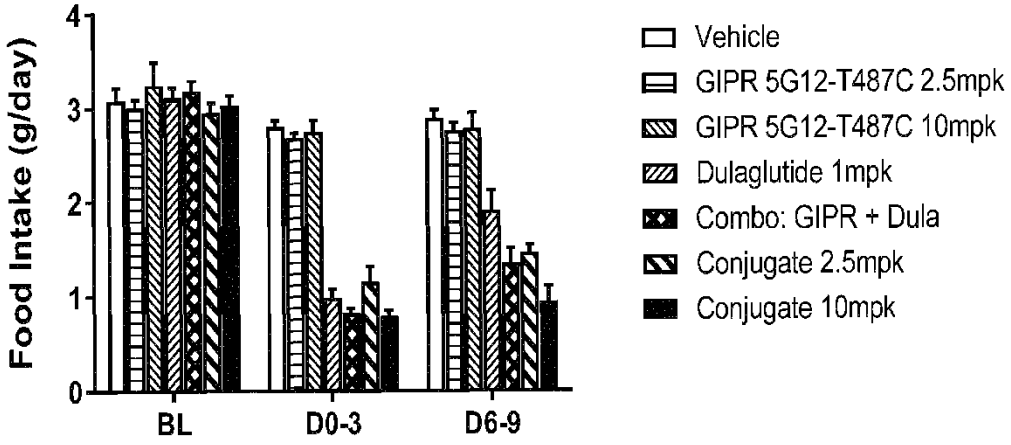
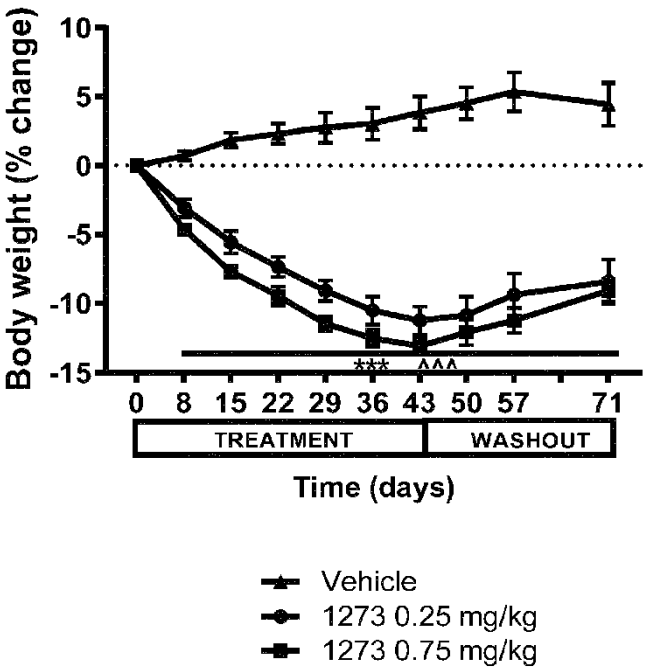
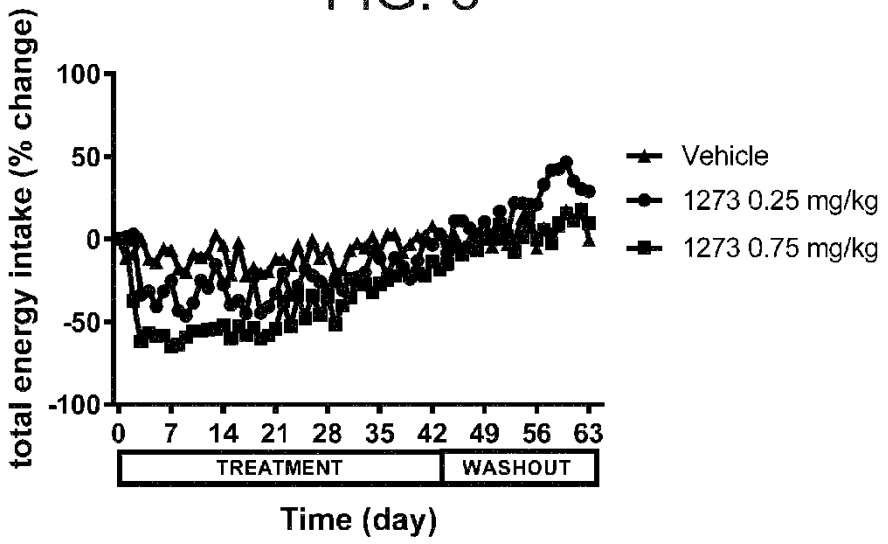

Food Intake (g/day)
4
3
2
1
0
BL
D0-3
D6-9
Vehicle
GIPR 5G12-T487C 2.5mpk
GIPR 5G12-T487C 10mpk
Dulaglutide 1mpk
Combo: GIPR + Dula
Conjugate 2.5mpk
Conjugate 10mpk

FIG. 7



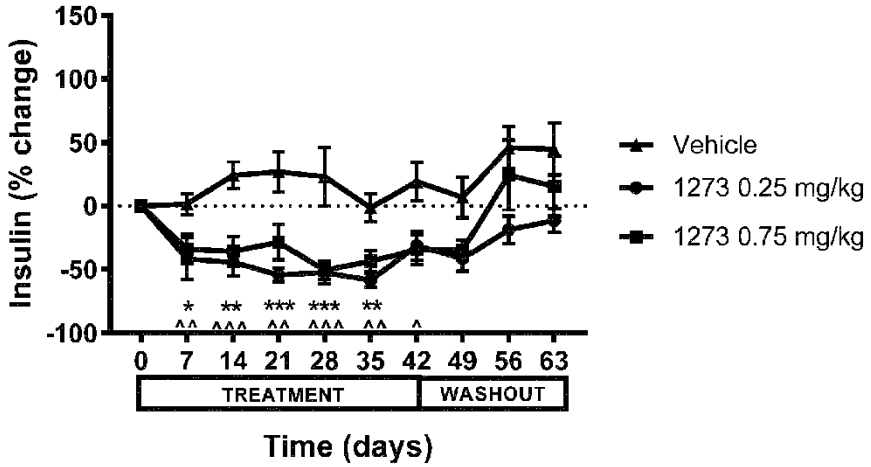
ANCOVA; ***p<0.001 vs vehicle for 0.25 mg/kg; ^^^p<0.001 vs vehicle for 0.75 mg/kg
Data represented as group mean ± SEM; n=8-9/group

FIG. 8



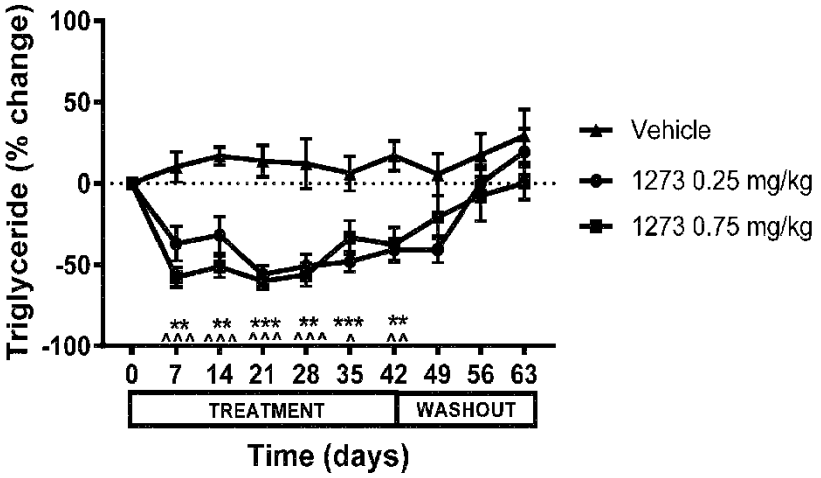
Statistical analysis not performed on total energy intake; error bars not shown; data represented as group mean; n=8-9/group

FIG. 9



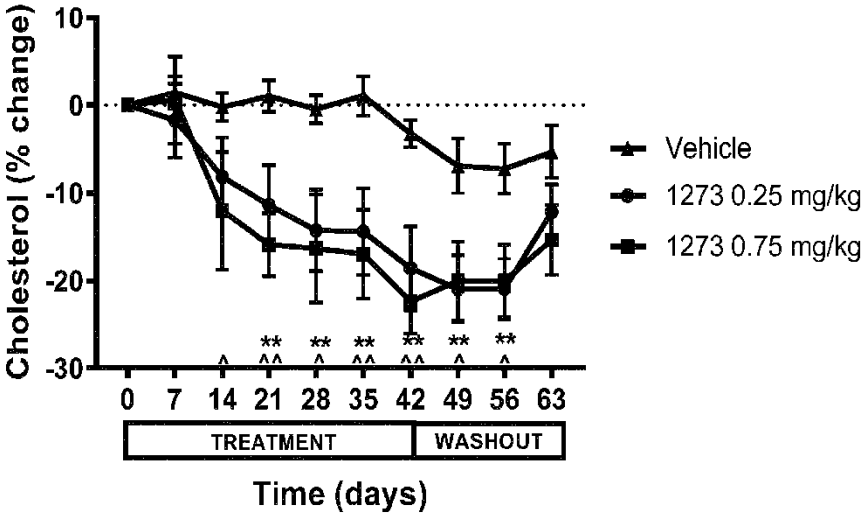
ANCOVA; *p<0.05, **p<0.01, ***p<0.001 vs vehicle for 0.25 mg/kg; ^p<0.05, ^^p<0.01, ^^^p<0.001 vs vehicle for 0.75 mg/kg Data represented as group mean ± SEM; n=8-9/group

FIG. 10



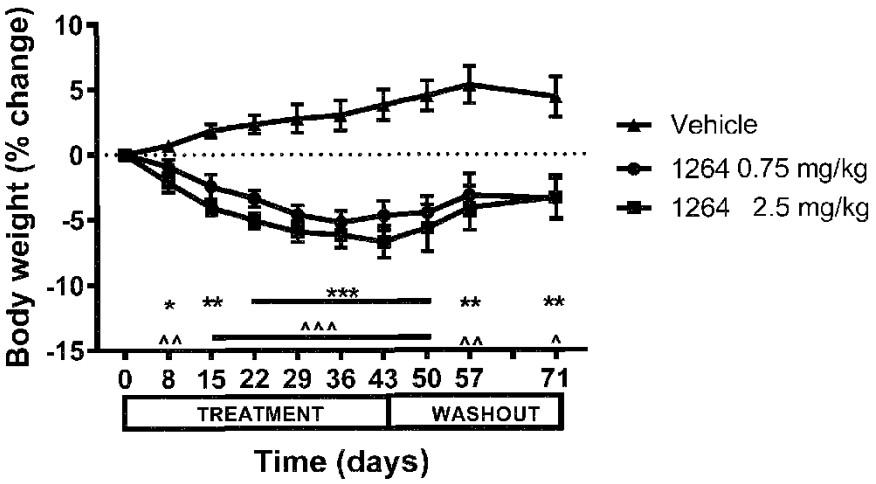
ANCOVA; **p<0.01, ***p<0.001 vs vehicle for 0.25 mg/kg; ^p<0.05, ^^p<0.01, ^^^p<0.001 vs vehicle or 0.75 mg/kg Data represented as group mean ± SEM; n=8-9/group

FIG. 11



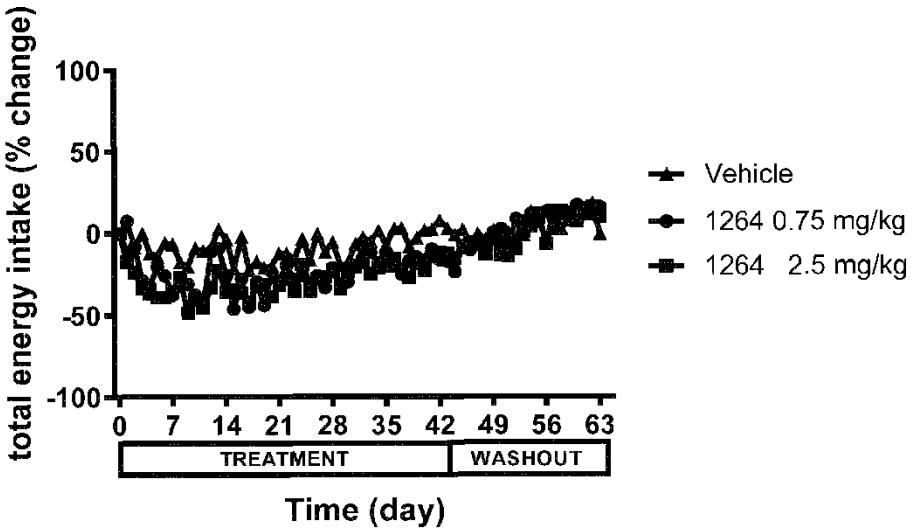
ANCOVA; **p<0.01 vs vehicle for 0.25 mg/kg; ^p<0.05, ^^p<0.01 vs vehicle for 0.75 mg/kg Data represented as group mean ± SEM; n=8-9/group

FIG. 12



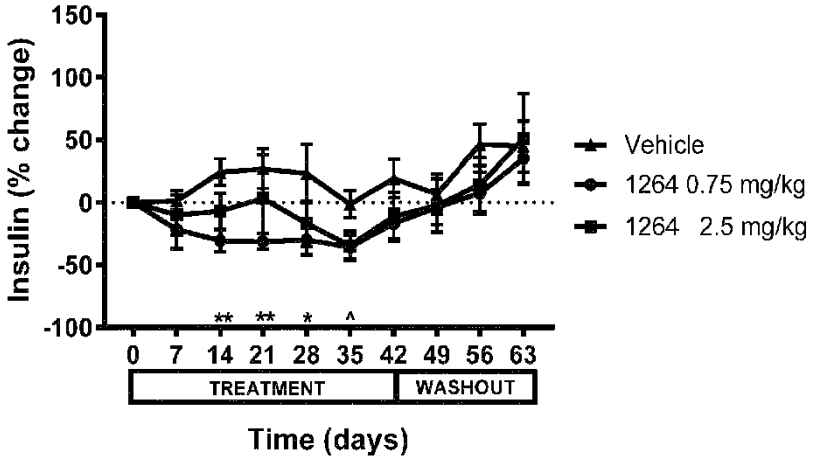
ANCOVA; *p<0.05, **p<0.01, ***p<0.001 vs vehicle for 0.75 mg/kg; ^p<0.05, ^^p<0.01, ^^^p<0.001 vs vehicle for 2.5 mg/kg Data represented as group mean ± SEM; n=9/group

FIG. 13



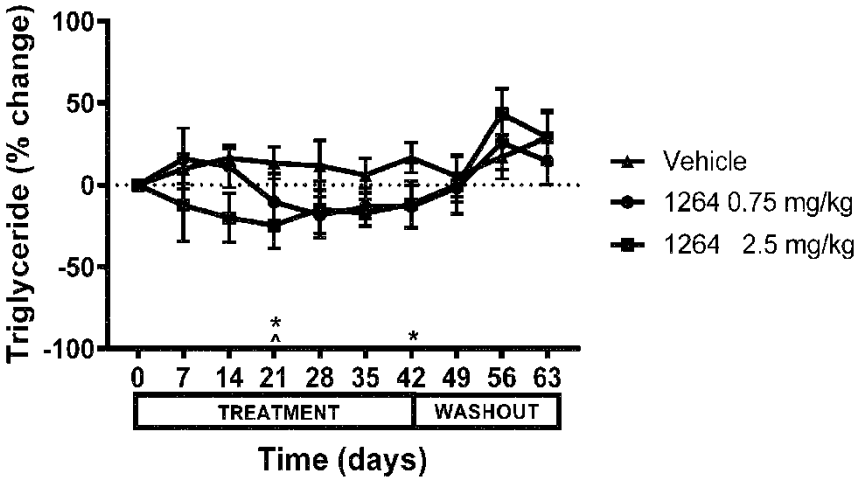
Statistical analysis not performed on total energy intake; error bars not shown; data represented as group mean; n=9/group

FIG. 14



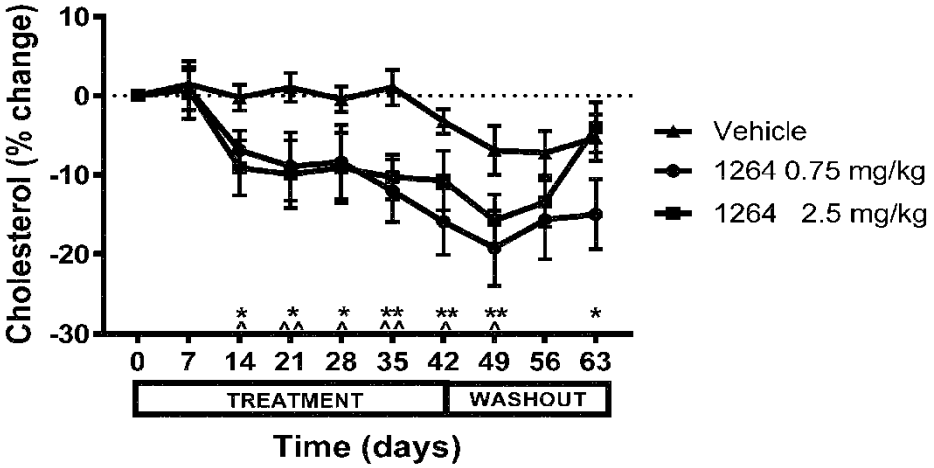
ANCOVA; *p<0.05, **p<0.01 vs vehicle for 0.75 mg/kg; ^p<0.05 vs vehicle for 2.5 mg/kg
Data represented as group mean ± SEM; n=9/group

FIG. 15



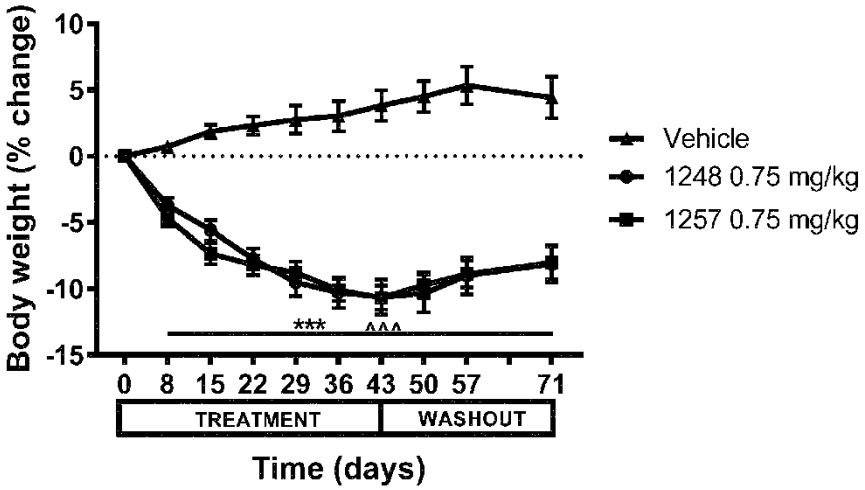
ANCOVA; *p<0.05 vs vehicle for 0.75 mg/kg; ^p<0.05 vs vehicle for 2.5 mg/kg
Data represented as group mean ± SEM; n=9/group

FIG. 16



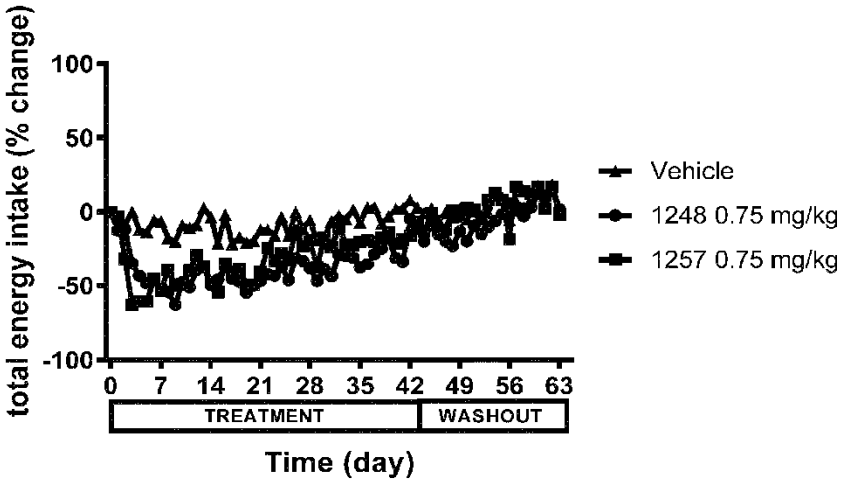
ANCOVA; *p<0.05, **p<0.01 vs vehicle for 0.75 mg/kg; ^p<0.05, ^^p<0.01 vs vehicle for 2.5 mg/kg Data represented as group mean ± SEM; n=9/group

FIG. 17



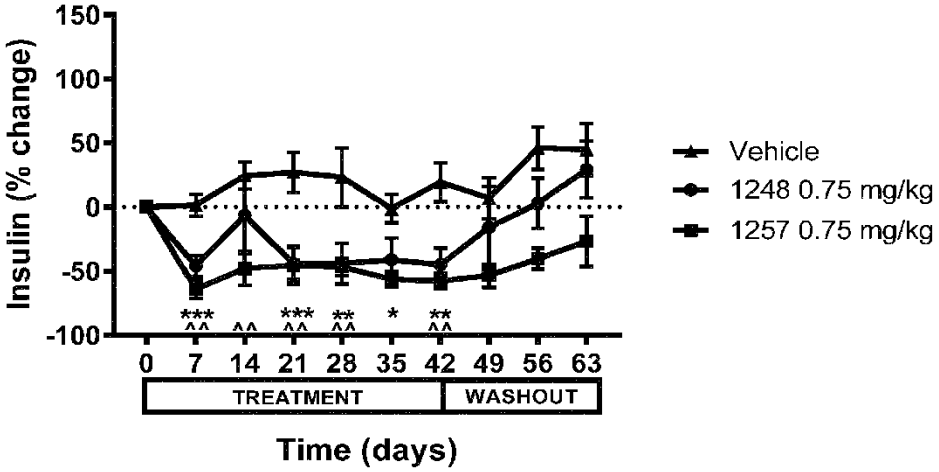
ANCOVA; ***p<0.001 vs vehicle for 1248 0.75 mg/kg; ^^^p<0.001 vs vehicle for 1257 0.75 mg/kg Data represented as group mean ± SEM; n=7-10/group

FIG. 18



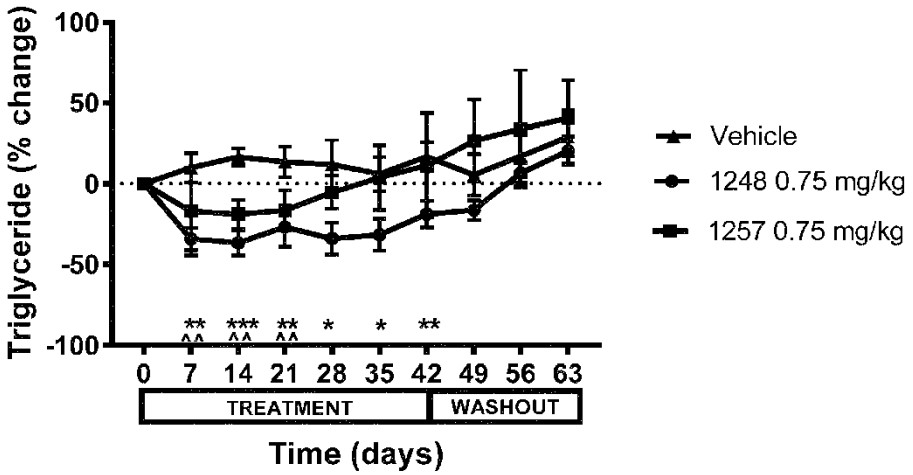
ANCOVA; ***p<0.001 vs vehicle for 1248 0.75 mg/kg; ^^^p<0.001 vs vehicle for 1257 0.75 mg/kgData represented as group mean ± SEM; n=7-10/group

FIG. 19



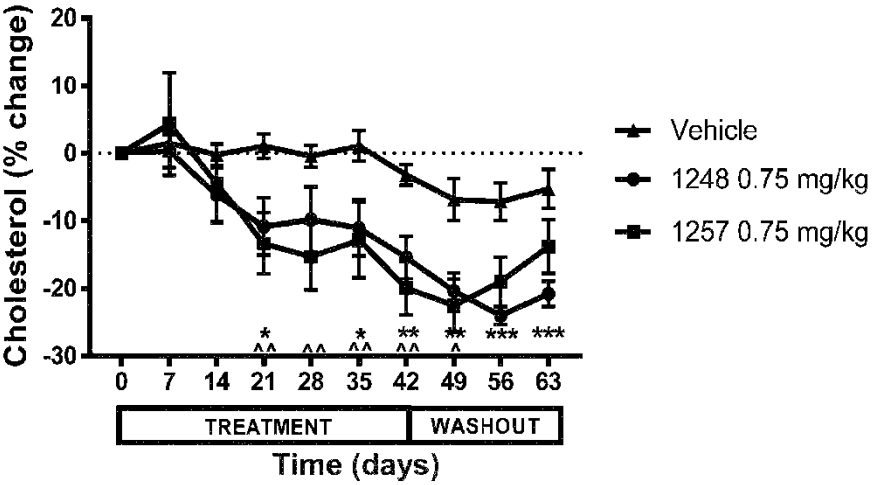
ANCOVA; *p<0.05, **p<0.01, ***p<0.001 vs vehicle for 1248 0.75 mg/kg; ^^p<0.01 vs vehicle for 1257 0.75 mg/kg
Data represented as group mean ± SEM; n=7-10/group

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

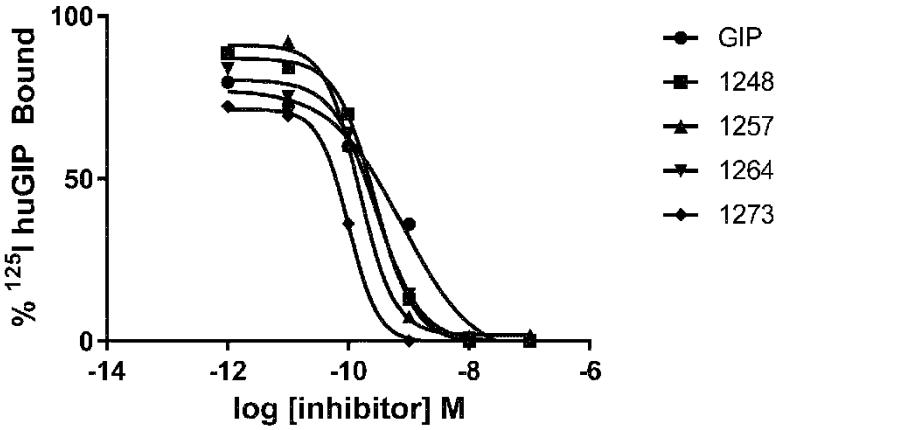
FIG. 21



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

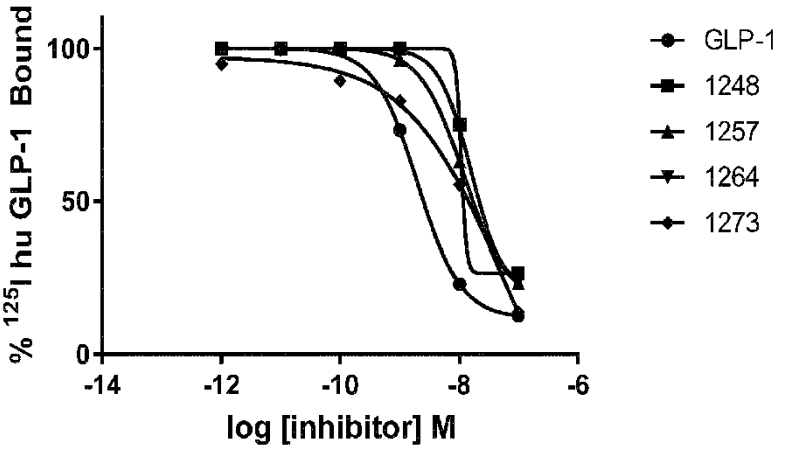
^{125}I huGIP Radioligand Binding Assay



	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

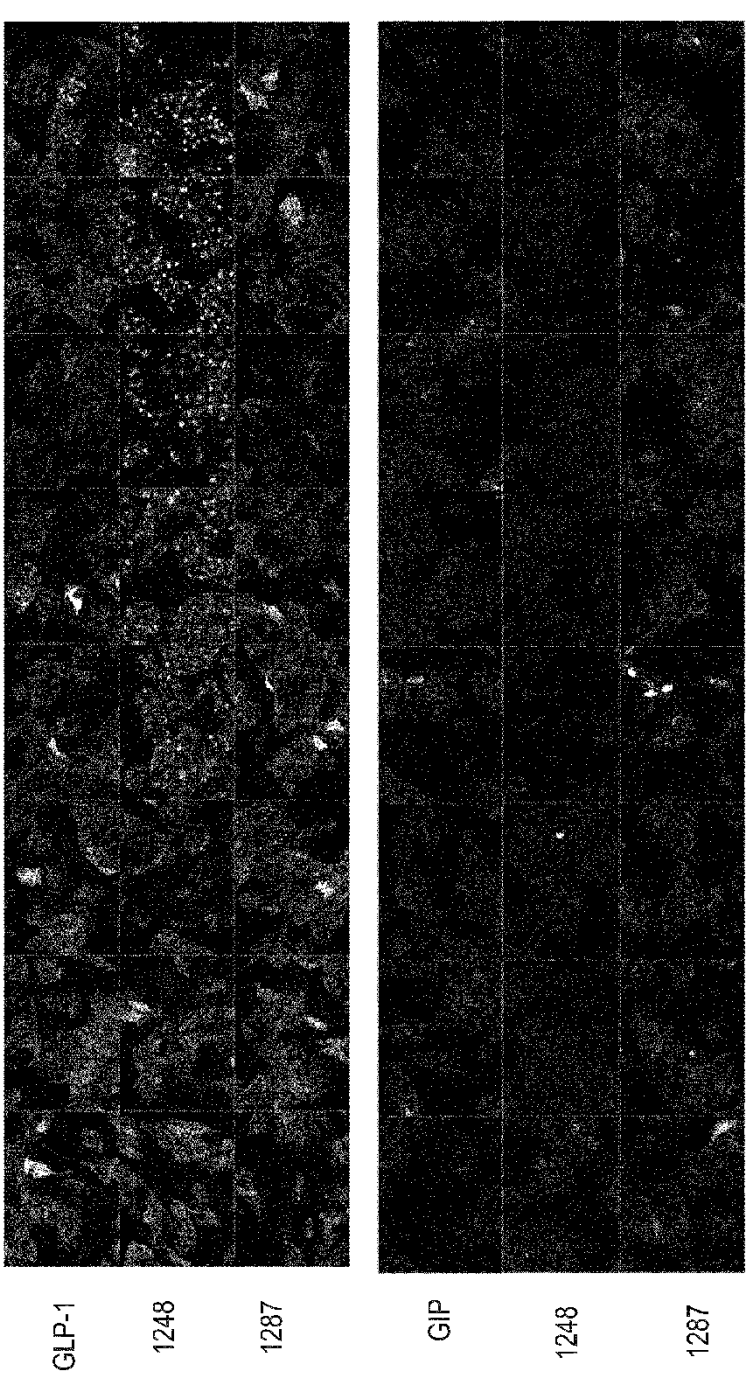


FIG. 24A

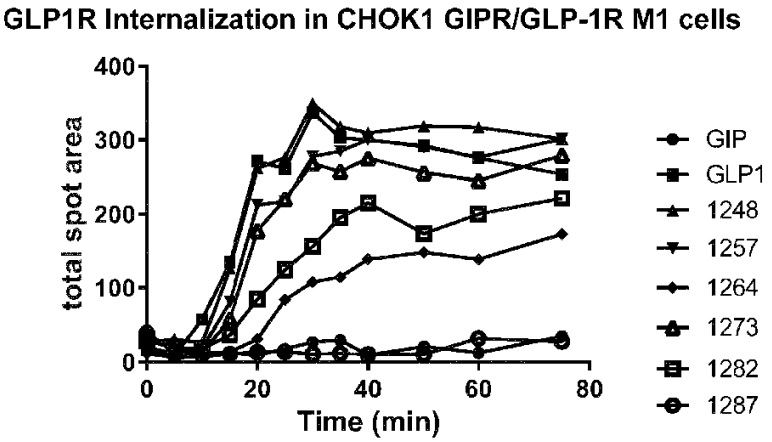
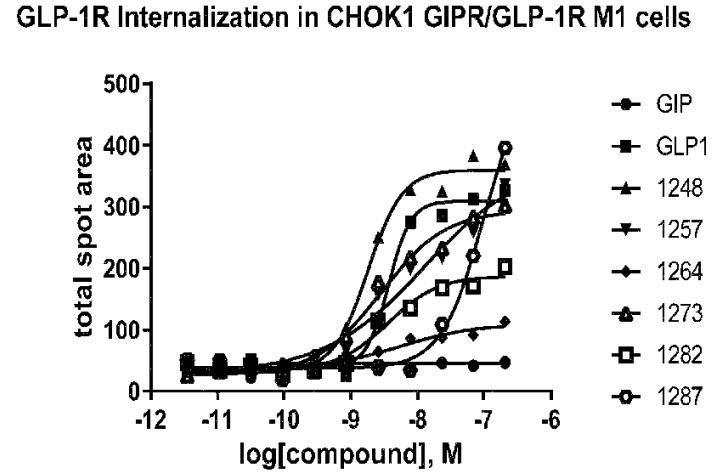


FIG. 24B



	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

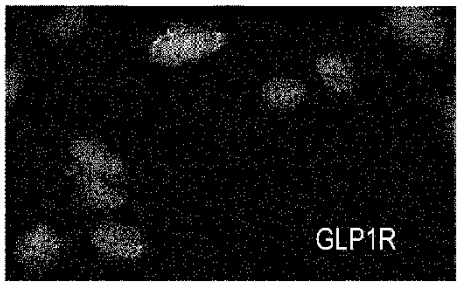


FIG. 25B

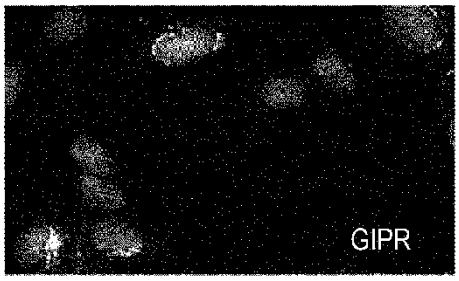


FIG. 25C

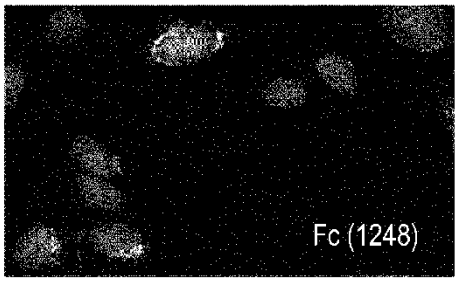


FIG. 25D

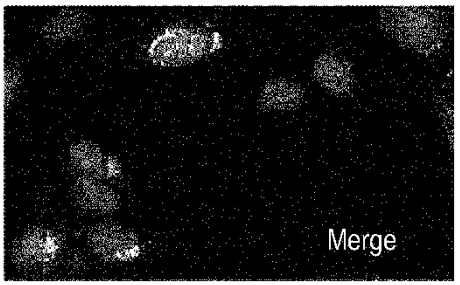


FIG. 26A

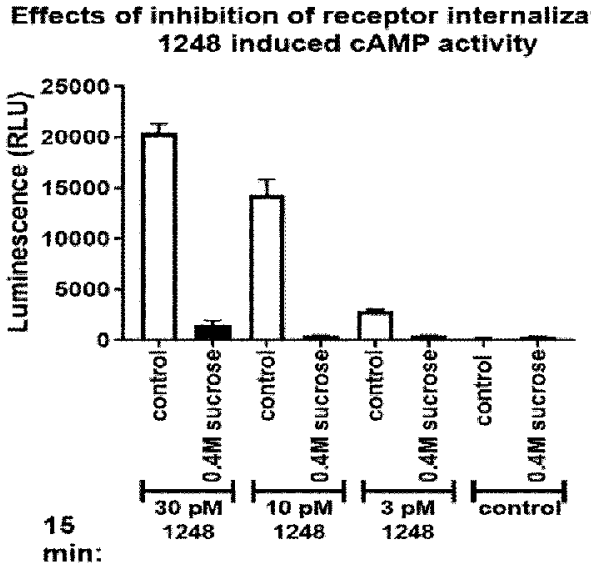


FIG. 26B

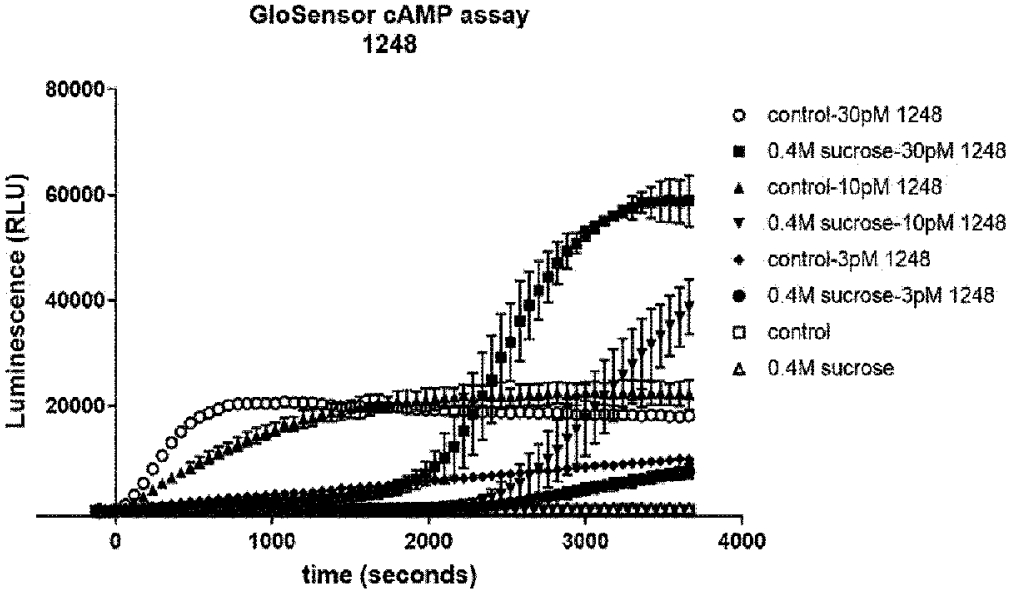


FIG. 27A

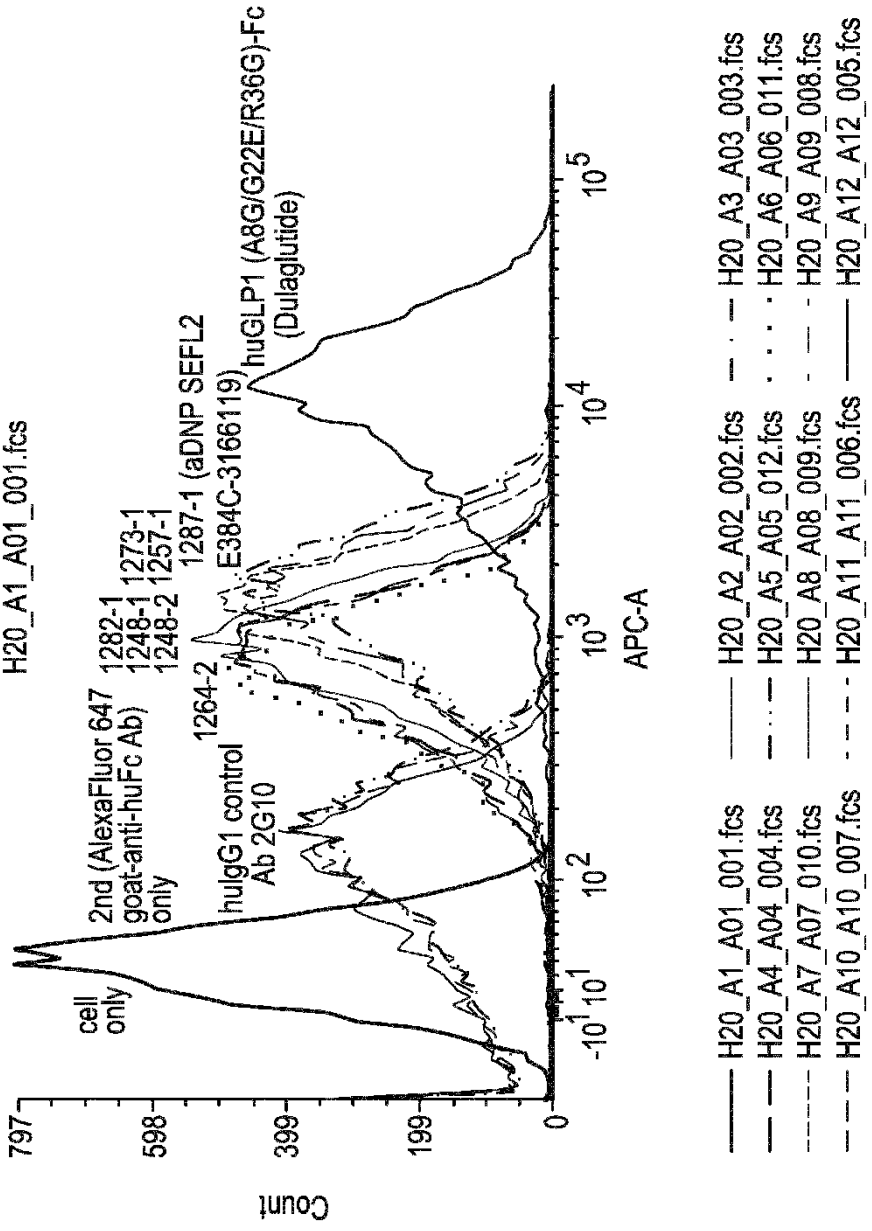
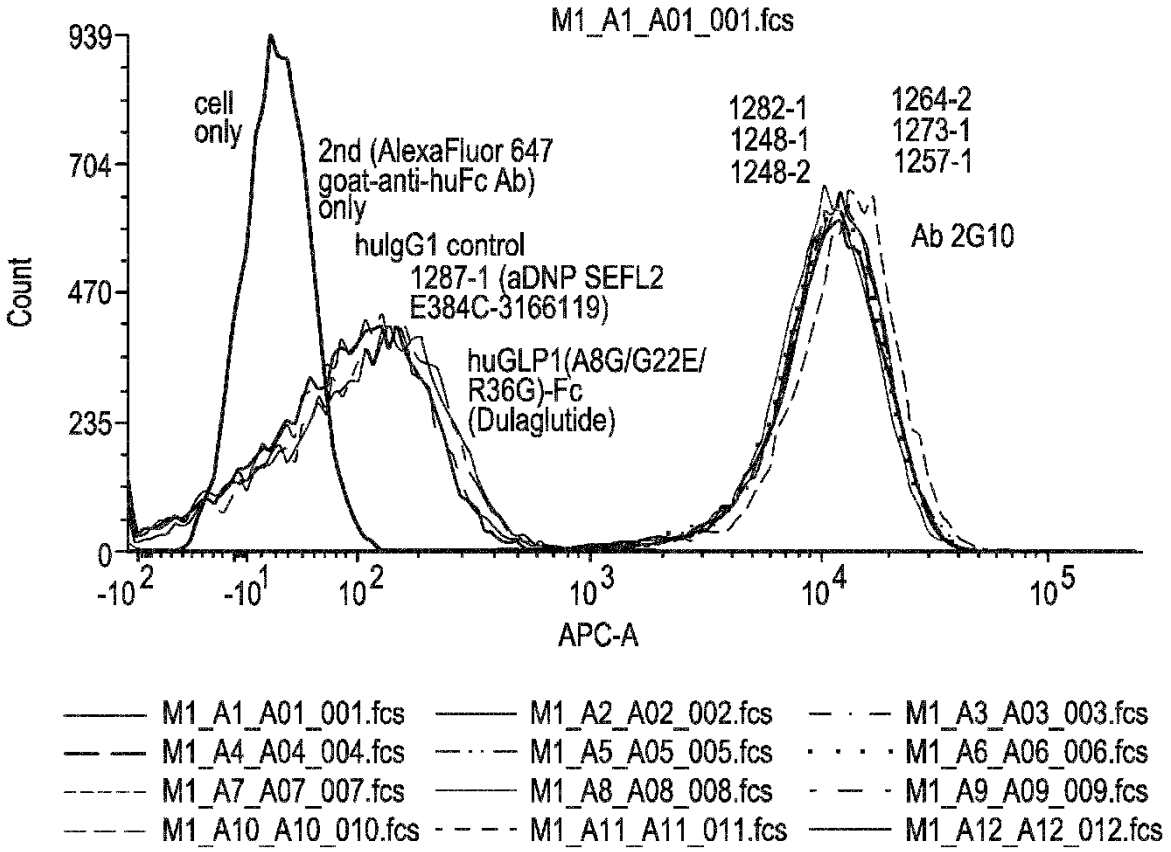

CHOK1-hGLP1R H20
H20_A1_A01_001.fcs
cell only
2nd (AlexaFluor 647 goat-anti-huFc Ab) only
hulgG1 control Ab 2G10
1264-2
1282-1
1248-1
1248-2
1273-1
1257-1
1287-1 (aDNP SEFL2 E384C-3166119)
huGLP1 (A8G/G22E/R36G)-Fc (Dulaglutide)
Count
APC-A
797
598
399
199
0
-10^1
10^1
10^2
10^3
10^4
10^5
H20_A1_A01_001.fcs
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



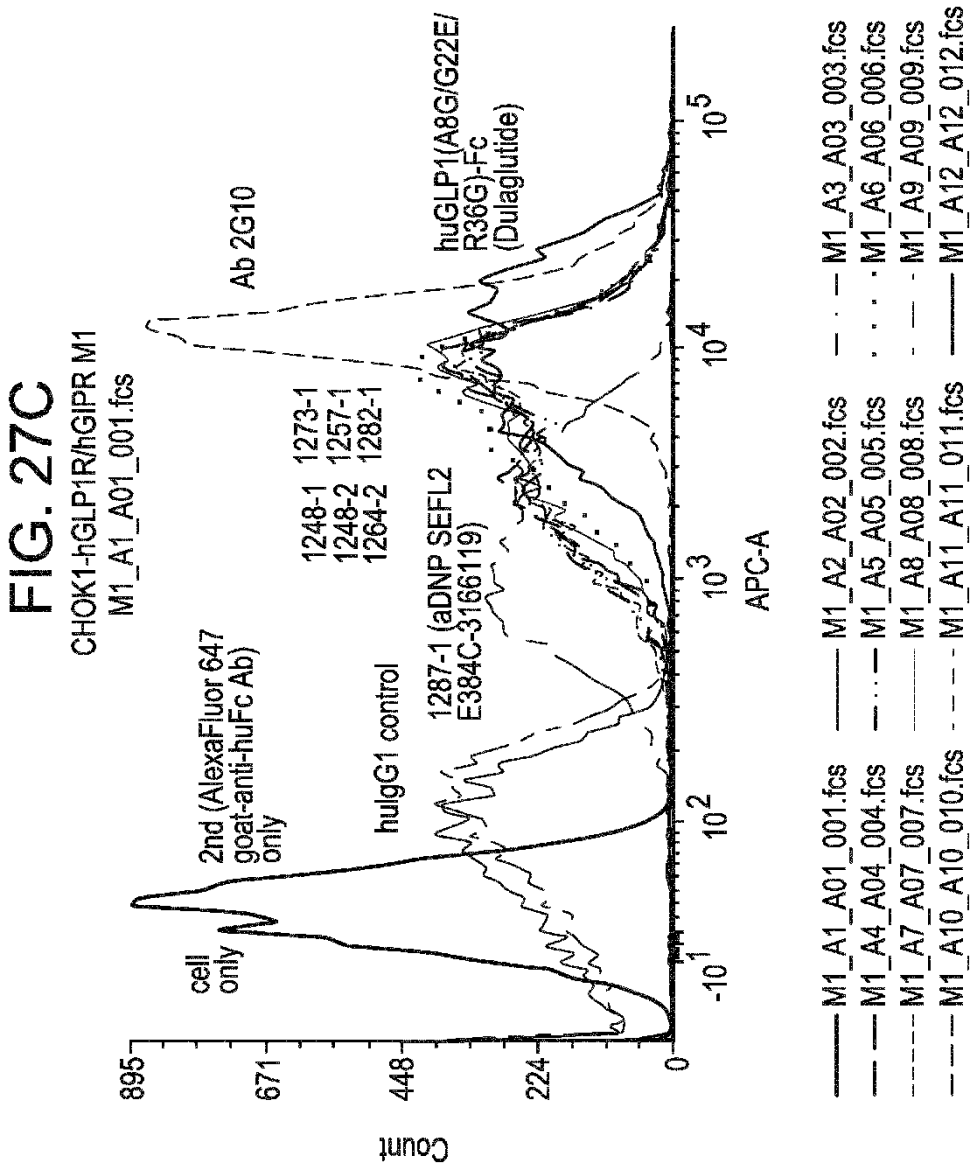
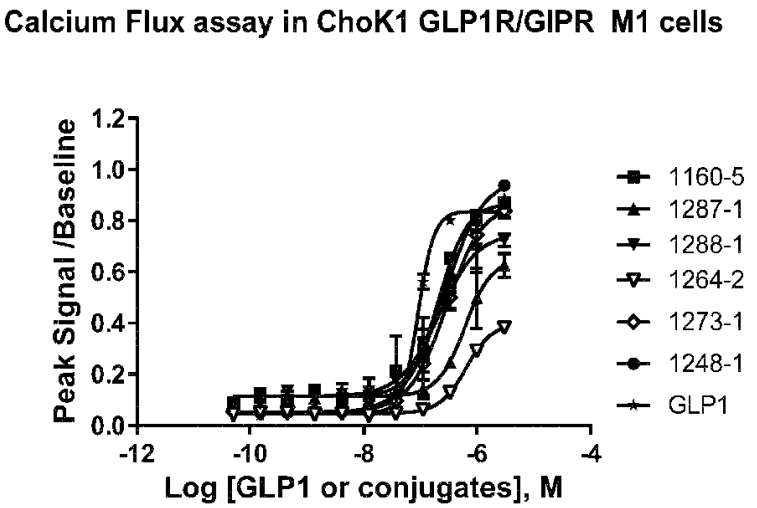
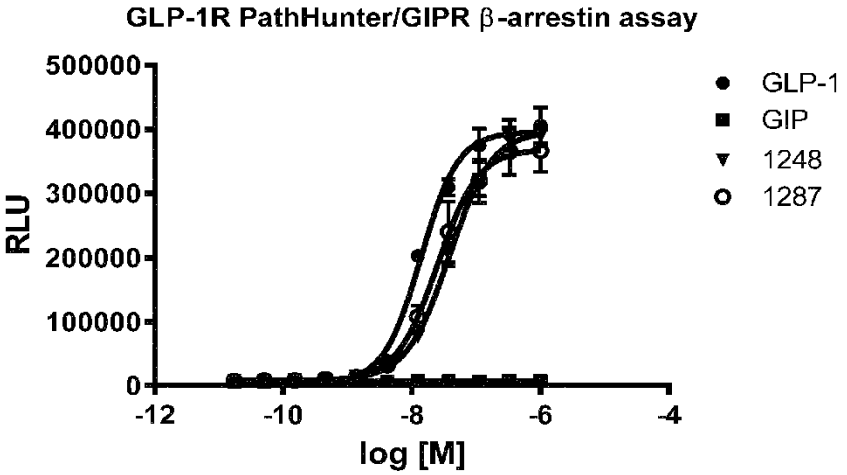

FIG. 27C
CHOK1-hGLP1R/hGIPR M1
M1_A1_A01_001.fcs
Count
APC-A
cell only
2nd (AlexaFluor 647 goat-anti-huFc Ab) only
hulgG1 control
1287-1 (aDNP SEFL2 E384C-3166119)
1248-1 1273-1
1248-2 1257-1
1264-2 1282-1
Ab 2G10
huGLP1(A8G/G22E/ R36G)-Fc (Dulaglutide)
M1_A1_A01_001.fcs
M1_A4_A04_004.fcs
M1_A7_A07_007.fcs
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



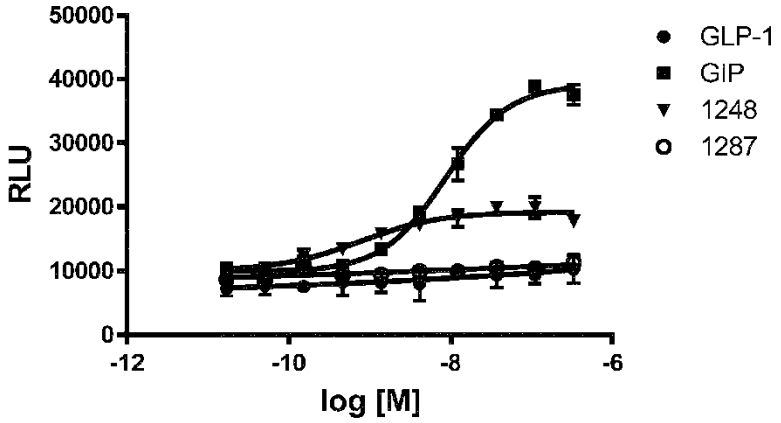
	1160-5	1287-1	1288-1	1264-2	1273-1	1248-1	GLP1
EC50	2.098e-007	6.152e-007	2.141e-007	6.485e-007	2.862e-007	2.594e-007	9.123e-008

FIG. 29A



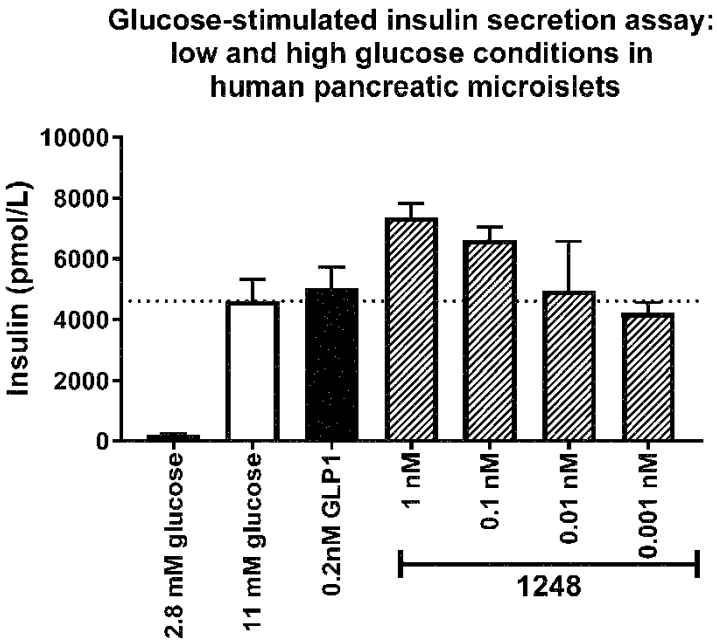
	GIP	GLP-1	1248	1287
EC50	1.974e-010	1.379e-008	3.83e-008	2.493e-008

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