(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
04 October 2018 (04.10.2018)

WIPO | PCT

(10) International Publication Number
WO 2018/183376 A1

(51) International Patent Classification:
C07K 16/28 (2006.01) *C07K 16/46* (2006.01)
C07K 16/42 (2006.01)

(21) International Application Number:
PCT/US2018/024632

(22) International Filing Date:
27 March 2018 (27.03.2018)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
62/477,911 28 March 2017 (28.03.2017) US

(71) Applicant: **RIGEL PHARMACEUTICALS, INC.** [US/US]; 1180 Veterans Boulevard, South San Francisco, California 94080 (US).

(72) Inventors: **KINSELLA, Todd M.**; Rigel Pharmaceuticals, Inc., 1180 Veterans Boulevard, South San Francisco, California 94080 (US). **BHATT, Ramesh**; Rigel Pharmaceuticals, Inc., South San Francisco, California 94080 (US). **BALTGALVIS, Kristen**; Rigel Pharmaceuticals, Inc., 1180 Veterans Boulevard, South San Francisco, California 94080 (US).

(74) Agent: **KEDDIE, James S.**; 201 Redwood Shores Parkway, Suite 200, Redwood City, California 94065 (US).

(81) Designated States *(unless otherwise indicated, for every kind of national protection available)*: AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DJ, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IR, IS, JO, JP, KE, KG, KH, KN, KP, KR, KW, KZ, LA, LC, LK, LR, LS, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SA, SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

(84) Designated States *(unless otherwise indicated, for every kind of regional protection available)*: ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, ST, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, KM, ML, MR, NE, SN, TD, TG).

Published:
— *with international search report (Art. 21(3))*
— *before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments (Rule 48.2(h))*
— *with sequence listing part of description (Rule 5.2(a))*

(54) Title: ACVR2A-SPECIFIC ANTIBODY AND METHOD OF USE THEREOF

(57) Abstract: The present disclosure provides antibodies that specifically bind to and block signaling by ACVR2A, i.e., ACVR2A but not ACVR2B, as well as methods for using the same. The antibodies may be used for the treatment of a number of conditions associated with muscle atrophy, as well as other conditions.

WO 2018/183376 A1

ACVR2A-SPECIFIC ANTIBODY AND METHOD OF USE THEREOF

CROSS-REFERENCING

This application claims the benefit of US provisional application serial no. 62/477,911, filed on March 28, 2017, which application is incorporated herein in its entirety.

BACKGROUND

The activin receptor, type II A (ACVR2A) is a high affinity receptor for the activin proteins as well as other members of the TGF-beta superfamily. ACVR2A is generally thought to transduce signals that lead to the phosphorylation of one or more SMAD transcription factors, particularly SMADs 1, 2, 3 and 5. ACVR2A has been implicated in the regulation of a wide range of biological processes, including bone formation, muscle formation, red blood cell formation, tumor growth, immune function and the production of reproductive hormones.

There is a need for reagents, e.g., antibodies, that specifically bind to ACVR2A and inhibit ACVR2A signaling.

SUMMARY OF THE INVENTION

The present disclosure provides antibodies that specifically bind to and block signaling by ACVR2A, i.e., ACVR2A but not ACVR2B. The antibodies are useful in various treatment, diagnostic, and monitoring applications. In some embodiments, an antibody may comprise: (a) a variable domain comprising: i. heavy chain CDR1, CDR2 and CDR3 regions that are identical the heavy chain CDR1, CDR2 and CDR3 regions of an antibody selected from any of Tables 2A-2F; and ii. light chain CDR1, CDR2 and CDR3 regions that are identical the light chain CDR1, CDR2 and CDR3 regions of the antibody selected from any of Tables 2A-2F; or (b) a variant of said variable domain of (a) that is otherwise identical to said antibody variable domain except for up to 15 amino acid substitutions in said CDR regions.

In some embodimens, an antibody may comprise: (a) a heavy chain variable domain comprising a heavy chain framework, a CDR1 region, a CDR2 region, and a CDR3 region of sequence ARSATWHDTXLD (SEQ ID NO:6538) or a variant of ARSATWHDTXLD (SEQ ID NO:6538) that comprises up to three amino acid substitutions, and (b) a light chain variable domain comprising a light chain framework, a CDR1 region, a CDR2 region, and a CDR3 region.

DEFINITIONS

The terms "antibodies" and "immunoglobulin" include antibodies or immunoglobulins of any isotype, fragments of antibodies which retain specific binding to antigen, including, but not limited to, Fab, Fv, scFv, and Fd fragments, chimeric antibodies, humanized antibodies, single-chain antibodies, and fusion proteins comprising an antigen-binding portion of an antibody and a non-antibody protein. The antibodies may be detectably labeled, *e.g.*, with a radioisotope, an enzyme which generates a detectable product, a fluorescent protein, and the like. The antibodies may be further conjugated to other moieties, such as members of specific binding pairs, *e.g.*, biotin (member of biotin-avidin specific binding pair), and the like. The antibodies may also be bound to a solid support, including, but not limited to, polystyrene plates or beads, and the like. Also encompassed by the term are Fab', Fv, $F(ab')_2$, and or other antibody fragments that retain specific binding to antigen, and monoclonal antibodies. An antibody may be monovalent or bivalent.

"Antibody fragments" comprise a portion of an intact antibody, for example, the antigen binding or variable region of the intact antibody. Examples of antibody fragments include Fab, Fab', $F(ab')_2$, and Fv fragments; diabodies; linear antibodies (Zapata et al., Protein Eng. 8(10): 1057-1062 (1995)); single-chain antibody molecules; and multispecific antibodies formed from antibody fragments. Papain digestion of antibodies produces two identical antigen-binding fragments, called "Fab" fragments, each with a single antigen-binding site, and a residual "Fc" fragment, a designation reflecting the ability to crystallize readily. Pepsin treatment yields an $F(ab')_2$ fragment that has two antigen combining sites and is still capable of cross-linking antigen.

"Fv" is the minimum antibody fragment which contains a complete antigen-recognition and -binding site. This region consists of a dimer of one heavy- and one light-chain variable domain in tight, non-covalent association. It is in this configuration that the three CDRS of each variable domain interact to define an antigen-binding site on the surface of the V_H-V_L dimer. Collectively, the six CDRs confer antigen-binding specificity to the antibody. However, even a single variable domain (or half of an Fv comprising only three CDRs specific for an antigen) has the ability to recognize and bind antigen, although at a lower affinity than the entire binding site.

The "Fab" fragment also contains the constant domain of the light chain and the first constant domain (CH_1) of the heavy chain. Fab fragments differ from Fab' fragments by the addition of a few residues at the carboxyl terminus of the heavy chain CH_1 domain including one or more cysteines from the antibody hinge region. Fab'-SH is the designation herein for Fab' in which the cysteine residue(s) of the constant domains bear a free thiol group. $F(ab')_2$ antibody fragments originally were produced as pairs of Fab' fragments which have hinge cysteines between them. Other chemical couplings of antibody fragments are also known.

The "light chains" of antibodies (immunoglobulins) from any vertebrate species can be assigned to one of two clearly distinct types, called kappa and lambda, based on the amino acid sequences of their constant domains. Depending on the amino acid sequence of the constant domain of their heavy chains, immunoglobulins can be assigned to different classes. There are five major classes of immunoglobulins: IgA, IgD, IgE, IgG, and IgM, and several of these may be further divided into subclasses (isotypes), e.g., IgG1, IgG2, IgG3, IgG4, IgA, and IgA2.

"Single-chain Fv" or "sFv" antibody fragments comprise the V_H and V_L domains of antibody, wherein these domains are present in a single polypeptide chain. In some embodiments, the Fv polypeptide further comprises a polypeptide linker between the V_H and V_L domains, which enables the sFv to form the desired structure for antigen binding. For a review of sFv, see *Pluckthun in The Pharmacology of Monoclonal Antibodies, vol. 113, Rosenburg and Moore eds., Springer-Verlag, New York, pp. 269-315 (1994)*.

The term "diabodies" refers to small antibody fragments with two antigen-binding sites, which fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) in the same polypeptide chain (V_H-V_L). By using a linker that is too short to allow pairing between the two domains on the same chain, the domains are forced to pair with the complementary domains of another chain and create two antigen-binding sites. Diabodies are described more fully in, for example, EP 404,097; WO 93/11161; and *Hollinger et al., Proc. Natl. Acad. Sci. USA, 90:6444-6448 (1993).*

As used herein, the term "affinity" refers to the equilibrium constant for the reversible binding of two agents and is expressed as a dissociation constant (Kd). Affinity can be at least 1-fold greater, at least 2-fold greater, at least 3-fold greater, at least 4-fold greater, at least 5-fold greater, at least 6-fold greater, at least 7-fold greater, at least 8-fold greater, at least 9-fold greater, at least 10-fold greater, at least 20-fold greater, at least 30-fold greater, at least 40-fold greater, at least 50-fold greater, at least 60-fold greater, at least 70-fold greater, at least 80-fold greater, at least 90-fold greater, at least 100-fold greater, or at least 1000-fold greater, or more, than the affinity of an antibody for unrelated amino acid sequences. Affinity of an antibody to a target protein can be, for example, from about 100 nanomolar (nM) to about 0.1 nM, from about 100 nM to about 1 picomolar (pM), or from about 100 nM to about 1 femtomolar (fM) or more. As used herein, the term “avidity” refers to the resistance of a complex of two or more agents to dissociation after dilution. The terms “immunoreactive” and “preferentially binds” are used interchangeably herein with respect to antibodies and/or antigen-binding fragments.

The term “binding” refers to a direct association between two molecules, due to, for example, covalent, electrostatic, hydrophobic, and ionic and/or hydrogen-bond interactions, including interactions such as salt bridges and water bridges. An ACVR2A-specific antibody antibodies binds specifically to an

epitope within a ACVR2A polypeptide. Non-specific binding would refer to binding with an affinity of less than about 10^{-7} M, e.g., binding with an affinity of 10^{-6} M, 10^{-5} M, 10^{-4} M, etc.

As used herein, the term "CDR" or "complementarity determining region" is intended to mean the non-contiguous antigen combining sites found within the variable region of both heavy and light chain polypeptides. CDRs have been described by Kabat et al., J. Biol. Chem. 252:6609-6616 (1977); Kabat et al., U.S. Dept. of Health and Human Services, "Sequences of proteins of immunological interest" (1991); by Chothia et al., J. Mol. Biol. 196:901-917 (1987); and MacCallum et al., J. Mol. Biol. 262:732-745 (1996), where the definitions include overlapping or subsets of amino acid residues when compared against each other. Nevertheless, application of either definition to refer to a CDR of an antibody or grafted antibodies or variants thereof is intended to be within the scope of the term as defined and used herein. The amino acid residues which encompass the CDRs as defined by each of the above cited references are set forth below in Table 1 as a comparison.

Table 1: CDR Definitions

	Kabat[1]	Chothia[2]	MacCallum[3]
V_H CDR1	31-35	26-32	30-35
V_H CDR2	50-65	53-55	47-58
V_H CDR3	95-102	96-101	93-101
V_L CDR1	24-34	26-32	30-36
V_L CDR2	50-56	50-52	46-55
V_L CDR3	89-97	91-96	89-96

[1] Residue numbering follows the nomenclature of Kabat et al., *supra*
[2] Residue numbering follows the nomenclature of Chothia et al., *supra*
[3] Residue numbering follows the nomenclature of MacCallum et al., *supra*

As used herein, the term "framework" when used in reference to an antibody variable region is intended to mean all amino acid residues outside the CDR regions within the variable region of an antibody. A variable region framework is generally a discontinuous amino acid sequence between about 100-120 amino acids in length but is intended to reference only those amino acids outside of the CDRs. As used herein, the term "framework region" is intended to mean each domain of the framework that is separated by the CDRs.

An "isolated" antibody is one that has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials that would interfere with diagnostic or therapeutic uses for the antibody, and may include enzymes, hormones, and other proteinaceous or nonproteinaceous solutes. In some embodiments, the antibody will be purified (1) to greater than 90%, greater than 95%, or greater than 98%, by weight of antibody as determined by the Lowry method, for example, more than 99% by weight, (2) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup

sequenator, or (3) to homogeneity by sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) under reducing or nonreducing conditions using Coomassie blue or silver stain. Isolated antibody includes the antibody in situ within recombinant cells since at least one component of the antibody's natural environment will not be present. In some instances, isolated antibody will be prepared by at least one purification step.

As used herein, the terms "treatment," "treating," and the like, refer to obtaining a desired pharmacologic and/or physiologic effect. The effect may be prophylactic in terms of completely or partially preventing a disease or symptom thereof and/or may be therapeutic in terms of a partial or complete cure for a disease and/or adverse effect attributable to the disease. "Treatment," as used herein, covers any treatment of a disease in a mammal, particularly in a human, and includes: (a) preventing the disease from occurring in a subject which may be predisposed to the disease but has not yet been diagnosed as having it; (b) inhibiting the disease, i.e., arresting its development; and (c) relieving the disease, i.e., causing regression of the disease.

The terms “individual,” “subject,” “host,” and “patient,” used interchangeably herein, refer to a mammal, including, but not limited to, murines (rats, mice), non-human primates, humans, canines, felines, ungulates (e.g., equines, bovines, ovines, porcines, caprines), etc.

A “therapeutically effective amount” or “efficacious amount” refers to the amount of an ACVR2A-specific antibody that, when administered to a mammal or other subject for treating a disease, is sufficient to effect such treatment for the disease. The “therapeutically effective amount” will vary depending on the ACVR2A-specific antibody, the disease and its severity and the age, weight, etc., of the subject to be treated.

A “biological sample” encompasses a variety of sample types obtained from an individual and can be used in a diagnostic or monitoring assay. The definition encompasses blood and other liquid samples of biological origin, solid tissue samples such as a biopsy specimen or tissue cultures or cells derived therefrom and the progeny thereof. The definition also includes samples that have been manipulated in any way after their procurement, such as by treatment with reagents, solubilization, or enrichment for certain components, such as polynucleotides. The term “biological sample” encompasses a clinical sample, and also includes cells in culture, cell supernatants, cell lysates, serum, plasma, biological fluid, and tissue samples.

The present disclosure may make use of consensus sequences. If an amino acid sequence is indicated as being “of sequence Y”, where Y is a consensus sequence, the amino acid sequence falls within the consensus sequence. In a consensus sequence, the amino acid “X” can be any amino acid.

Before the present invention is further described, it is to be understood that this invention is not limited to particular embodiments described, as such may, of course, vary. It is also to be understood that

the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to be limiting, since the scope of the present invention will be limited only by the appended claims.

Where a range of values is provided, it is understood that each intervening value, to the tenth of the unit of the lower limit unless the context clearly dictates otherwise, between the upper and lower limit of that range and any other stated or intervening value in that stated range, is encompassed within the invention. The upper and lower limits of these smaller ranges may independently be included in the smaller ranges, and are also encompassed within the invention, subject to any specifically excluded limit in the stated range. Where the stated range includes one or both of the limits, ranges excluding either or both of those included limits are also included in the invention.

Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although any methods and materials similar or equivalent to those described herein can also be used in the practice or testing of the present invention, the preferred methods and materials are now described. All publications mentioned herein are incorporated herein by reference to disclose and describe the methods and/or materials in connection with which the publications are cited.

It must be noted that as used herein and in the appended claims, the singular forms "a," "an," and "the" include plural referents unless the context clearly dictates otherwise. Thus, for example, reference to "an antibody" includes a plurality of such antibodies and reference to "the ACVR2A-specific antibody" includes reference to one or more ACVR2A-specific antibodies and equivalents thereof known to those skilled in the art, and so forth. It is further noted that the claims may be drafted to exclude any optional element. As such, this statement is intended to serve as antecedent basis for use of such exclusive terminology as "solely," "only" and the like in connection with the recitation of claim elements, or use of a "negative" limitation.

The publications discussed herein are provided solely for their disclosure prior to the filing date of the present application. Nothing herein is to be construed as an admission that the present invention is not entitled to antedate such publication by virtue of prior invention. Further, the dates of publication provided may be different from the actual publication dates which may need to be independently confirmed.

DETAILED DESCRIPTION

The present disclosure provides antibodies that specifically bind to and block signaling by ACVR2A, i.e., ACVR2A but not ACVR2B. In some embodiments, the antibody may comprise (a) a variable domain comprising: i. heavy chain CDR1, CDR2 and CDR3 regions that are identical the heavy

chain CDR1, CDR2 and CDR3 regions of an antibody selected from any of Tables 2A-2F; and ii. light chain CDR1, CDR2 and CDR3 regions that are identical the light chain CDR1, CDR2 and CDR3 regions of the antibody selected from any of Tables 2A-2F; or (b) a variant of the variable domain of (a) that is otherwise identical to the antibody variable domain of (a) except for up to 15 amino acid substitutions in the CDR regions, e.g., up to 15, up to 14, up to 13, up to 12, up to 11, up to 10, up to 9, up to 8, up to 7, up to 6, up to 5, up to 4, up to 3, up to 2 amino acid substitutions in the CDR regions.

In some embodiments, the antibody may comprise: a heavy chain variable domain comprising: a heavy chain framework, a CDR1 region, a CDR2 region, and a CDR3 region of sequence AxxAxWHDTxLD; and a light chain variable domain comprising: a light chain framework, a CDR1 region, a CDR2 region, and a CDR3 region. For example, in some embodiments, the heavy chain variable domain of the antibody may comprise a CDR3 region of sequence ARSATWHDTxLD (SEQ ID NO: 6538) (e.g., ARAANWHDTA/HLD (SEQ ID NO: 6539)), ARAATWHDTxLD (SEQ ID NO: 6540) (e.g., ARAATWHDTH/ALD (SEQ ID NO: 6541)), ARGANWHDTxLD (SEQ ID NO: 6542) (e.g., ARGANWHDTA/HLD (SEQ ID NO: 6543)), ARGATWHDTxLD (SEQ ID NO: 6544) (e.g., ARGATWHDTH/ALD (SEQ ID NO: 6545)), ARSANWHDTxLD (SEQ ID NO: 6546) (e.g., AR/KSANWHDTA/HLD (SEQ ID NO: 6547)) or ARSATWHDTxLD (SEQ ID NO: 6548) (e.g., ARSATWHDTH/ALD (SEQ ID NO: 6549)).

As will be shown below, there is considerable diversity in the heavy chain CDR1, heavy chain CDR2, light chain CDR1, light chain CDR2 and light chain CDR3 regions in the present antibodies. Therefore, consistent with Barrios et al (Mol. Recognit. 2004 17: 332-8) and Bowers et al (J. Biol. Chem. 2013 288: 7688-96) the heavy chain CDR3 is believed primarily responsible for antigen binding in the present antibody.

In some embodiments, the antibody may comprise a heavy chain variable domain comprising: i . a CDR1 region that has a sequence of D/SS/DYG/SMH/N (SEQ ID NO: 6550), ii . a CDR2 region that has a sequence of WVA/SS/G/NINYNG/SGYT/KS/G (SEQ ID NO: 6551), and iii . a CDR3 region that has a sequence of ARAANWHDTA/HLD (SEQ ID NO: 6552); and a light chain variable domain comprising: i . a CDR1 region that has a sequence of XXYL/VNWY (SEQ ID NO: 6553) (e.g., L/V/I/SS/T/RYL/VNWY (SEQ ID NO: 6554)), ii . a CDR2 region that has a sequence of LV/LIYXXXS/NR/LX (SEQ ID NO: 6555)(e.g., LV/LIYA/Y/VA/V/TT/S/NS/NR/LA/H/Q/P (SEQ ID NO: 6556)), and iii . a CDR3 region that has a sequence of QQ/HSY/DXXPL (SEQ ID NO: 6557) (e.g., QQ/HSY/DD/E/S /NL/N/S/TPL (SEQ ID NO: 6558)).

In some embodiments, the antibody may comprise a heavy chain variable domain comprising: i . a CDR1 region that has a sequence of D/SS/DYG/SMH/N (SEQ ID NO: 6550), ii . a CDR2 region that has a sequence of WVA/SS/G/NINYNG/SGYT/KS/G (SEQ ID NO: 6551), and iii . a CDR3 region that

has a sequence of ARAATWHDTH/ALD (SEQ ID NO: 6559); and a light chain variable domain comprising: i . a CDR1 region that has a sequence of XS/TYL/VNWY (SEQ ID NO: 6560) (e.g., L/V/I/SS/TYL/VNWY (SEQ ID NO: 6561)), ii . a CDR2 region that has a sequence of LL/VIYA/YXXS/NR/LX (SEQ ID NO: 6562)(e.g., LL/VIYA/YA/T/VT/S/NS/NR/LA/P/Q (SEQ ID NO: 6563)), and iii . a CDR3 region that has a sequence of QQSY/D/NXXPL (SEQ ID NO: 6564) (e.g., QQSY/D/ND/E/S/NL/S/T/NPL (SEQ ID NO: 6565)).

In some embodiments, the antibody may comprise a heavy chain variable domain comprising: i . a CDR1 region that has a sequence of S/DS/DYS/GMN/H (SEQ ID NO: 6566), ii . a CDR2 region that has a sequence of WVS/AG/S/NINYNG/SGYT/KS/G (SEQ ID NO: 6567), and iii . a CDR3 region that has a sequence of ARGANWHDTA/HLD (SEQ ID NO: 6543); and a light chain variable domain comprising: i . a CDR1 region that has a sequence of XS/TYL/VNWY (SEQ ID NO: 6568) (e.g., L/V/S/IS/TYL/VNWY (SEQ ID NO: 6569)), ii . a CDR2 region that has a sequence of LL/VIYAXT/SSR/LX (SEQ ID NO: 6570) (e.g., LL/VIYAA/V/TT/SSR/LA/H/Q (SEQ ID NO: 6571)), and iii . a CDR3 region that has a sequence of QQSY/DXXPL (SEQ ID NO: 6572) (e.g., QQSY/DD/E/S/NS/T/N/LPL (SEQ ID NO: 6573)).

In some embodiments, the antibody may comprise a heavy chain variable domain comprising: i . a CDR1 region that has a sequence of S/DS/DYS/GMN/H (SEQ ID NO: 6574), ii . a CDR2 region that has a sequence of WVA/SG/N/SINYNG/SGYT/KS/G (SEQ ID NO: 6575), and iii . a CDR3 region that has a sequence of ARGATWHDTH/ALD (SEQ ID NO: 6544); and a light chain variable domain comprising: i . a CDR1 region that has a sequence of XS/TYL/VNWY (SEQ ID NO: 6568) (e.g., L/I/V/SS/TYL/VNWY (SEQ ID NO: 6576)), ii . a CDR2 region that has a sequence of LL/VIYAXT/SSR/LX (SEQ ID NO: 6570) (e.g., LL/VIYAA/V/TT/SSR/LA/H/Q (SEQ ID NO: 6571)), and iii . a CDR3 region that has a sequence of QQSY/DXXPL (SEQ ID NO: 6572) (e.g., QQSY/DD/E/S/NT/S/N/LPL (SEQ ID NO: 6577)).

In some embodiments, the antibody may comprise a heavy chain variable domain comprising: i . a CDR1 region that has a sequence of S/DS/DYG/SMN/H (SEQ ID NO: 6578), ii . a CDR2 region that has a sequence of WVS/AG/N/SINYNG/SGYT/KS/G (SEQ ID NO: 6579), and iii . a CDR3 region that has a sequence of AR/KSANWHDTA/HLD (SEQ ID NO: 6580); and a light chain variable domain comprising: i . a CDR1 region that has a sequence of XS/TYL/VNWY (SEQ ID NO: 6568) (e.g., L/V/I/SS/TYL/VNWY (SEQ ID NO: 6561)), ii . a CDR2 region that has a sequence of LL/VIYA/YXT/SS/NR/LX (SEQ ID NO: 6581) (e.g., LL/VIYA/YA/V/TT/SS/NR/LA/H/Q (SEQ ID NO: 6582)), and iii . a CDR3 region that has a sequence of QQSY/DXXPL (SEQ ID NO: 6572) (e.g., QQSY/DD/E/N/S S/T/L/NPL (SEQ ID NO: 6583)).

In some embodiments, the antibody may comprise a heavy chain variable domain comprising: i . a CDR1 region that has a sequence of D/SS/DYS/GMN/H (SEQ ID NO: 6584), ii . a CDR2 region that has a sequence of WVA/SG/N/SINYNG/SGYT/KS/G (SEQ ID NO: 6585), and iii . a CDR3 region that has a sequence of ARSATWHDTH/ALD (SEQ ID NO: 6586); and a light chain variable domain comprising: i . a CDR1 region that has a sequence of XXYL/VNWY (SEQ ID NO: 6587) (e.g., L/V/I/SS/T/RYL/VNWY (SEQ ID NO: 6588)), ii . a CDR2 region that has a sequence of LL/VIYA/YXT/SS/NR/LX (SEQ ID NO: 6589) (e.g., LL/VIYA/YA/V/TT/SS/NR/LA/H/Q (SEQ ID NO: 6590)), and iii . a CDR3 region that has a sequence of QQSY/DXXPL (SEQ ID NO: 6572) (e.g., QQSY/DD/E/S/NL/N/T/SPL (SEQ ID NO: 6591)).

In some embodiments the antibody may comprise: a heavy chain variable domain comprising an amino acid sequence that is at least 80% identical to (e.g., at least 90%, at least 95%, at least 98%, at least 99%, or 100% identical to) the amino acid sequence of the heavy chain variable domain of an antibody selected from any of Tables 2A-2F; and a light chain variable domain comprising an amino acid sequence that is at least 80% identical to (e.g., at least 90%, at least 95%, at least 98%, at least 99%, or 100% identical to) the light chain variable domain of the antibody selected from any of Tables 2A-2F.

Tables 2A-2F provides the amino acid sequences of the heavy and light variable domains of some examples of the present antibody.

Table 2A: Group I Antibody Sequences

Ab	VH sequence	VL sequence
365_B04	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMHWVRQAPGKGLEWVASINYNSGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQK PGKAPKLLIYAATSRHSGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSDESPLTFGGGTKVEIK (SEQ ID NO: 58)
365_B10	EVQLLESGGGLVQPGGSLRLSCAASGFTFDDY SMHWVRQAPGKGLEWVASINYNSGYKGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 2)	DIQMTQSPSSLSASVGDRVTITCRASQSILRYLNWYQQK PGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSDNLPLTFGGGTKVEIK (SEQ ID NO: 59)
365_C03	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMHWVRQAPGKGLEWVAGINYNSGYKGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 3)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVNWYQQK PGKAPKLVIYATTSLASGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSYNTPLTFGGGTKVEIK (SEQ ID NO: 60)
365_C06	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDY GMHWVRQAPGKGLEWVSGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 4)	DIQMTQSPSSLSASVGDRVTITCRASQSISTYVNWYQQK PGKAPKLLIYAVTSLASGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSYDNPLTFGGGTKVEIK (SEQ ID NO: 61)
365_D04	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDY GMHWVRQAPGKGLEWVAGINYNGGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 5)	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQK PGKAPKLVIYAVTSRASGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSYDLPLTFGGGTKVEIK (SEQ ID NO: 62)
365_E04	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVNWYQQK

	GMHWVRQAPGKGLEWVASINYNGGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 6)	PGKAPKLLIYAATSLASGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSYELPLTFGGGTKVEIK (SEQ ID NO: 63)
365_F11	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY SMNWVRQAPGKGLEWVSGINYNSGYKGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 7)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYVNWYQQK PGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSYNTPLTFGGGTKVEIK (SEQ ID NO: 64)
365_G07	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMHWVRQAPGKGLEWVSSINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 8)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYLNWYQQK PGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSYDNPLTFGGGTKVEIK (SEQ ID NO: 65)
365_H08	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMHWVRQAPGKGLEWVASINYNGGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 9)	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQK PGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSYSTPLTFGGGTKVEIK (SEQ ID NO: 66)
366_A02	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMNWVRQAPGKGLEWVASINYNSGYKGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 10)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVNWYQQK PGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSYDLPLTFGGGTKVEIK (SEQ ID NO: 67)
366_A04	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMNWVRQAPGKGLEWVAGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 11)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQK PGKAPKLVIYAATSLASGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSDDSPLTFGGGTKVEIK (SEQ ID NO: 68)
366_D01	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMHWVRQAPGKGLEWVSSINYNGGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 12)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVNWYQQK PGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSYENPLTFGGGTKVEIK (SEQ ID NO: 69)
366_D03	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMHWVRQAPGKGLEWVSSINYNGGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 13)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVNWYQQK PGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSYDLPLTFGGGTKVEIK (SEQ ID NO: 70)
366_F10	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY SMNWVRQAPGKGLEWVAGINYNGGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 14)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYLNWYQQK PGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSYDTPLTFGGGTKVEIK (SEQ ID NO: 71)
366_G06	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMHWVRQAPGKGLEWVASINYNGGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 15)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVNWYQQK PGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSYDNPLTFGGGTKVEIK (SEQ ID NO: 72)
367_B09	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMHWVRQAPGKGLEWVASINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 16)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVNWYQQK PGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSYENPLTFGGGTKVEIK (SEQ ID NO: 73)
367_B11	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDY SMHWVRQAPGKGLEWVANINYNSGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 17)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLNWYQQK PGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSYSTPLTFGGGTKVEIK (SEQ ID NO: 74)
367_C09	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMHWVRQAPGKGLEWVASINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVNWYQQK PGKAPKLVIYAATSRHSGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSYNTPLTFGGGTKVEIK (SEQ ID

	ARAANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 18)	NO: 75)
367_D11	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMHWVRQAPGKGLEWVSNINYNGGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 19)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYLNWYQQK PGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSYDSPLTFGGGTKVEIK (SEQ ID NO: 76)
367_F06	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMNWVRQAPGKGLEWVSSINYNSGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 20)	DIQMTQSPSSLSASVGDRVTITCRASQSISSYVNWYQQK PGKAPKLLIYAVTSRASGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSYDSPLTFGGGTKVEIK (SEQ ID NO: 77)
367_H01	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMNWVRQAPGKGLEWVSGINYNGGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 21)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQK PGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSYDNPLTFGGGTKVEIK (SEQ ID NO: 78)
368_A02	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMNWVRQAPGKGLEWVAGINYNGGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 22)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYVNWYQQK PGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSYDTPLTFGGGTKVEIK (SEQ ID NO: 79)
368_A06	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY SMHWVRQAPGKGLEWVAGINYNSGYKGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 23)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVNWYQQK PGKAPKLLIYAATSRHSGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSYNSPLTFGGGTKVEIK (SEQ ID NO: 80)
368_A12	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY SMHWVRQAPGKGLEWVSSINYNSGYKGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 24)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQK PGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSYDSPLTFGGGTKVEIK (SEQ ID NO: 81)
368_B03	EVQLLESGGGLVQPGGSLRLSCAASGFTFDDY GMNWVRQAPGKGLEWVSGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 25)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQK PGKAPKLVIYAATSLASGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQHSYENPLTFGGGTKVEIK (SEQ ID NO: 82)
368_B08	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMNWVRQAPGKGLEWVSSINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 26)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVNWYQQK PGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSYENPLTFGGGTKVEIK (SEQ ID NO: 83)
368_B10	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMHWVRQAPGKGLEWVASINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 27)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQK PGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSDELPLTFGGGTKVEIK (SEQ ID NO: 84)
368_B11	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMHWVRQAPGKGLEWVSGINYNGGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 28)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLNWYQQK PGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSYDSPLTFGGGTKVEIK (SEQ ID NO: 85)
368_C09	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMHWVRQAPGKGLEWVSNINYNGGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 29)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVNWYQQK PGKAPKLLIYAATSLASGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSYDLPLTFGGGTKVEIK (SEQ ID NO: 86)
368_D09	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMHWVRQAPGKGLEWVAGINYNSGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 30)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVNWYQQK PGKAPKLLIYAATSLASGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSYDNPLTFGGGTKVEIK (SEQ ID NO: 87)

368_F02	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMNWVRQAPGKGLEWVASINYNSGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 31)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLNWYQQK PGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSYSLPLTFGGGTKVEIK (SEQ ID NO: 88)
368_F10	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMNWVRQAPGKGLEWVAGINYNSGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 32)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVNWYQQK PGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSYDTPLTFGGGTKVEIK (SEQ ID NO: 89)
369_B03	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMHWVRQAPGKGLEWVAGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 33)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVNWYQQK PGKAPKLVIYAATSLASGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSYELPLTFGGGTKVEIK (SEQ ID NO: 90)
369_G10	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMHWVRQAPGKGLEWVASINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 34)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLNWYQQK PGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSYDSPLTFGGGTKVEIK (SEQ ID NO: 91)
369_H03	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMHWVRQAPGKGLEWVASINYNSGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 35)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYLNWYQQK PGKAPKLLIYATTSRASGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSYDTPLTFGGGTKVEIK (SEQ ID NO: 92)
370_B01	EVQLLESGGGLVQPGGSLRLSCAASGFTFDDY GMHWVRQAPGKGLEWVSGINYNGGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 36)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVNWYQQK PGKAPKLLIYVASSRASGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSYSLPLTFGGGTKVEIK (SEQ ID NO: 93)
370_D06	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMNWVRQAPGKGLEWVASINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 37)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYLNWYQQK PGKAPKLVIYAATSLASGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSYSSPLTFGGGTKVEIK (SEQ ID NO: 94)
370_G04	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMHWVRQAPGKGLEWVSGINYNGGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 38)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVNWYQQK PGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSYSTPLTFGGGTKVEIK (SEQ ID NO: 95)
370_H08	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMHWVRQAPGKGLEWVASINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 39)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVNWYQQK PGKAPKLLIYAATSRHSGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSYSLPLTFGGGTKVEIK (SEQ ID NO: 96)
371_A04	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMNWVRQAPGKGLEWVSSINYNSGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 40)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQK PGKAPKLLIYAVTSRASGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSYDTPLTFGGGTKVEIK (SEQ ID NO: 97)
371_A09	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMNWVRQAPGKGLEWVSGINYNGGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 41)	DIQMTQSPSSLSASVGDRVTITCRASQSIVTYVNWYQQK PGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSYDSPLTFGGGTKVEIK (SEQ ID NO: 98)
371_D07	EVQLLESGGGLVQPGGSLRLSCAASGFTFDDY GMNWVRQAPGKGLEWVANINYNGGYKGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 42)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQK PGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSYELPLTFGGGTKVEIK (SEQ ID NO: 99)
371_D12	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMNWVRQAPGKGLEWVSGINYNGGYKSYADSV	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLNWYQQK PGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTISSL

	KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 43)	QPEDFATYYCQQSYELPLTFGGGTKVEIK (SEQ ID NO: 100)
371_H02	EVQLLESGGGLVQPGGSLRLSCAASGFTFDDY SMNWVRQAPGKGLEWVSGINYNGGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 44)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYLNWYQQK PGKAPKLVIYAATSLASGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSYENPLTFGGGTKVEIK (SEQ ID NO: 101)
372_A09	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMNWVRQAPGKGLEWVSGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 45)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLNWYQQK PGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSYNSPLTFGGGTKVEIK (SEQ ID NO: 102)
372_B11	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMHWVRQAPGKGLEWVAGINYNSGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 46)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVNWYQQK PGKAPKLVIYAATSLASGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSYDTPLTFGGGTKVEIK (SEQ ID NO: 103)
372_E02	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMNWVRQAPGKGLEWVASINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 47)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYVNWYQQK PGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSYDLPLTFGGGTKVEIK (SEQ ID NO: 104)
373_E11	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMHWVRQAPGKGLEWVASINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 48)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYLNWYQQK PGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSYDSPLTFGGGTKVEIK (SEQ ID NO: 105)
373_H02	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMHWVRQAPGKGLEWVAGINYNSGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 49)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVNWYQQK PGKAPKLLIYAATSRHSGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSYXNPLTFGGGTKVEIK (SEQ ID NO: 106)
374_B02	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY SMHWVRQAPGKGLEWVAGINYNSGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 50)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYLNWYQQK PGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSYDSPLTFGGGTKVEIK (SEQ ID NO: 107)
374_F03	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMNWVRQAPGKGLEWVASINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 51)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYVNWYQQK PGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSYDTPLTFGGGTKVEIK (SEQ ID NO: 108)
375_A04	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMNWVRQAPGKGLEWVAGINYNGGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 52)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQK PGKAPKLVIYYVNNLPSGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSYNSPLTFGGGTKVEIK (SEQ ID NO: 109)
375_A11	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDY GMHWVRQAPGKGLEWVSSINYNSGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 53)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYLNWYQQK PGKAPKLLIYYVTNLASGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSYDNPLTFGGGTKVEIK (SEQ ID NO: 110)
375_C10	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMHWVRQAPGKGLEWVASINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 54)	DIQMTQSPSSLSASVGDRVTITCRASQSISTYLNWYQQK PGKAPKLVIYAASSLQSGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSYSTPLTFGGGTKVEIK (SEQ ID NO: 111)
375_F12	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMHWVRQAPGKGLEWVASINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAANWHDTALDYWGQGTLVTVSS (SEQ ID	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQK PGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSDELPLTFGGGTKVEIK (SEQ ID NO: 112)

	NO: 55)	
375_H01	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDY SMNWVRQAPGKGLEWVAGINYNSGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 56)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQK PGKAPKLLIYAATSRHSGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSYSNPLTFGGGTKVEIK (SEQ ID NO: 113)
376_G02	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDY GMNWVRQAPGKGLEWVSGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 57)	DIQMTQSPSSLSASVGDRVTITCRASQSISRYLNWYQQK PGKAPKLVIYAATSLASGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSYDNPLTFGGGTKVEIK (SEQ ID NO: 114)

Table 3A provides the amino acid sequences of the CDRs of the antibodies shown in Table 2A.

Table 3A: CDR sequences for Group I antibodies

Ab	HCDR1	HCDR2	HCDR3	LCDR1	LCDR2	LCDR3
365_B04	SSYGMH (SEQ ID NO: 115)	WVASINYNSGYTS (SEQ ID NO: 172)	ARAANWHDTALD (SEQ ID NO: 229)	LTYLNWY (SEQ ID NO: 286)	LLIYAATSRH (SEQ ID NO: 343)	QQSDESPL (SEQ ID NO: 400)
365_B10	DDYSMH (SEQ ID NO: 116)	WVASINYNSGYKG (SEQ ID NO: 173)	ARAANWHDTALD (SEQ ID NO: 230)	LRYLNWY (SEQ ID NO: 287)	LLIYAATSRA (SEQ ID NO: 344)	QQSDNLPL (SEQ ID NO: 401)
365_C03	SSYGMH (SEQ ID NO: 117)	WVAGINYNSGYKG (SEQ ID NO: 174)	ARAANWHDTHLD (SEQ ID NO: 231)	LTYVNWY (SEQ ID NO: 288)	LVIYATTSLA (SEQ ID NO: 345)	QQSYNTPL (SEQ ID NO: 402)
365_C06	SDYGMH (SEQ ID NO: 118)	WVSGINYNGGYTS (SEQ ID NO: 175)	ARAANWHDTALD (SEQ ID NO: 232)	STYVNWY (SEQ ID NO: 289)	LLIYAVTSLA (SEQ ID NO: 346)	QQSYDNPL (SEQ ID NO: 403)
365_D04	SDYGMH (SEQ ID NO: 119)	WVAGINYNGGYKS (SEQ ID NO: 176)	ARAANWHDTALD (SEQ ID NO: 233)	SSYLNWY (SEQ ID NO: 290)	LVIYAVTSRA (SEQ ID NO: 347)	QQSYDLPL (SEQ ID NO: 404)
365_E04	DSYGMH (SEQ ID NO: 120)	WVASINYNGGYKS (SEQ ID NO: 177)	ARAANWHDTALD (SEQ ID NO: 234)	LSYVNWY (SEQ ID NO: 291)	LLIYAATSLA (SEQ ID NO: 348)	QQSYELPL (SEQ ID NO: 405)
365_F11	DSYSMN (SEQ ID NO: 121)	WVSGINYNSGYKG (SEQ ID NO: 178)	ARAANWHDTHLD (SEQ ID NO: 235)	ISYVNWY (SEQ ID NO: 292)	LLIYAATSRA (SEQ ID NO: 349)	QQSYNTPL (SEQ ID NO: 406)
365_G07	DSYGMH (SEQ ID NO: 122)	WVSSINYNGGYTS (SEQ ID NO: 179)	ARAANWHDTALD (SEQ ID NO: 236)	VSYLNWY (SEQ ID NO: 293)	LLIYAATSRA (SEQ ID NO: 350)	QQSYDNPL (SEQ ID NO: 407)
365_H08	SSYGMH (SEQ ID NO: 123)	WVASINYNGGYKS (SEQ ID NO: 180)	ARAANWHDTALD (SEQ ID NO: 237)	SSYLNWY (SEQ ID NO: 294)	LLIYAASSLQ (SEQ ID NO: 351)	QQSYSTPL (SEQ ID NO: 408)
366_A02	DSYGMN (SEQ	WVASINYNSGYKG (SEQ ID NO:	ARAANWHDTHLD (SEQ ID NO:	VSYVNWY (SEQ ID	LLIYAATSRA (SEQ ID	QQSYDLPL (SEQ ID

	ID NO: 124)	181)	238)	NO: 295)	NO: 352)	NO: 409)
366_A04	SSYGMN (SEQ ID NO: 125)	WVAGINYNGGYTS (SEQ ID NO: 182)	ARAANWHDTALD (SEQ ID NO: 239)	LTYLNWY (SEQ ID NO: 296)	LVIYAATSLA (SEQ ID NO: 353)	QQSDDSPL (SEQ ID NO: 410)
366_D01	SSYGMH (SEQ ID NO: 126)	WVSSINYNGGYTG (SEQ ID NO: 183)	ARAANWHDTHLD (SEQ ID NO: 240)	LTYVNWY (SEQ ID NO: 297)	LLIYAATSRA (SEQ ID NO: 354)	QQSYENPL (SEQ ID NO: 411)
366_D03	DSYGMH (SEQ ID NO: 127)	WVSSINYNGGYTG (SEQ ID NO: 184)	ARAANWHDTHLD (SEQ ID NO: 241)	LSYVNWY (SEQ ID NO: 298)	LLIYAATSRA (SEQ ID NO: 355)	QQSYDLPL (SEQ ID NO: 412)
366_F10	DSYSMN (SEQ ID NO: 128)	WVAGINYNGGYTG (SEQ ID NO: 185)	ARAANWHDTHLD (SEQ ID NO: 242)	VSYLNWY (SEQ ID NO: 299)	LVIYAATSRA (SEQ ID NO: 356)	QQSYDTPL (SEQ ID NO: 413)
366_G06	SSYGMH (SEQ ID NO: 129)	WVASINYNGGYTG (SEQ ID NO: 186)	ARAANWHDTHLD (SEQ ID NO: 243)	VSYVNWY (SEQ ID NO: 300)	LVIYAATSRA (SEQ ID NO: 357)	QQSYDNPL (SEQ ID NO: 414)
367_B09	DSYGMH (SEQ ID NO: 130)	WVASINYNGGYTS (SEQ ID NO: 187)	ARAANWHDTALD (SEQ ID NO: 244)	LSYVNWY (SEQ ID NO: 301)	LVIYAATSRA (SEQ ID NO: 358)	QQSYENPL (SEQ ID NO: 415)
367_B11	SDYSMH (SEQ ID NO: 131)	WVANINYNSGYTS (SEQ ID NO: 188)	ARAANWHDTALD (SEQ ID NO: 245)	LSYLNWY (SEQ ID NO: 302)	LVIYAATSRA (SEQ ID NO: 359)	QQSYSTPL (SEQ ID NO: 416)
367_C09	DSYGMH (SEQ ID NO: 132)	WVASINYNGGYTS (SEQ ID NO: 189)	ARAANWHDTHLD (SEQ ID NO: 246)	LSYVNWY (SEQ ID NO: 303)	LVIYAATSRH (SEQ ID NO: 360)	QQSYNTPL (SEQ ID NO: 417)
367_D11	DSYGMH (SEQ ID NO: 133)	WVSNINYNGGYKS (SEQ ID NO: 190)	ARAANWHDTALD (SEQ ID NO: 247)	ISYLNWY (SEQ ID NO: 304)	LLIYAATSRA (SEQ ID NO: 361)	QQSYDSPL (SEQ ID NO: 418)
367_F06	SSYGMN (SEQ ID NO: 134)	WVSSINYNSGYTS (SEQ ID NO: 191)	ARAANWHDTALD (SEQ ID NO: 248)	SSYVNWY (SEQ ID NO: 305)	LLIYAVTSRA (SEQ ID NO: 362)	QQSYDSPL (SEQ ID NO: 419)
367_H01	DSYGMN (SEQ ID NO: 135)	WVSGINYNGGYKS (SEQ ID NO: 192)	ARAANWHDTALD (SEQ ID NO: 249)	LTYLNWY (SEQ ID NO: 306)	LVIYAATSRA (SEQ ID NO: 363)	QQSYDNPL (SEQ ID NO: 420)
368_A02	DSYGMN (SEQ ID NO: 136)	WVAGINYNGGYKS (SEQ ID NO: 193)	ARAANWHDTHLD (SEQ ID NO: 250)	ISYVNWY (SEQ ID NO: 307)	LVIYAATSRA (SEQ ID NO: 364)	QQSYDTPL (SEQ ID NO: 421)
368_A06	DSYSMH (SEQ ID NO: 137)	WVAGINYNSGYKG (SEQ ID NO: 194)	ARAANWHDTHLD (SEQ ID NO: 251)	LSYVNWY (SEQ ID NO: 308)	LLIYAATSRH (SEQ ID NO: 365)	QQSYNSPL (SEQ ID NO: 422)
368_A12	DSYSMH (SEQ	WVSSINYNSGYKG (SEQ ID NO:	ARAANWHDTALD (SEQ ID NO:	LTYLNWY (SEQ ID	LVIYAATSRA (SEQ ID	QQSYDSPL (SEQ ID

	ID NO: 138)	195)	252)	NO: 309)	NO: 366)	NO: 423)
368_B03	DDYGMN (SEQ ID NO: 139)	WVSGINYNGGYTS (SEQ ID NO: 196)	ARAANWHDTALD (SEQ ID NO: 253)	LTYLNWY (SEQ ID NO: 310)	LVIYAATSLA (SEQ ID NO: 367)	QHSYENPL (SEQ ID NO: 424)
368_B08	DSYGMN (SEQ ID NO: 140)	WVSSINYNGGYTS (SEQ ID NO: 197)	ARAANWHDTHLD (SEQ ID NO: 254)	LTYVNWY (SEQ ID NO: 311)	LVIYAATSRA (SEQ ID NO: 368)	QQSYENPL (SEQ ID NO: 425)
368_B10	DSYGMH (SEQ ID NO: 141)	WVASINYNGGYTS (SEQ ID NO: 198)	ARAANWHDTALD (SEQ ID NO: 255)	LTYLNWY (SEQ ID NO: 312)	LVIYAATSRA (SEQ ID NO: 369)	QQSDELPL (SEQ ID NO: 426)
368_B11	DSYGMH (SEQ ID NO: 142)	WVSGINYNGGYKS (SEQ ID NO: 199)	ARAANWHDTHLD (SEQ ID NO: 256)	LSYLNWY (SEQ ID NO: 313)	LLIYAASSLQ (SEQ ID NO: 370)	QQSYDSPL (SEQ ID NO: 427)
368_C09	SSYSMH (SEQ ID NO: 143)	WVSNINYNGGYTG (SEQ ID NO: 200)	ARAANWHDTHLD (SEQ ID NO: 257)	LTYVNWY (SEQ ID NO: 314)	LLIYAATSLA (SEQ ID NO: 371)	QQSYDLPL (SEQ ID NO: 428)
368_D09	DSYGMH (SEQ ID NO: 144)	WVAGINYNSGYKS (SEQ ID NO: 201)	ARAANWHDTHLD (SEQ ID NO: 258)	VSYVNWY (SEQ ID NO: 315)	LLIYAATSLA (SEQ ID NO: 372)	QQSYDNPL (SEQ ID NO: 429)
368_F02	SSYGMN (SEQ ID NO: 145)	WVASINYNSGYTS (SEQ ID NO: 202)	ARAANWHDTHLD (SEQ ID NO: 259)	LSYLNWY (SEQ ID NO: 316)	LLIYAASSLQ (SEQ ID NO: 373)	QQSYSLPL (SEQ ID NO: 430)
368_F10	SSYGMN (SEQ ID NO: 146)	WVAGINYNSGYTS (SEQ ID NO: 203)	ARAANWHDTHLD (SEQ ID NO: 260)	VSYVNWY (SEQ ID NO: 317)	LLIYAATSRA (SEQ ID NO: 374)	QQSYDTPL (SEQ ID NO: 431)
369_B03	SSYGMH (SEQ ID NO: 147)	WVAGINYNGGYTS (SEQ ID NO: 204)	ARAANWHDTALD (SEQ ID NO: 261)	LTYVNWY (SEQ ID NO: 318)	LVIYAATSLA (SEQ ID NO: 375)	QQSYELPL (SEQ ID NO: 432)
369_G10	SSYGMH (SEQ ID NO: 148)	WVASINYNGGYTS (SEQ ID NO: 205)	ARAANWHDTALD (SEQ ID NO: 262)	LSYLNWY (SEQ ID NO: 319)	LVIYAATSRA (SEQ ID NO: 376)	QQSYDSPL (SEQ ID NO: 433)
369_H03	SSYSMH (SEQ ID NO: 149)	WVASINYNSGYKS (SEQ ID NO: 206)	ARAANWHDTALD (SEQ ID NO: 263)	VSYLNWY (SEQ ID NO: 320)	LLIYATTSRA (SEQ ID NO: 377)	QQSYDTPL (SEQ ID NO: 434)
370_B01	DDYGMH (SEQ ID NO: 150)	WVSGINYNGGYKS (SEQ ID NO: 207)	ARAANWHDTALD (SEQ ID NO: 264)	LSYVNWY (SEQ ID NO: 321)	LLIYVASSRA (SEQ ID NO: 378)	QQSYSLPL (SEQ ID NO: 435)
370_D06	SSYGMN (SEQ ID NO: 151)	WVASINYNGGYTS (SEQ ID NO: 208)	ARAANWHDTHLD (SEQ ID NO: 265)	ISYLNWY (SEQ ID NO: 322)	LVIYAATSLA (SEQ ID NO: 379)	QQSYSSPL (SEQ ID NO: 436)
370_G04	SSYGMH (SEQ	WVSGINYNGGYTG (SEQ ID NO:	ARAANWHDTALD (SEQ ID NO:	LSYVNWY (SEQ ID	LLIYAATSRA (SEQ ID	QQSYSTPL (SEQ ID

	ID NO: 152)	209)	266)	NO: 323)	NO: 380)	NO: 437)
370_H08	SSYGMH (SEQ ID NO: 153)	WVASINYNGGYTS (SEQ ID NO: 210)	ARAANWHDTHLD (SEQ ID NO: 267)	LSYVNWY (SEQ ID NO: 324)	LLIYAATSRH (SEQ ID NO: 381)	QQSYSLPL (SEQ ID NO: 438)
371_A04	DSYGMN (SEQ ID NO: 154)	WVSSINYNSGYTG (SEQ ID NO: 211)	ARAANWHDTALD (SEQ ID NO: 268)	LTYLNWY (SEQ ID NO: 325)	LLIYAVTSRA (SEQ ID NO: 382)	QQSYDTPL (SEQ ID NO: 439)
371_A09	SSYGMN (SEQ ID NO: 155)	WVSGINYNGGYKS (SEQ ID NO: 212)	ARAANWHDTALD (SEQ ID NO: 269)	VTYVNWY (SEQ ID NO: 326)	LVIYAATSRA (SEQ ID NO: 383)	QQSYDSPL (SEQ ID NO: 440)
371_D07	DDYGMN (SEQ ID NO: 156)	WVANINYNGGYKG (SEQ ID NO: 213)	ARAANWHDTHLD (SEQ ID NO: 270)	LTYLNWY (SEQ ID NO: 327)	LVIYAATSRA (SEQ ID NO: 384)	QQSYELPL (SEQ ID NO: 441)
371_D12	DSYGMN (SEQ ID NO: 157)	WVSGINYNGGYKS (SEQ ID NO: 214)	ARAANWHDTALD (SEQ ID NO: 271)	LSYLNWY (SEQ ID NO: 328)	LLIYAATSRA (SEQ ID NO: 385)	QQSYELPL (SEQ ID NO: 442)
371_H02	DDYSMN (SEQ ID NO: 158)	WVSGINYNGGYKS (SEQ ID NO: 215)	ARAANWHDTHLD (SEQ ID NO: 272)	ISYLNWY (SEQ ID NO: 329)	LVIYAATSLA (SEQ ID NO: 386)	QQSYENPL (SEQ ID NO: 443)
372_A09	DSYGMN (SEQ ID NO: 159)	WVSGINYNGGYTS (SEQ ID NO: 216)	ARAANWHDTALD (SEQ ID NO: 273)	LSYLNWY (SEQ ID NO: 330)	LVIYAATSRA (SEQ ID NO: 387)	QQSYNSPL (SEQ ID NO: 444)
372_B11	SSYSMH (SEQ ID NO: 160)	WVAGINYNSGYTS (SEQ ID NO: 217)	ARAANWHDTHLD (SEQ ID NO: 274)	LTYVNWY (SEQ ID NO: 331)	LVIYAATSLA (SEQ ID NO: 388)	QQSYDTPL (SEQ ID NO: 445)
372_E02	SSYGMN (SEQ ID NO: 161)	WVASINYNGGYTS (SEQ ID NO: 218)	ARAANWHDTALD (SEQ ID NO: 275)	ISYVNWY (SEQ ID NO: 332)	LVIYAATSRA (SEQ ID NO: 389)	QQSYDLPL (SEQ ID NO: 446)
373_E11	DSYGMH (SEQ ID NO: 162)	WVASINYNGGYTS (SEQ ID NO: 219)	ARAANWHDTALD (SEQ ID NO: 276)	VSYLNWY (SEQ ID NO: 333)	LVIYAATSRA (SEQ ID NO: 390)	QQSYDSPL (SEQ ID NO: 447)
373_H02	SSYGMH (SEQ ID NO: 163)	WVAGINYNSGYTS (SEQ ID NO: 220)	ARAANWHDTALD (SEQ ID NO: 277)	VSYVNWY (SEQ ID NO: 334)	LLIYAATSRH (SEQ ID NO: 391)	QQSYXNPL (SEQ ID NO: 448)
374_B02	DSYSMH (SEQ ID NO: 164)	WVAGINYNSGYTS (SEQ ID NO: 221)	ARAANWHDTHLD (SEQ ID NO: 278)	ISYLNWY (SEQ ID NO: 335)	LLIYAATSRA (SEQ ID NO: 392)	QQSYDSPL (SEQ ID NO: 449)
374_F03	SSYGMN (SEQ ID NO: 165)	WVASINYNGGYTS (SEQ ID NO: 222)	ARAANWHDTHLD (SEQ ID NO: 279)	ISYVNWY (SEQ ID NO: 336)	LVIYAATSRA (SEQ ID NO: 393)	QQSYDTPL (SEQ ID NO: 450)
375_A04	DSYGMN (SEQ	WVAGINYNGGYKS (SEQ ID NO:	ARAANWHDTALD (SEQ ID NO:	LTYLNWY (SEQ ID	LVIYYVNNLP (SEQ ID	QQSYNSPL (SEQ ID

	ID NO: 166)	223)	280)	NO: 337)	NO: 394)	NO: 451)
375_A11	SDYGMH (SEQ ID NO: 167)	WVSSINYNSGYKS (SEQ ID NO: 224)	ARAANWHDTALD (SEQ ID NO: 281)	VSYLNWY (SEQ ID NO: 338)	LLIYYVTNLA (SEQ ID NO: 395)	QQSYDNPL (SEQ ID NO: 452)
375_C10	SSYGMH (SEQ ID NO: 168)	WVASINYNGGYTS (SEQ ID NO: 225)	ARAANWHDTALD (SEQ ID NO: 282)	STYLNWY (SEQ ID NO: 339)	LVIYAASSLQ (SEQ ID NO: 396)	QQSYSTPL (SEQ ID NO: 453)
375_F12	DSYGMH (SEQ ID NO: 169)	WVASINYNGGYTS (SEQ ID NO: 226)	ARAANWHDTALD (SEQ ID NO: 283)	LTYLNWY (SEQ ID NO: 340)	LVIYAATSRA (SEQ ID NO: 397)	QQSDELPL (SEQ ID NO: 454)
375_H01	SDYSMN (SEQ ID NO: 170)	WVAGINYNSGYTS (SEQ ID NO: 227)	ARAANWHDTHLD (SEQ ID NO: 284)	LTYLNWY (SEQ ID NO: 341)	LLIYAATSRH (SEQ ID NO: 398)	QQSYSNPL (SEQ ID NO: 455)
376_G02	SDYGMN (SEQ ID NO: 171)	WVSGINYNGGYTS (SEQ ID NO: 228)	ARAANWHDTALD (SEQ ID NO: 285)	SRYLNWY (SEQ ID NO: 342)	LVIYAATSLA (SEQ ID NO: 399)	QQSYDNPL (SEQ ID NO: 456)

The consensus sequences for each of these CDRs shown in Fig. 3A are as follows:

HCDR1: D/SS/DYG/SMH/N (SEQ ID NO: 6550)

HCDR2: WVA/SS/G/NINYNG/SGYT/KS/G (SEQ ID NO: 6551)

HCDR3: ARAANWHDTA/HLD (SEQ ID NO: 6552)

LCDR1: L/V/I/SS/T/RYL/VNWY (SEQ ID NO: 6554)

LCDR2: LV/LIYA/Y/VA/V/TT/S/NS/NR/LA/H/Q/P (SEQ ID NO: 6592)

LCDR3 QQ/HSY/DD/E/S/NL/N/S/TPL (SEQ ID NO: 6593)

Table 2B: Group II Antibody Sequences

Ab	VH sequence	VL sequence
365_A05	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMHWVRQAPGKGLEWVSSINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 457)	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQ KPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYSTPLTFGGGTKVEIK (SEQ ID NO: 528)
365_B08	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMNWVRQAPGKGLEWVSNINYNSGYKGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 458)	DIQMTQSPSSLSASVGDRVTITCRASQSIVTYLNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYSSPLTFGGGTKVEIK (SEQ ID NO: 529)
365_B12	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDY GMHWVRQAPGKGLEWVSGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 459)	DIQMTQSPSSLSASVGDRVTITCRASQSISTYVNWYQQ KPGKAPKLLIYAVTSLHSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDNPLTFGGGTKVEIK (SEQ ID NO: 530)
365_D03	EVQLLESGGGLVQPGGSLRLSCAASGFTFDDY SMHWVRQAPGKGLEWVASINYNGGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYLNWYQQ KPGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDSPLTFGGGTKVEIK (SEQ

	ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 460)	ID NO: 531)
365_D08	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY SMHWVRQAPGKGLEWVSSINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 461)	DIQMTQSPSSLSASVGDRVTITCRASQSIITYVNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDTPLTFGGGTKVEIK (SEQ ID NO: 532)
365_E06	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMNWVRQAPGKGLEWVSGINYNGGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 462)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQ KPGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYNTPLTFGGGTKVEIK (SEQ ID NO: 533)
365_F10	EVQLLESGGGLVQPGGSLRLSCAASGFTFDDY GMHWVRQAPGKGLEWVSGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 463)	DIQMTQSPSSLSASVGDRVTITCRASQSIVTYVNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYELPLTFGGGTKVEIK (SEQ ID NO: 534)
365_G06	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMHWVRQAPGKGLEWVAGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 464)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLNWYQQ KPGKAPKLLIYAATSLASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSDSTPLTFGGGTKVEIK (SEQ ID NO: 535)
365_G08	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMHWVRQAPGKGLEWVASINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 465)	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQ KPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYETPLTFGGGTKVEIK (SEQ ID NO: 536)
366_B09	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDY GMHWVRQAPGKGLEWVSSINYNSGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 466)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQ KPGKAPKLVIYAATSRHSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDSPLTFGGGTKVEIK (SEQ ID NO: 537)
366_C05	EVQLLESGGGLVQPGGSLRLSCAASGFTFDDY GMHWVRQAPGKGLEWVSSINYNGGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 467)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYLNWYQQ KPGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDSPLTFGGGTKVEIK (SEQ ID NO: 538)
366_E07	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMHWVRQAPGKGLEWVAGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTALDYWGQGTLVTVSS (SEQ ID NO: 468)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQ KPGKAPKLVIYAATSRHSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSDNSPLTFGGGTKVEIK (SEQ ID NO: 539)
366_G02	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMHWVRQAPGKGLEWVSSINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 469)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQ KPGKAPKLLIYAATSRHSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSDDNPLTFGGGTKVEIK (SEQ ID NO: 540)
366_H01	EVQLLESGGGLVQPGGSLRLSCAASGFTFDDY SMHWVRQAPGKGLEWVANINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 470)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQ KPGKAPKLVIYATTSRHSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYESPLTFGGGTKVEIK (SEQ ID NO: 541)
367_C06	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY SMHWVRQAPGKGLEWVASINYNGGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 471)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQ KPGKAPKLVIYAATSLHSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDTPLTFGGGTKVEIK (SEQ ID NO: 542)
367_C12	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMHWVRQAPGKGLEWVSGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 472)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVNWYQQ KPGKAPKLLIYATTSRHSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYESPLTFGGGTKVEIK (SEQ ID NO: 543)

367_E08	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDY GMNWVRQAPGKGLEWVASINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 473)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLNWYQQ KPGKAPKLLIYATTSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDNPLTFGGGTKVEIK (SEQ ID NO: 544)
367_E10	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMHWVRQAPGKGLEWVSSINYNGGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 474)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYELPLTFGGGTKVEIK (SEQ ID NO: 545)
367_F08	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMHWVRQAPGKGLEWVSSINYNSGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 475)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVNWYQQ KPGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSNELPLTFGGGTKVEIK (SEQ ID NO: 546)
367_F10	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMNWVRQAPGKGLEWVSGINYNSGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 476)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDTPLTFGGGTKVEIK (SEQ ID NO: 547)
367_G03	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY SMHWVRQAPGKGLEWVANINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 477)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVNWYQQ KPGKAPKLVIYAATSRHSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDLPLTFGGGTKVEIK (SEQ ID NO: 548)
367_G11	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMHWVRQAPGKGLEWVASINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 478)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQ KPGKAPKLLIYAATSRHSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSDDSPLTFGGGTKVEIK (SEQ ID NO: 549)
367_H08	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMNWVRQAPGKGLEWVSSINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 479)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVNWYQQ KPGKAPKLLIYAATSRHSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYNLPLTFGGGTKVEIK (SEQ ID NO: 550)
368_B04	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMHWVRQAPGKGLEWVSSINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 480)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYLNWYQQ KPGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYENPLTFGGGTKVEIK (SEQ ID NO: 551)
368_B12	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMHWVRQAPGKGLEWVSGINYNSGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 481)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDLPLTFGGGTKVEIK (SEQ ID NO: 552)
368_C04	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMHWVRQAPGKGLEWVSNINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 482)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYSTPLTFGGGTKVEIK (SEQ ID NO: 553)
368_C07	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMHWVRQAPGKGLEWVAGINYNSGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 483)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVNWYQQ KPGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYENPLTFGGGTKVEIK (SEQ ID NO: 554)
368_C12	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMHWVRQAPGKGLEWVASINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 484)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSDSNPLTFGGGTKVEIK (SEQ ID NO: 555)
368_D03	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDY SMHWVRQAPGKGLEWVASINYNGGYTSYADSV	DIQMTQSPSSLSASVGDRVTITCRASQSIITYVNWYQQ KPGKAPKLLIYATTSRASGVPSRFSGSGSGTDFTLTIS

	KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 485)	SLQPEDFATYYCQQSYDLPLTFGGGTKVEIK (SEQ ID NO: 556)
368_D06	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMNWVRQAPGKGLEWVSNINYNGGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 486)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVNWYQQ KPGKAPKLVIYAATSRHSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYENPLTFGGGTKVEIK (SEQ ID NO: 557)
368_D07	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMHWVRQAPGKGLEWVASINYNGGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 487)	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQ KPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYSTPLTFGGGTKVEIK (SEQ ID NO: 558)
368_E05	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY SMHWVRQAPGKGLEWVSSINYNGGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 488)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLNWYQQ KPGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYSSPLTFGGGTKVEIK (SEQ ID NO: 559)
368_E08	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMHWVRQAPGKGLEWVANINYNSGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 489)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVNWYQQ KPGKAPKLVIYAATSLHSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYETPLTFGGGTKVEIK (SEQ ID NO: 560)
368_G11	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMHWVRQAPGKGLEWVSGINYNSGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTALDYWGQGTLVTVSS (SEQ ID NO: 490)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSDNTPLTFGGGTKVEIK (SEQ ID NO: 561)
368_H03	EVQLLESGGGLVQPGGSLRLSCAASGFTFDDY SMHWVRQAPGKGLEWVASINYNGGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 491)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVNWYQQ KPGKAPKLVIYAVTSRHSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYSNPLTFGGGTKVEIK (SEQ ID NO: 562)
369_A04	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMHWVRQAPGKGLEWVASINYNGGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 492)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVNWYQQ KPGKAPKLVIYAATSLASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDLPLTFGGGTKVEIK (SEQ ID NO: 563)
369_A12	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMHWVRQAPGKGLEWVASINYNSGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 493)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQ KPGKAPKLLIYAATSRHSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDLPLTFGGGTKVEIK (SEQ ID NO: 564)
369_B07	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMHWVRQAPGKGLEWVANINYNGGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 494)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVNWYQQ KPGKAPKLVIYAATSLASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDLPLTFGGGTKVEIK (SEQ ID NO: 565)
369_B08	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMHWVRQAPGKGLEWVSSINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 495)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYESPLTFGGGTKVEIK (SEQ ID NO: 566)
369_C06	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMHWVRQAPGKGLEWVSSINYNGGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 496)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDSPLTFGGGTKVEIK (SEQ ID NO: 567)
369_C09	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMHWVRQAPGKGLEWVSSINYNGGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYLNWYQQ KPGKAPKLVIYAATSRHSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDLPLTFGGGTKVEIK (SEQ ID NO: 568)

	NO: 497)	
369_C11	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDY GMHWVRQAPGKGLEWVAGINYNGGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 498)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLNWYQQ KPGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDTPLTFGGGTKVEIK (SEQ ID NO: 569)
369_E03	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMHWVRQAPGKGLEWVAGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 499)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVNWYQQ KPGKAPKLLIYAATSLASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYENPLTFGGGTKVEIK (SEQ ID NO: 570)
370_B06	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMHWVRQAPGKGLEWVAGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 500)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVNWYQQ KPGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYETPLTFGGGTKVEIK (SEQ ID NO: 571)
370_B07	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMHWVRQAPGKGLEWVANINYNSGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 501)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVNWYQQ KPGKAPKLLIYAATSRHSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYSSPLTFGGGTKVEIK (SEQ ID NO: 572)
370_E12	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMHWVRQAPGKGLEWVAGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 502)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYENPLTFGGGTKVEIK (SEQ ID NO: 573)
370_H05	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMHWVRQAPGKGLEWVSNINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 503)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLNWYQQ KPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSDSLPLTFGGGTKVEIK (SEQ ID NO: 574)
371_A05	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMHWVRQAPGKGLEWVSNINYNGGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 504)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSDNLPLTFGGGTKVEIK (SEQ ID NO: 575)
371_B02	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMNWVRQAPGKGLEWVSNINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 505)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVNWYQQ KPGKAPKLVIYAATSLASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYNNPLTFGGGTKVEIK (SEQ ID NO: 576)
371_B11	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMHWVRQAPGKGLEWVASINYNSGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 506)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYELPLTFGGGTKVEIK (SEQ ID NO: 577)
371_C02	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMHWVRQAPGKGLEWVAGINYNSGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 507)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVNWYQQ KPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDTPLTFGGGTKVEIK (SEQ ID NO: 578)
371_D05	EVQLLESGGGLVQPGGSLRLSCAASGFTFDDY GMHWVRQAPGKGLEWVSGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 508)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQ KPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDSPLTFGGGTKVEIK (SEQ ID NO: 579)
371_F07	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMHWVRQAPGKGLEWVAGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 509)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQ KPGKAPKLLIYAATSLASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSDSNPLTFGGGTKVEIK (SEQ ID NO: 580)

371_G07	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDY GMHWVRQAPGKGLEWVAGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 510)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVNWYQQ KPGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYSLPLTFGGGTKVEIK (SEQ ID NO: 581)
372_D07	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMNWVRQAPGKGLEWVAGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 511)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYESPLTFGGGTKVEIK (SEQ ID NO: 582)
373_B01	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMHWVRQAPGKGLEWVSGINYNGGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 512)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVNWYQQ KPGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDLPLTFGGGTKVEIK (SEQ ID NO: 583)
373_D11	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMHWVRQAPGKGLEWVAGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 513)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDNPLTFGGGTKVEIK (SEQ ID NO: 584)
373_G06	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMHWVRQAPGKGLEWVASINYNSGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 514)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVNWYQQ KPGKAPKLLIYAATSLASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYNLPLTFGGGTKVEIK (SEQ ID NO: 585)
374_A10	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMHWVRQAPGKGLEWVSGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 515)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDTPLTFGGGTKVEIK (SEQ ID NO: 586)
374_A12	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMHWVRQAPGKGLEWVSSINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 516)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSDSNPLTFGGGTKVEIK (SEQ ID NO: 587)
374_B01	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMHWVRQAPGKGLEWVAGINYNSGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 517)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLNWYQQ KPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDSPLTFGGGTKVEIK (SEQ ID NO: 588)
374_B07	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMHWVRQAPGKGLEWVSSINYNGGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 518)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYLNWYQQ KPGKAPKLLIYAATSLASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYESPLTFGGGTKVEIK (SEQ ID NO: 589)
374_H02	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMHWVRQAPGKGLEWVASINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 519)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVNWYQQ KPGKAPKLLIYAATSLASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDTPLTFGGGTKVEIK (SEQ ID NO: 590)
375_C03	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY SMHWVRQAPGKGLEWVSGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 520)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVNWYQQ KPGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYESPLTFGGGTKVEIK (SEQ ID NO: 591)
375_C05	EVQLLESGGGLVQPGGSLRLSCAASGFTFXSY GMNWVRQAPGKGLEWVASINYNGGYKGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 521)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYELPLTFGGGTKVEIK (SEQ ID NO: 592)
375_D02	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVSNINYNGGYTSYADSV	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQ KPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTIS

	KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 522)	SLQPEDFATYYCQQSYELPLTFGGGTKVEIK (SEQ ID NO: 593)
375_G08	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMHWVRQAPGKGLEWVSGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 523)	DIQMTQSPSSLSASVGDRVTITCRASQSISSYVNWYQQ KPGKAPKLLIYAVTSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYSTPLTFGGGTKVEIK (SEQ ID NO: 594)
375_H04	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMHWVRQAPGKGLEWVAGINYNSGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 524)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLNWYQQ KPGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYSNPLTFGGGTKVEIK (SEQ ID NO: 595)
376_D08	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMNWVRQAPGKGLEWVANINYNSGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTALDYWGQGTLVTVSS (SEQ ID NO: 525)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQ KPGKAPKLVIYYANNRPSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYSNPLTFGGGTKVEIK (SEQ ID NO: 596)
376_F09	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY SMHWVRQAPGKGLEWVSSINYNGGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 526)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVNWYQQ KPGKAPKLLIYAVTSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDTPLTFGGGTKVEIK (SEQ ID NO: 597)
376_H12	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDY GMHWVRQAPGKGLEWVASINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARAATWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 527)	DIQMTQSPSSLSASVGDRVTITCRASQSIITYLNWYQQ KPGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYESPLTFGGGTKVEIK (SEQ ID NO: 598)

Table 3B provides the amino acid sequences of the CDRs of the antibodies shown in Table 2B.

Table 3B: CDR sequences for Group II antibodies

Ab	HCDR1	HCDR2	HCDR3	LCDR1	LCDR2	LCDR3
365_A05	SSYGMH (SEQ ID NO: 599)	WVSSINYNGGYTS (SEQ ID NO: 670)	ARAATWHDTHLD (SEQ ID NO: 742)	SSYLNWY (SEQ ID NO: 813)	LLIYAASSLQ (SEQ ID NO: 884)	QQSYSTPL (SEQ ID NO: 955)
365_B08	DSYGMN (SEQ ID NO: 600)	WVSNINYNSGYKG (SEQ ID NO: 671)	ARAATWHDTHLD (SEQ ID NO: 743)	VTYLNWY (SEQ ID NO: 814)	LLIYAATSRA (SEQ ID NO: 885)	QQSYSSPL (SEQ ID NO: 956)
365_B12	SDYGMH (SEQ ID NO: 601)	WVSGINYNGGYTS (SEQ ID NO: 672)	ARAATWHDTHLD (SEQ ID NO: 744)	STYVNWY (SEQ ID NO: 815)	LLIYAVTSLH (SEQ ID NO: 886)	QQSYDNPL (SEQ ID NO: 957)
365_D03	DDYSMH (SEQ ID NO: 602)	WVASINYNGGYKS (SEQ ID NO: 673)	ARAATWHDTHLD (SEQ ID NO: 745)	VSYLNWY (SEQ ID NO: 816)	LVIYAATSRA (SEQ ID NO: 887)	QQSYDSPL (SEQ ID NO: 958)
365_D08	DSYSMH (SEQ ID NO: 603)	WVSSINYNGGYTS (SEQ ID NO: 674)	ARAATWHDTHLD (SEQ ID NO: 746)	ITYVNWY (SEQ ID NO: 817)	LLIYAATSRA (SEQ ID NO: 888)	QQSYDTPL (SEQ ID NO: 959)
365_E06	DSYGMN (SEQ ID NO: 604)	WVSGINYNGGYTG (SEQ ID NO: 675)	ARAATWHDTHLD (SEQ ID NO: 747)	LTYLNWY (SEQ ID NO: 818)	LVIYAATSRA (SEQ ID NO: 889)	QQSYNTPL (SEQ ID NO: 960)
365_F10	DDYGMH (SEQ ID NO: 605)	WVSGINYNGGYTS (SEQ ID NO: 676)	ARAATWHDTHLD (SEQ ID NO: 748)	VTYVNWY (SEQ ID NO: 819)	LLIYAATSRA (SEQ ID NO: 890)	QQSYELPL (SEQ ID NO: 961)
365_G06	DSYGMH (SEQ ID NO: 606)	WVAGINYNGGYTS (SEQ ID NO: 677)	ARAATWHDTHLD (SEQ ID NO: 749)	LSYLNWY (SEQ ID NO: 820)	LLIYAATSLA (SEQ ID NO: 891)	QQSDSTPL (SEQ ID NO: 962)
365_G08	SSYGMH (SEQ	WVASINYNGGYTS (SEQ ID NO:	ARAATWHDTHLD (SEQ ID NO:	SSYLNWY (SEQ ID	LLIYAASSLQ (SEQ ID	QQSYETPL (SEQ ID

	ID NO: 607)	678)	750)	NO: 821)	NO: 892)	NO: 963)
366_B09	SDYGMH (SEQ ID NO: 608)	WVSSINYNSGYKS (SEQ ID NO: 679)	ARAATWHDTHLD (SEQ ID NO: 751)	LTYLNWY (SEQ ID NO: 822)	LVIYAATSRH (SEQ ID NO: 893)	QQSYDSPL (SEQ ID NO: 964)
366_C05	DDYGMH (SEQ ID NO: 609)	WVSSINYNGGYTG (SEQ ID NO: 680)	ARAATWHDTHLD (SEQ ID NO: 752)	ISYLNWY (SEQ ID NO: 823)	LVIYAATSRA (SEQ ID NO: 894)	QQSYDSPL (SEQ ID NO: 965)
366_E07	DSYGMH (SEQ ID NO: 610)	WVAGINYNGGYTS (SEQ ID NO: 681)	ARAATWHDTALD (SEQ ID NO: 753)	LTYLNWY (SEQ ID NO: 824)	LVIYAATSRH (SEQ ID NO: 895)	QQSDNSPL (SEQ ID NO: 966)
366_G02	DSYGMH (SEQ ID NO: 611)	WVSSINYNGGYTS (SEQ ID NO: 682)	ARAATWHDTHLD (SEQ ID NO: 754)	LTYLNWY (SEQ ID NO: 825)	LLIYAATSRH (SEQ ID NO: 896)	QQSDDNPL (SEQ ID NO: 967)
366_H01	DDYSMH (SEQ ID NO: 612)	WVANINYNGGYTS (SEQ ID NO: 683)	ARAATWHDTHLD (SEQ ID NO: 755)	LTYLNWY (SEQ ID NO: 826)	LVIYATTSRH (SEQ ID NO: 897)	QQSYESPL (SEQ ID NO: 968)
367_C06	DSYSMH (SEQ ID NO: 613)	WVASINYNGGYKS (SEQ ID NO: 684)	ARAATWHDTHLD (SEQ ID NO: 756)	LTYLNWY (SEQ ID NO: 827)	LVIYAATSLH (SEQ ID NO: 898)	QQSYDTPL (SEQ ID NO: 969)
367_C12	SSYGMH (SEQ ID NO: 614)	WVSGINYNGGYTS (SEQ ID NO: 685)	ARAATWHDTHLD (SEQ ID NO: 757)	LSYVNWY (SEQ ID NO: 828)	LLIYATTSRH (SEQ ID NO: 899)	QQSYESPL (SEQ ID NO: 970)
367_E08	SDYGMN (SEQ ID NO: 615)	WVASINYNGGYTS (SEQ ID NO: 686)	ARAATWHDTHLD (SEQ ID NO: 758)	LSYLNWY (SEQ ID NO: 829)	LLIYATTSRA (SEQ ID NO: 900)	QQSYDNPL (SEQ ID NO: 971)
367_E10	SSYGMH (SEQ ID NO: 616)	WVSSINYNGGYTG (SEQ ID NO: 687)	ARAATWHDTHLD (SEQ ID NO: 759)	LSYVNWY (SEQ ID NO: 830)	LLIYAATSRA (SEQ ID NO: 901)	QQSYELPL (SEQ ID NO: 972)
367_F08	SSYGMH (SEQ	WVSSINYNSGYTS (SEQ ID NO:	ARAATWHDTHLD (SEQ ID NO:	LSYVNWY (SEQ ID	LVIYAATSRA (SEQ ID	QQSNELPL (SEQ ID NO: 973)

	ID NO: 617)	688)	760)	NO: 831)	NO: 902)	
367_F10	DSYGMN (SEQ ID NO: 618)	WVSGINYNSGYTS (SEQ ID NO: 689)	ARAATWHDTHLD (SEQ ID NO: 761)	LTYLNWY (SEQ ID NO: 832)	LLIYAATSRA (SEQ ID NO: 903)	QQSYDTPL (SEQ ID NO: 974)
367_G03	DSYSMH (SEQ ID NO: 619)	WVANINYNGGYTS (SEQ ID NO: 690)	ARAATWHDTHLD (SEQ ID NO: 762)	VSYVNWY (SEQ ID NO: 833)	LVIYAATSRH (SEQ ID NO: 904)	QQSYDLPL (SEQ ID NO: 975)
367_G11	SSYGMH (SEQ ID NO: 620)	WVASINYNGGYTS (SEQ ID NO: 691)	ARAATWHDTHLD (SEQ ID NO: 763)	LTYLNWY (SEQ ID NO: 834)	LLIYAATSRH (SEQ ID NO: 905)	QQSDDSPL (SEQ ID NO: 976)
367_H08	DSYGMN (SEQ ID NO: 621)	WVSSINYNGGYTS (SEQ ID NO: 692)	ARAATWHDTHLD (SEQ ID NO: 764)	LTYVNWY (SEQ ID NO: 835)	LLIYAATSRH (SEQ ID NO: 906)	QQSYNLPL (SEQ ID NO: 977)
368_B04	DSYGMH (SEQ ID NO: 622)	WVSSINYNGGYTS (SEQ ID NO: 693)	ARAATWHDTHLD (SEQ ID NO: 765)	VSYLNWY (SEQ ID NO: 836)	LVIYAATSRA (SEQ ID NO: 907)	QQSYENPL (SEQ ID NO: 978)
368_B12	DSYGMH (SEQ ID NO: 623)	WVSGINYNSGYTS (SEQ ID NO: 694)	ARAATWHDTHLD (SEQ ID NO: 766)	VSYVNWY (SEQ ID NO: 837)	LLIYAATSRA (SEQ ID NO: 908)	QQSYDLPL (SEQ ID NO: 979)
368_C04	DSYGMH (SEQ ID NO: 624)	WVSNINYNGGYTS (SEQ ID NO: 695)	ARAATWHDTHLD (SEQ ID NO: 767)	LSYVNWY (SEQ ID NO: 838)	LLIYAATSRA (SEQ ID NO: 909)	QQSYSTPL (SEQ ID NO: 980)
368_C07	SSYGMH (SEQ ID NO: 625)	WVAGINYNSGYTS (SEQ ID NO: 696)	ARAATWHDTHLD (SEQ ID NO: 768)	VSYVNWY (SEQ ID NO: 839)	LVIYAATSRA (SEQ ID NO: 910)	QQSYENPL (SEQ ID NO: 981)
368_C12	DSYGMH (SEQ ID NO: 626)	WVASINYNGGYTS (SEQ ID NO: 697)	ARAATWHDTHLD (SEQ ID NO: 769)	LTYLNWY (SEQ ID NO: 840)	LLIYAATSRA (SEQ ID NO: 911)	QQSDSNPL (SEQ ID NO: 982)
368_D03	SDYSMH (SEQ	WVASINYNGGYTS (SEQ ID NO:	ARAATWHDTHLD (SEQ ID NO:	ITYVNWY (SEQ ID	LLIYATTSRA (SEQ ID	QQSYDLPL (SEQ ID NO: 983)

	ID NO: 627)	698)	770)	NO: 841)	NO: 912)	
368_D06	SSYGMN (SEQ ID NO: 628)	WVSNINYNGGYTG (SEQ ID NO: 699)	ARAATWHDTHLD (SEQ ID NO: 771)	LSYVNWY (SEQ ID NO: 842)	LVIYAATSRH (SEQ ID NO: 913)	QQSYENPL (SEQ ID NO: 984)
368_D07	DSYGMH (SEQ ID NO: 629)	WVASINYNGGYTG (SEQ ID NO: 700)	ARAATWHDTHLD (SEQ ID NO: 772)	SSYLNWY (SEQ ID NO: 843)	LLIYAASSLQ (SEQ ID NO: 914)	QQSYSTPL (SEQ ID NO: 985)
368_E05	DSYSMH (SEQ ID NO: 630)	WVSSINYNGGYKS (SEQ ID NO: 701)	ARAATWHDTHLD (SEQ ID NO: 773)	LSYLNWY (SEQ ID NO: 844)	LVIYAATSRA (SEQ ID NO: 915)	QQSYSSPL (SEQ ID NO: 986)
368_E08	DSYGMH (SEQ ID NO: 631)	WVANINYNSGYTG (SEQ ID NO: 702)	ARAATWHDTHLD (SEQ ID NO: 774)	LSYVNWY (SEQ ID NO: 845)	LVIYAATSLH (SEQ ID NO: 916)	QQSYETPL (SEQ ID NO: 987)
368_G11	DSYGMH (SEQ ID NO: 632)	WVSGINYNSGYKS (SEQ ID NO: 703)	ARAATWHDTALD (SEQ ID NO: 775)	LTYLNWY (SEQ ID NO: 846)	LLIYAATSRA (SEQ ID NO: 917)	QQSDNTPL (SEQ ID NO: 988)
368_H03	DDYSMH (SEQ ID NO: 633)	WVASINYNGGYTG (SEQ ID NO: 704)	ARAATWHDTHLD (SEQ ID NO: 776)	LSYVNWY (SEQ ID NO: 847)	LVIYAVTSRH (SEQ ID NO: 918)	QQSYSNPL (SEQ ID NO: 989)
369_A04	DSYGMH (SEQ ID NO: 634)	WVASINYNGGYKS (SEQ ID NO: 705)	ARAATWHDTHLD (SEQ ID NO: 777)	VSYVNWY (SEQ ID NO: 848)	LVIYAATSLA (SEQ ID NO: 919)	QQSYDLPL (SEQ ID NO: 990)
369_A12	SSYSMH (SEQ ID NO: 635)	WVASINYNSGYTG (SEQ ID NO: 706)	ARAATWHDTHLD (SEQ ID NO: 778)	LTYLNWY (SEQ ID NO: 849)	LLIYAATSRH (SEQ ID NO: 920)	QQSYDLPL (SEQ ID NO: 991)
369_B07	DSYGMH (SEQ ID NO: 636)	WVANINYNGGYKS (SEQ ID NO: 707)	ARAATWHDTHLD (SEQ ID NO: 779)	VSYVNWY (SEQ ID NO: 850)	LVIYAATSLA (SEQ ID NO: 921)	QQSYDLPL (SEQ ID NO: 992)
369_B08	DSYGMH (SEQ	WVSSINYNGGYTS (SEQ ID NO:	ARAATWHDTHLD (SEQ ID NO:	LSYVNWY (SEQ ID	LLIYAATSRA (SEQ ID	QQSYESPL (SEQ ID NO: 993)

	ID NO: 637)	708)	780)	NO: 851)	NO: 922)	
369_C06	SSYSMH (SEQ ID NO: 638)	WVSSINYNGGYKS (SEQ ID NO: 709)	ARAATWHDTHLD (SEQ ID NO: 781)	LSYVNWY (SEQ ID NO: 852)	LLIYAATSRA (SEQ ID NO: 923)	QQSYDSPL (SEQ ID NO: 994)
369_C09	SSYGMH (SEQ ID NO: 639)	WVSSINYNGGYTG (SEQ ID NO: 710)	ARAATWHDTHLD (SEQ ID NO: 782)	VSYLNWY (SEQ ID NO: 853)	LVIYAATSRH (SEQ ID NO: 924)	QQSYDLPL (SEQ ID NO: 995)
369_C11	SDYGMH (SEQ ID NO: 640)	WVAGINYNGGYTG (SEQ ID NO: 711)	ARAATWHDTHLD (SEQ ID NO: 783)	LSYLNWY (SEQ ID NO: 854)	LVIYAATSRA (SEQ ID NO: 925)	QQSYDTPL (SEQ ID NO: 996)
369_E03	SSYGMH (SEQ ID NO: 641)	WVAGINYNGGYTS (SEQ ID NO: 712)	ARAATWHDTHLD (SEQ ID NO: 784)	LSYVNWY (SEQ ID NO: 855)	LLIYAATSLA (SEQ ID NO: 926)	QQSYENPL (SEQ ID NO: 997)
370_B06	SSYGMH (SEQ ID NO: 642)	WVAGINYNGGYTS (SEQ ID NO: 713)	ARAATWHDTHLD (SEQ ID NO: 785)	VSYVNWY (SEQ ID NO: 856)	LVIYAATSRA (SEQ ID NO: 927)	QQSYETPL (SEQ ID NO: 998)
370_B07	SSYGMH (SEQ ID NO: 643)	WVANINYNSGYKS (SEQ ID NO: 714)	ARAATWHDTHLD (SEQ ID NO: 786)	LTYVNWY (SEQ ID NO: 857)	LLIYAATSRH (SEQ ID NO: 928)	QQSYSSPL (SEQ ID NO: 999)
370_E12	DSYGMH (SEQ ID NO: 644)	WVAGINYNGGYTS (SEQ ID NO: 715)	ARAATWHDTHLD (SEQ ID NO: 787)	LSYVNWY (SEQ ID NO: 858)	LLIYAATSRA (SEQ ID NO: 929)	QQSYENPL (SEQ ID NO: 1000)
370_H05	SSYGMH (SEQ ID NO: 645)	WVSNINYNGGYTS (SEQ ID NO: 716)	ARAATWHDTHLD (SEQ ID NO: 788)	LSYLNWY (SEQ ID NO: 859)	LLIYAASSLQ (SEQ ID NO: 930)	QQSDSLPL (SEQ ID NO: 1001)
371_A05	SSYGMH (SEQ ID NO: 646)	WVSNINYNGGYKS (SEQ ID NO: 717)	ARAATWHDTHLD (SEQ ID NO: 789)	LTYLNWY (SEQ ID NO: 860)	LLIYAATSRA (SEQ ID NO: 931)	QQSDNLPL (SEQ ID NO: 1002)
371_B02	DSYGMN (SEQ	WVSNINYNGGYTS (SEQ ID NO:	ARAATWHDTHLD (SEQ ID NO:	LTYVNWY (SEQ ID	LVIYAATSLA (SEQ ID	QQSYNNPL (SEQ ID NO:

	ID NO: 647)	718)	790)	NO: 861)	NO: 932)	1003)
371_B11	SSYSMH (SEQ ID NO: 648)	WVASINYNSGYTS (SEQ ID NO: 719)	ARAATWHDTHLD (SEQ ID NO: 791)	LTYLNWY (SEQ ID NO: 862)	LLIYAATSRA (SEQ ID NO: 933)	QQSYELPL (SEQ ID NO: 1004)
371_C02	DSYGMH (SEQ ID NO: 649)	WVAGINYNSGYTG (SEQ ID NO: 720)	ARAATWHDTHLD (SEQ ID NO: 792)	LTYVNWY (SEQ ID NO: 863)	LLIYAASSLQ (SEQ ID NO: 934)	QQSYDTPL (SEQ ID NO: 1005)
371_D05	DDYGMH (SEQ ID NO: 650)	WVSGINYNGGYTS (SEQ ID NO: 721)	ARAATWHDTHLD (SEQ ID NO: 793)	LTYLNWY (SEQ ID NO: 864)	LLIYAASSLQ (SEQ ID NO: 935)	QQSYDSPL (SEQ ID NO: 1006)
371_F07	SSYGMH (SEQ ID NO: 651)	WVAGINYNGGYTS (SEQ ID NO: 722)	ARAATWHDTHLD (SEQ ID NO: 794)	LTYLNWY (SEQ ID NO: 865)	LLIYAATSLA (SEQ ID NO: 936)	QQSDSNPL (SEQ ID NO: 1007)
371_G07	SDYGMH (SEQ ID NO: 652)	WVAGINYNGGYTS (SEQ ID NO: 723)	ARAATWHDTHLD (SEQ ID NO: 795)	VSYVNWY (SEQ ID NO: 866)	LVIYAATSRA (SEQ ID NO: 937)	QQSYSLPL (SEQ ID NO: 1008)
372_D07	SSYGMN (SEQ ID NO: 653)	WVAGINYNGGYTS (SEQ ID NO: 724)	ARAATWHDTHLD (SEQ ID NO: 796)	LSYLNWY (SEQ ID NO: 867)	LLIYAATSRA (SEQ ID NO: 938)	QQSYESPL (SEQ ID NO: 1009)
373_B01	DSYGMH (SEQ ID NO: 654)	WVSGINYNGGYKS (SEQ ID NO: 725)	ARAATWHDTHLD (SEQ ID NO: 797)	LSYVNWY (SEQ ID NO: 868)	LVIYAATSRA (SEQ ID NO: 939)	QQSYDLPL (SEQ ID NO: 1010)
373_D11	SSYGMH (SEQ ID NO: 655)	WVAGINYNGGYTS (SEQ ID NO: 726)	ARAATWHDTHLD (SEQ ID NO: 798)	LTYVNWY (SEQ ID NO: 869)	LLIYAATSRA (SEQ ID NO: 940)	QQSYDNPL (SEQ ID NO: 1011)
373_G06	SSYGMH (SEQ ID NO: 656)	WVASINYNSGYTG (SEQ ID NO: 727)	ARAATWHDTHLD (SEQ ID NO: 799)	LSYVNWY (SEQ ID NO: 870)	LLIYAATSLA (SEQ ID NO: 941)	QQSYNLPL (SEQ ID NO: 1012)
374_A10	SSYGMH (SEQ	WVSGINYNGGYTS (SEQ ID NO:	ARAATWHDTHLD (SEQ ID NO:	LSYVNWY (SEQ ID	LLIYAATSRA (SEQ ID	QQSYDTPL (SEQ ID NO:

	ID NO: 657)	728)	800)	NO: 871)	NO: 942)	1013)
374_A12	DSYGMH (SEQ ID NO: 658)	WVSSINYNGGYTS (SEQ ID NO: 729)	ARAATWHDTHLD (SEQ ID NO: 801)	LTYLNWY (SEQ ID NO: 872)	LLIYAATSRA (SEQ ID NO: 943)	QQSDSNPL (SEQ ID NO: 1014)
374_B01	DSYGMH (SEQ ID NO: 659)	WVAGINYNSGYTS (SEQ ID NO: 730)	ARAATWHDTHLD (SEQ ID NO: 802)	LSYLNWY (SEQ ID NO: 873)	LLIYAASSLQ (SEQ ID NO: 944)	QQSYDSPL (SEQ ID NO: 1015)
374_B07	SSYGMH (SEQ ID NO: 660)	WVSSINYNGGYKS (SEQ ID NO: 731)	ARAATWHDTHLD (SEQ ID NO: 803)	ISYLNWY (SEQ ID NO: 874)	LLIYAATSLA (SEQ ID NO: 945)	QQSYESPL (SEQ ID NO: 1016)
374_H02	SSYGMH (SEQ ID NO: 661)	WVASINYNGGYTS (SEQ ID NO: 732)	ARAATWHDTHLD (SEQ ID NO: 804)	LSYVNWY (SEQ ID NO: 875)	LLIYAATSLA (SEQ ID NO: 946)	QQSYDTPL (SEQ ID NO: 1017)
375_C03	DSYSMH (SEQ ID NO: 662)	WVSGINYNGGYTS (SEQ ID NO: 733)	ARAATWHDTHLD (SEQ ID NO: 805)	LSYVNWY (SEQ ID NO: 876)	LVIYAATSRA (SEQ ID NO: 947)	QQSYESPL (SEQ ID NO: 1018)
375_C05	XSYGMN (SEQ ID NO: 663)	WVASINYNGGYKG (SEQ ID NO: 734)	ARAATWHDTHLD (SEQ ID NO: 806)	LSYLNWY (SEQ ID NO: 877)	LLIYAATSRA (SEQ ID NO: 948)	QQSYELPL (SEQ ID NO: 1019)
375_D02	SSYSMN (SEQ ID NO: 664)	WVSNINYNGGYTS (SEQ ID NO: 735)	ARAATWHDTHLD (SEQ ID NO: 807)	LTYLNWY (SEQ ID NO: 878)	LLIYAASSLQ (SEQ ID NO: 949)	QQSYELPL (SEQ ID NO: 1020)
375_G08	SSYGMH (SEQ ID NO: 665)	WVSGINYNGGYTS (SEQ ID NO: 736)	ARAATWHDTHLD (SEQ ID NO: 808)	SSYVNWY (SEQ ID NO: 879)	LLIYAVTSRA (SEQ ID NO: 950)	QQSYSTPL (SEQ ID NO: 1021)
375_H04	SSYGMH (SEQ ID NO: 666)	WVAGINYNSGYTG (SEQ ID NO: 737)	ARAATWHDTHLD (SEQ ID NO: 809)	LSYLNWY (SEQ ID NO: 880)	LVIYAATSRA (SEQ ID NO: 951)	QQSYSNPL (SEQ ID NO: 1022)
376_D08	DSYGMN (SEQ	WVANINYNSGYKS (SEQ ID NO:	ARAATWHDTALD (SEQ ID NO:	LTYLNWY (SEQ ID	LVIYYANNRP (SEQ ID	QQSYSNPL (SEQ ID NO:

	ID NO: 667)	738)	810)	NO: 881)	NO: 952)	1023)
376_F09	DSYSMH (SEQ ID NO: 668)	WVSSINYNGGYKS (SEQ ID NO: 739)	ARAATWHDTHLD (SEQ ID NO: 811)	LTYVNWY (SEQ ID NO: 882)	LLIYAVTSRA (SEQ ID NO: 953)	QQSYDTPL (SEQ ID NO: 1024)
376_H12	SDYGMH (SEQ ID NO: 669)	WVASINYNGGYTS (SEQ ID NO: 740)	ARAATWHDTHLD (SEQ ID NO: 812)	ITYLNWY (SEQ ID NO: 883)	LVIYAATSRA (SEQ ID NO: 954)	QQSYESPL (SEQ ID NO: 1025)

The consensus sequences for each of these CDRs shown in Fig. 3B are as follows:

HCDR1: D/SS/DYG/SMH/N (SEQ ID NO: 6550)

HCDR2: WVA/SS/G/NINYNG/SGYT/KS/G (SEQ ID NO: 6551)

HCDR3: ARAATWHDTH/ALD (SEQ ID NO: 6559)

LCDR1: L/V/I/SS/TYL/VNWY (SEQ ID NO: 6561)

LCDR2: LL/VIYA/YA/T/VT/S/NS/NR/LA/P/Q (SEQ ID NO: 6563)

LCDR3: QQSY/D/ND/E/S/NL/S/T/NPL (SEQ ID NO: 6565)

Table 2C: Group III Antibody Sequences

Ab	VH sequence	VL sequence
365_C05	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDY SMNWVRQAPGKGLEWVSGINYNGGYKGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1026)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQ KPGKAPKLLIYAATSRHSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYNSPLTFGGGTKVEIK (SEQ ID NO: 1205)
365_E10	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY SMNWVRQAPGKGLEWVSSINYNSGYKGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1027)	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQ KPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYSTPLTFGGGTKVEIK (SEQ ID NO: 1206)
365_E12	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDY GMNWVRQAPGKGLEWVSNINYNGGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1028)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYETPLTFGGGTKVEIK (SEQ ID NO: 1207)
365_F02	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVSGINYNGGYKGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1029)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVNWYQQ KPGKAPKLLIYAATSRHSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDTPLTFGGGTKVEIK (SEQ ID NO: 1208)
365_F03	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY SMNWVRQAPGKGLEWVSSINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1030)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDNPLTFGGGTKVEIK (SEQ ID NO: 1209)
365_G03	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMNWVRQAPGKGLEWVAGINYNSGYKGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1031)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYLNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYNTPLTFGGGTKVEIK (SEQ ID NO: 1210)
365_G04	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY SMNWVRQAPGKGLEWVAGINYNGGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1032)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVNWYQQ KPGKAPKLVIYAATSLASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDTPLTFGGGTKVEIK (SEQ ID NO: 1211)
365_G05	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMNWVRQAPGKGLEWVSGINYNGGYKGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1033)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLNWYQQ KPGKAPKLVIYAATSLASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYENPLTFGGGTKVEIK (SEQ ID NO: 1212)
365_G09	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVSGINYNGGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID	DIQMTQSPSSLSASVGDRVTITCRASQSIITYLNWYQQ KPGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYNSPLTFGGGTKVEIK (SEQ ID NO: 1213)

	NO: 1034)	
365_H07	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY SMNWVRQAPGKGLEWVSGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1035)	DIQMTQSPSSLSASVGDRVTITCRASQSISTYVNWYQQ KPGKAPKLLIYAATSRHSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYENPLTFGGGTKVEIK (SEQ ID NO: 1214)
366_A06	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDY SMNWVRQAPGKGLEWVASINYNGGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1036)	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQ KPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYSTPLTFGGGTKVEIK (SEQ ID NO: 1215)
366_A08	EVQLLESGGGLVQPGGSLRLSCAASGFTFDDY SMNWVRQAPGKGLEWVSGINYNSGYKGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1037)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVNWYQQ KPGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYNSPLTFGGGTKVEIK (SEQ ID NO: 1216)
366_B05	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDY SMNWVRQAPGKGLEWVSGINYNSGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1038)	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQ KPGKAPKLVIYAVTSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYELPLTFGGGTKVEIK (SEQ ID NO: 1217)
366_B07	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDY GMNWVRQAPGKGLEWVSGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1039)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYLNWYQQ KPGKAPKLVIYATTSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYNSPLTFGGGTKVEIK (SEQ ID NO: 1218)
366_E01	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMNWVRQAPGKGLEWVSNINYNGGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1040)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYSSPLTFGGGTKVEIK (SEQ ID NO: 1219)
366_E08	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDY SMNWVRQAPGKGLEWVSNINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1041)	DIQMTQSPSSLSASVGDRVTITCRASQSIVTYLNWYQQ KPGKAPKLLIYAATSRHSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYSNPLTFGGGTKVEIK (SEQ ID NO: 1220)
366_F02	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMNWVRQAPGKGLEWVSGINYNSGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1042)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQ KPGKAPKLVIYAATSRHSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDNPLTFGGGTKVEIK (SEQ ID NO: 1221)
366_G12	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMHWVRQAPGKGLEWVSGINYNSGYKGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1043)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLNWYQQ KPGKAPKLLIYAATSRHSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYNTPLTFGGGTKVEIK (SEQ ID NO: 1222)
366_H04	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMNWVRQAPGKGLEWVSNINYNGGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1044)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYSSPLTFGGGTKVEIK (SEQ ID NO: 1223)
367_A03	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMNWVRQAPGKGLEWVAGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1045)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVNWYQQ KPGKAPKLLIYATTSRHSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDSPLTFGGGTKVEIK (SEQ ID NO: 1224)
367_A06	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMNWVRQAPGKGLEWVASINYNGGYKGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1046)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVNWYQQ KPGKAPKLLIYAATSRHSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDTPLTFGGGTKVEIK (SEQ ID NO: 1225)

367_A08	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMNWVRQAPGKGLEWVAGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1047)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQ KPGKAPKLLIYAVTSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDSPLTFGGGTKVEIK (SEQ ID NO: 1226)
367_A10	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMNWVRQAPGKGLEWVAGINYNSGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1048)	DIQMTQSPSSLSASVGDRVTITCRASQSIITYVNWYQQ KPGKAPKLLIYAATSLASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDLPLTFGGGTKVEIK (SEQ ID NO: 1227)
367_A12	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMNWVRQAPGKGLEWVSGINYNSGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1049)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLNWYQQ KPGKAPKLLIYAATSLHSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYNNPLTFGGGTKVEIK (SEQ ID NO: 1228)
367_B01	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVAGINYNGGYKGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1050)	DIQMTQSPSSLSASVGDRVTITCRASQSISSYVNWYQQ KPGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYSTPLTFGGGTKVEIK (SEQ ID NO: 1229)
367_B04	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY SMNWVRQAPGKGLEWVSGINYNSGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1051)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYELPLTFGGGTKVEIK (SEQ ID NO: 1230)
367_B12	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMHWVRQAPGKGLEWVASINYNGGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1052)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVNWYQQ KPGKAPKLVIYAATSLASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDTPLTFGGGTKVEIK (SEQ ID NO: 1231)
367_C07	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVSSINYNSGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1053)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYNLPLTFGGGTKVEIK (SEQ ID NO: 1232)
367_C10	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY SMNWVRQAPGKGLEWVSGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1054)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVNWYQQ KPGKAPKLLIYAVTSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYETPLTFGGGTKVEIK (SEQ ID NO: 1233)
367_D03	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY SMNWVRQAPGKGLEWVSSINYNGGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1055)	DIQMTQSPSSLSASVGDRVTITCRASQSIITYLNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDTPLTFGGGTKVEIK (SEQ ID NO: 1234)
367_D06	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY SMNWVRQAPGKGLEWVAGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1056)	DIQMTQSPSSLSASVGDRVTITCRASQSISTYLNWYQQ KPGKAPKLVIYAATSLASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYNSPLTFGGGTKVEIK (SEQ ID NO: 1235)
367_D08	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDY SMNWVRQAPGKGLEWVAGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1057)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLNWYQQ KPGKAPKLVIYAATSRHSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSDDLPLTFGGGTKVEIK (SEQ ID NO: 1236)
367_D12	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVSSINYNGGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1058)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVNWYQQ KPGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYESPLTFGGGTKVEIK (SEQ ID NO: 1237)
367_E05	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMNWVRQAPGKGLEWVAGINYNGGYTSYADSV	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLNWYQQ KPGKAPKLLIYAATSRHSGVPSRFSGSGSGTDFTLTIS

	KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1059)	SLQPEDFATYYCQQSYDSPLTFGGGTKVEIK (SEQ ID NO: 1238)
367_F01	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY SMNWVRQAPGKGLEWVSNINYNGGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1060)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYLNWYQQ KPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYSTPLTFGGGTKVEIK (SEQ ID NO: 1239)
367_G01	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMNWVRQAPGKGLEWVASINYNSGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1061)	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQ KPGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDLPLTFGGGTKVEIK (SEQ ID NO: 1240)
367_G04	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVAGINYNSGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1062)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLNWYQQ KPGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDSPLTFGGGTKVEIK (SEQ ID NO: 1241)
367_H02	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMNWVRQAPGKGLEWVSSINYNGGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1063)	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQ KPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYSTPLTFGGGTKVEIK (SEQ ID NO: 1242)
367_H03	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMNWVRQAPGKGLEWVAGINYNSGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1064)	DIQMTQSPSSLSASVGDRVTITCRASQSIITYVNWYQQ KPGKAPKLLIYAATSLASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDLPLTFGGGTKVEIK (SEQ ID NO: 1243)
368_A03	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVSGINYNGGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1065)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYLNWYQQ KPGKAPKLLIYAVTSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYENPLTFGGGTKVEIK (SEQ ID NO: 1244)
368_A04	EVQLLESGGGLVQPGGSLRLSCAASGFTFDDY SMNWVRQAPGKGLEWVAGINYNGGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1066)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQ KPGKAPKLVIYAVTSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYELPLTFGGGTKVEIK (SEQ ID NO: 1245)
368_B09	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMNWVRQAPGKGLEWVSNINYNGGYKGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1067)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLNWYQQ KPGKAPKLLIYAATSRHSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDTPLTFGGGTKVEIK (SEQ ID NO: 1246)
368_C02	EVQLLESGGGLVQPGGSLRLSCAASGFTFDDY SMNWVRQAPGKGLEWVANINYNGGYKGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1068)	DIQMTQSPSSLSASVGDRVTITCRASQSISTYVNWYQQ KPGKAPKLLIYAATSLASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYSTPLTFGGGTKVEIK (SEQ ID NO: 1247)
368_C08	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDY SMNWVRQAPGKGLEWVSGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1069)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVNWYQQ KPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYSTPLTFGGGTKVEIK (SEQ ID NO: 1248)
368_E12	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDY GMNWVRQAPGKGLEWVAGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1070)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVNWYQQ KPGKAPKLVIYAVTSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDSPLTFGGGTKVEIK (SEQ ID NO: 1249)
368_F09	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMNWVRQAPGKGLEWVSGINYNSGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQ KPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYETPLTFGGGTKVEIK (SEQ ID NO: 1250)

	NO: 1071)	
368_H02	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMNWVRQAPGKGLEWVAGINYNSGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1072)	DIQMTQSPSSLSASVGDRVTITCRASQSIVTYLNWYQQ KPGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYESPLTFGGGTKVEIK (SEQ ID NO: 1251)
368_H05	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVANINYNGGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1073)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVNWYQQ KPGKAPKLVIYATTSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYESPLTFGGGTKVEIK (SEQ ID NO: 1252)
369_A07	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVAGINYNGGYKGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1074)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLNWYQQ KPGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYESPLTFGGGTKVEIK (SEQ ID NO: 1253)
369_B05	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY SMNWVRQAPGKGLEWVSGINYNGGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1075)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYLNWYQQ KPGKAPKLLIYAATSLASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDTPLTFGGGTKVEIK (SEQ ID NO: 1254)
369_C05	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY SMNWVRQAPGKGLEWVAGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1076)	DIQMTQSPSSLSASVGDRVTITCRASQSISSYVNWYQQ KPGKAPKLVIYATTSRHSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYNSPLTFGGGTKVEIK (SEQ ID NO: 1255)
369_D03	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVSGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1077)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQ KPGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYENPLTFGGGTKVEIK (SEQ ID NO: 1256)
369_D07	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMNWVRQAPGKGLEWVSGINYNGGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1078)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYLNWYQQ KPGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDLPLTFGGGTKVEIK (SEQ ID NO: 1257)
369_D09	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDY GMNWVRQAPGKGLEWVSNINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1079)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDSPLTFGGGTKVEIK (SEQ ID NO: 1258)
369_E06	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMNWVRQAPGKGLEWVSGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1080)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYLNWYQQ KPGKAPKLVIYAATSRHSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDSPLTFGGGTKVEIK (SEQ ID NO: 1259)
369_F08	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDY GMHWVRQAPGKGLEWVSGINYNSGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1081)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLNWYQQ KPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDLPLTFGGGTKVEIK (SEQ ID NO: 1260)
369_G08	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY SMNWVRQAPGKGLEWVSSINYNGGYKGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1082)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQ KPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYSTPLTFGGGTKVEIK (SEQ ID NO: 1261)
370_A02	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMNWVRQAPGKGLEWVAGINYNGGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1083)	DIQMTQSPSSLSASVGDRVTITCRASQSIVTYLNWYQQ KPGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDSPLTFGGGTKVEIK (SEQ ID NO: 1262)

370_B03	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVANINYNGGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1084)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLNWYQQ KPGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYNNPLTFGGGTKVEIK (SEQ ID NO: 1263)
370_B11	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY SMNWVRQAPGKGLEWVSGINYNSGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1085)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLNWYQQ KPGKAPKLVIYAATSRHSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQGYDLPLTFGGGTKVEIK (SEQ ID NO: 1264)
370_B12	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDY SMNWVRQAPGKGLEWVSGINYNGGYKGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1086)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVNWYQQ KPGKAPKLVIYATTSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYETPLTFGGGTKVEIK (SEQ ID NO: 1265)
370_D01	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVSSINYNGGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1087)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLNWYQQ KPGKAPKLLIYAATSRHSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYNTPLTFGGGTKVEIK (SEQ ID NO: 1266)
370_D05	EVQLLESGGGLVQPGGSLRLSCAASGFTFDDY SMNWVRQAPGKGLEWVSNINYNGGYKGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1088)	DIQMTQSPSSLSASVGDRVTITCRASQSIITYLNWYQQ KPGKAPKLVIYAATSRHSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDTPLTFGGGTKVEIK (SEQ ID NO: 1267)
370_F03	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMNWVRQAPGKGLEWVSSINYNSGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1089)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYENPLTFGGGTKVEIK (SEQ ID NO: 1268)
370_H02	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY SMNWVRQAPGKGLEWVSGINYNSGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1090)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYESPLTFGGGTKVEIK (SEQ ID NO: 1269)
370_H07	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVAGINYNGGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1091)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLNWYQQ KPGKAPKLLIYAATSLASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSDSSPLTFGGGTKVEIK (SEQ ID NO: 1270)
371_A10	EVQLLESGGGLVQPGGSLRLSCAASGFTFDDY SMNWVRQAPGKGLEWVSGINYNGGYKGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1092)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYLNWYQQ KPGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYENPLTFGGGTKVEIK (SEQ ID NO: 1271)
371_B03	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMHWVRQAPGKGLEWVASINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1093)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVNWYQQ KPGKAPKLLIYATTSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDNPLTFGGGTKVEIK (SEQ ID NO: 1272)
371_B04	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVSGINYNGGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1094)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLNWYQQ KPGKAPKLVIYAVTSRHSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDSPLTFGGGTKVEIK (SEQ ID NO: 1273)
371_B09	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVAGINYNSGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1095)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVNWYQQ KPGKAPKLVIYATTSLASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDTPLTFGGGTKVEIK (SEQ ID NO: 1274)
371_B12	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDY SMNWVRQAPGKGLEWVAGINYNSGYTSYADSV	DIQMTQSPSSLSASVGDRVTITCRASQSIVTYLNWYQQ KPGKAPKLVIYAATSRHSGVPSRFSGSGSGTDFTLTIS

	KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1096)	SLQPEDFATYYCQQSYNNPLTFGGGTKVEIK (SEQ ID NO: 1275)
371_C01	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMHWVRQAPGKGLEWVSSINYNGGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1097)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYLNWYQQ KPGKAPKLLIYAATSRHSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDNPLTFGGGTKVEIK (SEQ ID NO: 1276)
371_C04	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMNWVRQAPGKGLEWVSGINYNSGYKGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1098)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYSTPLTFGGGTKVEIK (SEQ ID NO: 1277)
371_C05	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDY GMHWVRQAPGKGLEWVANINYNGGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1099)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDSPLTFGGGTKVEIK (SEQ ID NO: 1278)
371_C12	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVAGINYNSGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1100)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDTPLTFGGGTKVEIK (SEQ ID NO: 1279)
371_D02	EVQLLESGGGLVQPGGSLRLSCAASGFTFDDY SMNWVRQAPGKGLEWVAGINYNGGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1101)	DIQMTQSPSSLSASVGDRVTITCRASQSIVTYLNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDSPLTFGGGTKVEIK (SEQ ID NO: 1280)
371_D04	EVQLLESGGGLVQPGGSLRLSCAASGFTFDDY SMNWVRQAPGKGLEWVAGINYNGGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1102)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVNWYQQ KPGKAPKLLIYAATSLASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYENPLTFGGGTKVEIK (SEQ ID NO: 1281)
371_E06	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVSGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1103)	DIQMTQSPSSLSASVGDRVTITCRASQSISTYLNWYQQ KPGKAPKLLIYAVTSLHSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYESPLTFGGGTKVEIK (SEQ ID NO: 1282)
371_E07	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY SMNWVRQAPGKGLEWVAGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1104)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYLNWYQQ KPGKAPKLLIYAATSLASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYESPLTFGGGTKVEIK (SEQ ID NO: 1283)
371_E10	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY SMNWVRQAPGKGLEWVAGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1105)	DIQMTQSPSSLSASVGDRVTITCRASQSISTYLNWYQQ KPGKAPKLLIYAVTSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYNSPLTFGGGTKVEIK (SEQ ID NO: 1284)
371_F10	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMNWVRQAPGKGLEWVSGINYNSGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1106)	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQ KPGKAPKLVIYAVTSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYESPLTFGGGTKVEIK (SEQ ID NO: 1285)
371_F11	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVSGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1107)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYVNWYQQ KPGKAPKLLIYAVTSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDLPLTFGGGTKVEIK (SEQ ID NO: 1286)
371_G02	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMNWVRQAPGKGLEWVASINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDLPLTFGGGTKVEIK (SEQ ID NO: 1287)

	NO: 1108)	
371_G04	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY SMNWVRQAPGKGLEWVSGINYNGGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1109)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLNWYQQ KPGKAPKLLIYAATSLHSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYESPLTFGGGTKVEIK (SEQ ID NO: 1288)
371_G09	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVANINYNGGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1110)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLNWYQQ KPGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSDSTPLTFGGGTKVEIK (SEQ ID NO: 1289)
371_G11	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMNWVRQAPGKGLEWVSNINYNSGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1111)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVNWYQQ KPGKAPKLLIYAATSLASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDSPLTFGGGTKVEIK (SEQ ID NO: 1290)
371_H04	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMNWVRQAPGKGLEWVSNINYNGGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1112)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYNSPLTFGGGTKVEIK (SEQ ID NO: 1291)
371_H05	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMNWVRQAPGKGLEWVSGINYNSGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1113)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYLNWYQQ KPGKAPKLLIYAATSLASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYSLPLTFGGGTKVEIK (SEQ ID NO: 1292)
371_H06	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMNWVRQAPGKGLEWVSGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1114)	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQ KPGKAPKLVIYAVTSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDLPLTFGGGTKVEIK (SEQ ID NO: 1293)
371_H08	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMNWVRQAPGKGLEWVASINYNGGYKGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1115)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYVNWYQQ KPGKAPKLVIYAVTSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDTPLTFGGGTKVEIK (SEQ ID NO: 1294)
371_H10	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVAGINYNSGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1116)	DIQMTQSPSSLSASVGDRVTITCRASQSISTYLNWYQQ KPGKAPKLLIYAATSRHSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYENPLTFGGGTKVEIK (SEQ ID NO: 1295)
372_B02	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVSGINYNSGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1117)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVNWYQQ KPGKAPKLLIYAVTSLASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYETPLTFGGGTKVEIK (SEQ ID NO: 1296)
372_C06	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDY SMNWVRQAPGKGLEWVSGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1118)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYSSPLTFGGGTKVEIK (SEQ ID NO: 1297)
372_D03	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVAGINYNSGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1119)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVNWYQQ KPGKAPKLVIYAVTSRHSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDSPLTFGGGTKVEIK (SEQ ID NO: 1298)
372_E01	EVQLLESGGGLVQPGGSLRLSCAASGFTFDDY SMNWVRQAPGKGLEWVSGINYNGGYKGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1120)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYLNWYQQ KPGKAPKLVIYAATSRHSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDSPLTFGGGTKVEIK (SEQ ID NO: 1299)

372_G12	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY SMNWVRQAPGKGLEWVAGINYNGGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1121)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQ KPGKAPKLVIYAATSRHSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDSPLTFGGGTKVEIK (SEQ ID NO: 1300)
373_A01	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMNWVRQAPGKGLEWVSNINYNGGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1122)	DIQMTQSPSSLSASVGDRVTITCRASQSIVTYLNWYQQ KPGKAPKLVIYATTSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYNLPLTFGGGTKVEIK (SEQ ID NO: 1301)
373_A03	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDY SMNWVRQAPGKGLEWVANINYNGGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1123)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLNWYQQ KPGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDNPLTFGGGTKVEIK (SEQ ID NO: 1302)
373_A05	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDY SMNWVRQAPGKGLEWVSGINYNSGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1124)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVNWYQQ KPGKAPKLVIYAATSRHSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYESPLTFGGGTKVEIK (SEQ ID NO: 1303)
373_A09	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY SMNWVRQAPGKGLEWVAGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1125)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQ KPGKAPKLLIYAATSLASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDTPLTFGGGTKVEIK (SEQ ID NO: 1304)
373_A11	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNY GMNWVRQAPGKGLEWVANINYNGGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1126)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDLPLTFGGGTKVEIK (SEQ ID NO: 1305)
373_A12	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVSSINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1127)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQ KPGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDTPLTFGGGTKVEIK (SEQ ID NO: 1306)
373_B05	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDY SMNWVRQAPGKGLEWVSNINYNGGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1128)	DIQMTQSPSSLSASVGDRVTITCRASQSIVTYLNWYQQ KPGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYSNPLTFGGGTKVEIK (SEQ ID NO: 1307)
373_B07	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY SMNWVRQAPGKGLEWVSGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1129)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVNWYQQ KPGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYELPLTFGGGTKVEIK (SEQ ID NO: 1308)
373_C03	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVSGINYNGGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1130)	DIQMTQSPSSLSASVGDRVTITCRASQSIVTYLNWYQQ KPGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDSPLTFGGGTKVEIK (SEQ ID NO: 1309)
373_C07	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY SMNWVRQAPGKGLEWVAGINYNSGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1131)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQ KPGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYETPLTFGGGTKVEIK (SEQ ID NO: 1310)
373_C10	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVAGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1132)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDNPLTFGGGTKVEIK (SEQ ID NO: 1311)
373_D03	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVSGINYNGGYTSYADSV	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYLNWYQQ KPGKAPKLLIYAATSLASGVPSRFSGSGSGTDFTLTIS

	KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1133)	SLQPEDFATYYCQQSYDTPLTFGGGTKVEIK (SEQ ID NO: 1312)
373_D12	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY SMNWVRQAPGKGLEWVSSINYNSGYKGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1134)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYSLPLTFGGGTKVEIK (SEQ ID NO: 1313)
373_E10	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDY SMNWVRQAPGKGLEWVSGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1135)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVNWYQQ KPGKAPKLVIYAATSRHSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYETPLTFGGGTKVEIK (SEQ ID NO: 1314)
373_F08	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVSGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1136)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDTPLTFGGGTKVEIK (SEQ ID NO: 1315)
373_F11	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMHWVRQAPGKGLEWVSGINYNSGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1137)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYNLPLTFGGGTKVEIK (SEQ ID NO: 1316)
373_F12	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVSNINYNGGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1138)	DIQMTQSPSSLSASVGDRVTITCRASQSISTYLNWYQQ KPGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYETPLTFGGGTKVEIK (SEQ ID NO: 1317)
373_G08	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY SMNWVRQAPGKGLEWVSNINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1139)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQ KPGKAPKLLIYAATSLASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDSPLTFGGGTKVEIK (SEQ ID NO: 1318)
373_H03	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVSGINYNSGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1140)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLNWYQQ KPGKAPKLLIYATTSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYENPLTFGGGTKVEIK (SEQ ID NO: 1319)
373_H07	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVAGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1141)	DIQMTQSPSSLSASVGDRVTITCRASQSIVTYLNWYQQ KPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDSPLTFGGGTKVEIK (SEQ ID NO: 1320)
373_H09	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMNWVRQAPGKGLEWVASINYNSGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1142)	DIQMTQSPSSLSASVGDRVTITCRASQSIITYLNWYQQ KPGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSDDSPLTFGGGTKVEIK (SEQ ID NO: 1321)
374_A06	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVSSINYNSGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1143)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLNWYQQ KPGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDSPLTFGGGTKVEIK (SEQ ID NO: 1322)
374_A09	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVSSINYNGGYKGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1144)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVNWYQQ KPGKAPKLLIYAATSLASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDSPLTFGGGTKVEIK (SEQ ID NO: 1323)
374_B03	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY SMNWVRQAPGKGLEWVSGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQ KPGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDSPLTFGGGTKVEIK (SEQ ID NO: 1324)

	NO: 1145)	
374_B05	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY SMNWVRQAPGKGLEWVSGINYNSGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1146)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYLNWYQQ KPGKAPKLLIYAATSRHSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYESPLTFGGGTKVEIK (SEQ ID NO: 1325)
374_B08	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY SMNWVRQAPGKGLEWVAGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1147)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVNWYQQ KPGKAPKLLIYAATSRHSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYELPLTFGGGTKVEIK (SEQ ID NO: 1326)
374_B10	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVSSINYNSGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1148)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVNWYQQ KPGKAPKLVIYAATSLASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDTPLTFGGGTKVEIK (SEQ ID NO: 1327)
374_C01	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMNWVRQAPGKGLEWVSGINYNSGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1149)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYETPLTFGGGTKVEIK (SEQ ID NO: 1328)
374_C09	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMNWVRQAPGKGLEWVSSINYNGGYKGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1150)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYLNWYQQ KPGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYELPLTFGGGTKVEIK (SEQ ID NO: 1329)
374_C12	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVAGINYNGGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1151)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQ KPGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSDNSPLTFGGGTKVEIK (SEQ ID NO: 1330)
374_D03	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY SMNWVRQAPGKGLEWVAGINYNGGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1152)	DIQMTQSPSSLSASVGDRVTITCRASQSIVTYLNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDTPLTFGGGTKVEIK (SEQ ID NO: 1331)
374_D05	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY SMNWVRQAPGKGLEWVSGINYNSGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1153)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDTPLTFGGGTKVEIK (SEQ ID NO: 1332)
374_D06	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVSGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1154)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVNWYQQ KPGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDSPLTFGGGTKVEIK (SEQ ID NO: 1333)
374_D07	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY SMNWVRQAPGKGLEWVSGINYNSGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1155)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYLNWYQQ KPGKAPKLVIYAATSLASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYNSPLTFGGGTKVEIK (SEQ ID NO: 1334)
374_D10	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMHWVRQAPGKGLEWVASINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1156)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDNPLTFGGGTKVEIK (SEQ ID NO: 1335)
374_E10	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVSGINYNGGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1157)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLNWYQQ KPGKAPKLLIYAATSRHSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDSPLTFGGGTKVEIK (SEQ ID NO: 1336)

374_E12	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVSGINYNGGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1158)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLNWYQQ KPGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDNPLTFGGGTKVEIK (SEQ ID NO: 1337)
374_F06	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVSGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1159)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYVNWYQQ KPGKAPKLVIYAATSLHSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYSTPLTFGGGTKVEIK (SEQ ID NO: 1338)
374_F07	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY SMNWVRQAPGKGLEWVASINYNGGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1160)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLNWYQQ KPGKAPKLVIYAVTSLASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYESPLTFGGGTKVEIK (SEQ ID NO: 1339)
374_F08	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY SMNWVRQAPGKGLEWVSGINYNGGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1161)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVNWYQQ KPGKAPKLVIYAVTSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDTPLTFGGGTKVEIK (SEQ ID NO: 1340)
374_G03	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDY SMNWVRQAPGKGLEWVSGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1162)	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQ KPGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSDDTPLTFGGGTKVEIK (SEQ ID NO: 1341)
374_G08	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY SMNWVRQAPGKGLEWVSGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1163)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVNWYQQ KPGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDSPLTFGGGTKVEIK (SEQ ID NO: 1342)
374_G09	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVAGINYNGGYKGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1164)	DIQMTQSPSSLSASVGDRVTITCRASQSIVRYLNWYQQ KPGKAPKLVIYAATSLASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYELPLTFGGGTKVEIK (SEQ ID NO: 1343)
374_G10	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVSSINYNSGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1165)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYLNWYQQ KPGKAPKLVIYAVTSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDSPLTFGGGTKVEIK (SEQ ID NO: 1344)
374_G11	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDY SMNWVRQAPGKGLEWVSGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1166)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYVNWYQQ KPGKAPKLVIYAATSLASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDSPLTFGGGTKVEIK (SEQ ID NO: 1345)
374_H01	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY SMNWVRQAPGKGLEWVAGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1167)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLNWYQQ KPGKAPKLVIYAATSLASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYENPLTFGGGTKVEIK (SEQ ID NO: 1346)
374_H11	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVSGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1168)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYVNWYQQ KPGKAPKLVIYAATSLHSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYSNPLTFGGGTKVEIK (SEQ ID NO: 1347)
375_A01	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY SMNWVRQAPGKGLEWVAGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1169)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLNWYQQ KPGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYNTPLTFGGGTKVEIK (SEQ ID NO: 1348)
375_A07	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY SMNWVRQAPGKGLEWVSSINYNSGYTGYADSV	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS

	KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1170)	SLQPEDFATYYCQQSYDTPLTFGGGTKVEIK (SEQ ID NO: 1349)
375_A08	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVAGINYNGGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1171)	DIQMTQSPSSLSASVGDRVTITCRASQSIVTYLNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYESPLTFGGGTKVEIK (SEQ ID NO: 1350)
375_A12	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVSGINYNSGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1172)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLNWYQQ KPGKAPKLVIYAVTSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYETPLTFGGGTKVEIK (SEQ ID NO: 1351)
375_B12	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY SMNWVRQAPGKGLEWVAGINYNGGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1173)	DIQMTQSPSSLSASVGDRVTITCRASQSIVTYLNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDTPLTFGGGTKVEIK (SEQ ID NO: 1352)
375_C04	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDY SMNWVRQAPGKGLEWVAGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1174)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQ KPGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYESPLTFGGGTKVEIK (SEQ ID NO: 1353)
375_D01	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVSGINYNGGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1175)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQ KPGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYETPLTFGGGTKVEIK (SEQ ID NO: 1354)
375_D10	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVAGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1176)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSDDSPLTFGGGTKVEIK (SEQ ID NO: 1355)
375_E02	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDY SMNWVRQAPGKGLEWVAGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1177)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYSSPLTFGGGTKVEIK (SEQ ID NO: 1356)
375_E03	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDY SMNWVRQAPGKGLEWVANINYNGGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1178)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQ KPGKAPKLVIYAATSLASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDNPLTFGGGTKVEIK (SEQ ID NO: 1357)
375_E05	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVAGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1179)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLNWYQQ KPGKAPKLVIYAATSLASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYSSPLTFGGGTKVEIK (SEQ ID NO: 1358)
375_E06	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVSGINYNGGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1180)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLNWYQQ KPGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDSPLTFGGGTKVEIK (SEQ ID NO: 1359)
375_E10	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVSGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1181)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLNWYQQ KPGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDNPLTFGGGTKVEIK (SEQ ID NO: 1360)
375_F02	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVASINYNSGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDSPLTFGGGTKVEIK (SEQ ID NO: 1361)

	NO: 1182)	
375_F07	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDY SMNWVRQAPGKGLEWVSNINYNGGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1183)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDSPLTFGGGTKVEIK (SEQ ID NO: 1362)
375_F08	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMNWVRQAPGKGLEWVSSINYNSGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1184)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLNWYQQ KPGKAPKLLIYAATSRHSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDNPLTFGGGTKVEIK (SEQ ID NO: 1363)
375_G04	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMNWVRQAPGKGLEWVASINYNSGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1185)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVNWYQQ KPGKAPKLLIYAATSLASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDSPLTFGGGTKVEIK (SEQ ID NO: 1364)
375_G05	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVAGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1186)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYLNWYQQ KPGKAPKLLIYAVTSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDSPLTFGGGTKVEIK (SEQ ID NO: 1365)
375_H05	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVSNINYNGGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1187)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDTPLTFGGGTKVEIK (SEQ ID NO: 1366)
375_H07	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVAGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1188)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLNWYQQ KPGKAPKLLIYAATSLASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYSSPLTFGGGTKVEIK (SEQ ID NO: 1367)
376_A03	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMNWVRQAPGKGLEWVAGINYNGGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1189)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYSTPLTFGGGTKVEIK (SEQ ID NO: 1368)
376_B03	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVAGINYNSGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1190)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVNWYQQ KPGKAPKLVIYAVTSRHSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDSPLTFGGGTKVEIK (SEQ ID NO: 1369)
376_B10	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDY SMNWVRQAPGKGLEWVAGINYNGGYKGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1191)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLNWYQQ KPGKAPKLVIYAATSLASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYSTPLTFGGGTKVEIK (SEQ ID NO: 1370)
376_C04	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMNWVRQAPGKGLEWVSNINYNGGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1192)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVNWYQQ KPGKAPKLLIYAVTSRHSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDNPLTFGGGTKVEIK (SEQ ID NO: 1371)
376_C08	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY SMNWVRQAPGKGLEWVAGINYNSGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1193)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLNWYQQ KPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYSTPLTFGGGTKVEIK (SEQ ID NO: 1372)
376_D07	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY SMNWVRQAPGKGLEWVSGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1194)	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQ KPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYSTPLTFGGGTKVEIK (SEQ ID NO: 1373)

376_E02	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVAGINYNGGYKGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1195)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVNWYQQ KPGKAPKLVIYAATSRHSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSDNTPLTFGGGTKVEIK (SEQ ID NO: 1374)
376_E11	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVSGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1196)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVNWYQQ KPGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYELPLTFGGGTKVEIK (SEQ ID NO: 1375)
376_F01	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDY SMNWVRQAPGKGLEWVAGINYNGGYKSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1197)	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQ KPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYSTPLTFGGGTKVEIK (SEQ ID NO: 1376)
376_F06	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMNWVRQAPGKGLEWVSGINYNGGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1198)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVNWYQQ KPGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYETPLTFGGGTKVEIK (SEQ ID NO: 1377)
376_G05	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVAGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1199)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYVNWYQQ KPGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYESPLTFGGGTKVEIK (SEQ ID NO: 1378)
376_G06	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMNWVRQAPGKGLEWVAGINYNGGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTHLDYWGQGTLVTVSS (SEQ ID NO: 1200)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVNWYQQ KPGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYNSPLTFGGGTKVEIK (SEQ ID NO: 1379)
376_G10	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY GMNWVRQAPGKGLEWVAGINYNGGYTSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1201)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYESPLTFGGGTKVEIK (SEQ ID NO: 1380)
376_H01	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDY SMNWVRQAPGKGLEWVAGINYNGGYKGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1202)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLNWYQQ KPGKAPKLLIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYSTPLTFGGGTKVEIK (SEQ ID NO: 1381)
376_H04	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY SMNWVRQAPGKGLEWVAGINYNGGYKGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1203)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVNWYQQ KPGKAPKLVIYAATSRASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYDLPLTFGGGTKVEIK (SEQ ID NO: 1382)
376_H11	EVQLLESGGGLVQPGGSLRLSCAASGFTFDSY SMNWVRQAPGKGLEWVSNINYNGGYTGYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARGANWHDTALDYWGQGTLVTVSS (SEQ ID NO: 1204)	DIQMTQSPSSLSASVGDRVTITCRASQSISRYLNWYQQ KPGKAPKLLIYAVTSLASGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQSYESPLTFGGGTKVEIK (SEQ ID NO: 1383)

Table 3C provides the amino acid sequences of the CDRs of the antibodies shown in Table 2C.

Table 3C: CDR sequences for Group III antibodies

Ab	HCDR1	HCDR2	HCDR3	LCDR1	LCDR2	LCDR3
365_C05	SDYSMN (SEQ ID NO: 5464)	WVSGINYNGGYKG (SEQ ID NO: 5643)	ARGANWHDTHLD (SEQ ID NO:5822)	LTYLNWY (SEQ ID NO: 6001)	LLIYAATSRH (SEQ ID NO: 6180)	QQSYNSPL (SEQ ID NO: 6359)
365_E10	DSYSMN (SEQ ID NO: 5465)	WVSSINYNSGYKG (SEQ ID NO: 5644)	ARGANWHDTHLD (SEQ ID NO:5823)	SSYLNWY (SEQ ID NO: 6002)	LLIYAASSLQ (SEQ ID NO: 6181)	QQSYSTPL (SEQ ID NO: 6360)
365_E12	SDYGMN (SEQ ID NO: 5466)	WVSNINYNGGYTG (SEQ ID NO: 5645)	ARGANWHDTALD (SEQ ID NO:5824)	LTYLNWY (SEQ ID NO: 6003)	LLIYAATSRA (SEQ ID NO: 6182)	QQSYETPL (SEQ ID NO: 6361)
365_F02	SSYSMN (SEQ ID NO: 5467)	WVSGINYNGGYKG (SEQ ID NO: 5646)	ARGANWHDTHLD (SEQ ID NO:5825)	LTYVNWY (SEQ ID NO: 6004)	LLIYAATSRH (SEQ ID NO: 6183)	QQSYDTPL (SEQ ID NO: 6362)
365_F03	DSYSMN (SEQ ID NO: 5468)	WVSSINYNGGYTS (SEQ ID NO: 5647)	ARGANWHDTHLD (SEQ ID NO:5826)	LSYLNWY (SEQ ID NO: 6005)	LLIYAATSRA (SEQ ID NO: 6184)	QQSYDNPL (SEQ ID NO: 6363)
365_G03	SSYGMN (SEQ ID NO: 5469)	WVAGINYNSGYKG (SEQ ID NO: 5648)	ARGANWHDTHLD (SEQ ID NO:5827)	VSYLNWY (SEQ ID NO: 6006)	LLIYAATSRA (SEQ ID NO: 6185)	QQSYNTPL (SEQ ID NO: 6364)
365_G04	DSYSMN (SEQ ID NO: 5470)	WVAGINYNGGYTG (SEQ ID NO: 5649)	ARGANWHDTHLD (SEQ ID NO:5828)	VSYVNWY (SEQ ID NO: 6007)	LVIYAATSLA (SEQ ID NO: 6186)	QQSYDTPL (SEQ ID NO: 6365)
365_G05	SSYGMN (SEQ ID NO: 5471)	WVSGINYNGGYKG (SEQ ID NO: 5650)	ARGANWHDTALD (SEQ ID NO:5829)	LSYLNWY (SEQ ID NO: 6008)	LVIYAATSLA (SEQ ID NO: 6187)	QQSYENPL (SEQ ID NO: 6366)
365_G09	SSYSMN (SEQ	WVSGINYNGGYKS (SEQ ID NO:	ARGANWHDTHLD (SEQ ID	ITYLNWY (SEQ ID	LVIYAATSRA (SEQ ID	QQSYNSPL (SEQ ID

	ID NO: 5472)	5651)	NO:5830)	NO: 6009)	NO: 6188)	NO: 6367)
365_H07	DSYSMN (SEQ ID NO: 5473)	WVSGINYNGGYTS (SEQ ID NO: 5652)	ARGANWHDTHLD (SEQ ID NO:5831)	STYVNWY (SEQ ID NO: 6010)	LLIYAATSRH (SEQ ID NO: 6189)	QQSYENPL (SEQ ID NO: 6368)
366_A06	SDYSMN (SEQ ID NO: 5474)	WVASINYNGGYKS (SEQ ID NO: 5653)	ARGANWHDTHLD (SEQ ID NO:5832)	SSYLNWY (SEQ ID NO: 6011)	LLIYAASSLQ (SEQ ID NO: 6190)	QQSYSTPL (SEQ ID NO: 6369)
366_A08	DDYSMN (SEQ ID NO: 5475)	WVSGINYNSGYKG (SEQ ID NO: 5654)	ARGANWHDTHLD (SEQ ID NO:5833)	VSYVNWY (SEQ ID NO: 6012)	LVIYAATSRA (SEQ ID NO: 6191)	QQSYNSPL (SEQ ID NO: 6370)
366_B05	SDYSMN (SEQ ID NO: 5476)	WVSGINYNSGYKS (SEQ ID NO: 5655)	ARGANWHDTALD (SEQ ID NO:5834)	SSYLNWY (SEQ ID NO: 6013)	LVIYAVTSRA (SEQ ID NO: 6192)	QQSYELPL (SEQ ID NO: 6371)
366_B07	SDYGMN (SEQ ID NO: 5477)	WVSGINYNGGYTS (SEQ ID NO: 5656)	ARGANWHDTHLD (SEQ ID NO:5835)	VSYLNWY (SEQ ID NO: 6014)	LVIYATTSRA (SEQ ID NO: 6193)	QQSYNSPL (SEQ ID NO: 6372)
366_E01	DSYGMN (SEQ ID NO: 5478)	WVSNINYNGGYKS (SEQ ID NO: 5657)	ARGANWHDTHLD (SEQ ID NO:5836)	LTYLNWY (SEQ ID NO: 6015)	LLIYAATSRA (SEQ ID NO: 6194)	QQSYSSPL (SEQ ID NO: 6373)
366_E08	SDYSMN (SEQ ID NO: 5479)	WVSNINYNGGYTS (SEQ ID NO: 5658)	ARGANWHDTHLD (SEQ ID NO:5837)	VTYLNWY (SEQ ID NO: 6016)	LLIYAATSRH (SEQ ID NO: 6195)	QQSYSNPL (SEQ ID NO: 6374)
366_F02	SSYGMN (SEQ ID NO: 5480)	WVSGINYNSGYTG (SEQ ID NO: 5659)	ARGANWHDTHLD (SEQ ID NO:5838)	LTYLNWY (SEQ ID NO: 6017)	LVIYAATSRH (SEQ ID NO: 6196)	QQSYDNPL (SEQ ID NO: 6375)
366_G12	SSYGMH (SEQ ID NO: 5481)	WVSGINYNSGYKG (SEQ ID NO: 5660)	ARGANWHDTHLD (SEQ ID NO:5839)	LSYLNWY (SEQ ID NO: 6018)	LLIYAATSRH (SEQ ID NO: 6197)	QQSYNTPL (SEQ ID NO: 6376)
366_H04	DSYGMN (SEQ	WVSNINYNGGYKS (SEQ ID NO:	ARGANWHDTHLD (SEQ ID	LTYLNWY (SEQ ID	LLIYAATSRA (SEQ ID	QQSYSSPL (SEQ ID

	ID NO: 5482)	5661)	NO:5840)	NO: 6019)	NO: 6198)	NO: 6377)
367_A03	DSYGMN (SEQ ID NO: 5483)	WVAGINYNGGYTS (SEQ ID NO: 5662)	ARGANWHDTALD (SEQ ID NO:5841)	LTYVNWY (SEQ ID NO: 6020)	LLIYATTSRH (SEQ ID NO: 6199)	QQSYDSPL (SEQ ID NO: 6378)
367_A06	DSYGMN (SEQ ID NO: 5484)	WVASINYNGGYKG (SEQ ID NO: 5663)	ARGANWHDTHLD (SEQ ID NO:5842)	LSYVNWY (SEQ ID NO: 6021)	LLIYAATSRH (SEQ ID NO: 6200)	QQSYDTPL (SEQ ID NO: 6379)
367_A08	DSYGMN (SEQ ID NO: 5485)	WVAGINYNGGYTS (SEQ ID NO: 5664)	ARGANWHDTHLD (SEQ ID NO:5843)	LTYLNWY (SEQ ID NO: 6022)	LLIYAVTSRA (SEQ ID NO: 6201)	QQSYDSPL (SEQ ID NO: 6380)
367_A10	SSYGMN (SEQ ID NO: 5486)	WVAGINYNSGYTS (SEQ ID NO: 5665)	ARGANWHDTHLD (SEQ ID NO:5844)	ITYVNWY (SEQ ID NO: 6023)	LLIYAATSLA (SEQ ID NO: 6202)	QQSYDLPL (SEQ ID NO: 6381)
367_A12	SSYGMN (SEQ ID NO: 5487)	WVSGINYNSGYTS (SEQ ID NO: 5666)	ARGANWHDTHLD (SEQ ID NO:5845)	LSYLNWY (SEQ ID NO: 6024)	LLIYAATSLH (SEQ ID NO: 6203)	QQSYNNPL (SEQ ID NO: 6382)
367_B01	SSYSMN (SEQ ID NO: 5488)	WVAGINYNGGYKG (SEQ ID NO: 5667)	ARGANWHDTALD (SEQ ID NO:5846)	SSYVNWY (SEQ ID NO: 6025)	LVIYAATSRA (SEQ ID NO: 6204)	QQSYSTPL (SEQ ID NO: 6383)
367_B04	DSYSMN (SEQ ID NO: 5489)	WVSGINYNSGYKS (SEQ ID NO: 5668)	ARGANWHDTHLD (SEQ ID NO:5847)	LSYLNWY (SEQ ID NO: 6026)	LLIYAATSRA (SEQ ID NO: 6205)	QQSYELPL (SEQ ID NO: 6384)
367_B12	SSYGMH (SEQ ID NO: 5490)	WVASINYNGGYKS (SEQ ID NO: 5669)	ARGANWHDTHLD (SEQ ID NO:5848)	LSYVNWY (SEQ ID NO: 6027)	LVIYAATSLA (SEQ ID NO: 6206)	QQSYDTPL (SEQ ID NO: 6385)
367_C07	SSYSMN (SEQ ID NO: 5491)	WVSSINYNSGYTG (SEQ ID NO: 5670)	ARGANWHDTHLD (SEQ ID NO:5849)	LTYVNWY (SEQ ID NO: 6028)	LLIYAATSRA (SEQ ID NO: 6207)	QQSYNLPL (SEQ ID NO: 6386)
367_C10	DSYSMN (SEQ	WVSGINYNGGYTS (SEQ ID NO:	ARGANWHDTALD (SEQ ID	VSYVNWY (SEQ ID	LLIYAVTSRA (SEQ ID	QQSYETPL (SEQ ID

	ID NO: 5492)	5671)	NO:5850)	NO: 6029)	NO: 6208)	NO: 6387)
367_D03	DSYSMN (SEQ ID NO: 5493)	WVSSINYNGGYTG (SEQ ID NO: 5672)	ARGANWHDTHLD (SEQ ID NO:5851)	ITYLNWY (SEQ ID NO: 6030)	LLIYAATSRA (SEQ ID NO: 6209)	QQSYDTPL (SEQ ID NO: 6388)
367_D06	DSYSMN (SEQ ID NO: 5494)	WVAGINYNGGYTS (SEQ ID NO: 5673)	ARGANWHDTHLD (SEQ ID NO:5852)	STYLNWY (SEQ ID NO: 6031)	LVIYAATSLA (SEQ ID NO: 6210)	QQSYNSPL (SEQ ID NO: 6389)
367_D08	SDYSMN (SEQ ID NO: 5495)	WVAGINYNGGYTS (SEQ ID NO: 5674)	ARGANWHDTHLD (SEQ ID NO:5853)	LSYLNWY (SEQ ID NO: 6032)	LVIYAATSRH (SEQ ID NO: 6211)	QQSDDLPL (SEQ ID NO: 6390)
367_D12	SSYSMN (SEQ ID NO: 5496)	WVSSINYNGGYTG (SEQ ID NO: 5675)	ARGANWHDTHLD (SEQ ID NO:5854)	VSYVNWY (SEQ ID NO: 6033)	LVIYAATSRA (SEQ ID NO: 6212)	QQSYESPL (SEQ ID NO: 6391)
367_E05	SSYGMN (SEQ ID NO: 5497)	WVAGINYNGGYTS (SEQ ID NO: 5676)	ARGANWHDTHLD (SEQ ID NO:5855)	LSYLNWY (SEQ ID NO: 6034)	LLIYAATSRH (SEQ ID NO: 6213)	QQSYDSPL (SEQ ID NO: 6392)
367_F01	DSYSMN (SEQ ID NO: 5498)	WVSNINYNGGYKS (SEQ ID NO: 5677)	ARGANWHDTHLD (SEQ ID NO:5856)	ISYLNWY (SEQ ID NO: 6035)	LLIYAASSLQ (SEQ ID NO: 6214)	QQSYSTPL (SEQ ID NO: 6393)
367_G01	DSYGMN (SEQ ID NO: 5499)	WVASINYNSGYTG (SEQ ID NO: 5678)	ARGANWHDTHLD (SEQ ID NO:5857)	SSYLNWY (SEQ ID NO: 6036)	LVIYAATSRA (SEQ ID NO: 6215)	QQSYDLPL (SEQ ID NO: 6394)
367_G04	SSYSMN (SEQ ID NO: 5500)	WVAGINYNSGYTS (SEQ ID NO: 5679)	ARGANWHDTHLD (SEQ ID NO:5858)	LSYLNWY (SEQ ID NO: 6037)	LVIYAATSRA (SEQ ID NO: 6216)	QQSYDSPL (SEQ ID NO: 6395)
367_H02	DSYGMN (SEQ ID NO: 5501)	WVSSINYNGGYTG (SEQ ID NO: 5680)	ARGANWHDTHLD (SEQ ID NO:5859)	SSYLNWY (SEQ ID NO: 6038)	LLIYAASSLQ (SEQ ID NO: 6217)	QQSYSTPL (SEQ ID NO: 6396)
367_H03	SSYGMN (SEQ	WVAGINYNSGYTS (SEQ ID NO:	ARGANWHDTHLD (SEQ ID	ITYVNWY (SEQ ID	LLIYAATSLA (SEQ ID	QQSYDLPL (SEQ ID

	ID NO: 5502)	5681)	NO:5860)	NO: 6039)	NO: 6218)	NO: 6397)
368_A03	SSYSMN (SEQ ID NO: 5503)	WVSGINYNGGYTG (SEQ ID NO: 5682)	ARGANWHDTHLD (SEQ ID NO:5861)	ISYLNWY (SEQ ID NO: 6040)	LLIYAVTSRA (SEQ ID NO: 6219)	QQSYENPL (SEQ ID NO: 6398)
368_A04	DDYSMN (SEQ ID NO: 5504)	WVAGINYNGGYKS (SEQ ID NO: 5683)	ARGANWHDTHLD (SEQ ID NO:5862)	LTYLNWY (SEQ ID NO: 6041)	LVIYAVTSRA (SEQ ID NO: 6220)	QQSYELPL (SEQ ID NO: 6399)
368_B09	DSYGMN (SEQ ID NO: 5505)	WVSNINYNGGYKG (SEQ ID NO: 5684)	ARGANWHDTHLD (SEQ ID NO:5863)	LSYLNWY (SEQ ID NO: 6042)	LLIYAATSRH (SEQ ID NO: 6221)	QQSYDTPL (SEQ ID NO: 6400)
368_C02	DDYSMN (SEQ ID NO: 5506)	WVANINYNGGYKG (SEQ ID NO: 5685)	ARGANWHDTHLD (SEQ ID NO:5864)	STYVNWY (SEQ ID NO: 6043)	LLIYAATSLA (SEQ ID NO: 6222)	QQSYSTPL (SEQ ID NO: 6401)
368_C08	SDYSMN (SEQ ID NO: 5507)	WVSGINYNGGYTS (SEQ ID NO: 5686)	ARGANWHDTHLD (SEQ ID NO:5865)	LTYVNWY (SEQ ID NO: 6044)	LLIYAASSLQ (SEQ ID NO: 6223)	QQSYSTPL (SEQ ID NO: 6402)
368_E12	SDYGMN (SEQ ID NO: 5508)	WVAGINYNGGYTS (SEQ ID NO: 5687)	ARGANWHDTHLD (SEQ ID NO:5866)	VSYVNWY (SEQ ID NO: 6045)	LVIYAVTSRA (SEQ ID NO: 6224)	QQSYDSPL (SEQ ID NO: 6403)
368_F09	SSYGMN (SEQ ID NO: 5509)	WVSGINYNSGYTS (SEQ ID NO: 5688)	ARGANWHDTHLD (SEQ ID NO:5867)	LTYLNWY (SEQ ID NO: 6046)	LLIYAASSLQ (SEQ ID NO: 6225)	QQSYETPL (SEQ ID NO: 6404)
368_H02	SSYGMN (SEQ ID NO: 5510)	WVAGINYNSGYTS (SEQ ID NO: 5689)	ARGANWHDTALD (SEQ ID NO:5868)	VTYLNWY (SEQ ID NO: 6047)	LVIYAATSRA (SEQ ID NO: 6226)	QQSYESPL (SEQ ID NO: 6405)
368_H05	SSYSMN (SEQ ID NO: 5511)	WVANINYNGGYKS (SEQ ID NO: 5690)	ARGANWHDTHLD (SEQ ID NO:5869)	VSYVNWY (SEQ ID NO: 6048)	LVIYATTSRA (SEQ ID NO: 6227)	QQSYESPL (SEQ ID NO: 6406)
369_A07	SSYSMN (SEQ	WVAGINYNGGYKG (SEQ ID NO:	ARGANWHDTALD (SEQ ID	LSYLNWY (SEQ ID	LVIYAATSRA (SEQ ID	QQSYESPL (SEQ ID

	ID NO: 5512)	5691)	NO:5870)	NO: 6049)	NO: 6228)	NO: 6407)
369_B05	DSYSMN (SEQ ID NO: 5513)	WVSGINYNGGYKS (SEQ ID NO: 5692)	ARGANWHDTHLD (SEQ ID NO:5871)	ISYLNWY (SEQ ID NO: 6050)	LLIYAATSLA (SEQ ID NO: 6229)	QQSYDTPL (SEQ ID NO: 6408)
369_C05	DSYSMN (SEQ ID NO: 5514)	WVAGINYNGGYTS (SEQ ID NO: 5693)	ARGANWHDTALD (SEQ ID NO:5872)	SSYVNWY (SEQ ID NO: 6051)	LVIYATTSRH (SEQ ID NO: 6230)	QQSYNSPL (SEQ ID NO: 6409)
369_D03	SSYSMN (SEQ ID NO: 5515)	WVSGINYNGGYTS (SEQ ID NO: 5694)	ARGANWHDTHLD (SEQ ID NO:5873)	LTYLNWY (SEQ ID NO: 6052)	LVIYAATSRA (SEQ ID NO: 6231)	QQSYENPL (SEQ ID NO: 6410)
369_D07	SSYGMN (SEQ ID NO: 5516)	WVSGINYNGGYKS (SEQ ID NO: 5695)	ARGANWHDTHLD (SEQ ID NO:5874)	VSYLNWY (SEQ ID NO: 6053)	LVIYAATSRA (SEQ ID NO: 6232)	QQSYDLPL (SEQ ID NO: 6411)
369_D09	SDYGMN (SEQ ID NO: 5517)	WVSNINYNGGYTS (SEQ ID NO: 5696)	ARGANWHDTALD (SEQ ID NO:5875)	LTYLNWY (SEQ ID NO: 6054)	LLIYAATSRA (SEQ ID NO: 6233)	QQSYDSPL (SEQ ID NO: 6412)
369_E06	SSYGMN (SEQ ID NO: 5518)	WVSGINYNGGYTS (SEQ ID NO: 5697)	ARGANWHDTALD (SEQ ID NO:5876)	ISYLNWY (SEQ ID NO: 6055)	LVIYAATSRH (SEQ ID NO: 6234)	QQSYDSPL (SEQ ID NO: 6413)
369_F08	SDYGMH (SEQ ID NO: 5519)	WVSGINYNSGYTS (SEQ ID NO: 5698)	ARGANWHDTALD (SEQ ID NO:5877)	LSYLNWY (SEQ ID NO: 6056)	LLIYAASSLQ (SEQ ID NO: 6235)	QQSYDLPL (SEQ ID NO: 6414)
369_G08	DSYSMN (SEQ ID NO: 5520)	WVSSINYNGGYKG (SEQ ID NO: 5699)	ARGANWHDTHLD (SEQ ID NO:5878)	LTYLNWY (SEQ ID NO: 6057)	LLIYAASSLQ (SEQ ID NO: 6236)	QQSYSTPL (SEQ ID NO: 6415)
370_A02	DSYGMN (SEQ ID NO: 5521)	WVAGINYNGGYTG (SEQ ID NO: 5700)	ARGANWHDTALD (SEQ ID NO:5879)	VTYLNWY (SEQ ID NO: 6058)	LVIYAATSRA (SEQ ID NO: 6237)	QQSYDSPL (SEQ ID NO: 6416)
370_B03	SSYSMN (SEQ	WVANINYNGGYTG (SEQ ID NO:	ARGANWHDTALD (SEQ ID	LSYLNWY (SEQ ID	LVIYAATSRA (SEQ ID	QQSYNNPL (SEQ ID

	ID NO: 5522)	5701)	NO:5880)	NO: 6059)	NO: 6238)	NO: 6417)
370_B11	DSYSMN (SEQ ID NO: 5523)	WVSGINYNSGYTS (SEQ ID NO: 5702)	ARGANWHDTHLD (SEQ ID NO:5881)	LSYLNWY (SEQ ID NO: 6060)	LVIYAATSRH (SEQ ID NO: 6239)	QQGYDLPL (SEQ ID NO: 6418)
370_B12	SDYSMN (SEQ ID NO: 5524)	WVSGINYNGGYKG (SEQ ID NO: 5703)	ARGANWHDTALD (SEQ ID NO:5882)	LSYVNWY (SEQ ID NO: 6061)	LVIYATTSRA (SEQ ID NO: 6240)	QQSYETPL (SEQ ID NO: 6419)
370_D01	SSYSMN (SEQ ID NO: 5525)	WVSSINYNGGYTG (SEQ ID NO: 5704)	ARGANWHDTALD (SEQ ID NO:5883)	LSYLNWY (SEQ ID NO: 6062)	LLIYAATSRH (SEQ ID NO: 6241)	QQSYNTPL (SEQ ID NO: 6420)
370_D05	DDYSMN (SEQ ID NO: 5526)	WVSNINYNGGYKG (SEQ ID NO: 5705)	ARGANWHDTALD (SEQ ID NO:5884)	ITYLNWY (SEQ ID NO: 6063)	LVIYAATSRH (SEQ ID NO: 6242)	QQSYDTPL (SEQ ID NO: 6421)
370_F03	SSYGMN (SEQ ID NO: 5527)	WVSSINYNSGYKS (SEQ ID NO: 5706)	ARGANWHDTALD (SEQ ID NO:5885)	LSYVNWY (SEQ ID NO: 6064)	LLIYAATSRA (SEQ ID NO: 6243)	QQSYENPL (SEQ ID NO: 6422)
370_H02	DSYSMN (SEQ ID NO: 5528)	WVSGINYNSGYTS (SEQ ID NO: 5707)	ARGANWHDTHLD (SEQ ID NO:5886)	LTYLNWY (SEQ ID NO: 6065)	LLIYAATSRA (SEQ ID NO: 6244)	QQSYESPL (SEQ ID NO: 6423)
370_H07	SSYSMN (SEQ ID NO: 5529)	WVAGINYNGGYKS (SEQ ID NO: 5708)	ARGANWHDTALD (SEQ ID NO:5887)	LSYLNWY (SEQ ID NO: 6066)	LLIYAATSLA (SEQ ID NO: 6245)	QQSDSSPL (SEQ ID NO: 6424)
371_A10	DDYSMN (SEQ ID NO: 5530)	WVSGINYNGGYKG (SEQ ID NO: 5709)	ARGANWHDTALD (SEQ ID NO:5888)	VSYLNWY (SEQ ID NO: 6067)	LVIYAATSRA (SEQ ID NO: 6246)	QQSYENPL (SEQ ID NO: 6425)
371_B03	SSYGMH (SEQ ID NO: 5531)	WVASINYNGGYTS (SEQ ID NO: 5710)	ARGANWHDTHLD (SEQ ID NO:5889)	LSYVNWY (SEQ ID NO: 6068)	LLIYATTSRA (SEQ ID NO: 6247)	QQSYDNPL (SEQ ID NO: 6426)
371_B04	SSYSMN (SEQ	WVSGINYNGGYKS (SEQ ID NO:	ARGANWHDTALD (SEQ ID	LSYLNWY (SEQ ID	LVIYAVTSRH (SEQ ID	QQSYDSPL (SEQ ID

	ID NO: 5532)	5711)	NO:5890)	NO: 6069)	NO: 6248)	NO: 6427)
371_B09	SSYSMN (SEQ ID NO: 5533)	WVAGINYNSGYTG (SEQ ID NO: 5712)	ARGANWHDTHLD (SEQ ID NO:5891)	LSYVNWY (SEQ ID NO: 6070)	LVIYATTSLA (SEQ ID NO: 6249)	QQSYDTPL (SEQ ID NO: 6428)
371_B12	SDYSMN (SEQ ID NO: 5534)	WVAGINYNSGYTS (SEQ ID NO: 5713)	ARGANWHDTALD (SEQ ID NO:5892)	VTYLNWY (SEQ ID NO: 6071)	LVIYAATSRH (SEQ ID NO: 6250)	QQSYNNPL (SEQ ID NO: 6429)
371_C01	SSYGMH (SEQ ID NO: 5535)	WVSSINYNGGYTG (SEQ ID NO: 5714)	ARGANWHDTHLD (SEQ ID NO:5893)	VSYLNWY (SEQ ID NO: 6072)	LLIYAATSRH (SEQ ID NO: 6251)	QQSYDNPL (SEQ ID NO: 6430)
371_C04	DSYGMN (SEQ ID NO: 5536)	WVSGINYNSGYKG (SEQ ID NO: 5715)	ARGANWHDTALD (SEQ ID NO:5894)	LSYLNWY (SEQ ID NO: 6073)	LLIYAATSRA (SEQ ID NO: 6252)	QQSYSTPL (SEQ ID NO: 6431)
371_C05	SDYGMH (SEQ ID NO: 5537)	WVANINYNGGYTG (SEQ ID NO: 5716)	ARGANWHDTALD (SEQ ID NO:5895)	LSYLNWY (SEQ ID NO: 6074)	LLIYAATSRA (SEQ ID NO: 6253)	QQSYDSPL (SEQ ID NO: 6432)
371_C12	SSYSMN (SEQ ID NO: 5538)	WVAGINYNSGYKS (SEQ ID NO: 5717)	ARGANWHDTHLD (SEQ ID NO:5896)	VSYVNWY (SEQ ID NO: 6075)	LLIYAATSRA (SEQ ID NO: 6254)	QQSYDTPL (SEQ ID NO: 6433)
371_D02	DDYSMN (SEQ ID NO: 5539)	WVAGINYNGGYKS (SEQ ID NO: 5718)	ARGANWHDTALD (SEQ ID NO:5897)	VTYLNWY (SEQ ID NO: 6076)	LLIYAATSRA (SEQ ID NO: 6255)	QQSYDSPL (SEQ ID NO: 6434)
371_D04	DDYSMN (SEQ ID NO: 5540)	WVAGINYNGGYTG (SEQ ID NO: 5719)	ARGANWHDTHLD (SEQ ID NO:5898)	VSYVNWY (SEQ ID NO: 6077)	LLIYAATSLA (SEQ ID NO: 6256)	QQSYENPL (SEQ ID NO: 6435)
371_E06	SSYSMN (SEQ ID NO: 5541)	WVSGINYNGGYTS (SEQ ID NO: 5720)	ARGANWHDTALD (SEQ ID NO:5899)	STYLNWY (SEQ ID NO: 6078)	LLIYAVTSLH (SEQ ID NO: 6257)	QQSYESPL (SEQ ID NO: 6436)
371_E07	DSYSMN (SEQ	WVAGINYNGGYTS (SEQ ID NO:	ARGANWHDTALD (SEQ ID	ISYLNWY (SEQ ID	LLIYAATSLA (SEQ ID	QQSYESPL (SEQ ID

	ID NO: 5542)	5721)	NO:5900)	NO: 6079)	NO: 6258)	NO: 6437)
371_E10	DSYSMN (SEQ ID NO: 5543)	WVAGINYNGGYTS (SEQ ID NO: 5722)	ARGANWHDTALD (SEQ ID NO:5901)	STYLNWY (SEQ ID NO: 6080)	LLIYAVTSRA (SEQ ID NO: 6259)	QQSYNSPL (SEQ ID NO: 6438)
371_F10	DSYGMN (SEQ ID NO: 5544)	WVSGINYNSGYTS (SEQ ID NO: 5723)	ARGANWHDTALD (SEQ ID NO:5902)	SSYLNWY (SEQ ID NO: 6081)	LVIYAVTSRA (SEQ ID NO: 6260)	QQSYESPL (SEQ ID NO: 6439)
371_F11	SSYSMN (SEQ ID NO: 5545)	WVSGINYNGGYTS (SEQ ID NO: 5724)	ARGANWHDTALD (SEQ ID NO:5903)	ISYVNWY (SEQ ID NO: 6082)	LLIYAVTSRA (SEQ ID NO: 6261)	QQSYDLPL (SEQ ID NO: 6440)
371_G02	DSYGMN (SEQ ID NO: 5546)	WVASINYNGGYTS (SEQ ID NO: 5725)	ARGANWHDTHLD (SEQ ID NO:5904)	LSYLNWY (SEQ ID NO: 6083)	LLIYAATSRA (SEQ ID NO: 6262)	QQSYDLPL (SEQ ID NO: 6441)
371_G04	DSYSMN (SEQ ID NO: 5547)	WVSGINYNGGYKS (SEQ ID NO: 5726)	ARGANWHDTALD (SEQ ID NO:5905)	LSYLNWY (SEQ ID NO: 6084)	LLIYAATSLH (SEQ ID NO: 6263)	QQSYESPL (SEQ ID NO: 6442)
371_G09	SSYSMN (SEQ ID NO: 5548)	WVANINYNGGYTG (SEQ ID NO: 5727)	ARGANWHDTALD (SEQ ID NO:5906)	LSYLNWY (SEQ ID NO: 6085)	LVIYAATSRA (SEQ ID NO: 6264)	QQSDSTPL (SEQ ID NO: 6443)
371_G11	SSYGMN (SEQ ID NO: 5549)	WVSNINYNSGYTS (SEQ ID NO: 5728)	ARGANWHDTALD (SEQ ID NO:5907)	LSYVNWY (SEQ ID NO: 6086)	LLIYAATSLA (SEQ ID NO: 6265)	QQSYDSPL (SEQ ID NO: 6444)
371_H04	SSYGMN (SEQ ID NO: 5550)	WVSNINYNGGYTG (SEQ ID NO: 5729)	ARGANWHDTALD (SEQ ID NO:5908)	LTYLNWY (SEQ ID NO: 6087)	LLIYAATSRA (SEQ ID NO: 6266)	QQSYNSPL (SEQ ID NO: 6445)
371_H05	SSYGMN (SEQ ID NO: 5551)	WVSGINYNSGYKS (SEQ ID NO: 5730)	ARGANWHDTALD (SEQ ID NO:5909)	ISYLNWY (SEQ ID NO: 6088)	LLIYAATSLA (SEQ ID NO: 6267)	QQSYSLPL (SEQ ID NO: 6446)
371_H06	DSYGMN (SEQ	WVSGINYNGGYTS (SEQ ID NO:	ARGANWHDTALD (SEQ ID	SSYLNWY (SEQ ID	LVIYAVTSRA (SEQ ID	QQSYDLPL (SEQ ID

	ID NO: 5552)	5731)	NO:5910)	NO: 6089)	NO: 6268)	NO: 6447)
371_H08	SSYGMN (SEQ ID NO: 5553)	WVASINYNGGYKG (SEQ ID NO: 5732)	ARGANWHDTHLD (SEQ ID NO:5911)	ISYVNWY (SEQ ID NO: 6090)	LVIYAVTSRA (SEQ ID NO: 6269)	QQSYDTPL (SEQ ID NO: 6448)
371_H10	SSYSMN (SEQ ID NO: 5554)	WVAGINYNSGYKS (SEQ ID NO: 5733)	ARGANWHDTHLD (SEQ ID NO:5912)	STYLNWY (SEQ ID NO: 6091)	LLIYAATSRH (SEQ ID NO: 6270)	QQSYENPL (SEQ ID NO: 6449)
372_B02	SSYSMN (SEQ ID NO: 5555)	WVSGINYNSGYTS (SEQ ID NO: 5734)	ARGANWHDTALD (SEQ ID NO:5913)	LSYVNWY (SEQ ID NO: 6092)	LLIYAVTSLA (SEQ ID NO: 6271)	QQSYETPL (SEQ ID NO: 6450)
372_C06	SDYSMN (SEQ ID NO: 5556)	WVSGINYNGGYTS (SEQ ID NO: 5735)	ARGANWHDTALD (SEQ ID NO:5914)	VSYVNWY (SEQ ID NO: 6093)	LLIYAATSRA (SEQ ID NO: 6272)	QQSYSSPL (SEQ ID NO: 6451)
372_D03	SSYSMN (SEQ ID NO: 5557)	WVAGINYNSGYKS (SEQ ID NO: 5736)	ARGANWHDTALD (SEQ ID NO:5915)	LSYVNWY (SEQ ID NO: 6094)	LVIYAVTSRH (SEQ ID NO: 6273)	QQSYDSPL (SEQ ID NO: 6452)
372_E01	DDYSMN (SEQ ID NO: 5558)	WVSGINYNGGYKG (SEQ ID NO: 5737)	ARGANWHDTALD (SEQ ID NO:5916)	VSYLNWY (SEQ ID NO: 6095)	LVIYAATSRH (SEQ ID NO: 6274)	QQSYDSPL (SEQ ID NO: 6453)
372_G12	DSYSMN (SEQ ID NO: 5559)	WVAGINYNGGYTG (SEQ ID NO: 5738)	ARGANWHDTHLD (SEQ ID NO:5917)	LTYLNWY (SEQ ID NO: 6096)	LVIYAATSRH (SEQ ID NO: 6275)	QQSYDSPL (SEQ ID NO: 6454)
373_A01	SSYGMN (SEQ ID NO: 5560)	WVSNINYNGGYTG (SEQ ID NO: 5739)	ARGANWHDTHLD (SEQ ID NO:5918)	VTYLNWY (SEQ ID NO: 6097)	LVIYATTSRA (SEQ ID NO: 6276)	QQSYNLPL (SEQ ID NO: 6455)
373_A03	SDYSMN (SEQ ID NO: 5561)	WVANINYNGGYTG (SEQ ID NO: 5740)	ARGANWHDTALD (SEQ ID NO:5919)	LSYLNWY (SEQ ID NO: 6098)	LVIYAATSRA (SEQ ID NO: 6277)	QQSYDNPL (SEQ ID NO: 6456)
373_A05	SDYSMN (SEQ	WVSGINYNSGYKS (SEQ ID NO:	ARGANWHDTHLD (SEQ ID	LSYVNWY (SEQ ID	LVIYAATSRH (SEQ ID	QQSYESPL (SEQ ID

	ID NO: 5562)	5741)	NO:5920)	NO: 6099)	NO: 6278)	NO: 6457)
373_A09	DSYSMN (SEQ ID NO: 5563)	WVAGINYNGGYTS (SEQ ID NO: 5742)	ARGANWHDTALD (SEQ ID NO:5921)	LTYLNWY (SEQ ID NO: 6100)	LLIYAATSLA (SEQ ID NO: 6279)	QQSYDTPL (SEQ ID NO: 6458)
373_A11	SNYGMN (SEQ ID NO: 5564)	WVANINYNGGYTG (SEQ ID NO: 5743)	ARGANWHDTALD (SEQ ID NO:5922)	LTYLNWY (SEQ ID NO: 6101)	LLIYAATSRA (SEQ ID NO: 6280)	QQSYDLPL (SEQ ID NO: 6459)
373_A12	SSYSMN (SEQ ID NO: 5565)	WVSSINYNGGYTS (SEQ ID NO: 5744)	ARGANWHDTALD (SEQ ID NO:5923)	LTYLNWY (SEQ ID NO: 6102)	LVIYAATSRA (SEQ ID NO: 6281)	QQSYDTPL (SEQ ID NO: 6460)
373_B05	SDYSMN (SEQ ID NO: 5566)	WVSNINYNGGYKS (SEQ ID NO: 5745)	ARGANWHDTALD (SEQ ID NO:5924)	VTYLNWY (SEQ ID NO: 6103)	LVIYAATSRA (SEQ ID NO: 6282)	QQSYSNPL (SEQ ID NO: 6461)
373_B07	DSYSMN (SEQ ID NO: 5567)	WVSGINYNGGYTS (SEQ ID NO: 5746)	ARGANWHDTALD (SEQ ID NO:5925)	LTYVNWY (SEQ ID NO: 6104)	LVIYAATSRA (SEQ ID NO: 6283)	QQSYELPL (SEQ ID NO: 6462)
373_C03	SSYSMN (SEQ ID NO: 5568)	WVSGINYNGGYKS (SEQ ID NO: 5747)	ARGANWHDTALD (SEQ ID NO:5926)	VTYLNWY (SEQ ID NO: 6105)	LVIYAATSRA (SEQ ID NO: 6284)	QQSYDSPL (SEQ ID NO: 6463)
373_C07	DSYSMN (SEQ ID NO: 5569)	WVAGINYNSGYTS (SEQ ID NO: 5748)	ARGANWHDTHLD (SEQ ID NO:5927)	LTYLNWY (SEQ ID NO: 6106)	LVIYAATSRA (SEQ ID NO: 6285)	QQSYETPL (SEQ ID NO: 6464)
373_C10	SSYSMN (SEQ ID NO: 5570)	WVAGINYNGGYTS (SEQ ID NO: 5749)	ARGANWHDTALD (SEQ ID NO:5928)	LTYVNWY (SEQ ID NO: 6107)	LLIYAATSRA (SEQ ID NO: 6286)	QQSYDNPL (SEQ ID NO: 6465)
373_D03	SSYSMN (SEQ ID NO: 5571)	WVSGINYNGGYTS (SEQ ID NO: 5750)	ARGANWHDTALD (SEQ ID NO:5929)	VSYLNWY (SEQ ID NO: 6108)	LLIYAATSLA (SEQ ID NO: 6287)	QQSYDTPL (SEQ ID NO: 6466)
373_D12	DSYSMN (SEQ	WVSSINYNSGYKG (SEQ ID NO:	ARGANWHDTHLD (SEQ ID	LSYVNWY (SEQ ID	LLIYAATSRA (SEQ ID	QQSYSLPL (SEQ ID

	ID NO: 5572)	5751)	NO:5930)	NO: 6109)	NO: 6288)	NO: 6467)
373_E10	SDYSMN (SEQ ID NO: 5573)	WVSGINYNGGYTS (SEQ ID NO: 5752)	ARGANWHDTALD (SEQ ID NO:5931)	LTYVNWY (SEQ ID NO: 6110)	LVIYAATSRH (SEQ ID NO: 6289)	QQSYETPL (SEQ ID NO: 6468)
373_F08	SSYSMN (SEQ ID NO: 5574)	WVSGINYNGGYTS (SEQ ID NO: 5753)	ARGANWHDTALD (SEQ ID NO:5932)	LTYLNWY (SEQ ID NO: 6111)	LLIYAATSRA (SEQ ID NO: 6290)	QQSYDTPL (SEQ ID NO: 6469)
373_F11	DSYGMH (SEQ ID NO: 5575)	WVSGINYNSGYTS (SEQ ID NO: 5754)	ARGANWHDTHLD (SEQ ID NO:5933)	VSYVNWY (SEQ ID NO: 6112)	LLIYAATSRA (SEQ ID NO: 6291)	QQSYNLPL (SEQ ID NO: 6470)
373_F12	SSYSMN (SEQ ID NO: 5576)	WVSNINYNGGYTG (SEQ ID NO: 5755)	ARGANWHDTALD (SEQ ID NO:5934)	STYLNWY (SEQ ID NO: 6113)	LVIYAATSRA (SEQ ID NO: 6292)	QQSYETPL (SEQ ID NO: 6471)
373_G08	DSYSMN (SEQ ID NO: 5577)	WVSNINYNGGYTS (SEQ ID NO: 5756)	ARGANWHDTALD (SEQ ID NO:5935)	LTYLNWY (SEQ ID NO: 6114)	LLIYAATSLA (SEQ ID NO: 6293)	QQSYDSPL (SEQ ID NO: 6472)
373_H03	SSYSMN (SEQ ID NO: 5578)	WVSGINYNSGYKS (SEQ ID NO: 5757)	ARGANWHDTALD (SEQ ID NO:5936)	LSYLNWY (SEQ ID NO: 6115)	LLIYATTSRA (SEQ ID NO: 6294)	QQSYENPL (SEQ ID NO: 6473)
373_H07	SSYSMN (SEQ ID NO: 5579)	WVAGINYNGGYTS (SEQ ID NO: 5758)	ARGANWHDTHLD (SEQ ID NO:5937)	VTYLNWY (SEQ ID NO: 6116)	LLIYAASSLQ (SEQ ID NO: 6295)	QQSYDSPL (SEQ ID NO: 6474)
373_H09	SSYGMN (SEQ ID NO: 5580)	WVASINYNSGYKS (SEQ ID NO: 5759)	ARGANWHDTHLD (SEQ ID NO:5938)	ITYLNWY (SEQ ID NO: 6117)	LVIYAATSRA (SEQ ID NO: 6296)	QQSDDSPL (SEQ ID NO: 6475)
374_A06	SSYSMN (SEQ ID NO: 5581)	WVSSINYNSGYTS (SEQ ID NO: 5760)	ARGANWHDTHLD (SEQ ID NO:5939)	LSYLNWY (SEQ ID NO: 6118)	LVIYAATSRA (SEQ ID NO: 6297)	QQSYDSPL (SEQ ID NO: 6476)
374_A09	SSYSMN (SEQ	WVSSINYNGGYKG (SEQ ID NO:	ARGANWHDTHLD (SEQ ID	LTYVNWY (SEQ ID	LLIYAATSLA (SEQ ID	QQSYDSPL (SEQ ID

	ID NO: 5582)	5761)	NO:5940)	NO: 6119)	NO: 6298)	NO: 6477)
374_B03	DSYSMN (SEQ ID NO: 5583)	WVSGINYNGGYTS (SEQ ID NO: 5762)	ARGANWHDTALD (SEQ ID NO:5941)	LTYLNWY (SEQ ID NO: 6120)	LVIYAATSRA (SEQ ID NO: 6299)	QQSYDSPL (SEQ ID NO: 6478)
374_B05	DSYSMN (SEQ ID NO: 5584)	WVSGINYNSGYTS (SEQ ID NO: 5763)	ARGANWHDTALD (SEQ ID NO:5942)	VSYLNWY (SEQ ID NO: 6121)	LLIYAATSRH (SEQ ID NO: 6300)	QQSYESPL (SEQ ID NO: 6479)
374_B08	DSYSMN (SEQ ID NO: 5585)	WVAGINYNGGYTS (SEQ ID NO: 5764)	ARGANWHDTALD (SEQ ID NO:5943)	VSYVNWY (SEQ ID NO: 6122)	LLIYAATSRH (SEQ ID NO: 6301)	QQSYELPL (SEQ ID NO: 6480)
374_B10	SSYSMN (SEQ ID NO: 5586)	WVSSINYNSGYTS (SEQ ID NO: 5765)	ARGANWHDTHLD (SEQ ID NO:5944)	LTYVNWY (SEQ ID NO: 6123)	LVIYAATSLA (SEQ ID NO: 6302)	QQSYDTPL (SEQ ID NO: 6481)
374_C01	DSYGMN (SEQ ID NO: 5587)	WVSGINYNSGYKS (SEQ ID NO: 5766)	ARGANWHDTALD (SEQ ID NO:5945)	LTYLNWY (SEQ ID NO: 6124)	LLIYAATSRA (SEQ ID NO: 6303)	QQSYETPL (SEQ ID NO: 6482)
374_C09	DSYGMN (SEQ ID NO: 5588)	WVSSINYNGGYKG (SEQ ID NO: 5767)	ARGANWHDTHLD (SEQ ID NO:5946)	VSYLNWY (SEQ ID NO: 6125)	LVIYAATSRA (SEQ ID NO: 6304)	QQSYELPL (SEQ ID NO: 6483)
374_C12	SSYSMN (SEQ ID NO: 5589)	WVAGINYNGGYKS (SEQ ID NO: 5768)	ARGANWHDTALD (SEQ ID NO:5947)	LTYLNWY (SEQ ID NO: 6126)	LVIYAATSRA (SEQ ID NO: 6305)	QQSDNSPL (SEQ ID NO: 6484)
374_D03	DSYSMN (SEQ ID NO: 5590)	WVAGINYNGGYKS (SEQ ID NO: 5769)	ARGANWHDTHLD (SEQ ID NO:5948)	VTYLNWY (SEQ ID NO: 6127)	LLIYAATSRA (SEQ ID NO: 6306)	QQSYDTPL (SEQ ID NO: 6485)
374_D05	DSYSMN (SEQ ID NO: 5591)	WVSGINYNSGYTG (SEQ ID NO: 5770)	ARGANWHDTHLD (SEQ ID NO:5949)	LTYLNWY (SEQ ID NO: 6128)	LLIYAATSRA (SEQ ID NO: 6307)	QQSYDTPL (SEQ ID NO: 6486)
374_D06	SSYSMN (SEQ	WVSGINYNGGYTS (SEQ ID NO:	ARGANWHDTALD (SEQ ID	LSYVNWY (SEQ ID	LVIYAATSRA (SEQ ID	QQSYDSPL (SEQ ID

	ID NO: 5592)	5771)	NO:5950)	NO: 6129)	NO: 6308)	NO: 6487)
374_D07	DSYSMN (SEQ ID NO: 5593)	WVSGINYNSGYKS (SEQ ID NO: 5772)	ARGANWHDTALD (SEQ ID NO:5951)	VSYLNWY (SEQ ID NO: 6130)	LVIYAATSLA (SEQ ID NO: 6309)	QQSYNSPL (SEQ ID NO: 6488)
374_D10	SSYGMH (SEQ ID NO: 5594)	WVASINYNGGYTS (SEQ ID NO: 5773)	ARGANWHDTHLD (SEQ ID NO:5952)	LTYVNWY (SEQ ID NO: 6131)	LLIYAATSRA (SEQ ID NO: 6310)	QQSYDNPL (SEQ ID NO: 6489)
374_E10	SSYSMN (SEQ ID NO: 5595)	WVSGINYNGGYKS (SEQ ID NO: 5774)	ARGANWHDTALD (SEQ ID NO:5953)	LSYLNWY (SEQ ID NO: 6132)	LLIYAATSRH (SEQ ID NO: 6311)	QQSYDSPL (SEQ ID NO: 6490)
374_E12	SSYSMN (SEQ ID NO: 5596)	WVSGINYNGGYKS (SEQ ID NO: 5775)	ARGANWHDTALD (SEQ ID NO:5954)	LSYLNWY (SEQ ID NO: 6133)	LVIYAATSRA (SEQ ID NO: 6312)	QQSYDNPL (SEQ ID NO: 6491)
374_F06	SSYSMN (SEQ ID NO: 5597)	WVSGINYNGGYTS (SEQ ID NO: 5776)	ARGANWHDTALD (SEQ ID NO:5955)	ISYVNWY (SEQ ID NO: 6134)	LVIYAATSLH (SEQ ID NO: 6313)	QQSYSTPL (SEQ ID NO: 6492)
374_F07	DSYSMN (SEQ ID NO: 5598)	WVASINYNGGYTG (SEQ ID NO: 5777)	ARGANWHDTHLD (SEQ ID NO:5956)	LSYLNWY (SEQ ID NO: 6135)	LVIYAVTSLA (SEQ ID NO: 6314)	QQSYESPL (SEQ ID NO: 6493)
374_F08	DSYSMN (SEQ ID NO: 5599)	WVSGINYNGGYKS (SEQ ID NO: 5778)	ARGANWHDTALD (SEQ ID NO:5957)	LTYVVNWY (SEQ ID NO: 6136)	LVIYAVTSRA (SEQ ID NO: 6315)	QQSYDTPL (SEQ ID NO: 6494)
374_G03	SDYSMN (SEQ ID NO: 5600)	WVSGINYNGGYTS (SEQ ID NO: 5779)	ARGANWHDTALD (SEQ ID NO:5958)	SSYLNWY (SEQ ID NO: 6137)	LVIYAATSRA (SEQ ID NO: 6316)	QQSDDTPL (SEQ ID NO: 6495)
374_G08	DSYSMN (SEQ ID NO: 5601)	WVSGINYNGGYTS (SEQ ID NO: 5780)	ARGANWHDTALD (SEQ ID NO:5959)	LTYVNWY (SEQ ID NO: 6138)	LVIYAATSRA (SEQ ID NO: 6317)	QQSYDSPL (SEQ ID NO: 6496)
374_G09	SSYSMN (SEQ	WVAGINYNGGYKG (SEQ ID NO:	ARGANWHDTHLD (SEQ ID	VRYLNWY (SEQ ID	LVIYAATSLA (SEQ ID	QQSYELPL (SEQ ID

	ID NO: 5602)	5781)	NO:5960)	NO: 6139)	NO: 6318)	NO: 6497)
374_G10	SSYSMN (SEQ ID NO: 5603)	WVSSINYNSGYTS (SEQ ID NO: 5782)	ARGANWHDTHLD (SEQ ID NO:5961)	VSYLNWY (SEQ ID NO: 6140)	LVIYAVTSRA (SEQ ID NO: 6319)	QQSYDSPL (SEQ ID NO: 6498)
374_G11	SDYSMN (SEQ ID NO: 5604)	WVSGINYNGGYTS (SEQ ID NO: 5783)	ARGANWHDTALD (SEQ ID NO:5962)	ISYVNWY (SEQ ID NO: 6141)	LVIYAATSLA (SEQ ID NO: 6320)	QQSYDSPL (SEQ ID NO: 6499)
374_H01	DSYSMN (SEQ ID NO: 5605)	WVAGINYNGGYTS (SEQ ID NO: 5784)	ARGANWHDTHLD (SEQ ID NO:5963)	LSYLNWY (SEQ ID NO: 6142)	LVIYAATSLA (SEQ ID NO: 6321)	QQSYENPL (SEQ ID NO: 6500)
374_H11	SSYSMN (SEQ ID NO: 5606)	WVSGINYNGGYTS (SEQ ID NO: 5785)	ARGANWHDTALD (SEQ ID NO:5964)	ISYVNWY (SEQ ID NO: 6143)	LVIYAATSLH (SEQ ID NO: 6322)	QQSYSNPL (SEQ ID NO: 6501)
375_A01	DSYSMN (SEQ ID NO: 5607)	WVAGINYNGGYTS (SEQ ID NO: 5786)	ARGANWHDTALD (SEQ ID NO:5965)	LSYLNWY (SEQ ID NO: 6144)	LVIYAATSRA (SEQ ID NO: 6323)	QQSYNTPL (SEQ ID NO: 6502)
375_A07	DSYSMN (SEQ ID NO: 5608)	WVSSINYNSGYTG (SEQ ID NO: 5787)	ARGANWHDTHLD (SEQ ID NO:5966)	LTYLNWY (SEQ ID NO: 6145)	LLIYAATSRA (SEQ ID NO: 6324)	QQSYDTPL (SEQ ID NO: 6503)
375_A08	SSYSMN (SEQ ID NO: 5609)	WVAGINYNGGYTG (SEQ ID NO: 5788)	ARGANWHDTALD (SEQ ID NO:5967)	VTYLNWY (SEQ ID NO: 6146)	LLIYAATSRA (SEQ ID NO: 6325)	QQSYESPL (SEQ ID NO: 6504)
375_A12	SSYSMN (SEQ ID NO: 5610)	WVSGINYNSGYKS (SEQ ID NO: 5789)	ARGANWHDTALD (SEQ ID NO:5968)	LSYLNWY (SEQ ID NO: 6147)	LVIYAVTSRA (SEQ ID NO: 6326)	QQSYETPL (SEQ ID NO: 6505)
375_B12	DSYSMN (SEQ ID NO: 5611)	WVAGINYNGGYKS (SEQ ID NO: 5790)	ARGANWHDTALD (SEQ ID NO:5969)	VTYLNWY (SEQ ID NO: 6148)	LLIYAATSRA (SEQ ID NO: 6327)	QQSYDTPL (SEQ ID NO: 6506)
375_C04	SDYSMN (SEQ	WVAGINYNGGYTS (SEQ ID NO:	ARGANWHDTALD (SEQ ID	LTYLNWY (SEQ ID	LVIYAATSRA (SEQ ID	QQSYESPL (SEQ ID

	ID NO: 5612)	5791)	NO:5970)	NO: 6149)	NO: 6328)	NO: 6507)
375_D01	SSYSMN (SEQ ID NO: 5613)	WVSGINYNGGYTG (SEQ ID NO: 5792)	ARGANWHDTALD (SEQ ID NO:5971)	LTYLNWY (SEQ ID NO: 6150)	LVIYAATSRA (SEQ ID NO: 6329)	QQSYETPL (SEQ ID NO: 6508)
375_D10	SSYSMN (SEQ ID NO: 5614)	WVAGINYNGGYTS (SEQ ID NO: 5793)	ARGANWHDTALD (SEQ ID NO:5972)	LTYVNWY (SEQ ID NO: 6151)	LLIYAATSRA (SEQ ID NO: 6330)	QQSDDSPL (SEQ ID NO: 6509)
375_E02	SDYSMN (SEQ ID NO: 5615)	WVAGINYNGGYTS (SEQ ID NO: 5794)	ARGANWHDTALD (SEQ ID NO:5973)	LTYLNWY (SEQ ID NO: 6152)	LLIYAATSRA (SEQ ID NO: 6331)	QQSYSSPL (SEQ ID NO: 6510)
375_E03	SDYSMN (SEQ ID NO: 5616)	WVANINYNGGYTG (SEQ ID NO: 5795)	ARGANWHDTHLD (SEQ ID NO:5974)	LTYLNWY (SEQ ID NO: 6153)	LVIYAATSLA (SEQ ID NO: 6332)	QQSYDNPL (SEQ ID NO: 6511)
375_E05	SSYSMN (SEQ ID NO: 5617)	WVAGINYNGGYTS (SEQ ID NO: 5796)	ARGANWHDTALD (SEQ ID NO:5975)	LSYLNWY (SEQ ID NO: 6154)	LVIYAATSLA (SEQ ID NO: 6333)	QQSYSSPL (SEQ ID NO: 6512)
375_E06	SSYSMN (SEQ ID NO: 5618)	WVSGINYNGGYKS (SEQ ID NO: 5797)	ARGANWHDTALD (SEQ ID NO:5976)	LSYLNWY (SEQ ID NO: 6155)	LVIYAATSRA (SEQ ID NO: 6334)	QQSYDSPL (SEQ ID NO: 6513)
375_E10	SSYSMN (SEQ ID NO: 5619)	WVSGINYNGGYTS (SEQ ID NO: 5798)	ARGANWHDTALD (SEQ ID NO:5977)	LSYLNWY (SEQ ID NO: 6156)	LVIYAATSRA (SEQ ID NO: 6335)	QQSYDNPL (SEQ ID NO: 6514)
375_F02	SSYSMN (SEQ ID NO: 5620)	WVASINYNSGYTS (SEQ ID NO: 5799)	ARGANWHDTHLD (SEQ ID NO:5978)	LSYLNWY (SEQ ID NO: 6157)	LLIYAATSRA (SEQ ID NO: 6336)	QQSYDSPL (SEQ ID NO: 6515)
375_F07	SDYSMN (SEQ ID NO: 5621)	WVSNINYNGGYTG (SEQ ID NO: 5800)	ARGANWHDTALD (SEQ ID NO:5979)	LSYLNWY (SEQ ID NO: 6158)	LLIYAATSRA (SEQ ID NO: 6337)	QQSYDSPL (SEQ ID NO: 6516)
375_F08	SSYGMN (SEQ	WVSSINYNSGYKS (SEQ ID NO:	ARGANWHDTHLD (SEQ ID	LSYLNWY (SEQ ID	LLIYAATSRH (SEQ ID	QQSYDNPL (SEQ ID

	ID NO: 5622)	5801)	NO:5980)	NO: 6159)	NO: 6338)	NO: 6517)
375_G04	SSYGMN (SEQ ID NO: 5623)	WVASINYNSGYTG (SEQ ID NO: 5802)	ARGANWHDTHLD (SEQ ID NO:5981)	VSYVNWY (SEQ ID NO: 6160)	LLIYAATSLA (SEQ ID NO: 6339)	QQSYDSPL (SEQ ID NO: 6518)
375_G05	SSYSMN (SEQ ID NO: 5624)	WVAGINYNGGYTS (SEQ ID NO: 5803)	ARGANWHDTALD (SEQ ID NO:5982)	VSYLNWY (SEQ ID NO: 6161)	LLIYAVTSRA (SEQ ID NO: 6340)	QQSYDSPL (SEQ ID NO: 6519)
375_H05	SSYSMN (SEQ ID NO: 5625)	WVSNINYNGGYTG (SEQ ID NO: 5804)	ARGANWHDTALD (SEQ ID NO:5983)	LSYVNWY (SEQ ID NO: 6162)	LLIYAATSRA (SEQ ID NO: 6341)	QQSYDTPL (SEQ ID NO: 6520)
375_H07	SSYSMN (SEQ ID NO: 5626)	WVAGINYNGGYTS (SEQ ID NO: 5805)	ARGANWHDTALD (SEQ ID NO:5984)	LSYLNWY (SEQ ID NO: 6163)	LLIYAATSLA (SEQ ID NO: 6342)	QQSYSSPL (SEQ ID NO: 6521)
376_A03	SSYGMN (SEQ ID NO: 5627)	WVAGINYNGGYTG (SEQ ID NO: 5806)	ARGANWHDTALD (SEQ ID NO:5985)	LTYLNWY (SEQ ID NO: 6164)	LLIYAATSRA (SEQ ID NO: 6343)	QQSYSTPL (SEQ ID NO: 6522)
376_B03	SSYSMN (SEQ ID NO: 5628)	WVAGINYNSGYKS (SEQ ID NO: 5807)	ARGANWHDTALD (SEQ ID NO:5986)	LSYVNWY (SEQ ID NO: 6165)	LVIYAVTSRH (SEQ ID NO: 6344)	QQSYDSPL (SEQ ID NO: 6523)
376_B10	SDYSMN (SEQ ID NO: 5629)	WVAGINYNGGYKG (SEQ ID NO: 5808)	ARGANWHDTALD (SEQ ID NO:5987)	LSYLNWY (SEQ ID NO: 6166)	LVIYAATSLA (SEQ ID NO: 6345)	QQSYSTPL (SEQ ID NO: 6524)
376_C04	SSYGMN (SEQ ID NO: 5630)	WVSNINYNGGYTG (SEQ ID NO: 5809)	ARGANWHDTALD (SEQ ID NO:5988)	LSYVNWY (SEQ ID NO: 6167)	LLIYAVTSRH (SEQ ID NO: 6346)	QQSYDNPL (SEQ ID NO: 6525)
376_C08	DSYSMN (SEQ ID NO: 5631)	WVAGINYNSGYTG (SEQ ID NO: 5810)	ARGANWHDTHLD (SEQ ID NO:5989)	LSYLNWY (SEQ ID NO: 6168)	LLIYAASSLQ (SEQ ID NO: 6347)	QQSYSTPL (SEQ ID NO: 6526)
376_D07	DSYSMN (SEQ	WVSGINYNGGYTS (SEQ ID NO:	ARGANWHDTHLD (SEQ ID	SSYLNWY (SEQ ID	LLIYAASSLQ (SEQ ID	QQSYSTPL (SEQ ID

	ID NO: 5632)	5811)	NO:5990)	NO: 6169)	NO: 6348)	NO: 6527)
376_E02	SSYSMN (SEQ ID NO: 5633)	WVAGINYNGGYKG (SEQ ID NO: 5812)	ARGANWHDTALD (SEQ ID NO:5991)	LSYVNWY (SEQ ID NO: 6170)	LVIYAATSRH (SEQ ID NO: 6349)	QQSDNTPL (SEQ ID NO: 6528)
376_E11	SSYSMN (SEQ ID NO: 5634)	WVSGINYNGGYTS (SEQ ID NO: 5813)	ARGANWHDTALD (SEQ ID NO:5992)	LTYVNWY (SEQ ID NO: 6171)	LVIYAATSRA (SEQ ID NO: 6350)	QQSYELPL (SEQ ID NO: 6529)
376_F01	SDYSMN (SEQ ID NO: 5635)	WVAGINYNGGYKS (SEQ ID NO: 5814)	ARGANWHDTALD (SEQ ID NO:5993)	SSYLNWY (SEQ ID NO: 6172)	LLIYAASSLQ (SEQ ID NO: 6351)	QQSYSTPL (SEQ ID NO: 6530)
376_F06	SSYCMN (SEQ ID NO: 5636)	WVSGINYNGGYTG (SEQ ID NO: 5815)	ARGANWHDTHLD (SEQ ID NO:5994)	LTYVNWY (SEQ ID NO: 6173)	LVIYAATSRA (SEQ ID NO: 6352)	QQSYETPL (SEQ ID NO: 6531)
376_G05	SSYSMN (SEQ ID NO: 5637)	WVAGINYNGGYTS (SEQ ID NO: 5816)	ARGANWHDTALD (SEQ ID NO:5995)	ISYVNWY (SEQ ID NO: 6174)	LVIYAATSRA (SEQ ID NO: 6353)	QQSYESPL (SEQ ID NO: 6532)
376_G06	SSYGMN (SEQ ID NO: 5638)	WVAGINYNGGYTG (SEQ ID NO: 5817)	ARGANWHDTHLD (SEQ ID NO:5996)	VSYVNWY (SEQ ID NO: 6175)	LVIYAATSRA (SEQ ID NO: 6354)	QQSYNSPL (SEQ ID NO: 6533)
376_G10	DSYGMN (SEQ ID NO: 5639)	WVAGINYNGGYTS (SEQ ID NO: 5818)	ARGANWHDTALD (SEQ ID NO:5997)	LSYVNWY (SEQ ID NO: 6176)	LLIYAATSRA (SEQ ID NO: 6355)	QQSYESPL (SEQ ID NO: 6534)
376_H01	SDYSMN (SEQ ID NO: 5640)	WVAGINYNGGYKG (SEQ ID NO: 5819)	ARGANWHDTALD (SEQ ID NO:5998)	LTYLNWY (SEQ ID NO: 6177)	LLIYAATSRA (SEQ ID NO: 6356)	QQSYSTPL (SEQ ID NO: 6535)
376_H04	SSYSMN (SEQ ID NO: 5641)	WVAGINYNGGYKG (SEQ ID NO: 5820)	ARGANWHDTALD (SEQ ID NO:5999)	LTYVNWY (SEQ ID NO: 6178)	LVIYAATSRA (SEQ ID NO: 6357)	QQSYDLPL (SEQ ID NO: 6536)
376_H11	DSYSMN (SEQ	WVSNINYNGGYTG (SEQ ID NO:	ARGANWHDTALD (SEQ ID	SRYLNWY (SEQ ID	LLIYAVTSLA (SEQ ID	QQSYESPL (SEQ ID

	ID NO: 5642)	5821)	NO:6000)	NO: 6179)	NO: 6358)	NO: 6537)

The consensus sequences for each of these CDRs shown in Fig. 3C are as follows:

HCDR1: S/DS/DYS/GMN/H (SEQ ID NO: 6566)

HCDR2: WVS/AG/S/NINYNG/SGYT/KS/G (SEQ ID NO: 6594)

HCDR3: ARGANWHDTA/HLD (SEQ ID NO: 6543)

LCDR1: L/V/S/IS/TYL/VNWY (SEQ ID NO: 6569)

LCDR2: LL/VIYAA/V/TT/SSR/LA/H/Q (SEQ ID NO:)

LCDR3: QQSY/DD/E/S/NS/T/N/LPL (SEQ ID NO: 6571)

Table 2D: Group IV Antibody Sequences

Ab	VH sequence	VL sequence
365_A08	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYSMNWVRQAPGKGLEWVASINYNGGYK SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1384)	DIQMTQSPSSLSASVGDRVTITCRASQSIITYLN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSDNTPLTFGGGT KVEIK (SEQ ID NO: 1477)
365_A09	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYGMHWVRQAPGKGLEWVASINYNGGYT SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1385)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 1478)
365_C02	EVQLLESGGGLVQPGGSLRLSCAASGFTF DSYSMNWVRQAPGKGLEWVSNINYNGGYK GYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1386)	DIQMTQSPSSLSASVGDRVTITCRASQSISTYLN WYQQKPGKAPKLVIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYENPLTFGGGT KVEIK (SEQ ID NO: 1479)
365_C04	EVQLLESGGGLVQPGGSLRLSCAASGFTF DSYSMNWVRQAPGKGLEWVANINYNGGYK GYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1387)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLVIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 1480)
365_D02	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYSMHWVRQAPGKGLEWVASINYNGGYT SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1388)	DIQMTQSPSSLSASVGDRVTITCRASQSIVTYLN WYQQKPGKAPKLLIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDNPLTFGGGT KVEIK (SEQ ID NO: 1481)
365_D07	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYGMNWVRQAPGKGLEWVSSINYNSGYK SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1389)	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLN WYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSTPLTFGGGT KVEIK (SEQ ID NO: 1482)
365_D10	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYSMNWVRQAPGKGLEWVAGINYNGGYT GYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1390)	DIQMTQSPSSLSASVGDRVTITCRASQSISTYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYESPLTFGGGT KVEIK (SEQ ID NO: 1483)
365_E11	EVQLLESGGGLVQPGGSLRLSCAASGFTF DDYSMNWVRQAPGKGLEWVSSINYNGGYK SYADSVKGRFTISRDNSKNTLYLQMNSLR	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLN WYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNTPLTFGGGT

	AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1391)	KVEIK (SEQ ID NO: 1484)
365_F05	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYGMNWVRQAPGKGLEWVASINYNGGYT SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1392)	DIQMTQSPSSLSASVGDRVTITCRASQSIVTYVN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYETPLTFGGGT KVEIK (SEQ ID NO: 1485)
365_H05	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYGMNWVRQAPGKGLEWVAGINYNGGYT SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1393)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLLIYAATSLHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSTPLTFGGGT KVEIK (SEQ ID NO: 1486)
366_D08	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYGMHWVRQAPGKGLEWVSNINYNGGYK SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1394)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLVIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYENPLTFGGGT KVEIK (SEQ ID NO: 1487)
366_F08	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYGMNWVRQAPGKGLEWVSSINYNGGYT SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1395)	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLN WYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSTPLTFGGGT KVEIK (SEQ ID NO: 1488)
366_G09	EVQLLESGGGLVQPGGSLRLSCAASGFTF DDYSMNWVRQAPGKGLEWVASINYNSGYT GYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1396)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 1489)
367_A02	EVQLLESGGGLVQPGGSLRLSCAASGFTF DSYGMNWVRQAPGKGLEWVSSINYNSGYK GYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1397)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYLN WYQQKPGKAPKLLIYAVTSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 1490)
367_B06	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYSMNWVRQAPGKGLEWVANINYNGGYT GYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1398)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYVN WYQQKPGKAPKLVIYAATSLHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNSPLTFGGGT KVEIK (SEQ ID NO: 1491)
367_C08	EVQLLESGGGLVQPGGSLRLSCAASGFTF DSYSMHWVRQAPGKGLEWVAGINYNGGYT SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1399)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLLIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSDSNPLTFGGGT KVEIK (SEQ ID NO: 1492)
367_D05	EVQLLESGGGLVQPGGSLRLSCAASGFTF SDYSMNWVRQAPGKGLEWVSSINYNGGYK SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1400)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYVN WYQQKPGKAPKLVIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 1493)
367_D09	EVQLLESGGGLVQPGGSLRLSCAASGFTF DSYGMNWVRQAPGKGLEWVASINYNGGYK SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1401)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLLIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDNPLTFGGGT KVEIK (SEQ ID NO: 1494)
367_E07	EVQLLESGGGLVQPGGSLRLSCAASGFTF SDYSMNWVRQAPGKGLEWVSSINYNGGYK GYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYENPLTFGGGT KVEIK (SEQ ID NO: 1495)

	TVSS (SEQ ID NO: 1402)	
367_E12	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYGMHWVRQAPGKGLEWVASINYNGGYT SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1403)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNSPLTFGGGT KVEIK (SEQ ID NO: 1496)
367_F09	EVQLLESGGGLVQPGGSLRLSCAASGFTF DSYSMHWVRQAPGKGLEWVAGINYNGGYT SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1404)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLLIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSDSNPLTFGGGT KVEIK (SEQ ID NO: 1497)
367_H05	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYGMHWVRQAPGKGLEWVASINYNSGYK SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1405)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSTPLTFGGGT KVEIK (SEQ ID NO: 1498)
367_H10	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYGMNWVRQAPGKGLEWVASINYNGGYT GYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1406)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYELPLTFGGGT KVEIK (SEQ ID NO: 1499)
368_B02	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYGMNWVRQAPGKGLEWVSGINYNSGYK SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1407)	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLN WYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSTPLTFGGGT KVEIK (SEQ ID NO: 1500)
368_C11	EVQLLESGGGLVQPGGSLRLSCAASGFTF SDYSMNWVRQAPGKGLEWVSSINYNSGYK SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1408)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDNPLTFGGGT KVEIK (SEQ ID NO: 1501)
368_D02	EVQLLESGGGLVQPGGSLRLSCAASGFTF DDYGMNWVRQAPGKGLEWVSNINYNGGYT GYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1409)	DIQMTQSPSSLSASVGDRVTITCRASQSISTYLN WYQQKPGKAPKLVIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 1502)
368_D12	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYGMNWVRQAPGKGLEWVSSINYNGGYT SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1410)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNNPLTFGGGT KVEIK (SEQ ID NO: 1503)
368_F06	EVQLLESGGGLVQPGGSLRLSCAASGFTF DDYSMHWVRQAPGKGLEWVANINYNSGYT GYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1411)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLVIYATTSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYENPLTFGGGT KVEIK (SEQ ID NO: 1504)
368_G03	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYSMNWVRQAPGKGLEWVSGINYNSGYT SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTALDYWGQGTLV TVSS (SEQ ID NO: 1412)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 1505)
368_G10	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYSMHWVRQAPGKGLEWVSSINYNGGYT SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1413)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 1506)

368_H06	EVQLLESGGGLVQPGGSLRLSCAASGFTF DSYGMHWVRQAPGKGLEWVANINYNGGYK SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1414)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLLIYATTSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDNPLTFGGGT KVEIK (SEQ ID NO: 1507)
368_H11	EVQLLESGGGLVQPGGSLRLSCAASGFTF DSYGMHWVRQAPGKGLEWVASINYNGGYT SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1415)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSDDTPLTFGGGT KVEIK (SEQ ID NO: 1508)
369_A11	EVQLLESGGGLVQPGGSLRLSCAASGFTF DSYGMNWVRQAPGKGLEWVANINYNGGYK GYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1416)	DIQMTQSPSSLSASVGDRVTITCRASQSIITYLN WYQQKPGKAPKLVIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYESPLTFGGGT KVEIK (SEQ ID NO: 1509)
369_C12	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYGMNWVRQAPGKGLEWVANINYNGGYK GYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1417)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLLIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 1510)
369_D08	EVQLLESGGGLVQPGGSLRLSCAASGFTF SDYSMNWVRQAPGKGLEWVASINYNGGYK GYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1418)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 1511)
369_E05	EVQLLESGGGLVQPGGSLRLSCAASGFTF SDYGMNWVRQAPGKGLEWVANINYNGGYK SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1419)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLLIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYETPLTFGGGT KVEIK (SEQ ID NO: 1512)
369_E08	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYSMNWVRQAPGKGLEWVASINYNSGYT GYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1420)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 1513)
369_F05	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYSMNWVRQAPGKGLEWVSGINYNGGYK SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1421)	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLN WYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQGYDSPLTFGGGT KVEIK (SEQ ID NO: 1514)
369_F09	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYGMHWVRQAPGKGLEWVAGINYNGGYT SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1422)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 1515)
369_G05	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYSMNWVRQAPGKGLEWVAGINYNGGYT SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1423)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYLN WYQQKPGKAPKLLIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 1516)
369_H02	EVQLLESGGGLVQPGGSLRLSCAASGFTF DDYSMNWVRQAPGKGLEWVSNINYNGGYK SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1424)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 1517)
369_H08	EVQLLESGGGLVQPGGSLRLSCAASGFTF	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN

	SSYSMNWVRQAPGKGLEWVAGINYNSGYK SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1425)	WYQQKPGKAPKLVIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYESPLTFGGGT KVEIK (SEQ ID NO: 1518)
369_H12	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYSMNWVRQAPGKGLEWVAGINYNGGYK SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1426)	DIQMTQSPSSLSASVGDRVTITCRASQSIVTYVN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 1519)
370_B08	EVQLLESGGGLVQPGGSLRLSCAASGFTF SDYSMNWVRQAPGKGLEWVANINYNGGYT GYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1427)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 1520)
370_C06	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYSMNWVRQAPGKGLEWVANINYNGGYK SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1428)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSTPLTFGGGT KVEIK (SEQ ID NO: 1521)
370_C07	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYSMNWVRQAPGKGLEWVANINYNGGYK SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1429)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLLIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYESPLTFGGGT KVEIK (SEQ ID NO: 1522)
370_C10	EVQLLESGGGLVQPGGSLRLSCAASGFTF DSYSMNWVRQAPGKGLEWVSNINYNSGYK GYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1430)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVN WYQQKPGKAPKLLIYATTSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSSPLTFGGGT KVEIK (SEQ ID NO: 1523)
370_D03	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYSMNWVRQAPGKGLEWVASINYNGGYT SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1431)	DIQMTQSPSSLSASVGDRVTITCRASQSIITYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 1524)
370_D09	EVQLLESGGGLVQPGGSLRLSCAASGFTF SDYSMNWVRQAPGKGLEWVSGINYNSGYT SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1432)	DIQMTQSPSSLSASVGDRVTITCRASQSIVTYLN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 1525)
370_E04	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYSMNWVRQAPGKGLEWVANINYNGGYK GYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1433)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLLIYAVTSLHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYETPLTFGGGT KVEIK (SEQ ID NO: 1526)
370_E05	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYGMNWVRQAPGKGLEWVSNINYNGGYK GYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1434)	DIQMTQSPSSLSASVGDRVTITCRASQSISTYLN WYQQKPGKAPKLVIYAVTSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNSPLTFGGGT KVEIK (SEQ ID NO: 1527)
370_F01	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYGMNWVRQAPGKGLEWVSNINYNGGYT SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1435)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 1528)
370_F02	EVQLLESGGGLVQPGGSLRLSCAASGFTF DSYGMNWVRQAPGKGLEWVANINYNGGYT	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLLIYAVTSRHSGVPSRFSGSGSG

	GYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1436)	TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 1529)
370_F12	EVQLLESGGGLVQPGGSLRLSCAASGFTF SDYSMNWVRQAPGKGLEWVANINYNGGYT GYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1437)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 1530)
370_G08	EVQLLESGGGLVQPGGSLRLSCAASGFTF SDYSMNWVRQAPGKGLEWVAGINYNGGYT GYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1438)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYESPLTFGGGT KVEIK (SEQ ID NO: 1531)
370_H04	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYSMNWVRQAPGKGLEWVSNINYNGGYT GYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1439)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 1532)
370_H06	EVQLLESGGGLVQPGGSLRLSCAASGFTF DDYSMNWVRQAPGKGLEWVANINYNGGYT GYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1440)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYETPLTFGGGT KVEIK (SEQ ID NO: 1533)
371_B01	EVQLLESGGGLVQPGGSLRLSCAASGFTF DSYSMNWVRQAPGKGLEWVSNINYNSGYT GYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1441)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLLIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 1534)
371_C06	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYSMNWVRQAPGKGLEWVSSINYNGGYT SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1442)	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLN WYQQKPGKAPKLLIYAVTSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 1535)
371_C07	EVQLLESGGGLVQPGGSLRLSCAASGFTF DSYGMNWVRQAPGKGLEWVSNINYNGGYT GYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTALDYWGQGTLV TVSS (SEQ ID NO: 1443)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLLIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 1536)
371_E05	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYSMNWVRQAPGKGLEWVAGINYNGGYT SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1444)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYLN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSSPLTFGGGT KVEIK (SEQ ID NO: 1537)
371_E08	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYSMNWVRQAPGKGLEWVSNINYNSGYK SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1445)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVN WYQQKPGKAPKLVIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 1538)
371_E09	EVQLLESGGGLVQPGGSLRLSCAASGFTF SDYSMNWVRQAPGKGLEWVSGINYNSGYT SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1446)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNSPLTFGGGT KVEIK (SEQ ID NO: 1539)
371_E12	EVQLLESGGGLVQPGGSLRLSCAASGFTF DSYSMNWVRQAPGKGLEWVSGINYNSGYK SYADSVKGRFTISRDNSKNTLYLQMNSLR	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLLIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT

	AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1447)	KVEIK (SEQ ID NO: 1540)
371_F03	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYSMNWVRQAPGKGLEWVSGINYNGGYT SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1448)	DIQMTQSPSSLSASVGDRVTITCRASQSIITYLN WYQQKPGKAPKLLIYAATSLHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDNPLTFGGGT KVEIK (SEQ ID NO: 1541)
371_F09	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYSMNWVRQAPGKGLEWVAGINYNGGYT SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1449)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDNPLTFGGGT KVEIK (SEQ ID NO: 1542)
371_G01	EVQLLESGGGLVQPGGSLRLSCAASGFTF SDYSMNWVRQAPGKGLEWVSNINYNGGYT SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1450)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLLIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 1543)
371_H11	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYSMNWVRQAPGKGLEWVSGINYNGGYK GYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1451)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLLIYATTSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYESPLTFGGGT KVEIK (SEQ ID NO: 1544)
372_B09	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYSMNWVRQAPGKGLEWVSSINYNSGYT SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1452)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYETPLTFGGGT KVEIK (SEQ ID NO: 1545)
372_E08	EVQLLESGGGLVQPGGSLRLSCAASGFTF SDYSMNWVRQAPGKGLEWVSNINYNGGYT SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1453)	DIQMTQSPSSLSASVGDRVTITCRASQSIITYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNLPLTFGGGT KVEIK (SEQ ID NO: 1546)
372_F02	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYGMHWVRQAPGKGLEWVASINYNGGYT SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1454)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLVIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 1547)
372_H11	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYGMHWVRQAPGKGLEWVAGINYNGGYT SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1455)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYENPLTFGGGT KVEIK (SEQ ID NO: 1548)
373_A06	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYSMNWVRQAPGKGLEWVSGINYNGGYK SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1456)	DIQMTQSPSSLSASVGDRVTITCRASQSIVTYLN WYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSTPLTFGGGT KVEIK (SEQ ID NO: 1549)
373_B09	EVQLLESGGGLVQPGGSLRLSCAASGFTF DSYSMNWVRQAPGKGLEWVSGINYNGGYK SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1457)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLVIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYETPLTFGGGT KVEIK (SEQ ID NO: 1550)
373_D06	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYSMNWVRQAPGKGLEWVAGINYNGGYT SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV	DIQMTQSPSSLSASVGDRVTITCRASQSIVTYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 1551)

	TVSS (SEQ ID NO: 1458)	
373_F07	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYSMNWVRQAPGKGLEWVSGINYNSGYK SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1459)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLLIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYETPLTFGGGT KVEIK (SEQ ID NO: 1552)
373_G02	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYSMNWVRQAPGKGLEWVSGINYNGGYT SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1460)	DIQMTQSPSSLSASVGDRVTITCRASQSIITYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSSPLTFGGGT KVEIK (SEQ ID NO: 1553)
374_A04	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYSMNWVRQAPGKGLEWVAGINYNGGYT SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1461)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 1554)
374_A05	EVQLLESGGGLVQPGGSLRLSCAASGFTF SDYGMNWVRQAPGKGLEWVANINYNGGYK GYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1462)	DIQMTQSPSSLSASVGDRVTITCRASQSIVRYLN WYQQKPGKAPKLVIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYELPLTFGGGT KVEIK (SEQ ID NO: 1555)
374_C10	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYSMNWVRQAPGKGLEWVSSINYNGGYK GYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1463)	DIQMTQSPSSLSASVGDRVTITCRASQSIVTYLN WYQQKPGKAPKLLIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNTPLTFGGGT KVEIK (SEQ ID NO: 1556)
374_D04	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYSMNWVRQAPGKGLEWVAGINYNGGYT SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1464)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLVIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 1557)
374_D09	EVQLLESGGGLVQPGGSLRLSCAASGFTF DSYGMNWVRQAPGKGLEWVANINYNGGYK GYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1465)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYVN WYQQKPGKAPKLLIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 1558)
374_G05	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYSMNWVRQAPGKGLEWVSNINYNSGYK GYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1466)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 1559)
374_H05	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYSMNWVRQAPGKGLEWVAGINYNGGYT SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1467)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDNPLTFGGGT KVEIK (SEQ ID NO: 1560)
375_A03	EVQLLESGGGLVQPGGSLRLSCAASGFTF DSYSMNWVRQAPGKGLEWVAGINYNGGYT SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1468)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLLIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDNPLTFGGGT KVEIK (SEQ ID NO: 1561)
375_B03	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYSMNWVRQAPGKGLEWVAGINYNGGYT SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1469)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 1562)

375_C01	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYGMNWVRQAPGKGLEWVSSINYNGGYK GYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1470)	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLN WYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSTPLTFGGGT KVEIK (SEQ ID NO: 1563)
375_C11	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYSMNWVRQAPGKGLEWVSSINYNGGYT SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1471)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLLIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 1564)
375_F10	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYSMNWVRQAPGKGLEWVSGINYNGGYT GYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1472)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 1565)
375_H08	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYSMNWVRQAPGKGLEWVSGINYNGGYT SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1473)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLLIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 1566)
376_A02	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYSMNWVRQAPGKGLEWVAGINYNGGYK SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1474)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 1567)
376_A05	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYSMNWVRQAPGKGLEWVAGINYNSGYK GYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1475)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNTPLTFGGGT KVEIK (SEQ ID NO: 1568)
376_A07	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYSMNWVRQAPGKGLEWVSGINYNGGYK SYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGATWHDTHLDYWGQGTLV TVSS (SEQ ID NO: 1476)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 1569)

Table 3D provides the amino acid sequences of the CDRs of the antibodies shown in Table 2D.

Table 3D: CDR sequences for Group IV antibodies

Ab	HCDR1	HCDR2	HCDR3	LCDR1	LCDR2	LCDR3
365_A08	SSYSMN (SEQ ID NO: 1570)	WVASINYNGGYKS (SEQ ID NO: 1663)	ARGATWHDTHLD (SEQ ID NO: 1756)	ITYLNWY (SEQ ID NO: 1849)	LVIYAATSRA (SEQ ID NO: 1942)	QQSDNTPL (SEQ ID NO: 2035)
365_A09	SSYGMH (SEQ ID NO: 1571)	WVASINYNGGYTS (SEQ ID NO: 1664)	ARGATWHDTHLD (SEQ ID NO: 1757)	LSYVNWY (SEQ ID NO: 1850)	LLIYAATSRA (SEQ ID NO: 1943)	QQSYDLPL (SEQ ID NO: 2036)
365_C02	DSYSMN (SEQ ID NO: 1572)	WVSNINYNGGYKG (SEQ ID NO: 1665)	ARGATWHDTHLD (SEQ ID NO: 1758)	STYLNWY (SEQ ID NO: 1851)	LVIYAATSRH (SEQ ID NO: 1944)	QQSYENPL (SEQ ID NO: 2037)
365_C04	DSYSMN (SEQ ID NO: 1573)	WVANINYNGGYKG (SEQ ID NO: 1666)	ARGATWHDTHLD (SEQ ID NO: 1759)	LTYLNWY (SEQ ID NO: 1852)	LVIYAATSLA (SEQ ID NO: 1945)	QQSYDTPL (SEQ ID NO: 2038)
365_D02	SSYSMH (SEQ ID NO: 1574)	WVASINYNGGYTS (SEQ ID NO: 1667)	ARGATWHDTHLD (SEQ ID NO: 1760)	VTYLNWY (SEQ ID NO: 1853)	LLIYAATSLA (SEQ ID NO: 1946)	QQSYDNPL (SEQ ID NO: 2039)
365_D07	SSYGMN (SEQ ID NO: 1575)	WVSSINYNSGYKS (SEQ ID NO: 1668)	ARGATWHDTHLD (SEQ ID NO: 1761)	SSYLNWY (SEQ ID NO: 1854)	LLIYAASSLQ (SEQ ID NO: 1947)	QQSYSTPL (SEQ ID NO: 2040)
365_D10	SSYSMN (SEQ ID NO: 1576)	WVAGINYNGGYTG (SEQ ID NO: 1669)	ARGATWHDTHLD (SEQ ID NO: 1762)	STYLNWY (SEQ ID NO: 1855)	LLIYAATSRA (SEQ ID NO: 1948)	QQSYESPL (SEQ ID NO: 2041)
365_E11	DDYSMN (SEQ ID NO: 1577)	WVSSINYNGGYKS (SEQ ID NO: 1670)	ARGATWHDTHLD (SEQ ID NO: 1763)	SSYLNWY (SEQ ID NO: 1856)	LLIYAASSLQ (SEQ ID NO: 1949)	QQSYNTPL (SEQ ID NO: 2042)

	1577)			1856)		2042)
365_F05	SSYGMN (SEQ ID NO: 1578)	WVASINYNGGYTS (SEQ ID NO: 1671)	ARGATWHDTHLD (SEQ ID NO: 1764)	VTYVNWY (SEQ ID NO: 1857)	LLIYAATSRA (SEQ ID NO: 1950)	QQSYETPL (SEQ ID NO: 2043)
365_H05	SSYGMN (SEQ ID NO: 1579)	WVAGINYNGGYTS (SEQ ID NO: 1672)	ARGATWHDTHLD (SEQ ID NO: 1765)	LTYVNWY (SEQ ID NO: 1858)	LLIYAATSLH (SEQ ID NO: 1951)	QQSYSTPL (SEQ ID NO: 2044)
366_D08	SSYGMH (SEQ ID NO: 1580)	WVSNINYNGGYKS (SEQ ID NO: 1673)	ARGATWHDTHLD (SEQ ID NO: 1766)	LSYVNWY (SEQ ID NO: 1859)	LVIYAATSLA (SEQ ID NO: 1952)	QQSYENPL (SEQ ID NO: 2045)
366_F08	SSYGMN (SEQ ID NO: 1581)	WVSSINYNGGYTS (SEQ ID NO: 1674)	ARGATWHDTHLD (SEQ ID NO: 1767)	SSYLNWY (SEQ ID NO: 1860)	LLIYAASSLQ (SEQ ID NO: 1953)	QQSYSTPL (SEQ ID NO: 2046)
366_G09	DDYSMN (SEQ ID NO: 1582)	WVASINYNSGYTG (SEQ ID NO: 1675)	ARGATWHDTHLD (SEQ ID NO: 1768)	LSYVNWY (SEQ ID NO: 1861)	LVIYAATSRA (SEQ ID NO: 1954)	QQSYDLPL (SEQ ID NO: 2047)
367_A02	DSYGMN (SEQ ID NO: 1583)	WVSSINYNSGYKG (SEQ ID NO: 1676)	ARGATWHDTHLD (SEQ ID NO: 1769)	ISYLNWY (SEQ ID NO: 1862)	LLIYAVTSRA (SEQ ID NO: 1955)	QQSYDTPL (SEQ ID NO: 2048)
367_B06	SSYSMN (SEQ ID NO: 1584)	WVANINYNGGYTG (SEQ ID NO: 1677)	ARGATWHDTHLD (SEQ ID NO: 1770)	ISYVNWY (SEQ ID NO: 1863)	LVIYAATSLH (SEQ ID NO: 1956)	QQSYNSPL (SEQ ID NO: 2049)
367_C08	DSYSMH (SEQ ID NO: 1585)	WVAGINYNGGYTS (SEQ ID NO: 1678)	ARGATWHDTHLD (SEQ ID NO: 1771)	LTYLNWY (SEQ ID NO: 1864)	LLIYAATSLA (SEQ ID NO: 1957)	QQSDSNPL (SEQ ID NO: 2050)
367_D05	SDYSMN (SEQ ID NO: 1586)	WVSSINYNGGYKS (SEQ ID NO: 1679)	ARGATWHDTHLD (SEQ ID NO: 1772)	ISYVNWY (SEQ ID NO: 1865)	LVIYAATSLA (SEQ ID NO: 1958)	QQSYDSPL (SEQ ID NO: 2051)
367_D09	DSYGMN (SEQ ID NO: 1680)	WVASINYNGGYKS (SEQ ID NO: 1680)	ARGATWHDTHLD (SEQ ID NO: 1773)	LTYLNWY (SEQ ID NO:	LLIYAATSLA (SEQ ID NO: 1959)	QQSYDNPL (SEQ ID NO:

	1587)			1866)		2052)
367_E07	SDYSMN (SEQ ID NO: 1588)	WVSSINYNGGYKG (SEQ ID NO: 1681)	ARGATWHDTHLD (SEQ ID NO: 1774)	LSYVNWY (SEQ ID NO: 1867)	LVIYAATSRA (SEQ ID NO: 1960)	QQSYENPL (SEQ ID NO: 2053)
367_E12	SSYGMH (SEQ ID NO: 1589)	WVASINYNGGYTS (SEQ ID NO: 1682)	ARGATWHDTHLD (SEQ ID NO: 1775)	LTYVNWY (SEQ ID NO: 1868)	LLIYAASSLQ (SEQ ID NO: 1961)	QQSYNSPL (SEQ ID NO: 2054)
367_F09	DSYSMH (SEQ ID NO: 1590)	WVAGINYNGGYTS (SEQ ID NO: 1683)	ARGATWHDTHLD (SEQ ID NO: 1776)	LTYLNWY (SEQ ID NO: 1869)	LLIYAATSLA (SEQ ID NO: 1962)	QQSDSNPL (SEQ ID NO: 2055)
367_H05	SSYGMH (SEQ ID NO: 1591)	WVASINYNSGYKS (SEQ ID NO: 1684)	ARGATWHDTHLD (SEQ ID NO: 1777)	LSYVNWY (SEQ ID NO: 1870)	LLIYAASSLQ (SEQ ID NO: 1963)	QQSYSTPL (SEQ ID NO: 2056)
367_H10	SSYGMN (SEQ ID NO: 1592)	WVASINYNGGYTG (SEQ ID NO: 1685)	ARGATWHDTHLD (SEQ ID NO: 1778)	LSYVNWY (SEQ ID NO: 1871)	LVIYAATSRA (SEQ ID NO: 1964)	QQSYELPL (SEQ ID NO: 2057)
368_B02	SSYGMN (SEQ ID NO: 1593)	WVSGINYNSGYKS (SEQ ID NO: 1686)	ARGATWHDTHLD (SEQ ID NO: 1779)	SSYLNWY (SEQ ID NO: 1872)	LLIYAASSLQ (SEQ ID NO: 1965)	QQSYSTPL (SEQ ID NO: 2058)
368_C11	SDYSMN (SEQ ID NO: 1594)	WVSSINYNSGYKS (SEQ ID NO: 1687)	ARGATWHDTHLD (SEQ ID NO: 1780)	ISYLNWY (SEQ ID NO: 1873)	LLIYAATSRA (SEQ ID NO: 1966)	QQSYDNPL (SEQ ID NO: 2059)
368_D02	DDYGMN (SEQ ID NO: 1595)	WVSNINYNGGYTG (SEQ ID NO: 1688)	ARGATWHDTHLD (SEQ ID NO: 1781)	STYLNWY (SEQ ID NO: 1874)	LVIYAATSRH (SEQ ID NO: 1967)	QQSYDTPL (SEQ ID NO: 2060)
368_D12	SSYGMN (SEQ ID NO: 1596)	WVSSINYNGGYTS (SEQ ID NO: 1689)	ARGATWHDTHLD (SEQ ID NO: 1782)	LSYVNWY (SEQ ID NO: 1875)	LVIYAATSRA (SEQ ID NO: 1968)	QQSYNNPL (SEQ ID NO: 2061)
368_F06	DDYSMH (SEQ ID NO: 1590)	WVANINYNSGYTG (SEQ ID NO: 1690)	ARGATWHDTHLD (SEQ ID NO: 1783)	LSYLNWY (SEQ ID NO:	LVIYATTSRA (SEQ ID NO: 1969)	QQSYENPL (SEQ ID NO:

	1597)			1876)		2062)
368_G03	SSYSMN (SEQ ID NO: 1598)	WVSGINYNSGYTS (SEQ ID NO: 1691)	ARGATWHDTALD (SEQ ID NO: 1784)	LSYLNWY (SEQ ID NO: 1877)	LVIYAATSRA (SEQ ID NO: 1970)	QQSYDTPL (SEQ ID NO: 2063)
368_G10	SSYSMH (SEQ ID NO: 1599)	WVSSINYNGGYTS (SEQ ID NO: 1692)	ARGATWHDTHLD (SEQ ID NO: 1785)	VSYVNWY (SEQ ID NO: 1878)	LVIYAATSRA (SEQ ID NO: 1971)	QQSYDTPL (SEQ ID NO: 2064)
368_H06	DSYGMH (SEQ ID NO: 1600)	WVANINYNGGYKS (SEQ ID NO: 1693)	ARGATWHDTHLD (SEQ ID NO: 1786)	LTYVNWY (SEQ ID NO: 1879)	LLIYATTSRA (SEQ ID NO: 1972)	QQSYDNPL (SEQ ID NO: 2065)
368_H11	DSYGMH (SEQ ID NO: 1601)	WVASINYNGGYTS (SEQ ID NO: 1694)	ARGATWHDTHLD (SEQ ID NO: 1787)	LSYLNWY (SEQ ID NO: 1880)	LLIYAATSRA (SEQ ID NO: 1973)	QQSDDTPL (SEQ ID NO: 2066)
369_A11	DSYGMN (SEQ ID NO: 1602)	WVANINYNGGYKG (SEQ ID NO: 1695)	ARGATWHDTHLD (SEQ ID NO: 1788)	ITYLNWY (SEQ ID NO: 1881)	LVIYAATSRH (SEQ ID NO: 1974)	QQSYESPL (SEQ ID NO: 2067)
369_C12	SSYGMN (SEQ ID NO: 1603)	WVANINYNGGYKG (SEQ ID NO: 1696)	ARGATWHDTHLD (SEQ ID NO: 1789)	LTYLNWY (SEQ ID NO: 1882)	LLIYAATSRH (SEQ ID NO: 1975)	QQSYDTPL (SEQ ID NO: 2068)
369_D08	SDYSMN (SEQ ID NO: 1604)	WVASINYNGGYKG (SEQ ID NO: 1697)	ARGATWHDTHLD (SEQ ID NO: 1790)	LTYLNWY (SEQ ID NO: 1883)	LLIYAATSRA (SEQ ID NO: 1976)	QQSYDTPL (SEQ ID NO: 2069)
369_E05	SDYGMN (SEQ ID NO: 1605)	WVANINYNGGYKS (SEQ ID NO: 1698)	ARGATWHDTHLD (SEQ ID NO: 1791)	LTYLNWY (SEQ ID NO: 1884)	LLIYAATSLA (SEQ ID NO: 1977)	QQSYETPL (SEQ ID NO: 2070)
369_E08	SSYSMN (SEQ ID NO: 1606)	WVASINYNSGYTG (SEQ ID NO: 1699)	ARGATWHDTHLD (SEQ ID NO: 1792)	LTYVNWY (SEQ ID NO: 1885)	LLIYAATSRA (SEQ ID NO: 1978)	QQSYDSPL (SEQ ID NO: 2071)
369_F05	SSYSMN (SEQ ID NO: 1700)	WVSGINYNGGYKS (SEQ ID NO: 1793)	ARGATWHDTHLD (SEQ ID NO: 1793)	SSYLNWY (SEQ ID NO:	LLIYAASSLQ (SEQ ID NO: 1979)	QQGYDSPL (SEQ ID NO:

	1607)			1886)		2072)
369_F09	SSYGMH (SEQ ID NO: 1608)	WVAGINYNGGYTS (SEQ ID NO: 1701)	ARGATWHDTHLD (SEQ ID NO: 1794)	LTYVNWY (SEQ ID NO: 1887)	LLIYAATSRA (SEQ ID NO: 1980)	QQSYDSPL (SEQ ID NO: 2073)
369_G05	SSYSMN (SEQ ID NO: 1609)	WVAGINYNGGYTS (SEQ ID NO: 1702)	ARGATWHDTHLD (SEQ ID NO: 1795)	VSYLNWY (SEQ ID NO: 1888)	LLIYAATSRH (SEQ ID NO: 1981)	QQSYDSPL (SEQ ID NO: 2074)
369_H02	DDYSMN (SEQ ID NO: 1610)	WVSNINYNGGYKS (SEQ ID NO: 1703)	ARGATWHDTHLD (SEQ ID NO: 1796)	ISYLNWY (SEQ ID NO: 1889)	LLIYAATSRA (SEQ ID NO: 1982)	QQSYDSPL (SEQ ID NO: 2075)
369_H08	SSYSMN (SEQ ID NO: 1611)	WVAGINYNSGYKS (SEQ ID NO: 1704)	ARGATWHDTHLD (SEQ ID NO: 1797)	LSYVNWY (SEQ ID NO: 1890)	LVIYAATSLA (SEQ ID NO: 1983)	QQSYESPL (SEQ ID NO: 2076)
369_H12	SSYSMN (SEQ ID NO: 1612)	WVAGINYNGGYKS (SEQ ID NO: 1705)	ARGATWHDTHLD (SEQ ID NO: 1798)	VTYVNWY (SEQ ID NO: 1891)	LVIYAATSRA (SEQ ID NO: 1984)	QQSYDSPL (SEQ ID NO: 2077)
370_B08	SDYSMN (SEQ ID NO: 1613)	WVANINYNGGYTG (SEQ ID NO: 1706)	ARGATWHDTHLD (SEQ ID NO: 1799)	LSYLNWY (SEQ ID NO: 1892)	LLIYAASSLQ (SEQ ID NO: 1985)	QQSYDSPL (SEQ ID NO: 2078)
370_C06	SSYSMN (SEQ ID NO: 1614)	WVANINYNGGYKS (SEQ ID NO: 1707)	ARGATWHDTHLD (SEQ ID NO: 1800)	LTYVNWY (SEQ ID NO: 1893)	LLIYAASSLQ (SEQ ID NO: 1986)	QQSYSTPL (SEQ ID NO: 2079)
370_C07	SSYSMN (SEQ ID NO: 1615)	WVANINYNGGYKS (SEQ ID NO: 1708)	ARGATWHDTHLD (SEQ ID NO: 1801)	LSYLNWY (SEQ ID NO: 1894)	LLIYAATSRH (SEQ ID NO: 1987)	QQSYESPL (SEQ ID NO: 2080)
370_C10	DSYSMN (SEQ ID NO: 1616)	WVSNINYNSGYKG (SEQ ID NO: 1709)	ARGATWHDTHLD (SEQ ID NO: 1802)	VSYVNWY (SEQ ID NO: 1895)	LLIYATTSRA (SEQ ID NO: 1988)	QQSYSSPL (SEQ ID NO: 2081)
370_D03	SSYSMN (SEQ ID NO: 1610)	WVASINYNGGYTS (SEQ ID NO: 1710)	ARGATWHDTHLD (SEQ ID NO: 1803)	ITYLNWY (SEQ ID NO:	LLIYAATSRA (SEQ ID NO: 1989)	QQSYDLPL (SEQ ID NO:

	1617)		1896)		2082)
370_D09	SDYSMN (SEQ ID NO: 1618)	WVSGINYNSGYTS (SEQ ID NO: 1711)	ARGATWHDTHLD (SEQ ID NO: 1804)	VTYLNWY (SEQ ID NO: 1897)	LVIYAATSRA (SEQ ID NO: 1990)	QQSYDTPL (SEQ ID NO: 2083)
370_E04	SSYSMN (SEQ ID NO: 1619)	WVANINYNGGYKG (SEQ ID NO: 1712)	ARGATWHDTHLD (SEQ ID NO: 1805)	LTYLNWY (SEQ ID NO: 1898)	LLIYAVTSLH (SEQ ID NO: 1991)	QQSYETPL (SEQ ID NO: 2084)
370_E05	SSYGMN (SEQ ID NO: 1620)	WVSNINYNGGYKG (SEQ ID NO: 1713)	ARGATWHDTHLD (SEQ ID NO: 1806)	STYLNWY (SEQ ID NO: 1899)	LVIYAVTSRA (SEQ ID NO: 1992)	QQSYNSPL (SEQ ID NO: 2085)
370_F01	SSYGMN (SEQ ID NO: 1621)	WVSNINYNGGYTS (SEQ ID NO: 1714)	ARGATWHDTHLD (SEQ ID NO: 1807)	VSYLNWY (SEQ ID NO: 1900)	LLIYAATSRA (SEQ ID NO: 1993)	QQSYDSPL (SEQ ID NO: 2086)
370_F02	DSYGMN (SEQ ID NO: 1622)	WVANINYNGGYTG (SEQ ID NO: 1715)	ARGATWHDTHLD (SEQ ID NO: 1808)	LSYLNWY (SEQ ID NO: 1901)	LLIYAVTSRH (SEQ ID NO: 1994)	QQSYDSPL (SEQ ID NO: 2087)
370_F12	SDYSMN (SEQ ID NO: 1623)	WVANINYNGGYTG (SEQ ID NO: 1716)	ARGATWHDTHLD (SEQ ID NO: 1809)	LSYLNWY (SEQ ID NO: 1902)	LLIYAASSLQ (SEQ ID NO: 1995)	QQSYDSPL (SEQ ID NO: 2088)
370_G08	SDYSMN (SEQ ID NO: 1624)	WVAGINYNGGYTG (SEQ ID NO: 1717)	ARGATWHDTHLD (SEQ ID NO: 1810)	LTYLNWY (SEQ ID NO: 1903)	LVIYAATSRA (SEQ ID NO: 1996)	QQSYESPL (SEQ ID NO: 2089)
370_H04	SSYSMN (SEQ ID NO: 1625)	WVSNINYNGGYTG (SEQ ID NO: 1718)	ARGATWHDTHLD (SEQ ID NO: 1811)	LSYVNWY (SEQ ID NO: 1904)	LLIYAATSRA (SEQ ID NO: 1997)	QQSYDLPL (SEQ ID NO: 2090)
370_H06	DDYSMN (SEQ ID NO: 1626)	WVANINYNGGYTG (SEQ ID NO: 1719)	ARGATWHDTHLD (SEQ ID NO: 1812)	LTYLNWY (SEQ ID NO: 1905)	LLIYAATSRA (SEQ ID NO: 1998)	QQSYETPL (SEQ ID NO: 2091)
371_B01	DSYSMN (SEQ ID NO: 1720)	WVSNINYNSGYTG (SEQ ID NO: 1813)	ARGATWHDTHLD (SEQ ID NO: 1906)	LSYVNWY (SEQ ID NO: 1999)	LLIYAATSLA (SEQ ID NO: 2092)	QQSYDLPL (SEQ ID NO: 2185)

	1627)			1906)		2092)
371_C06	SSYSMN (SEQ ID NO: 1628)	WVSSINYNGGYTS (SEQ ID NO: 1721)	ARGATWHDTHLD (SEQ ID NO: 1814)	SSYLNWY (SEQ ID NO: 1907)	LLIYAVTSRA (SEQ ID NO: 2000)	QQSYDLPL (SEQ ID NO: 2093)
371_C07	DSYGMN (SEQ ID NO: 1629)	WVSNINYNGGYTG (SEQ ID NO: 1722)	ARGATWHDTALD (SEQ ID NO: 1815)	LSYLNWY (SEQ ID NO: 1908)	LLIYAATSLA (SEQ ID NO: 2001)	QQSYDTPL (SEQ ID NO: 2094)
371_E05	SSYSMN (SEQ ID NO: 1630)	WVAGINYNGGYTS (SEQ ID NO: 1723)	ARGATWHDTHLD (SEQ ID NO: 1816)	ISYLNWY (SEQ ID NO: 1909)	LVIYAATSRA (SEQ ID NO: 2002)	QQSYSSPL (SEQ ID NO: 2095)
371_E08	SSYSMN (SEQ ID NO: 1631)	WVSNINYNSGYKS (SEQ ID NO: 1724)	ARGATWHDTHLD (SEQ ID NO: 1817)	VSYVNWY (SEQ ID NO: 1910)	LVIYAATSRH (SEQ ID NO: 2003)	QQSYDLPL (SEQ ID NO: 2096)
371_E09	SDYSMN (SEQ ID NO: 1632)	WVSGINYNSGYTS (SEQ ID NO: 1725)	ARGATWHDTHLD (SEQ ID NO: 1818)	LTYLNWY (SEQ ID NO: 1911)	LLIYAATSRA (SEQ ID NO: 2004)	QQSYNSPL (SEQ ID NO: 2097)
371_E12	DSYSMN (SEQ ID NO: 1633)	WVSGINYNSGYKS (SEQ ID NO: 1726)	ARGATWHDTHLD (SEQ ID NO: 1819)	LSYLNWY (SEQ ID NO: 1912)	LLIYAATSLA (SEQ ID NO: 2005)	QQSYDTPL (SEQ ID NO: 2098)
371_F03	SSYSMN (SEQ ID NO: 1634)	WVSGINYNGGYTS (SEQ ID NO: 1727)	ARGATWHDTHLD (SEQ ID NO: 1820)	ITYLNWY (SEQ ID NO: 1913)	LLIYAATSLH (SEQ ID NO: 2006)	QQSYDNPL (SEQ ID NO: 2099)
371_F09	SSYSMN (SEQ ID NO: 1635)	WVAGINYNGGYTS (SEQ ID NO: 1728)	ARGATWHDTHLD (SEQ ID NO: 1821)	LTYLNWY (SEQ ID NO: 1914)	LLIYAATSRA (SEQ ID NO: 2007)	QQSYDNPL (SEQ ID NO: 2100)
371_G01	SDYSMN (SEQ ID NO: 1636)	WVSNINYNGGYTS (SEQ ID NO: 1729)	ARGATWHDTHLD (SEQ ID NO: 1822)	LTYLNWY (SEQ ID NO: 1915)	LLIYAATSLA (SEQ ID NO: 2008)	QQSYDLPL (SEQ ID NO: 2101)
371_H11	SSYSMN (SEQ ID NO:	WVSGINYNGGYKG (SEQ ID NO: 1730)	ARGATWHDTHLD (SEQ ID NO: 1823)	LTYLNWY (SEQ ID NO:	LLIYATTSRH (SEQ ID NO: 2009)	QQSYESPL (SEQ ID NO:

	1637)			1916)		2102)
372_B09	SSYSMN (SEQ ID NO: 1638)	WVSSINYNSGYTS (SEQ ID NO: 1731)	ARGATWHDTHLD (SEQ ID NO: 1824)	LTYLNWY (SEQ ID NO: 1917)	LLIYAATSRA (SEQ ID NO: 2010)	QQSYETPL (SEQ ID NO: 2103)
372_E08	SDYSMN (SEQ ID NO: 1639)	WVSNINYNGGYTS (SEQ ID NO: 1732)	ARGATWHDTHLD (SEQ ID NO: 1825)	ITYLNWY (SEQ ID NO: 1918)	LLIYAATSRA (SEQ ID NO: 2011)	QQSYNLPL (SEQ ID NO: 2104)
372_F02	SSYGMH (SEQ ID NO: 1640)	WVASINYNGGYTS (SEQ ID NO: 1733)	ARGATWHDTHLD (SEQ ID NO: 1826)	LTYLNWY (SEQ ID NO: 1919)	LVIYAATSRH (SEQ ID NO: 2012)	QQSYDLPL (SEQ ID NO: 2105)
372_H11	SSYGMH (SEQ ID NO: 1641)	WVAGINYNGGYTS (SEQ ID NO: 1734)	ARGATWHDTHLD (SEQ ID NO: 1827)	LSYVNWY (SEQ ID NO: 1920)	LLIYAATSRA (SEQ ID NO: 2013)	QQSYENPL (SEQ ID NO: 2106)
373_A06	SSYSMN (SEQ ID NO: 1642)	WVSGINYNGGYKS (SEQ ID NO: 1735)	ARGATWHDTHLD (SEQ ID NO: 1828)	VTYLNWY (SEQ ID NO: 1921)	LLIYAASSLQ (SEQ ID NO: 2014)	QQSYSTPL (SEQ ID NO: 2107)
373_B09	DSYSMN (SEQ ID NO: 1643)	WVSGINYNGGYKS (SEQ ID NO: 1736)	ARGATWHDTHLD (SEQ ID NO: 1829)	LSYLNWY (SEQ ID NO: 1922)	LVIYAATSLA (SEQ ID NO: 2015)	QQSYETPL (SEQ ID NO: 2108)
373_D06	SSYSMN (SEQ ID NO: 1644)	WVAGINYNGGYTS (SEQ ID NO: 1737)	ARGATWHDTHLD (SEQ ID NO: 1830)	VTYLNWY (SEQ ID NO: 1923)	LLIYAATSRA (SEQ ID NO: 2016)	QQSYDTPL (SEQ ID NO: 2109)
373_F07	SSYSMN (SEQ ID NO: 1645)	WVSGINYNSGYKS (SEQ ID NO: 1738)	ARGATWHDTHLD (SEQ ID NO: 1831)	LSYLNWY (SEQ ID NO: 1924)	LLIYAATSLA (SEQ ID NO: 2017)	QQSYETPL (SEQ ID NO: 2110)
373_G02	SSYSMN (SEQ ID NO: 1646)	WVSGINYNGGYTS (SEQ ID NO: 1739)	ARGATWHDTHLD (SEQ ID NO: 1832)	ITYLNWY (SEQ ID NO: 1925)	LLIYAATSRA (SEQ ID NO: 2018)	QQSYSSPL (SEQ ID NO: 2111)
374_A04	SSYSMN (SEQ ID NO:	WVAGINYNGGYTS (SEQ ID NO: 1740)	ARGATWHDTHLD (SEQ ID NO: 1833)	LTYLNWY (SEQ ID NO:	LVIYAATSRA (SEQ ID NO: 2019)	QQSYDTPL (SEQ ID NO:

	1647)			1926)		2112)
374_A05	SDYGMN (SEQ ID NO: 1648)	WVANINYNGGYKG (SEQ ID NO: 1741)	ARGATWHDTHLD (SEQ ID NO: 1834)	VRYLNWY (SEQ ID NO: 1927)	LVIYAATSLA (SEQ ID NO: 2020)	QQSYELPL (SEQ ID NO: 2113)
374_C10	SSYSMN (SEQ ID NO: 1649)	WVSSINYNGGYKG (SEQ ID NO: 1742)	ARGATWHDTHLD (SEQ ID NO: 1835)	VTYLNWY (SEQ ID NO: 1928)	LLIYAATSLA (SEQ ID NO: 2021)	QQSYNTPL (SEQ ID NO: 2114)
374_D04	SSYSMN (SEQ ID NO: 1650)	WVAGINYNGGYTS (SEQ ID NO: 1743)	ARGATWHDTHLD (SEQ ID NO: 1836)	LSYLNWY (SEQ ID NO: 1929)	LVIYAATSRH (SEQ ID NO: 2022)	QQSYDTPL (SEQ ID NO: 2115)
374_D09	DSYGMN (SEQ ID NO: 1651)	WVANINYNGGYKG (SEQ ID NO: 1744)	ARGATWHDTHLD (SEQ ID NO: 1837)	ISYVNWY (SEQ ID NO: 1930)	LLIYAATSLA (SEQ ID NO: 2023)	QQSYDTPL (SEQ ID NO: 2116)
374_G05	SSYSMN (SEQ ID NO: 1652)	WVSNINYNSGYKG (SEQ ID NO: 1745)	ARGATWHDTHLD (SEQ ID NO: 1838)	ISYLNWY (SEQ ID NO: 1931)	LLIYAATSRA (SEQ ID NO: 2024)	QQSYDLPL (SEQ ID NO: 2117)
374_H05	SSYSMN (SEQ ID NO: 1653)	WVAGINYNGGYTS (SEQ ID NO: 1746)	ARGATWHDTHLD (SEQ ID NO: 1839)	LSYVNWY (SEQ ID NO: 1932)	LVIYAATSRA (SEQ ID NO: 2025)	QQSYDNPL (SEQ ID NO: 2118)
375_A03	DSYSMN (SEQ ID NO: 1654)	WVAGINYNGGYTS (SEQ ID NO: 1747)	ARGATWHDTHLD (SEQ ID NO: 1840)	LTYLNWY (SEQ ID NO: 1933)	LLIYAATSRH (SEQ ID NO: 2026)	QQSYDNPL (SEQ ID NO: 2119)
375_B03	SSYSMN (SEQ ID NO: 1655)	WVAGINYNGGYTS (SEQ ID NO: 1748)	ARGATWHDTHLD (SEQ ID NO: 1841)	LTYLNWY (SEQ ID NO: 1934)	LLIYAATSRA (SEQ ID NO: 2027)	QQSYDSPL (SEQ ID NO: 2120)
375_C01	SSYGMN (SEQ ID NO: 1656)	WVSSINYNGGYKG (SEQ ID NO: 1749)	ARGATWHDTHLD (SEQ ID NO: 1842)	SSYLNWY (SEQ ID NO: 1935)	LLIYAASSLQ (SEQ ID NO: 2028)	QQSYSTPL (SEQ ID NO: 2121)
375_C11	SSYSMN (SEQ ID NO: 1650)	WVSSINYNGGYTS (SEQ ID NO: 1750)	ARGATWHDTHLD (SEQ ID NO: 1843)	LSYVNWY (SEQ ID NO:	LLIYAATSRH (SEQ ID NO: 2029)	QQSYDTPL (SEQ ID NO:

	1657)			1936)		2122)
375_F10	SSYSMN (SEQ ID NO: 1658)	WVSGINYNGGYTG (SEQ ID NO: 1751)	ARGATWHDTHLD (SEQ ID NO: 1844)	LTYLNWY (SEQ ID NO: 1937)	LVIYAATSRA (SEQ ID NO: 2030)	QQSYDTPL (SEQ ID NO: 2123)
375_H08	SSYSMN (SEQ ID NO: 1659)	WVSGINYNGGYTS (SEQ ID NO: 1752)	ARGATWHDTHLD (SEQ ID NO: 1845)	LTYLNWY (SEQ ID NO: 1938)	LLIYAATSLA (SEQ ID NO: 2031)	QQSYDSPL (SEQ ID NO: 2124)
376_A02	SSYSMN (SEQ ID NO: 1660)	WVAGINYNGGYKS (SEQ ID NO: 1753)	ARGATWHDTHLD (SEQ ID NO: 1846)	LSYLNWY (SEQ ID NO: 1939)	LLIYAATSRA (SEQ ID NO: 2032)	QQSYDLPL (SEQ ID NO: 2125)
376_A05	SSYSMN (SEQ ID NO: 1661)	WVAGINYNSGYKG (SEQ ID NO: 1754)	ARGATWHDTHLD (SEQ ID NO: 1847)	LTYLNWY (SEQ ID NO: 1940)	LLIYAATSRA (SEQ ID NO: 2033)	QQSYNTPL (SEQ ID NO: 2126)
376_A07	SSYSMN (SEQ ID NO: 1662)	WVSGINYNGGYKS (SEQ ID NO: 1755)	ARGATWHDTHLD (SEQ ID NO: 1848)	LTYLNWY (SEQ ID NO: 1941)	LLIYAATSRA (SEQ ID NO: 2034)	QQSYDSPL (SEQ ID NO: 2127)

The consensus sequences for each of these CDRs shown in Fig. 3D are as follows:

HCDR1: S/DS/DYS/GMN/H (SEQ ID NO: 6574)

HCDR2: WVA/SG/N/SINYNG/SGYT/KS/G (SEQ ID NO: 6575)

HCDR3: ARGATWHDTH/ALD (SEQ ID NO: 6595)

LCDR1: L/I/V/SS/TYL/VNWY (SEQ ID NO: 6596)

LCDR2: LL/VIYAA/V/TT/SSR/LA/H/Q (SEQ ID NO: 6571)

LCDR3: QQSY/DD/E/S/NT/S/N/LPL (SEQ ID NO: 6577)

Table 2E: Group V Antibody Sequences

Ab	VH sequence	VL sequence
365_A03	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVAGINYNSG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2128)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLVIYAVTSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 2376)
365_A11	EVQLLESGGGLVQPGGSLRLSCAASGFT FDDYGMNWVRQAPGKGLEWVSGINYNSG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2129)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLVIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYESPLTFGGGT KVEIK (SEQ ID NO: 2377)
365_A12	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMHWVRQAPGKGLEWVAGINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCAKSANWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 2130)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLLIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYENPLTFGGGT KVEIK (SEQ ID NO: 2378)
365_B01	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYGMHWVRQAPGKGLEWVASINYNSG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2131)	DIQMTQSPSSLSASVGDRVTITCRASQSISSYVN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYESPLTFGGGT KVEIK (SEQ ID NO: 2379)
365_B06	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYGMHWVRQAPGKGLEWVSNINYNGG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2132)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLLIYATTSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 2380)
365_B07	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMHWVRQAPGKGLEWVASINYNSG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2133)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYENPLTFGGGT KVEIK (SEQ ID NO: 2381)
365_B11	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMHWVRQAPGKGLEWVAGINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2134)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYLN WYQQKPGKAPKLVIYATTSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 2382)

365_C01	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYGMNWVRQAPGKGLEWVSSINYNSG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 2135)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYLN WYQQKPGKAPKLVIYAVTSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYESPLTFGGGT KVEIK (SEQ ID NO: 2383)
365_C10	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMHWVRQAPGKGLEWVASINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2136)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLLIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYESPLTFGGGT KVEIK (SEQ ID NO: 2384)
365_C11	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVAGINYNGG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 2137)	DIQMTQSPSSLSASVGDRVTITCRASQSIITYLN WYQQKPGKAPKLVIYAVTSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSLPLTFGGGT KVEIK (SEQ ID NO: 2385)
365_C12	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVAGINYNSG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2138)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVN WYQQKPGKAPKLVIYAVTSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 2386)
365_D09	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMHWVRQAPGKGLEWVSGINYNSG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2139)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSDESPLTFGGGT KVEIK (SEQ ID NO: 2387)
365_D11	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYGMNWVRQAPGKGLEWVSNINYNSG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2140)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYLN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSSPLTFGGGT KVEIK (SEQ ID NO: 2388)
365_D12	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYGMNWVRQAPGKGLEWVSNINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2141)	DIQMTQSPSSLSASVGDRVTITCRASQSIVTYLN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 2389)
365_E01	EVQLLESGGGLVQPGGSLRLSCAASGFT FSDYSMNWVRQAPGKGLEWVSGINYNSG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2142)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 2390)
365_E05	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMHWVRQAPGKGLEWVAGINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2143)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVN WYQQKPGKAPKLLIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDNPLTFGGGT KVEIK (SEQ ID NO: 2391)
365_E07	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYGMHWVRQAPGKGLEWVSGINYNSG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCAKSANWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 2144)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDNPLTFGGGT KVEIK (SEQ ID NO: 2392)
365_E09	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMHWVRQAPGKGLEWVASINYNSG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2145)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSDDSPLTFGGGT KVEIK (SEQ ID NO: 2393)

365_F01	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVSGINYNSG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 2146)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYLN WYQQKPGKAPKLVIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYELPLTFGGGT KVEIK (SEQ ID NO: 2394)
365_F06	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVAGINYNSG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2147)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSDNLPLTFGGGT KVEIK (SEQ ID NO: 2395)
365_F12	EVQLLESGGGLVQPGGSLRLSCAASGFT FSDYSMNWVRQAPGKGLEWVSGINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 2148)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLVIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYETPLTFGGGT KVEIK (SEQ ID NO: 2396)
365_G01	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYGMNWVRQAPGKGLEWVAGINYNSG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2149)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLLIYATTSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 2397)
365_G11	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVANINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2150)	DIQMTQSPSSLSASVGDRVTITCRASQSIITYVN WYQQKPGKAPKLLIYAVTSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNSPLTFGGGT KVEIK (SEQ ID NO: 2398)
365_H02	EVQLLESGGGLVQPGGSLRLSCAASGFT FSDYGMNWVRQAPGKGLEWVSSINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 2151)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYENPLTFGGGT KVEIK (SEQ ID NO: 2399)
365_H03	EVQLLESGGGLVQPGGSLRLSCAASGFT FDDYGMNWVRQAPGKGLEWVAGINYNGG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2152)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLVIYAATSLHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNNPLTFGGGT KVEIK (SEQ ID NO: 2400)
365_H06	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVSGINYNSG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2153)	DIQMTQSPSSLSASVGDRVTITCRASQSISSYVN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSTPLTFGGGT KVEIK (SEQ ID NO: 2401)
365_H10	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYGMNWVRQAPGKGLEWVAGINYNSG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 2154)	DIQMTQSPSSLSASVGDRVTITCRASQSIVTYVN WYQQKPGKAPKLVIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNTPLTFGGGT KVEIK (SEQ ID NO: 2402)
365_H11	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVSGINYNSG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2155)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 2403)
365_H12	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVSNINYNGG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 2156)	DIQMTQSPSSLSASVGDRVTITCRASQSIITYVN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSTPLTFGGGT KVEIK (SEQ ID NO: 2404)

366_A07	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMHWVRQAPGKGLEWVASINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2157)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVN WYQQKPGKAPKLVIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYESPLTFGGGT KVEIK (SEQ ID NO: 2405)
366_B08	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYGMNWVRQAPGKGLEWVSNINYNGG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 2158)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYLN WYQQKPGKAPKLLIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDNPLTFGGGT KVEIK (SEQ ID NO: 2406)
366_B10	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVSGINYNSG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2159)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDNPLTFGGGT KVEIK (SEQ ID NO: 2407)
366_B12	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVAGINYNSG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2160)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDNPLTFGGGT KVEIK (SEQ ID NO: 2408)
366_D04	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVSGINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2161)	DIQMTQSPSSLSASVGDRVTITCRASQSISSYVN WYQQKPGKAPKLLIYATTSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYETPLTFGGGT KVEIK (SEQ ID NO: 2409)
366_E10	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYGMNWVRQAPGKGLEWVSGINYNGG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 2162)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLVIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSLPLTFGGGT KVEIK (SEQ ID NO: 2410)
366_F04	EVQLLESGGGLVQPGGSLRLSCAASGFT FSDYGMNWVRQAPGKGLEWVSGINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2163)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLVIYATTSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYESPLTFGGGT KVEIK (SEQ ID NO: 2411)
366_F05	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVANINYNSG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 2164)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSDNTPLTFGGGT KVEIK (SEQ ID NO: 2412)
366_F07	EVQLLESGGGLVQPGGSLRLSCAASGFT FSDYSMNWVRQAPGKGLEWVAGINYNSG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 2165)	DIQMTQSPSSLSASVGDRVTITCRASQSIITYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYETPLTFGGGT KVEIK (SEQ ID NO: 2413)
366_G04	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVSGINYNSG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2166)	DIQMTQSPSSLSASVGDRVTITCRASQSIITYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSDDTPLTFGGGT KVEIK (SEQ ID NO: 2414)
366_G05	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYGMNWVRQAPGKGLEWVSNINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2167)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYVN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYENPLTFGGGT KVEIK (SEQ ID NO: 2415)

366_H06	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVSSINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2168)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLLIYATTSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 2416)
366_H07	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMHWVRQAPGKGLEWVSGINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2169)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYVN WYQQKPGKAPKLVIYAVTSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYENPLTFGGGT KVEIK (SEQ ID NO: 2417)
366_H08	EVQLLESGGGLVQPGGSLRLSCAASGFT FSDYGMNWVRQAPGKGLEWVASINYNSG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 2170)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLLIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNNPLTFGGGT KVEIK (SEQ ID NO: 2418)
366_H09	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYGMNWVRQAPGKGLEWVSNINYNSG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2171)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVN WYQQKPGKAPKLVIYATTSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSSPLTFGGGT KVEIK (SEQ ID NO: 2419)
367_A04	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVSNINYNSG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2172)	DIQMTQSPSSLSASVGDRVTITCRASQSIITYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSDDSPLTFGGGT KVEIK (SEQ ID NO: 2420)
367_A05	EVQLLESGGGLVQPGGSLRLSCAASGFT FSDYGMNWVRQAPGKGLEWVSSINYNGG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2173)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLVIYAVTSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 2421)
367_B02	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYGMNWVRQAPGKGLEWVSSINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2174)	DIQMTQSPSSLSASVGDRVTITCRASQSIVTYLN WYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSTPLTFGGGT KVEIK (SEQ ID NO: 2422)
367_B03	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVAGINYNGG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2175)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLLIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNLPLTFGGGT KVEIK (SEQ ID NO: 2423)
367_B07	EVQLLESGGGLVQPGGSLRLSCAASGFT FSDYSMNWVRQAPGKGLEWVAGINYNSG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 2176)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYVN WYQQKPGKAPKLLIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNLPLTFGGGT KVEIK (SEQ ID NO: 2424)
367_B08	EVQLLESGGGLVQPGGSLRLSCAASGFT FSDYGMNWVRQAPGKGLEWVSGINYNGG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2177)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDNPLTFGGGT KVEIK (SEQ ID NO: 2425)
367_C01	EVQLLESGGGLVQPGGSLRLSCAASGFT FDDYSMNWVRQAPGKGLEWVSGINYNGG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 2178)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLVIYATTSLHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 2426)

367_C05	EVQLLESGGGLVQPGGSLRLSCAASGFT FDDYGMNWVRQAPGKGLEWVSSINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 2179)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLVIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 2427)
367_C11	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVSSINYNSG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 2180)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLVIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNTPLTFGGGT KVEIK (SEQ ID NO: 2428)
367_D10	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYGMNWVRQAPGKGLEWVSNINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2181)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYLN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 2429)
367_E01	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVAGINYNGG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2182)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLLIYATTSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 2430)
367_E04	EVQLLESGGGLVQPGGSLRLSCAASGFT FSDYSMNWVRQAPGKGLEWVSSINYNGG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 2183)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYESPLTFGGGT KVEIK (SEQ ID NO: 2431)
367_E06	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVSSINYNSG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 2184)	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLN WYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSTPLTFGGGT KVEIK (SEQ ID NO: 2432)
367_E09	EVQLLESGGGLVQPGGSLRLSCAASGFT FSDYGMNWVRQAPGKGLEWVASINYNSG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2185)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLVIYATTSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYETPLTFGGGT KVEIK (SEQ ID NO: 2433)
367_E11	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYGMNWVRQAPGKGLEWVSSINYNSG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 2186)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVN WYQQKPGKAPKLVIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 2434)
367_F03	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVAGINYNSG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2187)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLVIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSDDTPLTFGGGT KVEIK (SEQ ID NO: 2435)
367_F07	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYGMHWVRQAPGKGLEWVANINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2188)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYVN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYETPLTFGGGT KVEIK (SEQ ID NO: 2436)
367_F11	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVAGINYNSG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 2189)	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLN WYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSTPLTFGGGT KVEIK (SEQ ID NO: 2437)

367_G05	EVQLLESGGGLVQPGGSLRLSCAASGFT FSDYGMNWVRQAPGKGLEWVANINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2190)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYLN WYQQKPGKAPKLVIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 2438)
367_G06	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVSGINYNSG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 2191)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLLIYATTSLHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 2439)
367_G10	EVQLLESGGGLVQPGGSLRLSCAASGFT FDDYGMNWVRQAPGKGLEWVSGINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2192)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYVN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 2440)
367_H06	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVSNINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 2193)	DIQMTQSPSSLSASVGDRVTITCRASQSIITYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 2441)
367_H11	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVAGINYNGG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2194)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYVN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNSPLTFGGGT KVEIK (SEQ ID NO: 2442)
368_A01	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVSNINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2195)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYLN WYQQKPGKAPKLLIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDNPLTFGGGT KVEIK (SEQ ID NO: 2443)
368_A05	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVAGINYNSG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2196)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYLN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 2444)
368_A07	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVAGINYNSG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 2197)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLVIYATTSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSNELPLTFGGGT KVEIK (SEQ ID NO: 2445)
368_A09	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVSGINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 2198)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLLIYAVTSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 2446)
368_B01	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVSGINYNSG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2199)	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYETPLTFGGGT KVEIK (SEQ ID NO: 2447)
368_B06	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYGMHWVRQAPGKGLEWVSGINYNSG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2200)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYLN WYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSTPLTFGGGT KVEIK (SEQ ID NO: 2448)

368_B07	EVQLLESGGGLVQPGGSLRLSCAASGFT FSDYSMNWVRQAPGKGLEWVSNINYNGG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2201)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYLN WYQQKPGKAPKLLIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSSPLTFGGGT KVEIK (SEQ ID NO: 2449)
368_C05	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYGMNWVRQAPGKGLEWVSGINYNSG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2202)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSDSNPLTFGGGT KVEIK (SEQ ID NO: 2450)
368_D01	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMHWVRQAPGKGLEWVANINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2203)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSDSTPLTFGGGT KVEIK (SEQ ID NO: 2451)
368_D04	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVSGINYNGG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2204)	DIQMTQSPSSLSASVGDRVTITCRASQSISTYVN WYQQKPGKAPKLVIYAVTSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 2452)
368_D05	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVSGINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2205)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSDDSPLTFGGGT KVEIK (SEQ ID NO: 2453)
368_D11	EVQLLESGGGLVQPGGSLRLSCAASGFT FDDYGMNWVRQAPGKGLEWVSNINYNGG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2206)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 2454)
368_E01	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVASINYNSG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 2207)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLLIYAVTSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSLPLTFGGGT KVEIK (SEQ ID NO: 2455)
368_E02	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVAGINYNSG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 2208)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSSPLTFGGGT KVEIK (SEQ ID NO: 2456)
368_E04	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVANINYNSG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2209)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLLIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDNPLTFGGGT KVEIK (SEQ ID NO: 2457)
368_E06	EVQLLESGGGLVQPGGSLRLSCAASGFT FSDYGMHWVRQAPGKGLEWVSGINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2210)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLVIYGATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 2458)
368_E07	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVAGINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCAKSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2211)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLLIYAVTSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYENPLTFGGGT KVEIK (SEQ ID NO: 2459)

368_F03	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVAGINYNSG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCAKSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2212)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYLN WYQQKPGKAPKLVIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 2460)
368_F11	EVQLLESGGGLVQPGGSLRLSCAASGFT FSDYGMNWVRQAPGKGLEWVSGINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 2213)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNNPLTFGGGT KVEIK (SEQ ID NO: 2461)
368_G01	EVQLLESGGGLVQPGGSLRLSCAASGFT FSDYGMHWVRQAPGKGLEWVASINYNSG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2214)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNLPLTFGGGT KVEIK (SEQ ID NO: 2462)
368_G12	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVASINYNSG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2215)	DIQMTQSPSSLSASVGDRVTITCRASQSISSYVN WYQQKPGKAPKLVIYAVTSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYETPLTFGGGT KVEIK (SEQ ID NO: 2463)
368_H04	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVAGINYNSG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCAKSANWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 2216)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 2464)
369_A02	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVAGINYNSG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 2217)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 2465)
369_A03	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVSNINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2218)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLLIYAVTSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQGYDLPLTFGGGT KVEIK (SEQ ID NO: 2466)
369_B01	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVSGINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2219)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLLIYAVTSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYENPLTFGGGT KVEIK (SEQ ID NO: 2467)
369_C02	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVSNINYNGG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2220)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYELPLTFGGGT KVEIK (SEQ ID NO: 2468)
369_C03	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVSNINYNGG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2221)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 2469)
369_C04	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVSNINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2222)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLLIYTTTSLHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNNPLTFGGGT KVEIK (SEQ ID NO: 2470)

369_D01	EVQLLESGGGLVQPGGSLRLSCAASGFT FSDYGMNWVRQAPGKGLEWVASINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2223)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSNPLTFGGGT KVEIK (SEQ ID NO: 2471)
369_D02	EVQLLESGGGLVQPGGSLRLSCAASGFT FSDYSMNWVRQAPGKGLEWVSNINYNSG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2224)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLVIYAVTSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 2472)
369_D04	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYGMNWVRQAPGKGLEWVSGINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2225)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNLPLTFGGGT KVEIK (SEQ ID NO: 2473)
369_D12	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVAGINYNSG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2226)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLLIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 2474)
369_E02	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYGMNWVRQAPGKGLEWVSNINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2227)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVN WYQQKPGKAPKLLIYATTSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDNPLTFGGGT KVEIK (SEQ ID NO: 2475)
369_E11	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVSNINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2228)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYLN WYQQKPGKAPKLLIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 2476)
369_E12	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMHWVRQAPGKGLEWVASINYNSG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2229)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYESPLTFGGGT KVEIK (SEQ ID NO: 2477)
369_F01	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVSGINYNGG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2230)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYELPLTFGGGT KVEIK (SEQ ID NO: 2478)
369_F02	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVASINYNSG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2231)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYLN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 2479)
369_F03	EVQLLESGGGLVQPGGSLRLSCAASGFT FSDYGMNWVRQAPGKGLEWVSGINYNSG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2232)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVN WYQQKPGKAPKLLIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 2480)
369_F06	EVQLLESGGGLVQPGGSLRLSCAASGFT FDDYSMNWVRQAPGKGLEWVAGINYNGG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2233)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 2481)

369_F10	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYGMNWVRQAPGKGLEWVSNINYNSG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2234)	DIQMTQSPSSLSASVGDRVTITCRASQSIVTYLN WYQQKPGKAPKLLIYAVTSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 2482)
369_F11	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYGMNWVRQAPGKGLEWVSNINYNSG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2235)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 2483)
369_G01	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVSNINYNSG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2236)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSSPLTFGGGT KVEIK (SEQ ID NO: 2484)
369_G04	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVSGINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2237)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLLIYATTSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYETPLTFGGGT KVEIK (SEQ ID NO: 2485)
369_G06	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYGMNWVRQAPGKGLEWVAGINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2238)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYENPLTFGGGT KVEIK (SEQ ID NO: 2486)
369_G11	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVANINYNSG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2239)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLLIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYESPLTFGGGT KVEIK (SEQ ID NO: 2487)
369_G12	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVANINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2240)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLVIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSDNTPLTFGGGT KVEIK (SEQ ID NO: 2488)
369_H05	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVANINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2241)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSNPLTFGGGT KVEIK (SEQ ID NO: 2489)
369_H06	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVANINYNGG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2242)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 2490)
369_H09	EVQLLESGGGLVQPGGSLRLSCAASGFT FDDYSMNWVRQAPGKGLEWVSGINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2243)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLLIYAVTSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYESPLTFGGGT KVEIK (SEQ ID NO: 2491)
370_A01	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVSGINYNSG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2244)	DIQMTQSPSSLSASVGDRVTITCRASQSISTYLN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNLPLTFGGGT KVEIK (SEQ ID NO: 2492)

370_A03	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVSNINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2245)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 2493)
370_A04	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVSGINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2246)	DIQMTQSPSSLSASVGDRVTITCRASQSIITYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDNPLTFGGGT KVEIK (SEQ ID NO: 2494)
370_A12	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVAGINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2247)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLLIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 2495)
370_C01	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVSGINYNSG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2248)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLVIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 2496)
370_C03	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVAGINYNGG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2249)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLLIYYVTNRQSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSSPLTFGGGT KVEIK (SEQ ID NO: 2497)
370_C05	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVAGINYNSG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2250)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNSPLTFGGGT KVEIK (SEQ ID NO: 2498)
370_C08	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVAGINYNGG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2251)	DIQMTQSPSSLSASVGDRVTITCRASQSISNYLN WYQQKPGKAPKLLIYAVTSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 2499)
370_C09	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYGMNWVRQAPGKGLEWVSGINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2252)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYLN WYQQKPGKAPKLVIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSTPLTFGGGT KVEIK (SEQ ID NO: 2500)
370_D04	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVANINYNSG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2253)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDNPLTFGGGT KVEIK (SEQ ID NO: 2501)
370_D11	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVSGINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2254)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 2502)
370_E03	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVSSINYNGG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2255)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLVIYYASNRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 2503)

370_E06	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVSGINYNSG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2256)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLVIYATTSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 2504)
370_E09	EVQLLESGGGLVQPGGSLRLSCAASGFT FDDSSMHWVRQAPGKGLEWVSNINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCAKSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2257)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYELPLTFGGGT KVEIK (SEQ ID NO: 2505)
370_F05	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVSGINYNSG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2258)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYETPLTFGGGT KVEIK (SEQ ID NO: 2506)
370_F07	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVSNINYNGG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2259)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNLPLTFGGGT KVEIK (SEQ ID NO: 2507)
370_F10	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVAGINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2260)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYLN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNSPLTFGGGT KVEIK (SEQ ID NO: 2508)
370_G02	EVQLLESGGGLVQPGGSLRLSCAASGFT FSDYSMNWVRQAPGKGLEWVANINYNGG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2261)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYLN WYQQKPGKAPKLLIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 2509)
370_G03	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVANINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2262)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLVIYATTSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNNPLTFGGGT KVEIK (SEQ ID NO: 2510)
370_G06	EVQLLESGGGLVQPGGSLRLSCAASGFT FSDYGMHWVRQAPGKGLEWVSSINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2263)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSDNTPLTFGGGT KVEIK (SEQ ID NO: 2511)
370_G09	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVAGINYNGG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2264)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYESPLTFGGGT KVEIK (SEQ ID NO: 2512)
370_G10	EVQLLESGGGLVQPGGSLRLSCAASGFT FSDYGMNWVRQAPGKGLEWVSGINYNSG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2265)	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLN WYQQKPGKAPKLLIYVVNNRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYENPLTFGGGT KVEIK (SEQ ID NO: 2513)
370_G11	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVASINYNSG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 2266)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYLN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSLPLTFGGGT KVEIK (SEQ ID NO: 2514)

370_H01	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVSGINYNSG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2267)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYLN WYQQKPGKAPKLLIYAVTSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 2515)
370_H09	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVANINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2268)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDNPLTFGGGT KVEIK (SEQ ID NO: 2516)
371_A03	EVQLLESGGGLVQPGGSLRLSCAASGFT FSDYGMNWVRQAPGKGLEWVANINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2269)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLVIYATTSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYESPLTFGGGT KVEIK (SEQ ID NO: 2517)
371_A06	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVAGINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2270)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLVIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 2518)
371_A07	EVQLLESGGGLVQPGGSLRLSCAASGFT FSDYSMNWVRQAPGKGLEWVSNINYNGG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2271)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLVIYATTSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 2519)
371_A08	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMHWVRQAPGKGLEWVSSINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2272)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYELPLTFGGGT KVEIK (SEQ ID NO: 2520)
371_A12	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVAGINYNSG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2273)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLVIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 2521)
371_B06	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVAGINYNGG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2274)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLVIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNLPLTFGGGT KVEIK (SEQ ID NO: 2522)
371_B07	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVAGINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2275)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYELPLTFGGGT KVEIK (SEQ ID NO: 2523)
371_C03	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVSNINYNGG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2276)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLVIYATTSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSTPLTFGGGT KVEIK (SEQ ID NO: 2524)
371_D06	EVQLLESGGGLVQPGGSLRLSCAASGFT FDDYSMNWVRQAPGKGLEWVAGINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2277)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYVN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSTPLTFGGGT KVEIK (SEQ ID NO: 2525)

371_D09	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVSNINYNSG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2278)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNNPLTFGGGT KVEIK (SEQ ID NO: 2526)
371_F01	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVAGINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2279)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLVIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNNPLTFGGGT KVEIK (SEQ ID NO: 2527)
371_F04	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVAGINYNSG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2280)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLLIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNNPLTFGGGT KVEIK (SEQ ID NO: 2528)
371_F06	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVANINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2281)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYLN WYQQKPGKAPKLVIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNSPLTFGGGT KVEIK (SEQ ID NO: 2529)
371_F08	EVQLLESGGGLVQPGGSLRLSCAASGFT FDDYSMNWVRQAPGKGLEWVSGINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2282)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVN WYQQKPGKAPKLVIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYESPLTFGGGT KVEIK (SEQ ID NO: 2530)
371_G05	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVSGINYNSG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2283)	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLN WYQQKPGKAPKLLIYAVTSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSSPLTFGGGT KVEIK (SEQ ID NO: 2531)
371_G10	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVSGINYNGG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2284)	DIQMTQSPSSLSASVGDRVTITCRASQSISSYVN WYQQKPGKAPKLLIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSDDSPLTFGGGT KVEIK (SEQ ID NO: 2532)
371_H09	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVSNINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2285)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLVIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 2533)
372_A04	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVSGINYNSG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2286)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYETPLTFGGGT KVEIK (SEQ ID NO: 2534)
372_B04	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYGMNWVRQAPGKGLEWVANINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2287)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLVIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 2535)
372_C07	EVQLLESGGGLVQPGGSLRLSCAASGFT FSDYSMNWVRQAPGKGLEWVSNINYNSG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 2288)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLVIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSDNTPLTFGGGT KVEIK (SEQ ID NO: 2536)

372_D02	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMHWVRQAPGKGLEWVAGINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2289)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDNPLTFGGGT KVEIK (SEQ ID NO: 2537)
372_F03	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVAGINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2290)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 2538)
372_F06	EVQLLESGGGLVQPGGSLRLSCAASGFT FSDYGMNWVRQAPGKGLEWVAGINYNGG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2291)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLLIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYETPLTFGGGT KVEIK (SEQ ID NO: 2539)
372_F08	EVQLLESGGGLVQPGGSLRLSCAASGFT FSDYSMNWVRQAPGKGLEWVSNINYNSG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2292)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 2540)
372_F09	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVANINYNSG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2293)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLVIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSSPLTFGGGT KVEIK (SEQ ID NO: 2541)
373_A02	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYGMNWVRQAPGKGLEWVSGINYNGG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2294)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLVIYATTSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNTPLTFGGGT KVEIK (SEQ ID NO: 2542)
373_A08	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYGMNWVRQAPGKGLEWVSNINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2295)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVN WYQQKPGKAPKLLIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSLPLTFGGGT KVEIK (SEQ ID NO: 2543)
373_A10	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVSGINYNSG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2296)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 2544)
373_B04	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVAGINYNSG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2297)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYETPLTFGGGT KVEIK (SEQ ID NO: 2545)
373_B06	EVQLLESGGGLVQPGGSLRLSCAASGFT FSDYSMNWVRQAPGKGLEWVAGINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2298)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLVIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYESPLTFGGGT KVEIK (SEQ ID NO: 2546)
373_B10	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYGMNWVRQAPGKGLEWVSNINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2299)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 2547)

373_B12	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYGMNWVRQAPGKGLEWVSSINYNSG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2300)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 2548)
373_C02	EVQLLESGGGLVQPGGSLRLSCAASGFT FDDYSMNWVRQAPGKGLEWVSGINYNSG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2301)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNTPLTFGGGT KVEIK (SEQ ID NO: 2549)
373_C04	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVANINYNSG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2302)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYVN WYQQKPGKAPKLVIYAVTSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNSPLTFGGGT KVEIK (SEQ ID NO: 2550)
373_C06	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVAGINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2303)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 2551)
373_C08	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVANINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2304)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYLN WYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNNPLTFGGGT KVEIK (SEQ ID NO: 2552)
373_C11	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVSGINYNSG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2305)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLVIYAVTSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYETPLTFGGGT KVEIK (SEQ ID NO: 2553)
373_D01	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVSGINYNSG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 2306)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 2554)
373_D04	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVSGINYNSG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2307)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLLIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 2555)
373_D05	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVSGINYNSG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2308)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 2556)
373_D08	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVSGINYNGG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2309)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 2557)
373_D10	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVSNINYNSG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2310)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 2558)

373_E01	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVSGINYNGG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2311)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVN WYQQKPGKAPKLLIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNNPLTFGGGT KVEIK (SEQ ID NO: 2559)
373_E05	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYGMNWVRQAPGKGLEWVSNINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2312)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLLIYAVTSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 2560)
373_E07	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVANINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2313)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLLIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYETPLTFGGGT KVEIK (SEQ ID NO: 2561)
373_E12	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVANINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2314)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 2562)
373_G10	EVQLLESGGGLVQPGGSLRLSCAASGFT FSDYGMNWVRQAPGKGLEWVSNINYNGG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2315)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 2563)
373_G12	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVSNINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2316)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLLIYATTSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNSPLTFGGGT KVEIK (SEQ ID NO: 2564)
373_H01	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVANINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2317)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDNPLTFGGGT KVEIK (SEQ ID NO: 2565)
373_H05	EVQLLESGGGLVQPGGSLRLSCAASGFT FSDYSMNWVRQAPGKGLEWVANINYNGG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2318)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYETPLTFGGGT KVEIK (SEQ ID NO: 2566)
374_A07	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVSGINYNSG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2319)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLLIYAVTSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 2567)
374_B04	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVSNINYNSG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2320)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYLN WYQQKPGKAPKLLIYAVTSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYESPLTFGGGT KVEIK (SEQ ID NO: 2568)
374_B06	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVAGINYNSG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 2321)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 2569)

374_B12	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVAGINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 2322)	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDNPLTFGGGT KVEIK (SEQ ID NO: 2570)
374_C03	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVSGINYNSG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2323)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 2571)
374_C06	EVQLLESGGGLVQPGGSLRLSCAASGFT FDDYSMNWVRQAPGKGLEWVSSINYNSG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2324)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNSPLTFGGGT KVEIK (SEQ ID NO: 2572)
374_D01	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVSGINYNSG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2325)	DIQMTQSPSSLSASVGDRVTITCRASQSIITYVN WYQQKPGKAPKLLIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSSPLTFGGGT KVEIK (SEQ ID NO: 2573)
374_D08	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYGMNWVRQAPGKGLEWVSGINYNSG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 2326)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLLIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYESPLTFGGGT KVEIK (SEQ ID NO: 2574)
374_E01	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVAGINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2327)	DIQMTQSPSSLSASVGDRVTITCRASQSISSYVN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSTPLTFGGGT KVEIK (SEQ ID NO: 2575)
374_E02	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVSGINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2328)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLLIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 2576)
374_E05	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVAGINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2329)	DIQMTQSPSSLSASVGDRVTITCRASQSILSFVN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNLPLTFGGGT KVEIK (SEQ ID NO: 2577)
374_E07	EVQLLESGGGLVQPGGSLRLSCAASGFT FSDYSMNWVRQAPGKGLEWVAGINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2330)	DIQMTQSPSSLSASVGDRVTITCRASQSIITYVN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNTPLTFGGGT KVEIK (SEQ ID NO: 2578)
374_E08	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVAGINYNGG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2331)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLLIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 2579)
374_E11	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVSNINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2332)	DIQMTQSPSSLSASVGDRVTITCRASQSIVTYLN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 2580)

374_F01	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVSNINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2333)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLVIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYENPLTFGGGT KVEIK (SEQ ID NO: 2581)
374_F02	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVANINYNSG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2334)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYLN WYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYELPLTFGGGT KVEIK (SEQ ID NO: 2582)
374_F04	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVSGINYNSG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2335)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNSPLTFGGGT KVEIK (SEQ ID NO: 2583)
374_F10	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVSGINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2336)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDNPLTFGGGT KVEIK (SEQ ID NO: 2584)
374_F11	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVSNINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2337)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLLIYAVTSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYESPLTFGGGT KVEIK (SEQ ID NO: 2585)
374_G04	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVAGINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2338)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLVIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDNPLTFGGGT KVEIK (SEQ ID NO: 2586)
374_G06	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMHWVRQAPGKGLEWVASINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2339)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLLIYAVTSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 2587)
374_G07	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVSGINYNSG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2340)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 2588)
374_H03	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVSGINYNSG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2341)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 2589)
374_H04	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVSGINYNSG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2342)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDNPLTFGGGT KVEIK (SEQ ID NO: 2590)
374_H06	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVSNINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2343)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNLPLTFGGGT KVEIK (SEQ ID NO: 2591)

374_H07	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYGMNWVRQAPGKGLEWVANINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2344)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYETPLTFGGGT KVEIK (SEQ ID NO: 2592)
374_H09	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVANINYNSG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2345)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLVIYAVTSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 2593)
375_A05	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVANINYNGG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2346)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 2594)
375_C06	EVQLLESGGGLVQPGGSLRLSCAASGFT FDDYGMHWVRQAPGKGLEWVASINYNSG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2347)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLVIYATTSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 2595)
375_D04	EVQLLESGGGLVQPGGSLRLSCAASGFT FDDSSMHWVRQAPGKGLEWVSNINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCAKSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2348)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYELPLTFGGGT KVEIK (SEQ ID NO: 2596)
375_D05	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVASINYNSG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 2349)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYLN WYQQKPGKAPKLLIYAATSLHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 2597)
375_D07	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVANINYNSG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2350)	DIQMTQSPSSLSASVGDRVTITCRASQSIITYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 2598)
375_D08	EVQLLESGGGLVQPGGSLRLSCAASGFT FSDYGMNWVRQAPGKGLEWVSGINYNSG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2351)	DIQMTQSPSSLSASVGDRVTITCRASQSIITYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSTPLTFGGGT KVEIK (SEQ ID NO: 2599)
375_D12	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYGMNWVRQAPGKGLEWVSSINYNSG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2352)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYETPLTFGGGT KVEIK (SEQ ID NO: 2600)
375_E01	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVSGINYNSG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2353)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSDDSPLTFGGGT KVEIK (SEQ ID NO: 2601)
375_E07	EVQLLESGGGLVQPGGSLRLSCAASGFT FSDYSMNWVRQAPGKGLEWVAGINYNSG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2354)	DIQMTQSPSSLSASVGDRVTITCRASQSIVTYLN WYQQKPGKAPKLLIYVVTNRESGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYETPLTFGGGT KVEIK (SEQ ID NO: 2602)

375_H12	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVAGINYNGG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2355)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLLIYYVTNRQSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSIPLTFGGGT KVEIK (SEQ ID NO: 2603)
376_A04	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVSNINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2356)	DIQMTQSPSSLSASVGDRVTITCRASQSIVTYLN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 2604)
376_A10	EVQLLESGGGLVQPGGSLRLSCAASGFT FSDYGMNWVRQAPGKGLEWVSNINYNSG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2357)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYESPLTFGGGT KVEIK (SEQ ID NO: 2605)
376_A12	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVANINYNSG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2358)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 2606)
376_B04	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYGMHWVRQAPGKGLEWVASINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2359)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 2607)
376_B05	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVANINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2360)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYVN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYELPLTFGGGT KVEIK (SEQ ID NO: 2608)
376_B09	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVANINYNSG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2361)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 2609)
376_B11	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVSGINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2362)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 2610)
376_C01	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVAGINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2363)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLLIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDNPLTFGGGT KVEIK (SEQ ID NO: 2611)
376_C02	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYGMNWVRQAPGKGLEWVSGINYNSG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2364)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYLN WYQQKPGKAPKLVIYAVTSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 2612)
376_C12	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVAGINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2365)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 2613)

376_D05	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVSNINYNGG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2366)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVN WYQQKPGKAPKLLIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 2614)
376_D11	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVANINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2367)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNNPLTFGGGT KVEIK (SEQ ID NO: 2615)
376_E03	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVANINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2368)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLVIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 2616)
376_E08	EVQLLESGGGLVQPGGSLRLSCAASGFT FSDYGMNWVRQAPGKGLEWVAGINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2369)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 2617)
376_F03	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYGMNWVRQAPGKGLEWVANINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2370)	DIQMTQSPSSLSASVGDRVTITCRASQSIITYVN WYQQKPGKAPKLVIYATTSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSSPLTFGGGT KVEIK (SEQ ID NO: 2618)
376_F04	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVSNINYNSG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2371)	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLN WYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSTPLTFGGGT KVEIK (SEQ ID NO: 2619)
376_G08	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYGMNWVRQAPGKGLEWVANINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2372)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 2620)
376_G09	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVSGINYNSG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2373)	DIQMTQSPSSLSASVGDRVTITCRASQSISYYLN WYQQKPGKAPKLLIYAVTSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDNPLTFGGGT KVEIK (SEQ ID NO: 2621)
376_H09	EVQLLESGGGLVQPGGSLRLSCAASGFT FSDYSMNWVRQAPGKGLEWVANINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2374)	DIQMTQSPSSLSASVGDRVTITCRASQSIITYLN WYQQKPGKAPKLVIYYVSNLPSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 2622)
376_H10	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVSGINYNSG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSANWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 2375)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLVIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 2623)

Table 3E provides the amino acid sequences of the CDRs of the antibodies shown in Table 2E.

Table 3E: CDR sequences for Group V antibodies

Ab	HCDR1	HCDR2	HCDR3	LCDR1	LCDR2	LCDR3
365_A03	SSYSMN (SEQ ID NO: 2624)	WVAGINYNSGYKG (SEQ ID NO: 2872)	ARSANWHDTALD (SEQ ID NO: 3120)	LSYLNWY (SEQ ID NO: 3368)	LVIYAVTSRA (SEQ ID NO: 3616)	QQSYDSPL (SEQ ID NO: 3864)
365_A11	DDYGMN (SEQ ID NO: 2625)	WVSGINYNSGYTS (SEQ ID NO: 2873)	ARSANWHDTALD (SEQ ID NO: 3121)	LSYLNWY (SEQ ID NO: 3369)	LVIYAATSLA (SEQ ID NO: 3617)	QQSYESPL (SEQ ID NO: 3865)
365_A12	SSYGMH (SEQ ID NO: 2626)	WVAGINYNGGYTS (SEQ ID NO: 2874)	AKSANWHDTHLD (SEQ ID NO: 3122)	LTYVNWY (SEQ ID NO: 3370)	LLIYAATSRH (SEQ ID NO: 3618)	QQSYENPL (SEQ ID NO: 3866)
365_B01	DSYGMH (SEQ ID NO: 2627)	WVASINYNSGYTS (SEQ ID NO: 2875)	ARSANWHDTALD (SEQ ID NO: 3123)	SSYVNWY (SEQ ID NO: 3371)	LVIYAATSRA (SEQ ID NO: 3619)	QQSYESPL (SEQ ID NO: 3867)
365_B06	DSYGMH (SEQ ID NO: 2628)	WVSNINYNGGYKS (SEQ ID NO: 2876)	ARSANWHDTALD (SEQ ID NO: 3124)	LTYVNWY (SEQ ID NO: 3372)	LLIYATTSLA (SEQ ID NO: 3620)	QQSYDLPL (SEQ ID NO: 3868)
365_B07	SSYGMH (SEQ ID NO: 2629)	WVASINYNSGYTS (SEQ ID NO: 2877)	ARSANWHDTALD (SEQ ID NO: 3125)	LTYLNWY (SEQ ID NO: 3373)	LLIYAATSRA (SEQ ID NO: 3621)	QQSYENPL (SEQ ID NO: 3869)
365_B11	SSYGMH (SEQ ID NO: 2630)	WVAGINYNGGYTS (SEQ ID NO: 2878)	ARSANWHDTALD (SEQ ID NO: 3126)	ISYLNWY (SEQ ID NO: 3374)	LVIYATTSRH (SEQ ID NO: 3622)	QQSYDSPL (SEQ ID NO: 3870)
365_C01	DSYGMN (SEQ ID NO: 2631)	WVSSINYNSGYKS (SEQ ID NO: 2879)	ARSANWHDTHLD (SEQ ID NO: 3127)	VSYLNWY (SEQ ID NO: 3375)	LVIYAVTSRA (SEQ ID NO: 3623)	QQSYESPL (SEQ ID NO: 3871)
365_C10	SSYGMH (SEQ ID NO: 2632)	WVASINYNGGYTS (SEQ ID NO: 2880)	ARSANWHDTALD (SEQ ID NO: 3128)	LSYVNWY (SEQ ID NO: 3376)	LLIYAATSLA (SEQ ID NO: 3624)	QQSYESPL (SEQ ID NO: 3872)
365_C11	SSYSMN (SEQ ID NO: 2633)	WVAGINYNGGYKS (SEQ ID NO: 2881)	ARSANWHDTHLD (SEQ ID NO: 3129)	ITYLNWY (SEQ ID NO: 3377)	LVIYAVTSRA (SEQ ID NO: 3625)	QQSYSLPL (SEQ ID NO: 3873)
365_C12	SSYGMN (SEQ ID NO: 2634)	WVAGINYNSGYKS (SEQ ID NO: 2882)	ARSANWHDTALD (SEQ ID NO: 3130)	VSYVNWY (SEQ ID NO: 3378)	LVIYAVTSLA (SEQ ID NO: 3626)	QQSYDTPL (SEQ ID NO: 3874)
365_D09	SSYGMH (SEQ ID NO: 2635)	WVSGINYNSGYTS (SEQ ID NO: 2883)	ARSANWHDTALD (SEQ ID NO: 3131)	LSYLNWY (SEQ ID NO: 3379)	LLIYAATSRA (SEQ ID NO: 3627)	QQSDESPL (SEQ ID NO: 3875)
365_D11	DSYGMN (SEQ ID NO: 2636)	WVSNINYNSGYTS (SEQ ID NO: 2884)	ARSANWHDTALD (SEQ ID NO: 3132)	VSYLNWY (SEQ ID NO: 3380)	LVIYAATSRA (SEQ ID NO: 3628)	QQSYSSPL (SEQ ID NO: 3876)
365_D12	DSYGMN (SEQ ID NO:	WVSNINYNGGYTG (SEQ ID NO: 2885)	ARSANWHDTALD (SEQ ID NO: 3133)	VTYLNWY (SEQ ID NO:	LVIYAATSRA (SEQ ID NO: 3629)	QQSYDTPL (SEQ ID NO:

	2637)			3381)		3877)
365_E01	SDYSMN (SEQ ID NO: 2638)	WVSGINYNSGYKG (SEQ ID NO: 2886)	ARSANWHDTALD (SEQ ID NO: 3134)	ISYLNWY (SEQ ID NO: 3382)	LLIYAATSRA (SEQ ID NO: 3630)	QQSYDSPL (SEQ ID NO: 3878)
365_E05	SSYGMH (SEQ ID NO: 2639)	WVAGINYNGGYTS (SEQ ID NO: 2887)	ARSANWHDTALD (SEQ ID NO: 3135)	VSYVNWY (SEQ ID NO: 3383)	LLIYAATSLA (SEQ ID NO: 3631)	QQSYDNPL (SEQ ID NO: 3879)
365_E07	DSYGMH (SEQ ID NO: 2640)	WVSGINYNSGYTS (SEQ ID NO: 2888)	AKSANWHDTHLD (SEQ ID NO: 3136)	LSYLNWY (SEQ ID NO: 3384)	LLIYAATSRA (SEQ ID NO: 3632)	QQSYDNPL (SEQ ID NO: 3880)
365_E09	SSYGMH (SEQ ID NO: 2641)	WVASINYNSGYKS (SEQ ID NO: 2889)	ARSANWHDTALD (SEQ ID NO: 3137)	LTYVNWY (SEQ ID NO: 3385)	LVIYAATSRA (SEQ ID NO: 3633)	QQSDDSPL (SEQ ID NO: 3881)
365_F01	DSYSMN (SEQ ID NO: 2642)	WVSGINYNSGYKG (SEQ ID NO: 2890)	ARSANWHDTHLD (SEQ ID NO: 3138)	VSYLNWY (SEQ ID NO: 3386)	LVIYAATSLA (SEQ ID NO: 3634)	QQSYELPL (SEQ ID NO: 3882)
365_F06	SSYGMN (SEQ ID NO: 2643)	WVAGINYNSGYKS (SEQ ID NO: 2891)	ARSANWHDTALD (SEQ ID NO: 3139)	LSYVNWY (SEQ ID NO: 3387)	LLIYAATSRA (SEQ ID NO: 3635)	QQSDNLPL (SEQ ID NO: 3883)
365_F12	SDYSMN (SEQ ID NO: 2644)	WVSGINYNGGYTS (SEQ ID NO: 2892)	ARSANWHDTHLD (SEQ ID NO: 3140)	LTYVNWY (SEQ ID NO: 3388)	LVIYAATSRH (SEQ ID NO: 3636)	QQSYETPL (SEQ ID NO: 3884)
365_G01	DSYGMN (SEQ ID NO: 2645)	WVAGINYNSGYKS (SEQ ID NO: 2893)	ARSANWHDTALD (SEQ ID NO: 3141)	LTYVNWY (SEQ ID NO: 3389)	LLIYATTSRA (SEQ ID NO: 3637)	QQSYDSPL (SEQ ID NO: 3885)
365_G11	SSYGMN (SEQ ID NO: 2646)	WVANINYNGGYTG (SEQ ID NO: 2894)	ARSANWHDTALD (SEQ ID NO: 3142)	ITYVNWY (SEQ ID NO: 3390)	LLIYAVTSRH (SEQ ID NO: 3638)	QQSYNSPL (SEQ ID NO: 3886)
365_H02	SDYGMN (SEQ ID NO: 2647)	WVSSINYNGGYTG (SEQ ID NO: 2895)	ARSANWHDTHLD (SEQ ID NO: 3143)	LTYLNWY (SEQ ID NO: 3391)	LLIYAATSRA (SEQ ID NO: 3639)	QQSYENPL (SEQ ID NO: 3887)
365_H03	DDYGMN (SEQ ID NO: 2648)	WVAGINYNGGYKS (SEQ ID NO: 2896)	ARSANWHDTALD (SEQ ID NO: 3144)	LSYVNWY (SEQ ID NO: 3392)	LVIYAATSLH (SEQ ID NO: 3640)	QQSYNNPL (SEQ ID NO: 3888)
365_H06	SSYGMN (SEQ ID NO: 2649)	WVSGINYNSGYTG (SEQ ID NO: 2897)	ARSANWHDTALD (SEQ ID NO: 3145)	SSYVNWY (SEQ ID NO: 3393)	LLIYAATSRA (SEQ ID NO: 3641)	QQSYSTPL (SEQ ID NO: 3889)
365_H10	DSYGMN (SEQ ID NO: 2650)	WVAGINYNSGYKS (SEQ ID NO: 2898)	ARSANWHDTHLD (SEQ ID NO: 3146)	VTYVNWY (SEQ ID NO: 3394)	LVIYAATSLA (SEQ ID NO: 3642)	QQSYNTPL (SEQ ID NO: 3890)
365_H11	SSYSMN (SEQ ID NO:	WVSGINYNSGYTG (SEQ ID NO: 2899)	ARSANWHDTALD (SEQ ID NO: 3147)	LTYLNWY (SEQ ID NO:	LLIYAATSRA (SEQ ID NO: 3643)	QQSYDSPL (SEQ ID NO:

	2651)			3395)		3891)
365_H12	SSYSMN (SEQ ID NO: 2652)	WVSNINYNGGYKS (SEQ ID NO: 2900)	ARSANWHDTHLD (SEQ ID NO: 3148)	ITYVNWY (SEQ ID NO: 3396)	LLIYAATSRA (SEQ ID NO: 3644)	QQSYSTPL (SEQ ID NO: 3892)
366_A07	SSYGMH (SEQ ID NO: 2653)	WVASINYNGGYTG (SEQ ID NO: 2901)	ARSANWHDTALD (SEQ ID NO: 3149)	VSYVNWY (SEQ ID NO: 3397)	LVIYAATSRH (SEQ ID NO: 3645)	QQSYESPL (SEQ ID NO: 3893)
366_B08	DSYGMN (SEQ ID NO: 2654)	WVSNINYNGGYKG (SEQ ID NO: 2902)	ARSANWHDTHLD (SEQ ID NO: 3150)	VSYLNWY (SEQ ID NO: 3398)	LLIYAATSRH (SEQ ID NO: 3646)	QQSYDNPL (SEQ ID NO: 3894)
366_B10	SSYGMN (SEQ ID NO: 2655)	WVSGINYNSGYTS (SEQ ID NO: 2903)	ARSANWHDTALD (SEQ ID NO: 3151)	ISYLNWY (SEQ ID NO: 3399)	LLIYAATSRA (SEQ ID NO: 3647)	QQSYDNPL (SEQ ID NO: 3895)
366_B12	SSYSMN (SEQ ID NO: 2656)	WVAGINYNSGYKG (SEQ ID NO: 2904)	ARSANWHDTALD (SEQ ID NO: 3152)	LTYVNWY (SEQ ID NO: 3400)	LLIYAATSRA (SEQ ID NO: 3648)	QQSYDNPL (SEQ ID NO: 3896)
366_D04	SSYSMN (SEQ ID NO: 2657)	WVSGINYNGGYTS (SEQ ID NO: 2905)	ARSANWHDTALD (SEQ ID NO: 3153)	SSYVNWY (SEQ ID NO: 3401)	LLIYATTSRA (SEQ ID NO: 3649)	QQSYETPL (SEQ ID NO: 3897)
366_E10	DSYGMN (SEQ ID NO: 2658)	WVSGINYNGGYKG (SEQ ID NO: 2906)	ARSANWHDTHLD (SEQ ID NO: 3154)	LSYVNWY (SEQ ID NO: 3402)	LVIYAATSRH (SEQ ID NO: 3650)	QQSYSLPL (SEQ ID NO: 3898)
366_F04	SDYGMN (SEQ ID NO: 2659)	WVSGINYNGGYTS (SEQ ID NO: 2907)	ARSANWHDTALD (SEQ ID NO: 3155)	LSYVNWY (SEQ ID NO: 3403)	LVIYATTSRH (SEQ ID NO: 3651)	QQSYESPL (SEQ ID NO: 3899)
366_F05	SSYSMN (SEQ ID NO: 2660)	WVANINYNSGYKS (SEQ ID NO: 2908)	ARSANWHDTHLD (SEQ ID NO: 3156)	LTYLNWY (SEQ ID NO: 3404)	LLIYAATSRA (SEQ ID NO: 3652)	QQSDNTPL (SEQ ID NO: 3900)
366_F07	SDYSMN (SEQ ID NO: 2661)	WVAGINYNSGYTS (SEQ ID NO: 2909)	ARSANWHDTHLD (SEQ ID NO: 3157)	ITYLNWY (SEQ ID NO: 3405)	LLIYAATSRA (SEQ ID NO: 3653)	QQSYETPL (SEQ ID NO: 3901)
366_G04	SSYSMN (SEQ ID NO: 2662)	WVSGINYNSGYTS (SEQ ID NO: 2910)	ARSANWHDTALD (SEQ ID NO: 3158)	ITYLNWY (SEQ ID NO: 3406)	LLIYAATSRA (SEQ ID NO: 3654)	QQSDDTPL (SEQ ID NO: 3902)
366_G05	DSYGMN (SEQ ID NO: 2663)	WVSNINYNGGYTS (SEQ ID NO: 2911)	ARSANWHDTALD (SEQ ID NO: 3159)	ISYVNWY (SEQ ID NO: 3407)	LVIYAATSRA (SEQ ID NO: 3655)	QQSYENPL (SEQ ID NO: 3903)
366_H06	SSYGMN (SEQ ID NO: 2664)	WVSSINYNGGYTG (SEQ ID NO: 2912)	ARSANWHDTALD (SEQ ID NO: 3160)	LSYLNWY (SEQ ID NO: 3408)	LLIYATTSRA (SEQ ID NO: 3656)	QQSYDTPL (SEQ ID NO: 3904)
366_H07	SSYGMH (SEQ ID NO:	WVSGINYNGGYTS (SEQ ID NO: 2913)	ARSANWHDTALD (SEQ ID NO: 3161)	ISYVNWY (SEQ ID NO:	LVIYAVTSRA (SEQ ID NO: 3657)	QQSYENPL (SEQ ID NO:

	2665)			3409)		3905)
366_H08	SDYGMN (SEQ ID NO: 2666)	WVASINYNSGYTS (SEQ ID NO: 2914)	ARSANWHDTHLD (SEQ ID NO: 3162)	LSYVNWY (SEQ ID NO: 3410)	LLIYAATSRH (SEQ ID NO: 3658)	QQSYNNPL (SEQ ID NO: 3906)
366_H09	DSYGMN (SEQ ID NO: 2667)	WVSNINYNSGYKG (SEQ ID NO: 2915)	ARSANWHDTALD (SEQ ID NO: 3163)	VSYVNWY (SEQ ID NO: 3411)	LVIYATTSRA (SEQ ID NO: 3659)	QQSYSSPL (SEQ ID NO: 3907)
367_A04	SSYSMN (SEQ ID NO: 2668)	WVSNINYNSGYKS (SEQ ID NO: 2916)	ARSANWHDTALD (SEQ ID NO: 3164)	ITYLNWY (SEQ ID NO: 3412)	LLIYAATSRA (SEQ ID NO: 3660)	QQSDDSPL (SEQ ID NO: 3908)
367_A05	SDYGMN (SEQ ID NO: 2669)	WVSSINYNGGYKG (SEQ ID NO: 2917)	ARSANWHDTALD (SEQ ID NO: 3165)	LSYLNWY (SEQ ID NO: 3413)	LVIYAVTSRA (SEQ ID NO: 3661)	QQSYDSPL (SEQ ID NO: 3909)
367_B02	DSYGMN (SEQ ID NO: 2670)	WVSSINYNGGYTS (SEQ ID NO: 2918)	ARSANWHDTALD (SEQ ID NO: 3166)	VTYLNWY (SEQ ID NO: 3414)	LLIYAASSLQ (SEQ ID NO: 3662)	QQSYSTPL (SEQ ID NO: 3910)
367_B03	SSYGMN (SEQ ID NO: 2671)	WVAGINYNGGYKS (SEQ ID NO: 2919)	ARSANWHDTALD (SEQ ID NO: 3167)	LTYLNWY (SEQ ID NO: 3415)	LLIYAATSLA (SEQ ID NO: 3663)	QQSYNLPL (SEQ ID NO: 3911)
367_B07	SDYSMN (SEQ ID NO: 2672)	WVAGINYNSGYTG (SEQ ID NO: 2920)	ARSANWHDTHLD (SEQ ID NO: 3168)	ISYVNWY (SEQ ID NO: 3416)	LLIYAATSLA (SEQ ID NO: 3664)	QQSYNLPL (SEQ ID NO: 3912)
367_B08	SDYGMN (SEQ ID NO: 2673)	WVSGINYNGGYKG (SEQ ID NO: 2921)	ARSANWHDTALD (SEQ ID NO: 3169)	LTYLNWY (SEQ ID NO: 3417)	LVIYAATSRA (SEQ ID NO: 3665)	QQSYDNPL (SEQ ID NO: 3913)
367_C01	DDYSMN (SEQ ID NO: 2674)	WVSGINYNGGYKS (SEQ ID NO: 2922)	ARSANWHDTHLD (SEQ ID NO: 3170)	LTYLNWY (SEQ ID NO: 3418)	LVIYATTSLH (SEQ ID NO: 3666)	QQSYDTPL (SEQ ID NO: 3914)
367_C05	DDYGMN (SEQ ID NO: 2675)	WVSSINYNGGYTG (SEQ ID NO: 2923)	ARSANWHDTHLD (SEQ ID NO: 3171)	LSYVNWY (SEQ ID NO: 3419)	LVIYAATSRH (SEQ ID NO: 3667)	QQSYDLPL (SEQ ID NO: 3915)
367_C11	DSYSMN (SEQ ID NO: 2676)	WVSSINYNSGYTG (SEQ ID NO: 2924)	ARSANWHDTHLD (SEQ ID NO: 3172)	LSYLNWY (SEQ ID NO: 3420)	LVIYAATSRH (SEQ ID NO: 3668)	QQSYNTPL (SEQ ID NO: 3916)
367_D10	DSYGMN (SEQ ID NO: 2677)	WVSNINYNGGYTS (SEQ ID NO: 2925)	ARSANWHDTALD (SEQ ID NO: 3173)	ISYLNWY (SEQ ID NO: 3421)	LVIYAATSRA (SEQ ID NO: 3669)	QQSYDTPL (SEQ ID NO: 3917)
367_E01	SSYGMN (SEQ ID NO: 2678)	WVAGINYNGGYKS (SEQ ID NO: 2926)	ARSANWHDTALD (SEQ ID NO: 3174)	LSYVNWY (SEQ ID NO: 3422)	LLIYATTSRA (SEQ ID NO: 3670)	QQSYDLPL (SEQ ID NO: 3918)
367_E04	SDYSMN (SEQ ID NO:	WVSSINYNGGYKG (SEQ ID NO: 2927)	ARSANWHDTHLD (SEQ ID NO: 3175)	LSYLNWY (SEQ ID NO:	LLIYAATSRA (SEQ ID NO: 3671)	QQSYESPL (SEQ ID NO:

	2679)			3423)		3919)
367_E06	DSYSMN (SEQ ID NO: 2680)	WVSSINYNSGYKG (SEQ ID NO: 2928)	ARSANWHDTHLD (SEQ ID NO: 3176)	SSYLNWY (SEQ ID NO: 3424)	LLIYAASSLQ (SEQ ID NO: 3672)	QQSYSTPL (SEQ ID NO: 3920)
367_E09	SDYGMN (SEQ ID NO: 2681)	WVASINYNSGYKG (SEQ ID NO: 2929)	ARSANWHDTALD (SEQ ID NO: 3177)	LSYLNWY (SEQ ID NO: 3425)	LVIYATTSRA (SEQ ID NO: 3673)	QQSYETPL (SEQ ID NO: 3921)
367_E11	DSYGMN (SEQ ID NO: 2682)	WVSSINYNSGYKG (SEQ ID NO: 2930)	ARSANWHDTHLD (SEQ ID NO: 3178)	VSYVNWY (SEQ ID NO: 3426)	LVIYAATSRH (SEQ ID NO: 3674)	QQSYDTPL (SEQ ID NO: 3922)
367_F03	SSYSMN (SEQ ID NO: 2683)	WVAGINYNSGYKS (SEQ ID NO: 2931)	ARSANWHDTALD (SEQ ID NO: 3179)	LSYVNWY (SEQ ID NO: 3427)	LVIYAATSLA (SEQ ID NO: 3675)	QQSDDTPL (SEQ ID NO: 3923)
367_F07	DSYGMH (SEQ ID NO: 2684)	WVANINYNGGYTG (SEQ ID NO: 2932)	ARSANWHDTALD (SEQ ID NO: 3180)	ISYVNWY (SEQ ID NO: 3428)	LLIYAATSRA (SEQ ID NO: 3676)	QQSYETPL (SEQ ID NO: 3924)
367_F11	SSYSMN (SEQ ID NO: 2685)	WVAGINYNSGYTG (SEQ ID NO: 2933)	ARSANWHDTHLD (SEQ ID NO: 3181)	SSYLNWY (SEQ ID NO: 3429)	LLIYAASSLQ (SEQ ID NO: 3677)	QQSYSTPL (SEQ ID NO: 3925)
367_G05	SDYGMN (SEQ ID NO: 2686)	WVANINYNGGYTS (SEQ ID NO: 2934)	ARSANWHDTALD (SEQ ID NO: 3182)	VSYLNWY (SEQ ID NO: 3430)	LVIYAATSLA (SEQ ID NO: 3678)	QQSYDTPL (SEQ ID NO: 3926)
367_G06	SSYGMN (SEQ ID NO: 2687)	WVSGINYNSGYKS (SEQ ID NO: 2935)	ARSANWHDTHLD (SEQ ID NO: 3183)	LTYVNWY (SEQ ID NO: 3431)	LLIYATTSLH (SEQ ID NO: 3679)	QQSYDTPL (SEQ ID NO: 3927)
367_G10	DDYGMN (SEQ ID NO: 2688)	WVSGINYNGGYTS (SEQ ID NO: 2936)	ARSANWHDTALD (SEQ ID NO: 3184)	ISYVNWY (SEQ ID NO: 3432)	LLIYAATSRA (SEQ ID NO: 3680)	QQSYDSPL (SEQ ID NO: 3928)
367_H06	SSYGMN (SEQ ID NO: 2689)	WVSNINYNGGYTG (SEQ ID NO: 2937)	ARSANWHDTHLD (SEQ ID NO: 3185)	ITYLNWY (SEQ ID NO: 3433)	LLIYAATSRA (SEQ ID NO: 3681)	QQSYDTPL (SEQ ID NO: 3929)
367_H11	SSYGMN (SEQ ID NO: 2690)	WVAGINYNGGYKG (SEQ ID NO: 2938)	ARSANWHDTALD (SEQ ID NO: 3186)	ISYVNWY (SEQ ID NO: 3434)	LVIYAATSRA (SEQ ID NO: 3682)	QQSYNSPL (SEQ ID NO: 3930)
368_A01	SSYGMN (SEQ ID NO: 2691)	WVSNINYNGGYTS (SEQ ID NO: 2939)	ARSANWHDTALD (SEQ ID NO: 3187)	ISYLNWY (SEQ ID NO: 3435)	LLIYAATSRH (SEQ ID NO: 3683)	QQSYDNPL (SEQ ID NO: 3931)
368_A05	SSYSMN (SEQ ID NO: 2692)	WVAGINYNSGYTG (SEQ ID NO: 2940)	ARSANWHDTALD (SEQ ID NO: 3188)	VSYLNWY (SEQ ID NO: 3436)	LVIYAATSRA (SEQ ID NO: 3684)	QQSYDSPL (SEQ ID NO: 3932)
368_A07	SSYSMN (SEQ ID NO:	WVAGINYNSGYTS (SEQ ID NO: 2941)	ARSANWHDTHLD (SEQ ID NO: 3189)	LTYLNWY (SEQ ID NO:	LVIYATTSRA (SEQ ID NO: 3685)	QQSNELPL (SEQ ID NO:

	2693)			3437)		3933)
368_A09	DSYSMN (SEQ ID NO: 2694)	WVSGINYNGGYTS (SEQ ID NO: 2942)	ARSANWHDTHLD (SEQ ID NO: 3190)	LSYVNWY (SEQ ID NO: 3438)	LLIYAVTSRA (SEQ ID NO: 3686)	QQSYDSPL (SEQ ID NO: 3934)
368_B01	SSYGMN (SEQ ID NO: 2695)	WVSGINYNSGYKS (SEQ ID NO: 2943)	ARSANWHDTALD (SEQ ID NO: 3191)	SSYLNWY (SEQ ID NO: 3439)	LLIYAATSRA (SEQ ID NO: 3687)	QQSYETPL (SEQ ID NO: 3935)
368_B06	DSYGMH (SEQ ID NO: 2696)	WVSGINYNSGYTS (SEQ ID NO: 2944)	ARSANWHDTALD (SEQ ID NO: 3192)	ISYLNWY (SEQ ID NO: 3440)	LLIYAASSLQ (SEQ ID NO: 3688)	QQSYSTPL (SEQ ID NO: 3936)
368_B07	SDYSMN (SEQ ID NO: 2697)	WVSNINYNGGYKS (SEQ ID NO: 2945)	ARSANWHDTALD (SEQ ID NO: 3193)	VSYLNWY (SEQ ID NO: 3441)	LLIYAATSLA (SEQ ID NO: 3689)	QQSYSSPL (SEQ ID NO: 3937)
368_C05	DSYGMN (SEQ ID NO: 2698)	WVSGINYNSGYTS (SEQ ID NO: 2946)	ARSANWHDTALD (SEQ ID NO: 3194)	LSYLNWY (SEQ ID NO: 3442)	LVIYAATSRA (SEQ ID NO: 3690)	QQSDSNPL (SEQ ID NO: 3938)
368_D01	SSYGMH (SEQ ID NO: 2699)	WVANINYNGGYTS (SEQ ID NO: 2947)	ARSANWHDTALD (SEQ ID NO: 3195)	LSYLNWY (SEQ ID NO: 3443)	LVIYAATSRA (SEQ ID NO: 3691)	QQSDSTPL (SEQ ID NO: 3939)
368_D04	SSYGMN (SEQ ID NO: 2700)	WVSGINYNGGYKS (SEQ ID NO: 2948)	ARSANWHDTALD (SEQ ID NO: 3196)	STYVNWY (SEQ ID NO: 3444)	LVIYAVTSRH (SEQ ID NO: 3692)	QQSYDSPL (SEQ ID NO: 3940)
368_D05	SSYSMN (SEQ ID NO: 2701)	WVSGINYNGGYTS (SEQ ID NO: 2949)	ARSANWHDTALD (SEQ ID NO: 3197)	LTYLNWY (SEQ ID NO: 3445)	LVIYAATSRA (SEQ ID NO: 3693)	QQSDDSPL (SEQ ID NO: 3941)
368_D11	DDYGMN (SEQ ID NO: 2702)	WVSNINYNGGYKS (SEQ ID NO: 2950)	ARSANWHDTALD (SEQ ID NO: 3198)	LTYLNWY (SEQ ID NO: 3446)	LVIYAATSRA (SEQ ID NO: 3694)	QQSYDLPL (SEQ ID NO: 3942)
368_E01	SSYSMN (SEQ ID NO: 2703)	WVASINYNSGYTG (SEQ ID NO: 2951)	ARSANWHDTHLD (SEQ ID NO: 3199)	LSYLNWY (SEQ ID NO: 3447)	LLIYAVTSRH (SEQ ID NO: 3695)	QQSYSLPL (SEQ ID NO: 3943)
368_E02	DSYSMN (SEQ ID NO: 2704)	WVAGINYNSGYTS (SEQ ID NO: 2952)	ARSANWHDTHLD (SEQ ID NO: 3200)	LTYLNWY (SEQ ID NO: 3448)	LLIYAATSRA (SEQ ID NO: 3696)	QQSYSSPL (SEQ ID NO: 3944)
368_E04	SSYSMN (SEQ ID NO: 2705)	WVANINYNSGYTG (SEQ ID NO: 2953)	ARSANWHDTALD (SEQ ID NO: 3201)	LSYVNWY (SEQ ID NO: 3449)	LLIYAATSRH (SEQ ID NO: 3697)	QQSYDNPL (SEQ ID NO: 3945)
368_E06	SDYGMH (SEQ ID NO: 2706)	WVSGINYNGGYTG (SEQ ID NO: 2954)	ARSANWHDTALD (SEQ ID NO: 3202)	LSYLNWY (SEQ ID NO: 3450)	LVIYGATSRA (SEQ ID NO: 3698)	QQSYDSPL (SEQ ID NO: 3946)
368_E07	SSYGMN (SEQ ID NO:	WVAGINYNGGYTS (SEQ ID NO: 2955)	AKSANWHDTALD (SEQ ID NO: 3203)	LSYLNWY (SEQ ID NO:	LLIYAVTSRA (SEQ ID NO: 3699)	QQSYENPL (SEQ ID NO:

	2707)			3451)		3947)
368_F03	DSYSMN (SEQ ID NO: 2708)	WVAGINYNSGYTG (SEQ ID NO: 2956)	AKSANWHDTALD (SEQ ID NO: 3204)	ISYLNWY (SEQ ID NO: 3452)	LVIYAATSRH (SEQ ID NO: 3700)	QQSYDSPL (SEQ ID NO: 3948)
368_F11	SDYGMN (SEQ ID NO: 2709)	WVSGINYNGGYTS (SEQ ID NO: 2957)	ARSANWHDTHLD (SEQ ID NO: 3205)	VSYVNWY (SEQ ID NO: 3453)	LVIYAATSRA (SEQ ID NO: 3701)	QQSYNNPL (SEQ ID NO: 3949)
368_G01	SDYGMH (SEQ ID NO: 2710)	WVASINYNSGYTS (SEQ ID NO: 2958)	ARSANWHDTALD (SEQ ID NO: 3206)	LTYLNWY (SEQ ID NO: 3454)	LVIYAATSRA (SEQ ID NO: 3702)	QQSYNLPL (SEQ ID NO: 3950)
368_G12	SSYGMN (SEQ ID NO: 2711)	WVASINYNSGYTG (SEQ ID NO: 2959)	ARSANWHDTALD (SEQ ID NO: 3207)	SSYVNWY (SEQ ID NO: 3455)	LVIYAVTSRA (SEQ ID NO: 3703)	QQSYETPL (SEQ ID NO: 3951)
368_H04	SSYSMN (SEQ ID NO: 2712)	WVAGINYNSGYKG (SEQ ID NO: 2960)	AKSANWHDTHLD (SEQ ID NO: 3208)	VSYVNWY (SEQ ID NO: 3456)	LLIYAATSRA (SEQ ID NO: 3704)	QQSYDSPL (SEQ ID NO: 3952)
369_A02	SSYSMN (SEQ ID NO: 2713)	WVAGINYNSGYTG (SEQ ID NO: 2961)	ARSANWHDTHLD (SEQ ID NO: 3209)	LSYVNWY (SEQ ID NO: 3457)	LLIYAATSRA (SEQ ID NO: 3705)	QQSYDLPL (SEQ ID NO: 3953)
369_A03	SSYGMN (SEQ ID NO: 2714)	WVSNINYNGGYTG (SEQ ID NO: 2962)	ARSANWHDTALD (SEQ ID NO: 3210)	LTYLNWY (SEQ ID NO: 3458)	LLIYAVTSRH (SEQ ID NO: 3706)	QQGYDLPL (SEQ ID NO: 3954)
369_B01	SSYSMN (SEQ ID NO: 2715)	WVSGINYNGGYTS (SEQ ID NO: 2963)	ARSANWHDTALD (SEQ ID NO: 3211)	LSYLNWY (SEQ ID NO: 3459)	LLIYAVTSRA (SEQ ID NO: 3707)	QQSYENPL (SEQ ID NO: 3955)
369_C02	DSYSMN (SEQ ID NO: 2716)	WVSNINYNGGYKS (SEQ ID NO: 2964)	ARSANWHDTALD (SEQ ID NO: 3212)	LTYLNWY (SEQ ID NO: 3460)	LVIYAATSRA (SEQ ID NO: 3708)	QQSYELPL (SEQ ID NO: 3956)
369_C03	SSYGMN (SEQ ID NO: 2717)	WVSNINYNGGYKS (SEQ ID NO: 2965)	ARSANWHDTALD (SEQ ID NO: 3213)	LTYLNWY (SEQ ID NO: 3461)	LVIYAATSRA (SEQ ID NO: 3709)	QQSYDSPL (SEQ ID NO: 3957)
369_C04	SSYSMN (SEQ ID NO: 2718)	WVSNINYNGGYTG (SEQ ID NO: 2966)	ARSANWHDTALD (SEQ ID NO: 3214)	LTYVNWY (SEQ ID NO: 3462)	LLIYTTTSLH (SEQ ID NO: 3710)	QQSYNNPL (SEQ ID NO: 3958)
369_D01	SDYGMN (SEQ ID NO: 2719)	WVASINYNGGYTG (SEQ ID NO: 2967)	ARSANWHDTALD (SEQ ID NO: 3215)	LTYLNWY (SEQ ID NO: 3463)	LLIYAATSRA (SEQ ID NO: 3711)	QQSYSNPL (SEQ ID NO: 3959)
369_D02	SDYSMN (SEQ ID NO: 2720)	WVSNINYNSGYTG (SEQ ID NO: 2968)	ARSANWHDTALD (SEQ ID NO: 3216)	LSYLNWY (SEQ ID NO: 3464)	LVIYAVTSRA (SEQ ID NO: 3712)	QQSYDTPL (SEQ ID NO: 3960)
369_D04	DSYGMN (SEQ ID NO:	WVSGINYNGGYTS (SEQ ID NO: 2969)	ARSANWHDTALD (SEQ ID NO: 3217)	LSYVNWY (SEQ ID NO:	LVIYAATSRA (SEQ ID NO: 3713)	QQSYNLPL (SEQ ID NO:

	2721)			3465)		3961)
369_D12	DSYSMN (SEQ ID NO: 2722)	WVAGINYNSGYTS (SEQ ID NO: 2970)	ARSANWHDTALD (SEQ ID NO: 3218)	LSYLNWY (SEQ ID NO: 3466)	LLIYAATSLA (SEQ ID NO: 3714)	QQSYDTPL (SEQ ID NO: 3962)
369_E02	DSYGMN (SEQ ID NO: 2723)	WVSNINYNGGYTG (SEQ ID NO: 2971)	ARSANWHDTALD (SEQ ID NO: 3219)	VSYVNWY (SEQ ID NO: 3467)	LLIYATTSRH (SEQ ID NO: 3715)	QQSYDNPL (SEQ ID NO: 3963)
369_E11	SSYGMN (SEQ ID NO: 2724)	WVSNINYNGGYTS (SEQ ID NO: 2972)	ARSANWHDTALD (SEQ ID NO: 3220)	ISYLNWY (SEQ ID NO: 3468)	LLIYAATSLA (SEQ ID NO: 3716)	QQSYDTPL (SEQ ID NO: 3964)
369_E12	SSYGMH (SEQ ID NO: 2725)	WVASINYNSGYTS (SEQ ID NO: 2973)	ARSANWHDTALD (SEQ ID NO: 3221)	ISYLNWY (SEQ ID NO: 3469)	LLIYAATSRA (SEQ ID NO: 3717)	QQSYESPL (SEQ ID NO: 3965)
369_F01	SSYGMN (SEQ ID NO: 2726)	WVSGINYNGGYKS (SEQ ID NO: 2974)	ARSANWHDTALD (SEQ ID NO: 3222)	LTYVNWY (SEQ ID NO: 3470)	LLIYAATSRA (SEQ ID NO: 3718)	QQSYELPL (SEQ ID NO: 3966)
369_F02	SSYGMN (SEQ ID NO: 2727)	WVASINYNSGYKS (SEQ ID NO: 2975)	ARSANWHDTALD (SEQ ID NO: 3223)	VSYLNWY (SEQ ID NO: 3471)	LVIYAATSRA (SEQ ID NO: 3719)	QQSYDTPL (SEQ ID NO: 3967)
369_F03	SDYGMN (SEQ ID NO: 2728)	WVSGINYNSGYTS (SEQ ID NO: 2976)	ARSANWHDTALD (SEQ ID NO: 3224)	VSYVNWY (SEQ ID NO: 3472)	LLIYAATSLA (SEQ ID NO: 3720)	QQSYDSPL (SEQ ID NO: 3968)
369_F06	DDYSMN (SEQ ID NO: 2729)	WVAGINYNGGYKG (SEQ ID NO: 2977)	ARSANWHDTALD (SEQ ID NO: 3225)	VSYVNWY (SEQ ID NO: 3473)	LVIYAATSRA (SEQ ID NO: 3721)	QQSYDSPL (SEQ ID NO: 3969)
369_F10	DSYGMN (SEQ ID NO: 2730)	WVSNINYNSGYKS (SEQ ID NO: 2978)	ARSANWHDTALD (SEQ ID NO: 3226)	VTYLNWY (SEQ ID NO: 3474)	LLIYAVTSRA (SEQ ID NO: 3722)	QQSYDLPL (SEQ ID NO: 3970)
369_F11	DSYGMN (SEQ ID NO: 2731)	WVSNINYNSGYKS (SEQ ID NO: 2979)	ARSANWHDTALD (SEQ ID NO: 3227)	ISYLNWY (SEQ ID NO: 3475)	LLIYAATSRA (SEQ ID NO: 3723)	QQSYDLPL (SEQ ID NO: 3971)
369_G01	SSYSMN (SEQ ID NO: 2732)	WVSNINYNSGYKS (SEQ ID NO: 2980)	ARSANWHDTALD (SEQ ID NO: 3228)	LSYVNWY (SEQ ID NO: 3476)	LLIYAATSRA (SEQ ID NO: 3724)	QQSYSSPL (SEQ ID NO: 3972)
369_G04	DSYSMN (SEQ ID NO: 2733)	WVSGINYNGGYTS (SEQ ID NO: 2981)	ARSANWHDTALD (SEQ ID NO: 3229)	LTYVNWY (SEQ ID NO: 3477)	LLIYATTSRH (SEQ ID NO: 3725)	QQSYETPL (SEQ ID NO: 3973)
369_G06	DSYGMN (SEQ ID NO: 2734)	WVAGINYNGGYTS (SEQ ID NO: 2982)	ARSANWHDTALD (SEQ ID NO: 3230)	LSYVNWY (SEQ ID NO: 3478)	LVIYAATSRA (SEQ ID NO: 3726)	QQSYENPL (SEQ ID NO: 3974)
369_G11	SSYSMN (SEQ ID NO:	WVANINYNSGYKG (SEQ ID NO: 2983)	ARSANWHDTALD (SEQ ID NO: 3231)	LTYLNWY (SEQ ID NO:	LLIYAATSLA (SEQ ID NO: 3727)	QQSYESPL (SEQ ID NO:

	2735)			3479)		3975)
369_G12	SSYSMN (SEQ ID NO: 2736)	WVANINYNGGYTG (SEQ ID NO: 2984)	ARSANWHDTALD (SEQ ID NO: 3232)	LTYVNWY (SEQ ID NO: 3480)	LVIYAATSRH (SEQ ID NO: 3728)	QQSDNTPL (SEQ ID NO: 3976)
369_H05	SSYGMN (SEQ ID NO: 2737)	WVANINYNGGYTG (SEQ ID NO: 2985)	ARSANWHDTALD (SEQ ID NO: 3233)	VSYVNWY (SEQ ID NO: 3481)	LLIYAATSRA (SEQ ID NO: 3729)	QQSYSNPL (SEQ ID NO: 3977)
369_H06	SSYGMN (SEQ ID NO: 2738)	WVANINYNGGYKS (SEQ ID NO: 2986)	ARSANWHDTALD (SEQ ID NO: 3234)	VSYVNWY (SEQ ID NO: 3482)	LLIYAATSRA (SEQ ID NO: 3730)	QQSYDTPL (SEQ ID NO: 3978)
369_H09	DDYSMN (SEQ ID NO: 2739)	WVSGINYNGGYTS (SEQ ID NO: 2987)	ARSANWHDTALD (SEQ ID NO: 3235)	LSYVNWY (SEQ ID NO: 3483)	LLIYAVTSLA (SEQ ID NO: 3731)	QQSYESPL (SEQ ID NO: 3979)
370_A01	SSYSMN (SEQ ID NO: 2740)	WVSGINYNSGYKS (SEQ ID NO: 2988)	ARSANWHDTALD (SEQ ID NO: 3236)	STYLNWY (SEQ ID NO: 3484)	LVIYAATSRA (SEQ ID NO: 3732)	QQSYNLPL (SEQ ID NO: 3980)
370_A03	SSYSMN (SEQ ID NO: 2741)	WVSNINYNGGYTS (SEQ ID NO: 2989)	ARSANWHDTALD (SEQ ID NO: 3237)	LSYLNWY (SEQ ID NO: 3485)	LLIYAATSRA (SEQ ID NO: 3733)	QQSYDSPL (SEQ ID NO: 3981)
370_A04	DSYSMN (SEQ ID NO: 2742)	WVSGINYNGGYTS (SEQ ID NO: 2990)	ARSANWHDTALD (SEQ ID NO: 3238)	ITYLNWY (SEQ ID NO: 3486)	LLIYAATSRA (SEQ ID NO: 3734)	QQSYDNPL (SEQ ID NO: 3982)
370_A12	SSYGMN (SEQ ID NO: 2743)	WVAGINYNGGYTS (SEQ ID NO: 2991)	ARSANWHDTALD (SEQ ID NO: 3239)	LTYLNWY (SEQ ID NO: 3487)	LLIYAATSLA (SEQ ID NO: 3735)	QQSYDSPL (SEQ ID NO: 3983)
370_C01	DSYSMN (SEQ ID NO: 2744)	WVSGINYNSGYTG (SEQ ID NO: 2992)	ARSANWHDTALD (SEQ ID NO: 3240)	LTYLNWY (SEQ ID NO: 3488)	LVIYAATSLA (SEQ ID NO: 3736)	QQSYDTPL (SEQ ID NO: 3984)
370_C03	SSYGMN (SEQ ID NO: 2745)	WVAGINYNGGYKG (SEQ ID NO: 2993)	ARSANWHDTALD (SEQ ID NO: 3241)	LTYLNWY (SEQ ID NO: 3489)	LLIYYVTNRQ (SEQ ID NO: 3737)	QQSYSSPL (SEQ ID NO: 3985)
370_C05	SSYSMN (SEQ ID NO: 2746)	WVAGINYNSGYTG (SEQ ID NO: 2994)	ARSANWHDTALD (SEQ ID NO: 3242)	LSYVNWY (SEQ ID NO: 3490)	LVIYAATSRA (SEQ ID NO: 3738)	QQSYNSPL (SEQ ID NO: 3986)
370_C08	SSYGMN (SEQ ID NO: 2747)	WVAGINYNGGYKG (SEQ ID NO: 2995)	ARSANWHDTALD (SEQ ID NO: 3243)	SNYLNWY (SEQ ID NO: 3491)	LLIYAVTSRA (SEQ ID NO: 3739)	QQSYDSPL (SEQ ID NO: 3987)
370_C09	DSYGMN (SEQ ID NO: 2748)	WVSGINYNGGYTS (SEQ ID NO: 2996)	ARSANWHDTALD (SEQ ID NO: 3244)	ISYLNWY (SEQ ID NO: 3492)	LVIYAATSLA (SEQ ID NO: 3740)	QQSYSTPL (SEQ ID NO: 3988)
370_D04	DSYSMN (SEQ ID NO:	WVANINYNSGYKG (SEQ ID NO: 2997)	ARSANWHDTALD (SEQ ID NO: 3245)	LTYLNWY (SEQ ID NO:	LVIYAATSRA (SEQ ID NO: 3741)	QQSYDNPL (SEQ ID NO:

	2749)			3493)		3989)
370_D11	DSYSMN (SEQ ID NO: 2750)	WVSGINYNGGYTG (SEQ ID NO: 2998)	ARSANWHDTALD (SEQ ID NO: 3246)	VSYLNWY (SEQ ID NO: 3494)	LLIYAATSRA (SEQ ID NO: 3742)	QQSYDTPL (SEQ ID NO: 3990)
370_E03	SSYGMN (SEQ ID NO: 2751)	WVSSINYNGGYKG (SEQ ID NO: 2999)	ARSANWHDTALD (SEQ ID NO: 3247)	LTYLNWY (SEQ ID NO: 3495)	LVIYYASNRA (SEQ ID NO: 3743)	QQSYDSPL (SEQ ID NO: 3991)
370_E06	SSYGMN (SEQ ID NO: 2752)	WVSGINYNSGYKS (SEQ ID NO: 3000)	ARSANWHDTALD (SEQ ID NO: 3248)	LSYLNWY (SEQ ID NO: 3496)	LVIYATTSLA (SEQ ID NO: 3744)	QQSYDTPL (SEQ ID NO: 3992)
370_E09	DDSSMH (SEQ ID NO: 2753)	WVSNINYNGGYTG (SEQ ID NO: 3001)	AKSANWHDTALD (SEQ ID NO: 3249)	LSYVNWY (SEQ ID NO: 3497)	LVIYAATSRA (SEQ ID NO: 3745)	QQSYELPL (SEQ ID NO: 3993)
370_F05	SSYGMN (SEQ ID NO: 2754)	WVSGINYNSGYTS (SEQ ID NO: 3002)	ARSANWHDTALD (SEQ ID NO: 3250)	VSYVNWY (SEQ ID NO: 3498)	LVIYAATSRA (SEQ ID NO: 3746)	QQSYETPL (SEQ ID NO: 3994)
370_F07	DSYSMN (SEQ ID NO: 2755)	WVSNINYNGGYKG (SEQ ID NO: 3003)	ARSANWHDTALD (SEQ ID NO: 3251)	LSYLNWY (SEQ ID NO: 3499)	LLIYAATSRA (SEQ ID NO: 3747)	QQSYNLPL (SEQ ID NO: 3995)
370_F10	SSYSMN (SEQ ID NO: 2756)	WVAGINYNGGYTS (SEQ ID NO: 3004)	ARSANWHDTALD (SEQ ID NO: 3252)	VSYLNWY (SEQ ID NO: 3500)	LVIYAATSRA (SEQ ID NO: 3748)	QQSYNSPL (SEQ ID NO: 3996)
370_G02	SDYSMN (SEQ ID NO: 2757)	WVANINYNGGYKG (SEQ ID NO: 3005)	ARSANWHDTALD (SEQ ID NO: 3253)	VSYLNWY (SEQ ID NO: 3501)	LLIYAATSRH (SEQ ID NO: 3749)	QQSYDSPL (SEQ ID NO: 3997)
370_G03	SSYSMN (SEQ ID NO: 2758)	WVANINYNGGYTG (SEQ ID NO: 3006)	ARSANWHDTALD (SEQ ID NO: 3254)	LTYVNWY (SEQ ID NO: 3502)	LVIYATTSRA (SEQ ID NO: 3750)	QQSYNNPL (SEQ ID NO: 3998)
370_G06	SDYGMH (SEQ ID NO: 2759)	WVSSINYNGGYTS (SEQ ID NO: 3007)	ARSANWHDTALD (SEQ ID NO: 3255)	LSYVNWY (SEQ ID NO: 3503)	LVIYAATSRA (SEQ ID NO: 3751)	QQSDNTPL (SEQ ID NO: 3999)
370_G09	SSYGMN (SEQ ID NO: 2760)	WVAGINYNGGYKS (SEQ ID NO: 3008)	ARSANWHDTALD (SEQ ID NO: 3256)	LSYVNWY (SEQ ID NO: 3504)	LVIYAATSRA (SEQ ID NO: 3752)	QQSYESPL (SEQ ID NO: 4000)
370_G10	SDYGMN (SEQ ID NO: 2761)	WVSGINYNSGYTS (SEQ ID NO: 3009)	ARSANWHDTALD (SEQ ID NO: 3257)	SSYLNWY (SEQ ID NO: 3505)	LLIYVVNNRA (SEQ ID NO: 3753)	QQSYENPL (SEQ ID NO: 4001)
370_G11	SSYSMN (SEQ ID NO: 2762)	WVASINYNSGYTS (SEQ ID NO: 3010)	ARSANWHDTHLD (SEQ ID NO: 3258)	VSYLNWY (SEQ ID NO: 3506)	LVIYAATSRA (SEQ ID NO: 3754)	QQSYSLPL (SEQ ID NO: 4002)
370_H01	SSYSMN (SEQ ID NO:	WVSGINYNSGYKG (SEQ ID NO: 3011)	ARSANWHDTALD (SEQ ID NO: 3259)	ISYLNWY (SEQ ID NO:	LLIYAVTSRA (SEQ ID NO: 3755)	QQSYDTPL (SEQ ID NO:

	2763)			3507)		4003)
370_H09	SSYGMN (SEQ ID NO: 2764)	WVANINYNGGYTS (SEQ ID NO: 3012)	ARSANWHDTALD (SEQ ID NO: 3260)	VSYVNWY (SEQ ID NO: 3508)	LLIYAATSRA (SEQ ID NO: 3756)	QQSYDNPL (SEQ ID NO: 4004)
371_A03	SDYGMN (SEQ ID NO: 2765)	WVANINYNGGYTG (SEQ ID NO: 3013)	ARSANWHDTALD (SEQ ID NO: 3261)	LSYLNWY (SEQ ID NO: 3509)	LVIYATTSRA (SEQ ID NO: 3757)	QQSYESPL (SEQ ID NO: 4005)
371_A06	SSYGMN (SEQ ID NO: 2766)	WVAGINYNGGYTS (SEQ ID NO: 3014)	ARSANWHDTALD (SEQ ID NO: 3262)	LTYLNWY (SEQ ID NO: 3510)	LVIYAATSRH (SEQ ID NO: 3758)	QQSYDSPL (SEQ ID NO: 4006)
371_A07	SDYSMN (SEQ ID NO: 2767)	WVSNINYNGGYKS (SEQ ID NO: 3015)	ARSANWHDTALD (SEQ ID NO: 3263)	LSYLNWY (SEQ ID NO: 3511)	LVIYATTSRA (SEQ ID NO: 3759)	QQSYDLPL (SEQ ID NO: 4007)
371_A08	SSYGMH (SEQ ID NO: 2768)	WVSSINYNGGYTS (SEQ ID NO: 3016)	ARSANWHDTALD (SEQ ID NO: 3264)	LSYLNWY (SEQ ID NO: 3512)	LVIYAATSRA (SEQ ID NO: 3760)	QQSYELPL (SEQ ID NO: 4008)
371_A12	DSYSMN (SEQ ID NO: 2769)	WVAGINYNSGYTS (SEQ ID NO: 3017)	ARSANWHDTALD (SEQ ID NO: 3265)	LSYVNWY (SEQ ID NO: 3513)	LVIYAATSLA (SEQ ID NO: 3761)	QQSYDTPL (SEQ ID NO: 4009)
371_B06	DSYSMN (SEQ ID NO: 2770)	WVAGINYNGGYKS (SEQ ID NO: 3018)	ARSANWHDTALD (SEQ ID NO: 3266)	LTYVNWY (SEQ ID NO: 3514)	LVIYAATSRH (SEQ ID NO: 3762)	QQSYNLPL (SEQ ID NO: 4010)
371_B07	DSYSMN (SEQ ID NO: 2771)	WVAGINYNGGYTS (SEQ ID NO: 3019)	ARSANWHDTALD (SEQ ID NO: 3267)	LTYVNWY (SEQ ID NO: 3515)	LLIYAATSRA (SEQ ID NO: 3763)	QQSYELPL (SEQ ID NO: 4011)
371_C03	SSYSMN (SEQ ID NO: 2772)	WVSNINYNGGYKG (SEQ ID NO: 3020)	ARSANWHDTALD (SEQ ID NO: 3268)	LSYLNWY (SEQ ID NO: 3516)	LVIYATTSRA (SEQ ID NO: 3764)	QQSYSTPL (SEQ ID NO: 4012)
371_D06	DDYSMN (SEQ ID NO: 2773)	WVAGINYNGGYTS (SEQ ID NO: 3021)	ARSANWHDTALD (SEQ ID NO: 3269)	ISYVNWY (SEQ ID NO: 3517)	LLIYAATSRA (SEQ ID NO: 3765)	QQSYSTPL (SEQ ID NO: 4013)
371_D09	SSYSMN (SEQ ID NO: 2774)	WVSNINYNSGYTG (SEQ ID NO: 3022)	ARSANWHDTALD (SEQ ID NO: 3270)	LTYLNWY (SEQ ID NO: 3518)	LVIYAATSRA (SEQ ID NO: 3766)	QQSYNNPL (SEQ ID NO: 4014)
371_F01	SSYSMN (SEQ ID NO: 2775)	WVAGINYNGGYTG (SEQ ID NO: 3023)	ARSANWHDTALD (SEQ ID NO: 3271)	LTYVNWY (SEQ ID NO: 3519)	LVIYAATSLA (SEQ ID NO: 3767)	QQSYNNPL (SEQ ID NO: 4015)
371_F04	DSYSMN (SEQ ID NO: 2776)	WVAGINYNSGYKG (SEQ ID NO: 3024)	ARSANWHDTALD (SEQ ID NO: 3272)	LSYLNWY (SEQ ID NO: 3520)	LLIYAATSRH (SEQ ID NO: 3768)	QQSYNNPL (SEQ ID NO: 4016)
371_F06	DSYSMN (SEQ ID NO:	WVANINYNGGYTS (SEQ ID NO: 3025)	ARSANWHDTALD (SEQ ID NO: 3273)	VSYLNWY (SEQ ID NO:	LVIYAATSRH (SEQ ID NO: 3769)	QQSYNSPL (SEQ ID NO:

	2777)			3521)		4017)
371_F08	DDYSMN (SEQ ID NO: 2778)	WVSGINYNGGYTG (SEQ ID NO: 3026)	ARSANWHDTALD (SEQ ID NO: 3274)	VSYVNWY (SEQ ID NO: 3522)	LVIYAATSRH (SEQ ID NO: 3770)	QQSYESPL (SEQ ID NO: 4018)
371_G05	DSYSMN (SEQ ID NO: 2779)	WVSGINYNSGYTG (SEQ ID NO: 3027)	ARSANWHDTALD (SEQ ID NO: 3275)	SSYLNWY (SEQ ID NO: 3523)	LLIYAVTSRA (SEQ ID NO: 3771)	QQSYSSPL (SEQ ID NO: 4019)
371_G10	SSYSMN (SEQ ID NO: 2780)	WVSGINYNGGYKS (SEQ ID NO: 3028)	ARSANWHDTALD (SEQ ID NO: 3276)	SSYVNWY (SEQ ID NO: 3524)	LLIYAATSRH (SEQ ID NO: 3772)	QQSDDSPL (SEQ ID NO: 4020)
371_H09	DSYSMN (SEQ ID NO: 2781)	WVSNINYNGGYTS (SEQ ID NO: 3029)	ARSANWHDTALD (SEQ ID NO: 3277)	LTYVNWY (SEQ ID NO: 3525)	LVIYAATSLA (SEQ ID NO: 3773)	QQSYDSPL (SEQ ID NO: 4021)
372_A04	DSYSMN (SEQ ID NO: 2782)	WVSGINYNSGYTS (SEQ ID NO: 3030)	ARSANWHDTALD (SEQ ID NO: 3278)	LTYLNWY (SEQ ID NO: 3526)	LVIYAATSRA (SEQ ID NO: 3774)	QQSYETPL (SEQ ID NO: 4022)
372_B04	DSYGMN (SEQ ID NO: 2783)	WVANINYNGGYTS (SEQ ID NO: 3031)	ARSANWHDTALD (SEQ ID NO: 3279)	LSYVNWY (SEQ ID NO: 3527)	LVIYAATSLA (SEQ ID NO: 3775)	QQSYDSPL (SEQ ID NO: 4023)
372_C07	SDYSMN (SEQ ID NO: 2784)	WVSNINYNSGYTS (SEQ ID NO: 3032)	ARSANWHDTHLD (SEQ ID NO: 3280)	LSYLNWY (SEQ ID NO: 3528)	LVIYAATSRH (SEQ ID NO: 3776)	QQSDNTPL (SEQ ID NO: 4024)
372_D02	SSYGMH (SEQ ID NO: 2785)	WVAGINYNGGYTG (SEQ ID NO: 3033)	ARSANWHDTALD (SEQ ID NO: 3281)	LTYLNWY (SEQ ID NO: 3529)	LVIYAATSRA (SEQ ID NO: 3777)	QQSYDNPL (SEQ ID NO: 4025)
372_F03	SSYGMN (SEQ ID NO: 2786)	WVAGINYNGGYTS (SEQ ID NO: 3034)	ARSANWHDTALD (SEQ ID NO: 3282)	LSYLNWY (SEQ ID NO: 3530)	LVIYAATSRA (SEQ ID NO: 3778)	QQSYDTPL (SEQ ID NO: 4026)
372_F06	SDYGMN (SEQ ID NO: 2787)	WVAGINYNGGYKS (SEQ ID NO: 3035)	ARSANWHDTALD (SEQ ID NO: 3283)	LSYVNWY (SEQ ID NO: 3531)	LLIYAATSLA (SEQ ID NO: 3779)	QQSYETPL (SEQ ID NO: 4027)
372_F08	SDYSMN (SEQ ID NO: 2788)	WVSNINYNSGYTG (SEQ ID NO: 3036)	ARSANWHDTALD (SEQ ID NO: 3284)	LTYVNWY (SEQ ID NO: 3532)	LVIYAATSRA (SEQ ID NO: 3780)	QQSYDTPL (SEQ ID NO: 4028)
372_F09	DSYSMN (SEQ ID NO: 2789)	WVANINYNSGYKG (SEQ ID NO: 3037)	ARSANWHDTALD (SEQ ID NO: 3285)	LTYLNWY (SEQ ID NO: 3533)	LVIYAATSLA (SEQ ID NO: 3781)	QQSYSSPL (SEQ ID NO: 4029)
373_A02	DSYGMN (SEQ ID NO: 2790)	WVSGINYNGGYKG (SEQ ID NO: 3038)	ARSANWHDTALD (SEQ ID NO: 3286)	LSYVNWY (SEQ ID NO: 3534)	LVIYATTSLA (SEQ ID NO: 3782)	QQSYNTPL (SEQ ID NO: 4030)
373_A08	DSYGMN (SEQ ID NO:	WVSNINYNGGYTG (SEQ ID NO: 3039)	ARSANWHDTALD (SEQ ID NO: 3287)	VSYVNWY (SEQ ID NO:	LLIYAATSLA (SEQ ID NO: 3783)	QQSYSLPL (SEQ ID NO:

	2791)			3535)		4031)
373_A10	SSYGMN (SEQ ID NO: 2792)	WVSGINYNSGYTS (SEQ ID NO: 3040)	ARSANWHDTALD (SEQ ID NO: 3288)	LSYLNWY (SEQ ID NO: 3536)	LVIYAATSRA (SEQ ID NO: 3784)	QQSYDLPL (SEQ ID NO: 4032)
373_B04	SSYGMN (SEQ ID NO: 2793)	WVAGINYNSGYKG (SEQ ID NO: 3041)	ARSANWHDTALD (SEQ ID NO: 3289)	LTYLNWY (SEQ ID NO: 3537)	LLIYAATSRA (SEQ ID NO: 3785)	QQSYETPL (SEQ ID NO: 4033)
373_B06	SDYSMN (SEQ ID NO: 2794)	WVAGINYNGGYTG (SEQ ID NO: 3042)	ARSANWHDTALD (SEQ ID NO: 3290)	LTYVNWY (SEQ ID NO: 3538)	LVIYAATSRH (SEQ ID NO: 3786)	QQSYESPL (SEQ ID NO: 4034)
373_B10	DSYGMN (SEQ ID NO: 2795)	WVSNINYNGGYTS (SEQ ID NO: 3043)	ARSANWHDTALD (SEQ ID NO: 3291)	LSYLNWY (SEQ ID NO: 3539)	LLIYAATSRA (SEQ ID NO: 3787)	QQSYDLPL (SEQ ID NO: 4035)
373_B12	DSYGMN (SEQ ID NO: 2796)	WVSSINYNSGYTS (SEQ ID NO: 3044)	ARSANWHDTALD (SEQ ID NO: 3292)	VSYVNWY (SEQ ID NO: 3540)	LLIYAATSRA (SEQ ID NO: 3788)	QQSYDSPL (SEQ ID NO: 4036)
373_C02	DDYSMN (SEQ ID NO: 2797)	WVSGINYNSGYKG (SEQ ID NO: 3045)	ARSANWHDTALD (SEQ ID NO: 3293)	LSYVNWY (SEQ ID NO: 3541)	LLIYAATSRA (SEQ ID NO: 3789)	QQSYNTPL (SEQ ID NO: 4037)
373_C04	SSYSMN (SEQ ID NO: 2798)	WVANINYNSGYTG (SEQ ID NO: 3046)	ARSANWHDTALD (SEQ ID NO: 3294)	ISYVNWY (SEQ ID NO: 3542)	LVIYAVTSRA (SEQ ID NO: 3790)	QQSYNSPL (SEQ ID NO: 4038)
373_C06	SSYSMN (SEQ ID NO: 2799)	WVAGINYNGGYTG (SEQ ID NO: 3047)	ARSANWHDTALD (SEQ ID NO: 3295)	VSYVNWY (SEQ ID NO: 3543)	LVIYAATSRA (SEQ ID NO: 3791)	QQSYDTPL (SEQ ID NO: 4039)
373_C08	SSYSMN (SEQ ID NO: 2800)	WVANINYNGGYTS (SEQ ID NO: 3048)	ARSANWHDTALD (SEQ ID NO: 3296)	ISYLNWY (SEQ ID NO: 3544)	LLIYAASSLQ (SEQ ID NO: 3792)	QQSYNNPL (SEQ ID NO: 4040)
373_C11	SSYSMN (SEQ ID NO: 2801)	WVSGINYNSGYTG (SEQ ID NO: 3049)	ARSANWHDTALD (SEQ ID NO: 3297)	LTYVNWY (SEQ ID NO: 3545)	LVIYAVTSRA (SEQ ID NO: 3793)	QQSYETPL (SEQ ID NO: 4041)
373_D01	DSYSMN (SEQ ID NO: 2802)	WVSGINYNSGYKS (SEQ ID NO: 3050)	ARSANWHDTHLD (SEQ ID NO: 3298)	LSYVNWY (SEQ ID NO: 3546)	LVIYAATSRA (SEQ ID NO: 3794)	QQSYDSPL (SEQ ID NO: 4042)
373_D04	DSYSMN (SEQ ID NO: 2803)	WVSGINYNSGYKG (SEQ ID NO: 3051)	ARSANWHDTALD (SEQ ID NO: 3299)	LSYLNWY (SEQ ID NO: 3547)	LLIYAATSRH (SEQ ID NO: 3795)	QQSYDSPL (SEQ ID NO: 4043)
373_D05	SSYSMN (SEQ ID NO: 2804)	WVSGINYNSGYKG (SEQ ID NO: 3052)	ARSANWHDTALD (SEQ ID NO: 3300)	LSYLNWY (SEQ ID NO: 3548)	LVIYAATSRA (SEQ ID NO: 3796)	QQSYDSPL (SEQ ID NO: 4044)
373_D08	SSYSMN (SEQ ID NO:	WVSGINYNGGYKS (SEQ ID NO: 3053)	ARSANWHDTALD (SEQ ID NO: 3301)	LSYVNWY (SEQ ID NO:	LLIYAATSRA (SEQ ID NO: 3797)	QQSYDSPL (SEQ ID NO:

	2805)			3549)		4045)
373_D10	DSYSMN (SEQ ID NO: 2806)	WVSNINYNSGYKG (SEQ ID NO: 3054)	ARSANWHDTALD (SEQ ID NO: 3302)	LSYVNWY (SEQ ID NO: 3550)	LLIYAATSRA (SEQ ID NO: 3798)	QQSYDLPL (SEQ ID NO: 4046)
373_E01	SSYGMN (SEQ ID NO: 2807)	WVSGINYNGGYKG (SEQ ID NO: 3055)	ARSANWHDTALD (SEQ ID NO: 3303)	VSYVNWY (SEQ ID NO: 3551)	LLIYAATSRH (SEQ ID NO: 3799)	QQSYNNPL (SEQ ID NO: 4047)
373_E05	DSYGMN (SEQ ID NO: 2808)	WVSNINYNGGYTS (SEQ ID NO: 3056)	ARSANWHDTALD (SEQ ID NO: 3304)	LSYVNWY (SEQ ID NO: 3552)	LLIYAVTSRA (SEQ ID NO: 3800)	QQSYDLPL (SEQ ID NO: 4048)
373_E07	SSYGMN (SEQ ID NO: 2809)	WVANINYNGGYTS (SEQ ID NO: 3057)	ARSANWHDTALD (SEQ ID NO: 3305)	LTYVNWY (SEQ ID NO: 3553)	LLIYAATSLA (SEQ ID NO: 3801)	QQSYETPL (SEQ ID NO: 4049)
373_E12	SSYSMN (SEQ ID NO: 2810)	WVANINYNGGYTG (SEQ ID NO: 3058)	ARSANWHDTALD (SEQ ID NO: 3306)	LSYVNWY (SEQ ID NO: 3554)	LVIYAATSRA (SEQ ID NO: 3802)	QQSYDTPL (SEQ ID NO: 4050)
373_G10	SDYGMN (SEQ ID NO: 2811)	WVSNINYNGGYKS (SEQ ID NO: 3059)	ARSANWHDTALD (SEQ ID NO: 3307)	VSYVNWY (SEQ ID NO: 3555)	LLIYAATSRA (SEQ ID NO: 3803)	QQSYDLPL (SEQ ID NO: 4051)
373_G12	SSYSMN (SEQ ID NO: 2812)	WVSNINYNGGYTS (SEQ ID NO: 3060)	ARSANWHDTALD (SEQ ID NO: 3308)	LSYLNWY (SEQ ID NO: 3556)	LLIYATTSLA (SEQ ID NO: 3804)	QQSYNSPL (SEQ ID NO: 4052)
373_H01	DSYSMN (SEQ ID NO: 2813)	WVANINYNGGYTG (SEQ ID NO: 3061)	ARSANWHDTALD (SEQ ID NO: 3309)	LSYLNWY (SEQ ID NO: 3557)	LVIYAATSRA (SEQ ID NO: 3805)	QQSYDNPL (SEQ ID NO: 4053)
373_H05	SDYSMN (SEQ ID NO: 2814)	WVANINYNGGYKG (SEQ ID NO: 3062)	ARSANWHDTALD (SEQ ID NO: 3310)	LTYVNWY (SEQ ID NO: 3558)	LVIYAATSRA (SEQ ID NO: 3806)	QQSYETPL (SEQ ID NO: 4054)
374_A07	SSYSMN (SEQ ID NO: 2815)	WVSGINYNSGYKG (SEQ ID NO: 3063)	ARSANWHDTALD (SEQ ID NO: 3311)	LSYVNWY (SEQ ID NO: 3559)	LLIYAVTSRA (SEQ ID NO: 3807)	QQSYDLPL (SEQ ID NO: 4055)
374_B04	SSYSMN (SEQ ID NO: 2816)	WVSNINYNSGYTG (SEQ ID NO: 3064)	ARSANWHDTALD (SEQ ID NO: 3312)	VSYLNWY (SEQ ID NO: 3560)	LLIYAVTSRA (SEQ ID NO: 3808)	QQSYESPL (SEQ ID NO: 4056)
374_B06	DSYSMN (SEQ ID NO: 2817)	WVAGINYNSGYKG (SEQ ID NO: 3065)	ARSANWHDTHLD (SEQ ID NO: 3313)	LTYVNWY (SEQ ID NO: 3561)	LLIYAATSRA (SEQ ID NO: 3809)	QQSYDTPL (SEQ ID NO: 4057)
374_B12	DSYSMN (SEQ ID NO: 2818)	WVAGINYNGGYTG (SEQ ID NO: 3066)	ARSANWHDTHLD (SEQ ID NO: 3314)	SSYLNWY (SEQ ID NO: 3562)	LVIYAATSRA (SEQ ID NO: 3810)	QQSYDNPL (SEQ ID NO: 4058)
374_C03	DSYSMN (SEQ ID NO:	WVSGINYNSGYTS (SEQ ID NO: 3067)	ARSANWHDTALD (SEQ ID NO: 3315)	LTYLNWY (SEQ ID NO:	LLIYAATSRA (SEQ ID NO: 3811)	QQSYDSPL (SEQ ID NO:

	2819)			3563)		4059)
374_C06	DDYSMN (SEQ ID NO: 2820)	WVSSINYNSGYKG (SEQ ID NO: 3068)	ARSANWHDTALD (SEQ ID NO: 3316)	LTYVNWY (SEQ ID NO: 3564)	LLIYAATSRA (SEQ ID NO: 3812)	QQSYNSPL (SEQ ID NO: 4060)
374_D01	DSYSMN (SEQ ID NO: 2821)	WVSGINYNSGYKG (SEQ ID NO: 3069)	ARSANWHDTALD (SEQ ID NO: 3317)	ITYVNWY (SEQ ID NO: 3565)	LLIYAATSLA (SEQ ID NO: 3813)	QQSYSSPL (SEQ ID NO: 4061)
374_D08	DSYGMN (SEQ ID NO: 2822)	WVSGINYNSGYTG (SEQ ID NO: 3070)	ARSANWHDTHLD (SEQ ID NO: 3318)	LTYLNWY (SEQ ID NO: 3566)	LLIYAATSRH (SEQ ID NO: 3814)	QQSYESPL (SEQ ID NO: 4062)
374_E01	SSYGMN (SEQ ID NO: 2823)	WVAGINYNGGYTS (SEQ ID NO: 3071)	ARSANWHDTALD (SEQ ID NO: 3319)	SSYVNWY (SEQ ID NO: 3567)	LLIYAATSRA (SEQ ID NO: 3815)	QQSYSTPL (SEQ ID NO: 4063)
374_E02	SSYSMN (SEQ ID NO: 2824)	WVSGINYNGGYTS (SEQ ID NO: 3072)	ARSANWHDTALD (SEQ ID NO: 3320)	LSYLNWY (SEQ ID NO: 3568)	LLIYAATSLA (SEQ ID NO: 3816)	QQSYDLPL (SEQ ID NO: 4064)
374_E05	SSYSMN (SEQ ID NO: 2825)	WVAGINYNGGYTS (SEQ ID NO: 3073)	ARSANWHDTALD (SEQ ID NO: 3321)	LSFVNWY (SEQ ID NO: 3569)	LVIYAATSRA (SEQ ID NO: 3817)	QQSYNLPL (SEQ ID NO: 4065)
374_E07	SDYSMN (SEQ ID NO: 2826)	WVAGINYNGGYTS (SEQ ID NO: 3074)	ARSANWHDTALD (SEQ ID NO: 3322)	ITYVNWY (SEQ ID NO: 3570)	LVIYAATSRA (SEQ ID NO: 3818)	QQSYNTPL (SEQ ID NO: 4066)
374_E08	SSYGMN (SEQ ID NO: 2827)	WVAGINYNGGYKS (SEQ ID NO: 3075)	ARSANWHDTALD (SEQ ID NO: 3323)	LSYLNWY (SEQ ID NO: 3571)	LLIYAATSRH (SEQ ID NO: 3819)	QQSYDLPL (SEQ ID NO: 4067)
374_E11	SSYGMN (SEQ ID NO: 2828)	WVSNINYNGGYTS (SEQ ID NO: 3076)	ARSANWHDTALD (SEQ ID NO: 3324)	VTYLNWY (SEQ ID NO: 3572)	LVIYAATSRA (SEQ ID NO: 3820)	QQSYDSPL (SEQ ID NO: 4068)
374_F01	DSYSMN (SEQ ID NO: 2829)	WVSNINYNGGYTG (SEQ ID NO: 3077)	ARSANWHDTALD (SEQ ID NO: 3325)	LSYVNWY (SEQ ID NO: 3573)	LVIYAATSRH (SEQ ID NO: 3821)	QQSYENPL (SEQ ID NO: 4069)
374_F02	DSYSMN (SEQ ID NO: 2830)	WVANINYNSGYTS (SEQ ID NO: 3078)	ARSANWHDTALD (SEQ ID NO: 3326)	VSYLNWY (SEQ ID NO: 3574)	LLIYAASSLQ (SEQ ID NO: 3822)	QQSYELPL (SEQ ID NO: 4070)
374_F04	SSYGMN (SEQ ID NO: 2831)	WVSGINYNSGYKS (SEQ ID NO: 3079)	ARSANWHDTALD (SEQ ID NO: 3327)	LTYVNWY (SEQ ID NO: 3575)	LLIYAATSRA (SEQ ID NO: 3823)	QQSYNSPL (SEQ ID NO: 4071)
374_F10	SSYSMN (SEQ ID NO: 2832)	WVSGINYNGGYTS (SEQ ID NO: 3080)	ARSANWHDTALD (SEQ ID NO: 3328)	LSYLNWY (SEQ ID NO: 3576)	LVIYAATSRA (SEQ ID NO: 3824)	QQSYDNPL (SEQ ID NO: 4072)
374_F11	DSYSMN (SEQ ID NO:	WVSNINYNGGYTG (SEQ ID NO: 3081)	ARSANWHDTALD (SEQ ID NO: 3329)	LSYLNWY (SEQ ID NO:	LLIYAVTSLA (SEQ ID NO: 3825)	QQSYESPL (SEQ ID NO:

	2833)			3577)		4073)
374_G04	SSYSMN (SEQ ID NO: 2834)	WVAGINYNGGYTG (SEQ ID NO: 3082)	ARSANWHDTALD (SEQ ID NO: 3330)	LTYLNWY (SEQ ID NO: 3578)	LVIYAATSLA (SEQ ID NO: 3826)	QQSYDNPL (SEQ ID NO: 4074)
374_G06	SSYGMH (SEQ ID NO: 2835)	WVASINYNGGYTS (SEQ ID NO: 3083)	ARSANWHDTALD (SEQ ID NO: 3331)	LSYLNWY (SEQ ID NO: 3579)	LLIYAVTSRA (SEQ ID NO: 3827)	QQSYDLPL (SEQ ID NO: 4075)
374_G07	SSYSMN (SEQ ID NO: 2836)	WVSGINYNSGYKS (SEQ ID NO: 3084)	ARSANWHDTALD (SEQ ID NO: 3332)	ISYLNWY (SEQ ID NO: 3580)	LLIYAATSRA (SEQ ID NO: 3828)	QQSYDSPL (SEQ ID NO: 4076)
374_H03	SSYGMN (SEQ ID NO: 2837)	WVSGINYNSGYKS (SEQ ID NO: 3085)	ARSANWHDTALD (SEQ ID NO: 3333)	LSYVNWY (SEQ ID NO: 3581)	LVIYAATSRA (SEQ ID NO: 3829)	QQSYDSPL (SEQ ID NO: 4077)
374_H04	DSYSMN (SEQ ID NO: 2838)	WVSGINYNSGYTS (SEQ ID NO: 3086)	ARSANWHDTALD (SEQ ID NO: 3334)	LTYLNWY (SEQ ID NO: 3582)	LLIYAATSRA (SEQ ID NO: 3830)	QQSYDNPL (SEQ ID NO: 4078)
374_H06	SSYGMN (SEQ ID NO: 2839)	WVSNINYNGGYTG (SEQ ID NO: 3087)	ARSANWHDTALD (SEQ ID NO: 3335)	VSYVNWY (SEQ ID NO: 3583)	LVIYAATSRA (SEQ ID NO: 3831)	QQSYNLPL (SEQ ID NO: 4079)
374_H07	DSYGMN (SEQ ID NO: 2840)	WVANINYNGGYTG (SEQ ID NO: 3088)	ARSANWHDTALD (SEQ ID NO: 3336)	LTYLNWY (SEQ ID NO: 3584)	LLIYAATSRA (SEQ ID NO: 3832)	QQSYETPL (SEQ ID NO: 4080)
374_H09	SSYSMN (SEQ ID NO: 2841)	WVANINYNSGYKS (SEQ ID NO: 3089)	ARSANWHDTALD (SEQ ID NO: 3337)	LSYLNWY (SEQ ID NO: 3585)	LVIYAVTSLA (SEQ ID NO: 3833)	QQSYDLPL (SEQ ID NO: 4081)
375_A05	SSYGMN (SEQ ID NO: 2842)	WVANINYNGGYKG (SEQ ID NO: 3090)	ARSANWHDTALD (SEQ ID NO: 3338)	LSYLNWY (SEQ ID NO: 3586)	LLIYAATSRA (SEQ ID NO: 3834)	QQSYDLPL (SEQ ID NO: 4082)
375_C06	DDYGMH (SEQ ID NO: 2843)	WVASINYNSGYTS (SEQ ID NO: 3091)	ARSANWHDTALD (SEQ ID NO: 3339)	LTYVNWY (SEQ ID NO: 3587)	LVIYATTSRA (SEQ ID NO: 3835)	QQSYDSPL (SEQ ID NO: 4083)
375_D04	DDSSMH (SEQ ID NO: 2844)	WVSNINYNGGYTG (SEQ ID NO: 3092)	AKSANWHDTALD (SEQ ID NO: 3340)	LSYVNWY (SEQ ID NO: 3588)	LVIYAATSRA (SEQ ID NO: 3836)	QQSYELPL (SEQ ID NO: 4084)
375_D05	SSYSMN (SEQ ID NO: 2845)	WVASINYNSGYTS (SEQ ID NO: 3093)	ARSANWHDTHLD (SEQ ID NO: 3341)	VSYLNWY (SEQ ID NO: 3589)	LLIYAATSLH (SEQ ID NO: 3837)	QQSYDTPL (SEQ ID NO: 4085)
375_D07	SSYGMN (SEQ ID NO: 2846)	WVANINYNSGYTG (SEQ ID NO: 3094)	ARSANWHDTALD (SEQ ID NO: 3342)	ITYLNWY (SEQ ID NO: 3590)	LLIYAATSRA (SEQ ID NO: 3838)	QQSYDTPL (SEQ ID NO: 4086)
375_D08	SDYGMN (SEQ ID NO:	WVSGINYNSGYKG (SEQ ID NO: 3095)	ARSANWHDTALD (SEQ ID NO: 3343)	ITYLNWY (SEQ ID NO:	LLIYAATSRA (SEQ ID NO: 3839)	QQSYSTPL (SEQ ID NO:

	2847)			3591)		4087)
375_D12	DSYGMN (SEQ ID NO: 2848)	WVSSINYNSGYTS (SEQ ID NO: 3096)	ARSANWHDTALD (SEQ ID NO: 3344)	LTYVNWY (SEQ ID NO: 3592)	LVIYAATSRA (SEQ ID NO: 3840)	QQSYETPL (SEQ ID NO: 4088)
375_E01	SSYSMN (SEQ ID NO: 2849)	WVSGINYNSGYKS (SEQ ID NO: 3097)	ARSANWHDTALD (SEQ ID NO: 3345)	LTYLNWY (SEQ ID NO: 3593)	LVIYAATSRA (SEQ ID NO: 3841)	QQSDDSPL (SEQ ID NO: 4089)
375_E07	SDYSMN (SEQ ID NO: 2850)	WVAGINYNSGYKG (SEQ ID NO: 3098)	ARSANWHDTALD (SEQ ID NO: 3346)	VTYLNWY (SEQ ID NO: 3594)	LLIYVVTNRE (SEQ ID NO: 3842)	QQSYETPL (SEQ ID NO: 4090)
375_H12	SSYGMN (SEQ ID NO: 2851)	WVAGINYNGGYKG (SEQ ID NO: 3099)	ARSANWHDTALD (SEQ ID NO: 3347)	LTYLNWY (SEQ ID NO: 3595)	LLIYYVTNRQ (SEQ ID NO: 3843)	QQSYSIPL (SEQ ID NO: 4091)
376_A04	DSYSMN (SEQ ID NO: 2852)	WVSNINYNGGYTS (SEQ ID NO: 3100)	ARSANWHDTALD (SEQ ID NO: 3348)	VTYLNWY (SEQ ID NO: 3596)	LVIYAATSRA (SEQ ID NO: 3844)	QQSYDSPL (SEQ ID NO: 4092)
376_A10	SDYGMN (SEQ ID NO: 2853)	WVSNINYNSGYKG (SEQ ID NO: 3101)	ARSANWHDTALD (SEQ ID NO: 3349)	LSYLNWY (SEQ ID NO: 3597)	LLIYAATSRA (SEQ ID NO: 3845)	QQSYESPL (SEQ ID NO: 4093)
376_A12	SSYSMN (SEQ ID NO: 2854)	WVANINYNSGYKG (SEQ ID NO: 3102)	ARSANWHDTALD (SEQ ID NO: 3350)	LSYVNWY (SEQ ID NO: 3598)	LVIYAATSRA (SEQ ID NO: 3846)	QQSYDTPL (SEQ ID NO: 4094)
376_B04	DSYGMH (SEQ ID NO: 2855)	WVASINYNGGYTG (SEQ ID NO: 3103)	ARSANWHDTALD (SEQ ID NO: 3351)	VSYVNWY (SEQ ID NO: 3599)	LVIYAATSRA (SEQ ID NO: 3847)	QQSYDTPL (SEQ ID NO: 4095)
376_B05	SSYSMN (SEQ ID NO: 2856)	WVANINYNGGYTG (SEQ ID NO: 3104)	ARSANWHDTALD (SEQ ID NO: 3352)	ISYVNWY (SEQ ID NO: 3600)	LLIYAATSRA (SEQ ID NO: 3848)	QQSYELPL (SEQ ID NO: 4096)
376_B09	DSYSMN (SEQ ID NO: 2857)	WVANINYNSGYKG (SEQ ID NO: 3105)	ARSANWHDTALD (SEQ ID NO: 3353)	LTYVNWY (SEQ ID NO: 3601)	LVIYAATSRA (SEQ ID NO: 3849)	QQSYDLPL (SEQ ID NO: 4097)
376_B11	SSYSMN (SEQ ID NO: 2858)	WVSGINYNGGYTS (SEQ ID NO: 3106)	ARSANWHDTALD (SEQ ID NO: 3354)	LSYVNWY (SEQ ID NO: 3602)	LVIYAATSRA (SEQ ID NO: 3850)	QQSYDLPL (SEQ ID NO: 4098)
376_C01	DSYSMN (SEQ ID NO: 2859)	WVAGINYNGGYTS (SEQ ID NO: 3107)	ARSANWHDTALD (SEQ ID NO: 3355)	LTYLNWY (SEQ ID NO: 3603)	LLIYAATSLA (SEQ ID NO: 3851)	QQSYDNPL (SEQ ID NO: 4099)
376_C02	DSYGMN (SEQ ID NO: 2860)	WVSGINYNSGYTS (SEQ ID NO: 3108)	ARSANWHDTALD (SEQ ID NO: 3356)	VSYLNWY (SEQ ID NO: 3604)	LVIYAVTSRA (SEQ ID NO: 3852)	QQSYDSPL (SEQ ID NO: 4100)
376_C12	SSYSMN (SEQ ID NO:	WVAGINYNGGYTG (SEQ ID NO: 3109)	ARSANWHDTALD (SEQ ID NO: 3357)	LTYVNWY (SEQ ID NO:	LLIYAATSRA (SEQ ID NO: 3853)	QQSYDSPL (SEQ ID NO:

	2861)			3605)		4101)
376_D05	SSYSMN (SEQ ID NO: 2862)	WVSNINYNGGYKG (SEQ ID NO: 3110)	ARSANWHDTALD (SEQ ID NO: 3358)	VSYVNWY (SEQ ID NO: 3606)	LLIYAATSLA (SEQ ID NO: 3854)	QQSYDTPL (SEQ ID NO: 4102)
376_D11	SSYGMN (SEQ ID NO: 2863)	WVANINYNGGYTG (SEQ ID NO: 3111)	ARSANWHDTALD (SEQ ID NO: 3359)	LSYLNWY (SEQ ID NO: 3607)	LVIYAATSRA (SEQ ID NO: 3855)	QQSYNNPL (SEQ ID NO: 4103)
376_E03	SSYGMN (SEQ ID NO: 2864)	WVANINYNGGYTG (SEQ ID NO: 3112)	ARSANWHDTALD (SEQ ID NO: 3360)	LSYVNWY (SEQ ID NO: 3608)	LVIYAATSLA (SEQ ID NO: 3856)	QQSYDLPL (SEQ ID NO: 4104)
376_E08	SDYGMN (SEQ ID NO: 2865)	WVAGINYNGGYTS (SEQ ID NO: 3113)	ARSANWHDTALD (SEQ ID NO: 3361)	VSYVNWY (SEQ ID NO: 3609)	LVIYAATSRA (SEQ ID NO: 3857)	QQSYDSPL (SEQ ID NO: 4105)
376_F03	DSYGMN (SEQ ID NO: 2866)	WVANINYNGGYTG (SEQ ID NO: 3114)	ARSANWHDTALD (SEQ ID NO: 3362)	ITYVNWY (SEQ ID NO: 3610)	LVIYATTSLA (SEQ ID NO: 3858)	QQSYSSPL (SEQ ID NO: 4106)
376_F04	DSYSMN (SEQ ID NO: 2867)	WVSNINYNSGYTG (SEQ ID NO: 3115)	ARSANWHDTALD (SEQ ID NO: 3363)	SSYLNWY (SEQ ID NO: 3611)	LLIYAASSLQ (SEQ ID NO: 3859)	QQSYSTPL (SEQ ID NO: 4107)
376_G08	DSYGMN (SEQ ID NO: 2868)	WVANINYNGGYTS (SEQ ID NO: 3116)	ARSANWHDTALD (SEQ ID NO: 3364)	LSYVNWY (SEQ ID NO: 3612)	LVIYAATSRA (SEQ ID NO: 3860)	QQSYDTPL (SEQ ID NO: 4108)
376_G09	DSYSMN (SEQ ID NO: 2869)	WVSGINYNSGYKG (SEQ ID NO: 3117)	ARSANWHDTALD (SEQ ID NO: 3365)	SYYLNWY (SEQ ID NO: 3613)	LLIYAVTSRA (SEQ ID NO: 3861)	QQSYDNPL (SEQ ID NO: 4109)
376_H09	SDYSMN (SEQ ID NO: 2870)	WVANINYNGGYTG (SEQ ID NO: 3118)	ARSANWHDTALD (SEQ ID NO: 3366)	ITYLNWY (SEQ ID NO: 3614)	LVIYYVSNLP (SEQ ID NO: 3862)	QQSYDSPL (SEQ ID NO: 4110)
376_H10	DSYSMN (SEQ ID NO: 2871)	WVSGINYNSGYKS (SEQ ID NO: 3119)	ARSANWHDTALD (SEQ ID NO: 3367)	LTYLNWY (SEQ ID NO: 3615)	LVIYAATSRH (SEQ ID NO: 3863)	QQSYDSPL (SEQ ID NO: 4111)

The consensus sequences for each of these CDRs shown in Fig. 3E are as follows:

HCDR1: S/DS/DYG/SMN/H (SEQ ID NO: 6578)

HCDR2: WVS/AG/N/SINYNG/SGYT/KS/G (SEQ ID NO: 6579)

HCDR3: AR/KSANWHDTA/HLD (SEQ ID NO: 6597)

LCDR1: L/V/I/SS/TYL/VNWY (SEQ ID NO: 6561)

LCDR2: LL/VIYA/YA/V/TT/SS/NR/LA/H/Q (SEQ ID NO: 6582)

LCDR3: QQSY/DD/E/N/SS/T/L/NPL (SEQ ID NO: 6598)

Table 2F: Group IV Antibody Sequences

Ab	VH sequence	VL sequence
365_E02	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVANINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCAKSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4112)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYENPLTFGGGT KVEIK (SEQ ID NO: 4281)
370_G12	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVAGINYNGG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 4113)	DIQMTQSPSSLSASVGDRVTITCRASQSIITYLN WYQQKPGKAPKLLIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSDESPLTFGGGT KVEIK (SEQ ID NO: 4282)
368_C01	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYGMNWVRQAPGKGLEWVAGINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 4114)	DIQMTQSPSSLSASVGDRVTITCRASQSIITYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 4283)
376_C06	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVAGINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 4115)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 4284)
368_D10	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYGMNWVRQAPGKGLEWVAGINYNSG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 4116)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 4285)
365_G12	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVAGINYNSG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 4117)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSNPLTFGGGT KVEIK (SEQ ID NO: 4286)
367_C03	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVANINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 4118)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLVIYATTSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYENPLTFGGGT KVEIK (SEQ ID NO: 4287)
367_H07	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVANINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 4119)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLVIYATTSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYENPLTFGGGT KVEIK (SEQ ID NO: 4288)
371_D03	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYGMNWVRQAPGKGLEWVANINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 4120)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLVIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNTPLTFGGGT KVEIK (SEQ ID NO: 4289)
369_C10	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVANINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 4121)	DIQMTQSPSSLSASVGDRVTITCRASQSIVTYLN WYQQKPGKAPKLLIYAATSLHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSDSLPLTFGGGT KVEIK (SEQ ID NO: 4290)
367_F05	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVASINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSSPLTFGGGT

	SLRAEDTAVYYCARSATWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 4122)	KVEIK (SEQ ID NO: 4291)
365_C07	EVQLLESGGGLVQPGGSLRLSCAASGFT FSDYGMNWVRQAPGKGLEWVASINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 4123)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 4292)
374_C08	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYGMNWVRQAPGKGLEWVSGINYNSG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 4124)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLLIYAVTSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 4293)
376_A06	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVSGINYNSG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 4125)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLVIYYVSNRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDNPLTFGGGT KVEIK (SEQ ID NO: 4294)
376_B07	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVSGINYNSG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 4126)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLVIYYVSNRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDNPLTFGGGT KVEIK (SEQ ID NO: 4295)
365_F07	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVSNINYNGG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 4127)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 4296)
369_E10	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVSNINYNGG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 4128)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 4297)
373_E03	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYGMNWVRQAPGKGLEWVSNINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTALDYWGQ GTLVTVSS (SEQ ID NO: 4129)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 4298)
366_B04	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVAGINYNGG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4130)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLVIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 4299)
376_F12	EVQLLESGGGLVQPGGSLRLSCAASGFT FDDYSMNWVRQAPGKGLEWVAGINYNGG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4131)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYVN WYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSTPLTFGGGT KVEIK (SEQ ID NO: 4300)
369_F07	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVAGINYNGG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4132)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYESPLTFGGGT KVEIK (SEQ ID NO: 4301)
368_C06	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVAGINYNGG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLN WYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSTPLTFGGGT KVEIK (SEQ ID NO: 4302)

	GTLVTVSS (SEQ ID NO: 4133)	
376_E12	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVAGINYNGG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4134)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSTPLTFGGGT KVEIK (SEQ ID NO: 4303)
371_H01	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVAGINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4135)	DIQMTQSPSSLSASVGDRVTITCRASQSIITYLN WYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSTPLTFGGGT KVEIK (SEQ ID NO: 4304)
367_E02	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVAGINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4136)	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLN WYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSTPLTFGGGT KVEIK (SEQ ID NO: 4305)
365_F04	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVAGINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4137)	DIQMTQSPSSLSASVGDRVTITCRASQSIVTYVN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 4306)
370_A09	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVAGINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4138)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 4307)
365_B03	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVAGINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4139)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYENPLTFGGGT KVEIK (SEQ ID NO: 4308)
369_A05	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVAGINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4140)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYESPLTFGGGT KVEIK (SEQ ID NO: 4309)
373_H10	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVAGINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4141)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSLPLTFGGGT KVEIK (SEQ ID NO: 4310)
367_A09	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYGMNWVRQAPGKGLEWVAGINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4142)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLVIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 4311)
370_F08	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVAGINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4143)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYVN WYQQKPGKAPKLLIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNLPLTFGGGT KVEIK (SEQ ID NO: 4312)
376_B01	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVAGINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4144)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNLPLTFGGGT KVEIK (SEQ ID NO: 4313)

365_D05	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVAGINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4145)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNSPLTFGGGT KVEIK (SEQ ID NO: 4314)
373_E04	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVAGINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4146)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNSPLTFGGGT KVEIK (SEQ ID NO: 4315)
368_G05	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVAGINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4147)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLLIYAATSLHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNTPLTFGGGT KVEIK (SEQ ID NO: 4316)
365_A01	EVQLLESGGGLVQPGGSLRLSCAASGFT FSDYGMNWVRQAPGKGLEWVAGINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4148)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLVIYATTSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSTPLTFGGGT KVEIK (SEQ ID NO: 4317)
373_H06	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMHWVRQAPGKGLEWVAGINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4149)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYVN WYQQKPGKAPKLLIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 4318)
369_G07	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVAGINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4150)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDNPLTFGGGT KVEIK (SEQ ID NO: 4319)
373_G05	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVAGINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4151)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLLIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYELPLTFGGGT KVEIK (SEQ ID NO: 4320)
372_F07	EVQLLESGGGLVQPGGSLRLSCAASGFT FDDYSMNWVRQAPGKGLEWVAGINYNSG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4152)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYELPLTFGGGT KVEIK (SEQ ID NO: 4321)
370_H03	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVAGINYNSG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4153)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLLIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 4322)
366_A03	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVAGINYNSG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4154)	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLN WYQQKPGKAPKLLIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSNPLTFGGGT KVEIK (SEQ ID NO: 4323)
365_A07	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVAGINYNSG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4155)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNLPLTFGGGT KVEIK (SEQ ID NO: 4324)
376_B06	EVQLLESGGGLVQPGGSLRLSCAASGFT	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN

	FSSYSMNWVRQAPGKGLEWVAGINYNSG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4156)	WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 4325)
374_C11	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVAGINYNSG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4157)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYESPLTFGGGT KVEIK (SEQ ID NO: 4326)
375_A06	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVAGINYNSG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4158)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSTPLTFGGGT KVEIK (SEQ ID NO: 4327)
365_B09	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVAGINYNSG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4159)	DIQMTQSPSSLSASVGDRVTITCRASQSILRYLN WYQQKPGKAPKLLIYAATSLHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDNPLTFGGGT KVEIK (SEQ ID NO: 4328)
373_E06	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVAGINYNSG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4160)	DIQMTQSPSSLSASVGDRVTITCRASQSILRYLN WYQQKPGKAPKLLIYAATSLHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDNPLTFGGGT KVEIK (SEQ ID NO: 4329)
374_C05	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVAGINYNSG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4161)	DIQMTQSPSSLSASVGDRVTITCRASQSIIRYLN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDNPLTFGGGT KVEIK (SEQ ID NO: 4330)
376_C11	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVAGINYNSG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4162)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDNPLTFGGGT KVEIK (SEQ ID NO: 4331)
373_C09	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVAGINYNSG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4163)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYELPLTFGGGT KVEIK (SEQ ID NO: 4332)
368_H01	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVAGINYNSG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4164)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLLIYATTSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDNPLTFGGGT KVEIK (SEQ ID NO: 4333)
373_B03	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVAGINYNSG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4165)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLVIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDNPLTFGGGT KVEIK (SEQ ID NO: 4334)
374_C04	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVAGINYNSG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4166)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYELPLTFGGGT KVEIK (SEQ ID NO: 4335)
371_F05	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVAGINYNSG	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLLIYAATSRHSGVPSRFSGSGSG

	YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4167)	TDFTLTISSLQPEDFATYYCQQSYENPLTFGGGT KVEIK (SEQ ID NO: 4336)
369_A10	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVAGINYNSG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4168)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYELPLTFGGGT KVEIK (SEQ ID NO: 4337)
366_A05	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVAGINYNSG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4169)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLVIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNTPLTFGGGT KVEIK (SEQ ID NO: 4338)
375_G07	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVAGINYNSG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4170)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLVIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 4339)
374_D02	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVAGINYNSG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4171)	DIQMTQSPSSLSASVGDRVTITCRASQSISTYVN WYQQKPGKAPKLLIYAVTSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 4340)
365_A10	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMHWVRQAPGKGLEWVAGINYNSG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4172)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLVIYAVTSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 4341)
375_A02	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVAGINYNSG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4173)	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLN WYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSTPLTFGGGT KVEIK (SEQ ID NO: 4342)
371_G03	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVANINYNGG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4174)	DIQMTQSPSSLSASVGDRVTITCRASQSIVTYVN WYQQKPGKAPKLVIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNLPLTFGGGT KVEIK (SEQ ID NO: 4343)
370_E07	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVANINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4175)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDNPLTFGGGT KVEIK (SEQ ID NO: 4344)
375_B04	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVANINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4176)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDNPLTFGGGT KVEIK (SEQ ID NO: 4345)
367_G07	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVANINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4177)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDNPLTFGGGT KVEIK (SEQ ID NO: 4346)
366_C02	EVQLLESGGGLVQPGGSLRLSCAASGFT FSDYSMNWVRQAPGKGLEWVANINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDNPLTFGGGT

	SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4178)	KVEIK (SEQ ID NO: 4347)
375_C12	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVANINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4179)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 4348)
365_F08	EVQLLESGGGLVQPGGSLRLSCAASGFT FDDYGMNWVRQAPGKGLEWVANINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4180)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLLIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSLPLTFGGGT KVEIK (SEQ ID NO: 4349)
368_G09	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYGMHWVRQAPGKGLEWVANINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4181)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYLN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 4350)
368_E11	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYGMHWVRQAPGKGLEWVANINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4182)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYVN WYQQKPGKAPKLLIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYELPLTFGGGT KVEIK (SEQ ID NO: 4351)
367_F02	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVANINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4183)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYVN WYQQKPGKAPKLLIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYESPLTFGGGT KVEIK (SEQ ID NO: 4352)
373_B08	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVANINYNSG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4184)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLVIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYENPLTFGGGT KVEIK (SEQ ID NO: 4353)
374_A11	EVQLLESGGGLVQPGGSLRLSCAASGFT FSDYSMNWVRQAPGKGLEWVANINYNSG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4185)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSSPLTFGGGT KVEIK (SEQ ID NO: 4354)
373_B11	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVANINYNSG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4186)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDNPLTFGGGT KVEIK (SEQ ID NO: 4355)
373_F03	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVANINYNSG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4187)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLLIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 4356)
372_D04	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVANINYNSG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4188)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLLIYAATSLHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 4357)
366_C01	EVQLLESGGGLVQPGGSLRLSCAASGFT FSDYGMNWVRQAPGKGLEWVASINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ	DIQMTQSPSSLSASVGDRVTITCRASQSIVTYLN WYQQKPGKAPKLLIYAATSPASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYELPLTFGGGT KVEIK (SEQ ID NO: 4358)

	GTLVTVSS (SEQ ID NO: 4189)	
367_A01	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVASINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4190)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 4359)
366_H05	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYGMHWVRQAPGKGLEWVASINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4191)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLLIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 4360)
369_B09	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYGMHWVRQAPGKGLEWVASINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4192)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYENPLTFGGGT KVEIK (SEQ ID NO: 4361)
366_D07	EVQLLESGGGLVQPGGSLRLSCAASGFT FSDYGMHWVRQAPGKGLEWVASINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4193)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLLIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSSPLTFGGGT KVEIK (SEQ ID NO: 4362)
369_D11	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMHWVRQAPGKGLEWVASINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4194)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLVIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSDELPLTFGGGT KVEIK (SEQ ID NO: 4363)
370_B05	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVASINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4195)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYENPLTFGGGT KVEIK (SEQ ID NO: 4364)
366_D02	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVASINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4196)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLLIYATTSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 4365)
368_H12	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVASINYNSG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4197)	DIQMTQSPSSLSASVGDRVTITCRASQSIVTYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYESPLTFGGGT KVEIK (SEQ ID NO: 4366)
368_F12	EVQLLESGGGLVQPGGSLRLSCAASGFT FDDYSMNWVRQAPGKGLEWVASINYNSG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4198)	DIQMTQSPSSLSASVGDRVTITCRASQSIVTYLN WYQQKPGKAPKLVIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 4367)
370_A06	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVASINYNSG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4199)	DIQMTQSPSSLSASVGDRVTITCRASQSIVTYLN WYQQKPGKAPKLVIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 4368)
369_F12	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVASINYNSG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4200)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYLN WYQQKPGKAPKLLIYAVTSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYENPLTFGGGT KVEIK (SEQ ID NO: 4369)

366_A09	EVQLLESGGGLVQPGGSLRLSCAASGFT FSDYGMHWVRQAPGKGLEWVASINYNSG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4201)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLLIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYETPLTFGGGT KVEIK (SEQ ID NO: 4370)
368_H07	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMHWVRQAPGKGLEWVASINYNSG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4202)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYENPLTFGGGT KVEIK (SEQ ID NO: 4371)
370_C04	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVASINYNSG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4203)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYENPLTFGGGT KVEIK (SEQ ID NO: 4372)
373_E02	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYGMHWVRQAPGKGLEWVSGINYNGG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4204)	DIQMTQSPSSLSASVGDRVTITCRASQSIVRYLN WYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSTPLTFGGGT KVEIK (SEQ ID NO: 4373)
374_E09	EVQLLESGGGLVQPGGSLRLSCAASGFT FSDYSMNWVRQAPGKGLEWVSGINYNGG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4205)	DIQMTQSPSSLSASVGDRVTITCRASQSIVTYLN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 4374)
371_C09	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVSGINYNGG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4206)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDNPLTFGGGT KVEIK (SEQ ID NO: 4375)
369_B12	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVSGINYNGG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4207)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLLIYATTSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 4376)
369_B02	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVSGINYNGG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4208)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNLPLTFGGGT KVEIK (SEQ ID NO: 4377)
365_C09	EVQLLESGGGLVQPGGSLRLSCAASGFT FSDYGMNWVRQAPGKGLEWVSGINYNGG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4209)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 4378)
374_B09	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVSGINYNGG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4210)	DIQMTQSPSSLSASVGDRVTITCRASQSIVRYLN WYQQKPGKAPKLVIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYELPLTFGGGT KVEIK (SEQ ID NO: 4379)
374_D12	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVSGINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4211)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 4380)
374_C02	EVQLLESGGGLVQPGGSLRLSCAASGFT	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN

	FDSYSMNWVRQAPGKGLEWVSGINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4212)	WYQQKPGKAPKLLIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDSPLTFGGGT KVEIK (SEQ ID NO: 4381)
374_H08	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVSGINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4213)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLLIYAATSLHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYENPLTFGGGT KVEIK (SEQ ID NO: 4382)
369_D06	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVSGINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4214)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYETPLTFGGGT KVEIK (SEQ ID NO: 4383)
366_B06	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVSGINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4215)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLVIYAAPSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYXTPLTFGGGT KVEIK (SEQ ID NO: 4384)
367_A11	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMHWVRQAPGKGLEWVSGINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4216)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLVIYATTSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNSPLTFGGGT KVEIK (SEQ ID NO: 4385)
369_F04	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVSGINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4217)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYVN WYQQKPGKAPKLLIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDNPLTFGGGT KVEIK (SEQ ID NO: 4386)
369_A01	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVSGINYNSG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4218)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLVIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYELPLTFGGGT KVEIK (SEQ ID NO: 4387)
373_H12	EVQLLESGGGLVQPGGSLRLSCAASGFT FSDYSMNWVRQAPGKGLEWVSGINYNSG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4219)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNSPLTFGGGT KVEIK (SEQ ID NO: 4388)
376_C07	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVSGINYNSG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4220)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLLIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 4389)
366_E02	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVSGINYNSG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4221)	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLN WYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNSPLTFGGGT KVEIK (SEQ ID NO: 4390)
376_G01	EVQLLESGGGLVQPGGSLRLSCAASGFT FDDYSMNWVRQAPGKGLEWVSGINYNSG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4222)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLVIYAVTSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYELPLTFGGGT KVEIK (SEQ ID NO: 4391)
373_F02	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVSGINYNSG	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG

	YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4223)	TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 4392)
376_E09	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVSGINYNSG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4224)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLLIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 4393)
365_H04	EVQLLESGGGLVQPGGSLRLSCAASGFT FSDYGMNWVRQAPGKGLEWVSGINYNSG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4225)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYESPLTFGGGT KVEIK (SEQ ID NO: 4394)
369_E04	EVQLLESGGGLVQPGGSLRLSCAASGFT FSDYSMNWVRQAPGKGLEWVSGINYNSG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4226)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSLPLTFGGGT KVEIK (SEQ ID NO: 4395)
374_B11	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVSGINYNSG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4227)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 4396)
376_G11	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVSGINYNSG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4228)	DIQMTQSPSSLSASVGDRVTITCRASQSIVTYVN WYQQKPGKAPKLVIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNLPLTFGGGT KVEIK (SEQ ID NO: 4397)
374_E04	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVSGINYNSG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4229)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLLIYAVTSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNNPLTFGGGT KVEIK (SEQ ID NO: 4398)
373_E08	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYGMNWVRQAPGKGLEWVSGINYNSG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4230)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVN WYQQKPGKAPKLLIYAVTSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYESPLTFGGGT KVEIK (SEQ ID NO: 4399)
375_B10	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVSGINYNSG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4231)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLLIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 4400)
365_E08	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVSGINYNSG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4232)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYVN WYQQKPGKAPKLVIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 4401)
374_G02	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVSGINYNSG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4233)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 4402)
373_D09	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVSGINYNSG YTSYADSVKGRFTISRDNSKNTLYLQMN	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLVIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYENPLTFGGGT

	SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4234)	KVEIK (SEQ ID NO: 4403)
365_A04	EVQLLESGGGLVQPGGSLRLSCAASGFT FSDYSMNWVRQAPGKGLEWVSGINYNSG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4235)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVN WYQQKPGKAPKLVIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSTPLTFGGGT KVEIK (SEQ ID NO: 4404)
371_B05	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVSGINYNSG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4236)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLVIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSDETPLTFGGGT KVEIK (SEQ ID NO: 4405)
376_H08	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYGMNWVRQAPGKGLEWVSNINYNGG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4237)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLLIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSDSLPLTFGGGT KVEIK (SEQ ID NO: 4406)
367_G08	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYGMNWVRQAPGKGLEWVSNINYNGG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4238)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYENPLTFGGGT KVEIK (SEQ ID NO: 4407)
372_H03	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYGMNWVRQAPGKGLEWVSNINYNGG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4239)	DIQMTQSPSSLSASVGDRVTITCRASQSIITYVN WYQQKPGKAPKLLIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNLPLTFGGGT KVEIK (SEQ ID NO: 4408)
366_E03	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYGMNWVRQAPGKGLEWVSNINYNGG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4240)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLVIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSNPLTFGGGT KVEIK (SEQ ID NO: 4409)
371_F12	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVSNINYNGG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4241)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSNNLPLTFGGGT KVEIK (SEQ ID NO: 4410)
366_C03	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYGMNWVRQAPGKGLEWVSNINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4242)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSNPLTFGGGT KVEIK (SEQ ID NO: 4411)
376_A01	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYGMNWVRQAPGKGLEWVSNINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4243)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSTPLTFGGGT KVEIK (SEQ ID NO: 4412)
365_E03	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVSNINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4244)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLLIYAATSLHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSDERPLTFGGGT KVEIK (SEQ ID NO: 4413)
371_B10	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVSNINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 4414)

	GTLVTVSS (SEQ ID NO: 4245)	
369_G09	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVSNINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4246)	DIQMTQSPSSLSASVGDRVTITCRASQSIVTYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 4415)
369_A06	EVQLLESGGGLVQPGGSLRLSCAASGFT FSDYGMNWVRQAPGKGLEWVSNINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4247)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLLIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 4416)
369_C08	EVQLLESGGGLVQPGGSLRLSCAASGFT FSDYGMNWVRQAPGKGLEWVSNINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4248)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLVIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYENPLTFGGGT KVEIK (SEQ ID NO: 4417)
373_A07	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVSNINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4249)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSDNLPLTFGGGT KVEIK (SEQ ID NO: 4418)
367_D02	EVQLLESGGGLVQPGGSLRLSCAASGFT FDDYSMNWVRQAPGKGLEWVSNINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4250)	DIQMTQSPSSLSASVGDRVTITCRASQSIVTYVN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYENPLTFGGGT KVEIK (SEQ ID NO: 4419)
374_C07	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVSNINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4251)	DIQMTQSPSSLSASVGDRVTITCRASQSIISYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSDELPLTFGGGT KVEIK (SEQ ID NO: 4420)
374_A03	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVSNINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4252)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDNPLTFGGGT KVEIK (SEQ ID NO: 4421)
365_A02	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVSNINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4253)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNSPLTFGGGT KVEIK (SEQ ID NO: 4422)
365_D06	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVSNINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4254)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSLPLTFGGGT KVEIK (SEQ ID NO: 4423)
366_C07	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVSNINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4255)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNSPLTFGGGT KVEIK (SEQ ID NO: 4424)
367_F12	EVQLLESGGGLVQPGGSLRLSCAASGFT FDDYSMNWVRQAPGKGLEWVSNINYNSG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4256)	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLN WYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSTPLTFGGGT KVEIK (SEQ ID NO: 4425)

369_E09	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVSNINYNSG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4257)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 4426)
365_G02	EVQLLESGGGLVQPGGSLRLSCAASGFT FSDYSMNWVRQAPGKGLEWVSNINYNSG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4258)	DIQMTQSPSSLSASVGDRVTITCRASQSIVTYLN WYQQKPGKAPKLVIYAVTSLHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYELPLTFGGGT KVEIK (SEQ ID NO: 4427)
373_D02	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVSNINYNSG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4259)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLLIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 4428)
374_E03	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVSNINYNSG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4260)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLVIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 4429)
374_D11	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYGMNWVRQAPGKGLEWVSNINYNSG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4261)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYETPLTFGGGT KVEIK (SEQ ID NO: 4430)
370_D07	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVSNINYNSG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4262)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLVIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYESPLTFGGGT KVEIK (SEQ ID NO: 4431)
374_A08	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVSNINYNSG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4263)	DIQMTQSPSSLSASVGDRVTITCRASQSIVTYLN WYQQKPGKAPKLLIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 4432)
374_G01	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVSNINYNSG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4264)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLLIYATTSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNLPLTFGGGT KVEIK (SEQ ID NO: 4433)
374_G12	EVQLLESGGGLVQPGGSLRLSCAASGFT FDDYGMNWVRQAPGKGLEWVSSINYNGG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4265)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLVIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNSPLTFGGGT KVEIK (SEQ ID NO: 4434)
375_G10	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVSSINYNGG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4266)	DIQMTQSPSSLSASVGDRVTITCRASQSIVTYLN WYQQKPGKAPKLVIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 4435)
369_H11	EVQLLESGGGLVQPGGSLRLSCAASGFT FSDYGMNWVRQAPGKGLEWVSSINYNGG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4267)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLLIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 4436)
375_G12	EVQLLESGGGLVQPGGSLRLSCAASGFT	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVN

	FDSYGMHWVRQAPGKGLEWVSSINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4268)	WYQQKPGKAPKLLIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 4437)
366_F06	EVQLLESGGGLVQPGGSLRLSCAASGFT FSDYGMNWVRQAPGKGLEWVSSINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4269)	DIQMTQSPSSLSASVGDRVTITCRASQSISTYLN WYQQKPGKAPKLLIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSNPLTFGGGT KVEIK (SEQ ID NO: 4438)
368_G07	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMHWVRQAPGKGLEWVSSINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4270)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 4439)
367_H04	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVSSINYNGG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4271)	DIQMTQSPSSLSASVGDRVTITCRASQSILTYVN WYQQKPGKAPKLLIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSDNNPLTFGGGT KVEIK (SEQ ID NO: 4440)
374_E06	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVSSINYNSG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4272)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYLN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 4441)
370_A10	EVQLLESGGGLVQPGGSLRLSCAASGFT FSDYSMNWVRQAPGKGLEWVSSINYNSG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4273)	DIQMTQSPSSLSASVGDRVTITCRASQSILSYVN WYQQKPGKAPKLLIYAATSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDTPLTFGGGT KVEIK (SEQ ID NO: 4442)
368_H10	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVSSINYNSG YKGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4274)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVN WYQQKPGKAPKLVIYAVTSLASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYETPLTFGGGT KVEIK (SEQ ID NO: 4443)
368_G08	EVQLLESGGGLVQPGGSLRLSCAASGFT FDDYGMNWVRQAPGKGLEWVSSINYNSG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4275)	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYVN WYQQKPGKAPKLLIYAATSRHSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYNNPLTFGGGT KVEIK (SEQ ID NO: 4444)
365_H09	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVSSINYNSG YKSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4276)	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLN WYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSTPLTFGGGT KVEIK (SEQ ID NO: 4445)
370_A08	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVSSINYNSG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4277)	DIQMTQSPSSLSASVGDRVTITCRASQSIVTYLN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYDLPLTFGGGT KVEIK (SEQ ID NO: 4446)
368_B05	EVQLLESGGGLVQPGGSLRLSCAASGFT FDSYSMNWVRQAPGKGLEWVSSINYNSG YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4278)	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLN WYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSTPLTFGGGT KVEIK (SEQ ID NO: 4447)
375_F01	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYSMNWVRQAPGKGLEWVSSINYNSG	DIQMTQSPSSLSASVGDRVTITCRASQSIVSYLN WYQQKPGKAPKLVIYAATSRASGVPSRFSGSGSG

	YTGYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4279)	TDFTLTISSLQPEDFATYYCQQSYDNPLTFGGGT KVEIK (SEQ ID NO: 4448)
374_F09	EVQLLESGGGLVQPGGSLRLSCAASGFT FSSYGMNWVRQAPGKGLEWVSSINYNSG YTSYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARSATWHDTHLDYWGQ GTLVTVSS (SEQ ID NO: 4280)	DIQMTQSPSSLSASVGDRVTITCRASQSISSYVN WYQQKPGKAPKLLIYAATSRASGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQSYSTPLTFGGGT KVEIK (SEQ ID NO: 4449)

Table 3F provides the amino acid sequences of the CDRs of the antibodies shown in Table 2F.

Table 3F: CDR sequences for Group VI antibodies

Ab	HCDR1	HCDR2	HCDR3	LCDR1	LCDR2	LCDR3
365_E02	SSYSMN (SEQ ID NO: 4450)	WVANINYNGGYTS (SEQ ID NO: 4619)	AKSATWHDTHLD (SEQ ID NO: 4788)	ISYLNWY (SEQ ID NO: 4957)	LLIYAATSRA (SEQ ID NO: 5126)	QQSYENPL (SEQ ID NO: 5295)
370_G12	SSYSMN (SEQ ID NO: 4451)	WVAGINYNGGYKG (SEQ ID NO: 4620)	ARSATWHDTALD (SEQ ID NO: 4789)	ITYLNWY (SEQ ID NO: 4958)	LLIYAATSLA (SEQ ID NO: 5127)	QQSDESPL (SEQ ID NO: 5296)
368_C01	DSYGMN (SEQ ID NO: 4452)	WVAGINYNGGYTG (SEQ ID NO: 4621)	ARSATWHDTALD (SEQ ID NO: 4790)	ITYLNWY (SEQ ID NO: 4959)	LLIYAATSRA (SEQ ID NO: 5128)	QQSYDSPL (SEQ ID NO: 5297)
376_C06	SSYGMN (SEQ ID NO: 4453)	WVAGINYNGGYTS (SEQ ID NO: 4622)	ARSATWHDTALD (SEQ ID NO: 4791)	LSYLNWY (SEQ ID NO: 4960)	LVIYAATSRA (SEQ ID NO: 5129)	QQSYDSPL (SEQ ID NO: 5298)
368_D10	DSYGMN (SEQ ID NO: 4454)	WVAGINYNSGYTS (SEQ ID NO: 4623)	ARSATWHDTALD (SEQ ID NO: 4792)	LSYLNWY (SEQ ID NO: 4961)	LVIYAATSRA (SEQ ID NO: 5130)	QQSYDSPL (SEQ ID NO: 5299)
365_G12	SSYGMN (SEQ ID NO: 4455)	WVAGINYNSGYTS (SEQ ID NO: 4624)	ARSATWHDTALD (SEQ ID NO: 4793)	LSYVNWY (SEQ ID NO: 4962)	LVIYAATSRA (SEQ ID NO: 5131)	QQSYSNPL (SEQ ID NO: 5300)
367_C03	SSYSMN (SEQ ID NO: 4456)	WVANINYNGGYTG (SEQ ID NO: 4625)	ARSATWHDTALD (SEQ ID NO: 4794)	LSYVNWY (SEQ ID NO: 4963)	LVIYATTSRA (SEQ ID NO: 5132)	QQSYENPL (SEQ ID NO: 5301)
367_H07	SSYSMN (SEQ ID NO: 4457)	WVANINYNGGYTG (SEQ ID NO: 4626)	ARSATWHDTALD (SEQ ID NO: 4795)	LSYVNWY (SEQ ID NO: 4964)	LVIYATTSRA (SEQ ID NO: 5133)	QQSYENPL (SEQ ID NO: 5302)
371_D03	DSYGMN (SEQ ID NO: 4458)	WVANINYNGGYTS (SEQ ID NO: 4627)	ARSATWHDTALD (SEQ ID NO: 4796)	LTYVNWY (SEQ ID NO: 4965)	LVIYAATSLA (SEQ ID NO: 5134)	QQSYNTPL (SEQ ID NO: 5303)

369_C10	SSYSMN (SEQ ID NO: 4459)	WVANINYNGGYTS (SEQ ID NO: 4628)	ARSATWHDTALD (SEQ ID NO: 4797)	VTYLNWY (SEQ ID NO: 4966)	LLIYAATSLH (SEQ ID NO: 5135)	QQSDSLPL (SEQ ID NO: 5304)
367_F05	SSYGMN (SEQ ID NO: 4460)	WVASINYNGGYTG (SEQ ID NO: 4629)	ARSATWHDTALD (SEQ ID NO: 4798)	LSYVNWY (SEQ ID NO: 4967)	LLIYAATSRA (SEQ ID NO: 5136)	QQSYSSPL (SEQ ID NO: 5305)
365_C07	SDYGMN (SEQ ID NO: 4461)	WVASINYNGGYTS (SEQ ID NO: 4630)	ARSATWHDTALD (SEQ ID NO: 4799)	VSYVNWY (SEQ ID NO: 4968)	LLIYAATSRA (SEQ ID NO: 5137)	QQSYDTPL (SEQ ID NO: 5306)
374_C08	DSYGMN (SEQ ID NO: 4462)	WVSGINYNSGYKS (SEQ ID NO: 4631)	ARSATWHDTALD (SEQ ID NO: 4800)	LSYVNWY (SEQ ID NO: 4969)	LLIYAVTSRA (SEQ ID NO: 5138)	QQSYDSPL (SEQ ID NO: 5307)
376_A06	DSYSMN (SEQ ID NO: 4463)	WVSGINYNSGYTS (SEQ ID NO: 4632)	ARSATWHDTALD (SEQ ID NO: 4801)	LSYLNWY (SEQ ID NO: 4970)	LVIYYVSNRA (SEQ ID NO: 5139)	QQSYDNPL (SEQ ID NO: 5308)
376_B07	DSYSMN (SEQ ID NO: 4464)	WVSGINYNSGYTS (SEQ ID NO: 4633)	ARSATWHDTALD (SEQ ID NO: 4802)	LSYLNWY (SEQ ID NO: 4971)	LVIYYVSNRA (SEQ ID NO: 5140)	QQSYDNPL (SEQ ID NO: 5309)
365_F07	SSYSMN (SEQ ID NO: 4465)	WVSNINYNGGYKS (SEQ ID NO: 4634)	ARSATWHDTALD (SEQ ID NO: 4803)	LSYVNWY (SEQ ID NO: 4972)	LVIYAATSRA (SEQ ID NO: 5141)	QQSYDLPL (SEQ ID NO: 5310)
369_E10	SSYSMN (SEQ ID NO: 4466)	WVSNINYNGGYKS (SEQ ID NO: 4635)	ARSATWHDTALD (SEQ ID NO: 4804)	LSYVNWY (SEQ ID NO: 4973)	LVIYAATSRA (SEQ ID NO: 5142)	QQSYDLPL (SEQ ID NO: 5311)
373_E03	DSYGMN (SEQ ID NO: 4467)	WVSNINYNGGYTG (SEQ ID NO: 4636)	ARSATWHDTALD (SEQ ID NO: 4805)	LSYVNWY (SEQ ID NO: 4974)	LVIYAATSRA (SEQ ID NO: 5143)	QQSYDLPL (SEQ ID NO: 5312)
366_B04	DSYSMN (SEQ ID NO: 4468)	WVAGINYNGGYKG (SEQ ID NO: 4637)	ARSATWHDTHLD (SEQ ID NO: 4806)	LTYVNWY (SEQ ID NO: 4975)	LVIYAATSRH (SEQ ID NO: 5144)	QQSYDTPL (SEQ ID NO: 5313)

376_F12	DDYSMN (SEQ ID NO: 4469)	WVAGINYNGGYKS (SEQ ID NO: 4638)	ARSATWHDTHLD (SEQ ID NO: 4807)	ISYVNWY (SEQ ID NO: 4976)	LLIYAASSLQ (SEQ ID NO: 5145)	QQSYSTPL (SEQ ID NO: 5314)
369_F07	DSYSMN (SEQ ID NO: 4470)	WVAGINYNGGYKS (SEQ ID NO: 4639)	ARSATWHDTHLD (SEQ ID NO: 4808)	LSYVNWY (SEQ ID NO: 4977)	LVIYAATSRA (SEQ ID NO: 5146)	QQSYESPL (SEQ ID NO: 5315)
368_C06	DSYSMN (SEQ ID NO: 4471)	WVAGINYNGGYKS (SEQ ID NO: 4640)	ARSATWHDTHLD (SEQ ID NO: 4809)	SSYLNWY (SEQ ID NO: 4978)	LLIYAASSLQ (SEQ ID NO: 5147)	QQSYSTPL (SEQ ID NO: 5316)
376_E12	SSYSMN (SEQ ID NO: 4472)	WVAGINYNGGYKS (SEQ ID NO: 4641)	ARSATWHDTHLD (SEQ ID NO: 4810)	LSYLNWY (SEQ ID NO: 4979)	LLIYAASSLQ (SEQ ID NO: 5148)	QQSYSTPL (SEQ ID NO: 5317)
371_H01	DSYSMN (SEQ ID NO: 4473)	WVAGINYNGGYTG (SEQ ID NO: 4642)	ARSATWHDTHLD (SEQ ID NO: 4811)	ITYLNWY (SEQ ID NO: 4980)	LLIYAASSLQ (SEQ ID NO: 5149)	QQSYSTPL (SEQ ID NO: 5318)
367_E02	DSYSMN (SEQ ID NO: 4474)	WVAGINYNGGYTG (SEQ ID NO: 4643)	ARSATWHDTHLD (SEQ ID NO: 4812)	SSYLNWY (SEQ ID NO: 4981)	LLIYAASSLQ (SEQ ID NO: 5150)	QQSYSTPL (SEQ ID NO: 5319)
365_F04	SSYGMN (SEQ ID NO: 4475)	WVAGINYNGGYTG (SEQ ID NO: 4644)	ARSATWHDTHLD (SEQ ID NO: 4813)	VTYVNWY (SEQ ID NO: 4982)	LLIYAATSRA (SEQ ID NO: 5151)	QQSYDTPL (SEQ ID NO: 5320)
370_A09	SSYSMN (SEQ ID NO: 4476)	WVAGINYNGGYTG (SEQ ID NO: 4645)	ARSATWHDTHLD (SEQ ID NO: 4814)	LTYLNWY (SEQ ID NO: 4983)	LVIYAATSRA (SEQ ID NO: 5152)	QQSYDTPL (SEQ ID NO: 5321)
365_B03	SSYSMN (SEQ ID NO: 4477)	WVAGINYNGGYTG (SEQ ID NO: 4646)	ARSATWHDTHLD (SEQ ID NO: 4815)	VSYLNWY (SEQ ID NO: 4984)	LLIYAATSRA (SEQ ID NO: 5153)	QQSYENPL (SEQ ID NO: 5322)
369_A05	SSYSMN (SEQ ID NO: 4478)	WVAGINYNGGYTG (SEQ ID NO: 4647)	ARSATWHDTHLD (SEQ ID NO: 4816)	LTYVNWY (SEQ ID NO: 4985)	LVIYAATSRA (SEQ ID NO: 5154)	QQSYESPL (SEQ ID NO: 5323)

373_H10	SSYSMN (SEQ ID NO: 4479)	WVAGINYNGGYTG (SEQ ID NO: 4648)	ARSATWHDTHLD (SEQ ID NO: 4817)	LSYVNWY (SEQ ID NO: 4986)	LLIYAATSRA (SEQ ID NO: 5155)	QQSYSLPL (SEQ ID NO: 5324)
367_A09	DSYGMN (SEQ ID NO: 4480)	WVAGINYNGGYTS (SEQ ID NO: 4649)	ARSATWHDTHLD (SEQ ID NO: 4818)	LSYVNWY (SEQ ID NO: 4987)	LVIYAATSRH (SEQ ID NO: 5156)	QQSYDTPL (SEQ ID NO: 5325)
370_F08	DSYSMN (SEQ ID NO: 4481)	WVAGINYNGGYTS (SEQ ID NO: 4650)	ARSATWHDTHLD (SEQ ID NO: 4819)	ISYVNWY (SEQ ID NO: 4988)	LLIYAATSRH (SEQ ID NO: 5157)	QQSYNLPL (SEQ ID NO: 5326)
376_B01	DSYSMN (SEQ ID NO: 4482)	WVAGINYNGGYTS (SEQ ID NO: 4651)	ARSATWHDTHLD (SEQ ID NO: 4820)	LTYVNWY (SEQ ID NO: 4989)	LVIYAATSRA (SEQ ID NO: 5158)	QQSYNSPL (SEQ ID NO: 5327)
365_D05	DSYSMN (SEQ ID NO: 4483)	WVAGINYNGGYTS (SEQ ID NO: 4652)	ARSATWHDTHLD (SEQ ID NO: 4821)	LTYVNWY (SEQ ID NO: 4990)	LLIYAATSRA (SEQ ID NO: 5159)	QQSYNSPL (SEQ ID NO: 5328)
373_E04	DSYSMN (SEQ ID NO: 4484)	WVAGINYNGGYTS (SEQ ID NO: 4653)	ARSATWHDTHLD (SEQ ID NO: 4822)	LTYVNWY (SEQ ID NO: 4991)	LLIYAATSRA (SEQ ID NO: 5160)	QQSYNSPL (SEQ ID NO: 5329)
368_G05	DSYSMN (SEQ ID NO: 4485)	WVAGINYNGGYTS (SEQ ID NO: 4654)	ARSATWHDTHLD (SEQ ID NO: 4823)	LTYVNWY (SEQ ID NO: 4992)	LLIYAATSLH (SEQ ID NO: 5161)	QQSYNTPL (SEQ ID NO: 5330)
365_A01	SDYGMN (SEQ ID NO: 4486)	WVAGINYNGGYTS (SEQ ID NO: 4655)	ARSATWHDTHLD (SEQ ID NO: 4824)	LTYVNWY (SEQ ID NO: 4993)	LVIYATTSLA (SEQ ID NO: 5162)	QQSYSTPL (SEQ ID NO: 5331)
373_H06	SSYGMH (SEQ ID NO: 4487)	WVAGINYNGGYTS (SEQ ID NO: 4656)	ARSATWHDTHLD (SEQ ID NO: 4825)	ISYVNWY (SEQ ID NO: 4994)	LLIYAATSLA (SEQ ID NO: 5163)	QQSYDLPL (SEQ ID NO: 5332)
369_G07	SSYSMN (SEQ ID NO: 4488)	WVAGINYNGGYTS (SEQ ID NO: 4657)	ARSATWHDTHLD (SEQ ID NO: 4826)	LTYVNWY (SEQ ID NO: 4995)	LVIYAATSRA (SEQ ID NO: 5164)	QQSYDNPL (SEQ ID NO: 5333)

373_G05	SSYSMN (SEQ ID NO: 4489)	WVAGINYNGGYTS (SEQ ID NO: 4658)	ARSATWHDTHLD (SEQ ID NO: 4827)	LSYLNWY (SEQ ID NO: 4996)	LLIYAATSLA (SEQ ID NO: 5165)	QQSYELPL (SEQ ID NO: 5334)
372_F07	DDYSMN (SEQ ID NO: 4490)	WVAGINYNSGYKG (SEQ ID NO: 4659)	ARSATWHDTHLD (SEQ ID NO: 4828)	LTYLNWY (SEQ ID NO: 4997)	LVIYAATSRA (SEQ ID NO: 5166)	QQSYELPL (SEQ ID NO: 5335)
370_H03	DSYSMN (SEQ ID NO: 4491)	WVAGINYNSGYKG (SEQ ID NO: 4660)	ARSATWHDTHLD (SEQ ID NO: 4829)	LTYLNWY (SEQ ID NO: 4998)	LLIYAATSLA (SEQ ID NO: 5167)	QQSYDTPL (SEQ ID NO: 5336)
366_A03	DSYSMN (SEQ ID NO: 4492)	WVAGINYNSGYKG (SEQ ID NO: 4661)	ARSATWHDTHLD (SEQ ID NO: 4830)	SSYLNWY (SEQ ID NO: 4999)	LLIYAATSLA (SEQ ID NO: 5168)	QQSYSNPL (SEQ ID NO: 5337)
365_A07	SSYCMN (SEQ ID NO: 4493)	WVAGINYNSGYKG (SEQ ID NO: 4662)	ARSATWHDTHLD (SEQ ID NO: 4831)	VSYLNWY (SEQ ID NO: 5000)	LLIYAATSRA (SEQ ID NO: 5169)	QQSYNLPL (SEQ ID NO: 5338)
376_B06	SSYSMN (SEQ ID NO: 4494)	WVAGINYNSGYKG (SEQ ID NO: 4663)	ARSATWHDTHLD (SEQ ID NO: 4832)	LTYLNWY (SEQ ID NO: 5001)	LLIYAATSRA (SEQ ID NO: 5170)	QQSYDLPL (SEQ ID NO: 5339)
374_C11	SSYSMN (SEQ ID NO: 4495)	WVAGINYNSGYKG (SEQ ID NO: 4664)	ARSATWHDTHLD (SEQ ID NO: 4833)	LTYLNWY (SEQ ID NO: 5002)	LLIYAATSRA (SEQ ID NO: 5171)	QQSYESPL (SEQ ID NO: 5340)
375_A06	SSYSMN (SEQ ID NO: 4496)	WVAGINYNSGYKG (SEQ ID NO: 4665)	ARSATWHDTHLD (SEQ ID NO: 4834)	LTYVNWY (SEQ ID NO: 5003)	LLIYAASSLQ (SEQ ID NO: 5172)	QQSYSTPL (SEQ ID NO: 5341)
365_B09	DSYSMN (SEQ ID NO: 4497)	WVAGINYNSGYKS (SEQ ID NO: 4666)	ARSATWHDTHLD (SEQ ID NO: 4835)	LRYLNWY (SEQ ID NO: 5004)	LLIYAATSLH (SEQ ID NO: 5173)	QQSYDNPL (SEQ ID NO: 5342)
373_E06	DSYSMN (SEQ ID NO: 4498)	WVAGINYNSGYKS (SEQ ID NO: 4667)	ARSATWHDTHLD (SEQ ID NO: 4836)	LRYLNWY (SEQ ID NO: 5005)	LLIYAATSLH (SEQ ID NO: 5174)	QQSYDNPL (SEQ ID NO: 5343)

374_C05	DSYSMN (SEQ ID NO: 4499)	WVAGINYNSGYKS (SEQ ID NO: 4668)	ARSATWHDTHLD (SEQ ID NO: 4837)	IRYLNWY (SEQ ID NO: 5006)	LVIYAATSRA (SEQ ID NO: 5175)	QQSYDNPL (SEQ ID NO: 5344)
376_C11	DSYSMN (SEQ ID NO: 4500)	WVAGINYNSGYKS (SEQ ID NO: 4669)	ARSATWHDTHLD (SEQ ID NO: 4838)	LTYLNWY (SEQ ID NO: 5007)	LVIYAATSRA (SEQ ID NO: 5176)	QQSYDNPL (SEQ ID NO: 5345)
373_C09	DSYSMN (SEQ ID NO: 4501)	WVAGINYNSGYKS (SEQ ID NO: 4670)	ARSATWHDTHLD (SEQ ID NO: 4839)	LTYLNWY (SEQ ID NO: 5008)	LVIYAATSRA (SEQ ID NO: 5177)	QQSYELPL (SEQ ID NO: 5346)
368_H01	SSYSMN (SEQ ID NO: 4502)	WVAGINYNSGYKS (SEQ ID NO: 4671)	ARSATWHDTHLD (SEQ ID NO: 4840)	LSYLNWY (SEQ ID NO: 5009)	LLIYATTSLA (SEQ ID NO: 5178)	QQSYDNPL (SEQ ID NO: 5347)
373_B03	SSYSMN (SEQ ID NO: 4503)	WVAGINYNSGYKS (SEQ ID NO: 4672)	ARSATWHDTHLD (SEQ ID NO: 4841)	LTYLNWY (SEQ ID NO: 5010)	LVIYAATSLA (SEQ ID NO: 5179)	QQSYDNPL (SEQ ID NO: 5348)
374_C04	SSYSMN (SEQ ID NO: 4504)	WVAGINYNSGYKS (SEQ ID NO: 4673)	ARSATWHDTHLD (SEQ ID NO: 4842)	LTYLNWY (SEQ ID NO: 5011)	LLIYAASSLQ (SEQ ID NO: 5180)	QQSYELPL (SEQ ID NO: 5349)
371_F05	SSYSMN (SEQ ID NO: 4505)	WVAGINYNSGYKS (SEQ ID NO: 4674)	ARSATWHDTHLD (SEQ ID NO: 4843)	LSYLNWY (SEQ ID NO: 5012)	LLIYAATSRH (SEQ ID NO: 5181)	QQSYENPL (SEQ ID NO: 5350)
369_A10	DSYSMN (SEQ ID NO: 4506)	WVAGINYNSGYTG (SEQ ID NO: 4675)	ARSATWHDTHLD (SEQ ID NO: 4844)	LSYLNWY (SEQ ID NO: 5013)	LLIYAATSRA (SEQ ID NO: 5182)	QQSYELPL (SEQ ID NO: 5351)
366_A05	SSYSMN (SEQ ID NO: 4507)	WVAGINYNSGYTG (SEQ ID NO: 4676)	ARSATWHDTHLD (SEQ ID NO: 4845)	LTYVNWY (SEQ ID NO: 5014)	LVIYAATSLA (SEQ ID NO: 5183)	QQSYNTPL (SEQ ID NO: 5352)
375_G07	DSYSMN (SEQ ID NO: 4508)	WVAGINYNSGYTS (SEQ ID NO: 4677)	ARSATWHDTHLD (SEQ ID NO: 4846)	LSYLNWY (SEQ ID NO: 5015)	LVIYAATSLA (SEQ ID NO: 5184)	QQSYDLPL (SEQ ID NO: 5353)

374_D02	DSYSMN (SEQ ID NO: 4509)	WVAGINYNSGYTS (SEQ ID NO: 4678)	ARSATWHDTHLD (SEQ ID NO: 4847)	STYVNWY (SEQ ID NO: 5016)	LLIYAVTSLA (SEQ ID NO: 5185)	QQSYDSPL (SEQ ID NO: 5354)
365_A10	SSYGMH (SEQ ID NO: 4510)	WVAGINYNSGYTS (SEQ ID NO: 4679)	ARSATWHDTHLD (SEQ ID NO: 4848)	LTYLNWY (SEQ ID NO: 5017)	LVIYAVTSLA (SEQ ID NO: 5186)	QQSYDSPL (SEQ ID NO: 5355)
375_A02	SSYSMN (SEQ ID NO: 4511)	WVAGINYNSGYTS (SEQ ID NO: 4680)	ARSATWHDTHLD (SEQ ID NO: 4849)	SSYLNWY (SEQ ID NO: 5018)	LLIYAASSLQ (SEQ ID NO: 5187)	QQSYSTPL (SEQ ID NO: 5356)
371_G03	SSYGMN (SEQ ID NO: 4512)	WVANINYNGGYKG (SEQ ID NO: 4681)	ARSATWHDTHLD (SEQ ID NO: 4850)	VTYVNWY (SEQ ID NO: 5019)	LVIYAATSLA (SEQ ID NO: 5188)	QQSYNLPL (SEQ ID NO: 5357)
370_E07	DSYSMN (SEQ ID NO: 4513)	WVANINYNGGYTG (SEQ ID NO: 4682)	ARSATWHDTHLD (SEQ ID NO: 4851)	LTYLNWY (SEQ ID NO: 5020)	LLIYAATSRA (SEQ ID NO: 5189)	QQSYDNPL (SEQ ID NO: 5358)
375_B04	DSYSMN (SEQ ID NO: 4514)	WVANINYNGGYTG (SEQ ID NO: 4683)	ARSATWHDTHLD (SEQ ID NO: 4852)	LTYLNWY (SEQ ID NO: 5021)	LLIYAATSRA (SEQ ID NO: 5190)	QQSYDNPL (SEQ ID NO: 5359)
367_G07	DSYSMN (SEQ ID NO: 4515)	WVANINYNGGYTG (SEQ ID NO: 4684)	ARSATWHDTHLD (SEQ ID NO: 4853)	LTYVNWY (SEQ ID NO: 5022)	LLIYAATSRA (SEQ ID NO: 5191)	QQSYDNPL (SEQ ID NO: 5360)
366_C02	SDYSMN (SEQ ID NO: 4516)	WVANINYNGGYTG (SEQ ID NO: 4685)	ARSATWHDTHLD (SEQ ID NO: 4854)	VSYLNWY (SEQ ID NO: 5023)	LLIYAATSRA (SEQ ID NO: 5192)	QQSYDNPL (SEQ ID NO: 5361)
375_C12	SSYSMN (SEQ ID NO: 4517)	WVANINYNGGYTG (SEQ ID NO: 4686)	ARSATWHDTHLD (SEQ ID NO: 4855)	LTYLNWY (SEQ ID NO: 5024)	LLIYAATSRA (SEQ ID NO: 5193)	QQSYDLPL (SEQ ID NO: 5362)
365_F08	DDYGMN (SEQ ID NO: 4518)	WVANINYNGGYTS (SEQ ID NO: 4687)	ARSATWHDTHLD (SEQ ID NO: 4856)	LSYVNWY (SEQ ID NO: 5025)	LLIYAATSRH (SEQ ID NO: 5194)	QQSYSLPL (SEQ ID NO: 5363)

368_G09	DSYGMH (SEQ ID NO: 4519)	WVANINYNGGYTS (SEQ ID NO: 4688)	ARSATWHDTHLD (SEQ ID NO: 4857)	VSYLNWY (SEQ ID NO: 5026)	LVIYAATSRA (SEQ ID NO: 5195)	QQSYDTPL (SEQ ID NO: 5364)
368_E11	DSYGMH (SEQ ID NO: 4520)	WVANINYNGGYTS (SEQ ID NO: 4689)	ARSATWHDTHLD (SEQ ID NO: 4858)	ISYVNWY (SEQ ID NO: 5027)	LLIYAATSRH (SEQ ID NO: 5196)	QQSYELPL (SEQ ID NO: 5365)
367_F02	DSYSMN (SEQ ID NO: 4521)	WVANINYNGGYTS (SEQ ID NO: 4690)	ARSATWHDTHLD (SEQ ID NO: 4859)	ISYVNWY (SEQ ID NO: 5028)	LLIYAATSRH (SEQ ID NO: 5197)	QQSYESPL (SEQ ID NO: 5366)
373_B08	DSYSMN (SEQ ID NO: 4522)	WVANINYNSGYKG (SEQ ID NO: 4691)	ARSATWHDTHLD (SEQ ID NO: 4860)	LTYLNWY (SEQ ID NO: 5029)	LVIYAATSLA (SEQ ID NO: 5198)	QQSYENPL (SEQ ID NO: 5367)
374_A11	SDYSMN (SEQ ID NO: 4523)	WVANINYNSGYKG (SEQ ID NO: 4692)	ARSATWHDTHLD (SEQ ID NO: 4861)	LSYVNWY (SEQ ID NO: 5030)	LVIYAATSRA (SEQ ID NO: 5199)	QQSYSSPL (SEQ ID NO: 5368)
373_B11	SSYSMN (SEQ ID NO: 4524)	WVANINYNSGYKG (SEQ ID NO: 4693)	ARSATWHDTHLD (SEQ ID NO: 4862)	LSYLNWY (SEQ ID NO: 5031)	LLIYAATSRA (SEQ ID NO: 5200)	QQSYDNPL (SEQ ID NO: 5369)
373_F03	DSYSMN (SEQ ID NO: 4525)	WVANINYNSGYTG (SEQ ID NO: 4694)	ARSATWHDTHLD (SEQ ID NO: 4863)	LTYVNWY (SEQ ID NO: 5032)	LLIYAATSRH (SEQ ID NO: 5201)	QQSYDSPL (SEQ ID NO: 5370)
372_D04	SSYSMN (SEQ ID NO: 4526)	WVANINYNSGYTG (SEQ ID NO: 4695)	ARSATWHDTHLD (SEQ ID NO: 4864)	LTYLNWY (SEQ ID NO: 5033)	LLIYAATSLH (SEQ ID NO: 5202)	QQSYDLPL (SEQ ID NO: 5371)
366_C01	SDYGMN (SEQ ID NO: 4527)	WVASINYNGGYTG (SEQ ID NO: 4696)	ARSATWHDTHLD (SEQ ID NO: 4865)	VTYLNWY (SEQ ID NO: 5034)	LLIYAATSPA (SEQ ID NO: 5203)	QQSYELPL (SEQ ID NO: 5372)
367_A01	SSYSMN (SEQ ID NO: 4528)	WVASINYNGGYTG (SEQ ID NO: 4697)	ARSATWHDTHLD (SEQ ID NO: 4866)	LTYLNWY (SEQ ID NO: 5035)	LLIYAATSRA (SEQ ID NO: 5204)	QQSYDLPL (SEQ ID NO: 5373)

366_H05	DSYGMH (SEQ ID NO: 4529)	WVASINYNGGYTS (SEQ ID NO: 4698)	ARSATWHDTHLD (SEQ ID NO: 4867)	LSYVNWY (SEQ ID NO: 5036)	LLIYAATSLA (SEQ ID NO: 5205)	QQSYDLPL (SEQ ID NO: 5374)
369_B09	DSYGMH (SEQ ID NO: 4530)	WVASINYNGGYTS (SEQ ID NO: 4699)	ARSATWHDTHLD (SEQ ID NO: 4868)	LTYLNWY (SEQ ID NO: 5037)	LLIYAATSRA (SEQ ID NO: 5206)	QQSYENPL (SEQ ID NO: 5375)
366_D07	SDYGMH (SEQ ID NO: 4531)	WVASINYNGGYTS (SEQ ID NO: 4700)	ARSATWHDTHLD (SEQ ID NO: 4869)	LTYLNWY (SEQ ID NO: 5038)	LLIYAATSLA (SEQ ID NO: 5207)	QQSYSSPL (SEQ ID NO: 5376)
369_D11	SSYGMH (SEQ ID NO: 4532)	WVASINYNGGYTS (SEQ ID NO: 4701)	ARSATWHDTHLD (SEQ ID NO: 4870)	LTYLNWY (SEQ ID NO: 5039)	LVIYAATSLA (SEQ ID NO: 5208)	QQSDELPL (SEQ ID NO: 5377)
370_B05	SSYGMN (SEQ ID NO: 4533)	WVASINYNGGYTS (SEQ ID NO: 4702)	ARSATWHDTHLD (SEQ ID NO: 4871)	LTYVNWY (SEQ ID NO: 5040)	LVIYAATSRA (SEQ ID NO: 5209)	QQSYENPL (SEQ ID NO: 5378)
366_D02	SSYSMN (SEQ ID NO: 4534)	WVASINYNGGYTS (SEQ ID NO: 4703)	ARSATWHDTHLD (SEQ ID NO: 4872)	LSYVNWY (SEQ ID NO: 5041)	LLIYATTSLA (SEQ ID NO: 5210)	QQSYDLPL (SEQ ID NO: 5379)
368_H12	DSYSMN (SEQ ID NO: 4535)	WVASINYNSGYKG (SEQ ID NO: 4704)	ARSATWHDTHLD (SEQ ID NO: 4873)	VTYLNWY (SEQ ID NO: 5042)	LLIYAATSRA (SEQ ID NO: 5211)	QQSYESPL (SEQ ID NO: 5380)
368_F12	DDYSMN (SEQ ID NO: 4536)	WVASINYNSGYKS (SEQ ID NO: 4705)	ARSATWHDTHLD (SEQ ID NO: 4874)	VTYLNWY (SEQ ID NO: 5043)	LVIYAATSLA (SEQ ID NO: 5212)	QQSYDLPL (SEQ ID NO: 5381)
370_A06	SSYSMN (SEQ ID NO: 4537)	WVASINYNSGYKS (SEQ ID NO: 4706)	ARSATWHDTHLD (SEQ ID NO: 4875)	VTYLNWY (SEQ ID NO: 5044)	LVIYAATSLA (SEQ ID NO: 5213)	QQSYDLPL (SEQ ID NO: 5382)
369_F12	SSYSMN (SEQ ID NO: 4538)	WVASINYNSGYKS (SEQ ID NO: 4707)	ARSATWHDTHLD (SEQ ID NO: 4876)	ISYLNWY (SEQ ID NO: 5045)	LLIYAVTSLA (SEQ ID NO: 5214)	QQSYENPL (SEQ ID NO: 5383)

366_A09	SDYGMH (SEQ ID NO: 4539)	WVASINYNSGYTS (SEQ ID NO: 4708)	ARSATWHDTHLD (SEQ ID NO: 4877)	LTYLNWY (SEQ ID NO: 5046)	LLIYAATSRH (SEQ ID NO: 5215)	QQSYETPL (SEQ ID NO: 5384)
368_H07	SSYGMH (SEQ ID NO: 4540)	WVASINYNSGYTS (SEQ ID NO: 4709)	ARSATWHDTHLD (SEQ ID NO: 4878)	LSYLNWY (SEQ ID NO: 5047)	LLIYAATSRA (SEQ ID NO: 5216)	QQSYENPL (SEQ ID NO: 5385)
370_C04	SSYGMN (SEQ ID NO: 4541)	WVASINYNSGYTS (SEQ ID NO: 4710)	ARSATWHDTHLD (SEQ ID NO: 4879)	LSYLNWY (SEQ ID NO: 5048)	LLIYAASSLQ (SEQ ID NO: 5217)	QQSYENPL (SEQ ID NO: 5386)
373_E02	DSYGMH (SEQ ID NO: 4542)	WVSGINYNGGYKG (SEQ ID NO: 4711)	ARSATWHDTHLD (SEQ ID NO: 4880)	VRYLNWY (SEQ ID NO: 5049)	LLIYAASSLQ (SEQ ID NO: 5218)	QQSYSTPL (SEQ ID NO: 5387)
374_E09	SDYSMN (SEQ ID NO: 4543)	WVSGINYNGGYKG (SEQ ID NO: 4712)	ARSATWHDTHLD (SEQ ID NO: 4881)	VTYLNWY (SEQ ID NO: 5050)	LVIYAATSRA (SEQ ID NO: 5219)	QQSYDSPL (SEQ ID NO: 5388)
371_C09	DSYSMN (SEQ ID NO: 4544)	WVSGINYNGGYKS (SEQ ID NO: 4713)	ARSATWHDTHLD (SEQ ID NO: 4882)	LTYVNWY (SEQ ID NO: 5051)	LLIYAASSLQ (SEQ ID NO: 5220)	QQSYDNPL (SEQ ID NO: 5389)
369_B12	DSYSMN (SEQ ID NO: 4545)	WVSGINYNGGYKS (SEQ ID NO: 4714)	ARSATWHDTHLD (SEQ ID NO: 4883)	LTYVNWY (SEQ ID NO: 5052)	LLIYATTSLA (SEQ ID NO: 5221)	QQSYDSPL (SEQ ID NO: 5390)
369_B02	DSYSMN (SEQ ID NO: 4546)	WVSGINYNGGYKS (SEQ ID NO: 4715)	ARSATWHDTHLD (SEQ ID NO: 4884)	LSYLNWY (SEQ ID NO: 5053)	LVIYAATSRA (SEQ ID NO: 5222)	QQSYNLPL (SEQ ID NO: 5391)
365_C09	SDYGMN (SEQ ID NO: 4547)	WVSGINYNGGYKS (SEQ ID NO: 4716)	ARSATWHDTHLD (SEQ ID NO: 4885)	VSYVNWY (SEQ ID NO: 5054)	LLIYAATSRA (SEQ ID NO: 5223)	QQSYDTPL (SEQ ID NO: 5392)
374_B09	SSYSMN (SEQ ID NO: 4548)	WVSGINYNGGYKS (SEQ ID NO: 4717)	ARSATWHDTHLD (SEQ ID NO: 4886)	VRYLNWY (SEQ ID NO: 5055)	LVIYAATSLA (SEQ ID NO: 5224)	QQSYELPL (SEQ ID NO: 5393)

374_D12	DSYSMN (SEQ ID NO: 4549)	WVSGINYNGGYTG (SEQ ID NO: 4718)	ARSATWHDTHLD (SEQ ID NO: 4887)	VSYVNWY (SEQ ID NO: 5056)	LVIYAATSRA (SEQ ID NO: 5225)	QQSYDLPL (SEQ ID NO: 5394)
374_C02	DSYSMN (SEQ ID NO: 4550)	WVSGINYNGGYTG (SEQ ID NO: 4719)	ARSATWHDTHLD (SEQ ID NO: 4888)	LSYLNWY (SEQ ID NO: 5057)	LLIYAATSRH (SEQ ID NO: 5226)	QQSYDSPL (SEQ ID NO: 5395)
374_H08	DSYSMN (SEQ ID NO: 4551)	WVSGINYNGGYTG (SEQ ID NO: 4720)	ARSATWHDTHLD (SEQ ID NO: 4889)	LSYLNWY (SEQ ID NO: 5058)	LLIYAATSLH (SEQ ID NO: 5227)	QQSYENPL (SEQ ID NO: 5396)
369_D06	DSYSMN (SEQ ID NO: 4552)	WVSGINYNGGYTG (SEQ ID NO: 4721)	ARSATWHDTHLD (SEQ ID NO: 4890)	LTYLNWY (SEQ ID NO: 5059)	LLIYAATSRA (SEQ ID NO: 5228)	QQSYETPL (SEQ ID NO: 5397)
366_B06	DSYSMN (SEQ ID NO: 4553)	WVSGINYNGGYTS (SEQ ID NO: 4722)	ARSATWHDTHLD (SEQ ID NO: 4891)	LTYVNWY (SEQ ID NO: 5060)	LVIYAAPSLA (SEQ ID NO: 5229)	QQSYXTPL (SEQ ID NO: 5398)
367_A11	SSYGMH (SEQ ID NO: 4554)	WVSGINYNGGYTS (SEQ ID NO: 4723)	ARSATWHDTHLD (SEQ ID NO: 4892)	LSYVNWY (SEQ ID NO: 5061)	LVIYATTSLA (SEQ ID NO: 5230)	QQSYNSPL (SEQ ID NO: 5399)
369_F04	SSYGMN (SEQ ID NO: 4555)	WVSGINYNGGYTS (SEQ ID NO: 4724)	ARSATWHDTHLD (SEQ ID NO: 4893)	ISYVNWY (SEQ ID NO: 5062)	LLIYAATSRH (SEQ ID NO: 5231)	QQSYDNPL (SEQ ID NO: 5400)
369_A01	DSYSMN (SEQ ID NO: 4556)	WVSGINYNSGYKG (SEQ ID NO: 4725)	ARSATWHDTHLD (SEQ ID NO: 4894)	LTYVNWY (SEQ ID NO: 5063)	LVIYAATSLA (SEQ ID NO: 5232)	QQSYELPL (SEQ ID NO: 5401)
373_H12	SDYSMN (SEQ ID NO: 4557)	WVSGINYNSGYKG (SEQ ID NO: 4726)	ARSATWHDTHLD (SEQ ID NO: 4895)	LTYLNWY (SEQ ID NO: 5064)	LLIYAATSRA (SEQ ID NO: 5233)	QQSYNSPL (SEQ ID NO: 5402)
376_C07	SSYSMN (SEQ ID NO: 4558)	WVSGINYNSGYKG (SEQ ID NO: 4727)	ARSATWHDTHLD (SEQ ID NO: 4896)	LSYVNWY (SEQ ID NO: 5065)	LLIYAATSRH (SEQ ID NO: 5234)	QQSYDLPL (SEQ ID NO: 5403)

366_E02	SSYSMN (SEQ ID NO: 4559)	WVSGINYNSGYKG (SEQ ID NO: 4728)	ARSATWHDTHLD (SEQ ID NO: 4897)	SSYLNWY (SEQ ID NO: 5066)	LLIYAASSLQ (SEQ ID NO: 5235)	QQSYNSPL (SEQ ID NO: 5404)
376_G01	DDYSMN (SEQ ID NO: 4560)	WVSGINYNSGYKS (SEQ ID NO: 4729)	ARSATWHDTHLD (SEQ ID NO: 4898)	LSYVNWY (SEQ ID NO: 5067)	LVIYAVTSRA (SEQ ID NO: 5236)	QQSYELPL (SEQ ID NO: 5405)
373_F02	DSYSMN (SEQ ID NO: 4561)	WVSGINYNSGYKS (SEQ ID NO: 4730)	ARSATWHDTHLD (SEQ ID NO: 4899)	LTYLNWY (SEQ ID NO: 5068)	LLIYAATSRA (SEQ ID NO: 5237)	QQSYDTPL (SEQ ID NO: 5406)
376_E09	DSYSMN (SEQ ID NO: 4562)	WVSGINYNSGYKS (SEQ ID NO: 4731)	ARSATWHDTHLD (SEQ ID NO: 4900)	LTYLNWY (SEQ ID NO: 5069)	LLIYAATSRH (SEQ ID NO: 5238)	QQSYDTPL (SEQ ID NO: 5407)
365_H04	SDYCMN (SEQ ID NO: 4563)	WVSGINYNSGYKS (SEQ ID NO: 4732)	ARSATWHDTHLD (SEQ ID NO: 4901)	LTYVNWY (SEQ ID NO: 5070)	LVIYAATSRA (SEQ ID NO: 5239)	QQSYESPL (SEQ ID NO: 5408)
369_E04	SDYSMN (SEQ ID NO: 4564)	WVSGINYNSGYKS (SEQ ID NO: 4733)	ARSATWHDTHLD (SEQ ID NO: 4902)	LSYVNWY (SEQ ID NO: 5071)	LVIYAATSRA (SEQ ID NO: 5240)	QQSYSLPL (SEQ ID NO: 5409)
374_B11	SSYSMN (SEQ ID NO: 4565)	WVSGINYNSGYKS (SEQ ID NO: 4734)	ARSATWHDTHLD (SEQ ID NO: 4903)	LTYVNWY (SEQ ID NO: 5072)	LVIYAATSRA (SEQ ID NO: 5241)	QQSYDLPL (SEQ ID NO: 5410)
376_G11	SSYSMN (SEQ ID NO: 4566)	WVSGINYNSGYKS (SEQ ID NO: 4735)	ARSATWHDTHLD (SEQ ID NO: 4904)	VTYVNWY (SEQ ID NO: 5073)	LVIYAATSLA (SEQ ID NO: 5242)	QQSYNLPL (SEQ ID NO: 5411)
374_E04	SSYSMN (SEQ ID NO: 4567)	WVSGINYNSGYKS (SEQ ID NO: 4736)	ARSATWHDTHLD (SEQ ID NO: 4905)	LSYLNWY (SEQ ID NO: 5074)	LLIYAVTSRA (SEQ ID NO: 5243)	QQSYNNPL (SEQ ID NO: 5412)
373_E08	DSYGMN (SEQ ID NO: 4568)	WVSGINYNSGYTS (SEQ ID NO: 4737)	ARSATWHDTHLD (SEQ ID NO: 4906)	VSYVNWY (SEQ ID NO: 5075)	LLIYAVTSRA (SEQ ID NO: 5244)	QQSYESPL (SEQ ID NO: 5413)

375_B10	DSYSMN (SEQ ID NO: 4569)	WVSGINYNSGYTS (SEQ ID NO: 4738)	ARSATWHDTHLD (SEQ ID NO: 4907)	LSYLNWY (SEQ ID NO: 5076)	LLIYAATSRH (SEQ ID NO: 5245)	QQSYDLPL (SEQ ID NO: 5414)
365_E08	DSYSMN (SEQ ID NO: 4570)	WVSGINYNSGYTS (SEQ ID NO: 4739)	ARSATWHDTHLD (SEQ ID NO: 4908)	ISYVNWY (SEQ ID NO: 5077)	LVIYAATSLA (SEQ ID NO: 5246)	QQSYDLPL (SEQ ID NO: 5415)
374_G02	DSYSMN (SEQ ID NO: 4571)	WVSGINYNSGYTS (SEQ ID NO: 4740)	ARSATWHDTHLD (SEQ ID NO: 4909)	LTYLNWY (SEQ ID NO: 5078)	LLIYAASSLQ (SEQ ID NO: 5247)	QQSYDTPL (SEQ ID NO: 5416)
373_D09	DSYSMN (SEQ ID NO: 4572)	WVSGINYNSGYTS (SEQ ID NO: 4741)	ARSATWHDTHLD (SEQ ID NO: 4910)	LTYLNWY (SEQ ID NO: 5079)	LVIYAATSRH (SEQ ID NO: 5248)	QQSYENPL (SEQ ID NO: 5417)
365_A04	SDYSMN (SEQ ID NO: 4573)	WVSGINYNSGYTS (SEQ ID NO: 4742)	ARSATWHDTHLD (SEQ ID NO: 4911)	VSYVNWY (SEQ ID NO: 5080)	LVIYAATSLA (SEQ ID NO: 5249)	QQSYSTPL (SEQ ID NO: 5418)
371_B05	SSYSMN (SEQ ID NO: 4574)	WVSGINYNSGYTS (SEQ ID NO: 4743)	ARSATWHDTHLD (SEQ ID NO: 4912)	LTYLNWY (SEQ ID NO: 5081)	LVIYAATSLA (SEQ ID NO: 5250)	QQSDETPL (SEQ ID NO: 5419)
376_H08	DSYGMN (SEQ ID NO: 4575)	WVSNINYNGGYKG (SEQ ID NO: 4744)	ARSATWHDTHLD (SEQ ID NO: 4913)	LTYLNWY (SEQ ID NO: 5082)	LLIYAATSRH (SEQ ID NO: 5251)	QQSDSLPL (SEQ ID NO: 5420)
367_G08	DSYGMN (SEQ ID NO: 4576)	WVSNINYNGGYKG (SEQ ID NO: 4745)	ARSATWHDTHLD (SEQ ID NO: 4914)	LSYLNWY (SEQ ID NO: 5083)	LLIYAATSRA (SEQ ID NO: 5252)	QQSYENPL (SEQ ID NO: 5421)
372_H03	DSYGMN (SEQ ID NO: 4577)	WVSNINYNGGYKS (SEQ ID NO: 4746)	ARSATWHDTHLD (SEQ ID NO: 4915)	ITYVNWY (SEQ ID NO: 5084)	LLIYAATSLA (SEQ ID NO: 5253)	QQSYNLPL (SEQ ID NO: 5422)
366_E03	DSYGMN (SEQ ID NO: 4578)	WVSNINYNGGYKS (SEQ ID NO: 4747)	ARSATWHDTHLD (SEQ ID NO: 4916)	LTYLNWY (SEQ ID NO: 5085)	LVIYAATSRH (SEQ ID NO: 5254)	QQSYSNPL (SEQ ID NO: 5423)

371_F12	DSYSMN (SEQ ID NO: 4579)	WVSNINYNGGYKS (SEQ ID NO: 4748)	ARSATWHDTHLD (SEQ ID NO: 4917)	ISYLNWY (SEQ ID NO: 5086)	LLIYAATSRA (SEQ ID NO: 5255)	QQSNNLPL (SEQ ID NO: 5424)
366_C03	DSYGMN (SEQ ID NO: 4580)	WVSNINYNGGYTG (SEQ ID NO: 4749)	ARSATWHDTHLD (SEQ ID NO: 4918)	LSYLNWY (SEQ ID NO: 5087)	LVIYAATSRA (SEQ ID NO: 5256)	QQSYSNPL (SEQ ID NO: 5425)
376_A01	DSYGMN (SEQ ID NO: 4581)	WVSNINYNGGYTG (SEQ ID NO: 4750)	ARSATWHDTHLD (SEQ ID NO: 4919)	VSYLNWY (SEQ ID NO: 5088)	LLIYAATSRA (SEQ ID NO: 5257)	QQSYSTPL (SEQ ID NO: 5426)
365_E03	DSYSMN (SEQ ID NO: 4582)	WVSNINYNGGYTG (SEQ ID NO: 4751)	ARSATWHDTHLD (SEQ ID NO: 4920)	LTYVNWY (SEQ ID NO: 5089)	LLIYAATSLH (SEQ ID NO: 5258)	QQSDERPL (SEQ ID NO: 5427)
371_B10	DSYSMN (SEQ ID NO: 4583)	WVSNINYNGGYTG (SEQ ID NO: 4752)	ARSATWHDTHLD (SEQ ID NO: 4921)	VSYVNWY (SEQ ID NO: 5090)	LLIYAATSRA (SEQ ID NO: 5259)	QQSYDLPL (SEQ ID NO: 5428)
369_G09	DSYSMN (SEQ ID NO: 4584)	WVSNINYNGGYTG (SEQ ID NO: 4753)	ARSATWHDTHLD (SEQ ID NO: 4922)	VTYLNWY (SEQ ID NO: 5091)	LLIYAATSRA (SEQ ID NO: 5260)	QQSYDLPL (SEQ ID NO: 5429)
369_A06	SDYGMN (SEQ ID NO: 4585)	WVSNINYNGGYTG (SEQ ID NO: 4754)	ARSATWHDTHLD (SEQ ID NO: 4923)	LSYVNWY (SEQ ID NO: 5092)	LLIYAATSLA (SEQ ID NO: 5261)	QQSYDLPL (SEQ ID NO: 5430)
369_C08	SDYGMN (SEQ ID NO: 4586)	WVSNINYNGGYTG (SEQ ID NO: 4755)	ARSATWHDTHLD (SEQ ID NO: 4924)	LTYLNWY (SEQ ID NO: 5093)	LVIYAATSLA (SEQ ID NO: 5262)	QQSYENPL (SEQ ID NO: 5431)
373_A07	SSYSMN (SEQ ID NO: 4587)	WVSNINYNGGYTG (SEQ ID NO: 4756)	ARSATWHDTHLD (SEQ ID NO: 4925)	LTYVNWY (SEQ ID NO: 5094)	LLIYAATSRA (SEQ ID NO: 5263)	QQSDNLPL (SEQ ID NO: 5432)
367_D02	DDYSMN (SEQ ID NO: 4588)	WVSNINYNGGYTS (SEQ ID NO: 4757)	ARSATWHDTHLD (SEQ ID NO: 4926)	VTYVNWY (SEQ ID NO: 5095)	LLIYAATSRA (SEQ ID NO: 5264)	QQSYENPL (SEQ ID NO: 5433)

374_C07	DSYSMN (SEQ ID NO: 4589)	WVSNINYNGGYTS (SEQ ID NO: 4758)	ARSATWHDTHLD (SEQ ID NO: 4927)	ISYLNWY (SEQ ID NO: 5096)	LLIYAATSRA (SEQ ID NO: 5265)	QQSDELPL (SEQ ID NO: 5434)
374_A03	DSYSMN (SEQ ID NO: 4590)	WVSNINYNGGYTS (SEQ ID NO: 4759)	ARSATWHDTHLD (SEQ ID NO: 4928)	LTYLNWY (SEQ ID NO: 5097)	LLIYAATSRA (SEQ ID NO: 5266)	QQSYDNPL (SEQ ID NO: 5435)
365_A02	DSYSMN (SEQ ID NO: 4591)	WVSNINYNGGYTS (SEQ ID NO: 4760)	ARSATWHDTHLD (SEQ ID NO: 4929)	LTYVNWY (SEQ ID NO: 5098)	LLIYAATSRA (SEQ ID NO: 5267)	QQSYNSPL (SEQ ID NO: 5436)
365_D06	DSYSMN (SEQ ID NO: 4592)	WVSNINYNGGYTS (SEQ ID NO: 4761)	ARSATWHDTHLD (SEQ ID NO: 4930)	LTYVNWY (SEQ ID NO: 5099)	LLIYAATSRA (SEQ ID NO: 5268)	QQSYSLPL (SEQ ID NO: 5437)
366_C07	SSYSMN (SEQ ID NO: 4593)	WVSNINYNGGYTS (SEQ ID NO: 4762)	ARSATWHDTHLD (SEQ ID NO: 4931)	LTYVNWY (SEQ ID NO: 5100)	LLIYAATSRA (SEQ ID NO: 5269)	QQSYNSPL (SEQ ID NO: 5438)
367_F12	DDYSMN (SEQ ID NO: 4594)	WVSNINYNSGYKG (SEQ ID NO: 4763)	ARSATWHDTHLD (SEQ ID NO: 4932)	SSYLNWY (SEQ ID NO: 5101)	LLIYAASSLQ (SEQ ID NO: 5270)	QQSYSTPL (SEQ ID NO: 5439)
369_E09	DSYSMN (SEQ ID NO: 4595)	WVSNINYNSGYKG (SEQ ID NO: 4764)	ARSATWHDTHLD (SEQ ID NO: 4933)	LSYLNWY (SEQ ID NO: 5102)	LVIYAATSRA (SEQ ID NO: 5271)	QQSYDLPL (SEQ ID NO: 5440)
365_G02	SDYSMN (SEQ ID NO: 4596)	WVSNINYNSGYKG (SEQ ID NO: 4765)	ARSATWHDTHLD (SEQ ID NO: 4934)	VTYLNWY (SEQ ID NO: 5103)	LVIYAVTSLH (SEQ ID NO: 5272)	QQSYELPL (SEQ ID NO: 5441)
373_D02	SSYSMN (SEQ ID NO: 4597)	WVSNINYNSGYKG (SEQ ID NO: 4766)	ARSATWHDTHLD (SEQ ID NO: 4935)	LSYLNWY (SEQ ID NO: 5104)	LLIYAATSLA (SEQ ID NO: 5273)	QQSYDLPL (SEQ ID NO: 5442)
374_E03	SSYSMN (SEQ ID NO: 4598)	WVSNINYNSGYKG (SEQ ID NO: 4767)	ARSATWHDTHLD (SEQ ID NO: 4936)	LTYVNWY (SEQ ID NO: 5105)	LVIYAATSLA (SEQ ID NO: 5274)	QQSYDTPL (SEQ ID NO: 5443)

374_D11	DSYGMN (SEQ ID NO: 4599)	WVSNINYNSGYTG (SEQ ID NO: 4768)	ARSATWHDTHLD (SEQ ID NO: 4937)	LTYLNWY (SEQ ID NO: 5106)	LLIYAATSRA (SEQ ID NO: 5275)	QQSYETPL (SEQ ID NO: 5444)
370_D07	SSYGMN (SEQ ID NO: 4600)	WVSNINYNSGYTG (SEQ ID NO: 4769)	ARSATWHDTHLD (SEQ ID NO: 4938)	LSYVNWY (SEQ ID NO: 5107)	LVIYAATSLA (SEQ ID NO: 5276)	QQSYESPL (SEQ ID NO: 5445)
374_A08	DSYSMN (SEQ ID NO: 4601)	WVSNINYNSGYTS (SEQ ID NO: 4770)	ARSATWHDTHLD (SEQ ID NO: 4939)	VTYLNWY (SEQ ID NO: 5108)	LLIYAATSLA (SEQ ID NO: 5277)	QQSYDLPL (SEQ ID NO: 5446)
374_G01	DSYSMN (SEQ ID NO: 4602)	WVSNINYNSGYTS (SEQ ID NO: 4771)	ARSATWHDTHLD (SEQ ID NO: 4940)	LTYVNWY (SEQ ID NO: 5109)	LLIYATTSRH (SEQ ID NO: 5278)	QQSYNLPL (SEQ ID NO: 5447)
374_G12	DDYGMN (SEQ ID NO: 4603)	WVSSINYNGGYKS (SEQ ID NO: 4772)	ARSATWHDTHLD (SEQ ID NO: 4941)	LTYVNWY (SEQ ID NO: 5110)	LVIYAATSLA (SEQ ID NO: 5279)	QQSYNSPL (SEQ ID NO: 5448)
375_G10	SSYGMN (SEQ ID NO: 4604)	WVSSINYNGGYKS (SEQ ID NO: 4773)	ARSATWHDTHLD (SEQ ID NO: 4942)	VTYLNWY (SEQ ID NO: 5111)	LVIYAATSRH (SEQ ID NO: 5280)	QQSYDTPL (SEQ ID NO: 5449)
369_H11	SDYGMN (SEQ ID NO: 4605)	WVSSINYNGGYTG (SEQ ID NO: 4774)	ARSATWHDTHLD (SEQ ID NO: 4943)	LSYLNWY (SEQ ID NO: 5112)	LLIYAATSRH (SEQ ID NO: 5281)	QQSYDLPL (SEQ ID NO: 5450)
375_G12	DSYGMH (SEQ ID NO: 4606)	WVSSINYNGGYTS (SEQ ID NO: 4775)	ARSATWHDTHLD (SEQ ID NO: 4944)	VSYVNWY (SEQ ID NO: 5113)	LLIYAATSRH (SEQ ID NO: 5282)	QQSYDTPL (SEQ ID NO: 5451)
366_F06	SDYGMN (SEQ ID NO: 4607)	WVSSINYNGGYTS (SEQ ID NO: 4776)	ARSATWHDTHLD (SEQ ID NO: 4945)	STYLNWY (SEQ ID NO: 5114)	LLIYAATSLA (SEQ ID NO: 5283)	QQSYSNPL (SEQ ID NO: 5452)
368_G07	SSYSMH (SEQ ID NO: 4608)	WVSSINYNGGYTS (SEQ ID NO: 4777)	ARSATWHDTHLD (SEQ ID NO: 4946)	VSYVNWY (SEQ ID NO: 5115)	LVIYAATSRA (SEQ ID NO: 5284)	QQSYDTPL (SEQ ID NO: 5453)

367_H04	SSYSMN (SEQ ID NO: 4609)	WVSSINYNGGYTS (SEQ ID NO: 4778)	ARSATWHDTHLD (SEQ ID NO: 4947)	LTYVNWY (SEQ ID NO: 5116)	LLIYAATSRH (SEQ ID NO: 5285)	QQSDNNPL (SEQ ID NO: 5454)
374_E06	DSYSMN (SEQ ID NO: 4610)	WVSSINYNSGYKG (SEQ ID NO: 4779)	ARSATWHDTHLD (SEQ ID NO: 4948)	LSYLNWY (SEQ ID NO: 5117)	LLIYAATSRA (SEQ ID NO: 5286)	QQSYDLPL (SEQ ID NO: 5455)
370_A10	SDYSMN (SEQ ID NO: 4611)	WVSSINYNSGYKG (SEQ ID NO: 4780)	ARSATWHDTHLD (SEQ ID NO: 4949)	LSYVNWY (SEQ ID NO: 5118)	LLIYAATSLA (SEQ ID NO: 5287)	QQSYDTPL (SEQ ID NO: 5456)
368_H10	SSYSMN (SEQ ID NO: 4612)	WVSSINYNSGYKG (SEQ ID NO: 4781)	ARSATWHDTHLD (SEQ ID NO: 4950)	VSYVNWY (SEQ ID NO: 5119)	LVIYAVTSLA (SEQ ID NO: 5288)	QQSYETPL (SEQ ID NO: 5457)
368_G08	DDYCMN (SEQ ID NO: 4613)	WVSSINYNSGYKS (SEQ ID NO: 4782)	ARSATWHDTHLD (SEQ ID NO: 4951)	VSYVNWY (SEQ ID NO: 5120)	LLIYAATSRH (SEQ ID NO: 5289)	QQSYNNPL (SEQ ID NO: 5458)
365_H09	SSYGMN (SEQ ID NO: 4614)	WVSSINYNSGYKS (SEQ ID NO: 4783)	ARSATWHDTHLD (SEQ ID NO: 4952)	SSYLNWY (SEQ ID NO: 5121)	LLIYAASSLQ (SEQ ID NO: 5290)	QQSYSTPL (SEQ ID NO: 5459)
370_A08	DSYSMN (SEQ ID NO: 4615)	WVSSINYNSGYTG (SEQ ID NO: 4784)	ARSATWHDTHLD (SEQ ID NO: 4953)	VTYLNWY (SEQ ID NO: 5122)	LVIYAATSRA (SEQ ID NO: 5291)	QQSYDLPL (SEQ ID NO: 5460)
368_B05	DSYSMN (SEQ ID NO: 4616)	WVSSINYNSGYTG (SEQ ID NO: 4785)	ARSATWHDTHLD (SEQ ID NO: 4954)	SSYLNWY (SEQ ID NO: 5123)	LLIYAASSLQ (SEQ ID NO: 5292)	QQSYSTPL (SEQ ID NO: 5461)
375_F01	SSYSMN (SEQ ID NO: 4617)	WVSSINYNSGYTG (SEQ ID NO: 4786)	ARSATWHDTHLD (SEQ ID NO: 4955)	VSYLNWY (SEQ ID NO: 5124)	LVIYAATSRA (SEQ ID NO: 5293)	QQSYDNPL (SEQ ID NO: 5462)
374_F09	SSYGMN (SEQ ID NO: 4618)	WVSSINYNSGYTS (SEQ ID NO: 4787)	ARSATWHDTHLD (SEQ ID NO: 4956)	SSYVNWY (SEQ ID NO: 5125)	LLIYAATSRA (SEQ ID NO: 5294)	QQSYSTPL (SEQ ID NO: 5463)

The consensus sequences for each of these CDRs shown in Fig. 3F are as follows:

HCDR1: D/SS/DYS/GMN/H (SEQ ID NO: 6584)

HCDR2: WVA/SG/N/SINYNG/SGYT/KS/G (SEQ ID NO: 6585)

HCDR3: ARSATWHDTH/ALD (SEQ ID NO: 6586)

LCDR1: L/V/I/SS/T/RYL/VNWY (SEQ ID NO: 6588)

LCDR2: LL/VIYA/YA/V/TT/SS/NR/LA/H/Q (SEQ ID NO: 6590)

LCDR3: QQSY/DD/E/S/NL/N/T/SPL (SEQ ID NO: 6591)

The present antibody may exhibit high affinity binding to ACVR2A. For example, the antibody may binds to ACVR2 with an affinity of at least about 10^{-7} M, at least about 10^{-8} M, at least about 10^{-9} M, at least about 10^{-10} M, at least about 10^{-11} M, or at least about 10^{-12} M, or greater than 10^{-12} M. The present antibody binds to ACVR2A with a substantially lower affinity, e.g., at least 10 fold, 50 fold, 100 fold, 500 fold, 1000 fold, 5000 fold, 10,000 fold, 50,000 fold 100,000, or 500,000 fold lower affinity.

The present antibody may reduce binding of ACVR2A to GDF8 and/or other activins. For example, the antibody may reduce binding of ACVR2A to GDF8 and/or other activins by at least about 5%, at least about 10%, at least about 15%, at least about 20%, at least about 25%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or more, compared to the degree of binding between ACVR2A and GDF8 and/or other activins in the absence of the antibody.

In some embodiments, an antibody comprises one or more (e.g., one or two) heavy chain variable regions (VH) and/or one or more (e.g., one or two) light chain variable regions (VL), or subfragments thereof capable of binding an epitope. The VH and VL regions can be further subdivided into regions of hypervariability, termed "complementarity determining regions (CDR)", interspersed with regions that are more conserved, termed "framework regions (FR)". The extent of the FR and CDRs has been precisely defined (see, Kabat, et al. (1991) Sequences of Proteins of Immunological Interest, Fifth Edition, U.S. Department of Health and Human Services, NIH Publication No. 91-3242; Chothia et al. (1987) J. Mol. Biol. 196: 901-917). A VH can comprise three CDRs and four FRs arranged from N-terminus to C-terminus in the following order: FR1, CDR1, FR2, CDR2, FR3, CDR3, FR4. Similarly, a VL can comprise three CDRs and four FRs arranged from N-terminus to C-terminus in the following order: FR1, CDR1, FR2, CDR2, FR3, CDR3, FR4.

The VH or VL chain of an antibody can further include all or part of a heavy or light chain constant region, to thereby form a heavy or light immunoglobulin chain, respectively. In one embodiment, the antibody is a tetramer of two heavy and two light chains, wherein the heavy and light chains are interconnected by, for example, disulphide bonds. The heavy chain constant region is comprised of three

domains, CH1, CH2 and CH3. The light chain constant region is comprised of one domain, CL. The variable regions of the heavy and light chains comprise binding regions that interact with antigen. The constant regions of the antibodies typically mediate the binding of the antibody to host tissues and factors, including various cells of the immune system and the first component of the complement system. The term "antibody" includes intact immunoglobulins of types IgA, IgG, IgE, IgD, IgM and subtypes thereof. In some embodiments, a subject antibody is an IgG isotype.

As used herein the term "immunoglobulin" refers to a protein consisting of one or more polypeptides substantially encoded by immunoglobulin genes. The recognized human immunoglobulin genes include the kappa, lambda, alpha (IgA1 and IgA2), gamma (IgG1, IgG2, IgG3, IgG4), delta, epsilon and mu constant region genes; and numerous immunoglobulin variable region genes. Full-length immunoglobulin light chains (about 25 kD or 214 amino acids) are encoded by a variable region gene at the N-terminus (about 110 amino acids) and a kappa or lambda constant region at the C-terminus. Full-length immunoglobulin heavy chains (about 50 kD or 446 amino acids) are encoded by a variable region gene at the N-terminus (about 116 amino acids) and one of the other aforementioned constant region genes at the C-terminus, e.g. gamma (encoding about 330 amino acids). In some embodiments, a subject antibody comprises full-length immunoglobulin heavy chain and a full-length immunoglobulin light chain.

In some embodiments, a subject antibody does not comprise a full-length immunoglobulin heavy chain and a full-length immunoglobulin light chain, and instead comprises antigen-binding fragments of a full-length immunoglobulin heavy chain and a full-length immunoglobulin light chain. In some embodiments, the antigen-binding fragments are contained on separate polypeptide chains; in other embodiments, the antigen-binding fragments are contained within a single polypeptide chain. The term "antigen-binding fragment" refers to one or more fragments of a full-length antibody that are capable of specifically binding to ACVR2A as described above. Examples of binding fragments include (i) a Fab fragment (a monovalent fragment consisting of the VL, VH, CL and CH1 domains; (ii) a $F(ab')_2$ fragment (a bivalent fragment comprising two Fab fragments linked by a disulfide bridge at the hinge region; (iii) a Fd fragment (consisting of the VH and CH1 domains); (iv) a Fv fragment (consisting of the VH and VL domains of a single arm of an antibody); (v) a dAb fragment (consisting of the VH domain); (vi) an isolated CDR; (vii) a single chain Fv (scFv) (consisting of the VH and VL domains of a single arm of an antibody joined by a synthetic linker using recombinant means such that the VH and VL domains pair to form a monovalent molecule); (viii) diabodies (consisting of two scFvs in which the VH and VL domains are joined such that they do not pair to form a monovalent molecule; the VH of each one of the scFv pairs with the VL domain of the other scFv to form a bivalent molecule); (ix) bi-specific antibodies (consisting of at least two antigen binding regions, each region binding a different epitope). In some embodiments, a

subject antibody fragment is a Fab fragment. In some embodiments, a subject antibody fragment is a single-chain antibody (scFv).

In some embodiments, a subject antibody is a recombinant or modified antibody, e.g., a chimeric, humanized, deimmunized or an *in vitro* generated antibody. The term "recombinant" or "modified" antibody as used herein is intended to include all antibodies that are prepared, expressed, created, or isolated by recombinant means, such as (i) antibodies expressed using a recombinant expression vector transfected into a host cell; (ii) antibodies isolated from a recombinant, combinatorial antibody library; (iii) antibodies isolated from an animal (e.g. a mouse) that is transgenic for human immunoglobulin genes; or (iv) antibodies prepared, expressed, created, or isolated by any other means that involves splicing of human immunoglobulin gene sequences to other DNA sequences. Such recombinant antibodies include humanized, CDR grafted, chimeric, deimmunized, and *in vitro* generated antibodies; and can optionally include constant regions derived from human germline immunoglobulin sequences.

In some embodiments, a subject antibody comprises, in order from N-terminus to C-terminus: a light chain FR1 region; a CDR1; a light chain FR2 region; a CDR2; a light chain FR3 region; a CDR3; optionally a light chain FR4 region; a linker region; optionally a heavy chain FR1 region; a CDR1; a heavy chain FR2 region; a CDR2; a heavy chain FR3 region; a CDR3; and a heavy chain FR4 region. In some of these embodiments, each of the FR regions is a human FR region. The linker region can be from about 5 amino acids to about 50 amino acids in length, e.g., from about 5 aa to about 10 aa, from about 10 aa to about 15 aa, from about 15 aa to about 20 aa, from about 20 aa to about 25 aa, from about 25 aa to about 30 aa, from about 30 aa to about 35 aa, from about 35 aa to about 40 aa, from about 40 aa to about 45 aa, or from about 45 aa to about 50 aa in length.

Linkers suitable for use a subject antibody include “flexible linkers”. If present, the linker molecules are generally of sufficient length to permit some flexible movement between linked regions. The linker molecules are generally about 6-50 atoms long. The linker molecules may also be, for example, aryl acetylene, ethylene glycol oligomers containing 2-10 monomer units, diamines, diacids, amino acids, or combinations thereof. Other linker molecules which can bind to polypeptides may be used in light of this disclosure.

Suitable linkers can be readily selected and can be of any of a suitable of different lengths, such as from 1 amino acid (e.g., Gly) to 20 amino acids, from 2 amino acids to 15 amino acids, from 3 amino acids to 12 amino acids, including 4 amino acids to 10 amino acids, 5 amino acids to 9 amino acids, 6 amino acids to 8 amino acids, or 7 amino acids to 8 amino acids, and may be 1, 2, 3, 4, 5, 6, or 7 amino acids.

Exemplary flexible linkers include glycine polymers $(G)_n$, glycine-serine polymers (including, for example, $(GS)_n$, $GSGGS_n$ (SEQ ID NO: 6599) and $GGGS_n$ (SEQ ID NO: 6600), where n is an integer of

at least one), glycine-alanine polymers, alanine-serine polymers, and other flexible linkers known in the art. Glycine and glycine-serine polymers are of interest since both of these amino acids are relatively unstructured, and therefore may serve as a neutral tether between components. Glycine polymers are of particular interest since glycine accesses significantly more phi-psi space than even alanine, and is much less restricted than residues with longer side chains (see Scheraga, *Rev. Computational Chem.* 11173-142 (1992)). Exemplary flexible linkers include, but are not limited GGSG (SEQ ID NO:6601), GGSGG (SEQ ID NO:6602), GSGSG (SEQ ID NO: 6603), GSGGG (SEQ ID NO:6604), GGGSG (SEQ ID NO: 6605), GSSSG (SEQ ID NO: 6606), and the like. The ordinarily skilled artisan will recognize that design of a peptide conjugated to any elements described above can include linkers that are all or partially flexible, such that the linker can include a flexible linker as well as one or more portions that confer less flexible structure.

In some embodiments, a subject antibody is "humanized." The term "humanized antibody" refers to an antibody comprising at least one chain comprising variable region framework residues substantially from a human antibody chain (referred to as the acceptor immunoglobulin or antibody) and at least one CDR substantially from a mouse antibody, (referred to as the donor immunoglobulin or antibody). See, Queen et al., Proc. Natl. Acad. Sci. USA 86:10029 10033 (1989), U.S. Pat. No. 5,530,101, U.S. Pat. No. 5,585,089, U.S. Pat. No. 5,693,761, WO 90/07861, and U.S. Pat. No. 5,225,539. The constant region(s), if present, can also be substantially or entirely from a human immunoglobulin. In some embodiments, a subject antibody may comprise one or more CDRs and one or more FR regions from a human antibody. Methods of making humanized antibodies are known in the art. See, e.g., U.S. Patent No. 7,256,273.

The substitution of mouse CDRs into a human variable domain framework can result in retention of their correct spatial orientation where, e.g., the human variable domain framework adopts the same or similar conformation to the mouse variable framework from which the CDRs originated. This can be achieved by obtaining the human variable domains from human antibodies whose framework sequences exhibit a high degree of sequence identity with the murine variable framework domains from which the CDRs were derived. The heavy and light chain variable framework regions can be derived from the same or different human antibody sequences. The human antibody sequences can be the sequences of naturally occurring human antibodies or can be consensus sequences of several human antibodies. See Kettleborough et al., Protein Engineering 4:773 (1991); Kolbinger et al., Protein Engineering 6:971 (1993).

Having identified the complementarity determining regions of the murine donor immunoglobulin and appropriate human acceptor immunoglobulins, the next step is to determine which, if any, residues from these components should be substituted to optimize the properties of the resulting humanized antibody. In general, substitution of human amino acid residues with murine should be minimized,

because introduction of murine residues increases the risk of the antibody eliciting a human-anti-mouse-antibody (HAMA) response in humans. Art-recognized methods of determining immune response can be performed to monitor a HAMA response in a particular patient or during clinical trials. Patients administered humanized antibodies can be given an immunogenicity assessment at the beginning and throughout the administration of the therapy. The HAMA response is measured, for example, by detecting antibodies to the humanized therapeutic reagent, in serum samples from the patient using a method known to one in the art, including surface plasmon resonance technology (BIACORE) and/or solid-phase ELISA analysis. In many embodiments, a subject humanized antibody does not substantially elicit a HAMA response in a human subject.

Certain amino acids from the human variable region framework residues are selected for substitution based on their possible influence on CDR conformation and/or binding to antigen. The unnatural juxtaposition of murine CDR regions with human variable framework region can result in unnatural conformational restraints, which, unless corrected by substitution of certain amino acid residues, lead to loss of binding affinity.

The selection of amino acid residues for substitution can be determined, in part, by computer modeling. Computer hardware and software for producing three-dimensional images of immunoglobulin molecules are known in the art. In general, molecular models are produced starting from solved structures for immunoglobulin chains or domains thereof. The chains to be modeled are compared for amino acid sequence similarity with chains or domains of solved three-dimensional structures, and the chains or domains showing the greatest sequence similarity is/are selected as starting points for construction of the molecular model. Chains or domains sharing at least 50% sequence identity are selected for modeling, and preferably those sharing at least 60%, 70%, 80%, 90% sequence identity or more are selected for modeling. The solved starting structures are modified to allow for differences between the actual amino acids in the immunoglobulin chains or domains being modeled, and those in the starting structure. The modified structures are then assembled into a composite immunoglobulin. Finally, the model is refined by energy minimization and by verifying that all atoms are within appropriate distances from one another and that bond lengths and angles are within chemically acceptable limits.

CDR and framework regions are as defined by Kabat, Sequences of Proteins of Immunological Interest (National Institutes of Health, Bethesda, Md., 1987 and 1991). An alternative structural definition has been proposed by Chothia et al., J. Mol. Biol. 196:901 (1987); Nature 342:878 (1989); and J. Mol. Biol. 186:651 (1989) (collectively referred to as “Chothia”). When framework residues, as defined by Kabat, supra, constitute structural loop residues as defined by Chothia, supra, the amino acids present in the mouse antibody may be selected for substitution into the humanized antibody. Residues which are "adjacent to a CDR region" include amino acid residues in positions immediately adjacent to one or more

of the CDRs in the primary sequence of the humanized immunoglobulin chain, for example, in positions immediately adjacent to a CDR as defined by Kabat, or a CDR as defined by Chothia (See e.g., Chothia and Lesk JMB 196:901 (1987)). These amino acids are particularly likely to interact with the amino acids in the CDRs and, if chosen from the acceptor, to distort the donor CDRs and reduce affinity. Moreover, the adjacent amino acids may interact directly with the antigen (Amit et al., Science, 233:747 (1986)) and selecting these amino acids from the donor may be desirable to keep all the antigen contacts that provide affinity in the original antibody.

In some embodiments, a subject antibody comprises scFv multimers. For example, in some embodiments, a subject antibody is an scFv dimer (e.g., comprises two tandem scFv ($scFv_2$)), an scFv trimer (e.g., comprises three tandem scFv ($scFv_3$)), an scFv tetramer (e.g., comprises four tandem scFv ($scFv_4$)), or is a multimer of more than four scFv (e.g., in tandem). The scFv monomers can be linked in tandem via linkers of from about 2 amino acids to about 10 amino acids in length, e.g., 2 aa, 3 aa, 4 aa, 5 aa, 6 aa, 7 aa, 8 aa, 9 aa, or 10 aa in length. Suitable linkers include, e.g., $(Gly)_x$, where x is an integer from 2 to 10. Other suitable linkers are those discussed above. In some embodiments, each of the scFv monomers in a subject scFV multimer is humanized, as described above.

In some embodiments, a subject antibody comprises a constant region of an immunoglobulin (e.g., an Fc region). The Fc region, if present, can be a human Fc region. If constant regions are present, the antibody can contain both light chain and heavy chain constant regions. Suitable heavy chain constant region include CH1, hinge, CH2, CH3, and CH4 regions. The antibodies described herein include antibodies having all types of constant regions, including IgM, IgG, IgD, IgA and IgE, and any isotype, including IgG1, IgG2, IgG3 and IgG4. An example of a suitable heavy chain Fc region is a human isotype IgG1 Fc. Light chain constant regions can be lambda or kappa. A subject antibody (e.g., a subject humanized antibody) can comprise sequences from more than one class or isotype. Antibodies can be expressed as tetramers containing two light and two heavy chains, as separate heavy chains, light chains, as Fab, Fab' F(ab')2, and Fv, or as single chain antibodies in which heavy and light chain variable domains are linked through a spacer.

In some embodiments, a subject antibody comprises a free thiol (-SH) group at the carboxyl terminus, where the free thiol group can be used to attach the antibody to a second polypeptide (e.g., another antibody, including a subject antibody), a scaffold, a carrier, etc.

In some embodiments, a subject antibody comprises one or more non-naturally occurring amino acids. In some embodiments, the non-naturally encoded amino acid comprises a carbonyl group, an acetyl group, an aminooxy group, a hydrazine group, a hydrazide group, a semicarbazide group, an azide group, or an alkyne group. See, e.g., U.S. Patent No. 7,632,924 for suitable non-naturally occurring amino acids. Inclusion of a non-naturally occurring amino acid can provide for linkage to a polymer, a second

polypeptide, a scaffold, etc. For example, a subject antibody linked to a water-soluble polymer can be made by reacting a water-soluble polymer (e.g., PEG) that comprises a carbonyl group to an the subject antibody that comprises a non-naturally encoded amino acid that comprises an aminooxy, hydrazine, hydrazide or semicarbazide group. As another example, a subject antibody linked to a water-soluble polymer can be made by reacting a subject antibody that comprises an alkyne-containing amino acid with a water-soluble polymer (e.g., PEG) that comprises an azide moiety; in some embodiments, the azide or alkyne group is linked to the PEG molecule through an amide linkage. A "non-naturally encoded amino acid" refers to an amino acid that is not one of the 20 common amino acids or pyrolysine or selenocysteine. Other terms that may be used synonymously with the term "non-naturally encoded amino acid" are "non-natural amino acid," "unnatural amino acid," "non-naturally-occurring amino acid," and variously hyphenated and non-hyphenated versions thereof. The term "non-naturally encoded amino acid" also includes, but is not limited to, amino acids that occur by modification (e.g. post-translational modifications) of a naturally encoded amino acid (including but not limited to, the 20 common amino acids or pyrolysine and selenocysteine) but are not themselves naturally incorporated into a growing polypeptide chain by the translation complex. Examples of such non-naturally-occurring amino acids include, but are not limited to, N-acetylglucosaminyl-L-serine, N-acetylglucosaminyl-L-threonine, and O –phosphotyrosine.

In some embodiments, a subject antibody is linked (e.g., covalently linked) to a polymer (e.g., a polymer other than a polypeptide). Suitable polymers include, e.g., biocompatible polymers, and water-soluble biocompatible polymers. Suitable polymers include synthetic polymers and naturally-occurring polymers. Suitable polymers include, e.g., substituted or unsubstituted straight or branched chain polyalkylene, polyalkenylene or polyoxyalkylene polymers or branched or unbranched polysaccharides, e.g. a homo- or hetero-polysaccharide. Suitable polymers include, e.g., ethylene vinyl alcohol copolymer (commonly known by the generic name EVOH or by the trade name EVAL); polybutylmethacrylate; poly(hydroxyvalerate); poly(L-lactic acid); polycaprolactone; poly(lactide-co-glycolide); poly(hydroxybutyrate); poly(hydroxybutyrate-co-valerate); polydioxanone; polyorthoester; polyanhydride; poly(glycolic acid); poly(D,L-lactic acid); poly(glycolic acid-co-trimethylene carbonate); polyphosphoester; polyphosphoester urethane; poly(amino acids); cyanoacrylates; poly(trimethylene carbonate); poly(iminocarbonate); copoly(ether-esters) (e.g., poly(ethylene oxide)-poly(lactic acid) (PEO/PLA) co-polymers); polyalkylene oxalates; polyphosphazenes; biomolecules, such as fibrin, fibrinogen, cellulose, starch, collagen and hyaluronic acid; polyurethanes; silicones; polyesters; polyolefins; polyisobutylene and ethylene-alphaolefin copolymers; acrylic polymers and copolymers; vinyl halide polymers and copolymers, such as polyvinyl chloride; polyvinyl ethers, such as polyvinyl methyl ether; polyvinylidene halides, such as polyvinylidene fluoride and polyvinylidene chloride;

polyacrylonitrile; polyvinyl ketones; polyvinyl aromatics, such as polystyrene; polyvinyl esters, such as polyvinyl acetate; copolymers of vinyl monomers with each other and olefins, such as ethylene-methyl methacrylate copolymers, acrylonitrile-styrene copolymers, ABS resins, and ethylene-vinyl acetate copolymers; polyamides, such as Nylon 66 and polycaprolactam; alkyd resins; polycarbonates; polyoxymethylenes; polyimides; polyethers; epoxy resins; polyurethanes; rayon; rayon-triacetate; cellulose; cellulose acetate; cellulose butyrate; cellulose acetate butyrate; cellophane; cellulose nitrate; cellulose propionate; cellulose ethers; amorphous Teflon; poly(ethylene glycol); and carboxymethyl cellulose.

Suitable synthetic polymers include unsubstituted and substituted straight or branched chain poly(ethyleneglycol), poly(propyleneglycol) poly(vinylalcohol), and derivatives thereof, e.g., substituted poly(ethyleneglycol) such as methoxypoly(ethyleneglycol), and derivatives thereof. Suitable naturally-occurring polymers include, e.g., albumin, amylose, dextran, glycogen, and derivatives thereof.

Suitable polymers can have an average molecular weight in a range of from 500 Da to 50000 Da, e.g., from 5000 Da to 40000 Da, or from 25000 to 40000 Da. For example, in some embodiments, where a subject antibody comprises a poly(ethylene glycol) (PEG) or methoxypoly(ethyleneglycol) polymer, the PEG or methoxypoly(ethyleneglycol) polymer can have a molecular weight in a range of from about 0.5 kiloDaltons (kDa) to 1 kDa, from about 1 kDa to 5 kDa, from 5 kDa to 10 kDa, from 10 kDa to 25 kDa, from 25 kDa to 40 kDa, or from 40 kDa to 60 kDa.

As noted above, in some embodiments, a subject antibody is covalently linked to a PEG polymer. In some embodiments, a subject scFv multimer is covalently linked to a PEG polymer. See, e.g., Albrecht et al. (2006) *J. Immunol. Methods* 310:100. Methods and reagents suitable for PEGylation of a protein are well known in the art and may be found in, e.g., U.S. Pat. No. 5,849,860. PEG suitable for conjugation to a protein is generally soluble in water at room temperature, and has the general formula $R(O\text{-}CH_2\text{-}CH_2)_nO\text{-}R$, where R is hydrogen or a protective group such as an alkyl or an alkanol group, and where n is an integer from 1 to 1000. Where R is a protective group, it generally has from 1 to 8 carbons.

The PEG conjugated to the subject antibody can be linear. The PEG conjugated to the subject protein may also be branched. Branched PEG derivatives such as those described in U.S. Pat. No. 5,643,575, "star-PEG's" and multi-armed PEG's such as those described in Shearwater Polymers, Inc. catalog "Polyethylene Glycol Derivatives 1997-1998." Star PEGs are described in the art including, e.g., in U.S. Patent No. 6,046,305.

A subject antibody can be glycosylated, e.g., comprise a covalently linked carbohydrate or polysaccharide moiety. Glycosylation of antibodies is typically either N-linked or O-linked. N-linked refers to the attachment of the carbohydrate moiety to the side chain of an asparagine residue. The tripeptide sequences asparagine-X-serine and asparagine-X-threonine, where X is any amino acid except

proline, are the recognition sequences for enzymatic attachment of the carbohydrate moiety to the asparagine side chain. Thus, the presence of either of these tripeptide sequences in a polypeptide creates a potential glycosylation site. O-linked glycosylation refers to the attachment of one of the sugars N-acetylgalactosamine, galactose, or xylose to a hydroxyamino acid, most commonly serine or threonine, although 5-hydroxyproline or 5-hydroxylysine may also be used.

Addition of glycosylation sites to an antibody is conveniently accomplished by altering the amino acid sequence such that it contains one or more of the above-described tripeptide sequences (for N-linked glycosylation sites). The alteration may also be made by the addition of, or substitution by, one or more serine or threonine residues to the sequence of the original antibody (for O-linked glycosylation sites). Similarly, removal of glycosylation sites can be accomplished by amino acid alteration within the native glycosylation sites of an antibody.

A subject antibody will in some embodiments comprise a "radiopaque" label, e.g. a label that can be easily visualized using for example x-rays. Radiopaque materials are well known to those of skill in the art. The most common radiopaque materials include iodide, bromide or barium salts. Other radiopaque materials are also known and include, but are not limited to organic bismuth derivatives (see, e.g., U.S. Pat. No. 5,939,045), radiopaque multiurethanes (see U.S. Pat. No. 5,346,981), organobismuth composites (see, e.g., U.S. Pat. No. 5,256,334), radiopaque barium multimer complexes (see, e.g., U.S. Pat. No. 4,866,132), and the like.

A subject antibody can be covalently linked to a second moiety (e.g., a lipid, a polypeptide other than a subject antibody, a synthetic polymer, a carbohydrate, and the like) using for example, glutaraldehyde, a homobifunctional cross-linker, or a heterobifunctional cross-linker. Glutaraldehyde cross-links polypeptides via their amino moieties. Homobifunctional cross-linkers (e.g., a homobifunctional imidoester, a homobifunctional N-hydroxysuccinimidyl (NHS) ester, or a homobifunctional sulfhydryl reactive cross-linker) contain two or more identical reactive moieties and can be used in a one step reaction procedure in which the cross-linker is added to a solution containing a mixture of the polypeptides to be linked. Homobifunctional NHS ester and imido esters cross-link amine containing polypeptides. In a mild alkaline pH, imido esters react only with primary amines to form imidoamides, and overall charge of the cross-linked polypeptides is not affected. Homobifunctional sulfhydryl reactive cross-linkers includes bismaleimidhexane (BMH), 1,5-difluoro-2,4-dinitrobenzene (DFDNB), and 1,4-di-(3',2'-pyridyldithio) propinoamido butane (DPDPB).

Heterobifunctional cross-linkers have two or more different reactive moieties (e.g., amine reactive moiety and a sulfhydryl-reactive moiety) and are cross-linked with one of the polypeptides via the amine or sulfhydryl reactive moiety, then reacted with the other polypeptide via the non-reacted moiety. Multiple heterobifunctional haloacetyl cross-linkers are available, as are pyridyl disulfide cross-

linkers. Carbodiimides are a classic example of heterobifunctional cross-linking reagents for coupling carboxyls to amines, which results in an amide bond.

A subject antibody can be immobilized on a solid support. Suitable supports are well known in the art and comprise, inter alia, commercially available column materials, polystyrene beads, latex beads, magnetic beads, colloid metal particles, glass and/or silicon chips and surfaces, nitrocellulose strips, nylon membranes, sheets, duracytes, wells of reaction trays (e.g., multi-well plates), plastic tubes, etc. A solid support can comprise any of a variety of substances, including, e.g., glass, polystyrene, polyvinyl chloride, polypropylene, polyethylene, polycarbonate, dextran, nylon, amylose, natural and modified celluloses, polyacrylamides, agaroses, and magnetite. Suitable methods for immobilizing a subject antibody onto a solid support are well known and include, but are not limited to ionic, hydrophobic, covalent interactions and the like. Solid supports can be soluble or insoluble, e.g., in aqueous solution. In some embodiments, a suitable solid support is generally insoluble in an aqueous solution.

A subject antibody will in some embodiments comprise a detectable label. Suitable detectable labels include any composition detectable by spectroscopic, photochemical, biochemical, immunochemical, electrical, optical or chemical means. Suitable include, but are not limited to, magnetic beads (e.g. Dynabeads™), fluorescent dyes (e.g., fluorescein isothiocyanate, texas red, rhodamine, a green fluorescent protein, a red fluorescent protein, a yellow fluorescent protein, and the like), radiolabels (e.g., ^{3}H, ^{125}I, ^{35}S, ^{14}C, or ^{32}P), enzymes (e.g., horse radish peroxidase, alkaline phosphatase, luciferase, and others commonly used in an enzyme-linked immunosorbent assay (ELISA)), and colorimetric labels such as colloidal gold or colored glass or plastic (e.g. polystyrene, polypropylene, latex, etc.) beads.

In some embodiments, a subject antibody comprises a contrast agent or a radioisotope, where the contrast agent or radioisotope is one that is suitable for use in imaging, e.g., imaging procedures carried out on humans. Non-limiting examples of labels include radioisotope such as ^{1231}I (iodine), ^{18}F (fluorine), ^{99}Tc (technetium), ^{111}In (indium), and ^{67}Ga (gallium), and contrast agent such as gadolinium (Gd), dysprosium, and iron. Radioactive Gd isotopes (^{153}Gd) also are available and suitable for imaging procedures in non-human mammals. A subject antibody can be labeled using standard techniques. For example, a subject antibody can be iodinated using chloramine T or 1,3,4,6-tetrachloro-3α,6α-dephenylglycouril. For fluorination, fluorine is added to a subject antibody during the synthesis by a fluoride ion displacement reaction. See, Muller-Gartner, H., TIB Tech., 16:122-130 (1998) and Saji, H., Crit. Rev. Ther. Drug Carrier Syst., 16(2):209-244 (1999) for a review of synthesis of proteins with such radioisotopes. A subject antibody can also be labeled with a contrast agent through standard techniques. For example, a subject antibody can be labeled with Gd by conjugating low molecular Gd chelates such as Gd diethylene triamine pentaacetic acid (GdDTPA) or Gd tetraazacyclododecanetetraacetic (GdDOTA) to the antibody. See, Caravan et al., Chem. Rev. 99:2293-2352 (1999) and Lauffer et al., J.

Magn. Reson. Imaging, 3:11-16 (1985). A subject antibody can be labeled with Gd by, for example, conjugating polylysine-Gd chelates to the antibody. See, for example, Curtet et al., Invest. Radiol., 33(10):752-761 (1998). Alternatively, a subject antibody can be labeled with Gd by incubating paramagnetic polymerized liposomes that include Gd chelator lipid with avidin and biotinylated antibody. See, for example, Sipkins et al., Nature Med., 4:623-626 (1998).

Suitable fluorescent proteins that can be linked to a subject antibody include, but are not limited to, a green fluorescent protein from *Aequoria victoria* or a mutant or derivative thereof e.g., as described in U.S. Patent No. 6,066,476; 6,020,192; 5,985,577; 5,976,796; 5,968,750; 5,968,738; 5,958,713; 5,919,445; 5,874,304; e.g., Enhanced GFP, many such GFP which are available commercially, e.g., from Clontech, Inc.; a red fluorescent protein; a yellow fluorescent protein; any of a variety of fluorescent and colored proteins from Anthozoan species, as described in, e.g., Matz et al. (1999) *Nature Biotechnol.* 17:969-973; and the like.

A subject antibody will in some embodiments be linked to (e.g., covalently or non-covalently linked) a fusion partner, e.g., a ligand; an epitope tag; a peptide; a protein other than an antibody; and the like. Suitable fusion partners include peptides and polypeptides that confer enhanced stability *in vivo* (e.g., enhanced serum half-life); provide ease of purification, e.g., $(His)_n$, e.g., 6His, and the like; provide for secretion of the fusion protein from a cell; provide an epitope tag, e.g., GST, hemagglutinin (HA; e.g., CYPYDVPDYA; SEQ ID NO:6607), FLAG (e.g., DYKDDDDK; SEQ ID NO:6608), c-myc (e.g., CEQKLISEEDL; SEQ ID NO:6609), and the like; provide a detectable signal, e.g., an enzyme that generates a detectable product (e.g., β-galactosidase, luciferase), or a protein that is itself detectable, e.g., a green fluorescent protein, a red fluorescent protein, a yellow fluorescent protein, etc.; provides for multimerization, e.g., a multimerization domain such as an Fc portion of an immunoglobulin; and the like.

The fusion may also include an affinity domain, including peptide sequences that can interact with a binding partner, e.g., such as one immobilized on a solid support, useful for identification or purification. Consecutive single amino acids, such as histidine, when fused to a protein, can be used for one-step purification of the fusion protein by high affinity binding to a resin column, such as nickel sepharose. Exemplary affinity domains include His5 (HHHHH) (SEQ ID NO:6610), HisX6 (HHHHHH) (SEQ ID NO:6611), C-myc (EQKLISEEDL) (SEQ ID NO:6612), Flag (DYKDDDDK) (SEQ ID NO:6608), StrepTag (WSHPQFEK) (SEQ ID NO:6613), hemagglutinin, e.g., HA Tag (YPYDVPDYA; SEQ ID NO:6614), glutathinone-S-transferase (GST), thioredoxin, cellulose binding domain, RYIRS (SEQ ID NO:6615), Phe-His-His-Thr (SEQ ID NO:6616), chitin binding domain, S-peptide, T7 peptide, SH2 domain, C-end RNA tag, WEAAAREACCRECCARA (SEQ ID NO:6617), metal binding domains, e.g., zinc binding domains or calcium binding domains such as those from calcium-binding proteins, e.g.,

calmodulin, troponin C, calcineurin B, myosin light chain, recoverin, S-modulin, visinin, VILIP, neurocalcin, hippocalcin, frequenin, caltractin, calpain large-subunit, S100 proteins, parvalbumin, calbindin D9K, calbindin D28K, and calretinin, inteins, biotin, streptavidin, MyoD, leucine zipper sequences, and maltose binding protein.

A subject antibody will in some embodiments be fused to a polypeptide that binds to an endogenous blood brain barrier (BBB) receptor. Linking a subject antibody to a polypeptide that binds to an endogenous BBB receptor facilitates crossing the BBB, e.g., in a subject treatment method (see below) involving administration of a subject antibody to an individual in need thereof. Suitable polypeptides that bind to an endogenous BBB include antibodies, e.g., monoclonal antibodies, or antigen-binding fragments thereof, that specifically bind to an endogenous BBB receptor. Suitable endogenous BBB receptors include, but are not limited to, an insulin receptor, a transferrin receptor, a leptin receptor, a lipoprotein receptor, and an insulin-like growth factor receptor. See, e.g., U.S. Patent Publication No. 2009/0156498.

In some embodiments, a subject antibody comprises a polyamine modification. Polyamine modification of a subject antibody enhances permeability of the modified antibody at the BBB. A subject antibody can be modified with polyamines that are either naturally occurring or synthetic. See, for example, U.S. Pat. No. 5,670,477. Useful naturally occurring polyamines include putrescine, spermidine, spermine, 1,3-deaminopropane, norspermidine, syn-homospermidine, thermine, thermospermine, caldopentamine, homocaldopentamine, and canavalmine. Putrescine, spermidine and spermine are particularly useful. Synthetic polyamines are composed of the empirical formula $C_XH_YN_Z$, can be cyclic or acyclic, branched or unbranched, hydrocarbon chains of 3-12 carbon atoms that further include 1-6 NR or $N(R)_2$ moieties, wherein R is H, (C_1-C_4) alkyl, phenyl, or benzyl. Polyamines can be linked to an antibody using any standard crosslinking method.

In some embodiments, a subject antibody is modified to include a carbohydrate moiety, where the carbohydrate moiety can be covalently linked to the antibody. In some embodiments, a subject antibody is modified to include a lipid moiety, where the lipid moiety can be covalently linked to the antibody. Suitable lipid moieties include, e.g., an N-fatty acyl group such as N-lauroyl, N-oleoyl, etc.; a fatty amine such as dodecyl amine, oleoyl amine, etc.; a C3-C16 long-chain aliphatic lipid; and the like. See, e.g., U.S. Pat. No. 6,638,513). In some embodiments, a subject antibody is incorporated into a liposome.

Methods of producing a subject antibody

The present antibody can be produced by any known method, e.g., conventional synthetic methods for protein synthesis; recombinant DNA methods; etc.

Where a subject antibody is a single chain polypeptide, it can synthesized using standard chemical peptide synthesis techniques. Where a polypeptide is chemically synthesized, the synthesis may proceed via liquid-phase or solid-phase. Solid phase polypeptide synthesis (SPPS), in which the C-

terminal amino acid of the sequence is attached to an insoluble support followed by sequential addition of the remaining amino acids in the sequence, is an example of a suitable method for the chemical synthesis of a subject antibody. Various forms of SPPS, such as Fmoc and Boc, are available for synthesizing a subject antibody. Techniques for solid phase synthesis are described by Barany and Merrifield, Solid-Phase Peptide Synthesis; pp. 3-284 in The Peptides: Analysis, Synthesis, Biology. Vol. 2: Special Methods in Peptide Synthesis, Part A., Merrifield, et al. J. Am. Chem. Soc., 85: 2149-2156 (1963); Stewart et al., Solid Phase Peptide Synthesis, 2nd ed. Pierce Chem. Co., Rockford, Ill. (1984); and Ganesan A. 2006 *Mini Rev. Med Chem.* 6:3-10 and Camarero JA et al. 2005 *Protein Pept Lett.* 12:723-8. Briefly, small insoluble, porous beads are treated with functional units on which peptide chains are built. After repeated cycling of coupling/deprotection, the free N-terminal amine of a solid-phase attached is coupled to a single N-protected amino acid unit. This unit is then deprotected, revealing a new N-terminal amine to which a further amino acid may be attached. The peptide remains immobilized on the solid-phase and undergoes a filtration process before being cleaved off.

Standard recombinant methods can be used for production of a subject antibody. For example, nucleic acids encoding light and heavy chain variable regions, optionally linked to constant regions, are inserted into expression vectors. The light and heavy chains can be cloned in the same or different expression vectors. The DNA segments encoding immunoglobulin chains are operably linked to control sequences in the expression vector(s) that ensure the expression of immunoglobulin polypeptides. Expression control sequences include, but are not limited to, promoters (e.g., naturally-associated or heterologous promoters), signal sequences, enhancer elements, and transcription termination sequences. The expression control sequences can be eukaryotic promoter systems in vectors capable of transforming or transfecting eukaryotic host cells (e.g., COS or CHO cells). Once the vector has been incorporated into the appropriate host, the host is maintained under conditions suitable for high level expression of the nucleotide sequences, and the collection and purification of the antibodies.

Because of the degeneracy of the code, a variety of nucleic acid sequences can encode each immunoglobulin amino acid sequence. The desired nucleic acid sequences can be produced by de novo solid-phase DNA synthesis or by polymerase chain reaction (PCR) mutagenesis of an earlier prepared variant of the desired polynucleotide. Oligonucleotide-mediated mutagenesis is an example of a suitable method for preparing substitution, deletion and insertion variants of target polypeptide DNA. See Adelman et al., DNA 2:183 (1983). Briefly, the target polypeptide DNA is altered by hybridizing an oligonucleotide encoding the desired mutation to a single-stranded DNA template. After hybridization, a DNA polymerase is used to synthesize an entire second complementary strand of the template that incorporates the oligonucleotide primer, and encodes the selected alteration in the target polypeptide DNA.

Suitable expression vectors are typically replicable in the host organisms either as episomes or as an integral part of the host chromosomal DNA. Commonly, expression vectors contain selection markers (e.g., ampicillin-resistance, hygromycin-resistance, tetracycline resistance, kanamycin resistance or neomycin resistance) to permit detection of those cells transformed with the desired DNA sequences.

Escherichia coli is an example of a prokaryotic host cell that can be used for cloning a subject antibody-encoding polynucleotide. Other microbial hosts suitable for use include bacilli, such as *Bacillus subtilis*, and other enterobacteriaceae, such as Salmonella, Serratia, and various Pseudomonas species. In these prokaryotic hosts, one can also make expression vectors, which will typically contain expression control sequences compatible with the host cell (e.g., an origin of replication). In addition, any number of a variety of well-known promoters will be present, such as the lactose promoter system, a tryptophan (trp) promoter system, a beta-lactamase promoter system, or a promoter system from phage lambda. The promoters will typically control expression, optionally with an operator sequence, and have ribosome binding site sequences and the like, for initiating and completing transcription and translation.

Other microbes, such as yeast, are also useful for expression. Saccharomyces (e.g., *S. cerevisiae*) and Pichia are examples of suitable yeast host cells, with suitable vectors having expression control sequences (e.g., promoters), an origin of replication, termination sequences and the like as desired. Typical promoters include 3-phosphoglycerate kinase and other glycolytic enzymes. Inducible yeast promoters include, among others, promoters from alcohol dehydrogenase, isocytochrome C, and enzymes responsible for maltose and galactose utilization.

In addition to microorganisms, mammalian cells (e.g., mammalian cells grown in *in vitro* cell culture) can also be used to express and produce the polypeptides of the present invention (e.g., polynucleotides encoding immunoglobulins or fragments thereof). See Winnacker, From Genes to Clones, VCH Publishers, N.Y., N.Y. (1987). Suitable mammalian host cells include CHO cell lines, various Cos cell lines, HeLa cells, myeloma cell lines, and transformed B-cells or hybridomas. Expression vectors for these cells can include expression control sequences, such as an origin of replication, a promoter, and an enhancer (Queen et al., Immunol. Rev. 89:49 (1986)), and necessary processing information sites, such as ribosome binding sites, RNA splice sites, polyadenylation sites, and transcriptional terminator sequences. Examples of suitable expression control sequences are promoters derived from immunoglobulin genes, SV40, adenovirus, bovine papilloma virus, cytomegalovirus and the like. See Co et al., J. Immunol. 148:1149 (1992).

Once synthesized (either chemically or recombinantly), the whole antibodies, their dimers, individual light and heavy chains, or other forms of a subject antibody (e.g., scFv, etc.) can be purified according to standard procedures of the art, including ammonium sulfate precipitation, affinity columns, column chromatography, high performance liquid chromatography (HPLC) purification, gel

electrophoresis, and the like (see generally Scopes, Protein Purification (Springer-Verlag, N.Y., (1982)). A subject antibody can be substantially pure, e.g., at least about 80% to 85% pure, at least about 85% to 90% pure, at least about 90% to 95% pure, or 98% to 99%, or more, pure, e.g., free from contaminants such as cell debris, macromolecules other than a subject antibody, etc.

Compositions

The present disclosure provides a composition comprising a subject antibody. A subject antibody composition can comprise, in addition to a subject antibody, one or more of: a salt, e.g., NaCl, $MgCl_2$, KCl, $MgSO_4$, etc.; a buffering agent, e.g., a Tris buffer, N-(2-Hydroxyethyl)piperazine-N'-(2-ethanesulfonic acid) (HEPES), 2-(N-Morpholino)ethanesulfonic acid (MES), 2-(N-Morpholino)ethanesulfonic acid sodium salt (MES), 3-(N-Morpholino)propanesulfonic acid (MOPS), N-tris[Hydroxymethyl]methyl-3-aminopropanesulfonic acid (TAPS), etc.; a solubilizing agent; a detergent, e.g., a non-ionic detergent such as Tween-20, etc.; a protease inhibitor; glycerol; and the like.

Nucleic Acids

The present disclosure provides nucleic acids comprising nucleotide sequences encoding a subject antibody. A nucleotide sequence encoding a subject antibody can be operably linked to one or more regulatory elements, such as a promoter and enhancer, that allow expression of the nucleotide sequence in the intended target cells (e.g., a cell that is genetically modified to synthesize the encoded antibody).

Suitable promoter and enhancer elements are known in the art. For expression in a bacterial cell, suitable promoters include, but are not limited to, lacI, lacZ, T3, T7, gpt, lambda P and trc. For expression in a eukaryotic cell, suitable promoters include, but are not limited to, light and/or heavy chain immunoglobulin gene promoter and enhancer elements; cytomegalovirus immediate early promoter; herpes simplex virus thymidine kinase promoter; early and late SV40 promoters; promoter present in long terminal repeats from a retrovirus; mouse metallothionein-I promoter; and various art-known tissue specific promoters.

In some embodiments, e.g., for expression in a yeast cell, a suitable promoter is a constitutive promoter such as an ADH1 promoter, a PGK1 promoter, an ENO promoter, a PYK1 promoter and the like; or a regulatable promoter such as a GAL1 promoter, a GAL10 promoter, an ADH2 promoter, a PHO5 promoter, a CUP1 promoter, a GAL7 promoter, a MET25 promoter, a MET3 promoter, a CYC1 promoter, a HIS3 promoter, an ADH1 promoter, a PGK promoter, a GAPDH promoter, an ADC1 promoter, a TRP1 promoter, a URA3 promoter, a LEU2 promoter, an ENO promoter, a TP1 promoter, and AOX1 (e.g., for use in *Pichia*). Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art.

Suitable promoters for use in prokaryotic host cells include, but are not limited to, a bacteriophage T7 RNA polymerase promoter; a trp promoter; a lac operon promoter; a hybrid promoter, e.g., a lac/tac hybrid promoter, a tac/trc hybrid promoter, a trp/lac promoter, a T7/lac promoter; a trc promoter; a tac promoter, and the like; an araBAD promoter; *in vivo* regulated promoters, such as an *ssaG* promoter or a related promoter (*see*, e.g., U.S. Patent Publication No. 20040131637), a *pagC* promoter (Pulkkinen and Miller, *J. Bacteriol.*, 1991: 173(1): 86-93; Alpuche-Aranda et al., PNAS, 1992; 89(21): 10079-83), a *nirB* promoter (Harborne et al. (1992) *Mol. Micro.* 6:2805-2813), and the like (*see*, e.g., Dunstan et al. (1999) *Infect. Immun.* 67:5133-5141; McKelvie et al. (2004) *Vaccine* 22:3243-3255; and Chatfield et al. (1992) *Biotechnol.* 10:888-892); a sigma70 promoter, e.g., a consensus sigma70 promoter (see, e.g., GenBank Accession Nos. AX798980, AX798961, and AX798183); a stationary phase promoter, e.g., a *dps* promoter, an *spv* promoter, and the like; a promoter derived from the pathogenicity island SPI-2 (*see*, e.g., WO96/17951); an actA promoter (*see*, e.g., Shetron-Rama et al. (2002) *Infect. Immun.* 70:1087-1096); an rpsM promoter (*see*, e.g., Valdivia and Falkow (1996). *Mol. Microbiol.* 22:367); a tet promoter (*see*, e.g., Hillen,W. and Wissmann,A. (1989) In Saenger,W. and Heinemann,U. (eds), *Topics in Molecular and Structural Biology, Protein–Nucleic Acid Interaction*. Macmillan, London, UK, Vol. 10, pp. 143–162); an SP6 promoter (*see*, e.g., Melton et al. (1984) *Nucl. Acids Res.* 12:7035); and the like. Suitable strong promoters for use in prokaryotes such as *Escherichia coli* include, but are not limited to Trc, Tac, T5, T7, and $P_{Lambda.}$ Non-limiting examples of operators for use in bacterial host cells include a lactose promoter operator (LacI repressor protein changes conformation when contacted with lactose, thereby preventing the LacI repressor protein from binding to the operator), a tryptophan promoter operator (when complexed with tryptophan, TrpR repressor protein has a conformation that binds the operator; in the absence of tryptophan, the TrpR repressor protein has a conformation that does not bind to the operator), and a tac promoter operator (see, for example, deBoer et al. (1983) Proc. Natl. Acad. Sci. U.S.A. 80:21-25).

A nucleotide sequence encoding a subject antibody can be present in an expression vector and/or a cloning vector. Where a subject antibody comprises two separate polypeptides, nucleotide sequences encoding the two polypeptides can be cloned in the same or separate vectors. An expression vector can include a selectable marker, an origin of replication, and other features that provide for replication and/or maintenance of the vector.

Large numbers of suitable vectors and promoters are known to those of skill in the art; many are commercially available for generating a subject recombinant constructs. The following vectors are provided by way of example. Bacterial: pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene, La Jolla, Calif., USA); pTrc99A, pKK223-3, pKK233-3,

pDR540, and pRIT5 (Pharmacia, Uppsala, Sweden). Eukaryotic: pWLneo, pSV2cat, pOG44, PXR1, pSG (Stratagene) pSVK3, pBPV, pMSG and pSVL (Pharmacia).

Expression vectors generally have convenient restriction sites located near the promoter sequence to provide for the insertion of nucleic acid sequences encoding heterologous proteins. A selectable marker operative in the expression host may be present. Suitable expression vectors include, but are not limited to, viral vectors (e.g. viral vectors based on vaccinia virus; poliovirus; adenovirus (see, e.g., Li et al., Invest Opthalmol Vis Sci 35:2543 2549, 1994; Borras et al., Gene Ther 6:515 524, 1999; Li and Davidson, PNAS 92:7700 7704, 1995; Sakamoto et al., H Gene Ther 5:1088 1097, 1999; WO 94/12649, WO 93/03769; WO 93/19191; WO 94/28938; WO 95/11984 and WO 95/00655); adeno-associated virus (see, e.g., Ali et al., Hum Gene Ther 9:81 86, 1998, Flannery et al., PNAS 94:6916 6921, 1997; Bennett et al., Invest Opthalmol Vis Sci 38:2857 2863, 1997; Jomary et al., Gene Ther 4:683 690, 1997, Rolling et al., Hum Gene Ther 10:641 648, 1999; Ali et al., Hum Mol Genet 5:591 594, 1996; Srivastava in WO 93/09239, Samulski et al., J. Vir. (1989) 63:3822-3828; Mendelson et al., Virol. (1988) 166:154-165; and Flotte et al., PNAS (1993) 90:10613-10617); SV40; herpes simplex virus; human immunodeficiency virus (see, e.g., Miyoshi et al., PNAS 94:10319 23, 1997; Takahashi et al., J Virol 73:7812 7816, 1999); a retroviral vector (e.g., Murine Leukemia Virus, spleen necrosis virus, and vectors derived from retroviruses such as Rous Sarcoma Virus, Harvey Sarcoma Virus, avian leukosis virus, human immunodeficiency virus, myeloproliferative sarcoma virus, and mammary tumor virus); and the like.

As noted above, a subject nucleic acid comprises a nucleotide sequence encoding a subject antibody. A subject nucleic acid can comprise a nucleotide sequence encoding heavy- and light-chain CDRs. In some embodiments, a subject nucleic acid comprises a nucleotide sequence encoding heavy- and light-chain CDRs, where the CDR-encoding sequences are interspersed with FR-encoding nucleotide sequences. In some embodiments, the FR-encoding nucleotide sequences are human FR-encoding nucleotide sequences.

In some embodiments, a subject nucleic acid comprises a nucleotide sequence having at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, nucleotide sequence identity to the nucleotide sequence set forth in herein. In some embodiments, a subject nucleic acid comprises a nucleotide sequence having at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, nucleotide sequence identity to the nucleotide sequence set forth in herein.

Cells

The present disclosure provides isolated genetically modified host cells (e.g., *in vitro* cells) that are genetically modified with a subject nucleic acid. In some embodiments, a subject isolated genetically modified host cell can produce a subject antibody.

Suitable host cells include eukaryotic host cells, such as a mammalian cell, an insect host cell, a yeast cell; and prokaryotic cells, such as a bacterial cell. Introduction of a subject nucleic acid into the host cell can be effected, for example by calcium phosphate precipitation, DEAE dextran mediated transfection, liposome-mediated transfection, electroporation, or other known method.

Suitable mammalian cells include primary cells and immortalized cell lines. Suitable mammalian cell lines include human cell lines, non-human primate cell lines, rodent (e.g., mouse, rat) cell lines, and the like. Suitable mammalian cell lines include, but are not limited to, HeLa cells (e.g., American Type Culture Collection (ATCC) No. CCL-2), CHO cells (e.g., ATCC Nos. CRL9618, CCL61, CRL9096), 293 cells (e.g., ATCC No. CRL-1573), Vero cells, NIH 3T3 cells (e.g., ATCC No. CRL-1658), Huh-7 cells, BHK cells (e.g., ATCC No. CCL10), PC12 cells (ATCC No. CRL1721), COS cells, COS-7 cells (ATCC No. CRL1651), RAT1 cells, mouse L cells (ATCC No. CCLI.3), human embryonic kidney (HEK) cells (ATCC No. CRL1573), HLHepG2 cells, and the like.

Suitable yeast cells include, but are not limited to, Pichia pastoris, Pichia finlandica, Pichia trehalophila, Pichia koclamae, Pichia membranaefaciens, Pichia opuntiae, Pichia thermotolerans, Pichia salictaria, Pichia guercuum, Pichia pijperi, Pichia stiptis, Pichia methanolica, Pichia sp., Saccharomyces cerevisiae, Saccharomyces sp., Hansenula polymorpha, Kluyveromyces sp., Kluyveromyces lactis, Candida albicans, Aspergillus nidulans, Aspergillus niger, Aspergillus oryzae, Trichoderma reesei, Chrysosporium lucknowense, Fusarium sp., Fusarium gramineum, Fusarium venenatum, Neurospora crassa, Chlamydomonas reinhardtii, and the like.

Suitable prokaryotic cells include, but are not limited to, any of a variety of laboratory strains of *Escherichia coli*, *Lactobacillus* sp., *Salmonella* sp., *Shigella* sp., and the like. See, e.g., Carrier et al. (1992) *J. Immunol.* 148:1176-1181; U.S. Patent No. 6,447,784; and Sizemore et al. (1995) *Science* 270:299-302. Examples of Salmonella strains which can be employed in the present invention include, but are not limited to, *Salmonella typhi* and *S. typhimurium*. Suitable Shigella strains include, but are not limited to, *Shigella flexneri*, *Shigella sonnei*, and *Shigella disenteriae*. Typically, the laboratory strain is one that is non-pathogenic. Non-limiting examples of other suitable bacteria include, but are not limited to, *Bacillus subtilis*, *Pseudomonas pudita*, *Pseudomonas aeruginosa*, *Pseudomonas mevalonii*, *Rhodobacter sphaeroides*, *Rhodobacter capsulatus*, *Rhodospirillum rubrum*, *Rhodococcus* sp., and the like. In some embodiments, the host cell is *Escherichia coli*.

Compositions

The present disclosure provides compositions, including pharmaceutical compositions, comprising a subject antibody. In general, a formulation comprises an effective amount of a subject antibody. An "effective amount" means a dosage sufficient to produce a desired result, e.g., an increase of muscle mass or amelioration of a symptom of a disease. Generally, the desired result is at least a reduction in a symptom of an ACVR2A-associated conditino, as compared to a control. A subject antibody can be delivered in such a manner as to avoid the blood-brain barrier, as described in more detail below. A subject antibody can be formulated and/or modified to enable the antibody to cross the blood-brain barrier.

Formulations

In the subject methods, a subject antibody can be administered to the host using any convenient means capable of resulting in the desired therapeutic effect or diagnostic effect. Thus, the agent can be incorporated into a variety of formulations for therapeutic administration. More particularly, a subject antibody can be formulated into pharmaceutical compositions by combination with appropriate, pharmaceutically acceptable carriers or diluents, and may be formulated into preparations in solid, semi-solid, liquid or gaseous forms, such as tablets, capsules, powders, granules, ointments, solutions, suppositories, injections, inhalants and aerosols.

In pharmaceutical dosage forms, a subject antibody can be administered in the form of their pharmaceutically acceptable salts, or they may also be used alone or in appropriate association, as well as in combination, with other pharmaceutically active compounds. The following methods and excipients are merely exemplary and are in no way limiting.

For oral preparations, a subject antibody can be used alone or in combination with appropriate additives to make tablets, powders, granules or capsules, for example, with conventional additives, such as lactose, mannitol, corn starch or potato starch; with binders, such as crystalline cellulose, cellulose derivatives, acacia, corn starch or gelatins; with disintegrators, such as corn starch, potato starch or sodium carboxymethylcellulose; with lubricants, such as talc or magnesium stearate; and if desired, with diluents, buffering agents, moistening agents, preservatives and flavoring agents.

A subject antibody can be formulated into preparations for injection by dissolving, suspending or emulsifying them in an aqueous or nonaqueous solvent, such as vegetable or other similar oils, synthetic aliphatic acid glycerides, esters of higher aliphatic acids or propylene glycol; and if desired, with conventional additives such as solubilizers, isotonic agents, suspending agents, emulsifying agents, stabilizers and preservatives.

Pharmaceutical compositions comprising a subject antibody are prepared by mixing the antibody having the desired degree of purity with optional physiologically acceptable carriers, excipients, stabilizers, surfactants, buffers and/or tonicity agents. Acceptable carriers, excipients and/or stabilizers are

nontoxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid, glutathione, cysteine, methionine and citric acid; preservatives (such as ethanol, benzyl alcohol, phenol, m-cresol, p-chlor-m-cresol, methyl or propyl parabens, benzalkonium chloride, or combinations thereof); amino acids such as arginine, glycine, ornithine, lysine, histidine, glutamic acid, aspartic acid, isoleucine, leucine, alanine, phenylalanine, tyrosine, tryptophan, methionine, serine, proline and combinations thereof; monosaccharides, disaccharides and other carbohydrates; low molecular weight (less than about 10 residues) polypeptides; proteins, such as gelatin or serum albumin; chelating agents such as EDTA; sugars such as trehalose, sucrose, lactose, glucose, mannose, maltose, galactose, fructose, sorbose, raffinose, glucosamine, N-methylglucosamine, galactosamine, and neuraminic acid; and/or non-ionic surfactants such as Tween, Brij Pluronics, Triton-X, or polyethylene glycol (PEG).

The pharmaceutical composition may be in a liquid form, a lyophilized form or a liquid form reconstituted from a lyophilized form, wherein the lyophilized preparation is to be reconstituted with a sterile solution prior to administration. The standard procedure for reconstituting a lyophilized composition is to add back a volume of pure water (typically equivalent to the volume removed during lyophilization); however solutions comprising antibacterial agents may be used for the production of pharmaceutical compositions for parenteral administration; see also Chen (1992) Drug Dev Ind Pharm 18, 1311-54.

Exemplary antibody concentrations in a subject pharmaceutical composition may range from about 1 mg/mL to about 200 mg/ml or from about 50 mg/mL to about 200 mg/mL, or from about 150 mg/mL to about 200 mg/mL.

An aqueous formulation of the antibody may be prepared in a pH-buffered solution, e.g., at pH ranging from about 4.0 to about 7.0, or from about 5.0 to about 6.0, or alternatively about 5.5. Examples of buffers that are suitable for a pH within this range include phosphate-, histidine-, citrate-, succinate-, acetate-buffers and other organic acid buffers. The buffer concentration can be from about 1 mM to about 100 mM, or from about 5 mM to about 50 mM, depending, e.g., on the buffer and the desired tonicity of the formulation.

A tonicity agent may be included in the antibody formulation to modulate the tonicity of the formulation. Exemplary tonicity agents include sodium chloride, potassium chloride, glycerin and any component from the group of amino acids, sugars as well as combinations thereof. In some embodiments, the aqueous formulation is isotonic, although hypertonic or hypotonic solutions may be suitable. The term "isotonic" denotes a solution having the same tonicity as some other solution with which it is compared, such as physiological salt solution or serum. Tonicity agents may be used in an amount of about 5 mM to about 350 mM, e.g., in an amount of 100 mM to 350 nM.

A surfactant may also be added to the antibody formulation to reduce aggregation of the formulated antibody and/or minimize the formation of particulates in the formulation and/or reduce adsorption. Exemplary surfactants include polyoxyethylensorbitan fatty acid esters (Tween), polyoxyethylene alkyl ethers (Brij), alkylphenylpolyoxyethylene ethers (Triton-X), polyoxyethylene-polyoxypropylene copolymer (Poloxamer, Pluronic), and sodium dodecyl sulfate (SDS). Examples of suitable polyoxyethylenesorbitan-fatty acid esters are polysorbate 20, (sold under the trademark Tween 20™) and polysorbate 80 (sold under the trademark Tween 80™). Examples of suitable polyethylene-polypropylene copolymers are those sold under the names Pluronic® F68 or Poloxamer 188™. Examples of suitable Polyoxyethylene alkyl ethers are those sold under the trademark Brij™. Exemplary concentrations of surfactant may range from about 0.001% to about 1% w/v.

A lyoprotectant may also be added in order to protect the labile active ingredient (e.g. a protein) against destabilizing conditions during the lyophilization process. For example, known lyoprotectants include sugars (including glucose and sucrose); polyols (including mannitol, sorbitol and glycerol); and amino acids (including alanine, glycine and glutamic acid). Lyoprotectants can be included in an amount of about 10 mM to 500 nM.

In some embodiments, a subject formulation includes a subject antibody, and one or more of the above-identified agents (e.g., a surfactant, a buffer, a stabilizer, a tonicity agent) and is essentially free of one or more preservatives, such as ethanol, benzyl alcohol, phenol, m-cresol, p-chlor-m-cresol, methyl or propyl parabens, benzalkonium chloride, and combinations thereof. In other embodiments, a preservative is included in the formulation, e.g., at concentrations ranging from about 0.001 to about 2% (w/v).

For example, a subject formulation can be a liquid or lyophilized formulation suitable for parenteral administration, and can comprise: about 1 mg/mL to about 200 mg/mL of a subject antibody; about 0.001 % to about 1 % of at least one surfactant; about 1 mM to about 100 mM of a buffer; optionally about 10 mM to about 500 mM of a stabilizer; and about 5 mM to about 305 mM of a tonicity agent; and has a pH of about 4.0 to about 7.0.

As another example, a subject parenteral formulation is a liquid or lyophilized formulation comprising: about 1 mg/mL to about 200 mg/mL of a subject antibody; 0.04% Tween 20 w/v; 20 mM L-histidine; and 250 mM Sucrose; and has a pH of 5.5.

As another example, a subject parenteral formulation comprises a lyophilized formulation comprising: 1) 15 mg/mL of a subject antibody; 0.04% Tween 20 w/v; 20 mM L-histidine; and 250 mM sucrose; and has a pH of 5.5; or 2) 75 mg/mL of a subject antibody; 0.04% Tween 20 w/v; 20 mM L-histidine; and 250 mM sucrose; and has a pH of 5.5;or 3) 75 mg/mL of a subject antibody; 0.02% Tween 20 w/v; 20 mM L-histidine; and 250 mM Sucrose; and has a pH of 5.5; or 4) 75 mg/mL of a subject antibody; 0.04% Tween 20 w/v; 20 mM L-histidine; and 250 mM trehalose; and has a pH of 5.5; or 6) 75

mg/mL of a subject antibody; 0.02% Tween 20 w/v; 20 mM L-histidine; and 250 mM trehalose; and has a pH of 5.5.

As another example, a subject parenteral formulation is a liquid formulation comprising:1) 7.5 mg/mL of a subject antibody; 0.022% Tween 20 w/v; 120 mM L-histidine; and 250 125 mM sucrose; and has a pH of 5.5; or 2) 37.5 mg/mL of a subject antibody; 0.02% Tween 20 w/v; 10 mM L-histidine; and 125 mM sucrose; and has a pH of 5.5; or 3) 37.5 mg/mL of a subject antibody; 0.01% Tween 20 w/v; 10 mM L-histidine; and 125 mM sucrose; and has a pH of 5.5; or 4) 37.5 mg/mL of a subject antibody; 0.02% Tween 20 w/v; 10 mM L-histidine; 125 mM trehalose; and has a pH of 5.5; or 5) 37.5 mg/mL of a subject antibody; 0.01% Tween 20 w/v; 10 mM L-histidine; and 125 mM trehalose; and has a pH of 5.5; or 6) 5 mg/mL of a subject antibody; 0.02% Tween 20 w/v; 20 mM L-histidine; and 250 mM trehalose; and has a pH of 5.5; or 7) 75 mg/mL of a subject antibody; 0.02% Tween 20 w/v; 20 mM L-histidine; and 250 mM mannitol; and has a pH of 5.5; or 8) 75 mg/mL of a subject antibody; 0.02% Tween 20 w/v; 20 mM L histidine; and 140 mM sodium chloride; and has a pH of 5.5;or 9) 150 mg/mL of a subject antibody; 0.02% Tween 20 w/v; 20 mM L-histidine; and 250 mM trehalose; and has a pH of 5.5; or 10) 150 mg/mL of a subject antibody; 0.02% Tween 20 w/v; 20 mM L-histidine; and 250 mM mannitol; and has a pH of 5.5; or 11) 150 mg/mL of a subject antibody; 0.02% Tween 20 w/v; 20 mM L-histidine; and 140 mM sodium chloride; and has a pH of 5.5; or 12) 10 mg/mL of a subject antibody; 0.01% Tween 20 w/v; 20 mM L-histidine; and 40 mM sodium chloride; and has a pH of 5.5.

A subject antibody can be utilized in aerosol formulation to be administered via inhalation. A subject antibody can be formulated into pressurized acceptable propellants such as dichlorodifluoromethane, propane, nitrogen and the like.

Furthermore, a subject antibody can be made into suppositories by mixing with a variety of bases such as emulsifying bases or water-soluble bases. A subject antibody can be administered rectally via a suppository. The suppository can include vehicles such as cocoa butter, carbowaxes and polyethylene glycols, which melt at body temperature, yet are solidified at room temperature.

Unit dosage forms for oral or rectal administration such as syrups, elixirs, and suspensions may be provided wherein each dosage unit, for example, teaspoonful, tablespoonful, tablet or suppository, contains a predetermined amount of the composition containing one or more inhibitors. Similarly, unit dosage forms for injection or intravenous administration may comprise a subject antibody in a composition as a solution in sterile water, normal saline or another pharmaceutically acceptable carrier.

The term “unit dosage form,” as used herein, refers to physically discrete units suitable as unitary dosages for human and animal subjects, each unit containing a predetermined quantity of compounds of the present invention calculated in an amount sufficient to produce the desired effect in association with a pharmaceutically acceptable diluent, carrier or vehicle. The specifications for a subject antibody may

depend on the particular antibody employed and the effect to be achieved, and the pharmacodynamics associated with each antibody in the host.

Other modes of administration will also find use with the subject invention. For instance, a subject antibody can be formulated in suppositories and, in some cases, aerosol and intranasal compositions. For suppositories, the vehicle composition will include traditional binders and carriers such as, polyalkylene glycols, or triglycerides. Such suppositories may be formed from mixtures containing the active ingredient in the range of about 0.5% to about 10% (w/w), e.g., about 1% to about 2%.

Intranasal formulations will usually include vehicles that neither cause irritation to the nasal mucosa nor significantly disturb ciliary function. Diluents such as water, aqueous saline or other known substances can be employed with the subject invention. The nasal formulations may also contain preservatives such as, but not limited to, chlorobutanol and benzalkonium chloride. A surfactant may be present to enhance absorption of the subject proteins by the nasal mucosa.

A subject antibody can be administered as an injectable formulation. Typically, injectable compositions are prepared as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection may also be prepared. The preparation may also be emulsified or the antibody encapsulated in liposome vehicles.

Suitable excipient vehicles are, for example, water, saline, dextrose, glycerol, ethanol, or the like, and combinations thereof. In addition, if desired, the vehicle may contain minor amounts of auxiliary substances such as wetting or emulsifying agents or pH buffering agents. Actual methods of preparing such dosage forms are known, or will be apparent, to those skilled in the art. See, e.g., Remington's Pharmaceutical Sciences, Mack Publishing Company, Easton, Pennsylvania, 17th edition, 1985. The composition or formulation to be administered will, in any event, contain a quantity of a subject antibody adequate to achieve the desired state in the subject being treated.

The pharmaceutically acceptable excipients, such as vehicles, adjuvants, carriers or diluents, are readily available to the public. Moreover, pharmaceutically acceptable auxiliary substances, such as pH adjusting and buffering agents, tonicity adjusting agents, stabilizers, wetting agents and the like, are readily available to the public.

In some embodiments, a subject antibody is formulated in a controlled release formulation. Sustained-release preparations may be prepared using methods well known in the art. Suitable examples of sustained-release preparations include semipermeable matrices of solid hydrophobic polymers containing the antibody in which the matrices are in the form of shaped articles, e.g. films or microcapsules. Examples of sustained-release matrices include polyesters, copolymers of L-glutamic acid and ethyl-L-glutamate, non-degradable ethylene-vinyl acetate, hydrogels, polylactides, degradable lactic acid-glycolic acid copolymers and poly-D-(-)-3-hydroxybutyric acid. Possible loss of biological activity

and possible changes in immunogenicity of antibodies comprised in sustained-release preparations may be prevented by using appropriate additives, by controlling moisture content and by developing specific polymer matrix compositions.

Controlled release within the scope of this invention can be taken to mean any one of a number of extended release dosage forms. The following terms may be considered to be substantially equivalent to controlled release, for the purposes of the present invention: continuous release, controlled release, delayed release, depot, gradual release, long-term release, programmed release, prolonged release, proportionate release, protracted release, repository, retard, slow release, spaced release, sustained release, time coat, timed release, delayed action, extended action, layered-time action, long acting, prolonged action, repeated action, slowing acting, sustained action, sustained-action medications, and extended release. Further discussions of these terms may be found in Lesczek Krowczynski, Extended-Release Dosage Forms, 1987 (CRC Press, Inc.).

The various controlled release technologies cover a very broad spectrum of drug dosage forms. Controlled release technologies include, but are not limited to physical systems and chemical systems.

Physical systems include, but are not limited to, reservoir systems with rate-controlling membranes, such as microencapsulation, macroencapsulation, and membrane systems; reservoir systems without rate-controlling membranes, such as hollow fibers, ultra microporous cellulose triacetate, and porous polymeric substrates and foams; monolithic systems, including those systems physically dissolved in non-porous, polymeric, or elastomeric matrices (e.g., nonerodible, erodible, environmental agent ingression, and degradable), and materials physically dispersed in non-porous, polymeric, or elastomeric matrices (e.g., nonerodible, erodible, environmental agent ingression, and degradable); laminated structures, including reservoir layers chemically similar or dissimilar to outer control layers; and other physical methods, such as osmotic pumps, or adsorption onto ion-exchange resins.

Chemical systems include, but are not limited to, chemical erosion of polymer matrices (e.g., heterogeneous, or homogeneous erosion), or biological erosion of a polymer matrix (e.g., heterogeneous, or homogeneous). Additional discussion of categories of systems for controlled release may be found in Agis F. Kydonieus, Controlled Release Technologies: Methods, Theory and Applications, 1980 (CRC Press, Inc.).

There are a number of controlled release drug formulations that are developed for oral administration. These include, but are not limited to, osmotic pressure-controlled gastrointestinal delivery systems; hydrodynamic pressure-controlled gastrointestinal delivery systems; membrane permeation-controlled gastrointestinal delivery systems, which include microporous membrane permeation-controlled gastrointestinal delivery devices; gastric fluid-resistant intestine targeted controlled-release gastrointestinal delivery devices; gel diffusion-controlled gastrointestinal delivery systems; and ion-

exchange-controlled gastrointestinal delivery systems, which include cationic and anionic drugs. Additional information regarding controlled release drug delivery systems may be found in Yie W. Chien, Novel Drug Delivery Systems, 1992 (Marcel Dekker, Inc.)..

Dosages

A suitable dosage can be determined by an attending physician or other qualified medical personnel, based on various clinical factors. As is well known in the medical arts, dosages for any one patient depend upon many factors, including the patient's size, body surface area, age, the particular compound to be administered, sex of the patient, time, and route of administration, general health, and other drugs being administered concurrently. A subject antibody may be administered in amounts between 1 ng/kg body weight and 20 mg/kg body weight per dose, e.g. between 0.1 mg/kg body weight to 10 mg/kg body weight, e.g. between 0.5 mg/kg body weight to 5 mg/kg body weight; however, doses below or above this exemplary range are envisioned, especially considering the aforementioned factors. If the regimen is a continuous infusion, it can also be in the range of 1 μg to 10 mg per kilogram of body weight per minute.

Those of skill will readily appreciate that dose levels can vary as a function of the specific antibody, the severity of the symptoms and the susceptibility of the subject to side effects. Preferred dosages for a given compound are readily determinable by those of skill in the art by a variety of means.

Routes of administration

A subject antibody is administered to an individual using any available method and route suitable for drug delivery, including *in vivo* and *ex vivo* methods, as well as systemic and localized routes of administration.

Conventional and pharmaceutically acceptable routes of administration include intranasal, intramuscular, intratracheal, subcutaneous, intradermal, topical application, intravenous, intraarterial, rectal, nasal, oral, and other enteral and parenteral routes of administration. Routes of administration may be combined, if desired, or adjusted depending upon the antibody and/or the desired effect. A subject antibody composition can be administered in a single dose or in multiple doses. In some embodiments, a subject antibody composition is administered orally. In some embodiments, a subject antibody composition is administered via an inhalational route. In some embodiments, a subject antibody composition is administered intranasally. In some embodiments, a subject antibody composition is administered locally. In some embodiments, a subject antibody composition is administered intracranially. In some embodiments, a subject antibody composition is administered intravenously.

The agent can be administered to a host using any available conventional methods and routes suitable for delivery of conventional drugs, including systemic or localized routes. In general, routes of

administration contemplated by the invention include, but are not necessarily limited to, enteral, parenteral, or inhalational routes.

Parenteral routes of administration other than inhalation administration include, but are not necessarily limited to, topical, transdermal, subcutaneous, intramuscular, intraorbital, intracapsular, intraspinal, intrasternal, and intravenous routes, *i.e.*, any route of administration other than through the alimentary canal. Parenteral administration can be carried to effect systemic or local delivery of a subject antibody. Where systemic delivery is desired, administration typically involves invasive or systemically absorbed topical or mucosal administration of pharmaceutical preparations.

A subject antibody can also be delivered to the subject by enteral administration. Enteral routes of administration include, but are not necessarily limited to, oral and rectal (*e.g.*, using a suppository) delivery.

By treatment is meant at least an amelioration of the symptoms associated with the pathological condition afflicting the host, where amelioration is used in a broad sense to refer to at least a reduction in the magnitude of a parameter, e.g. symptom, associated with the pathological condition being treated, such as muscle atrophy. As such, treatment also includes situations where the pathological condition, or at least symptoms associated therewith, are completely inhibited, *e.g.* prevented from happening, or stopped, *e.g.* terminated, such that the host no longer suffers from the pathological condition, or at least the symptoms that characterize the pathological condition.

In some embodiments, a subject antibody is administered by injection and/or delivery, e.g., to a site in a brain artery or directly into brain tissue. A subject antibody can also be administered directly to a target site e.g., by biolistic delivery to the target site.

A variety of hosts (wherein the term "host" is used interchangeably herein with the terms "subject," "individual," and "patient") are treatable according to the subject methods. Generally such hosts are "mammals" or "mammalian," where these terms are used broadly to describe organisms which are within the class mammalia, including the orders carnivore (*e.g.*, dogs and cats), rodentia (*e.g.*, mice, guinea pigs, and rats), and primates (*e.g.,* humans, chimpanzees, and monkeys). In some embodiments, the hosts will be humans.

Kits with unit doses of a subject antibody, e.g. in oral or injectable doses, are provided. In such kits, in addition to the containers containing the unit doses will be an informational package insert describing the use and attendant benefits of the antibody in treating pathological condition of interest. Preferred compounds and unit doses are those described herein above.

Treatment Methods

The present disclosure provides methods of treating an ACVR2A-associated condition, the methods generally involving administering to an individual in need thereof (e.g., an individual having a

ACVR2A-associated condition) an effective amount of a subject antibody, alone (e.g., in monotherapy) or in combination (e.g., in combination therapy) with one or more additional therapeutic agents. In certain embodiments, an ACVR2A-specific antibody can be used for treating or preventing a disease or condition that can be treated by decreasing ACVR2A signaling. In certain embodiments, the present invention provides methods of treating or preventing a disease, disorder, or condition in an individual in need thereof through administering to the individual a therapeutically effective amount of an ACVR2A-specific antibody as described above. These methods are particularly aimed at therapeutic and prophylactic treatments of animals, and more particularly, humans.

Mice genetically deficient in the inhibin-α subunit are deficient in inhibin A and inhibin B, have gonadal tumors that overexpress activins A and B (Matzuk et al., 1992, Nature 360:313-319; Matzuk et al., 1994, Proc Natl Acad Sci USA 91:8817-8821). All such mice develop these tumors and eventually die of a cancer cachexia-like syndrome mediated by high levels of tumor-derived activin acting through ACVR2A (Coerver et al., 1996, Mol Endocrinol 10:534-543). While not wishing to limit the present invention, an antibody that specifically blocks binding of a ligand to ACVR2A may be useful for treating a variety of conditions that are related to muscle atrophy. For example, an ACVR2A-specific antibody may be used to reduce the effects of activin-producing tumors, alleviating activin-mediated cachexia, and prolonging patient survival. In some embodiments, the subject may have a muscle-wasting disorder such as insufficient lean body mass, a decrease in muscle mass or muscle function, cachexia or sarcopenia.

ACVR2A and ACVR2A-ligand complexes play essential roles in tissue growth as well as early developmental processes such as the correct formation of various structures or in one or more post-developmental capacities including sexual development, pituitary hormone production, and creation of bone and cartilage. Thus, ACVR2A-associated conditions include abnormal tissue growth and developmental defects. In addition, ACVR2A-associated conditions include, but are not limited to, disorders of cell growth and differentiation such as inflammation, allergy, autoimmune diseases, infectious diseases, and tumors.

Exemplary ACVR2A-associated conditions include neuromuscular disorders (e.g., muscular dystrophy and muscle atrophy), congestive obstructive pulmonary disease or pulmonary emphysema (and associated muscle wasting), muscle wasting syndrome, sarcopenia, cachexia, adipose tissue disorders (e.g., obesity), type 2 diabetes, and bone degenerative disease (e.g., osteoporosis). Other exemplary ACVR2A-associated conditions include musculodegenerative and neuromuscular disorders, tissue repair (e.g., wound healing), neurodegenerative diseases (e.g., amyotrophic lateral sclerosis), immunologic disorders (e.g., disorders related to abnormal proliferation or function of lymphocytes), and obesity or disorders related to abnormal proliferation of adipocytes.

In certain embodiments, an ACVR2A-specific antibody may be used as part of a treatment for a muscular dystrophy. The term "muscular dystrophy" refers to a group of degenerative muscle diseases

characterized by gradual weakening and deterioration of skeletal muscles and sometimes the heart and respiratory muscles. Muscular dystrophies are genetic disorders characterized by progressive muscle wasting and weakness that begin with microscopic changes in the muscle. As muscles degenerate over time, the person's muscle strength declines. Exemplary muscular dystrophies that can be treated with a regimen including the subject ACVR2A-specific antibodies include: Duchenne muscular dystrophy (DMD), Becker muscular dystrophy (BMD), Emery-Dreifuss muscular dystrophy (EDMD), limb-girdle muscular dystrophy (LGMD), fascioscapulohumeral muscular dystrophy (FSH or FSHD) (also known as Landouzy-Dejerine), myotonic muscular dystrophy (MMD) (also known as Steinert's Disease), oculopharyngeal muscular dystrophy (OPMD), distal muscular dystrophy (DD), congenital muscular dystrophy (CMD), and scapulohumeral muscular dystrophy (SMD).

Duchenne muscular dystrophy (DMD) was first described by the French neurologist Guillaume Benjamin Amand Duchenne in the 1860s. Becker muscular dystrophy (BMD) is named after the German doctor Peter Emil Becker, who first described this variant of DMD in the 1950s. DMD is one of the most frequent inherited diseases in males, affecting one in 3,500 boys. DMD occurs when the dystrophin gene, located on the short arm of the X chromosome, is broken. Since males only carry one copy of the X chromosome, they only have one copy of the dystrophin gene. Without the dystrophin protein, muscle is easily damaged during cycles of contraction and relaxation. While early in the disease muscle compensates by regeneration, later on muscle progenitor cells cannot keep up with the ongoing damage and healthy muscle is replaced by non-functional fibro-fatty tissue.

In other embodiments, ACVR2A-specific antibodies may also be used to treat or prevent muscular atrophy due to myopathies, examples of which include inflammatory myopathy, metabolic myopathy, and myotonia. Subject ACVR2A-specific antibodies have application in treating congenital myopathies such as myotubular myopathy, nemalene myopathy, and mitochondrial myopathy. The subject ACVR2A-specific antibodies may be used to treat inclusion body myositis, myoglobinurias, rhabdomyolysis, myositis ossificans, polymyositis, or dermatomyositis. In addition, ACVR2A-specific antibodies may treat or prevent muscle atrophy arising from glucocorticoid treatment, sarcopenia, prolonged bed rest, skeletal immobilization, sepsis, or congestive heart failure.

An ACVR2A-specific antibody may provide an effective means to increase muscle mass in other neuromuscular diseases or conditions that are in need of muscle growth. For example, amyotrophic lateral sclerosis (ALS, also known as Lou Gehrig's disease or motor neuron disease) is a chronic, incurable, and unstoppable CNS disorder that attacks the motor neurons, components of the CNS that connect the brain to the skeletal muscles. In ALS, the motor neurons deteriorate and eventually die, and though a person's brain normally remains fully functioning and alert, the command to move cannot reach the muscles. Most people who develop ALS are between 40 and 70 years old. The first motor neurons that weaken are those

leading to the arms or legs. Those with ALS may have trouble walking, they may drop things, fall, slur their speech, and laugh or cry uncontrollably. Eventually the muscles in the limbs begin to atrophy from disuse. This muscle weakness will become debilitating and a person will need a wheel chair or become unable to function out of bed. Most ALS patients die from respiratory failure or from complications of ventilator assistance like pneumonia, 3-5 years from disease onset. Other neuromuscular diseases in which ACVR2A-specific antibodies may be useful include paralysis due to spinal cord injury or stroke; denervation due to trauma or degenerative, metabolic, or inflammatory neuropathy; adult motor neuron disease; autoimmune motor neuropathy with multifocal conductor block; and infantile or juvenile spinal muscular atrophy.

Increased muscle mass induced by ACVR2A-specific antibodies might also benefit those suffering from muscle wasting diseases. Gonzalez-Cadavid et al. (1998, Proc. Natl. Acad. Sci. USA 95:14938-43) reported that that GDF8 expression correlates inversely with fat-free mass in humans and that increased expression of the GDF8 gene is associated with weight loss in men with AIDS wasting syndrome. By inhibiting the function of GDF8 in AIDS patients, at least certain symptoms of AIDS may be alleviated, if not completely eliminated, thus significantly improving quality of life in AIDS patients.

The cancer anorexia-cachexia syndrome is among the most debilitating and life-threatening aspects of cancer. Progressive weight loss in cancer anorexia-cachexia syndrome is a common feature of many types of cancer and is responsible not only for a poor quality of life and poor response to chemotherapy, but also a shorter survival time than is found in patients with comparable tumors without weight loss. Associated with anorexia, fat and muscle tissue wasting, psychological distress, and a lower quality of life, cachexia arises from a complex interaction between the cancer and the host. It is one of the most common causes of death among cancer patients and is present in 80% at death. It is a complex example of metabolic chaos effecting protein, carbohydrate, and fat metabolism. Tumors produce both direct and indirect abnormalities, resulting in anorexia and weight loss. Currently, there is no treatment to control or reverse the process. Cancer anorexia-cachexia syndrome affects cytokine production, release of lipid-mobilizing and proteolysis-inducing factors, and alterations in intermediary metabolism. Although anorexia is common, a decreased food intake alone is unable to account for the changes in body composition seen in cancer patients, and increasing nutrient intake is unable to reverse the wasting syndrome. Cachexia is generally suspected in patients with cancer if an involuntary weight loss of greater than five percent of premorbid weight occurs within a six-month period.

Since systemic overexpression of GDF8 in adult mice was found to induce profound muscle and fat loss analogous to that seen in human cachexia syndromes (Zimmers et al., 2002, Science 296:1486-1488), the subject ACVR2A-specific antibodies can be beneficially used to prevent, treat, or alleviate the

symptoms of the cachexia syndrome, where muscle growth is desired. This would include cachexia associated with cancer as well as cachexia associated with rheumatoid arthritis.

Combination therapy

In some embodiments, a subject treatment method involves administering a subject antibody and one or more additional therapeutic agents. Suitable additional therapeutic agents include, but are not limited to, anabolic steroids, deacetylase inhibitors and selective adrenergic receptor modulators (SARMs).

Subjects Suitable for Treatment

A variety of subjects are suitable for treatment with a subject method. Suitable subjects include any individual, e.g., a human, who has an ACVR2A-associated condition, who has been diagnosed with an ACVR2A-associated condition, who is at risk for developing an ACVR2A-associated condition, who has had an ACVR2A-associated condition and is at risk for recurrence of the an ACVR2A-associated condition, or who is recovering from an an ACVR2A-associated condition.

EXAMPLES

The following examples are put forth so as to provide those of ordinary skill in the art with a complete disclosure and description of how to make and use the present invention, and are not intended to limit the scope of what the inventors regard as their invention nor are they intended to represent that the experiments below are all or the only experiments performed. Efforts have been made to ensure accuracy with respect to numbers used (e.g. amounts, temperature, etc.) but some experimental errors and deviations should be accounted for. Unless indicated otherwise, parts are parts by weight, molecular weight is weight average molecular weight, temperature is in degrees Celsius, and pressure is at or near atmospheric. Standard abbreviations may be used, e.g., bp, base pair(s); kb, kilobase(s); pl, picoliter(s); s or sec, second(s); min, minute(s); h or hr, hour(s); aa, amino acid(s); kb, kilobase(s); bp, base pair(s); nt, nucleotide(s); i.m., intramuscular(ly); i.p., intraperitoneal(ly); s.c., subcutaneous(ly); and the like.

EXAMPLE 1

PHAGE DISPLAY SCREENING

Phagemid expression of diversified monovalent Fab libraries was accomplished by standard methods. TG-1 cells transformed with expression plasmids were grown to mid log (O.D. 600 .about.0.3) in 2-YT media supplemented with 100 mcg/ml ampicillin and 2% glucose repression and then infected with m13K07 helper phage and grown overnight in 2-YT media supplemented with 100 mcg ampicillin,

70 mcg/ml kanamycin, and 200 micromolar IPTG. Phage containing supernatants were precipitated using polyethylene glycol and PBS resuspended phage were used to pan on immobilized ACVR2.

Panning of the libraries was performed by using recombinant soluble extracellular domains of ACVR2 (Peprotech or R&D Systems) immobilized on the wells of a microtiter dish or biotinylated ACVR2 immobilized on streptavidin derivatized magnetic beads (Dynal - Life Technologies).

To identify phage clones that encoded ACVR2 -binding monovalent Fabs, a portion of the eluted phage were used to infect E. coli HB2151 allowing expression of periplasmic phage-encoded monovalent Fabs. Individual clones were picked into deep-well plates and grown overnight in 2YT containing ampicillin and 0.2 mM IPTG. Bacteria were lysed in BPERII and the lysates were applied to ACVR2 coated plates. Following washing, binding of antibodies was detected using an HRP-conjugated anti-human kappa and lambda light chain antibody (Bethyl). Daughter plates were also inoculated and grown in 2YT-Amp-glucose for Sanger-based sequencing to determine the antibody heavy and light chain sequences.

EXAMPLE 2

INITIAL ELISA ASSAYS

The binding of ACVR2A-specific monoclonal antibodies to human ACVR2A, mouse ACVR2A, biotinylated goat anti-human kappa light chain (positive control) and human Fc (negative control) were determined by ELISA.

The results of this assay are shown in Table 4 below. The values shown are optical densities. The data in this table shows that the antibodies listed I specifically bind to ACVR2A. The sequences of the heavy and light chains of the antibodies listed in Table 4 are shown above in Figs.2A-2F.

Table 4:

Ab	Human ACVR2A	Mouse ACVR2A	Goat anti-Human Kappa	Human Fc
365_B04	1.993	2.179	3.121	0.271
365_B10	2.819	2.782	3.212	0.322
365_C03	2.257	2.648	3.499	0.332
365_C06	1.785	2.229	3.447	0.318
365_D04	2.269	2.389	3.517	0.316
365_E04	2.342	2.401	3.54	0.46
365_F11	2.01	2.141	3.502	0.302
365_G07	2.424	2.596	3.467	0.331
365_H08	2.674	2.607	3.589	0.488
366_A02	2.448	2.687	3.583	0.336

366_A04	1.823	1.988	3.397	0.319
366_D01	2.361	2.46	3.484	0.374
366_D03	2.233	2.375	3.475	0.318
366_F10	2.048	2.211	3.518	0.28
366_G06	2.676	2.818	3.407	0.341
367_B09	2.422	2.429	3.365	0.476
367_B11	2.34	2.463	3.598	0.37
367_C09	2.413	2.771	3.445	0.263
367_D11	2.395	2.54	3.39	0.304
367_F06	2.008	2.045	3.345	0.265
367_H01	2.817	2.695	3.654	0.388
368_A02	2.573	2.741	3.691	0.376
368_A06	2.249	2.515	3.282	0.483
368_A12	3.009	2.781	3.693	0.425
368_B03	2.045	2.045	3.377	0.297
368_B08	1.979	2.182	3.208	0.314
368_B10	2.349	2.417	3.024	0.412
368_B11	2.14	2.35	3.607	0.286
368_C09	2.478	2.611	3.461	0.341
368_D09	2.194	2.11	3.461	0.212
368_F02	2.184	2.272	3.653	0.317
368_F10	2.254	2.602	3.522	0.328
369_B03	3.321	3.314	3.521	0.62
369_G10	3.37	3.295	3.491	0.423
369_H03	2.829	3.085	3.469	0.498
370_B01	3.375	3.473	3.752	0.47
370_D06	2.257	2.658	3.483	0.334
370_G04	1.825	2.125	3.513	0.423
370_H08	2.937	3.24	3.647	0.538
371_A04	1.008	1.173	3.532	0.315
371_A09	1.855	1.998	3.617	0.302
371_D07	2.661	2.902	3.59	0.299
371_D12	1.89	1.999	3.435	0.337
371_H02	1.881	2.026	3.623	0.388
372_A09	2.433	2.56	3.498	0.31
372_B11	2.309	2.575	3.73	0.438
372_E02	2.841	2.743	3.581	0.431
373_E11	3.301	3.361	3.172	0.243
373_H02	3.245	3.257	3.239	0.287

374_B02	3.421	3.537	3.024	0.179
374_F03	3.532	3.617	3.233	0.185
375_A04	3.72	3.734	3.101	0.177
375_A11	3.729	3.696	3.047	0.176
375_C10	3.459	3.596	3.333	0.294
375_F12	2.951	3.143	3.17	0.175
375_H01	2.787	3.059	3.104	0.216
376_G02	3.694	3.696	3.546	0.285
365_A05	2.34	2.229	3.454	0.331
365_B08	1.137	1.257	3.037	0.229
365_B12	2.334	2.289	3.427	0.307
365_D03	2.351	2.484	3.526	0.346
365_D08	2.264	2.355	3.614	0.35
365_E06	1.988	2.063	3.295	0.301
365_F10	2.752	2.789	3.655	0.386
365_G06	2.198	2.021	3.343	0.32
365_G08	2.527	2.581	3.498	0.346
366_B09	2.304	2.532	3.386	0.283
366_C05	2.007	2.362	3.405	0.269
366_E07	1.677	1.856	3.144	0.262
366_G02	2.163	2.316	3.565	0.357
366_H01	2.794	2.775	3.715	0.384
367_C06	2.119	2.513	3.496	0.29
367_C12	2.065	2.103	3.576	0.31
367_E08	2.042	2.372	3.426	0.299
367_E10	2.765	2.975	3.481	0.271
367_F08	2.079	2.193	3.539	0.299
367_F10	2.215	2.357	3.425	0.253
367_G03	2.591	2.632	3.595	0.341
367_G11	2.559	2.672	3.557	0.305
367_H08	2.266	2.473	3.544	0.312
368_B04	2.266	2.729	3.292	0.304
368_B12	2.514	2.471	3.486	0.567
368_C04	2.485	2.474	3.67	0.302
368_C07	2.577	2.367	3.309	0.282
368_C12	2.488	2.446	3.617	0.346
368_D03	2.394	2.552	3.494	0.374
368_D06	2.027	2.109	3.407	0.265
368_D07	2.2	2.463	3.262	0.309

368_E05	1.868	2.067	3.369	0.266
368_E08	2.267	2.669	3.5	0.255
368_G11	2.105	2.368	3.502	0.306
368_H03	2.44	2.727	3.558	0.343
369_A04	2.761	2.858	3.505	0.353
369_A12	3.175	3.243	3.721	0.461
369_B07	2.631	2.898	3.386	0.319
369_B08	2.751	2.879	3.29	0.309
369_C06	2.755	3.065	3.175	0.414
369_C09	2.883	3.054	3.412	0.32
369_C11	2.799	2.912	3.484	0.378
369_E03	3.147	3.356	3.373	0.63
370_B06	2.876	3.092	3.371	0.441
370_B07	1.914	2.196	3.482	0.336
370_E12	3.388	3.435	3.658	0.656
370_H05	2.939	3.138	3.612	0.364
371_A05	3.047	3.24	3.605	0.369
371_B02	2	2.279	3.59	0.449
371_B11	3.182	3.261	3.594	0.549
371_C02	2.918	2.877	3.656	0.372
371_D05	2.718	3.112	3.438	0.339
371_F07	2.784	2.893	3.342	0.425
371_G07	2.8	2.988	3.413	0.548
372_D07	2.684	2.993	3.704	0.472
373_B01	3.258	3.584	3.114	0.197
373_D11	3.572	3.546	3.202	0.364
373_G06	3.397	3.525	3.231	0.196
374_A10	3.557	3.587	2.999	0.23
374_A12	3.312	3.256	3.063	0.308
374_B01	3.143	3.369	2.918	0.173
374_B07	3.713	3.705	3.295	0.25
374_H02	3.263	3.257	3.183	0.197
375_C03	3.001	3.243	3.162	0.217
375_C05	3.457	3.584	3.316	0.193
375_D02	3.629	3.558	3.202	0.191
375_G08	3.332	3.432	3.267	0.259
375_H04	3.106	3.159	3.148	0.181
376_D08	3.815	3.711	3.471	0.232
376_F09	3.501	3.588	3.353	0.25

376_H12	3.234	3.082	3.487	0.344
365_C05	2.564	2.808	3.527	0.271
365_E10	1.823	2.053	3.337	0.273
365_E12	3.321	3.276	3.522	0.338
365_F02	2.781	3.049	3.396	0.326
365_F03	2.631	2.99	3.574	0.347
365_G03	2.242	2.543	3.543	0.321
365_G04	2.096	2.48	3.295	0.295
365_G05	2.442	2.539	3.352	0.319
365_G09	2.617	2.933	3.671	0.288
365_H07	2.514	2.745	3.431	0.33
366_A06	1.97	2.254	3.24	0.334
366_A08	1.653	1.734	3.23	0.243
366_B05	2.385	2.461	2.955	0.24
366_B07	1.796	1.915	3.222	0.215
366_E01	2.693	2.717	3.66	0.397
366_E08	1.973	2.002	3.349	0.272
366_F02	2.149	2.108	3.597	0.371
366_G12	2.713	2.828	3.586	0.372
366_H04	2.69	2.829	3.524	0.359
367_A03	2.576	2.451	3.438	0.347
367_A06	2.339	2.566	3.358	0.378
367_A08	2.057	2.091	3.337	0.252
367_A10	1.892	2.163	3.392	0.315
367_A12	2.439	2.416	3.647	0.39
367_B01	2.839	2.907	3.674	0.408
367_B04	2.664	3.099	3.342	0.265
367_B12	3.015	3.028	3.745	0.414
367_C07	2.468	2.516	3.414	0.387
367_C10	2.529	2.61	3.386	0.233
367_D03	2.594	2.451	3.455	0.29
367_D06	2.045	2.353	3.25	0.283
367_D08	2.183	2.373	3.501	0.237
367_D12	2.435	2.689	3.569	0.309
367_E05	2.353	2.639	3.466	0.333
367_F01	2.425	2.757	3.724	0.33
367_G01	1.8	1.944	3.578	0.356
367_G04	2.978	3.042	3.356	0.287
367_H02	1.077	1.199	3.616	0.378

367_H03	2.041	2.2	3.341	0.377
368_A03	2.834	2.833	3.411	0.348
368_A04	2.349	2.352	3.565	0.283
368_B09	2.543	2.808	3.434	0.258
368_C02	1.377	1.488	3.513	0.321
368_C08	2.259	2.432	3.383	0.289
368_E12	1.286	1.554	3.652	0.347
368_F09	2.389	2.449	3.578	0.242
368_H02	2.406	2.544	3.578	0.348
368_H05	1.954	2.197	3.342	0.277
369_A07	3.548	3.564	3.421	0.288
369_B05	2.777	3.057	3.44	0.314
369_C05	2.545	2.718	3.022	0.32
369_D03	3.277	3.554	3.606	0.391
369_D07	3.069	2.914	3.259	0.363
369_D09	3.303	3.051	3.446	0.287
369_E06	3.134	3.109	3.515	0.306
369_F08	0.503	0.589	3.099	0.302
369_G08	3.297	3.492	3.582	0.312
370_A02	2.901	2.907	3.624	0.425
370_B03	3.714	3.567	3.607	0.3
370_B11	2.076	2.449	3.685	0.326
370_B12	2.925	3.077	3.563	0.478
370_D01	3.137	3.17	3.664	0.382
370_D05	2.976	3.125	3.49	0.333
370_F03	1.136	1.25	3.301	0.373
370_H02	3.301	3.39	3.667	0.386
370_H07	3	3.245	3.511	0.403
371_A10	2.812	2.779	3.477	0.338
371_B03	1.634	1.935	3.482	0.367
371_B04	2.465	3.129	2.269	0.295
371_B09	0.825	0.827	2.702	0.292
371_B12	2.555	2.4	3.483	0.378
371_C01	2.001	2.273	3.594	0.402
371_C04	2.049	2.246	3.453	0.314
371_C05	1.24	1.355	3.079	0.269
371_C12	3.099	3.196	3.683	0.544
371_D02	2.939	2.991	3.578	0.385
371_D04	1.023	1.295	3.3	0.276

371_E06	3.003	3.029	3.443	0.33
371_E07	3.091	3.348	3.437	0.337
371_E10	3.062	3.052	3.486	0.341
371_F10	2.339	2.31	3.529	0.299
371_F11	3.039	3.253	3.676	0.331
371_G02	3.118	3.06	3.673	0.514
371_G04	3.625	3.577	3.544	0.325
371_G09	2.745	3.066	3.577	0.315
371_G11	2.84	2.752	3.666	0.399
371_H04	3.258	3.507	3.576	0.35
371_H05	1.202	1.245	3.271	0.321
371_H06	3.027	3.111	3.698	0.346
371_H08	1.662	2.039	3.472	0.309
371_H10	2.189	2.553	3.548	0.358
372_B02	3.172	3.509	3.665	0.371
372_C06	3.206	3.536	3.491	0.489
372_D03	3.042	3.289	3.603	0.319
372_E01	3.341	3.34	3.598	0.409
372_G12	2.409	2.725	3.495	0.439
373_A01	3.177	3.477	2.952	0.177
373_A03	3.647	3.634	3.079	0.189
373_A05	3.45	3.423	3.033	0.172
373_A09	3.66	3.615	3.107	0.248
373_A11	3.763	3.679	3.086	0.184
373_A12	3.59	3.315	3.093	0.179
373_B05	3.586	3.526	3.233	0.184
373_B07	3.661	3.61	3.304	0.208
373_C03	3.69	3.654	3.304	0.171
373_C07	3.569	3.578	3.298	0.206
373_C10	3.653	3.645	3.235	0.318
373_D03	3.745	3.694	3.18	0.18
373_D12	3.398	3.207	3.212	0.224
373_E10	3.722	3.636	3.2	0.188
373_F08	3.76	3.701	3.215	0.202
373_F11	3.354	3.46	3.319	0.204
373_F12	3.245	3.217	3.063	0.158
373_G08	3.651	3.673	3.284	0.172
373_H03	3.268	3.289	3.221	0.172
373_H07	3.253	3.27	3.233	0.199

373_H09	0.93	1.354	3.084	0.166
374_A06	3.775	3.747	2.999	0.173
374_A09	3.583	3.644	2.971	0.231
374_B03	3.687	3.697	3.066	0.166
374_B05	3.681	3.652	3.164	0.168
374_B08	3.6	3.629	3.124	0.188
374_B10	3.711	3.686	3.004	0.17
374_C01	2.685	2.929	3.078	0.167
374_C09	3.431	3.509	3.14	0.154
374_C12	3.667	3.326	3.145	0.308
374_D03	3.3	3.48	3.025	0.216
374_D05	3.434	3.565	3.148	0.171
374_D06	3.776	3.674	3.123	0.172
374_D07	3.71	3.684	3.26	0.176
374_D10	3.562	3.638	3.273	0.329
374_E10	3.736	3.768	3.375	0.165
374_E12	3.613	3.284	3.293	0.177
374_F06	3.723	3.704	3.179	0.201
374_F07	3.467	3.542	3.209	0.176
374_F08	3.671	3.676	3.176	0.211
374_G03	3.791	3.64	3.219	0.193
374_G08	3.706	3.704	3.211	0.206
374_G09	3.656	3.598	3.258	0.223
374_G10	3.681	3.737	3.233	0.173
374_G11	3.651	3.597	3.245	0.179
374_H01	3.084	3.261	3.068	0.251
374_H11	3.275	3.285	3.15	0.169
375_A01	3.281	3.676	2.908	0.196
375_A07	3.575	3.644	3.11	0.188
375_A08	3.676	3.687	3.14	0.205
375_A12	3.657	3.347	3.137	0.174
375_B12	3.654	3.338	3.28	0.223
375_C04	3.677	3.675	3.207	0.221
375_D01	3.298	3.608	3.1	0.182
375_D10	3.258	3.454	3.207	0.228
375_E02	3.582	3.691	3.199	0.496
375_E03	3.568	3.638	3.184	0.181
375_E05	3.669	3.709	3.283	0.296
375_E06	3.846	3.672	3.328	0.188

375_E10	3.689	3.792	3.293	0.187
375_F02	3.605	3.646	3.203	0.205
375_F07	3.675	3.707	3.216	0.172
375_F08	3.502	3.581	3.315	0.201
375_G04	2.909	3.294	3.193	0.161
375_G05	3.712	3.745	3.264	0.21
375_H05	3.355	3.331	3.171	0.167
375_H07	3.304	3.293	3.273	0.346
376_A03	3.613	3.65	3.231	0.328
376_B03	3.678	3.668	3.519	0.253
376_B10	3.595	3.665	3.457	0.232
376_C04	3.63	3.654	3.397	0.219
376_C08	3.612	3.627	3.462	0.246
376_D07	3.381	3.444	3.436	0.318
376_E02	3.298	3.376	3.408	0.222
376_E11	3.682	3.646	3.471	0.268
376_F01	2.769	3.015	3.177	0.199
376_F06	3.525	3.649	3.469	0.284
376_G05	3.745	3.773	3.489	0.252
376_G06	3.424	3.58	3.489	0.267
376_G10	3.545	3.524	3.542	0.321
376_H01	3.113	3.308	3.277	0.607
376_H04	3.309	3.338	3.513	0.34
376_A11	3.293	3.309	3.433	0.325
365_A08	1.584	1.593	3.2	0.256
365_A09	2.449	2.479	3.302	0.339
365_C02	2.155	2.332	3.447	0.362
365_C04	2.262	2.673	3.551	0.305
365_D02	2.539	2.699	3.518	0.486
365_D07	1.831	2.058	3.382	0.302
365_D10	2.393	2.236	3.272	0.641
365_E11	1.741	1.736	3.568	0.301
365_F05	2.141	2.232	3.416	0.376
365_H05	2.102	2.195	3.46	0.361
366_D08	2.166	2.463	3.65	0.312
366_F08	1.862	2.004	3.468	0.316
366_G09	1.855	2.041	3.435	0.291
367_A02	2.231	2.416	3.581	0.305
367_B06	1.817	1.889	3.019	0.378

367_C08	1.119	1.218	3.054	0.278
367_D05	1.26	1.373	3.341	0.265
367_D09	2.147	2.045	3.372	0.381
367_E07	1.935	2.055	3.215	0.221
367_E12	2.695	2.913	3.706	0.453
367_F09	1.795	1.818	3.455	0.289
367_H05	2.439	2.698	3.59	0.51
367_H10	2.577	2.353	3.55	0.326
368_B02	2.075	2.24	3.606	0.337
368_C11	2.027	2.209	3.558	0.275
368_D02	1.925	2.26	3.522	0.321
368_D12	2.254	2.283	3.568	0.329
368_F06	1.599	1.68	3.315	0.249
368_G03	2.726	2.746	3.392	0.312
368_G10	2.064	2.283	3.454	0.356
368_H06	2.351	2.654	3.612	0.311
368_H11	1.954	2.129	3.511	0.355
369_A11	2.643	2.774	3.286	0.366
369_C12	3.43	3.447	3.742	0.418
369_D08	2.942	3.127	3.063	0.241
369_E05	1.405	1.642	1.904	0.282
369_E08	1.028	1.227	1.116	0.272
369_F05	0.796	0.931	3.46	0.331
369_F09	3.227	3.381	3.601	0.5
369_G05	3.036	3.278	3.309	0.384
369_H02	3.088	3.29	3.572	0.408
369_H08	3.159	3.231	3.556	0.389
369_H12	3.463	3.42	3.652	0.414
370_B08	3.131	3.247	3.353	0.302
370_C06	3.141	3.414	3.55	0.303
370_C07	3.351	3.369	3.299	0.316
370_C10	1.3	1.383	3.352	0.332
370_D03	3.135	3.249	3.582	0.57
370_D09	2.924	2.531	3.484	0.287
370_E04	2.572	2.721	3.398	0.292
370_E05	2.585	2.768	3.519	0.427
370_F01	3.004	3.136	3.669	0.407
370_F02	2.682	2.891	3.627	0.376
370_F12	3.551	3.572	3.644	0.457

370_G08	3.212	3.326	3.564	0.364
370_H04	3.484	3.558	3.615	0.596
370_H06	3.22	3.394	3.514	0.358
371_B01	3.26	3.271	3.584	0.464
371_C06	2.486	3.012	3.435	0.308
371_C07	1.391	1.446	3.359	0.287
371_E05	2.989	3.178	3.446	0.59
371_E08	2.114	2.267	2.64	0.251
371_E09	2.078	2.283	3.155	0.306
371_E12	3.09	2.993	3.622	0.398
371_F03	1.19	1.302	1.819	0.252
371_F09	3.369	3.57	3.597	0.602
371_G01	2.014	2.242	1.786	0.375
371_H11	2.89	3.121	3.597	0.363
372_B09	3.108	3.011	3.502	0.308
372_E08	2.559	2.816	3.507	0.369
372_F02	3.006	3.094	3.695	0.411
372_H11	2.616	2.86	3.645	0.392
373_A06	3.636	3.624	3.073	0.193
373_B09	3.6	3.621	3.242	0.172
373_D06	3.633	3.574	3.208	0.192
373_F07	3.613	3.62	3.129	0.172
373_G02	3.59	3.559	3.223	0.226
374_A04	3.654	3.682	2.99	0.275
374_A05	3.604	3.6	2.923	0.159
374_C10	3.567	3.671	3.08	0.174
374_D04	3.629	3.649	3.053	0.179
374_D09	3.609	3.646	3.096	0.171
374_G05	3.658	3.667	3.003	0.158
374_H05	3.315	3.297	3.042	0.257
375_A03	3.615	3.619	3.087	0.203
375_B03	3.678	3.7	3.241	0.209
375_C01	2.962	3.27	3.136	0.191
375_C11	3.589	3.613	3.263	0.199
375_F10	3.691	3.767	3.295	0.21
375_H08	3.308	3.28	3.324	0.204
376_A02	3.716	3.634	3.194	0.22
376_A05	3.648	3.644	3.184	0.256
376_A07	3.7	3.722	3.193	0.221

365_A03	3.4	3.243	3.443	0.342
365_A11	2.039	1.937	3.267	0.299
365_A12	2.674	2.871	3.668	0.422
365_B01	2.386	2.646	3.491	0.445
365_B06	2.246	2.418	3.277	0.281
365_B07	2.112	2.213	3.229	0.269
365_B11	2.844	2.755	3.581	0.305
365_C01	2.869	3.025	3.626	0.376
365_C10	2.451	2.441	3.413	0.397
365_C11	2.656	2.781	3.668	0.296
365_C12	1.924	2.04	3.576	0.332
365_D09	1.523	1.35	3.375	0.302
365_D11	2.342	2.224	3.382	0.299
365_D12	2.567	2.613	3.53	0.34
365_E01	2.906	2.837	3.542	0.363
365_E05	2.181	2.437	3.36	0.379
365_E07	2.383	2.701	3.513	0.302
365_E09	1.906	2.16	3.474	0.322
365_F01	2.51	2.471	3.509	0.341
365_F06	1.953	2.082	3.397	0.329
365_F12	2.913	2.828	3.633	0.411
365_G01	2.483	2.647	3.447	0.39
365_G11	1.745	1.785	3.473	0.278
365_H02	2.732	2.908	3.58	0.407
365_H03	2.322	2.654	3.269	0.366
365_H06	2.244	2.459	3.437	0.367
365_H10	2.677	2.823	3.513	0.349
365_H11	3.239	3.353	3.614	0.375
365_H12	2.968	2.908	3.778	0.451
366_A07	2.417	2.679	3.365	0.309
366_B08	2.148	2.376	3.054	0.403
366_B10	2.328	2.444	3.059	0.424
366_B12	3.244	2.989	3.444	0.311
366_D04	2.079	2.125	3.463	0.338
366_E10	2.354	2.389	3.454	0.271
366_F04	1.726	1.912	3.366	0.281
366_F05	2.191	2.668	3.245	0.279
366_F07	2.386	2.534	3.473	0.353
366_G04	1.851	2.176	3.286	0.31

366_G05	2.212	2.496	3.262	0.28
366_H06	2.289	2.591	3.386	0.285
366_H07	2.526	2.673	3.605	0.285
366_H08	2.593	2.77	3.551	0.417
366_H09	2.095	2.437	3.423	0.328
367_A04	2.142	2.202	3.303	0.267
367_A05	2.218	2.384	3.381	0.269
367_B02	2.288	2.422	3.533	0.302
367_B03	2.479	2.659	3.445	0.318
367_B07	1.419	1.488	3.337	0.236
367_B08	2.128	2.245	3.033	0.37
367_C01	2.617	2.987	3.71	0.348
367_C05	2.215	2.856	3.424	0.255
367_C11	2.329	2.545	3.449	0.45
367_D10	2.699	2.667	3.38	0.251
367_E01	2.546	2.523	3.607	0.351
367_E04	2.406	2.573	3.501	0.284
367_E06	2.022	2.313	3.477	0.271
367_E09	1.664	1.81	3.329	0.249
367_E11	2.395	2.909	3.607	0.244
367_F03	2.1	2.392	3.446	0.301
367_F07	2.126	2.246	3.261	0.242
367_F11	1.714	1.873	3.477	0.267
367_G05	2.41	2.711	3.371	0.283
367_G06	2.641	2.81	3.348	0.28
367_G10	2.115	2.316	3.448	0.286
367_H06	2.695	3.083	3.651	0.313
367_H11	2.371	2.693	3.609	0.323
368_A01	2.994	2.9	3.683	0.396
368_A05	2.708	2.696	3.459	0.285
368_A07	2.11	2.312	3.65	0.261
368_A09	2.51	2.628	3.549	0.277
368_B01	2.607	2.588	3.705	0.365
368_B06	2.059	2.341	3.157	0.393
368_B07	1.909	2.065	3.135	0.344
368_C05	1.818	2.018	3.359	0.246
368_D01	2.751	2.971	3.647	0.319
368_D04	2.461	2.699	3.666	0.338
368_D05	2.857	2.868	3.385	0.282

368_D11	2.796	2.96	3.487	0.297
368_E01	2.566	2.849	3.736	0.392
368_E02	2.5	2.788	3.679	0.424
368_E04	3.08	3.232	3.476	0.32
368_E06	2.328	2.339	3.505	0.325
368_E07	1.067	1.169	3.453	0.251
368_F03	2.352	2.601	3.604	0.323
368_F11	2.578	2.726	3.526	0.338
368_G01	2.646	2.824	3.622	0.431
368_G12	2.457	2.535	3.518	0.341
368_H04	1.063	1.362	3.513	0.319
369_A02	3.147	3.457	3.493	0.383
369_A03	0.451	0.561	3.169	0.347
369_B01	3.358	3.457	3.588	0.487
369_C02	3.6	3.517	3.543	0.369
369_C03	3.371	3.649	3.516	0.323
369_C04	1.639	1.649	2.459	0.248
369_D01	3.127	3.317	3.63	0.595
369_D02	3.287	3.436	3.527	0.407
369_D04	3.054	2.968	3.589	0.435
369_D12	3.041	3.105	3.533	0.425
369_E02	2.144	2.341	3.429	0.365
369_E11	2.889	3.202	3.694	0.343
369_E12	2.464	2.692	3.667	0.452
369_F01	3.278	3.418	3.469	0.554
369_F02	3.071	3.35	3.556	0.478
369_F03	2.575	2.749	3.438	0.389
369_F06	3.109	3.066	3.51	0.353
369_F10	3.048	3.225	3.667	0.361
369_F11	3.196	3.373	3.657	0.37
369_G01	3.567	3.666	3.439	0.403
369_G04	2.365	2.685	3.316	0.385
369_G06	2.98	2.914	3.378	0.474
369_G11	3.028	3.06	2.594	0.331
369_G12	1.768	1.882	2.652	0.353
369_H05	3.249	3.342	3.54	0.457
369_H06	3.235	3.555	3.5	0.347
369_H09	2.364	2.643	3.507	0.365
370_A01	2.859	2.955	3.622	0.637

370_A03	3.544	3.633	3.564	0.424
370_A04	2.566	2.736	3.476	0.377
370_A12	3.062	3.188	3.719	0.674
370_C01	3.285	3.38	3.615	0.403
370_C03	3.592	3.773	3.571	0.35
370_C05	3.208	3.546	3.557	0.346
370_C08	2.73	2.967	3.111	0.381
370_C09	1.974	2.248	3.483	0.292
370_D04	3.59	3.737	3.6	0.371
370_D11	2.721	2.794	3.381	0.34
370_E03	3.636	3.738	3.57	0.361
370_E06	2.903	3.025	3.608	0.375
370_E09	3.45	3.555	3.597	0.338
370_F05	2.758	2.913	3.536	0.406
370_F07	3.451	3.534	3.515	0.384
370_F10	3.145	3.216	3.636	0.441
370_G02	2.982	3.22	3.625	0.388
370_G03	3.103	3.435	3.579	0.421
370_G06	2.191	2.334	3.408	0.356
370_G09	3.006	3.136	3.641	0.393
370_G10	2.985	2.744	3.49	0.315
370_G11	2.975	3.07	3.72	0.529
370_H01	3.31	3.179	3.651	0.436
370_H09	2.948	3.277	3.542	0.348
371_A03	2.843	2.622	3.563	0.354
371_A06	2.65	2.786	3.51	0.337
371_A07	2.875	3.059	3.651	0.336
371_A08	1.061	1.161	2.442	0.304
371_A12	3.168	3.299	3.631	0.483
371_B06	2.692	2.712	3.296	0.356
371_B07	2.779	3.045	3.329	0.308
371_C03	3.013	3.241	3.598	0.311
371_D06	1.477	1.555	3.322	0.295
371_D09	2.889	2.936	2.168	0.268
371_F01	2.41	2.618	3.678	0.41
371_F04	2.946	3.102	3.66	0.345
371_F06	2.414	2.795	3.456	0.289
371_F08	2.196	2.546	3.427	0.301
371_G05	1.249	1.329	3.082	0.313

371_G10	1.646	1.922	3.406	0.439
371_H09	2.962	3.225	3.656	0.32
372_A04	3.204	3.404	3.643	0.339
372_B04	2.611	3.122	3.59	0.333
372_C07	2.409	2.638	3.462	0.279
372_D02	2.657	2.907	3.579	0.433
372_F03	3.192	3.308	3.595	0.438
372_F06	2.259	2.539	3.483	0.38
372_F08	3.382	3.217	3.445	0.335
372_F09	3.166	3.043	3.474	0.268
373_A02	2.803	2.974	2.955	0.159
373_A08	3.301	3.309	3.112	0.195
373_A10	3.544	3.55	3.096	0.175
373_B04	3.605	3.617	3.255	0.176
373_B06	3.441	3.43	3.236	0.221
373_B10	3.655	3.597	3.15	0.174
373_B12	3.122	3.075	3.27	0.172
373_C02	3.452	3.466	3.146	0.17
373_C04	3.356	3.502	3.196	0.157
373_C06	3.545	3.531	3.163	0.163
373_C08	3.048	3.193	3.189	0.16
373_C11	3.49	3.468	3.168	0.171
373_D01	3.235	3.574	3.041	0.174
373_D04	3.678	3.646	3.154	0.168
373_D05	3.683	3.734	3.253	0.179
373_D08	3.656	3.665	3.241	0.182
373_D10	3.61	3.61	3.114	0.189
373_E01	2.347	2.56	2.986	0.16
373_E05	3.545	3.592	3.24	0.176
373_E07	3.483	3.536	3.231	0.294
373_E12	3.627	3.333	3.116	0.17
373_G10	3.538	3.563	3.261	0.2
373_G12	3.472	3.288	3.259	0.174
373_H01	3.104	3.28	3.123	0.198
373_H05	3.286	3.295	3.216	0.201
374_A07	3.624	3.712	3.072	0.206
374_B04	3.67	3.641	3.3	0.222
374_B06	3.482	3.595	3.084	0.157
374_B12	3.489	3.326	3.054	0.257

374_C03	3.583	3.612	3.056	0.208
374_C06	3.715	3.712	3.236	0.18
374_D01	3.244	3.578	2.935	0.198
374_D08	3.503	3.591	3.017	0.201
374_E01	3.238	3.556	3.037	0.235
374_E02	3.235	3.329	3.176	0.527
374_E05	3.561	3.568	3.176	0.244
374_E07	3.632	3.581	3.203	0.3
374_E08	3.496	3.524	3.263	0.251
374_E11	3.607	3.586	3.343	0.186
374_F01	3.291	3.597	3.026	0.165
374_F02	3.565	3.586	3.157	0.169
374_F04	3.576	3.645	3.228	0.163
374_F10	3.211	3.453	3.283	0.524
374_F11	3.657	3.608	3.151	0.191
374_G04	2.096	2.317	3.025	0.161
374_G06	3.256	3.421	3.289	0.25
374_G07	3.631	3.723	3.257	0.214
374_H03	3.265	3.268	3.065	0.162
374_H04	3.277	3.31	3.189	0.167
374_H06	3.297	3.264	3.081	0.166
374_H07	3.241	3.251	2.973	0.163
374_H09	3.249	3.264	3.039	0.158
375_A05	3.721	3.685	3.12	0.202
375_C06	2.646	3.212	3.289	0.2
375_D04	3.691	3.699	3.166	0.182
375_D05	3.465	3.609	3.215	0.202
375_D07	3.563	3.633	3.253	0.176
375_D08	3.287	3.403	3.302	0.234
375_D12	3.24	3.156	3.23	0.193
375_E01	3.159	3.627	3.111	0.164
375_E07	3.683	3.81	3.06	0.158
375_H12	3.256	3.104	3.263	0.188
376_A04	3.587	3.578	3.123	0.245
376_A10	3.676	3.642	3.174	0.279
376_A12	3.696	3.341	3.217	0.22
376_B04	3.409	3.479	3.577	0.293
376_B05	3.646	3.778	3.519	0.242
376_B09	3.777	3.717	3.506	0.227

376_B11	3.69	3.753	3.608	0.261
376_C01	3.264	3.599	3.198	0.324
376_C02	3.445	3.529	3.443	0.222
376_C12	3.698	3.322	3.391	0.438
376_D05	3.599	3.707	3.337	0.215
376_D11	3.698	3.621	3.433	0.267
376_E03	3.788	3.744	3.425	0.234
376_E08	3.64	3.638	3.473	0.332
376_F03	3.289	3.471	3.443	0.261
376_F04	3.066	3.29	3.415	0.222
376_G08	3.695	3.637	3.473	0.22
376_G09	3.678	3.646	3.446	0.23
376_H09	3.318	3.299	3.455	0.281
376_H10	3.28	3.293	3.538	0.318
365_E02	2.446	2.609	3.503	0.357
370_G12	1.337	1.6	3.523	0.418
368_C01	2.607	2.922	3.714	0.41
376_C06	3.487	3.563	3.43	0.29
368_D10	2.245	2.449	3.258	0.245
365_G12	2.742	2.748	3.548	0.556
367_C03	2.301	2.808	3.513	0.275
367_H07	2.719	2.684	3.463	0.297
371_D03	1.54	1.826	3.57	0.333
369_C10	2.48	2.456	3.373	0.32
367_F05	2.269	2.485	3.44	0.386
365_C07	1.943	1.917	3.171	0.311
374_C08	3.295	3.417	3.178	0.178
376_A06	3.694	3.742	3.162	0.262
376_B07	3.732	3.714	3.526	0.234
365_F07	3.122	3.184	3.393	0.331
369_E10	3.36	3.534	3.594	0.412
373_E03	3.465	3.465	3.247	0.194
366_B04	2.805	3.046	3.397	0.331
376_F12	3.131	3.247	3.441	0.323
369_F07	3.431	3.43	3.47	0.335
368_C06	0.738	1.034	3.524	0.255
376_E12	3.61	3.316	3.416	0.306
371_H01	3.027	2.995	3.693	0.471
367_E02	1.871	2.026	3.438	0.37

365_F04	2.26	2.509	3.471	0.403
370_A09	3.461	3.269	3.576	0.361
365_B03	2.645	2.53	3.377	0.444
369_A05	3.285	3.25	3.48	0.588
373_H10	3.243	3.251	3.189	0.2
367_A09	2.178	2.41	3.454	0.259
370_F08	2.339	2.994	3.587	0.495
376_B01	3.278	3.67	3.242	0.308
365_D05	2.578	2.72	3.514	0.357
373_E04	3.556	3.546	3.301	0.251
368_G05	2.175	2.421	3.354	0.245
365_A01	2.765	2.9	3.508	0.528
373_H06	3.004	3.151	3.3	0.2
369_G07	3.322	3.369	2.976	0.32
373_G05	3.612	3.615	3.224	0.273
372_F07	3.248	3.241	3.401	0.296
370_H03	3.426	3.565	3.558	0.381
366_A03	1.152	1.119	3.314	0.303
365_A07	2.244	2.255	3.407	0.284
376_B06	3.697	3.773	3.457	0.222
374_C11	3.641	3.593	3.215	0.471
375_A06	3.653	3.707	3.114	0.298
365_B09	3.264	3.319	3.282	0.272
373_E06	3.706	3.639	3.221	0.187
374_C05	3.698	3.693	3.176	0.175
376_C11	3.704	3.626	3.46	0.23
373_C09	3.64	3.597	3.22	0.17
368_H01	3.027	3.142	3.693	0.374
373_B03	3.638	3.621	3.161	0.18
374_C04	3.741	3.741	3.166	0.201
371_F05	2.89	3.149	3.33	0.297
369_A10	3.375	3.139	3.414	0.348
366_A05	2.624	2.596	3.477	0.284
375_G07	3.633	3.672	3.197	0.178
374_D02	3.06	3.2	2.994	0.204
365_A10	2.185	2.492	3.451	0.293
375_A02	2.977	3.178	3.066	0.186
371_G03	3.121	3.267	3.593	0.359
370_E07	3.442	3.496	3.453	0.379

375_B04	3.693	3.73	3.259	0.19
367_G07	3.019	3.197	3.287	0.295
366_C02	3.033	3.04	3.43	0.341
375_C12	3.662	3.328	3.266	0.197
365_F08	2.246	2.611	3.626	0.437
368_G09	2.438	2.815	3.62	0.281
368_E11	2.573	2.923	3.73	0.341
367_F02	2.375	2.268	3.522	0.315
373_B08	3.698	3.663	3.218	0.17
374_A11	3.645	3.722	2.806	0.15
373_B11	3.719	3.652	3.217	0.178
373_F03	3.652	3.603	3.213	0.179
372_D04	3.401	3.408	3.384	0.419
366_C01	2.307	2.406	3.601	0.382
367_A01	3.182	3.284	3.51	0.391
366_H05	2.445	2.737	3.47	0.418
369_B09	1.624	1.577	2.216	0.253
366_D07	2.413	2.623	3.383	0.418
369_D11	2.988	2.99	3.454	0.35
370_B05	2.839	3.111	3.492	0.593
366_D02	2.274	2.549	3.567	0.349
368_H12	2.636	2.693	3.572	0.381
368_F12	1.689	1.702	3.515	0.349
370_A06	2.594	2.769	3.471	0.331
369_F12	2.732	2.819	3.596	0.434
366_A09	1.787	1.926	3.277	0.266
368_H07	2.707	2.864	3.553	0.421
370_C04	2.319	2.632	3.6	0.334
373_E02	3.612	3.643	2.921	0.158
374_E09	3.671	3.578	3.157	0.162
371_C09	3.369	3.289	3.393	0.308
369_B12	2.666	2.759	3.562	0.4
369_B02	3.4	3.546	3.522	0.456
365_C09	2.052	2.178	3.272	0.266
374_B09	3.621	3.652	3.194	0.172
374_D12	3.55	3.28	3.087	0.235
374_C02	3.676	3.64	3.059	0.167
374_H08	3.307	3.271	3.089	0.199
369_D06	3.438	3.346	3.11	0.324

366_B06	2.474	2.453	3.104	0.415
367_A11	2.344	2.521	3.611	0.3
369_F04	1.949	2.171	3.459	0.369
369_A01	3.6	3.66	3.546	0.456
373_H12	3.061	2.985	3.004	0.162
376_C07	3.697	3.714	3.419	0.265
366_E02	2.257	2.581	3.456	0.37
376_G01	3.341	3.663	3.18	0.227
373_F02	3.623	3.6	3.149	0.175
376_E09	3.741	3.76	3.483	0.246
365_H04	2.471	2.588	3.495	0.371
369_E04	2.883	3.304	3.516	0.387
374_B11	3.692	3.657	3.175	0.17
376_G11	3.646	3.604	3.538	0.285
374_E04	3.74	3.716	3.187	0.169
373_E08	2.966	3.235	3.199	0.165
375_B10	3.651	3.74	3.138	0.17
365_E08	2.591	2.585	3.331	0.298
374_G02	3.515	3.538	3.174	0.175
373_D09	3.463	3.505	3.043	0.16
365_A04	1.487	1.405	3.28	0.25
371_B05	1.051	1.243	1.653	0.246
376_H08	3.305	3.279	3.527	0.274
367_G08	2.686	2.779	3.319	0.33
372_H03	2.322	2.697	3.642	0.437
366_E03	2.551	2.724	3.536	0.384
371_F12	2.474	2.304	3.616	0.413
366_C03	2.414	2.736	3.549	0.274
376_A01	3.243	3.661	2.985	0.239
365_E03	2.559	2.692	3.332	0.314
371_B10	3.313	3.36	3.441	0.387
369_G09	3.36	3.269	3.605	0.395
369_A06	2.891	3.012	3.32	0.394
369_C08	2.32	2.325	2.797	0.241
373_A07	3.525	3.594	3.114	0.177
367_D02	2.464	2.464	3.462	0.321
374_C07	3.651	3.698	3.22	0.225
374_A03	3.58	3.71	3.05	0.178
365_A02	3.028	2.962	3.492	0.374

365_D06	2.953	3.075	3.421	0.319
366_C07	3.016	3.06	3.368	0.301
367_F12	2.38	2.285	3.599	0.355
369_E09	3.627	3.767	3.483	0.278
365_G02	1.984	2.155	3.447	0.325
373_D02	3.729	3.645	3.187	0.18
374_E03	3.716	3.789	3.127	0.176
374_D11	3.639	3.579	2.905	0.162
370_D07	2.806	3.141	3.384	0.309
374_A08	3.589	3.673	2.944	0.16
374_G01	3.344	3.595	2.922	0.161
374_G12	3.195	3.215	3.149	0.214
375_G10	3.481	3.639	3.302	0.175
369_H11	1.445	1.639	2.21	0.382
375_G12	3.356	3.29	3.304	0.199
366_F06	1.874	2.155	3.445	0.394
368_G07	1.788	2.048	3.164	0.29
367_H04	1.623	1.849	3.395	0.289
374_E06	3.844	3.755	3.245	0.191
370_A10	2.581	2.878	3.467	0.434
368_H10	2.281	2.156	3.359	0.281
368_G08	1.603	1.752	3.291	0.329
365_H09	2.384	2.563	3.53	0.365
370_A08	2.406	2.335	3.522	0.319
368_B05	1.732	1.755	3.257	0.281
375_F01	3.16	3.455	2.956	0.166
374_F09	3.533	3.617	3.142	0.157

EXAMPLE 3

LIGAND COMPETITION ASSAYS

The ability of several of the antibodies identified in Example 2 to block Activin A and GDF8 binding to ACVR2A or ACVR2B was assessed by ELISA. Activin A (R&D systems) and GDF8 (R&D systems) were coated on 384-well Immunolon plates in 1x coating buffer (SurModics) at 0.5 μg/mL. Antibodies were serially diluted in a 10-point curve starting at 1 μM in 3-fold steps. ACVR2A and ACVR2B proteins were purchased from R&D Systems and biotinylated using the EZ-Link NHS-PEG4-biotin kit (Thermo Fisher). The antibodies were pre-incubated with biotinylated human ACVR2A-Fc, mouse ACVR2A-Fc, human ACVR2B-Fc, or mouse ACVR2B-Fc at a concentration of 500 ng/mL in 1%

BSA in PBST for 1 hour. The mixtures of antibodies and biotinylated receptors were added to the Activin A/GDF8-coated plates for 1 hour. The inhibition of ligand-receptor interaction was detected with streptavidin-HRP (Jackson ImmunoResearch) at a concentration of 10 ng/mL and TMB.

The results of this assay are shown in columns A-D of Table 5 below. The values shown are IC50 values. The data in this table shows that the antibodies can specifically block Activin A and GDF8 binding to ACVR2A.

EXAMPLE 4

ALK5/ACVR2B DIMERIZATION ASSAY

The ability of several of the antibodies identified in Example 2 to specifically block GDF8-induced dimerization between ACVR2A and ALK5 in U2OS cells was assessed using the DiscoverX receptor dimerization assay. In these assays, two receptors are tagged with ProLink™ (PK) or Enzyme Acceptor (EA). Upon ligand-induced activation, the receptors dimerize forcing the two β-gal components to complement and create an active enzyme. Active β-gal generates a chemiluminescent signal in the presence of substrate. In these assays, approximately 5000 U2OS cells were transferred into each well in total volume of 20ul, antibody was dispensed into each well in total volume of 5ul, the treated cells were incubated for 3hr at 37oC, 5ul of GDF8 was dispensed into wells in total volume of 5ul (final conc 100ng/ml), the cells were incubated for 16hr at 37oC and 30ul of 1X Flash detection reagent was added to each well. The reactions were incubated for 1hr at room temperature and then read on a plate reader.

The results of this assay are shown in columns E and F of Table 5 below. The values shown are IC50 values. The data in this table shows that the antibodies block GDF8-induced dimerization of ALK5/ACVR2A but not ALK5/ACVR2B.

EXAMPLE 5

QUANTITATIVE ELISA ASSAYS

The binding of several of the antibodies identified in Example 2 to human ACVR2A , mouse ACVR2A, human ACVR2B, and mouse ACVR2B were quantified by ELISA. His-tagged recombinant proteins (Sino Biological, Inc.) were His-tagged Human ACVR2A , Mouse ACVR2A, Human ACVR2B, or Mouse ACVR2B were coated on Immunolon 384-well plates at a concentration of 0.5 μg/mL in 1x coating buffer (SurModics). Antibodies were diluted to 1 μM in PBS buffer containing 1% BSA and diluted 3-fold in a 10-point curve. Detection of the antibody binding to the antigen was performed using biotinylated goat anti-human kappa light chain (Bethyl Laboratories). Detection of the secondary antibody was determined using streptavidin-HRP and TMB reagent. All assays were performed at room temperature. Curve-fitting software was used to determine the EC50 for each antibody (MatLab).

The results of this assay are shown in columns G-L of Table 5 below. The values shown are EC50 values. The data in this table shows that the antibodies specifically bind to ACVR2A, not ACVR2B.

EXAMPLE 6

ACTIVITY ON SKELETAL MUSCLE CELLS

The ability of several of the antibodies identified in Example 2 to alter SMAD3 activity in muscle cells was tested. Primary human myoblasts (Lonza) cultured in Ham's F-10 supplemented with SkGM-2 Single-Quots (Lonza). Myoblasts were differentiated in DMEM/F-12K (50:50) supplemented with 2% horse serum (Corning) and 1% Penicillin/Streptomycin. After 4 days of differentiation, myotubes were pre-treated with antibodies for 1 hour at a starting concentration of 1 μM and diluted serially 3-fold in a 10-point curve. GDF8 (R&D) was added for 1 hour at 100 ng/mL. Cells were lysed in 30 μL of PBS + 0.1% Triton-X + 1x Halt Protease/Phosphastase inhibitors (Thermo Fisher). Phospho-SMAD3 (Ser423/425) activity was assessed in primary human myotubes by AlphaLisa (Perkin-Elmer) according to manufacturer's instructions.

The results of this assay are shown in column M of Table 5 below. The data in this table shows that the antibodies reduce GDF8-induced SMAD3 phosphorylation in muscle cells.

EXAMPLE 7

SMAD REPORTER 293 ASSAY

The ability of several of the antibodies identified in Example 2 to specifically inhibit GDF8-induced SMAD activation in HEK293 was tested cells using a smad2/3 luciferase reporter construct. In these experiments, a smad2/3 luciferase reporter (SBI #TR203VA-P) was introduced into HEK293 cells. Endogenous ACVR2A and ACVR2B function was knocked out using custom made CRISPR/CAS9 targeting sequences. Finally, individual reporter lines were generated by reintroduction of ACVR2A or ACVR2B expression vectors. This method involved dispensing 30,000 cells into each well in total volume of 80ul, dispensing antibody into each well in total volume of 10ul, incubating the treated cells for 1hr at 37oC, dispensing GDF8 into wells in total volume of 10ul (final conc. 100ng/ml), incubating the stimulated cells for 24hr at 37oC, adding 100ul of 1X ONE-Glo detection reagent to each well, incubate the plate for 5min at room temperature and then reading luminescence using a plate reader.

The results of this assay are shown in column N of Table 5 below. The values shown are IC50 values. The data in this table shows that the antibodies inhibit GDF8-induced SMAD3 phosphorylation in HEK293 cells.

EXAMPLE 8

SMAD REPORTER 4E1 ASSAY

The ability of several of the antibodies identified in Example 2 to specifically inhibit GDF8-induced SMAD activation was tested cells using the following protocol. In this assay, HEK293 cells were infected with a lentiviral SMAD2/3/4 reporter (pGF-SMAD2/3/4-mCMV-EF1-Puro System Biosciences). The lentiviral based reporter expresses both GFP and luciferase under the control of a Smad3-responsive element $(CAGA)_{12}$. Cells were sorted for their responsiveness to GDF8 based on their GFP expression. Single cell clones were expanded and transcriptional activation was tested by GDF8-induced luciferase activity. Clone 4E1 was unresponsive to GDF8 or Activin A. This clone was further transfected with Human or Mouse ACVR2A or ACVR2B plasmids. The ability of the antibodies to inhibit luciferase induction by GDF8 or Activin A in these cell lines was tested.

The results of this assay are shown in column O of Table 5 below. These values are IC50 values. The data in this table shows that the antibodies inhibit GDF8 and Activin A-mediated induction of SMAD2/3/4 in HEK293 cells.

Table 3:

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
Ab	Comp ELISA Human ACVR2A Activin A	Comp ELISA Human ACVR2A GDF8	Comp ELISA Mouse ACVR2A Activin A	Comp ELISA Mouse ACVR2A GDF8	Dimer ALK5/ ACVR2A GDF8	Dimer ALK5/ ACVR2B GDF8	ELISA Human ACVR2A (10 pt)	ELISA-Human ACVR2A (8 pt)	ELISA-Human ACVR2B (10 pt)	ELISA Mouse ACVR2A (10 pt)	ELISA Mouse ACVR2A (8 pt)	ELISA Mouse ACVR2B (10 pt)	Phospho-SMAD3 Human Skeletal Muscle GDF8	SMAD 2/3/4 Reporter HEK293	Clone 4E1+Human ACVR2A, Activin A, 10pt
365_B10	0.0189	0.0079	0.0066	0.0002	0.6247	9999	0.0013	0.001	9999	0.001	0.0009	9999	0.031	0.3543	0.0364
365_E04								0.004			0.0048				
365_H08	0.4151	0.0116	0.1949	0.0044	9999	9999	0.1963	0.0029	9999	0.0959	0.0055	9999		9999	9999
366_D21	0.338	0.0292	0.1896	0.0133	6.372	9999	0.0017		9999	0.0011		9999	0.1323	0.4973	0.1006
366_G06								0.0035			0.0041				
367_H01	0.0363	0.0035	0.0125	0.0014	6.578	9999	0.0064	0.0029	9999	0.0054	0.0025	9999	0.0248	3.679	0.3607
368_A02								0.008			0.008				
368_A12	0.681	0.202	0.0348	0.0007	2.303	9999	0.0016	0.0028	9999	0.0015	0.0024	9999	0.046	0.9454	0.1142
368_B10	0.0077	0.0025	0.0084	0.0021	0.4969	9999	0.0053	0.0043	9999	0.0053	0.0045	9999	0.0469	1.387	0.0632
368_F10	0.1033	0.0069	0.1028	0.004	3.946	9999	0.0039		9999	0.0022		9999	0.2567	0.8681	0.2092
369_B03	0.0164	0.0044	0.0115	0.0033	1.761	9999	0.0051	0.0031	9999	0.006	0.0034	9999	0.0357	0.5055	0.1589
369_H03	0.1782	0.0017	0.0246	0.0003	8.179	9999	0.0073	0.003	9999	0.0052	0.01	9999	0.3262	9999	0.0957
370_B01	0.0036	0.0006	0.0027	0.0004	0.1589	9999	0.0004	0.0011	9999	0.0004	0.001	9999	0.0121	0.0535	0.0154
371_D07	0.0271	0.0032	0.0344	0.0035	1.182	9999	0.0093	0.013	9999	0.0057	0.01	9999	0.1265	4.187	0.2217
372_B11	0.0823	0.0059	0.0718	7.11E-05	2.191	9999	0.0042		9999	0.0032		9999	0.3973	4.276	0.2726
373_E11	0.0208	0.0012	0.021	8.31E-05	0.9392	9999	0.0013		9999	0.0012		9999	0.0229	0.4333	0.1403
373_H02	0.01	0.0036	0.006	0.0032	0.7633	9999	0.0032	0.001	9999	0.003	0.0011	9999	0.0145	0.3413	0.0351
374_B02	0.1374	0.0206	0.0771	0.0112	5.938	9999	0.0653	0.01	9999	0.0378	0.0032	9999	0.1183	9999	0.1766
375_A04	0.0025	0.0015	0.0018	0.0011	0.0481	9999	0.0007	0.0006	9999	0.0007	0.0004	9999	0.0076	0.0551	0.0071

375_A11	0.0167	0.0062	0.0305	0.0047	0.939	9999	0.0047	0.0009	9999	0.003	0.0007	9999	0.0127	0.5299	0.0359	
375_H01								0.015			0.015					
376_G02	0.0144	0.0051	0.0111	0.0041	0.8281	9999	0.0029	0.0018	9999	0.002	0.002	9999	0.1301	0.3337	0.0836	
365_G06	0.0151	0.0034	0.0225	0.0028	0.4743	9999	0.0035	0.0026	9999	0.0031	0.0073	9999	0.0875	0.2424	0.0329	
367_F10	0.0186	0.0035	0.0168	0.0026	2.249	9999	0.0019	0.0136	9999	0.0017	0.0119	9999	0.1178	0.4584	0.369	
368_B12	0.0074	0.0035	0.0128	0.0033	0.4249	9999	0.0047	0.0053	9999	0.0051	0.006	9999	0.0918	1.746	0.1613	
369_A12	0.0205	0.0005	0.0119	0.0002	0.3311	9999	0.001	0.0017	9999	0.0008	0.0014	9999	0.0119	0.0548	0.0311	
369_E03	0.0777	0.0006	0.0346	0.0049	0.8456	9999	0.001	0.0039	9999	0.0009	0.0043	5.543	0.0235	1.043	0.1325	
370_B06	0.018	0.0007	0.0107	0.0003	0.9481	9999	0.0032	0.0018	9999	0.0023	0.0015	9999	0.0061	0.3643	0.0467	
371_B11	0.0268	0.0036	0.0147	0.157	0.3699	9999	0.0011	0.0012	9999	0.001	0.0011	9999	0.015	0.2384	0.0316	
371_C02	0.0519	0.0043	0.0577	0.0007	3.394	9999	0.0025	0.0045	9999	0.0021	0.0045	9999	0.0488	1.01	0.0956	
373_D11	0.0037	0.0005	0.004	0.0001	0.1968	9999	0.0003		9999	0.0003		9999	0.0081	0.3066	0.0225	
373_G06	0.0478	0.0053	0.0325	0.0044	9999	9999	0.0052	0.0009	9999	0.0047	0.0021	9999	0.0231	1.963	0.0383	
376_D08	0.0027	0.0007	0.0019	0.0007	0.075	9999	0.0006		9999	0.0005		9999	0.0065	0.0243	0.41	
376_F09	0.0094	0.0015	0.0101	0.0016	0.3541	9999	0.0046	0.0045	9999	0.0041	0.0028	9999	0.0855	0.4007	0.0407	
365_E12								0.0019			0.0017					
365_F02	0.0077	0.0022	0.0078	0.0014	0.3793	9999	0.0006	0.0005	9999	0.0006	0.0005	9999	0.026	0.8487	0.0639	
365_G05								0.0073			0.0072					
367_A03								0.0136			0.0132					
367_C07	0.0298	0.0042	0.03	0.0041	1.082	9999	0.0008		9999	0.0007		9999	0.0716	9999	0.1569	
368_A07	0.0056	0.0039	0.0029	0.0013	0.5726	9999	0.001	0.0005	9999	0.0008	0.0006	9999	0.0149	0.1333	0.0135	
369_B05								0.0027			0.0018					
370_A02								0.0021			0.005					
370_H02	0.0254	0.0005	0.0123	1.00E-14	0.5495	9999	0.0009	0.0016	9999	0.0008	0.0012	9999	0.0226	0.6343	0.0355	
371_A10								0.0058			0.0056					
371_C12	0.043	0.0004	0.024	0.0043	0.3096	9999	0.0006	0.0011	9999	0.0005	0.0007	9999	0.0206	0.5658	0.0187	
371_D02								0.0018			0.0017					
371_G09								0.0019			0.0019					
371_G11	0.0052	0.0004	0.0066	0.0045	7.363	9999	0.0042	0.0039	9999	0.0034	0.0031	9999	0.1361	9999	0.3384	

372_B02	0.0029	0.0031	0.0045	0.0024	2.192	9999	0.0019	0.0026	9999	0.0014	0.0017	9999	0.1605	1.675	0.1778
372_C03	0.003	0.0024	0.0013	0.0006	0.7064	9999	0.0011	0.0012	9999	0.0029	0.0029	9999	0.058	0.1379	0.0466
373_A03	0.0053	0.0023	0.0031	0.0021	0.2914	9999	0.001	0.001	9999	0.0008	0.0007	9999	0.0148	0.559	0.009
373_A05								0.0032			0.0022				
373_A09								0.0012			0.0009				
373_A11								0.0009			0.0006				
373_B05								0.0022			0.0021				
373_C07	0.0126	0.004	0.0087	0.0011	1.215	9999	0.0028	0.0015	9999	0.0025	0.0014	9999	0.0048	1.208	0.0686
373_F08	0.0022	0.0015	0.0017	0.0004	0.0919	9999	0.0005	0.0007	2.32	0.0004	0.0005	2	0.005	0.3677	0.0315
373_F12								0.0016			0.0009				
374_G08	0.0042	0.0013	0.0033	0.001	0.2649	9999	0.0009	0.001	9999	0.0007	0.0009	9999	0.0057	0.3073	0.0711
374_H03	0.0139	0.0074	0.0117	0.0056	2.093	9999	0.003		9999	0.0024		9999	0.0129	0.808	0.1144
374_B03	0.0021	0.0015	0.002	0.0005	0.2057	9999	0.0008	0.0009	9999	0.0008	0.0006	9999	0.027	0.2394	0.0399
374_C01	0.3127	0.0191	0.2686	0.0033	9999	9999	0.012		9999	0.0163		9999	1.115	0.8145	4.942
374_C09	0.0467	0.0088	0.0496	0.0047	1.402	9999	0.011	0	9999	0.007	0.004	9999	0.1888	0.7011	0.2939
374_C12	0.0045	0.0023	0.0038	0.0026	0.2619	9999	0.0016	0.0005	0.4162	0.0012	0.0005	0.397	0.027	0.1579	0.083
374_D05	0.0392	0.0065	0.0258	0.0068	1.646	9999	0.0074	0.0022	9999	0.0066	0.0018	9999	0.0177	1.897	0.0851
374_D10	0.0781	0.0038	0.0653	0.0027	3.186	9999	0.0132		1.021	0.0022		1.053	0.1268	9999	4.658
374_G08	0.0056	0.0025	0.0056	0.0017	0.608	9999	0.0018	0.0005	9999	0.0014	0.0009	9999	0.034	0.542	0.0781
375_A01								0.0012			0.001				
375_A07	0.0097	0.0025	0.0221	0.0025	0.4117	9999	0.001		9999	0.001		9999	0.018	0.0154	0.0922
375_A12	0.0047	0.0014	0.0033	0.0003	0.3345	9999	0.0007		9999	0.0005		9999	0.0469	1.051	0.0415
375_D10								0.0023			0.0015				
375_E05								0.0009			0.0007				
375_E10	0.0035	0.002	0.0023	0.0009	0.2255	9999	0.0007	0.0008	9999	0.0007	0.0005	9999	0.0091	0.2237	0.0215
375_F02	0.0288	0.0034	0.0184	0.005	0.8957	9999	0.0037		9999	0.0028		9999	0.0075	0.6181	0.0247
375_G05	0.0008	0.0005	0.001	0.0004	0.1347	9999	0.0005	0.0007	2.852	0.0004	0.0005	2	0.0052	0.0108	0.0668
375_H05	0.0057	0.0019	0.0043	9.34E-05	0.4237	9999	0.0008	0.0006	9999	0.0007	0.0005	9999	0.0346	0.2948	0.0342
376_A03								0.0022			0.0014				

376_B10									0.0021			0.0017						
376_C08	0.0243	0.0046	0.6272	0.0046	0.9254	9999	0.0044			9999	0.0048		9999	0.0605	1.353	0.1794
376_F01	0.1328	0.0177	0.1264	0.0117	2.893	9999	0.0076	0.0082	0.0922	0.008	0.003	0.0924	0.3947	9999	9999	0.6449
376_F06	0.0352	0.0032	0.0221	0.002	0.3714	9999	0.0034	0.0024	9999	0.0032	0.0017	9999	0.0544	9999	9999	0.1295
376_G05	0.0281	0.0036	0.008	0.0032	0.9329	9999	0.0017	0.0006	9999	0.0014	0.0005	9999	0.0658	0.3712	9999	0.0755
376_G10								0.0031			0.0032							
376_H01	0.005	0.0025	0.0044	0.0013	0.5641	9999	0.001	0.0012	0.1094	0.0009	0.001	0.0981	0.0562	0.6002	0.6329			
376_H11	0.0008	0.0007	0.0013	0.0007	0.0368	9999	0.0004	0.0005	9999	0.0004	0.0004	9999	0.0042	0.0775	0.0084			
367_A02	0.5685	0.0168	0.0757	0.0117	1.404	9999	0.0039		9999	0.0053		9999	0.1591	2.765	0.065			
368_G03	0.1025	0.0013	0.0477	0.0003	6.811	9999	0.0003	0.0068	9999	0.0026	0.008	9999	0.199	1.678	0.4619			
368_H05								0.0138			0.0023							
369_C12	0.0022	0.0007	0.0016	0.0006	0.137	9999	0.0007	0.0008	9999	0.0007	0.0006	9999	0.0094	0.0821	0.0435			
369_E08								0.0028			0.0023							
369_F09	0.0204	0.0007	0.0156	0.0004	0.793	9999	0.0012		2	0.001		2	0.0325	1.095	0.1356			
369_H08	0.0721	0.0014	0.0431	0.0002	1.385	9999	0.0013	0.0034	9999	0.001	0.0026	9999	0.0308	0.7511	0.074			
369_H12	0.0154	0.001	0.0112	0.0001	1.812	9999	0.0006	0.0011	9999	0.0005	0.001	9999	0.0303	0.3774	0.0815			
370_C06	0.0146	0.0005	0.0083	6.83E-05	0.7631	9999	0.0005	0.0009	9999	0.0005	0.0008	9999	0.0111	4999	0.05			
370_C07	0.0219	0.0011	0.0084	0.0006	0.3774	9999	0.0006	0.0008	9999	0.0006	0.0005	9999	0.0044	0.1452	0.0213			
370_E03	0.0163	0.0025	0.0103	0.0042	0.8872	9999	0.0023	0.0017	9999	0.0017	0.0016	9999	0.0165	0.4708	0.0649			
370_E04	0.0067	0.0013	0.0066	0.0005	0.8152	9999	0.0008	0.0007	9999	0.0008	0.0006	9999	0.0135	0.3666	0.0416			
370_F12	0.005	0.0002	0.0025	2.65E-05	0.3859	9999	0.0009	0.0006	9999	0.0007	0.0005	9999	0.0066	0.1268	0.0096			
371_B01	0.003	0.0006	0.0024	0.0002	0.1859	9999	0.0005	0.0017	9999	0.0005	0.0018	9999	0.0076	0.0454	0.0091			
371_E12	0.0023	0.0043	0.0022	0.0024	0.5962	9999	0.0012		9999	0.0011		9999	0.0374	0.3135	0.1173			
371_F09	0.0054	0.0006	0.0047	0.0003	0.2882	9999	0.0006		9999	0.0005		9999	0.0311	0.31	0.0405			
371_G01											0.0012							
371_H11											0.0008							
372_B09	0.0021	0.0002	0.0007	0.0003	0.6034	9999	0.0006	0.0009	9999	0.0006	0.0008	9999	0.0182	0.4639	0.055			
373_D06	0.0085	0.001	0.0083	0.0003	0.3687	9999	0.0004		9999	0.0003		9999	0.0303	0.4069	0.0607			

373_F07	0.0081	0.002	0.0056	0.0039	3.811	9999	0.0015		9999	0.0014		9999	0.0068	0.397	0.0813
374_A05	0.0023	0.0002	0.0021	0.0005	0.0298	9999	0.0003	0.0008	9999	0.0003	0.0005	9999	0.0001	0.2037	0.0166
374_C03	0.0137	0.003	0.0064	0.0023	0.4673	9999	0.001	0.0013	9999	0.0007	0.001	9999	0.0582	0.0344	0.3012
374_G05	0.0074	0.002	0.0042	0.0027	0.5471	9999	0.0021	0.0005	9999	0.0017	0.0005	9999	0.0132	0.4163	0.0192
365_A12	0.3112	0.0015	0.1194	6.64E-05	9999	9999	0.0103	0.0064	0.7569	0.0059	0.0071	0.3945	0.9032	3.406	1.133
365_B11								0.003			0.0032				
365_E05	0.0435	0.0008	0.0528	0.0071	0.8445	9999	0.0045		9999	0.0042		9999	0.2437	0.367	0.0548
365_E07	0.3702	0.0105	0.1501	0.0122	9999	9999	0.011	0.008	9999	0.0048	0.0101	9999	0.3183	9999	0.9486
366_B12	0.0304	0.0115	0.0185	0.0114	0.8558	9999	0.0012	0.0013	9999	0.0009	0.001	9999	0.0392	0.3748	0.053
367_F03								0.01			0.007				
367_H06	0.0744	0.0035	0.0653	0.0034	0.8666	9999	0.0018		9999	0.0013		9999	0.108	0.9681	0.3793
367_H11	0.0389	0.0044	0.0256	0.0035	0.4515	9999	0.0057	0.004	9999	0.002	0.0028	9999	0.0703	1.207	0.118
368_F03	0.4171	0.0005	0.0313	0.0001	9999	9999	0.022	0.1	9999	0.0189	0.1503	9999	0.6118	3.239	3.216
369_B02	0.0031	0.0006	0.0039	2.58E-05	0.1671	9999	0.0004		9999	0.0004		9999	0.0135	0.1748	0.0252
369_F01	0.0147	0.0013	0.0147	0.0002	0.4998	9999	0.0008		9999	0.0007		9999	0.0317	0.3266	0.1112
369_F06								0.0038			0.0032				
369_G01	0.0112	0.0008	0.0061	0.0001	0.7538	9999	0.0004		9999	0.0004		9999	0.0116	0.1187	0.0275
369_H06	0.0106	0.0028	0.0082	3.81E-05	9999	9999	0.0006	0.0014	9999	0.0005	0.0012	9999	0.0058	9999	0.0225
370_A01								0.0046			0.0039				
370_A12	0.0061	0.0023	0.0136	0.0024	0.1245	9999	0.0009	0.0018	9999	0.0008	0.0015	9999	0.0032	0.031	0.0036
370_C01								0.0017			0.0015				
370_C03	0.0007	0.0004	0.0006	0.0004	0.0388	9999	0.0004	0.0003	9999	0.0004	0.0004	9999	0.0029	0.0133	0.0035
370_C05	0.0053	0.0032	0.0035	0.0024	0.927	9999	0.0012	0.0033	9999	0.0011	0.0024	9999	0.0082	0.2655	0.0343
370_C08								0.0021			0.0016				
370_D04	0.0055	0.0012	0.0038	0.0013	0.1029	9999	0.0005	0.0007	9999	0.0004	0.0008	9999	0.0074	0.0452	0.0133
370_E09	0.0043	0.0009	0.0021	0.0006	0.1656	9999	0.0006	0.0007	9999	0.0005	0.0006	9999	0.0093	0.1226	0.009
370_H01	0.0084	0.0006	0.0056	1.61E-06	2.84	9999	0.0005	0.0004	9999	0.0005	0.0003	9999	0.0093	4999	0.039

371_A06								0.0014		0.0014						
371_B07	0.0161	0.0013	0.0153	0.0003	1.236	9999	0.0012	0.0014	1.77	0.0011	0.0012	9999	0.0402	0.4851	0.0734	
371_F01								0.005			0.0046					
371_F04								0.0023			0.0021					
372_A04	0.0021	0.0028	0.0051	0.0022	0.3792	9999	0.0008		9999	0.0007		9999	0.0193	0.0367	0.0423	
372_D02								0.0029			0.0027					
372_F03	0.0047	0.0005	0.0041	0.0002	0.1903	9999	0.0003	0.0008	9999	0.0004	0.0008	9999	0.0046	0.1972	0.0233	
372_F08	0.0021	0.0113	0.0026	0.0113	0.373	9999	0.0009		9999	0.0008		9999	0.023	0.3148	0.0248	
372_F09	0.0053	0.0003	0.0113	0.0029	1.012	9999	0.001	0.0009	9999	0.0009	0.0008	9999	0.018	1.8	0.087	
373_A10	0.0028	0.002	0.0055	0.0018	0.3578	2.53	0.0006		9999	0.0006		9999	0.0111	0.0965	0.0334	
373_B04	0.0186	0.0023	0.0103	0.0031	1.262	9999	0.0026	0.0018	9999	0.0027	0.0013	9999	0.0093	1.028	0.1134	
373_C02	0.0302	0.0052	0.0179	0.0022	3.29	9999	0.0053		9999	0.0052		9999	0.0083	1.389	0.1045	
373_C06								0.001			0.001					
373_E04	0.0019	0.0013	0.0023	0.0012	0.1467	9999	0.0006		9999	0.0005		9999	0.0078	0.137	0.0183	
373_D10	0.0069	0.0018	0.0033	0.0004	0.2803	9999	0.0013	0.0008	9999	0.0012	0.0005	9999	0.006	0.0821	0.0175	
374_B04	0.0043	0.0018	0.0029	0.0016	0.2473	9999	0.0014	0.0023	9999	0.0015	0.0003	9999	0.0093	0.1014	0.0158	
374_B06	0.0614	0.0041	0.0513	0.0001	0.5987	9999	0.0011	0.004	9999	0.0009	0.004	9999	0.0407	0.3649	0.0717	
374_C03	0.0016	0.001	0.0026	0.0007	0.1284	9999	0.0005		9999	0.0004		9999	0.0094	0.0468	0.0144	
374_C06	0.0105	0.0039	0.0059	0.0032	0.5205	9999	0.0019	0.0008	9999	0.0015	0.0007	9999	0.0136	0.296	0.015	
374_D08	0.9536	0.0698	0.6104	0.0621	9999	9999	0.3558	0.01	9999	0.2008	0.01	9999	0.2299	9999	1.286	
374_E01								0.0013			0.001					
374_E05	0.0074	0.0023	0.0079	0.0019	0.3051	9999	0.0013	0.0016	0.1534	0.0014	0.0011	0.1414	0.0497	0.6496	2.729	
365_E02	0.4963	0.0046	0.1618	0.0012	13.07	9999	0.0095	0.008	9999	0.0047	0.0013	9999	0.3412	9999	0.4773	
376_C06	0.0349	0.0049	0.0238	0.0053	0.711	9999	0.0042	0.0016	9999	0.0022	0.001	9999	0.0107	0.1383	0.0817	
368_D10	0.0119	0.0045	0.0195	0.0033	0.4824	9999	0.0019		9999	0.0014		9999	0.0601	0.2942	0.0389	
374_C08	0.182	0.0335	0.194	0.0123	9999	9999	0.0462		9999	0.0285		9999	0.6246	9999	9999	
376_A06	0.0011	0.0006	0.0009	0.0004	0.0189	9999	0.0004	0.0004	9999	0.0004	0.0003	9999	0.0043	0.0203	0.0037	
365_F07	0.8044	0.0017	0.0037	0.0006	0.135	9999	0.0012	0.0008	9999	0.0013	0.0007	9999	0.011	0.0925	0.0354	

376_B01	0.0035	0.0006	0.0039	8.50E-05	0.2036	9999	0.0004	9999	0.0004		9999	0.0086	0.369	0.0383
365_D05	0.0146	0.0025	0.0149	0.0009	0.9169	9999	0.0008	9999	0.0008		9999	0.0209	0.6675	0.1617
369_G07	0.0068	0.001	0.0073	0.0001	9999	9999	0.0007	9999	0.0006		9999	0.012	0.0327	0.1333
373_G05	0.0023	0.0002	0.0021	0.0002	0.1636	9999	0.0003	9999	0.0002		9999	0.0059	0.1546	0.0202
376_B06	0.0016	0.001	0.0014	0.0007	0.0381	9999	0.0005	9999	0.0005	0.0004	9999	0.0042	0.0025	0.0164
374_C11	0.0192	0.0015	0.0185	0.0024	0.9402	9999	0.0018	0.3945	0.0015		0.3304	0.0266	0.6324	0.0328
375_A06	0.0032	0.0016	0.0025	0.0013	0.1302	9999	0.0012	0.0005	9999	0.0011	0.0004	9999	0.0318	0.1546	0.014
373_E06	0.0002	0.0002	0.0002	0.0001	0.0082	9999	0.0002	0.0002	9999	0.0002	0.0002	9999	0.0005	0.0025	0.0022
374_C05	0.0029	0.0005	0.0011	0.0004	0.1344	9999	0.0007	0.0005	9999	0.0007	0.0004	9999	0.0124	0.0142	9999
368_H01								0.0037			0.0014				
373_B03								0.0026			0.0005				
369_A10	0.017	0.0005	0.0077	8.47E-05	5000	9999	0.001	0.0015	9999	0.001	0.0005	9999	0.0076	5000	0.071
366_A05					0.7418	9999	0.0004	0.0006	9999	0.0005	0.0005	9999	0.0244	0.6492	0.0524
373_G07	0.0085	0.0032	0.0053	0.0031	0.7814	9999	0.0022	0.0012	9999	0.0016	0.001	9999	0.0112	0.2215	0.0786
371_G03								0.001			0.001				
370_E07	0.0009	0.0005	0.0013	0.0005	0.1001	9999	0.0007	0.0003	9999	0.0008	0.0003	9999	0.0046	0.0764	0.013
367_G07	0.0007	0.0009	0.0011	0.0007	0.1113	9999	0.0011	0.0005	9999	0.0009	0.0004	9999	0.0068	0.0843	0.0124
375_C12	0.0005	0.0003	0.0007	0.0004	0.0414	9999	0.0004	0.0003	0.4421	0.0004	0.0003	0.4194	0.0063	0.0237	0.2784
373_B08	0.003	0.0012	0.002	0.0012	0.3478	9999	0.0015	0.0005	9999	0.0017	0.0004	9999	0.0201	0.1231	0.017
374_A11	0.0038	0.0015	0.0027	0.0015	0.6038	9999	0.0013	0.0004	9999	0.0011	0.0003	9999	0.0086	0.075	0.0188
373_B11	0.0003	0.0002	0.0005	0.0003	0.0185	9999	0.0002		9999	0.0003		9999	0.0008	0.024	0.0036
372_D04	0.0022	0.0008	0.0026	0.0017	0.1255	9999	0.0009	0.0005	9999	0.0009	0.0005	9999	0.0014	0.0038	0.0179
367_A01	0.0021	0.0009	0.0041	0.0011	0.1471	9999	0.0012	0.0009	9999	0.0011	0.0007	9999	0.0063	0.1617	0.0355
373_E02	0.0034	0.0013	0.0021	0.0013	4999	9999	0.0012	0.0006	9999	0.0012	0.0005	9999	0.0049	4995	4999

While the present invention has been described with reference to the specific embodiments thereof, it should be understood by those skilled in the art that various changes may be made and equivalents may be substituted without departing from the true spirit and scope of the invention. In addition, many modifications may be made to adapt a particular situation, material, composition of matter, process, process step or steps, to the objective, spirit and scope of the present invention. All such modifications are intended to be within the scope of the claims appended hereto.

CLAIMS

What is claimed is:

1. An antibody that specifically binds to ACVR2A, wherein the antibody comprises:

(a) a variable domain comprising:

i. heavy chain CDR1, CDR2 and CDR3 regions that are identical the heavy chain CDR1, CDR2 and CDR3 regions of an antibody selected from any of Tables 2A-2F; and

ii. light chain CDR1, CDR2 and CDR3 regions that are identical the light chain CDR1, CDR2 and CDR3 regions of the antibody selected from any of Tables 2A-2F; or

(b) a variant of said variable domain of (a) that is otherwise identical to said antibody variable domain except for up to 15 amino acid substitutions in said CDR regions.

2. An antibody that specifically binds to ACVR2A, wherein the antibody comprises:

a heavy chain variable domain comprising: a heavy chain framework, a CDR1 region, a CDR2 region, and a CDR3 region of sequence AxxAxWHDTxLD (SEQ ID NO: 6618) ; and

a light chain variable domain comprising: a light chain framework, a CDR1 region, a CDR2 region, and a CDR3 region.

3. The antibody of any prior claim, wherein the heavy chain variable domain comprises a CDR3 region of sequence ARSATWHDTxLD (SEQ ID NO: 6549), ARAATWHDTxLD (SEQ ID NO: 6540), ARGANWHDTxLD (SEQ ID NO: 6542), ARGATWHDTxLD (SEQ ID NO: 6544), ARSANWHDTxLD (SEQ ID NO: 6546) or ARSATWHDTxLD (SEQ ID NO: 6548).

4. The antibody of any prior claim, wherein the antibody comprises:

a heavy chain variable domain comprising:

i. a CDR1 region that has a sequence of D/SS/DYG/SMH/N (SEQ ID NO: 6550) ,

ii. a CDR2 region that has a sequence of WVA/SS/G/NINYNG/SGYT/KS/G (SEQ ID NO: 6619), and

iii. a CDR3 region that has a sequence of ARAANWHDTA/HLD (SEQ ID NO: 6620); and

a light chain variable domain comprising:

i. a CDR1 region that has a sequence of L/V/I/SS/T/RYL/VNWY (SEQ ID NO: 6554),

ii. a CDR2 region that has a sequence of LV/LIYA/Y/VA/V/TT/S/NS/NR/LA/H/Q/P (SEQ ID NO: 6621), and

iii. a CDR3 region that has a sequence of QQ/HSY/DD/E/S/NL/N/S/TPL (SEQ ID NO: 6593).

5. The antibody of any of claims 1-3, wherein the antibody comprises:

a heavy chain variable domain comprising:

i. a CDR1 region that has a sequence of D/SS/DYG/SMH/N (SEQ ID NO: 6550),

ii. a CDR2 region that has a sequence of WVA/SS/G/NINYNG/SGYT/KS/G (SEQ ID NO: 6551) , and

iii. a CDR3 region that has a sequence of ARAATWHDTH/ALD (SEQ ID NO: 6559); and

a light chain variable domain comprising:

i. a CDR1 region that has a sequence of L/V/I/SS/TYL/VNWY (SEQ ID NO: 6561),

ii. a CDR2 region that has a sequence of LL/VIYA/YA/T/VT/S/NS/NR/LA/P/Q (SEQ ID NO: 6563), and

iii. a CDR3 region that has a sequence of QQSY/D/ND/E/S/NL/S/T/NPL (SEQ ID NO: 6565).

6. The antibody of any of claims 1-3, wherein the antibody comprises:

a heavy chain variable domain comprising:

i. a CDR1 region that has a sequence of S/DS/DYS/GMN/H (SEQ ID NO: 6566),

ii. a CDR2 region that has a sequence of WVS/AG/S/NINYNG/SGYT/KS/G (SEQ ID NO: 6567), and

iii. a CDR3 region that has a sequence of ARGANWHDTA/HLD (SEQ ID NO: 6543); and

a light chain variable domain comprising:

i. a CDR1 region that has a sequence of L/V/S/IS/TYL/VNWY (SEQ ID NO: 6569),

ii. a CDR2 region that has a sequence of LL/VIYAA/V/TT/SSR/LA/H/Q (SEQ ID NO: 6571), and

iii. a CDR3 region that has a sequence of QQSY/DD/E/S/NS/T/N/LPL (SEQ ID NO: 6573).

7. The antibody of any of claims 1-3, wherein the antibody comprises:

a heavy chain variable domain comprising:

i. a CDR1 region that has a sequence of S/DS/DYS/GMN/H (SEQ ID NO: 6574),

ii. a CDR2 region that has a sequence of WVA/SG/N/SINYNG/SGYT/KS/G (SEQ ID NO: 6575), and

iii. a CDR3 region that has a sequence of ARGATWHDTH/ALD (SEQ ID NO: 6595); and

a light chain variable domain comprising:

i. a CDR1 region that has a sequence of L/I/V/SS/TYL/VNWY (SEQ ID NO: 6596),

ii. a CDR2 region that has a sequence of LL/VIYAA/V/TT/SSR/LA/H/Q (SEQ ID NO: 6571), and

iii. a CDR3 region that has a sequence of QQSY/DD/E/S/NT/S/N/LPL (SEQ ID NO: 6577).

8. The antibody of any of claims 1-3, wherein the antibody comprises:

a heavy chain variable domain comprising:

i. a CDR1 region that has a sequence of S/DS/DYG/SMN/H (SEQ ID NO: 6578),

ii. a CDR2 region that has a sequence of WVS/AG/N/SINYNG/SGYT/KS/G (SEQ ID NO: 6579), and

iii. a CDR3 region that has a sequence of AR/KSANWHDTA/HLD (SEQ ID NO: 6580); and

a light chain variable domain comprising:

i. a CDR1 region that has a sequence of L/V/I/SS/TYL/VNWY (SEQ ID NO: 6561),

ii. a CDR2 region that has a sequence of LL/VIYA/YA/V/TT/SS/NR/LA/H/Q (SEQ ID NO: 6582), and

iii. a CDR3 region that has a sequence of QQSY/DD/E/N/SS/T/L/NPL (SEQ ID NO: 6598).

9. The antibody of any of claims 1-3, wherein the antibody comprises:

a heavy chain variable domain comprising:

i. a CDR1 region that has a sequence of D/SS/DYS/GMN/H (SEQ ID NO: 6584),

ii. a CDR2 region that has a sequence of WVA/SG/N/SINYNG/SGYT/KS/G (SEQ ID NO: 6585), and

iii. a CDR3 region that has a sequence of ARSATWHDTH/ALD (SEQ ID NO: 6586); and

a light chain variable domain comprising:

i. a CDR1 region that has a sequence of L/V/I/SS/T/RYL/VNWY (SEQ ID NO: 6588),

ii. a CDR2 region that has a sequence of LL/VIYA/YA/V/TT/SS/NR/LA/H/Q (SEQ ID NO: 6590), and

iii. a CDR3 region that has a sequence of QQSY/DD/E/S/NL/N/T/SPL (SEQ ID NO: 6591).

10. The antibody of any prior claim, wherein the antibody comprises:

a heavy chain variable domain comprising an amino acid sequence that is at least 80% identical to the amino acid sequence of the heavy chain variable domain of an antibody selected from any of Tables 2A-2F; and

a light chain variable domain comprising an amino acid sequence that is at least 80% identical to the light chain variable domain of the antibody selected from any of Tables 2A-2F.

11. The antibody of any prior claim, wherein the heavy chain variable domain and the light chain variable domain are present in separate polypeptides.

12. The antibody of any prior claim, wherein the heavy chain variable domain and the light chain variable domain are present in a single polypeptide.

13. The antibody of any prior claim, wherein the antibody binds ACVR2A with an affinity in the range of 10^7 M^{-1} to 10^{12} M^{-1}.

14. The antibody of any prior claim, wherein the antibody comprises a covalently linked non-peptide synthetic polymer.

15. The antibody of claim 14, wherein the synthetic polymer is poly(ethylene glycol) polymer.

16. The antibody of any prior claim, wherein the antibody comprises a covalently linked lipid or fatty acid moiety.

17. The antibody of any prior claim, wherein the antibody comprises a covalently linked polysaccharide or carbohydrate moiety.

18. The antibody of any prior claim, wherein the antibody is a single chain Fv (scFv) antibody.

19. The antibody of claim 18, wherein the scFv is multimerized.

20. A pharmaceutical composition comprising:
a) the antibody of any prior claim; and
b) a pharmaceutically acceptable carrier.

21. The pharmaceutical composition of claim 20, wherein the antibody is encapsulated in a liposome.

22. A method of decreasing ACVR2A-mediated signaling in a subject, the method comprising administering to the human patient an effective amount of the antibody of any prior antibody claim.

23. A method of treating a condition in a patient comprising administering to a patient in need thereof an effective amount of the antibody of any prior antibody claim.

24. The method according to claim 23, wherein the condition is associated with muscle atrophy.

25. The method according to claim 23, wherein the condition is characterized by a decrease in muscle mass or muscle function, or insufficient lean body mass..

26. The method according to claim 23, wherein the condition is cachexia or sarcopenia.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US18/24632

Box No. I Nucleotide and/or amino acid sequence(s) (Continuation of item 1.c of the first sheet)

1. With regard to any nucleotide and/or amino acid sequence disclosed in the international application, the international search was carried out on the basis of a sequence listing:

   a. ☒ forming part of the international application as filed:

      ☒ in the form of an Annex C/ST.25 text file.

      ☐ on paper or in the form of an image file.

   b. ☐ furnished together with the international application under PCT Rule 13*ter*.1(a) for the purposes of international search only in the form of an Annex C/ST.25 text file.

   c. ☐ furnished subsequent to the international filing date for the purposes of international search only:

      ☐ in the form of an Annex C/ST.25 text file (Rule 13*ter*.1(a)).

      ☐ on paper or in the form of an image file (Rule 13*ter*.1(b) and Administrative Instructions, Section 713).

2. ☐ In addition, in the case that more than one version or copy of a sequence listing has been filed or furnished, the required statements that the information in the subsequent or additional copies is identical to that forming part of the application as filed or does not go beyond the application as filed, as appropriate, were furnished.

3. Additional comments:

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US18/24632

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☒ Claims Nos.: 4-26
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
-***-Please See Supplemental Page-***-

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying additional fees, this Authority did not invite payment of additional fees.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
Groups I+, Claims 1-3; SEQ ID NO: 1 (VH), SEQ ID NO: 115 (HCDR1), SEQ ID NO: 172 (HCDR2), SEQ ID NO: 229 (HCDR3), SEQ ID NO: 58 (VL), SEQ ID NO: 286 (LCDR1), SEQ ID NO: 343 (LCDR2) and SEQ ID NO: 400 (LCDR3)

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.

☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.

☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US18/24632

A. CLASSIFICATION OF SUBJECT MATTER
IPC - C07K 16/28, 16/42, 16/46 (2018.01)
CPC - C07K 16/28, 16/42, 16/468, 16/2863

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
See Search History document

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched
See Search History document

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
See Search History document

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	US 2015/0152194 A1 (AMGEN, Inc.) June 4, 2015; paragraphs [0012], [0033], [0061], [0108], [0110], [0112]	1-3
A	US 2012/0201827 A1 (ELIAS et al.) August 9, 2012; column 41	1, 3
A	US 2016/0068601 A1 (BROGDON et al.) March 10, 2016; claim 105	1, 3
A	US 2007/0202566 A1 (BÖRNSCHEUER et al.) August 30, 2007; paragraph [0012]	2, 3
A	US 2003/0104569 A1 (ORITANI et al.) June 5, 2003; paragraph [0015]	2, 3

☐ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:
"A" document defining the general state of the art which is not considered to be of particular relevance
"E" earlier application or patent but published on or after the international filing date
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
"O" document referring to an oral disclosure, use, exhibition or other means
"P" document published prior to the international filing date but later than the priority date claimed
"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
12 June 2018 (12.06.2018)	01 AUG 2018
Name and mailing address of the ISA/ Mail Stop PCT, Attn: ISA/US, Commissioner for Patents P.O. Box 1450, Alexandria, Virginia 22313-1450 Facsimile No. 571-273-8300	Authorized officer Shane Thomas PCT Helpdesk: 571-272-4300 PCT OSP: 571-272-7774

Form PCT/ISA/210 (second sheet) (January 2015)

INTERNATIONAL SEARCH REPORT
Information on patent family members

International application No.
PCT/US18/24632

-***-Continued from Box No. III Observations where unity of invention is lacking: -***-

This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

Groups I+, Claims 1-3 and SEQ ID NOs: 1, (VH), 58 (VL), 115 (HCDR1), 172 (HCDR2), 229 (HCDR3), 286 (LCDR1), 343 (LCDR2) and 400 (LCDR3) are directed toward an antibody that specifically binds to ACVR2A.

The antibody will be searched to the extent it encompasses a heavy chain variable domain (VH) encompassing SEQ ID NO: 1 (first exemplary VH), with associated CDR1 encompassing SEQ ID NO: 115 (first exemplary HCDR1), CDR2 encompassing SEQ ID NO: 172 (first exemplary HCDR2), CDR3 encompassing SEQ ID NO: 229 (first exemplary HCDR3) and a light chain variable region (VL) encompassing SEQ ID NO: 58 (first exemplary VL), with associated CDR1 encompassing SEQ ID NO: 286 (first exemplary LCDR1), CDR2 encompassing SEQ ID NO: 343 (first exemplary LCDR2) and CDR3 encompassing SEQ ID NO: 400 (first exemplary LCDR3). Applicant is invited to elect additional set(s) of VH and VL sequence(s), with associated sequence(s) for the CDR region(s) thereof, with specified SEQ ID NO: for each, or with specified substitution(s) at specified site(s) of a SEQ ID NO., such that the sequence of each elected species is fully specified (i.e. no optional or variable residues or substituents), to be searched. Additional set(s) of fully specified VH and VL and (where applicable) associated CDR sequence(s) will be searched upon the payment of additional fees. It is believed that claims 1 (in-part) and 2 (in-part) encompass this first named invention and thus these claims will be searched without fee to the extent that they encompass SEQ ID NO: 1 (VH), SEQ ID NO: 115 (HCDR1), SEQ ID NO: 172 (HCDR2), SEQ ID NO: 229 (HCDR3), SEQ ID NO: 58 (VL), SEQ ID NO: 286 (LCDR1), SEQ ID NO: 343 (LCDR2) and SEQ ID NO: 400 (LCDR3). Applicants must specify the claims that encompass any additionally elected sequence(s). Applicants must further indicate, if applicable, the claims which encompass the first named invention, if different than what was indicated above for this group. Failure to clearly identify how any paid additional invention fees are to be applied to the "+" group(s) will result in only the first claimed invention to be searched/examined. An exemplary election would be an antibody encompassing SEQ ID NO: 2 (VH), SEQ ID NO: 116 (HCDR1), SEQ ID NO: 173 (HCDR2), SEQ ID NO: 230 (HCDR3), SEQ ID NO: 59 (VL), SEQ ID NO: 287 (LCDR1), SEQ ID NO: 344 (LCDR2) and SEQ ID NO: 401 (LCDR3).

No technical features are shared between the antibody variable region and/or CDR sequences of Groups I+ and, accordingly, these groups lack unity a priori.

Additionally, even if Groups I+ were considered to share the technical features including: an antibody that specifically binds to ACVR2A, wherein the antibody comprises: (a) a variable domain comprising: i. heavy chain CDR1, CDR2 and CDR3 regions; and ii. light chain CDR1, CDR2 and CDR3 regions; or (b) a variant of said variable domain of (a) that is otherwise identical to said antibody variable domain except for up to 15 amino acid substitutions in said CDR regions; and wherein the antibody comprises: a heavy chain variable domain comprising: a heavy chain framework; and a light chain variable domain comprising: a light chain framework; these shared technical features are previously disclosed by US 2015/0152194 A1 to Amgen, Inc. (hereinafter 'Amgen').

Amgen discloses an antibody that specifically binds to ACVR2A (an antibody that specifically binds to ACVR2A; paragraph [0012]), wherein the antibody comprises: (a) a variable domain comprising: i. heavy chain CDR1, CDR2 and CDR3 regions (wherein the antibody comprises: (a) a variable domain comprising: i. heavy chain CDR1, CDR2 and CDR3 regions; Fig. 1, paragraphs [0033], [0061], [0108]); and ii. light chain CDR1, CDR2 and CDR3 regions (and ii. light chain CDR1, CDR2 and CDR3 regions; fig. 1, paragraphs [0033], [0061], [0108]); and wherein the antibody comprises: a heavy chain variable domain comprising: a heavy chain framework (a heavy chain variable domain comprising: a heavy chain framework; paragraphs [0108], [0110], [0112]); and a light chain variable domain comprising: a light chain framework (a light chain variable domain comprising: a light chain framework; paragraphs [0108], [0110], [0112]).

Since none of the special technical features of the Groups I+ inventions is found in more than one of the inventions, and since all of the shared technical features are previously disclosed by the Amgen reference, unity of invention is lacking.