

[19]	INTELLECTUAL PROPERTY PHILIPPINES		
[12]	INVENTION PUBLICATION		
[11]	Publication Number:	12013502013	Document Code: B1
[22]	Publication Date:	16/12/2013	
[21]	Application Number:	12013502013	Document Code: A
[22]	Date Filed:	27/9/2013	
[54]	Title:	ANTIBODY POLYPEPTIDES THAT ANTAGONIZE CD40	
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[30]	Priority Data:	21/4/2011 US201161477904P	
[51]	International Class 8:	A61K 39/395 20060101AFI20190509BHPH; C07K 16/28 20060101ALI20190509BHPH;	
[57]	Abstract:	Antibody polypeptides that specifically bind a novel epitope of human CD40 are provided. The antibody polypeptides do not exhibit CD40 agonist activity. The antibody polypeptides are useful in the treatment of diseases involving CD40 activation, such as autoimmune diseases. The antibody polypeptides may be domain antibodies (dAbs) comprising a single VL or VH domain. The half-life of the antibody polypeptides may be increased by modifying the antibody polypeptides to be dual specific reagents that can also bind human serum albumin (HSA).	

atherosclerosis, autoimmune diseases of the ear, autoimmune diseases of the eye, autoimmune hepatitis, autoimmune parotitis, colitis, coronary heart disease, Crohn's disease, diabetes, including Type 1 and/or Type 2 diabetes, epididymitis, glomerulonephritis, Graves' disease, Guillain-Barre syndrome, Hashimoto's disease, hemolytic anemia, idiopathic
5 thrombocytopenic purpura, inflammatory bowel disease, immune response to recombinant drug products, systemic lupus erythematosus, male infertility, multiple sclerosis, myasthenia gravis, pemphigus, psoriasis, rheumatic fever, rheumatoid arthritis, sarcoidosis, scleroderma, Sjogren's syndrome, spondyloarthropathies, thyroiditis, transplant rejection, vasculitis, AIDS, atopic allergy, bronchial asthma, eczema, leprosy, schizophrenia, inherited depression,
10 transplantation of tissues and organs, chronic fatigue syndrome, Alzheimer's disease, Parkinson's disease, myocardial infarction, stroke, autism, epilepsy, Arthus's phenomenon, anaphylaxis, alcohol addiction, and drug addiction.

Provided is an antibody polypeptide comprising a first variable domain that specifically binds an epitope of human CD40 comprising the amino acid sequence of SEQ ID NO: 1,
15 wherein the antibody polypeptide competes with the binding of domain antibody (dAb) BMS3h-56-201 (SEQ ID NO: 9), or a pharmaceutically acceptable salt thereof, for use in the preparation of a medicament for treatment of an immune disease. The medicament can, for example, be administered in combination with an immunosuppressive/immunomodulatory and/or anti-inflammatory agent. The immune disease can be, for example, an autoimmune
20 disease or a graft-related disease. The immune disease can also be selected from the group consisting of selected from the group consisting of Addison's disease, allergies, ankylosing spondylitis, asthma, atherosclerosis, autoimmune diseases of the ear, autoimmune diseases of the eye, autoimmune hepatitis, autoimmune parotitis, colitis, coronary heart disease, Crohn's disease, diabetes, including Type 1 and/or Type 2 diabetes, epididymitis, glomerulonephritis,
25 Graves' disease, Guillain-Barre syndrome, Hashimoto's disease, hemolytic anemia, idiopathic thrombocytopenic purpura, inflammatory bowel disease, immune response to recombinant drug products, systemic lupus erythematosus, male infertility, multiple sclerosis, myasthenia gravis, pemphigus, psoriasis, rheumatic fever, rheumatoid arthritis, sarcoidosis, scleroderma, Sjogren's syndrome, spondyloarthropathies, thyroiditis, transplant rejection, vasculitis, AIDS,
30 atopic allergy, bronchial asthma, eczema, leprosy, schizophrenia, inherited depression, transplantation of tissues and organs, chronic fatigue syndrome, Alzheimer's disease,

Parkinson's disease, myocardial infarction, stroke, autism, epilepsy, Arthus's phenomenon, anaphylaxis, alcohol addiction, and drug addiction.

BRIEF DESCRIPTION OF THE FIGURES

5 The patent or application file contains at least one drawing executed in color. Copies of this patent or patent application publication with color drawing(s) will be provided by the Office upon request and payment of the necessary fee.

10 FIG. 1 depicts the binding modes of two different co-crystal structures of human CD40 (SEQ ID NO: 1), one with the dAb BMS3h-56-5 (SEQ ID NO: 321) and one with the Fab' of Chi220 antibody. The BMS3h-56-5 and Chi 220 Fab' molecules are shown as cartoons with β -strands (represented as arrows in the dAb) and non-repetitive secondary structure (represented as loops in th dAb). Complementarity-determining regions (CDRs) are also shown. CD40 is also shown as a cartoon with the BMS3h-56-5 epitope residues of human CD40. The Chi220 epitope residues are also shown. Disulfide bonds are also shown. The N-terminus (N) and C-terminus (C) of CD40 are labeled.

15 FIG. 2 depicts a space filling model of BMS3h-56-5 (SEQ ID NO: 321) contacting human CD40 (SEQ ID NO: 1), which is shown as a cartoon. Surface residues of the dAb BMS3h-56-5 that contact CD40 are shown. The BMS3h-56-5 CDR3 region and FR-2 residues Leu45, Arg47, Arg56 and Phe99 are labeled. Kabat numbering (Kabat et al., *Sequences of Immunological Interest*, 5th ed., U.S. Dept. Health & Human Services, Washington, D.C. (1991)) is used in this diagram and differs from sequential numbering in that insertion residues are used to keep the residue numbering of the β -strands identical. Thus for BMS3h-56-5, sequential residue 53 becomes residue 52A, sequential residues 84, 85, and 86 become, respectively, 82A, 82B, 82C and Kabat residue number 100 is missing (it would be between sequential residues 103 and 104); CD40 is also represented as a cartoon with non-repetitive secondary structure and the BMS3h-56-5 epitope. CD40 residues that differ between human and *Macaca fascicularis* (cynomolgus monkey), Ala115, Phe99, Ser126, His162, Leu121, and Trp109, are shown in stick representation. CD40 residues that differ between human and cynomolgus monkey that are part of the BMS3h-56-5 epitope are Trp109, Leu121, and His162.

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CD40 residues Trp109 and Leu121 lie in a cleft between the BMS3h-56-5 CDR3 and FR-2. Mutation of Trp109 either greatly reduces or ablates BMS3h-56-5 activity.

FIG. 3 depicts binding of a PEGylated anti-human CD40 dAb, BMS3h38-2C-P40Br, on blood samples from human and primate species. FIG. 3A shows BMS3h38-2C-P40Br binding to human and cynomolgus B cells; FIG. 3B shows BMS3h38-2C-P40Br binding to human, rhesus, and chimp B cells.

FIG. 4, FIG. 5, FIG. 6, and FIG. 7 show ClustalW2 alignments of representative domain antibody polypeptides from lineages BMS3h-56, BMS3h-37, BMS3h-38, and BMS3h-198, respectively.

10 DETAILED DESCRIPTION

Antibody polypeptides that specifically bind to human CD40 are provided. The antibody polypeptides do not exhibit CD40 agonist activity, and the antibody polypeptides are useful in the treatment of diseases involving CD40 activation, such as autoimmune diseases. The antibody polypeptides may be selected using a primary screen that utilizes cell binding assays, followed by one or more rounds of error-prone or degenerate oligonucleotide-directed affinity maturation. As a result, a genus of antibody polypeptides that specifically bind a single CD40 epitope are provided.

A "lineage" is a set of related antibody polypeptides that were prepared from a common precursor by error-prone or degenerate oligonucleotide-directed affinity maturation, as disclosed in the examples below, and that are expected to bind the same CD40 epitope. The nomenclature of the antibody polypeptides is used to designate the various lineages. The nomenclature "BMS3h-56," for example, refers to antibody polypeptides of lineage 56, which were raised against human CD40. "Lineage BMS3h-56" antibody polypeptides include BMS3h-56-1 through BMS3h-56-33, and BMS3h-56-202 through BMS3h-56-288.

Accordingly, in one aspect, an antibody polypeptide comprises a variable domain that specifically binds human CD40, where the antibody polypeptide competes with the binding of any one of the domain antibodies (dAbs) listed in TABLE 3. For example, the dAb may belong to a lineage selected from the group consisting of BMS3h-37, BMS3h-38, BMS3h-41, BMS3h-43, BMS3h-56, BMS3h-131, BMS3h-198, and BMS3h-202, such as the dAb BMS3h-56-5, BMS3h-56-201, or BMS3h-56-258, for instance. In another aspect, an antibody

polypeptide specifically binds the same human CD40 epitope as any one of the dAbs listed in TABLE 3. For example, the antibody polypeptide may comprise a variable domain that specifically binds the same human CD40 epitope as the dAb BMS3h-56-5, BMS3h-56-201, or BMS3h-56-258, for instance. As disclosed below, the human CD40 epitope may comprise amino acid residue Trp109 of SEQ ID NO: 1, for example.

The antibody polypeptides may be domain antibodies containing a single variable domain. The antibody polypeptides also may comprise additional domains, such as an Fc domain. For instance, the antibody polypeptide may comprise a second variable domain that specifically binds human serum albumin (HSA). Such dual specific antibody polypeptides may have an increased half-life, for example.

In the Sequence Listing, SEQ ID NO: 1 is the amino acid sequence of human CD40; SEQ ID NO: 2 is the amino acid sequence of *Macaca fascicularis* CD40. The amino acid sequence of the domain antibody BMS3h-56-5 is SEQ ID NO: 321.

As used herein, "specific binding" refers to the binding of an antigen by an antibody polypeptide with a dissociation constant (K_d) of about 1 μ M or lower as measured, for example, by surface plasmon resonance. Suitable assay systems include the BIAcoreTM surface plasmon resonance system and BIAcoreTM kinetic evaluation software (e.g., version 2.1). The affinity or K_d for a specific binding interaction may be about 500 nM or lower or about 300 nM or lower.

The term "about" will be understood by persons of ordinary skill in the art and will vary to some extent on the context in which it is used. Generally, about encompasses a range of values that are plus/minus 10% of a referenced value.

In accordance with this detailed description, the following abbreviations and definitions apply. It must be noted that as used herein, 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 dosage" includes reference to one or more dosages and equivalents thereof known to those skilled in the art, and so forth.

1. CD40 and CD40 Activities

Antibody polypeptides are provided that bind human CD40. CD40 is also known as B-cell surface antigen CD40, Bp50, CD40L receptor, CDw40, CDW40, MGC9013, p50, TNFRSF5, and Tumor necrosis factor receptor superfamily member 5. Relevant structural
5 information for human CD40 can be found, for example, at UniProt Accession Numbers P25942, Q9BYU0, and Q53GN5. "Human CD40" refers to the CD40 comprising the following amino acid sequence:

10 MVRLPLQCVL WGCLLTAVHP EPPTACREKQ YLINSQCCSL CQPGQKLVSD
CTEFTETECL PCGESEFLDT WNRETHCHQH KYCDPNLGLR VQQKGTSETD
TICTCEEGWH CTSEACESCV LHRSCSPGFG VKQIATGVSD TICEPCPVGF
FSNVSSAFEK CHPWTSCETK DLVVQQAGTN KTDVVCGPQD RLRALVVIPI
IFGILFAILL VLVFIKKVAK KPTNKAPHPK QEPQEINFPD DLPGSNTAAP
VQETLHGCQP VTQEDGKESR ISVQERQ (SEQ ID NO: 1).

CD40 also has been sequenced in *Mus musculus*, *Sus scrofa*, *Bos taurus*, *Gallus gallus*, *Canis
15 familiaris*, *Macaca fascicularis* (cynomolgus monkey), *Ovis aries*, *Equus caballus*, and *Rattus norvegicus*.

Binding of the present antibody polypeptides to CD40 antagonizes CD40 activity. "CD40 activities" include, but are not limited to, T cell activation (e.g., induction of T cell proliferation or cytokine secretion), macrophage activation (e.g., the induction of reactive
20 oxygen species and nitric oxide in the macrophage), and B cell activation (e.g., B cell proliferation, antibody isotype switching, or differentiation to plasma cells). CD40 activities can be mediated by interaction with other molecules. "CD40 activities" include the functional interaction between CD40 and the following molecules, which are identified by their Uniprot Accession Number in parentheses:

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CALR	(P27797);
ERP44	(Q9BS26);
FBL	(P22087);
POLR2H	(P52434);
RFC5	(P40937);
SGK1	(O00141);

SLC30A7 (Q8NEW0);
 SLC39A7 (Q92504);
 TRAF2 (Q5T1L5);
 TRAF3 (Q13114);
 5 TRAF6 (Q9Y4K3);
 TXN (Q5T937);
 UGGT1 (Q9NYU2); and
 USP15 (Q9Y4E8).

10 For example, a CD40 "activity" includes an interaction with TRAF2. CD40/TRAF2 interaction activates NF- κ B and JNK. See Davies et al., *Mol. Cell Biol.* 25: 9806-19 (2005). This CD40 activity thus can be determined by CD40-dependent cellular NF- κ B and JNK activation, relative to a reference.

As used herein, the terms "activate," "activates," and "activated" refer to an increase in
 15 a given measurable CD40 activity by at least 10% relative to a reference, for example, at least 10%, 25%, 50%, 75%, or even 100%, or more. A CD40 activity is "antagonized" if the activity is reduced by at least 10%, and in an exemplary embodiment, at least about 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, 97%, or even 100% (i.e., no detectable activity), relative to the absence of the antagonist. For example, an antibody polypeptide may
 20 antagonize some or all CD40 activity, while not activating CD40. In one embodiment, the antibody polypeptide does not activate B cell proliferation. In another embodiment, the antibody polypeptide does not activate cytokine secretion by T cells, where the cytokine is at least one cytokine selected from the group consisting of IL-2, IL-6, IL-10, IL-13, TNF- α , IFN- γ .

25 2. The CD40 Epitope

X-ray crystallography of a complex between human CD40 (SEQ ID NO: 1) and the dAb BMS3h-56-5 (SEQ ID NO: 321) was used to reveal an epitope recognized by the antibody polypeptides of the disclosure. Structural models of CD40 and BMS3h-56-5 were fitted to electron density data to yield seven models or versions of the CD40/BMS3h-56-5 complex,
 30 which come from three crystallographically independent complexes in one crystal form and four crystallographically independent complexes in a second crystal form. The versions have real space correlation coefficients of about 0.92 for main-chain atoms and 0.80 for side-chain atoms. The CD40 molecule has a certain amount of flexibility in the seven versions, but the

overall nature of the CD40/BMS3h-56-5 interaction is retained in all versions. The versions differ in the interaction between the CD40 residue Trp109 and BMS3h-56-5 Trp103 (Kabat Numbering, *see below*). BMS3h-56-5 Trp103 forms an edge-to-face interaction with CD40 Trp109 in one version, while forming a displaced stacking (*i.e.*, face-to-face) interaction in other versions.

The shape complementarity statistic, Sc , for the seven versions ranges from 0.70 – 0.77, which shows a higher degree of shape complementarity than for typical antibody/antigen complexes. For example, these values compare to ranges of 0.71 – 0.76 for four protease/protein inhibitor complexes, 0.70 – 0.74 for five oligomeric interfaces, and 0.64 – 0.68 for six antibody/antigen complexes. *See* Lawrence *et al.*, "Shape Complementarity at Protein/Protein Interfaces," *J. Mol. Biol.* 234: 946-950 (1993).

A model of the human CD40/BMS3H-56-5 complex is shown in FIG. 1. One BMS3h-56-5 dAb binds to one CD40 molecule. The BMS3h-56-5 epitope does not overlap the Chi220 Fab' fragment epitope. All versions of the complex define a set of CD40 residues that contact BMS3h-56-5: Trp109, Leu121, His122, Ser124, Ser156, Ala157, Phe158, Glu159, and His162 (with reference to SEQ ID NO: 1). CD40 residues that contact BMS3h-56-5 in some versions of the complex are Pro85, Asn86, Leu87, Gly88, Glu106, Glu107, Gly108, His110, Thr112, Cys119, Val120, Gln133, Ile134, Ala135, Thr136, Ser155, and Lys160. Val154 is a buried CD40 residue in all versions. Other CD40 residues buried in some versions are Ser118, Arg123, Thr141, Phe151, Asp153, Cys161, and Pro163.

As used herein, the term "in contact" refers to an interatomic distance whose maximum is determined by an atom type distance dependency as defined by Sheriff *et al.*, *J. Mol. Biol.* 197: 273-296 (1987) and Sheriff, *Immunomethods* 3: 191-196 (1993).

As used herein, the term "buried" refers to a residue that has a least one atom with surface area defined by the program MS (Connolly, *J. Appl. Crystallogr.* 16: 548-558 (1983)), a probe sphere of 1.7Å, and atom type dependent Van der Waals radii as defined by Sheriff, *Immunomethods* 3: 191-196 (1993).

FIG. 2 shows the surface of BMS3h-56-5 (SEQ ID NO: 321) including contacting residues and buried residues. CD40 (SEQ ID NO: 1) is represented as a ribbon diagram with orange representing non-repetitive secondary structure and magenta representing the epitope

residues. CD40 residues Trp109, Ala115, Leu121, Ser126, and His162, which are shown, differ in various non-human primate sequences. CD40 residues Ala115 and Ser126 are on the opposite side of the BMS3h-56-5 binding site. Trp109 and Leu121 bind in a cleft that lies between CDR3 and FR-2 (residues Leu45 and Arg47) of BMS3h-56-5. His162 interacts with residues in CDR2 of BMS3h-56-5, especially Lys 56. In summary, the CD40 epitope comprises one or more residues listed in TABLE 1, with reference to the numbering used in SEQ ID NO: 1.

TABLE 1

CD40 residues contacting BMS3h-56-5:
Trp109, Leu121, His122, Ser124, Ser156, Ala157, Phe158, Glu159, His162

BMS3h-56-5, like the other dAbs listed in TABLE 3, was prepared by a screening and affinity maturation method described in more detail below, using human CD40 as the antigen. It is expected that dAbs created by affinity maturation from a common precursor dAb will bind the same human CD40 epitope. Competition studies described below, for example, indicate that dAbs generated from a common precursor dAb by affinity maturation compete for binding with each other to human CD40. The same competition studies, however, show that the dAbs do not compete with at least the Chi220 or G28-5 antibodies.

3. Antibody Polypeptides

The antibody polypeptides comprise a variable domain. In one embodiment, the antibody polypeptides are in the form of a dAb that contains a single variable domain. Antibody polypeptides may be full-length anti-CD40 immunoglobulin molecules comprising two heavy (H) chains and two light (L) chains interconnected by disulfide bonds. In this embodiment, the amino terminal portion of each chain includes a variable domain (V_L or V_H) of about 100-110 amino acids primarily responsible for antigen recognition via the complementarity determining regions (CDRs) contained therein. The carboxy-terminal "half" of each heavy chain defines a constant region (Fc) primarily responsible for effector function.

Antibody polypeptides also may be "fragments" comprising a portion of the full-length anti-CD40 immunoglobulin molecule that comprises a variable domain that specifically binds CD40. Thus, the term "antibody polypeptides" includes an antigen-binding heavy chain, light chain, heavy chain-light chain dimer, Fab fragment, F(ab')₂ fragment, Fv fragment, single chain Fv (scFv), and dAb, for example. The term "antibody polypeptides" thus includes polypeptides made by recombinant engineering and expression, as well as monoclonal antibodies produced by natural recombination and secretion by hybridoma cell clones.

Light chains are classified as kappa (κ) or lambda (λ), and are characterized by a particular constant region, C_L, as known in the art. Heavy chains are classified as γ , μ , α , δ , or ϵ , and define the isotype of an antibody as IgG, IgM, IgA, IgD, or IgE, respectively. The heavy chain constant region is comprised of three domains (CH1, CH2, and CH3) for IgG, IgD, and IgA; and four domains (CH1, CH2, CH3, and CH4) for IgM and IgE. Anti-CD40 antibodies may have a heavy chain constant region selected from any of the immunoglobulin classes (IgA, IgD, IgG, IgM, and IgE).

Each light chain variable domain (V_L) and heavy chain variable domain (V_H) is composed of three CDRs and four framework regions (FRs), arranged from amino-terminus to carboxy-terminus in the following order: FR1, CDR1, FR2, CDR2, FR3, CDR3, FR4. The three CDRs of the light chain are referred to as "LCDR1, LCDR2, and LCDR3" and the three CDRs of the heavy chain are referred to as "HCDR1, HCDR2, and HCDR3."

As used herein, the term "Fc domain" refers to the constant region antibody sequences comprising CH2 and CH3 constant domains as delimited according to Kabat et al., *Sequences of Immunological Interest*, 5th ed., U.S. Dept. Health & Human Services, Washington, D.C. (1991). The Fc region may be derived from an IgG1 or an IgG4 Fc region, for example. A variable domain may be fused to an Fc domain. In this case, the carboxyl terminus of the variable domain (either a V_L or V_H domain, including dAbs) may be linked or fused to the amino terminus of the Fc CH2 domain. Alternatively, the carboxyl terminus of the variable domain may be linked or fused to the amino terminus of a CH1 domain, which itself is fused to the Fc CH2 domain. The protein may comprise the hinge region between the CH1 and CH2 domains in whole or in part.

The CDRs contain most of the residues that form specific interactions with the antigen. As shown in FIG. 2, for example, CDR2 and CDR3, plus FR4 residue Trp103, form most of the contacts between CD40 and the dAb BMS3h-56-5. For example, the variable domain of an antibody polypeptide comprises CDR1, CDR2, and CDR3 regions that have the same amino acid sequence as the CDR1, CDR2, and CDR3 regions of one of the dAbs listed in TABLE 3 or that each differ from the CDR1, CDR2, and CDR3 regions by one or two amino acids. For example, the antibody polypeptide may comprise CDR1, CDR2, and CDR3 regions that have the same amino acid sequence as the CDR1, CDR2, and CDR3 regions of BMS3h-56-5, BMS3h-56-258, or BMS3h-56-201, for example.

A "domain antibody" (dAb) comprises a single variable (V_L or V_H) domain that is capable of specifically and monovalently binding an antigen, such as CD40. For example, a dAb may have a V_{HH} structure, characteristic of a camelid dAb. A " V_H domain" as used herein is meant to include a V_{HH} structure. In another embodiment, the V_H domains of the present invention (including all features and combination of features presented as embodiments herein) are other than V_{HH} domains. dAbs may form homo- or heterodimers in solution. Bivalent anti-CD40 antibodies are believed to exhibit agonist activity because of the ability to cross-link bound CD40 molecules on the cell surface. While not limited by any particular theory, it is believed that monovalent dAbs do not activate CD40, because the dAbs do not cross-link CD40.

As used herein, the term "variable domain" refers to immunoglobulin variable domains defined by Kabat et al., *Sequences of Immunological Interest*, 5th ed., U.S. Dept. Health & Human Services, Washington, D.C. (1991). The numbering and positioning of CDR amino acid residues within the variable domains is in accordance with the well-known Kabat numbering convention. For example, the Kabat numbering for BMS3h-56-5 (SEQ ID NO: 321) is compared in TABLE 2 to the same sequence numbered sequentially. In the Kabat numbering, BMS3h-56-5 has insertion residues 52A, 82A, 82B, 82C, and is missing residue 100. In both numbering systems, the Ser and Thr at the N-terminus that are part of the expression construct are given negative numbers.

TABLE 2

[illegible]

The term “human,” when applied to antibody polypeptides, means that the antibody polypeptide has a sequence, e.g., FR and/or CH domains, derived from a human immunoglobulin. A sequence is “derived from” a human immunoglobulin coding sequence when the sequence is either: (a) isolated from a human individual or from a cell or cell line from a human individual; (b) isolated from a library of cloned human antibody gene sequences or of human antibody variable domain sequences; or (c) diversified by mutation and selection from one or more of the polypeptides above. An “isolated” compound as used herein means that the compound is removed from at least one component with which the compound is naturally associated with in nature.

Antibody polypeptides can be administered to human patients while largely avoiding the anti-antibody immune response often provoked by the administration of antibodies from other species, e.g., mouse. For example, murine antibodies can be “humanized” by grafting murine CDRs onto a human variable domain FR, according to procedures well known in the

art. Human antibodies as disclosed herein, however, can be produced without the need for genetic manipulation of a murine antibody sequence.

Variable domains may comprise one or more framework regions (FR) with the same amino acid sequence as a corresponding framework region encoded by a human germline antibody gene segment. For example, a domain antibody may comprise the V_H germline gene segments DP47, DP45, or DP38, the V_K germline gene segment DPK9, the J_H segment JH4b, or the J_K segment J_K1.

Changes may be made to antibody polypeptide sequences while retaining the ability to bind CD40 specifically. Specifically, the antibody polypeptides (e.g., a dAb) may comprise a variant variable domain that retains the function of specifically binding the same CD40 epitope as the dAb BMS3h-56-5. See TABLE 1. That is, the variant variable domain may bind a human CD40 epitope comprising at least one of Trp109, Leu121, His122, Ser124, Ser156, Ala157, Phe158, Glu159, and His162 of SEQ ID NO: 1. In one embodiment, the variant variable domain epitope may comprise Trp109, Leu121, His122, Ser124, Ser156, Ala157, Phe158, Glu159, and His162. Alternatively, the variant variable domain may specifically bind a CD40 epitope comprising CD40 residue Trp109. In yet another embodiment, the variant variable domain may compete with BMS3h-56-5 for specific binding to CD40. Error-prone affinity maturation, as disclosed in the examples below, provides one exemplary method for making and identifying antibody polypeptides with variant sequences that specifically bind the same CD40 epitope.

For example, a variant variable domain may differ from one of the variable domains listed in TABLE 3 by up to 10 amino acids or any integral value between, where the variant variable domain specifically binds CD40. Alternatively, the variant variable domain may have at least 90% sequence identity (e.g., at least 92%, 95%, or 98% sequence identity) relative to a sequence listed in the present Sequence Listing. Non-identical amino acid residues or amino acids that differ between two sequences may represent amino acid substitutions, additions, or deletions. Residues that differ between two sequences appear as non-identical positions, when the two sequences are aligned by any appropriate amino acid sequence alignment algorithm, such as BLAST.

It is provided that amino acid substitutions may be made to individual FR regions, such that one or more FR comprises up to two amino acid differences relative to the amino acid sequence of the corresponding FR encoded by a human germline antibody gene segment. It is further provided that the variant variable domain may contain one or two amino acid substitutions in one or more CDR. Representative variable domains that specifically bind CD40 are listed in TABLE 3.

ClustalW2 alignments between representative variable domains of antibody polypeptides from lineages BMS3h-56, BMS3h-37, BMS3h-38, and BMS3h-198 are shown in FIG. 4, FIG. 5, FIG. 6, and FIG. 7, respectively. As a general rule, the degree to which an amino acid is conserved in an alignment of related protein sequences is proportional to the relative importance of the amino acid position to the function of the protein. That is, amino acids that are common in all related sequences likely play an important role and cannot be easily substituted. On the other hand, positions that vary between the sequences likely can be substituted with other amino acids or otherwise modified, while maintaining the activity of the protein. The alignments shown in FIG. 4, FIG. 5, FIG. 6, and FIG. 7 and the structural relationships ascertained from FIG. 1 and FIG. 2, for example, can guide the construction of variant antibody polypeptides that specifically bind an epitope of human CD40 comprising the amino acid sequence of SEQ ID NO: 1, wherein the antibody polypeptide competes with the binding of dAb BMS3h-56-201 (SEQ ID NO: 9). Such variant antibody polypeptides include, but are not limited to, those with an amino acid modification corresponding to a substitution, insertion, or deletion with reference to any of the variable domains listed in TABLE 3. Variant antibody polypeptides also include those with an amino acid modification corresponding to an amino acid modification conserved between the sequences listed in TABLE 3.

The information regarding the boundaries of the V_L or V_H domains of heavy and light chain genes may be used to design PCR primers to amplify the variable domain from a cloned heavy or light chain coding sequence encoding an antibody polypeptide known to bind CD40. The amplified variable domain may be inserted into a suitable expression vector, e.g., pHEN-1 (Hoogenboom et al. (1991) *Nucleic Acids Res.* 19:4133-4137) and expressed, either alone or as a fusion with another polypeptide sequence, using techniques well known in the art. Based on the disclosed amino acid and polynucleotide sequences, the fusion protein can be produced and purified using only ordinary skill in any suitable mammalian host cell line, such as CHO, 293,

COS, NSO, and the like, followed by purification using one or a combination of methods, including protein A affinity chromatography, ion exchange, reverse phase techniques, or the like.

5 In one aspect, the antibody polypeptide is a "dual specific" antibody polypeptide comprising a first variable domain that specifically binds human CD40 comprising the amino acid sequence of SEQ ID NO: 1. Dual specific antibody polypeptides comprise a second variable domain that specifically binds a second antigen that is other than human CD40.

10 In another embodiment, the second antigen may be a cell surface molecule of an immune effector cell or a soluble molecule such as a cytokine, for example. Binding of the dual specificity antibody polypeptide could be used to antagonize CD40 and antagonize a biological activity of the second antigen. Cell surface molecules of immune effector cells include the cluster of differentiation (CD) molecules. Representative CD markers are listed on the Internet at [hypertext transfer protocol en.wikipedia.org/wiki/List_of_human_clusters_of](http://hypertexttransferprotocol.en.wikipedia.org/wiki/List_of_human_clusters_of_differentiation)
15 [_differentiation](http://hypertexttransferprotocol.en.wikipedia.org/wiki/List_of_human_clusters_of_differentiation) (last modified on February 22, 2012). Cell surface molecules of immune effector cells also include Major Histocompatibility Complex (MHC) Class II molecules. Antibodies against these cell surface molecules are known in the art and can be used as a source of a variable domain to construct a dual specific antibody polypeptide.

In one embodiment, antibody polypeptides of a dual specific ligand may be linked by an "amino acid linker" or "linker." For example, a dAb may be fused to the N-terminus of an amino acid linker, and another dAb may be fused to the C-terminus of the linker. Although
20 amino acid linkers can be any length and consist of any combination of amino acids, the linker length may be relatively short (e.g., five or fewer amino acids) to reduce interactions between the linked domains. The amino acid composition of the linker also may be adjusted to reduce the number of amino acids with bulky side chains or amino acids likely to introduce secondary
25 structure. Suitable amino acid linkers include, but are not limited to, those up to 3, 4, 5, 6, 7, 10, 15, 20, or 25 amino acids in length. Representative amino acid linker sequences include (GGGGS)_n (SEQ ID NO: 4), where n may be any integer between 1 and 5. Other suitable linker sequences may be selected from the group consisting of AST (SEQ ID NO: 5), TVAAPS (SEQ ID NO: 6), TVA (SEQ ID NO: 7), and ASTSGPS (SEQ ID NO: 8).

The binding of the second antigen can increase the *in vivo* half-life of the antibody polypeptide. For example, the second variable domain of the dual specific antibody polypeptide may specifically bind serum albumin (SA), e.g., human serum albumin (HSA). The antibody polypeptide formatted to bind HSA can have an increased *in vivo* t- α ("alpha half-life") or t- β ("beta half-life") half-life relative to the same unformatted antibody polypeptide. The t- α and t- β half-lives measure how quickly a substance is distributed in and eliminated from the body. The linkage to HSA may be accomplished by fusion of the antibody polypeptide with a second variable domain capable of specifically binding HSA, for example. Anti-human serum albumin antibodies are well-known in the art. *See, e.g.,* Abcam®, Human Serum Albumin antibodies ab10241, ab2406, and ab8940, available on the Internet at hypertext transfer protocol www.abcam.com/index.html, or GenWay, ALB antibody, available on the Internet at hypertext transfer protocol www.genwaybio.com. Variable domains that specifically bind HSA can be obtained from any of these antibodies, and then fused to an antibody polypeptide of the disclosure using recombinant techniques that are well known in the art.

Alternatively, the linking of the antibody polypeptide to HSA can be accomplished by directly fusing the antibody polypeptide sequence to an HSA coding sequence using techniques well known to the skilled artisan. The HSA coding sequences can be obtained by PCR using primers derived from the cDNA sequence available at GenBank Accession No. NM000477, for example.

In one embodiment, the t- α -half-life of the HSA-linked domain antibody composition is increased by 10% or more. In another embodiment, the t- α -half-life of the HSA-linked domain antibody composition is in the range of 0.25 hours to 6 hours. In another embodiment, the t- β -half-life of the HSA-linked domain antibody composition is increased by 10% or more. In another embodiment, the t- β -half-life of the HSA-linked domain antibody composition is in the range of 12 to 48 hours.

In another embodiment, an antibody polypeptide may be formatted to increase its *in vivo* half-life by PEGylation. In one embodiment, the PEG is covalently linked. In another embodiment, the PEG is linked to the antibody polypeptide at a cysteine or lysine residue. In yet another embodiment, the PEG-linked antibody polypeptide has a hydrodynamic size of at

least 24 kD. In yet another embodiment, the total PEG size is from 20 to 60 kD, inclusive. In yet another embodiment, the PEG-linked domain antibody has a hydrodynamic size of at least 200 kD.

PEGylation can be achieved using several PEG attachment moieties including, but not limited to N-hydroxysuccinimide active ester, succinimidyl propionate, maleimide, vinyl sulfone, or thiol. A PEG polymer can be linked to an antibody polypeptide at either a predetermined position, or can be randomly linked to the domain antibody molecule.

PEGylation can also be mediated through a peptide linker attached to a domain antibody. That is, the PEG moiety can be attached to a peptide linker fused to an antibody polypeptide, where the linker provides the site (e.g., a free cysteine or lysine) for PEG attachment. Methods of PEGylating antibodies are well known in the art, as disclosed in Chapman, et al., "PEGylated antibodies and antibody fragments for improved therapy: a review," *Adv. Drug Deliv. Rev.* 54(4):531-45 (2002), for example.

Antibody polypeptides also may be designed to form a dimer, trimer, tetramer, or other multimer. Antibody polypeptides, e.g., dAbs, can be linked to form a multimer by several methods known in the art, including, but not limited to, expression of monomers as a fusion protein, linkage of two or more monomers via a peptide linker between monomers, or by chemically joining monomers after translation, either to each other directly, or through a linker by disulfide bonds, or by linkage to a di-, tri- or multivalent linking moiety (e.g., a multi-arm PEG). In one embodiment, the multimer can bind a single molecule of CD40.

4. Pharmaceutical Compositions and Methods of Treatment

A pharmaceutical composition comprises a therapeutically-effective amount of one or more antibody polypeptides and optionally a pharmaceutically acceptable carrier.

Pharmaceutically acceptable carriers include, for example, water, saline, phosphate buffered saline, dextrose, glycerol, ethanol and the like, as well as combinations thereof.

Pharmaceutically acceptable carriers can further comprise minor amounts of auxiliary substances, such as wetting or emulsifying agents, preservatives, or buffers that enhance the shelf-life or effectiveness of the fusion protein. The compositions can be formulated to provide quick, sustained, or delayed release of the active ingredient(s) after administration.

Suitable pharmaceutical compositions and processes for preparing them are well known in the art. *See, e.g.,* Remington, THE SCIENCE AND PRACTICE OF PHARMACY, A. Gennaro, et al., eds., 21st ed., Mack Publishing Co. (2005).

The pharmaceutical composition further may comprise an immuno-
5 suppressive/immunomodulatory and/or anti-inflammatory agent. A method of treating an immune disease in a patient in need of such treatment may comprise administering to the patient a therapeutically effective amount of the pharmaceutical composition. Antagonizing CD40-mediated T cell activation could inhibit undesired T cell responses occurring during autoimmunity, transplant rejection, or allergic responses, for example. Inhibiting CD40-
10 mediated T cell activation could moderate the progression and/or severity of these diseases.

As used herein, a "patient" means an animal, e.g. mammal, including humans. The patient may be diagnosed with an immune disease. "Treatment" or "treat" or "treating" refers to the process involving alleviating the progression or severity of a symptom, disorder, condition, or disease. An "immune disease" refers to any disease associated with the
15 development of an immune reaction in an individual, including a cellular and/or a humoral immune reaction. Examples of immune diseases include, but are not limited to, inflammation, allergy, autoimmune disease, or graft-related disease. The autoimmune disease may be selected from the group consisting of systemic lupus erythematosus, multiple sclerosis, rheumatoid arthritis, diabetes, psoriasis, scleroderma, atherosclerosis, inflammatory bowel
20 disease, and ulcerative colitis.

Diseases that can be treated by administering the pharmaceutical composition may be selected from the group consisting of Addison's disease, allergies, ankylosing spondylitis, asthma, atherosclerosis, autoimmune diseases of the ear, autoimmune diseases of the eye, autoimmune hepatitis, autoimmune parotitis, colitis, coronary heart disease, Crohn's disease,
25 diabetes, including Type 1 and/or Type 2 diabetes, epididymitis, glomerulonephritis, Graves' disease, Guillain-Barre syndrome, Hashimoto's disease, hemolytic anemia, idiopathic thrombocytopenic purpura, inflammatory bowel disease, immune response to recombinant drug products (e.g., Factor VII in hemophiliacs), systemic lupus erythematosus, male infertility, multiple sclerosis, myasthenia gravis, pemphigus, psoriasis, rheumatic fever,
30 rheumatoid arthritis, sarcoidosis, scleroderma, Sjogren's syndrome, spondyloarthropathies,

thyroiditis, transplant rejection, and vasculitis. Autoimmune-mediated conditions include, but are not limited to, conditions in which the tissue affected is the primary target, and in some cases, the secondary target. Such conditions include, but are not limited to, AIDS, atopic allergy, bronchial asthma, eczema, leprosy, schizophrenia, inherited depression, transplantation of tissues and organs, chronic fatigue syndrome, Alzheimer's disease, Parkinson's disease, myocardial infarction, stroke, autism, epilepsy, Arthus' phenomenon, anaphylaxis, alcohol addiction, and drug addiction.

The pharmaceutical composition may be administered alone or in combination therapy, (i.e., simultaneously or sequentially) with an immunosuppressive/immunomodulatory and/or anti-inflammatory agent. Different immune diseases can require use of specific auxiliary compounds useful for treating immune diseases, which can be determined on a patient-to-patient basis. For example, the pharmaceutical composition may be administered in combination with one or more suitable adjuvants, e.g., cytokines (IL-10 and IL-13, for example) or other immune stimulators, e.g., chemokines, tumor-associated antigens, and peptides. Suitable adjuvants are known in the art.

Any suitable method or route can be used to administer the antibody polypeptide or the pharmaceutical composition. Routes of administration include, for example, oral, intravenous, intraperitoneal, subcutaneous, or intramuscular administration. A therapeutically effective dose of administered antibody polypeptide(s) depends on numerous factors, including, for example, the type and severity of the immune disease being treated, the use of combination therapy, the route of administration of the antibody polypeptide(s) or pharmaceutical composition, and the weight of the patient. A non-limiting range for a therapeutically effective amount of a domain antibody is 0.1-20 mg/kg, and in an aspect, 1-10 mg/kg, relative to the body weight of the patient. The dose of antibody polypeptide(s) can be further guided by the amount of antibody polypeptide(s) required for CD40 antagonism in *in vitro* and/or *in vivo* models of disease states. Representative models are described below and in the examples.

5. *In Vitro* and *In Vivo* Models

The ability of antibody polypeptides of the disclosure to antagonize CD40 can be tested in one of several available *in vitro* or *in vivo* model systems. Appropriate animal and cell model systems are described below. Further cell assay systems are described in the examples.

5.1. Inflammatory Bowel Disease (IBD) Models:

IBD is a multifactorial immune disorder of uncertain etiology. Several mouse models of mucosal inflammation that resemble IBD have provided insight into the mechanisms governing both normal and pathological mucosal immune function. IBD models include using the mucosal immunity and inflammation system of De Winter et al., *Am. J. Physiol.* 276: G1317-1321 (1999). In one aspect, the injection into immunodeficient mice of a subset of CD4(+) T lymphocytes, the CD4(+)CD45RB^{high} cells, leads to inflammation of the intestine. Pathogenesis is due in part to the secretion of proinflammatory cytokines. The induction of colitis can be prevented by co-transfer of another CD4(+) subpopulation, the CD4(+)CD45RB^{low} T cells. This population behaves analogously to the CD4(+)CD45RB^{high} population in terms of the acquisition of activation markers and homing to the host intestine. However, their lymphokine profile when activated is different, and anti-inflammatory cytokines secreted and/or induced by CD4(+)CD45RB^{low} T cells prevent colitis. De Winter et al. provide a description of the adoptive transfer model and the factors that promote and prevent colitis pathogenesis.

5.2. Spontaneous Arthritis Models:

A model of organ-specific disease provoked by systemic autoimmunity is provided by Kouskoff et al., *Cell* 87: 811-822 (1996). Rheumatoid arthritis (RA) is a chronic joint disease characterized by leukocyte invasion and synoviocyte activation followed by cartilage and bone destruction. Kouskoff et al. disclose a spontaneous mouse model of RA, generated by crossing a T cell receptor (TCR) transgenic line with the NOD strain. All offspring develop a joint disease highly reminiscent of RA in man. The trigger for the murine disorder is chance recognition of a NOD-derived major histocompatibility complex (MHC) class II molecule by the transgenic TCR; progression to arthritis involves CD4⁺ T, B, and probably myeloid cells.

5.3. Collagen Induced Arthritis (CIA) Model:

A mouse model of collagen-induced arthritis is provided by Brand et al., *Methods Mol. Med.* 102: 295-312 (2004). Collagen-induced arthritis (CIA) is an autoimmune disease that can be elicited in susceptible strains of rodents (rat and mouse) and non-human primates by immunization with type II collagen (CII), the major constituent protein of articular cartilage. After immunization, the animals develop an autoimmune polyarthritis that shares several clinical and histological features with RA. Susceptibility to CIA in rodents is linked to the class II molecules of the major histocompatibility complex (MHC), and the immune response to CII is characterized by both the stimulation of collagen-specific T cells and the production of high titers of antibody specific for both the immunogen (heterologous CII) and the autoantigen (mouse CII). Histologically, murine CIA is characterized by an intense synovitis that corresponds with the clinical onset of arthritis. This experimental data is useful evaluating CIA because of the pathological similarities between CIA and RA.

5.4. Antigen Induced T Cell Proliferation *In Vivo* Model:

The use of adoptive transfer of T cell receptor (TCR)-transgenic T cells provides an *in vivo* model for antigen-induced T-cell proliferation. Pape et al., *Immunol. Rev.* 156: 67-78 (1997) discloses adoptive transfer of TCR-transgenic T cells uniformly expressing an identifiable TCR of a known peptide/MHC specificity. The model can be used to monitor the *in vivo* behavior of antigen-specific T cells. Naive T cells are initially activated within T-cell zones of secondary lymphoid tissue to proliferate in a B7-dependent manner. If adjuvants or inflammatory cytokines are present during this period, enhanced numbers of T cells accumulate, migrate into B-cell-rich follicles, and acquire the capacity to produce IFN- γ and help B cells produce IgG2a. If inflammation is effectively antagonized, most of the initially activated antigen-specific T cells disappear without entering the follicles, and the survivors are poor producers of IL-2 and IFN- γ .

EXAMPLES

TABLE 3 lists representative anti-human CD40 variable domain amino acid sequences useful for the antibody polypeptides of the disclosure. TABLE 4 discloses representative nucleic acids that encode the variable domain sequences listed in TABLE 3. As is well known

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ANTIBODY POLYPEPTIDES THAT ANTAGONIZE CD40

TECHNICAL FIELD

Antibodies and fragments thereof that target CD40, and do not exhibit CD40 agonist activity, compositions comprising the same, and methods of using the same for treatment of diseases involving CD40 activity are provided.

SEQUENCE LISTING

The instant application contains a Sequence Listing in ASCII format and is hereby incorporated by reference in its entirety. Said ASCII copy, created on April 20, 2012, is named 200896WO.txt and is 1,188,533 bytes in size.

BACKGROUND

CD40 is a co-stimulatory molecule belonging to the tumor necrosis factor (TNF) receptor superfamily that is present on antigen presenting cells (APC), including dendritic cells, B cells, and macrophages. APCs are activated when CD40 binds its ligand, CD154 (CD40L), on T_H cells. CD40-mediated APC activation is involved in a variety of immune responses, including cytokine production, up-regulation of co-stimulatory molecules (such as CD86), and enhanced antigen presentation and B cell proliferation. CD40 can also be expressed by endothelial cells, smooth muscle cells, fibroblasts, and epithelial cells.

CD40 activation is also involved in a variety of undesired T cell responses related to autoimmunity, transplant rejection, or allergic responses, for example. One strategy for controlling undesirable T cell responses is to target CD40 with an antagonistic antibody. For example, monoclonal antibody HCD122 (Lucatumumab), formerly known as Chiron 1212, is currently in clinical trials for the treatment of certain CD40-mediated inflammatory diseases.

in the art, multiple codons can encode the same amino acid. Nucleic acids encoding a protein sequence thus include nucleic acids having codon degeneracy. The antibody polypeptides disclosed in TABLE 3 specifically bind CD40 and were made using the reiterative initial/primary screening and affinity maturation methodologies described in the examples that follow.

TABLE 3

Anti-Human CD40 Variable Domain Amino Acid Sequences

BMS3h-56-201

EVQLLES GGGGLVQP GGS LRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFYFQEWGQGT LVT VSS (SEQ ID NO: 9)

BMS3h-56-258

EVQLLES GGGGLVQP GGS LRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFYFHEWGQGT LVT VSS (SEQ ID NO: 10)

BMS3h-37

EVQLLES GGGGLVQP GGS LRLSCAASGFTFEWYEMQWVRQAPGKGLEWVSAISGDGYRTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKELGYFDYWGQGT LVT VSS (SEQ ID NO: 11)

BMS3h-38

EVQLLES GGGGLVQP GGS LRLSCAASGFTFEEEMIWVRQAPGKGLEWVSAISGSGGSTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPFRFDYWGQGT LVT VSS (SEQ ID NO: 12)

BMS3h-41

EVQLLES GGGGLVQP GGS LRLSCAASGFTFTEYEMIWVRQAPGKGLEWVSSISGNGANTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPLRFDYWGQGT LVT VSS (SEQ ID NO: 13)

BMS3h-43

EVQLLES GGGGLVQP GGS LRLSCTASGFTFNMYEMSWVRQAPGKGLEWVSGISRRGFTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPITYAMRYARFDYWGQGT LVT VSS (SEQ ID NO: 14)

BMS3h-56

EVQLLES GGGGLVQP GGS LRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFIFDYWGQGT LVT VSS (SEQ ID NO: 15)

BMS3h-106

EVQLLES GGGGLVQP GGS LRLSCAASGFTFSTYHMQWVRQAPGKGLEWVSMIDADGLGTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKPGPQFGQFDYWGQGT LVT VSS (SEQ ID NO: 16)

BMS3h-107

EVQLLES GGGGLVQP GGS LRLSCAASGFTFSGYDMQWVRQAPGKGLEWVSTISASGVFTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKYPNRFALNNFDYWGQGT LVT VSS (SEQ ID NO: 17)

BMS3h-131
 DIQMTQSPSSLSASVGDRVITITCRANSSILWALAWYQQKPGKAPKLLIESSSGLQSGVPSRFSGSGSGTDFTLTISSLQ
 PEDFATYYCVQNAGWPGTFGQGTKVEIKR (SEQ ID NO: 18)

5 BMS3h-193
 DIQMTQSPSSLSASVGDRVITITCRASQTIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGTDFTLTISSLQ
 PEDFATYYCHQYASPLTFGQGTKVEIKR (SEQ ID NO: 19)

10 BMS3h-198
 EVQLLES GGGGLVQPGGSLRLSCAASGFTFAGYEMWVRQAPGKGLERVS AISGSGGSTYYADSVKGRFTISRDDSKNTL
 YLQMNSLRAEDTAVYYCAKDPYSFDYWGQGT LVT VSS (SEQ ID NO: 20)

15 BMS3h-202
 EVQLLES GGGGLVQPGGSLRLSCAASGFTFPTAEMWVRQAPGKGLEWVSSISASGGSTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKEPVSYVATFDYWGQGT LVT VSS (SEQ ID NO: 21)

20 BMS3h-217
 DIQMTQSPSSLSASVGDRVITITCRASHFIGTLLSWYQQKPGKAPKLLITYGSL LQSGVPSRFSGSGSGTDFTLTISSLQ
 PEDFATYYCGQGVLPATFGQGTKVEIKR (SEQ ID NO: 22)

25 BMS3h-1
 EVQLLES GGGGLVQPGGSLRLSCAASGFTFPKNEMTWVRQAPGKGLEWVSAIESDGQATYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKNRIPDLVFDYWGQGT LVT VSS (SEQ ID NO: 23)

30 BMS3h-2
 EVQLLES GGGGLVQPGGSLRLSCAASGFTFDAGAMTWVRQAPGKGLEWVSSIDKEGLSTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKGRIPLVFDYWGQGT LVT VSS (SEQ ID NO: 24)

35 BMS3h-3
 EVQLLES GGGGLVQPGGSLRLSCAASGFTFGDAAMTWVRQAPGKGLEWVSAIQPMGDGTYADSVKGRFTVSRDN SKNTL
 YLQMNSLRAEDTAVYYCAKGRIPTLQFDYWGQGT LVT VSS (SEQ ID NO: 25)

40 BMS3h-4
 EVQLLES GGGGLVQPGGSLRLSCAASGFTFEDSPMTWVRQAPGKGLEWVSAITSNGYETYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKGRIPTLHFDYWGQGT LVT VSS (SEQ ID NO: 26)

45 BMS3h-5
 EVQLLES GGGGLVQPGGSLRLSCAASGFTFDEHDMWVRQAPGKGLEWVSRIGPDGFHTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKGRIPTLHFDYWGQGT LVT VSS (SEQ ID NO: 27)

50 BMS3h-6
 EVQLLES GGGGLVQPGGSLRLSCAASGFTFGEYHMSWVRQAPGKGLEWVSRITPLGTLTYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKGRIPLTFDYWGQGT LVT VSS (SEQ ID NO: 28)

55 BMS3h-7
 EVQLLES GGGGLVQPGGSLRLSCAASGFTFGTNAMSWVRQAPGKGLEWVSRISPGGDYTYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKGRVPDLLFDYWGQGT LVT VSS (SEQ ID NO: 29)

60 BMS3h-8
 EVQLLES GGGGLVQPGGSLRLSCAASGFTFPSEEMSWVRQAPGKGLEWVSRISADGANTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDA AVYYCAKGRVPDLLFDYWGQGT LVT VSS (SEQ ID NO: 30)

BMS3h-9
 EVQLLESGGGLVQPGGSLRLSCAASGFTFAEDDMTWVRQAPGKGLEWVSRIAVDGDRTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKGKVP SLHFDYWGQGT LVTVSS (SEQ ID NO: 31)

5 BMS3h-10
 EVQLLESGGGLVQPGGSLRLSCAASGFTFRTMDMSWVRQAPGKGLEWVSRTGDGMNTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKGVTPDLTFDYWGQGT LVTVSS (SEQ ID NO: 32)

10 BMS3h-11
 EVQLLESGGGLVQPGGSLRLSCAASGFTFERDDMTWVRQAPGKGLEWVSRIAGGVHTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKGVTPDLTFDYWGQGT LVTVSS (SEQ ID NO: 33)

15 BMS3h-12
 EVQLLESGGGLVQPGGSLRLSCAASGFTFDDDSMTWVRQAPGKGLEWVSRISSDGASTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKGVTPDLTFDYWGQGT LVTVSS (SEQ ID NO: 34)

20 BMS3h-13
 EVQLLESGGGLVQPGGSLRLSCAASGFTFTEEDMTWVRQAPGKGLEWVSRIIDSVGEGTYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKGVTPDLTFDYWGQGT LVTVSS (SEQ ID NO: 35)

25 BMS3h-14
 EVQLLESGGGLVQPGGSLRLSCAASGFTFSDSAMS WVRQAPGKGLEWVSRIIDNPGQHTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKGVTPDLTFDYWGQGT LVTVSS (SEQ ID NO: 36)

BMS3h-15
 EVQLLESGGGLVQPGGSLRLSCAASGFTFGQHSMTWVRQAPGKGLEWVSRIIDGGGYNTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKGEVPRSLHFDYWGQGT LVTVSS (SEQ ID NO: 37)

30 BMS3h-16
 EVQLLESGGGLVQPGGSLRLSCAASGFTFGQEPMTWVRQAPGKGLEWVSRIAYNGGDTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKGITPNLTFDYWGQGT LVTVSS (SEQ ID NO: 38)

35 BMS3h-17
 EVQLLESGGGLVQPGGSLRLSCAASGFTFENYPMSWVRQAPGKGLEWVSRIATGSITYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKGVIPHL MFDYWGQGT LVTVSS (SEQ ID NO: 39)

40 BMS3h-18
 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYDMSWVRQAPGKGLEWVSRIITGTGNSTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAQGVVPYLA FDYWGQGT LVTVSS (SEQ ID NO: 40)

45 BMS3h-19
 EVQLLESGGGLVQPGGSLRLSCAASGFTFEADAMTWVRQAPGKGLEWVSRIINV DGDRTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKGVPTLEFDYWGQGT LVTVSS (SEQ ID NO: 41)

BMS3h-21
 EVQLLESGGGLVQPGGSLRLSCAASGFTFDRADMTWVRQAPGKGLEWVSRIISGEGKCTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKGMV PNLVFDYWGQGT LVTVSS (SEQ ID NO: 42)

BMS3h-22
EVQLLESGGGLVQPGGSLRLSCAASGFTFHWEPMSWVRQAPGKGLEWVSRLNSSGWDITYADSVKGRFTISRDNKNTL
YLQMNSLRAEDTAVYYCAKGMVPLVFDYWGQGTLLTVSS (SEQ ID NO: 43)

5 BMS3h-24
EVQLLESGGGLVQPGGSLRLSCAASGFTFADEPMTWVRQAPGKGLEWVSRIPEGAPTYADSVKGRFTISRDNKNTL
YLQMNSLRAEDTAVYYCAKGITPNLTFDYWGQGTLLTVSS (SEQ ID NO: 44)

10 BMS3h-26
EVQLLESGGGLVQPGGSLRLSCAASGFTFHNHDMSWVRQAPGKGLEWVSRIIRGGLQTYADSVKGRFTISRDNKNTL
YLQMNSLRAEDTAVYYCAKGIVPDHFDYWGQGTLLTVSS (SEQ ID NO: 45)

15 BMS3h-27
EVQLLESGGGLVQPGGSLRLSCAASGFTFNEYPMWVRQAPGKGLEWVSRIIRGGLQTYADSVKGRFTISRDNKNTL
YLQMNSLRAEDTAVYYCAKGIIIPAMQFDYWGQGTLLTVSS (SEQ ID NO: 46)

20 BMS3h-28
EVQLLESGGGLVQPGGSLRLSCAASGFTFGDVPMSWVRQAPGKGLEWVSRIIDPYGSNTTYADSVKGRFTISRDNKNTL
YLQMNSLRAEDTAVYYCAKGIMPSLTFDYWGQGTLLTVSS (SEQ ID NO: 47)

BMS3h-29
EVQLLESGGGLVQPGGSLRLSCAASGFTFADYDMSWVRQAPGKGLEWVSRIISALGATTYYADSVKGRFTISRDNKNTL
YLQMNSLRAEDTAVYYCAKGQLPALEFDYWGQGTLLTVSS (SEQ ID NO: 48)

25 BMS3h-30
EVQLLESGGGLVQPGGSLRLSCAASGFTFKRYMTWVRQAPGKGLEWVSRIISALGATTYYADSVKGRFTISRDNKNTL
YLQMNSLRAEDTAVYYCAKGRIIDHFDYWGQGTLLTVSS (SEQ ID NO: 49)

30 BMS3h-31
EVQLLESGGGLVQPGGSLRLSCAASGFTFADYDMTWVRQAPGKGLEWVSRIISPTGGQTYADSVKGRFTISRDNKNTL
YLQMNSLRAEDTAVYYCAKGVIPYLSFSPFDYWGQGTLLTVSS (SEQ ID NO: 50)

35 BMS3h-32
EVQLLESGGGLVQPGGSLRLSCAASGFTFSKYWMGWARQAPGKGLEWVSRIISALGATTYYADSVKGRFTISRDNKNTL
YLQMNSLRAEDTAVYYCAKGAPKFTTYTFDYWGQGTLLTVSS (SEQ ID NO: 51)

40 BMS3h-33
EVQLLESGGGLVQPGGSLRLSCAASGFTFLSYPMHWVRQAPGKGLEWVSRIISALGATTYYADSVKGRFTISRDNKNTL
YLQMNSLRAEDTAVYYCAKGHSWTFDYWGQGTLLTVSS (SEQ ID NO: 52)

BMS3h-34
EVQLLESGGGLVQPGGSLRLSCAASGFTFANSNMTWVRQAPGKGLEWVSRIISALGATTYYADSVKGRFTISRDNKNTL
YLQMNSLRAEDTAVYYCAEGRIPTLHFDYWGQGTLLTVSS (SEQ ID NO: 53)

45 BMS3h-35
EVQLLESGGGLVQPGGSLRLSCAASGFTFGPRRMGWVRQAPGKGLEWVSRIISALGATTYYADSVKGRFTISRDNKNTL
YLQMNSLRAEDTAVYYCAEGAQGVLLFDYWGQGTLLTVSS (SEQ ID NO: 54)

50 BMS3h-36
EVQLLESGGGLVQPGGSLRLSCAASGFTFEDYRMWVRQAPGKGLEWVSRIISALGATTYYADSVKGRFTISRDNKNTL
YLQMNSLRAEDTAVYYCAETAGQFFDYWGQGTLLTVSS (SEQ ID NO: 55)

BMS3h-39
 EVQLLESGGGLVQPGGSLRLSCAASGFTFPEYEMVWRQAPGKGLEWVSAISREGRATYYADSVKGRFTISRDN SKNTL
 YLQMNNLRAEDTAVYYCAKEPVRFDYWGQGLTVTVSS (SEQ ID NO: 56)

5 BMS3h-40
 EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYEMLWRQAPGKGLEWSSISSSGNYTYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKEPLMFDYWGQGLTVTVSS (SEQ ID NO: 57)

10 BMS3h-42
 EVQLLESGGGLVQPGGSLRLSCAASGFTFDTEEMSWVRQAPGKGLEWVSAISPNGAFTFYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKEPILFDYWGQGLTVTVSS (SEQ ID NO: 58)

15 BMS3h-44
 EVQLLESGGGLVQPGGSLRLSCAASGFTFGHYDMVWRQAPGRGLEWSTINGAGLNTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAQSASRIFDYWGQGLTVTVSS (SEQ ID NO: 59)

20 BMS3h-45
 EVQLLESGGGLVQPGGSLRLSCAASGFTFRSYEMAWVRQAPGKGLEWSSISTLGTKTYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAQSSTHIFDYWGQGLTVTVSS (SEQ ID NO: 60)

25 BMS3h-46
 EVQLLESGGGLVQPGGSLRLSCAASGFTFIRYEMAWVRQAPGKGLEWSSISSSGWTTYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKSDAHIFDYWGQGLTVTVSS (SEQ ID NO: 61)

30 BMS3h-47
 EVQLLESGGGLVQPGGSLRLSCAASGFTFYAYEMAWVRQAPGKGLEWSSISDDGTRTYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKDLGQGFYWGQGLTVTVSS (SEQ ID NO: 62)

35 BMS3h-48
 EVQLLESGGGLVQPGGSLRLSCAASGFTFADHGMTWVRQAPGKGLEWVSGIGPSGEATYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKDRIPLNLFYWGQGLTVTVSS (SEQ ID NO: 63)

40 BMS3h-49
 EVQLLESGGGLVQPGGSLRLSCAASGFTFESQDMSWVRQAPGKGLEWVSGISPNGWDYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKDRSDFDYWGQGLTVTVSS (SEQ ID NO: 64)

45 BMS3h-50
 EVQLLESGGGLVQPGGSLRLSCAASGFTFGDYDMWVRQAPGKGLEWVSRIRHPGGVTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKAVPKGFDYWGQGLTVTVSS (SEQ ID NO: 65)

BMS3h-51
 EVQLLESGGGLVQPGGSLRLSCAASGFTFRVYWMWVRQAPGKGLEWVSSIDPQGGMTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKARIPNLEFDYWGQGLTVTVSS (SEQ ID NO: 66)

BMS3h-52
 EVQLLESGGGLVQPGESLRLSCAASGFTFSAYDMTWVRQAPGKGLEWVSRINPTGSYTYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKAKIPNLFYWGQGLTVTVSS (SEQ ID NO: 67)

BMS3h-53
EVQLLESGGGLVQPGGSLRLSCAASGFTFADSEMMWVRQAPGKGLEWVSGIAHNGGHTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKAGHPQQTEAFDYWGQGT LVTVSS (SEQ ID NO: 68)

5 BMS3h-54
EMQLLESGGGLVQPGGSLRLSCAASGFTFATYDMYWRQAPGKGLEWVSKISPNGWSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKYQTHFDYWGQGT LVTVSS (SEQ ID NO: 69)

10 BMS3h-55
EVQLLESGGGLVQPGGSLRLSCAASGFTFSVYDMRWVRQAPGKGLEWVSTISSSGTYTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKYPKNFDYWGQGT LVTVSS (SEQ ID NO: 70)

15 BMS3h-57
EVQLLESGGGLVQPGGSLRLSCAASGFTFSHEDMTWVRQAPGKGLEWVSSISPNGWDTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKRTRSKFDYWGQGT LVTVSS (SEQ ID NO: 71)

20 BMS3h-58
EVQLLESGGGLVQPGGSLRLSCAASGFTFEKYIMGWARQAPGKGLEWVSTIDYWGQHTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKRSHLIPLQFDYWGQGT LVTVSS (SEQ ID NO: 72)

BMS3h-59
EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYAMGWVRQAPGKGLEWVSTISYVGYTYTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKKALRGEAFTERFDYWGQGT LVTVSS (SEQ ID NO: 73)

25 BMS3h-60
EVQLLESGGGLVQPGGSLRLSCAASGFTFGPYMMHWVRQAPGKGLEWVSTIEVNGNRITYTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKWVGSKTSSDKSFDYWGQGT LVTVSS (SEQ ID NO: 74)

30 BMS3h-61
EVQLLESGGGLVQPGGSLRLSCAASGFTFGTTEMAWVRQAPGKGLEWVSSIGSAGAWTYTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKIGGHPQQGFDYWGQGT LVTVSS (SEQ ID NO: 75)

35 BMS3h-62
EVQLLESGGGLVQPGGSLRLSCAASGFTFPREWMWVRQAPGKGLEWVSSIQPMGQTTYTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKYSRNKGFFDYWGQGT LVTVSS (SEQ ID NO: 76)

40 BMS3h-63
EVQLLESGGGLVQPGGSLRLSCAASGFTFTSEYMGWVRQAPGKGLEWVSSIQRYGSTTYTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKHESNWETFDYWGQGT LVTVSS (SEQ ID NO: 77)

BMS3h-70
EVQLLESGGGLVQPGGSLRLSCAASGFTFSVYSMQWVRQAPGKGLEWVSAITPNGTRTYTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKTLGRGSYPGVDFDYWGQGT LVTVSS (SEQ ID NO: 78)

45 BMS3h-71
EVQLLESGGGLVQPGGSLRLSCAASGFTFPSYAMTWVRQAPGKGLEWVSRITADGTVTYTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKGSIPMLTFDYWGQGT LVTVSS (SEQ ID NO: 79)

50 BMS3h-72
EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYDMIWVRQAPGKGLEWVSAISPNGTGIYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKNQSVHHAVFDYWGQGT LVTVSS (SEQ ID NO: 80)

BMS3h-73
 EVQLLES GGG LVQP GGS LRLSCAASGFTFENYEMTWVRQAPGKGLEWVSRIAPHGRLTY YADSVKGRFTISRDN SKNTL
 5 YLQMNS LRAEDTAVYYCAKGQIPMLDFDYWGQGLTVTVSS (SEQ ID NO: 81)

BMS3h-74
 EVQLLES GGG LVQP GGS LRLSCAASGFTFSHYMMWVRQAPGKGLEWVSTISHFGDITY YADSVKGRFTISRDN SKNTL
 YLQMNS LRAEDTAVYYCAKNDMVMKNGGFDYWGQGLTVTVSS (SEQ ID NO: 82)

10 BMS3h-75
 EVQLLES GGG LVQP GGS LRLSCAASGFTFERYDMSWVRQAPGKGLEWVSRI DSRGWSTYYADSVKGRFTISRDN SKNTL
 YLQMNS LRAEDTAVYYCAKGLVPHLRFDYWGQGLTVTVSS (SEQ ID NO: 83)

15 BMS3h-76
 EVQLLES GGG LVQP GGS LRLSCAASGFTFANAQMTWVRQAPGKGLEWVSRI DAMGDATYYADSVKGRFTISRDN SKNTL
 YLQMNS LRAEDTAVYYCAKGKVP SIDYWGQGLTVTVSS (SEQ ID NO: 84)

20 BMS3h-77
 EVQLLES GGG LVQP GGS LRLSCAASGFTFANAQMTWVRQAPGKGLEWVSRI DAMGDATYYADSVKGRFTISRDN SKNTL
 YLQMNS LRAEDTAVYYCAKGVIPAFDYWGQGLTVTVSS (SEQ ID NO: 85)

25 BMS3h-78
 EVQLLES GGG LVQP GGS LRLSCAASGFTFQNDRMHWVRQAPGKGLEWVSSI SATGGDTYYADSVKGRFTISRDN SKNTL
 YLQMNS LRAEDTAVYYCAKQTGTNRFDYWGQGLTVTVSS (SEQ ID NO: 86)

BMS3h-79
 EVQLLES GGG LVQP GGS LRLSCAASGFTFNQPYMSWVRQAPGKGLEWVSSI DASGGTTYADSVKGRFTISRDN SKNTL
 YLQMNS LRAEDAAVYYCAKDRI PNLFDYWGQGLTVTVSS (SEQ ID NO: 87)

30 BMS3h-80
 EVQLLES GGG LVQP GGS LRLSCAASGFTFDNENMTWVRQAPGKGLEWVSRI DGGGYNTYYADSVKGRFTISRDN SKNTL
 YLQMNS LRAEDTAVYYCAKGQVPELLFDYWGQGLTVTVSS (SEQ ID NO: 88)

35 BMS3h-81
 EVQLLES GGG LVQP GGS LRLSCAASGFTFVSSNMTWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDN SKNTL
 YLQMNS LRAEDTAVYYCAKGRIPTLVFDYWGQGLTVTVSS (SEQ ID NO: 89)

40 BMS3h-82
 EVQLLES GGG LVQP GGS LRLSCAASGFTFVSSNMTWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDN SKNTL
 YLQMNS LRAEDTAVYYCAKDRI PNLFDYWGQGLTVTVSS (SEQ ID NO: 90)

45 BMS3h-83
 EVQLLES GGG LVQP GGS LRLSCAASGFTFSDDSMSWVRQAPGKGLEWVSRI NDAGSSTYYADSVKGRFTISRDN SKNTL
 YLQMNS LRAEDTAVYYCAKG TIPLLEFDYWGQGLTVTVSS (SEQ ID NO: 91)

BMS3h-84
 EMQLLES GGG LVQP GGS LRLSCAASGFTFVSDTMSWVRQAPGKGLEWVSRI DGTGGDTYYADSVKGRFTISRDN SKNTL
 YLQMNS LRAEDTAVYYCAKGLIPDLQFDYWGQGLTVTVSS (SEQ ID NO: 92)

BMS3h-85
EVQLLESGGGLVQPGGSLRLSCAASGFTFDEEEMTWVRQAPGKGLEWVSRIIGGGHETYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKGTIPLLEFDYWGQGLTVTVSS (SEQ ID NO: 93)

5 BMS3h-86
EVQLLESGGGLVQPGGSLRLSCAASGFTFDNENMTWVRQAPGKGLEWVSRIITERGDVTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKGTVP TLEFDYWGQGLTVTVSS (SEQ ID NO: 94)

10 BMS3h-87
EVQLLESGGGLVQPGGSLRLSCAASGFTFDEEEMTWVRQAPGKGLEWVSRIIGGGHETYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKGTVP TLEFDYWGQGLTVTVSS (SEQ ID NO: 95)

15 BMS3h-88
EVQLLESGGGLVQPGGSLRLSCAASGFTFHETEMTWVRQAPGKGLEWVSAINRLGQDTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKGRIPGLVFDYWGQGLTVTVSS (SEQ ID NO: 96)

20 BMS3h-89
EVQLLESGGGLVQPGGSLRLSCAASGFTFSDDSMSWVRQAPGKGLEWVSRIIDAGSSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKGTVP TLEFDYWGQGLTVTVSS (SEQ ID NO: 97)

25 BMS3h-90
EVQLLESGGGLVQPGGSLRLSCAASGFTFDNENMTWVRQAPGKGLEWVSRIITERGDVTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKGRIPTLVFDYWGQGLTVTVSS (SEQ ID NO: 98)

30 BMS3h-91
EVQLLESGGGLVQPGGSLRLSCAASGFTFSDDSMSWVRQAPGKGLEWVSRIIDAGSSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKGITPNLTFDYWGQGLTVTVSS (SEQ ID NO: 99)

35 BMS3h-92
EVQLLESGGGLVQPGGSLRLSCAASGFTFADEPMTWVRQAPGKGLEWVSRIIPPEGAPTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKGLIPDLQFDYWGQGLTVTVSS (SEQ ID NO: 100)

40 BMS3h-93
EVQLLESGGGLVQPGGSLRLSCAASGFTFQDSDMTWVRQAPGKGLEWVSAIAAPGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKDRIPNLRFDYWGQGLTVTVSS (SEQ ID NO: 101)

45 BMS3h-94
EVQLLESGGGLVQPGGSLRLSCAASGFTFVSDTMSWVRQAPGKGLEWVSRIIDGTGGDTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKGQVPELLFDYWGQGLTVTVSS (SEQ ID NO: 102)

50 BMS3h-95
EVQLLESGGGLVQPGGSLRLSCAASGFTFQDSDMTWVRQAPGKGLEWVSAIAAPGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKDRIPNLVFDYWGQGLTVTVSS (SEQ ID NO: 103)

55 BMS3h-96
EVQLLESGGGLVQPGGSLRLSCAAAGFTFDLAEMTWVRQAPGKGLEWVSRIIDEDGASTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDAAVYYCAEGVIPSLTFDYWGQGLTVTVSS (SEQ ID NO: 104)

60 BMS3h-97
EVQLLESGGGLVQPGGSLRLSCAASGFTFTDKHMSWVRQAPGKGLEWVSRIIDPDGTYTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDAAVYYCAEGVIPSLTFDYWGQGLTVTVSS (SEQ ID NO: 105)

BMS3h-98
 EVQLLESGGGLVQPGGSLRLSCAASGFTFAEDDMTWVRQAPGKGLEWVSRIAVDGDRTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRATEDAVYYCAKGKTPHLVFDYWGQGLTVTVSS (SEQ ID NO: 106)

5
 BMS3h-99
 EVQLLESGGGLVQPGGSLRLSCAAAGFTFDLAEMTWVRQAPGKGLEWVSRIDEDGASTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKGQVPALVFDYWGQGLTVTVSS (SEQ ID NO: 107)

10
 BMS3h-100
 EVQLLESGGGLVQPGGSLRLSCAASGFTFEDSMMSWVRQAPGKGLEWVSRIIDPGGAQTYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKGVTPDLTFDYWGQGLTVTVSS (SEQ ID NO: 108)

15
 BMS3h-101
 EVQLLESGGGLVQPGGSLRLSCAASGFTFEHADMSWVRQASGKGLEWVSRIIDNSGQSTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKGVTPDLTFDYWGQGLTVTVSS (SEQ ID NO: 109)

20
 BMS3h-102
 EVQLLESGGGLVQPGGSLRLSCAASGFTFSEAEMNWVRQAPGKGLEWVSRIITDGDSTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKGRIPTLHFDYWGQGLTVTVSS (SEQ ID NO: 110)

25
 BMS3h-103
 EVQLLESGGGLVQPGGSLRLSCAASGFTFDDSDMTWVRQAPGKSLEWVSIRGDDDETYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKNRIPDLVFDYWGQGLTVTVSS (SEQ ID NO: 111)

30
 BMS3h-108
 EVQLLESGGGLVQPGGSLRLSCAASGFTFNVADMWVRQAPGKGLEWVSSISPNGWDTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKHASTEGPTAFDYWGQGLTVTVSS (SEQ ID NO: 112)

35
 BMS3h-109
 EVQLLESGGGLVQPGGSLRLSCAASGFTFGPYDMGWVRQAPGKGLEWVSWISAHGSFTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKWPKFDYWGQGLTVTVSS (SEQ ID NO: 113)

40
 BMS3h-110
 EVQLLESGGGLVQPGGSLRLSCAASGFTFGSGSMSWVRQAPGKGLEWVSRIIGSNGADTYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKGMVPLVFDYWGQGLTVTVSS (SEQ ID NO: 114)

45
 BMS3h-111
 EVQLLESGGGLVQPGGSLRLSCAASGFTFNRFDMTWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKDRIPLVFDYWGQGLTVTVSS (SEQ ID NO: 115)

BMS3h-112
 EVQLLESGGGLVQPGGSLRLSCAASGFTFGESDMKWVRQAPGKGLEWVSSISPNGWDTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKSPSSRLKFDYWGQGLTVTVSS (SEQ ID NO: 116)

BMS3h-139
 EVQLLESGGGLVQPGGSLRLSCAASGFTFDSSEMSWVRQAPGKGLEWVSSIENQGGATYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKDRIPLVFDYWGQGLTVTVSS (SEQ ID NO: 117)

BMS3h-140
EVQLLESGGGLVQPGGSLRLSCAASGFTLDAYPMYWRQAPGKGLEWVSWIASGGGATYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKRTKNFDYWGQGT LVTVSS (SEQ ID NO: 118)

5 BMS3h-141
EVQLLESGGGLVQPGGSLRLSCAASGFTFMSYSMAWVRQAPGKGLEWVSGITSNGNRITYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKSTGANSRNFYWGQGT LVTVSS (SEQ ID NO: 119)

10 BMS3h-142
EVQLLESGGGLVQPGGSLRLSCAASGFTFEGYLSWVRQAPGKGLEWVSSIAANGMQTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKKPRGIWDGDFDYWGQGT LVTVSS (SEQ ID NO: 120)

15 BMS3h-143
EVQLLESGGGLVQPGGSLRLSCAASGFTFHESMTWVRQAPGKGLEWVSTIRHPGEFTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAGDTAVYYCAKGLIPDLQFDYWGQGT LVTVSS (SEQ ID NO: 121)

20 BMS3h-144
EVQLLESGGGLVQPGGSLRLSCAASGFTFAMYSMSWVRQAPGKGLEWVSSIAPPGGRITYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKQSLTGYSRSFDYWGQGT LVTVSS (SEQ ID NO: 122)

25 BMS3h-145
EVQLLESGGGLVQPGGSLRLSCAASGFTFSQNPMSWVRHAPGKGLEWVSTIPANGRPTSYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKYSQQPGRFDYWGQGT LVTVSS (SEQ ID NO: 123)

30 BMS3h-146
EVQLLESGGGLVQPGGSLRLSCAASGFTFANYHMTWVRQAPGKGLEWVSSIPDSGKQTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKGRIPLLFDYWGQGT LVTVSS (SEQ ID NO: 124)

35 BMS3h-147
EVQLLESGGGLVQPGGSLRLSCAASGFTFAQYHMRWVRQAPGKGLEWVSTINDIGSNTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKVGGRGSFSDYWGQGT LVTVSS (SEQ ID NO: 125)

40 BMS3h-148
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYDMKWVRQAPGKGLEWVSTISASGVFTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKREHAGQPPFDYWGQGT LVTVSS (SEQ ID NO: 126)

45 BMS3h-149
EVQLLESGGGLVQPGGSLRLSCAASGFTFNGYAMSWVRQAPGKGLEWVSTINANGKYTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKKLTLASNYFDYWGQGT LVTVSS (SEQ ID NO: 127)

50 BMS3h-150
EVQLLESGGGLVQPGGSLRLSCAASGFTFMDYDMKWVRQAPGKGLEWVSSITALGKKTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKDSVKYPLNLFDYWGQGT LVTVSS (SEQ ID NO: 128)

55 BMS3h-151
EVQLLESGGGLVQPGGSLRLSCAASGFTFPHYTMAWVRQAPGKGLEWVSSIQSPGWRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKYGDGLPLTFDYWGQGT LVTVSS (SEQ ID NO: 129)

60 BMS3h-167
EVQLLESGGGLVQPGGSLRLSCAASGFTFSGTPMSWVRQAPGKGLEWVSRIGDEGQETYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKGVTPDLTFDYWGQGT LVTVSS (SEQ ID NO: 130)

See "Study of HCD122 (Lucatumumab) and Bendamustine Combination Therapy in CD40⁺ Rituximab-Refractory Follicular Lymphoma," Clinical Trials Feeds, on the Internet at hypertext transfer protocol: clinicaltrialsfeeds.org/clinical-trials/show/NCT01275209 (last updated January 11, 2011). Monoclonal antibodies, however, can display agonist activity. For example, the usefulness of the anti-CD40 antibody Chi220 is limited by its weak stimulatory potential. See Adams, et al., "Development of a chimeric anti-CD40 monoclonal antibody that synergizes with LEA29Y to prolong islet allograft survival," *J. Immunol.* 174: 542-50 (2005).

SUMMARY

Anti-CD40 antibody antagonists that do not possess partial agonist activity are still needed in a clinical setting. Novel antibody polypeptides that specifically bind a novel epitope of human CD40 are provided. The CD40 epitope does not overlap the Chi220 epitope, as shown by competition analysis and by the structure derived from co-crystallization of an antibody polypeptide with CD40. The antibody polypeptides advantageously do not exhibit CD40 agonist activity. The antibody polypeptides are useful in the treatment of diseases involving CD40 activation, including autoimmune diseases, transplant rejection, and allergic responses. The antibody polypeptides comprise a variable domain. In one embodiment, the antibody polypeptides are in the form of a domain antibody (dAb) that contains a single variable domain. In another embodiment, the dAbs are bi-specific reagents that comprise a second variable domain that can bind human serum albumin (HSA), for example.

Provided is an antibody polypeptide comprising a first variable domain, where said antibody polypeptide specifically binds an epitope of human CD40, where the epitope comprises the amino acid sequence of SEQ ID NO: 1, where the antibody polypeptide competes with the binding of domain antibody (dAb) BMS3h-56-269 (SEQ ID NO: 417), and where the epitope comprises at least one CD40 amino acid residue selected from the group consisting of Trp109, Leu121, His122, Ser124, Ser156, Ala157, Phe158, Glu159, and His162.

Further provided is an antibody polypeptide where the first variable domain comprises the amino acid sequence of one of the antibody polypeptides selected from the lineage group consisting of BMS3h-37, BMS3h-38, BMS3h-56, and BMS3h-198, and where the first variable domain has an apparent binding constant of 1 pM to 100 nM. Further provided is an

BMS3h-168
 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSSSMSWVRQAPGKGLEWVSAIGSDGPSTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKGRIPTLHFDYWGQGT LVTVSS (SEQ ID NO: 131)

5

BMS3h-169
 EVQLLESGGGLVQPGGSLRLSCAASGFTFNP GEMTWVRQAPGKGLEWVSSIDGSGSSTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRADD TAVYYCAKGRIPTLHFDYWGQGT LVTVSS (SEQ ID NO: 132)

10

BMS3h-170
 EVQLLESGGGLVQPGGSLRLSCAASGFTFPESMMGWVRQAPGKGLEWVSSIGYPGATTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKGGSRDDNFDYWGQGT LVTVSS (SEQ ID NO: 133)

15

BMS3h-171
 EVQLLESGGGLVQPGGSLRLSCAASGFTFGQHS MHWVRQAPGKGLEWVSSISVPGPKTYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKSLRDLRPGDSKSF DYWGQGT LVTVSS (SEQ ID NO: 134)

20

BMS3h-197
 EVQLLESGGGLVQPGGSLRLSCAASGFTFGS AAMDWVRQAPGKGLEWVSSINDMGSNTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKQGRFDYWGQGT LVTVSS (SEQ ID NO: 135)

25

BMS3h-199
 EVQLLESGGGLVQPGGSLRLSCAASGFTFGYDRMAWVRQAPGKGLEWVSSIDGPGGATYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAEGRVPDFDYWGQGT LVTVSS (SEQ ID NO: 136)

30

BMS3h-200
 EVQLLESGGGLVQPGGSLRLSCAASGFTFGEYEMTWVRQAPGKGLEWVSRIDPFGSETYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAEGVVPDLNFDYWGQGT LVTVSS (SEQ ID NO: 137)

35

BMS3h-201
 EVQLLESGGGLVQPGGSLRLSCAASGFTFDKYVMGWVRQAPGKGLEWVSTIGSYGGATYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKRLTLSATKFDYWGQGT LVTVSS (SEQ ID NO: 138)

40

BMS3h-203
 EVQLLESGGGLVQPGGSLRLSCAASGFTFEDYVMGWVRQAPGKGLEWVSTIAHRGDITYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKRRRLSDYRFDYWGQGT LVTVSS (SEQ ID NO: 139)

45

BMS3h-204
 EVQLLESGGGLVQPGGSLRLSCAASGFTFGQFDMYVRQAPGKGLEWVSAISPAGTGTYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKAGDRSSLFDYRGQGT LVTVSS (SEQ ID NO: 140)

BMS3h-205
 EVQLLESGGGLVQPGGSLRLSCAASGFTFKDTGMTWVRQAPGKGLEWVSSISSYGRDYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDA AAVYYCAKLNAALGFDYWGQGT LVTVSS (SEQ ID NO: 141)

BMS3h-206
 EVQLLESGGGLVQPGGSLRLSCAASGFTFGPYPM SWVRQAPGKGLEWVSGINAPGTRTYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAQQMSSGVFDYWGQGT LVTVSS (SEQ ID NO: 142)

BMS3h-207
EVQLLESGGGLVQPGGSLRLSCAASGFTFSNQDMTWVRQAPGKGLEWSSIDSSGQLTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKVKSLARFDYWGQGLTVTVSS (SEQ ID NO: 143)

5 BMS3h-208
EVQLLESGGGLVQPGGSLRLSCAASGFTFPESDMKWVRQAPGKGLEWSSISPNGWDTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKPAQVLFYWGQGLTVTVSS (SEQ ID NO: 144)

10 BMS3h-209
EVQLLESGGGLVQPGGSLRLSCAASGFTFEQYVMGWVRQAPGKGLEWVSTIGTSGKYTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAQRRSLTRVHFDYWGQGLTVTVSS (SEQ ID NO: 145)

15 BMS3h-210
EVQLLESGGGLVQPGGSLRLSCAASGFTFGVEHMSWVRQAPGKGLEWVSAITGDGDRYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKTVSWNGRFDYWGQGLTVTVSS (SEQ ID NO: 146)

20 BMS3h-211
EVQLLESGGGLVQPGGSLRLSCAASGFTFAWYNMGWVRQAPGKGLEWVSRIAPSGIITYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKGLRGKFDYWGQGLTVTVSS (SEQ ID NO: 147)

BMS3h-212
EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYEMRWVRQAPGKGLEWSSISSAGTDYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKQSLNFDYWGQGLTVTVSS (SEQ ID NO: 148)

25 BMS3h-213
EVQLLESGGGLVQPGGSLRLSCVASGFTFDEEPMTWVRQAPGKGLEWVSIIDPGGGATYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKSNSMFDYWGQGLTVTVSS (SEQ ID NO: 149)

30 BMS3h-214
EVQLLESGGGLVQPGGSLRLSCAASGFTFSAYPMHWVRQAPGKGLEWVSSIASSGITTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKFTRLHFAQFDYWGQGLTVTVSS (SEQ ID NO: 150)

35 BMS3h-215
EVQLLESGGGLVQPGGSLRLSCAASGFTFADYAMGWVRQAPGKGLEWVSRISPEGSRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLRPYASKFDYWGQGLTVTVSS (SEQ ID NO: 151)

40 BMS3h-230
EVQLLESGGGLVQPGGSLRLSCAASGFTFRPYDMGWVRQAPGKGLEWVSTISHQGNRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKVSHHFDYWGQGLTVTVSS (SEQ ID NO: 152)

BMS3h-231
EVQLLESGGGLVQPGGSLRLSCAASGFTFSAYNMWWARQAPGKGLEWVSWINSTGSRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKNWHRGRFDYWGQGLTVTVSS (SEQ ID NO: 153)

45 BMS3h-232
EVQLLESGGGLVQPGGSLRLSCAASGFTFDYRMGWVRQAPGKGLEWVSTINRLGQSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKVKKHKFDYWGQGLTVTVSS (SEQ ID NO: 154)

50 BMS3h-233
EVQLLESGGGLVQPGGSLRLSCAASGFTFAHYNMWRQAPGKGLEWVSTITKTGFRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKAGQDFDYWGQGLTVTVSS (SEQ ID NO: 155)

BMS3h-234
 EVQLLES G GGLVQPGGSLRLSCAASGFTFYPYSMHWRQAPGKGLEWVSTIDGSGMFTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAEDSLKASFDYWGQGT LVT VSS (SEQ ID NO: 156)

5
 BMS3h-235
 EVQLLES G GGLVQPGGSLRLSCAASGFTFPLYGMWVRQAPGKGLEWVS YIGPYGHTTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKKRKKKFDYWGQGT LVT VSS (SEQ ID NO: 157)

10
 BMS3h-236
 EVQLLES G GGLVQPGGSLRLSCAASGFTFPRYRMSWVRQAPGKGLEWVS SITPYGAHTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKYGKWFYDYGQGT LVT VSS (SEQ ID NO: 158)

15
 BMS3h-237
 EVQLLES G GGLVQPGGSLRLSCAASGFTFNEYAMRWVRQAPGKGLEWVSTIDRLGLHTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKSGPFTFDYWGQGT LVT VSS (SEQ ID NO: 159)

20
 BMS3h-238
 EVQLLES G GGLVQPGGSLRLSCAASGFTFERYNMRWVRQAPGKGLEWVSTIDRLGLATYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKAGSWSFDYWGQGT LVT VSS (SEQ ID NO: 160)

25
 BMS3h-239
 EVQLLES G GGLVQPGGSLRLSCAASGFTFGIYDMKWVRQAPGKGLEWVSTISSSGHTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKYPQYPFDYWGQGT LVT VSS (SEQ ID NO: 161)

30
 BMS3h-240
 EVQLLES G GGLVQPGGSLRLSCAASGFTFWYDMRWVRQAPGKGLEWVSTISATGVHTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKYPAGRFDYWGQGT LVT VSS (SEQ ID NO: 162)

35
 BMS3h-241
 EVQLLES G GGLVQPGGSLRLSCAASGFTFSTYDMIWVRQAPGKGLEWVSAISPNGTGTYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKPPQVNTFDYRGQGT LVT VSS (SEQ ID NO: 163)

40
 BMS3h-243
 EVQLLES G GGLVQPGGSLRLSCAASGFTFEKEDMGWVRQAPGKGLEWVSHISPNGYATYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKSWSSFDYWGQGT LVT VSS (SEQ ID NO: 164)

45
 BMS3h-244
 EVQLLES G GGLVQPGGSLRLSCAASGFTFSATPMEWARQAPGKGLEWVSTISESGYSTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKWNSTTGFDYWGQGT LVT VSS (SEQ ID NO: 165)

BMS3h-245
 EVQLLES G GGLVQPGGSLRLSCAASGFTFNTVDMEWVRQAPGKGLEWVSSIPNGWDTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAEAPHRAFDYWGQGT LVT VSS (SEQ ID NO: 166)

BMS3h-246
 EVQLLES G GGLVQPGGSLRLSCAASGFTFEDKEMSWVRQAPGKGLEWVSRIDALGDSTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAEGMPRLKFDYWGQGT LVT VSS (SEQ ID NO: 167)

BMS3h-247
EVQLLESGGGLVQPGGSLRLSCAASGFTFSDHSMWVRQAPGKGLEWVSDIEPHGVHTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCANPTFDYWGGQGLTVTVSS (SEQ ID NO: 168)

5 BMS3h-248
EVQLLESGGGLVQPGGSLRLSCAASGFTFSPHTMHWVRQAPGKGLEWVSGIGPDGTTTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKRSYSWDRGWTFDYWGGQGLTVTVSS (SEQ ID NO: 169)

10 BMS3h-249
EVQLLESGGGLVQPGGSLRLSCAASGFTFYASDMKWVRQAPGKGLEWVSSIPNGWDTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKADYTYHSFDYWGGQGLTVTVSS (SEQ ID NO: 170)

15 BMS3h-250
EVQLLESGGGLVQPGGSLRLSCAASGFTFAHYNMWVRQAPGKGLEWVSTITKTGFRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKAGQFDFDYWGQGLTVTVSS (SEQ ID NO: 171)

20 BMS3h-251
EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYHMGWARQAPGKGLEWVSVIGPRGISTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKSPSRHRFDYWGGQGLTVTVSS (SEQ ID NO: 172)

25 BMS3h-252
EVQLLESGGGLVQPGGSLRLSCAASGFTFNEYAMRWVRQAPGKGLEWVSTIDRLGLHTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKSGPFTFDYWGGQGLTVTVSS (SEQ ID NO: 173)

30 BMS3h-253
EVQLLESGGGLVQPGGSLRLSCAASGFTFGNYSMKWARQAPGKGLEWVSTITPDGWYTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKVGDAVWGWIGGFDYWGGQGLTVTVSS (SEQ ID NO: 174)

35 BMS3h-254
EVQLLESGGGLVQPGGSLRLSCAASGFTFGDYGMKWVRQAPGKGLEWVSAITSNGDFTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKSLYKFDYWGGQGLTVTVSS (SEQ ID NO: 175)

40 BMS3h-255
EVQLLESGGGLVQPGGSLRLSCAGSGFTFPTYKMGWVRQAPGKGLEWVSFIDYWGWRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKSPYSWTHDSPHFDYWGGQGLTVTVSS (SEQ ID NO: 176)

45 BMS3h-256
EVQLLESGGGLVQPGGSLRLSCAASGFTFRPYTMCWARQAPGKGLEWVSCISDAGSFTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKRMSSFYWGQGLTVTVSS (SEQ ID NO: 177)

50 BMS3h-257
EVQLLESGGGLVQPGGSLRLSCAASGFTFQNYQMAWVRQAPGKGLEWVSTISGTGKNTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKTPQNYFSVRRFDYWGGQGLTVTVSS (SEQ ID NO: 178)

55 BMS3h-258
EVQLLESGGGLVQPGGSLRLSCAASGFTFGAYTMGWVRQAPGKGLEWVSKISTSGGQTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKPLNWWAFDYWGQGLTVTVSS (SEQ ID NO: 179)

60 BMS3h-272
EVQLLESGGGLVQPGGSLRLSCAASGFTFNAYPMTWVRQAPGKGLEWVSRIDGYGRHTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKGIIPNFDYWGGQGLTVTVSS (SEQ ID NO: 180)

BMS3h-273
 EVQLLESGGGLVQPGGSLRLSCAASGFTFGAVDMTWVRQAPGKGLEWWSAISPSSGATYYADSVKGRFTISRDNKNTL
 YLQMNSLRAEDTAVYYCAKGRVPLGFDYWGQGLTVTVSS (SEQ ID NO: 181)

5 BMS3h-274
 EVQLLESGGGLVQPGGSLRLSCAASGFTFDSYAMGWARQAPGKGLEWWSAIGAKGLSTYYADSVKGRFTISRDNKNTL
 YLQMNSLRAEDTAVYYCAKAARGKFDYWGQGLTVTVSS (SEQ ID NO: 182)

10 BMS3h-275
 EVQLLESGGGLVQPGGSLRLSCAASGFTFTRYQMGWVRQAPGKGLEWWSVINWGSSTYYADSVKGRFTISRDNKNTL
 YLQMNSLRAEDTAVYYCAKMSGKFAYWGQGLTVTVSS (SEQ ID NO: 183)

15 BMS3h-276
 EVQLLESGGGLVQPGGSLRLSCAASGFTFGNYSMWVRQAPGKGLEWVSTIIPAGTSTYYADSVKGRFTISRDNKNTL
 YLQMNSLRAEDTAVYYCAKPSIRLFDYWGQGLTVTVSS (SEQ ID NO: 184)

20 BMS3h-279
 EVQLLESGGGLVQPGGSLRLSCAASGFTFGAYDMGWVRQAPGKGLEWWSWISPNGYDTYYADSVKGRFTISRDNKNTL
 YLQMNSLRAEDTAVYYCAKGGVKFDYWGQGLTVTVSS (SEQ ID NO: 185)

25 BMS3h-282
 EVQLLESGGGLVQPGGSLRLSCAASGFTFVWYEMAWVRQAPGKGLEWVSTIQADGEQTYADSVKGRFTISRDNKNTL
 YLQMNSLRAEDTAVYYCAKASYALVYPPEEFDYWGQGLTVTVSS (SEQ ID NO: 186)

BMS3h-287
 EVQLLESGGGLVQPGGSLRLSCAASGFTFTNYRMSWVRQAPGKGLEWWSAIDDLGVSTYYADSVKGRFTISRDNKNTL
 YLQMNSLRAEDTAVYYCAKWRLKNSQPTDFDYWGQGLTVTVSS (SEQ ID NO: 187)

30 BMS3h-292
 EVQLLESGGGLVQPGGSLRLSCAASGFTFDQAHMWWVRQAPGKGLEWWSFINPSGYTYTYADSVKGRFTISRDNKNTL
 YLQMNSLRAEDTAVYYCAKPSLSPSSFDYWGQGLTVTVSS (SEQ ID NO: 188)

35 BMS3h-293
 EVQLLESGGGLVQPGGSLRLSCAASGFTFETGQMGWARQAPGKGLEWWSNIDGSGTYTYTYADSVKGRFTISRDNKNTL
 YLQMNSLRAEDTAVYYCAKSTQNYRFDYWGQGLTVTVSS (SEQ ID NO: 189)

40 BMS3h-296
 EVQLLESGGGLVQPGGSLRLSCAASGFTFGAYPMYWRQAPGKGLEWVSSIHKDGRITYTYADSVKGRFTISRDNKNTL
 YLQMNSLRAEDTAVYYCAKQGPVDGFDYWGQGLTVTVSS (SEQ ID NO: 190)

45 BMS3h-297
 EVQLLESGGGLVQPGGSLRLSCAASGFTFPDEGMTWVRQAPGKGLEWVSTIETGGTVTYTYADSVKGRFTISRDNKNTL
 YLQMNSLRAEDTAVYYCAKMDGSGTWQTFDYWGQGLTVTVSS (SEQ ID NO: 191)

BMS3h-298
 EVQLLESGGGLVQPGGSLRLSCAASGFTFDSLGMGWARQAPGKGLEWWSYIRAEGAYTYTYADSVKGRFTISRDNKNTL
 YLQMNSLRAEDTAVYYCAKYLADSDYWGQGLTVTVSS (SEQ ID NO: 192)

BMS3h-299
EVQLLES GGGGLVQPGGSLRLSCAASGFTFSESYMEWVRQAPGKGLEWVSGIDHIGGGTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKDDGRGGSMFDYWGQGT LVTVSS (SEQ ID NO: 193)

5 BMS3h-300
EVQLLES GGGGLVQPGGSLRLSCAASGFTFSGGYMWWVRQAPGKGLEWVSSIGASGAYTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKTGGRLDYWGQGT LVTVSS (SEQ ID NO: 194)

10 BMS3h-301
EVQLLES GGGGLVQPGGSLRLSCAASGFTFDEGHMGWVRQAPGKDLWVSYIGSLGLHTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKREFSNGGFDYWGQGT LVTVSS (SEQ ID NO: 195)

15 BMS3h-302
EVQLLES GGGGLVQPGGSLRLSCAASGFTFKTSPMYWVRQAPGKGLEWVSSIDRTGGHTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKQALLTDAKRFDYWGQGT LVTVSS (SEQ ID NO: 196)

20 BMS3h-303
EVQLLES GGGGLVQPGGSLRLSCAASGFTFDGRDMVWVRQAPGKGLEWVSAISPSGLDYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAERPQMLVTNFDYWGQGT LVTVSS (SEQ ID NO: 197)

25 BMS3h-304
EVQLLES GGGGLVQPGGSLRLSCAASGFTFGNDPMSWVRQAPGKGLEWVSGIGREGDSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKDSMRHQPFDYWGQGT LVTVSS (SEQ ID NO: 198)

30 BMS3h-305
EVQLLES GGGGLVQPGGSLRLSCAASGFTFDETYMKWVRQAPGKGLEWVSAIGASGADTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKFTHLNGRFDYWGQGT LVTVSS (SEQ ID NO: 199)

35 BMS3h-306
EVQLLES GGGGLVQPGGSLRLSCAASGFTFGGWPMGWVRQAPGKGLEWVSGIDIDGAPTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEEAGSWSFDYWGQGT LVTVSS (SEQ ID NO: 200)

40 BMS3h-307
EVQLLES GGGGLVQPGGSLRLSCAASGFTFSDQAMWWARQAPGKGLEWVSFIQGDGGFTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKPSKPFDYWGQGT LVTVSS (SEQ ID NO: 201)

45 BMS3h-308
EVQLLES GGGGLVQPGGSLRLSCAASGFTFETGQMWARQAPGKGLEWVSNIDGSGTYTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKAVRNFAFDYWGQGT LVTVSS (SEQ ID NO: 202)

50 BMS3h-309
EVQLLES GGGGLVQPGGSLRLSCAASGFTFSGHMSWVRQAPGKGLEWVSAISPHGHTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKGIRGWIGHDTQPFDYWGQGT LVTVSS (SEQ ID NO: 203)

55 BMS3h-310
EVQLLES GGGGLVQPGGSLRLSCAASGFTFESKDMLWVRQAPGKGLEWVSSISSDGHTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAQELGGSWQFDYWGQGT LVTVSS (SEQ ID NO: 204)

60 BMS3h-311
EVQLLES GGGGLVQPGGSLRLSCAASGFTFADRDMMWVRQAPGKGLEWVSGIGASGTSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDA AVYYCAKGGTGPTDLWDFDYWGQGT LVTVSS (SEQ ID NO: 205)

BMS3h-312
 EVQLLESGGGLVQPGGSLRLSCAASGFTFDDEKMLWVRQAPGKGLEWSSISVSLHTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKEEAGSWSFDYWGGTLTVSS (SEQ ID NO: 206)

5

BMS3h-313
 EVQLLESGGGLVQPGGSLRLSCAASGFTFGQERMIWVRQAPGKGLEWVSDISASGGTTYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKEEAGSWSFDYWGGTLTVSS (SEQ ID NO: 207)

10

BMS3h-37-1
 EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRQAPGKGLEWVSAISGDGYRTYYADSVKGRFTISRDN SMNTL
 YLQMNSLRAEDTAVYYCAKELGYFDYRGRGTLTVSS (SEQ ID NO: 208)

15

BMS3h-37-2
 EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWRRAPGKGLEWVSAISGDGYRTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKELGYFDYWGRGTLTVSS (SEQ ID NO: 209)

20

BMS3h-37-3
 EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWRRAPGKGLEWVSAISGDGYRTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKELGYFDYRVQGTTLTVSS (SEQ ID NO: 210)

25

BMS3h-37-4
 EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRKAPGKGLEWVSAISGDGYRTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKELGYFDYWGRGTLTVSS (SEQ ID NO: 211)

30

BMS3h-37-5
 EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRQAPGKGLEWISAISGDGYRTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKELGYFDYRVQGTTLTVSS (SEQ ID NO: 212)

35

BMS3h-37-6
 EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWRRAPGKGLEWVSAISGDGYRTYYADSVKGRFTISRDN SENTL
 YLQMNSLRAEDTAVYYCAKELGYFDYWGRGTLTVSS (SEQ ID NO: 213)

40

BMS3h-37-7
 EVQLLETGGGLVQPGGSLRLSCAASGFTFEWYEMQWRRAPGKGLEWVSAISGDGYRTYYADSVKGRFTISRDN SKNTL
 YLQMDSLRAEDTAVYYCAKELGYFDYWGRGTLTVTS (SEQ ID NO: 214)

45

BMS3h-37-8
 EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRQAPGKGLEWVSAISGDGYRTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKELGYFHYWGRGTLTVSS (SEQ ID NO: 215)

BMS3h-37-9
 EVQLLESGGGLVQPGGSLRLSCVASGFTFEWYEMQWVRQAPGNLEWISAISGDGYRTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKELGYFDYWGRGTLTVSS (SEQ ID NO: 216)

BMS3h-37-10
 EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWRRAPGKGLEWVSAISGDGYRTYYADSVKGRFTISRDN SKNTL
 YLLMNSLRAEDTAVYYCAKELGYFDYWGRGTLTVSS (SEQ ID NO: 217)

BMS3h-37-11
EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRKAPGKGLEWVSAISGDGYRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKELGYFDYRGRGTLVTVSS (SEQ ID NO: 218)

5 BMS3h-37-12
EVQLLESGGGLVQPGGSMRLSCAASGFTFEWYEMQWVRAPGKGLEWVSAISGDGYRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKELGYFDYRGRGTLVTVSS (SEQ ID NO: 219)

10 BMS3h-37-201
EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRAPGKGLEWVSMISGDGYRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKELGYFDYWGRGTLVTVSS (SEQ ID NO: 220)

15 BMS3h-37-202
EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRAPGKGLEWVSAISGDGWRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKELGYFDYWGRGTLVTVSS (SEQ ID NO: 221)

20 BMS3h-37-203
EVQLLESGGGLVQPGGSLRLSCAASGFTFGWYEMQWVRAPGKGLEWVSAISGDGYRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKELLYFDYWGRGTLVTVSS (SEQ ID NO: 222)

25 BMS3h-37-204
EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRAPGKGLEWVSAISGDGYRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKELGFFDYWGRGTLVTVSS (SEQ ID NO: 223)

30 BMS3h-37-205
EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRAPGKGLEWVSAISGDGYRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKELEYFDYWGRGTLVTVSS (SEQ ID NO: 224)

35 BMS3h-37-206
EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRAPGKGLEWVSAISGDGYRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLEYFDYWGRGTLVTVSS (SEQ ID NO: 225)

40 BMS3h-37-207
EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRAPGKGLEWVSAISGDGYRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKELAFFDYWGRGTLVTVSS (SEQ ID NO: 226)

45 BMS3h-37-208
EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRAPGKGLEWVSAISGDGYRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKELLYFDYWGRGTLVTVSS (SEQ ID NO: 227)

50 BMS3h-37-209
EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRAPGKGLEWVSAISGDGYRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKELEFFDYWGRGTLVTVSS (SEQ ID NO: 228)

55 BMS3h-37-210
EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRAPGKGLEWVSAISGDGYRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKELQFFDYWGRGTLVTVSS (SEQ ID NO: 229)

60 BMS3h-37-211
EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRAPGKGLEWVSAISGDGYRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKELLFFDYWGRGTLVTVSS (SEQ ID NO: 230)

BMS3h-37-212
 EVQLLESGGGLVRPGGSLRLSCAASGFTFEWYEMQWRRAPGKGLEWVSAISGDGYRTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKELEFFDYWGRGTLTVSS (SEQ ID NO: 231)

5 BMS3h-37-213
 EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWRRAPGKGLEWVSAISGDGYRTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKELLFFDYRGRGTLTVSS (SEQ ID NO: 232)

10 BMS3h-37-214
 EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWRRAPGKGLEWVSAISGDGYRTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKNLEYFDYWGRGTLTVSS (SEQ ID NO: 233)

15 BMS3h-37-215
 EVRLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWRRAPGKGLEWVSAISGDGYRTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKELQFFDYWGRGTLTVSS (SEQ ID NO: 234)

20 BMS3h-38-1
 EVQLLGSGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCSKEPFRFDYWGGTGLTVSS (SEQ ID NO: 235)

25 BMS3h-38-2
 EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCGKEPFRFDYWGGTGLTVSS (SEQ ID NO: 236)

BMS3h-38-3
 EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWISAISGSGGSTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCGKEPFRFDYWGGTGLTVSS (SEQ ID NO: 237)

30 BMS3h-38-4
 EVQLLDPGGGLVQPGGSLRLSCAASGFTFGKEEMIWVRQAPGKGLEWSSISGSGGSTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCGKEPFRFDYWGGTGLTVSS (SEQ ID NO: 238)

35 BMS3h-38-5
 EVQLLGSGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCGKEPFRFDYWGGTGLTVSS (SEQ ID NO: 239)

40 BMS3h-38-6
 EVQLLEPGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDN SKNTL
 YLLMNSLRAEDTAVYYCSKEPFRFDYWGGALTVSS (SEQ ID NO: 240)

45 BMS3h-38-7
 EVQLLDPGGGLVQPGGSLRLSCAASGFTFGKEEMIWVRQAPGKGLEWSSISGSGGSTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKEPLRFDYWGGTGLTVSS (SEQ ID NO: 241)

BMS3h-38-8
 EVQLLESGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWISAISGSGGSTYYADSVKGRFTIHRDN SKNTL
 YLQMNSLRAEDTAVYYCSKEPFRFDYRGLGTLTVSS (SEQ ID NO: 242)

BMS3h-38-9
EVQLLDPGGGLVQPGGSLRLSCAASGFTFGKEEMIWVRQAPGKGLEWSSISGSGGSTYYADSVKGRFTISRDNSENKNTLYLQMNSLRAEDTAVYYCAKEPLRFDYWGQGLTVTVSS (SEQ ID NO: 243)

5 BMS3h-38-10
EVQLLDGGGGLVQPGGSLRLSCAASGFTFEEEMIWVRQAPGKGLEWISAISGSGGSTYYADSVKGRFTISRDNSENKNTLYLQMNSLRAEDTAVYYCAKEPFRFDYWGQGLTVTVSS (SEQ ID NO: 244)

10 BMS3h-38-11
EVQLLDPGGGLVQPGGSLRLSCAASGFTFEEEMIWVRQAPGKGLEWISAISGSGGSTYYADSVKGRFTISRDNSENKNTLYLQMNSLRAEDTAVYYCGREPFRFDYWGQGLTVTVSS (SEQ ID NO: 245)

15 BMS3h-38-12
EVRLLSEGGGLVQPGGSLRLSCAASGFTFEEEMIWVRQAPGKGLEWISAISGSGGSTYYADSVKGRFTISRDNSENKNTLYLQMNSLRAEDTAVYYCGKEPFRFDYWGQGLTVTVSS (SEQ ID NO: 246)

20 BMS3h-38-13
EVQQLSEGGGLVQPGGSLRLSCAASGFTFEEEMIWVRQAPGKGLEWISAISGSGGSTYYADSVKGRFTISRDNSENKNTLYLQMNSLRAEDTAVYYCGKEPFRFDYWGQGLTVTVSS (SEQ ID NO: 247)

BMS3h-38-201
EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEMIWVRQAPGKGLEWISAISGSGGSTYYADSVKGRFTISRDNSENKNTLYLQMNSLRAEDTAVYYCGKEPFRFDYWGQGLTVTVSS (SEQ ID NO: 248)

25 BMS3h-38-202
EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEMIWVRQAPGKGLEWISAISGSGGSTYYADSVKGRFTISRDNSENKNTLYLQMNSLRAEDTAVYYCGKEPFRFDYWGQGLTVTVSS (SEQ ID NO: 249)

30 BMS3h-38-203
EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEMIWVRQAPGKGLEWISAISGSGGSTYYADSVKGRFTISRDNSENKNTLYLQMNSLRAEDTAVYYCGKEPFRFDYWGQGLTVTVSS (SEQ ID NO: 250)

35 BMS3h-38-204
EVQLLASGGGLVQPGGSLRLSCAASGFTFPQEEMIWVRQAPGKGLEWISAISGSGGSTYYADSVKGRFTISRDNSENKNTLYLQMNSLRAEDTAVYYCGKEPFRFDYWGQGLTVTVSS (SEQ ID NO: 251)

40 BMS3h-38-205
EVQLLASGGGLVQPGGSLRLSCAASGFTFFAAEMIWVRQAPGKGLEWISAISGSGGSTYYADSVKGRFTISRDNSENKNTLYLQMNSLRAEDTAVYYCGKEPFRFDYWGQGLTVTVSS (SEQ ID NO: 252)

BMS3h-38-206
EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEMIWVRQAPGKGLEWISAISRPGTSTYYADSVKGRFTISRDNSENKNTLYLQMNSLRAEDTAVYYCGKEPFRFDYWGQGLTVTVSS (SEQ ID NO: 253)

45 BMS3h-38-207
EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEMIWVRQAPGKGLEWISAISRMGSTYYADSVKGRFTISRDNSENKNTLYLQMNSLRAEDTAVYYCGKEPFRFDYWGQGLTVTVSS (SEQ ID NO: 254)

50 BMS3h-38-208
EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEMIWVRQAPGKGLEWISAISRWGHSTYYADSVKGRFTISRDNSENKNTLYLQMNSLRAEDTAVYYCGKEPFRFDYWGQGLTVTVSS (SEQ ID NO: 255)

antibody polypeptide where the first variable domain has an apparent binding constant of 1 pM to 10 nM.

Also provided is an antibody polypeptide where the amino acid sequence of the first variable domain comprises (a) a CDR1 region which differs from the CDR1 region of BMS3h-56-269 (SEQ ID NO: 417) by up to two amino acids, (b) a CDR2 region which differs from the CDR2 region of BMS3h-56-269 (SEQ ID NO: 417) by up to two amino acids, (c) a CDR3 region which differs from the CDR3 region of BMS3h-56-269 (SEQ ID NO: 417) by up to two amino acids, (d) a FR1 region which differs from the FR1 region of BMS3h-56-269 (SEQ ID NO: 417) by up to two amino acids, (e) a FR2 region which differs from the FR2 region of BMS3h-56-269 (SEQ ID NO: 417) by up to two amino acids, (f) a FR3 region which differs from the FR3 region of BMS3h-56-269 (SEQ ID NO: 417) by up to two amino acids, and (g) a FR4 region which differs from the FR4 region of BMS3h-56-269 (SEQ ID NO: 417) by up to two amino acids.

Also provided is an antibody polypeptide where the amino acid sequence of the first variable domain comprises (a) a CDR1 region which differs from the CDR1 region of BMS3h-56-269 (SEQ ID NO: 417) by up to two amino acids, (b) a CDR2 region which differs from the CDR2 region of BMS3h-56-269 (SEQ ID NO: 417) by up to two amino acids, (c) a CDR3 region which differs from the CDR3 region of BMS3h-56-269 (SEQ ID NO: 417) by up to two amino acids.

BMS3h-38-209
 EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISRLGWSTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCGKEPFRYDYWGQGLTVTVSS (SEQ ID NO: 256)

5 BMS3h-38-210
 EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISRWGASTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCGKEPFRYDYWGQGLTVTVSS (SEQ ID NO: 257)

10 BMS3h-38-211
 EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISRQGGSTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCGKEPFRYDYWGQGLTVTVSS (SEQ ID NO: 258)

15 BMS3h-38-212
 EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISVSGWSTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCGKEPFRYDYWGQGLTVTVSS (SEQ ID NO: 259)

20 BMS3h-38-213
 EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISRWGWSTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCGKEPFRYDYWGQGLTVTVSS (SEQ ID NO: 260)

25 BMS3h-38-214
 EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISRNLSTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCGKEPFRYDYWGQGLTVTVSS (SEQ ID NO: 261)

BMS3h-38-215
 EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISGLGWSTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCGKEPFRYDYWGQGLTVTVSS (SEQ ID NO: 262)

30 BMS3h-38-216
 EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISALGWSTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCGKEPFRYDYWGQGLTVTVSS (SEQ ID NO: 263)

35 BMS3h-38-217
 EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISRRGYSTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCGKEPFRYDYWGQGLTVTVSS (SEQ ID NO: 264)

40 BMS3h-38-218
 EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISRHWSTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCGKEPFRYDYWGQGLTVTVSS (SEQ ID NO: 265)

45 BMS3h-38-219
 EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSSISRSGGSTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCGKEPFRYDYWGQGLTVTVSS (SEQ ID NO: 266)

BMS3h-38-220
 EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISRIGNSTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCGKEPFRYDYWGQGLTVTVSS (SEQ ID NO: 267)

BMS3h-38-221

EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWWSAISGHGWSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFRYDYWGQGLTVTVSS (SEQ ID NO: 268)

5 BMS3h-38-222

EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWWSAISRWGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFRYDYWGQGLTVTVSS (SEQ ID NO: 269)

BMS3h-38-223

10 EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWWSAISGSGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFRYDYWGQGLTVTVSS (SEQ ID NO: 270)

BMS3h-38-224

15 EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWWSAISGSGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFRYDYWGQGLTVTVSS (SEQ ID NO: 271)

BMS3h-38-225

20 EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWWSAISGSGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFRYDYWGQGLTVTVSS (SEQ ID NO: 272)

BMS3h-38-226

EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWWSAISGSGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPLYDYWGQGLTVTVSS (SEQ ID NO: 273)

25 BMS3h-38-227

EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWWSAISGSGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPMYDYWGQGLTVTVSS (SEQ ID NO: 274)

BMS3h-38-228

30 EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWWSAISRNGFSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFRYDYWGQGLTVTVSS (SEQ ID NO: 275)

BMS3h-38-229

35 EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWWSAISRTGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFRYDYWGQGLTVTVSS (SEQ ID NO: 276)

BMS3h-38-230

40 EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWWSAISREGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFRYDYWGQGLTVTVSS (SEQ ID NO: 277)

BMS3h-38-231

EVQLLASGGGLVQPGGSLRLSCAASGFPFEEEEMIWVRQAPGKGLEWWSAISRQGWSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFRYDYWGQGLTVTVSS (SEQ ID NO: 278)

45 BMS3h-38-232

EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWWSAISRGGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFRYDYWGQGLTVTVSS (SEQ ID NO: 279)

BMS3h-38-233

50 EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWWSAISRTGYSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFRYDYWGQGLTVTVSS (SEQ ID NO: 280)

BMS3h-38-234
 EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISRNGRSTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCGKEPFRYDYGQGT LVTVSS (SEQ ID NO: 281)

5
 BMS3h-38-235
 EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISRNGYSTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCGKEPFRYDYGQGT LVTVSS (SEQ ID NO: 282)

10
 BMS3h-38-236
 EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISRKGSSTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCGKEPFRYDYGQGT LVTVSS (SEQ ID NO: 283)

15
 BMS3h-38-237
 EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISRGGWSTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCGKEPFRYDYGQGT LVTVSS (SEQ ID NO: 284)

20
 BMS3h-38-238
 EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISRSGYSTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCGKEPFRYDYGQGT LVTVSS (SEQ ID NO: 285)

25
 BMS3h-38-239
 EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISRNGMSTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCGKEPFRYDYGQGT LVTVSS (SEQ ID NO: 286)

30
 BMS3h-38-240
 EVQLLES GGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISRNGYSTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCGKEPFRYDYGQGT LVTVSS (SEQ ID NO: 287)

35
 BMS3h-41-1
 EVQLLES GGGLVQPGGSLRLSCAASGFTFTEHEMIWVRQAPGKGLEWSSISGNGANTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRPEDTAVYYCAKEPLRFDYWGQGT LVTVSS (SEQ ID NO: 288)

40
 BMS3h-41-2
 EVQLLES GGGLVQPGGSLRLSCAASGSTFTEYEMIWVRQAPGKGLEWISSISGNGANTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYFCAKEPLRFDYRGQGT LVTVSS (SEQ ID NO: 289)

45
 BMS3h-41-3
 EVQLLEPGGGGLVQPGGSLRLSCAASGFTFTEYEMIWVRKAPGKGMEWSSISGNGANTYYADSVKGRFTISRDN SKNML
 YLQMNSLRAEDTAVYYCAKEPLRFGYWGQGT LVTVSS (SEQ ID NO: 290)

BMS3h-41-4
 EVQLLD SGGGGLVQPGGSLRLSCAASGFTFTEYEMIWVRQAPGKGLEWSSISGNGANTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKEPLRFDYWGRT LVTVSS (SEQ ID NO: 291)

BMS3h-41-5
 EVQLLGSGGGGLVQPGGSLRLSCAASGFTFTEYEMIWVRQAPGKSLEWSSISGNGANTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKEPLRYDDWGQGT LVTVSS (SEQ ID NO: 292)

BMS3h-41-6
EVQPLESGGGLVQPGGSLRLSCASGFTFNEYEMIWVRQAPGKGLEWSSISGNGANTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPLRFDYWGQGLTVTVSS (SEQ ID NO: 293)

5 BMS3h-41-7
EVQLLESGEGLVQPGGSLRLSCAASGFTFAEYEMIWVRQAPGKGLEWSSISGNGANTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPLRFDYWGQGLTVTVSS (SEQ ID NO: 294)

10 BMS3h-41-8
EVQLLDPGGGLVQPGGSLRLSCAASGFTFTESEMIWVRQAPGKGLEWSSISGNGANTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPLRFDYWGQGLTVTVSS (SEQ ID NO: 295)

15 BMS3h-41-9
EVQLLEPGGGLVQPGGSLRLSCAASGFTFTEYEMIWVRKAPGKGMEWSSISGNGANTYYADSVKGRFTISRDN SKNTL
YLQMNSLRPEDTAVYYCAKEPLRFDWVGQGLTVTVSS (SEQ ID NO: 296)

20 BMS3h-41-10
EVQLLESGVGLVQPGGSLRLSCAASGFTFTEYEMIWVRKAPGKGLEWSSISGNGANTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPLRFDNWVGQGLTVTVSS (SEQ ID NO: 297)

25 BMS3h-41-11
EVQLLESRGGLVQPGGSLRLSCAASGFTFTEHEMIWVRQAPGKGLEWSSISGNGANTYYADSVKGRFSVSRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPLRFDYWGQGLTVTVSS (SEQ ID NO: 298)

30 BMS3h-41-12
EVQPLESGGGLVQPGGSLRLSCAASGFTFTEYEMIWVRQAPGKGLEWSSISGNGANTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPLRFDYWGQGLTVTVSS (SEQ ID NO: 299)

35 BMS3h-41-13
EVQLLESAGGLVQPGGSLRLSCAASGFTFAEYEMIWVRQAPGKGLEWSSISGNGANTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPLRFDYWGQGLTVTVSS (SEQ ID NO: 300)

40 BMS3h-41-14
EVQLLEPGGGLVQPGGSLRLSCAASGFTFTEYEMIWVRQAPGKGLEWSSISGNGANTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPLRFDNWVGQGLTVTVSS (SEQ ID NO: 301)

45 BMS3h-43-1
EVQLLESGGGLVQPGGSLRLSCTASGFTFNMYEMSWVRQAPGKGLEWVSGISRRGFTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPITYDLRYARFDYSGQGLTVTVSS (SEQ ID NO: 302)

50 BMS3h-43-2
EEQLLESGGGLVQPGGSLRLSCTASGFTFNMYEMSWVRQAPGKGLEWVSGISRRGFTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPITYATRYARFDYWGQGLTVTVSS (SEQ ID NO: 303)

55 BMS3h-43-3
EVQLLESGGGLVQPGGSLRLSCTASGFTFNMYEMSWVRQAPGKGLEWVSGISRRGFTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPITYDMRYARFDYGGQGLTVTVSS (SEQ ID NO: 304)

60 BMS3h-43-4
EVQLLESGGGLVQPGGSLRLSCTASGFTFNMYEMSWVRQAPGKGLEWVSGISRRGFTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPITYDMRYARFDNWVGQGLTVTVSN (SEQ ID NO: 305)

BMS3h-43-5
 EVQLLES GGGLVQPGGSLRLSCTASGFTFNMYEMSWVRQAPGKGLEWVSGISRRGFTTYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKEPITYDLRYARFDYSGQGLTVTVSS (SEQ ID NO: 306)

5 BMS3h-43-6
 EVQLMES GGGLVQPGGSLRLSCTASGFSFNMYEMSWVRQAPGKGLEWVSGISRRGYTTYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKEPITYDMRYARFDYWGRGTLTVTVSS (SEQ ID NO: 307)

10 BMS3h-43-7
 EVQLLES GGGLVQPGGSLRLSCTASGFAFNMYEMSWVRQAPGKGLEWVSGISRHGFTTYADSVKGRFTVSRDN SKNTL
 YLQMNSLRAEDTAVYYCAKEPITYDMRYARSDYWGGQGLTVTVSS (SEQ ID NO: 308)

15 BMS3h-43-8
 EVQLLES GGGLVQPGGSLRLSCTASGFTFNMYEMSWVRQAPGKGLEWVSGISRRGFTTYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYFCAKEPITYDMRYARSDYWGGQGLTVTVSS (SEQ ID NO: 309)

20 BMS3h-43-9
 EVQLLES GGGLVQPGGSLRLSCTASGFTFNMYEMSWVRQAPGKGLEWVSGISRRGFTTYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKEPITYSMRYARFDYSGGLTMVTVSS (SEQ ID NO: 310)

25 BMS3h-43-10
 EVQLLES GGGLVQPGGSLRLSCTASGFTFNMYEMSWVRQAPGKGLEWVSGISRRGFTTYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKEPITYDMRYARFDYSGQGLTVTVSS (SEQ ID NO: 311)

BMS3h-43-11
 EVQLLES GGGLVQPGGSLRLSCTASGFTFNMYEMSWVRKAPGKGLEWVSGISRHGFTTYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKEPITYDMRYARFDYWGGQGLTVTVSS (SEQ ID NO: 312)

30 BMS3h-43-12
 EVQLFES GGGLVQPGGSLRLSCTASGFTFNMYEMSWVRQAPGKGLEWVSGISRRGFTTYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKEPITYDMRYARFDYWGRGTLTVTVSS (SEQ ID NO: 313)

35 BMS3h-43-13
 EVQLLES GGGLVQPGGSLRLSCTASGFTFNMYEMSWVRQAPGKGLEWVSGISRRGFTTYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKEPITYDMRYARFDYWGRGTLTVTVSS (SEQ ID NO: 314)

BMS3h-43-14
 EVQLLES GGGSVQPGGSLRLSCTASGFSFNMYEMSWVRQAPGKGLEWVSGISRRGFTTYADSVKGRFTISRDN SKNTL
 40 YLQMNSLRAEDTAVYYCAKEPITYDMRYARFDYWGGQGLTVTVSG (SEQ ID NO: 315)

BMS3h-43-15
 EVQLLES GGGLVQPGGSLRLSCTASGFTFNMYEMSWVRKAPGKGLEWVSGISRRGFTTYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKEPITYDMRYARFDYWGGQGLTVTVSS (SEQ ID NO: 316)

45 BMS3h-56-1
 EVQLLES GGGLVQPGGSLRLS CAASGFTFRDYEMWVRQAPGKGLERVSAINPQGTRTYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKLPTFEDWGQGLTVTVSS (SEQ ID NO: 317)

BMS3h-56-2
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGT LVTVSS (SEQ ID NO: 318)

5 BMS3h-56-3
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCTKLPIFEYWGQGT LVTVSS (SEQ ID NO: 319)

10 BMS3h-56-4
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFMFDDRGQGT LVTVSS (SEQ ID NO: 320)

15 BMS3h-56-5
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTTYADSVMGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGT LVTVSS (SEQ ID NO: 321)

20 BMS3h-56-6
EVQLLESGGGLVQPGGSLRLSCAASGFSFRDYEMWWVRQAPGKGLERVSAINPQGTRTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFIFDNRGQGT LVTVSS (SEQ ID NO: 322)

25 BMS3h-56-7
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTSVYHCAKPPFIFGDWGP GT LVTVSS (SEQ ID NO: 323)

30 BMS3h-56-8
EVQLLESGGGLVQPGGSRRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFEDWGQGT LVTVSS (SEQ ID NO: 324)

35 BMS3h-56-9
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTTYADSVMGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFMFDDRGQGT LVTVSS (SEQ ID NO: 325)

40 BMS3h-56-10
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKVLERVSAINPQGTRTTYADSVKGRFTISRDN SKNML
YLQMNSLRAEDTAVYYCAKLPFMFDDRGQGT LVTVSS (SEQ ID NO: 326)

45 BMS3h-56-11
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFMFDDRGQGT LVTVSS (SEQ ID NO: 327)

50 BMS3h-56-12
EVQLLESGGGLIQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCLKLPFIFDYWGQGT LVTVSS (SEQ ID NO: 328)

55 BMS3h-56-13
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTTYADSVKGRFTISRDN SKNTL
YLQMNSLRADDTAVYHCTKLPIFDYWGQGT LVTVSS (SEQ ID NO: 329)

60 BMS3h-56-14
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGMVLERVSAINPQGTRTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFFFD SRGQGT LVTVSS (SEQ ID NO: 330)

BMS3h-56-15
 EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWRRAPGKGLERSAINPQGTRTTYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKL PFTFEDWGQGLTVTVSS (SEQ ID NO: 331)

5 BMS3h-56-16
 EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERSAINPQGTRTTYADSV MGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKL PFTFEDWGQGLTVTVSS (SEQ ID NO: 332)

10 BMS3h-56-17
 EVQLLES GGGGLVQPGGSLRLSCAASGFSFRDYEMWWYRQAPGKGLERSAINPQGTRTTYADSV KGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKL PFTFEDWGQGLTVTVSS (SEQ ID NO: 333)

15 BMS3h-56-18
 EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERSAINPQGTRTTYADSV KGRFTISRDN SKNML
 YLQMNSLRAEDTAVYYCAKL PFTFEDWGQGLTVTVSS (SEQ ID NO: 334)

20 BMS3h-56-19
 EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERSAINPQGTRTTYADSV KGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYHCAKL PFTFEDWGQGLTVTVSS (SEQ ID NO: 335)

25 BMS3h-56-20
 EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERSAINPQGTRTTYADSV KGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCTKL PFTFEDWGQGLTVTVSS (SEQ ID NO: 336)

BMS3h-56-21
 EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERSAINPQGTRTTYADSV KGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCKL PFTFEDWGQGLTVTVSS (SEQ ID NO: 337)

30 BMS3h-56-22
 EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERSAINPQGTRTTYADSV KGRFTISRDN SKNTL
 YLQMNSLRADDTAVYHCTKL PFI FEYWGQGLTVTVSS (SEQ ID NO: 338)

35 BMS3h-56-23
 EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERSAINPQGTRTTYADSV MGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKEPYSFDSWGQGLTVTVSS (SEQ ID NO: 339)

40 BMS3h-56-24
 EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERSAINPQGTRTTYADSV MGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYHCAKEPYSYDYGQGLTVTVSS (SEQ ID NO: 340)

45 BMS3h-56-25
 EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWRRAPGKGLERSAINPQGTRTTYADSV MGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKL PFTFDDWGQGLTVTVSS (SEQ ID NO: 341)

BMS3h-56-26
 EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWRRAPGKGLERSAINPQGTRTTYADSV MGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKL PFMFDDRQGLTVTVSS (SEQ ID NO: 342)

BMS3h-56-27
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYADSVMGFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFMFDDWGQGLVTVSS (SEQ ID NO: 343)

5 BMS3h-56-28
EVQLLESGGGLVQPGGSLRLSCAASGFTFAGYELWWVRQAPGKGLERVSAINPQGTRTYADSVMGFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGLVTVSS (SEQ ID NO: 344)

10 BMS3h-56-29
EVQLLESGGGLVQPGGSLRLSCAASGFTFAGYELWWVRQAPGKGLERVSAINPQGTRTYADSVMGFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFMFDDRQGLVTVSS (SEQ ID NO: 345)

15 BMS3h-56-30
EVQLLESGGGLVQPGGSLRLSCAASGFTFAGYEMWWFRQAPGKGLERVSAINPQGTRTYADSVMGFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGLVTVSS (SEQ ID NO: 346)

20 BMS3h-56-31
EVQLLESGGGLVQPGGSLRLSCAASGFTFAGYEMWWFRQAPGKGLERVSAINPQGTRTYADSVMGFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFMFDDRQGLVTVSS (SEQ ID NO: 347)

25 BMS3h-56-32
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLEWVSAINPQGTRTYADSVMGFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGLVTVSS (SEQ ID NO: 348)

30 BMS3h-56-33
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLEWVSAINPQGTRTYADSVMGFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFMFDDRQGLVTVSS (SEQ ID NO: 349)

35 BMS3h-56-202
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPTYFSRQGLVTVSS (SEQ ID NO: 350)

40 BMS3h-56-203
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPPFFFEWGQGLVTVSS (SEQ ID NO: 351)

45 BMS3h-56-204
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPTYFKDWGQGLVTVSS (SEQ ID NO: 352)

50 BMS3h-56-205
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPHYFSEWGQGLVTVSS (SEQ ID NO: 353)

55 BMS3h-56-206
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYHCAKLPMFFEDWGQGLVTVSN (SEQ ID NO: 354)

60 BMS3h-56-207
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPPFSEWGQGLVTVSS (SEQ ID NO: 355)

BMS3h-56-208
 EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYADSVKGRFTISRDN SKNTL
 YLQMDSLRAEDTAVYYCAKLPFYFSEWGQGLTVTVSS (SEQ ID NO: 356)

5 BMS3h-56-209
 EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPYGNLTYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKLPFTFEDWGQGLTVTVSS (SEQ ID NO: 357)

10 BMS3h-56-210
 EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPPGTLTYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKLPFTFEDRGQGLTVTVSS (SEQ ID NO: 358)

15 BMS3h-56-211
 EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGGLTYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKLPFTFEDWGQGLTVTVSS (SEQ ID NO: 359)

20 BMS3h-56-212
 EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPMGGFTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKLPFTFEDWGQGLTVTVSS (SEQ ID NO: 360)

25 BMS3h-56-213
 EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGSHTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKLPFTFEDWGQGLTVTVSS (SEQ ID NO: 361)

BMS3h-56-214
 EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPSGGLTYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKLPFTFDDRQGLTVTVSS (SEQ ID NO: 362)

30 BMS3h-56-215
 EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPHGSLTYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGLTVTVSS (SEQ ID NO: 363)

35 BMS3h-56-216
 EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPAGRLTYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKLPFTFEDWGQGLTVTVSS (SEQ ID NO: 364)

40 BMS3h-56-217
 EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGSLTYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKLPFTFEDWGQGLTVTVSS (SEQ ID NO: 365)

45 BMS3h-56-218
 EVQLLES GGGGLVQPGGSLRLSCAASGFTFPDYEMWWVRQAPGKGLERVSAINPQGTRTYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYHCAKLPFTFDDWGQGLTVTVSS (SEQ ID NO: 366)

BMS3h-56-219
 EVQLLES GGGGLVQPGGSLRLSCADSGFTFPPVEMWWVRQAPGKGLERVSAINPQGTRTYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKLPFTFEDWGQGLTVTVSS (SEQ ID NO: 367)

50 BMS3h-56-220

EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPYGGLTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGLTVTVSS (SEQ ID NO: 368)

5 BMS3h-56-221
EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGNHTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGLTVTVSS (SEQ ID NO: 369)

10 BMS3h-56-222
EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPHGGYTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGLTVTVSS (SEQ ID NO: 370)

15 BMS3h-56-223
EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGRGLERVSAINPPGMLTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGLTVTVSS (SEQ ID NO: 371)

20 BMS3h-56-224
EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGQLTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGLTVTVSS (SEQ ID NO: 372)

25 BMS3h-56-225
EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGGYTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGLTVTVSS (SEQ ID NO: 373)

30 BMS3h-56-226
EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPSGGLTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGLTVTVSS (SEQ ID NO: 374)

35 BMS3h-56-227
EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPSGGLTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGLTVTVSS (SEQ ID NO: 375)

40 BMS3h-56-228
EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPSGTLTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGLTVTVSS (SEQ ID NO: 376)

45 BMS3h-56-229
EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPYGSLTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGLTVTVSS (SEQ ID NO: 377)

50 BMS3h-56-230
EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGGYTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGLTVTVSS (SEQ ID NO: 378)

BMS3h-56-231
EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGGLTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGLTVTVSS (SEQ ID NO: 379)

BMS3h-56-232
EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGSHTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGLTVTVSS (SEQ ID NO: 380)

Further provided is an antibody polypeptide where the amino acid sequence of the first variable domain differs from the amino acid sequence of BMS3h-56-258 (SEQ ID NO: 10) or BMS3h-56-269 (SEQ ID NO: 417) by up to 10 amino acids.

5 Further provided is an antibody polypeptide where the amino acid sequence of the first variable domain differs from the amino acid sequence of BMS3h-56-258 (SEQ ID NO: 10) or BMS3h-56-269 (SEQ ID NO: 417) by up to 5 amino acids.

Further provided is an antibody polypeptide where the amino acid sequence of the first variable domain differs from the amino acid sequence of BMS3h-56-258 (SEQ ID NO: 10) or BMS3h-56-269 (SEQ ID NO: 417) by two amino acids.

10 Further provided is an antibody polypeptide where the amino acid sequence of the first variable domain differs from the amino acid sequence of BMS3h-56-258 (SEQ ID NO: 10) or BMS3h-56-269 (SEQ ID NO: 417) by one amino acid.

Further provided is an antibody polypeptide where the antibody polypeptide is selected from the lineage group of BMS3h-56, and where the amino acid sequence of the first variable domain further comprises: (a) a CDR1 region having a sequence X_1 -Tyr-Glu- Y_1 -Trp (SEQ ID NO: 1274), where X_1 is Asp or Gly, and Y_1 is Met or Leu; (b) a CDR2 region having a sequence Ala-Ile-Asn-Pro- X_2 -Gly- Y_2 - Z_2 -Thr-Tyr-Tyr-Ala-Asp-Ser-Val- A_2 -Gly (SEQ ID NO: 1275), where X_2 is Gln, Tyr, Pro, Trp, or Ala, Y_2 is Thr, Ser, Asn, Gly, Met, or Gln, Z_2 is Arg, Leu, Tyr, His, or Phe, and A_2 is Lys or Met; and (c) a CDR3 region having a sequence X_3 -Pro- Y_3 - Z_3 -Phe- A_3 - B_3 (SEQ ID NO: 1276), where X_3 is Leu or Pro, Y_3 is Phe, Gln, Thr, or Met, Z_3 is Tyr, Pro, Leu, Thr, Ile, Phe, or Met, A_3 is Gln, His, Asp, Ser, Lys, Glu, or Gly, and B_3 is Glu, Asp, or Tyr.

Further provided is an antibody polypeptide where the amino acid sequence of the first variable domain comprises: (a) a FR1 region having a sequence Glu-Val-Gln-Leu-Leu-Glu-Ser-Gly-Gly-Gly--Leu-Val-Gln-Pro-Gly-Gly-Ser- X_1 -Arg-Leu-Ser-Cys-Ala-Ala-Ser-Gly-Phe-Thr-Phe- Y_1 (SEQ ID NO: 1277), where X_1 is Leu or Arg, and Y_1 is Arg or Ala; (b) a FR2 region having a sequence Trp-Val-Arg- X_2 -Ala-Pro-Gly- Y_2 - Z_2 -Leu-Glu-Arg-Val-Ser (SEQ ID NO: 1278), where X_2 is Gln or Arg, Y_2 is Lys or Arg, and Z_2 is Gly or Val; (c) a FR3 region having a sequence Arg-Phe-Thr-Ile-Ser-Arg-Asp-Asn-Ser-Lys-Asn- X_3 -Lys-Tyr-Leu-Gln-Met-Asn-Ser-Leu-Arg-Ala- Y_3 -Asp-Thr- Z_3 -Val-Tyr- A_3 -Cys- B_3 -Lys (SEQ ID NO: 1279), where X_3 is Thr or Met, Y_3 is Glu or Asp, Z_3 is Ala or Ser, A_3 is Tyr or His, and B_3 is Ala or Thr; and (d)

BMS3h-56-233
EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGTLTYADSVKGRFTISRDN
SKNTLYLQMNSLRAEDTAVYYCAKLPFTFDDWGQGT LVTVSS (SEQ ID NO: 381)

5 BMS3h-56-234
EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPNGRLTYADSVKGRFTISRDN
SKNTLYLQMNSLRAEDTAVYYCAKLPFTFADWGQGT LVTVSS (SEQ ID NO: 382)

10 BMS3h-56-235
EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGQLTYADSVKGRFTISRDN
SKNTLYLQMNSLRAEDTAVYYCAKLPFTFDDWGQGT LVTVSS (SEQ ID NO: 383)

15 BMS3h-56-236
EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPHGGLTYADSVKGRFTISRDN
SKNTLYLQMNSLRAEDTAVYYCAKLPFTFDDWGQGT LVTVSS (SEQ ID NO: 384)

20 BMS3h-56-237
EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPAGMLTYADSVKGRFTISRDN
SKNTLYLQMNSLRAEDTAVYYCAKLPFTFDDWGQGT LVTVSS (SEQ ID NO: 385)

25 BMS3h-56-238
EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPHGTLTYADSVKGRFTISRDN
SKNTLYLQMNSLRAEDTAVYYCAKLPFTFDDWGQGT LVTVSS (SEQ ID NO: 386)

30 BMS3h-56-239
EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGSLTYADSVKGRFTISRDN
SKNTLYLQMNSLRAEDTAVYYCAKLPFTFDDWGQGT LVTVSS (SEQ ID NO: 387)

35 BMS3h-56-240
EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPYGGLTYADSVKGRFTISRDN
SKNTLYLQMNSLRAEDTAVYYCAKLPFTFDDWGQGT LVTVSS (SEQ ID NO: 388)

40 BMS3h-56-241
EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPAGFLTYYADSVKGRFTISRDN
SKNTLYLQMNSLRAEDTAVYYCAKLPFTFDDWGQGT LVTVSS (SEQ ID NO: 389)

45 BMS3h-56-242
EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPYGGLTYADSVKGRFTISRDN
SKNTLYLQMNSLRAEDTAVYYCAKLPFTFDDWGQGT LVTVSS (SEQ ID NO: 390)

50 BMS3h-56-243
EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGGFTYYADSVKGRFTISRDN
SKNTLYLQMNSLRAEDTAVYYCAKLPFTFDDWGQGT LVTVSS (SEQ ID NO: 391)

55 BMS3h-56-244
EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGGLTYADSVKGRFTISRDN
SKNTLYLQMNSLRAEDTAVYYCAKLPFTFDDWGQGT LVTVSS (SEQ ID NO: 392)

60 BMS3h-56-245
EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPYGGLTYADSVKGRFTISRDN
SKNTLYLQMNSLRAEDTAVYYCAKLPFTFDDWGQGT LVTVSS (SEQ ID NO: 393)

BMS3h-56-246
 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERSAINPWGTLTYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKLPFTFEDWGQGT LVTVSS (SEQ ID NO: 394)

5 BMS3h-56-247
 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERSAINPWGGYTYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKLPFTFEDWGRGT LVTVSS (SEQ ID NO: 395)

10 BMS3h-56-248
 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERSAINPYGNLTYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGT LVTVSS (SEQ ID NO: 396)

15 BMS3h-56-249
 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERSAINPHGGFTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKLPFTFEDWGQGT LVTVSS (SEQ ID NO: 397)

20 BMS3h-56-250
 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERSAINPAGFYTYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGT LVTVSS (SEQ ID NO: 398)

25 BMS3h-56-251
 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERSAINPAGGLTYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGT LVTVSS (SEQ ID NO: 399)

BMS3h-56-252
 EVQLLESGGGLVQPGGSLRLSCAASGFAFRDYEMWWVRQAPGKGLERSAINPHGSLTYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKLPFTFEDWGQGT LVTVSS (SEQ ID NO: 400)

30 BMS3h-56-253
 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERSAINPAGGYTYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYHCAKLPFTFEDWGQGT LVTVSS (SEQ ID NO: 401)

35 BMS3h-56-254
 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERSAINPQGTRTYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKLPFWFTEWGQGT LVTVSS (SEQ ID NO: 402)

40 BMS3h-56-255
 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERSAINPQGTRTYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKLPFMFSRQGQGT LVTVSS (SEQ ID NO: 403)

45 BMS3h-56-256
 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERSAINPQGTRTYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKLPFLFQEWGQGT LVTVSS (SEQ ID NO: 404)

BMS3h-56-257
 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERSAINPQGTRTYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKLPTRFEDWGQGT LVTVSS (SEQ ID NO: 405)

50 BMS3h-56-258

EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFYFHEWGQGT LVTVSS (SEQ ID NO: 406)

BMS3h-56-259

5 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFRDYWGQGT LVTVSS (SEQ ID NO: 407)

BMS3h-56-260

10 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPTFFKDWGQGT LVTVSS (SEQ ID NO: 408)

BMS3h-56-261

15 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKL PFFQEWGQGT LVTVSS (SEQ ID NO: 409)

BMS3h-56-262

EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKL PQLFHDRGQGT LVTVSS (SEQ ID NO: 410)

BMS3h-56-263

20 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKL PQLFEDWGQGT LVTVSS (SEQ ID NO: 411)

BMS3h-56-264

25 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYHCAKL PFGFSEWGQGT LVTVSS (SEQ ID NO: 412)

BMS3h-56-265

30 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKL PQLFQDWGQGT LVTVSS (SEQ ID NO: 413)

BMS3h-56-266

35 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKL PFFFHEWGQGT LVTVSS (SEQ ID NO: 414)

BMS3h-56-267

EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKL PHYFKDWGQGT LVTVSS (SEQ ID NO: 415)

BMS3h-56-268

40 EVQLLESGGGLVQSGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKL PFYFEWGQGT LVTVSS (SEQ ID NO: 416)

BMS3h-56-269

45 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKL PFRFSDRGQGT LVTVSS (SEQ ID NO: 417)

BMS3h-56-270

50 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKL PTLFQDWGQGT LVTVSS (SEQ ID NO: 418)

BMS3h-56-271
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERSAINPQGTRTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFYFSEWGQGT LVT VSN (SEQ ID NO: 419)

5 BMS3h-56-272
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERSAINPQGTRTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFWFQEWGQGT LVT VSS (SEQ ID NO: 420)

BMS3h-56-273
10 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERSAINPWGSLTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFYFQEWGQGT LVT VSS (SEQ ID NO: 421)

BMS3h-56-274
15 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERSAINPWGSLTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYHCAKLPMFFEDWGQGT LVT VSN (SEQ ID NO: 422)

BMS3h-56-275
20 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERSAINPWGSLTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFYFHEWGQGT LVT VSS (SEQ ID NO: 423)

BMS3h-56-276
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERSAINPWGSLTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKL PFF FQEWGQGT LVT VSS (SEQ ID NO: 424)

25 BMS3h-56-277
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERSAINPWGSLTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKL PFF FHEWGQGT LVT VSS (SEQ ID NO: 425)

BMS3h-56-278
30 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERSAINPWGGFTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFYFQEWGQGT LVT VSS (SEQ ID NO: 426)

BMS3h-56-279
35 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERSAINPWGGFTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYHCAKLPMFFEDWGQGT LVT VSN (SEQ ID NO: 427)

BMS3h-56-280
40 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERSAINPWGGFTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFYFHEWGQGT LVT VSS (SEQ ID NO: 428)

BMS3h-56-281
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERSAINPWGGFTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKL PFF FQEWGQGT LVT VSS (SEQ ID NO: 429)

45 BMS3h-56-282
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERSAINPWGGFTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKL PFF FHEWGQGT LVT VSS (SEQ ID NO: 430)

BMS3h-56-283
50 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERSAINPWGGLTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFYFQEWGQGT LVT VSS (SEQ ID NO: 431)

BMS3h-56-284
 EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGGLTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYHCAKLPFFEDWGQGT LVT VSN (SEQ ID NO: 432)

5

BMS3h-56-285
 EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGGLTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKLPFFYHEWGQGT LVT VSS (SEQ ID NO: 433)

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BMS3h-56-286
 EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGGLTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKLPFFFQEWGQGT LVT VSS (SEQ ID NO: 434)

15

BMS3h-56-287
 EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGGLTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKLPFFFHEWGQGT LVT VSS (SEQ ID NO: 435)

20

BMS3h-56-288
 EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGGLTYYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYHCAKLPFFEDWGQGT LVT VSS (SEQ ID NO: 436)

25

BMS3h-106-1
 EVQLLETGGGLVQPGGSLRLSCAASGFTFSTYHMQWVRAPGKGLEWVSMIDADGLGTYADPVKGRFTISRDN SKNTL
 YLQMNSLRAKDTAVYYCARPGPQFGQFDYLGQGT LVT VSS (SEQ ID NO: 437)

30

BMS3h-106-2
 EVQLFESGGGLVQTGGSLRLSCAASGFTFSTYHMQWVRAPGKGLEWVSMIDADGLGKYYADPVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCVKPGPQFGQYDWGQGT LVT VSS (SEQ ID NO: 438)

35

BMS3h-107-1
 EVQLLES GGGGLVQPGGSLRLSCSASGFTFSGYDMQWVRAPGKGLEWVSTISASGVYTYADSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCAKYPNRFALNSFDYRGRGT LVT VSS (SEQ ID NO: 439)

40

BMS3h-107-2
 EVQLLES GGGGLVQPGGSLRLSCAASGFTFSGYDMQWVRAPGRGLEWVSTISASGVYTYTDSVKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCTKYPNRFARNFDYWGQGT LVT VSS (SEQ ID NO: 440)

45

BMS3h-131-1
 DILMTQSPSSLSASVGDRVITITCRANSSILWALAWYQQKPGKAPKLLIESSSGLQSGVPSRFSGSGSGTDFTLTIS SLQ
 PEDFATYYCVQNAVWPGETFSQGTKVEIKR (SEQ ID NO: 441)

50

BMS3h-131-2
 DIQMTQSPSSLSASVGDRVITITCRADSSILWALAWYQQKPGKAPKLLIESSSGLQSGVPSRFSGSGSGTDFTLTIS SLQ
 PEDFATYYCVQNAVWPGETFGQGTKVEIKR (SEQ ID NO: 442)

BMS3h-131-3
 DIQMTVSPSSLSASVGDRVITITCRADSSILWALAWYQQKPGKAPKLLIESSSGLQSGVPSRFSGSGSGTDFTLTIS SLQ
 PEDFATYYCVQNAVWPGETFGQGTKVEIKR (SEQ ID NO: 443)

BMS3h-131-4

DIQMTQSPSSLSASVGDRVTITCRANSSILWALAWYQQKPGKAPKLLIESSGLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCVQNAVWPGTFDQGTKVEIKR (SEQ ID NO: 444)

5 BMS3h-131-5
DIQMTQSPSSLSASVGDRVTITCRANSSILWALAWYQQKPGKAPKLLIESSTGLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCVQNAVWPGTFGQGTKVEIKR (SEQ ID NO: 445)

10 BMS3h-131-6
DIQMTVSPSSLSASVGDRVTITCRANSSILWALAWYQQKPGKAPKLLIESSGLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCVQNAVWPGTFGQGTKVEIKR (SEQ ID NO: 446)

15 BMS3h-131-7
DIQMTQSPSSLSASVGDRVTITCRADSSILWALAWYQQKPGKAPKLLIESSGLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCVQNAVWPGTFDQGTKVEIKR (SEQ ID NO: 447)

BMS3h-131-8
DIQMTQSPSSLSASVGDRVTITCRANSSILWALAWYQQKPGKAPELLIESSTGLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCVQNAVWPGTFGQGTKVEIKR (SEQ ID NO: 448)

20 BMS3h-131-9
DIQMTQSPSSLSASVGDRVTITCRANSSILWALAWYQQKPGKAPKLLIESSGLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCVQNAVWPGTFGQGTKVENKR (SEQ ID NO: 449)

25 BMS3h-131-10
DIQMTQSPSSLSASVGDRVTITCRANSSILWALAWYQQKPGKAPKLLIESSGLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCVQNAVWPGTFGQGTKVEIKR (SEQ ID NO: 450)

30 BMS3h-131-11
DIQMTQSPSSLSASVGDRVTITCRANSSILWALAWYQQKPGKAPKLLIESSGLQSGIPSRFSGSGSGTDFTLTISLQ
PEDFATYYCVQNAVWPGTFGQGTKVEIKR (SEQ ID NO: 451)

35 BMS3h-131-12
DIQMTQSPSSLSASVGDRVTITCRANSSILWALAWYQQKPGKAPKLLIESSGLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCVQNAVWPGTFGQGTKVEIKR (SEQ ID NO: 452)

BMS3h-131-13
DILLTQSPSSLSASVGDRVTITCRANSSILWALAWYQQKPGKAPKLLIESSGLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCVQNAVWPGTFGQGTKVEIKR (SEQ ID NO: 453)

40 BMS3h-131-14
DIQMTQSPSSLSASVGDRVTITCRANSSILWALAWYQQKPGKAPKLLIESSGLQSGVPSRFSGSGTGTDFLTISGLQ
PEDFATYYCVQNAVWPGTFDQGTKVEIKR (SEQ ID NO: 454)

45 BMS3h-131-15
DIQMTQSPSSLSASVGDRVTIPCRANSSILWALAWYQQKPGKAPKLLIESSGLQSGVPSRFSGSASGTDFTLTISLQ
PEDFATYYCVQNAVWPGTFGQGTKVEIKR (SEQ ID NO: 455)

50 BMS3h-193-1
DIQMAQSPSSLSASVGDRVTITCRASQTIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCHQYASPLTLGQGTKVEIKR (SEQ ID NO: 456)

BMS3h-193-2

DIQMTQSPSSLSASVGDSVTITCRASQTIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGTDFTLTISSLQ
PEDFATYYCHQYASPLTFGQGTNVEIKR (SEQ ID NO: 457)

5 BMS3h-193-3

DIQMTQSPSSLSASVGDRVTITCRASQTIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGTDFTLTISSLQ
PEDFAAYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 458)

BMS3h-193-4

10 DIQMTQSPSSLSASVGDRVTITCRASRTIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGTDFTLTISSLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 459)

BMS3h-193-5

15 DIQMTQSPSSLSASVGERVTITCRASQTIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGTDFTLTISNLQ
PEDSATYYCHQYASPLTLGQGTKVEIKR (SEQ ID NO: 460)

BMS3h-193-6

20 DIQMTQSPSSLSASVGDRVTITCRASQTIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGTDFTLTISSLQ
PEDFATYYCHQYASPLTLGQGTKVEIKR (SEQ ID NO: 461)

BMS3h-193-7

DIQITQSPSSLSASVGDRVTITCRASQTIERRLNWYQQKPGKDPKLLIYLASRLQSGVPSRFSGSGSGTDFTLTISSLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 462)

25 BMS3h-193-8

DIQMTQSPSSLSASVGDRVTITCRASQTIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGTDFTLTISSLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKW (SEQ ID NO: 463)

BMS3h-193-9

30 DIQLTQSPSSLSASVGDRVTITCRASQTIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGTEFTLTISSLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 464)

BMS3h-193-10

35 DIQMSQSPSTLSASVGDRVTITCRASQTIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGTDFTLTISSLQ
PEDFATYYCHQYESPPLMFGQGTKVEIKR (SEQ ID NO: 465)

BMS3h-193-11

40 DIQMTQSPSSLSASVGDRVTITCRASQTIERRLNWYQQKPGKDPKLLIYLASRLQSGVPSRFSGSGSGTDFTLTISSLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 466)

BMS3h-193-12

DIQMTQSPSSLSASVGDRVTITCRASQTIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGTDFTLTISSLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 467)

45 BMS3h-193-13

DIQMTQSPSSLFASVGDRVTITCRASQTIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGTDFTLTISSLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 468)

BMS3h-193-14

50 DIQMTQYPSLSASVGDRVTITCRASQSIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGTDFTLTISSLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 469)

BMS3h-193-15
 DIQMTQSPSSLSASVGDRVTITCRASRTIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGDFTLTISLQ
 PEDFATYYCHPYESPPLTFGQGTKVEIKR (SEQ ID NO: 470)

5 BMS3h-193-16
 DIQMTQSPSSLSASVGDRVTITCRASQAIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGDFTLTISLQ
 PEDFATYYCHQYASPLTLGQGTKVEIKR (SEQ ID NO: 471)

10 BMS3h-193-17
 NIQMTQSPSSLSASVGDRVTITCRASQAIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGDFTLTISLQ
 PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 472)

15 BMS3h-193-18
 DIQMTQSPSSLSASVGDRVTITCRASQTIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGDFTLTISLQ
 PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 473)

20 BMS3h-193-19
 DIQMTQSPSSLSASVGDRVTITCRASQTIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGTEFTLTISLQ
 PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 474)

25 BMS3h-193-20
 DIQMTQSPSSLSASVGDRVTITCRASQTIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGDFTLTISLQ
 PEDFATYYCHQYESPPLTFGQGTKVVIKR (SEQ ID NO: 475)

BMS3h-193-21
 DIQMTQSPSSLSASVGDSVTITCRASQTIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGDFTLTISLQ
 PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 476)

30 BMS3h-193-22
 HIQMTQSPSSLSASVGDRVTITCRASQTIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGDFTLTISLQ
 PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 477)

35 BMS3h-193-23
 DVQMTQSPSSLSASVGDRVTITCRASQTIERRLNWYQQKPGKAPKLLIYLSRLQSGVPSRFSGSGSGDFTLTISLQ
 PEDFATYYCHQYASPLTFGQGTKVEIKR (SEQ ID NO: 478)

40 BMS3h-193-24
 DIQMTQSPSSLSASVGDRVTITCRASQTIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGDFTLTISLQ
 PEDFATYYCHQYESPPLTFGQGTKVVIKR (SEQ ID NO: 479)

45 BMS3h-193-25
 DIQMTQSPSSLSASVGDRVTITCRASQTIERRLNWYQQKPGKAPRLLIYLATRLQSGVPSRFSGSGSGDFTLTISLQ
 PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 480)

BMS3h-193-26
 DIQMTQSPSSLSASVGDRVTITCRASQPIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGDFTLTISLQ
 PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 481)

50 BMS3h-193-27

DIQMTQSPSSLSASVGDRVTITCRASQTIGRRNLNWWYQQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 482)

BMS3h-193-28

5 DIQMTQSPSSLSASVGDRVTITCRASQSIERRNLNWWYQQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCHQYESPPLTFGQGTKVEIIR (SEQ ID NO: 483)

BMS3h-193-29

10 DIQMTQSPSSLSASVGDRVTITCRASQTIERRNLNWWYQQKPGKAPKLLIYLATRLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 484)

BMS3h-193-30

15 DIQMTQSPSSLSASVGDRVTITCRASQSIERRNLNWWYQQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 485)

BMS3h-193-2501

DIQMTQSPSSLSASVGDRVTITCRASQTIERRNLNWWYQQKPGKAPRLLIYLATRLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCHQFEHPPLTFGQGTKVEIKR (SEQ ID NO: 486)

20 BMS3h-193-2502

DIQMTQSPSSLSASVGDRVTITCRASFPIDRRNLNWWYQQKPGKAPRLLIYLATRLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 487)

BMS3h-193-2503

25 DIQMTQSPSSLSASVGDRVTITCRASSTIGRRNLNWWYQQKPGKAPRLLIYLATRLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 488)

BMS3h-193-2504

30 DIQMTQSPSSLSASVGDRVTITCRASSQIGRRNLNWWYQQKPGKAPRLLIYLATRLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 489)

BMS3h-193-2505

35 DIQMTQSPSSLSASVGDRVTITCRASERIGRRNLNWWYQQKPGKAPRLLIYLATRLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 490)

BMS3h-193-2506

DIQMTQSPSSLSASVGDRVTITCRASQQIGRRNLNWWYQQKPGKAPRLLIYLATRLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 491)

40 BMS3h-193-2507

DIQMTQSPSSLSASVGDRVTITCRASQPIARRNLNWWYQQKPGKAPRLLIYLATRLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 492)

BMS3h-193-2508

45 DIQMTQSPSSLSASVGDRVTITCRASGNIGRRNLNWWYQQKPGKAPRLLIYLATRLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 493)

BMS3h-193-2509

50 DIQMTQSPSSLSASVGDRVTITCRASRNIDRRNLNWWYQQKPGKAPRLLIYLATRLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 494)

BMS3h-193-2510
 DIQMTQSPSSLSASVGDRVITITCRASQSIGRRLNWYQQKPGKAPRLLIYLATRLQSGVPSRFSGSGSGTDFTLTISLQ
 PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 495)

5 BMS3h-193-2511
 DIQMTQSPSSLSASVGDRVITITCRASQNIIGTRLNWYQQKPGKAPRLLIYLATRLQSGVPSRFSGSGSGTDFTLTISLQ
 PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 496)

10 BMS3h-193-2512
 DIQMTQSPSSLSASVGDRVITITCRASEVIGRRLNWYQQKPGKAPRLLIYLATRLQSGVPSRFSGSGSGTDFTLTISLQ
 PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 497)

15 BMS3h-193-2513
 DIQMTQSPSSLSASVGDRVITITCRASEAIGRRLNWYQQKPGKAPRLLIYLATRLQSGVPSRFSGSGSGTDFTLTISLQ
 PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 498)

20 BMS3h-193-2514
 DIQMTQSPSSLSASVGDRVITITCRASTSIARRLNWYQQKPGKAPRLLIYLATRLQSGVPSRFSGSGSGTDFTLTISLQ
 PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 499)

25 BMS3h-193-2515
 DIQMTQSPSSLSASVGDRVITITCRASLNIGRRLNWYQQKPGKAPRLLIYLATRLQSGVPSRFSGSGSGTDFTLTISLQ
 PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 500)

30 BMS3h-193-2516
 DIQMTQSPSSLSASVGDRVITITCRASQTIERRLNWYQQKPGKAPRLLIYLSSKLQSGVPSRFSGSGSGTDFTLTISLQ
 PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 501)

BMS3h-198-1
 EVQLLESGGGLVQPGGSLRLSCAASGSTIAGYEMWWVRQAPGKGLERVS AISGGSTYYADSVKGRFTISRDDSKNTL
 YLQMNSLRAEDTAVYYCARDPYSFDYWGQGLTVTVSS (SEQ ID NO: 502)

35 BMS3h-198-2
 EVQPLESGGGLVQPGGSLRLSCAASGFTFAGYEMWWVRQAPGKGLERISAISGGSTYYADSVKGRFTISRDDSKNTL
 YLQMNSLRAEDTAVYYCARDPYSFDYWGQGLTVTVSS (SEQ ID NO: 503)

40 BMS3h-198-3
 EVQLLESGGGSVQPGGSLRLSCAATGSTFAGYEMWWVRQAPGKGLERVS AISGGSTYYADSVKGRFTISRDDSKNTL
 YLQMNSLRAEDTAVYYCARDPYSYDWGQGLTVSVSS (SEQ ID NO: 504)

BMS3h-198-4
 EVQLLESGGGLVQPGGSLRLSCAASGLTFAGYEMWWVRQAPGKGLERVS AISGGSTYYADSVKGRFTISRDDSKNTL
 YLQMNSLRAEDTAVYHCARDPYSFDYWGQGLTVTVSS (SEQ ID NO: 505)

45 BMS3h-198-5
 EVQLLESGGGLVQPGGSLRLSCAASGFTFAGYEMWWVRQAPGKGLERVS AISGGSTYYADSVKGRFTISRDDSKNTL
 YLQMNSLRAEDTAVYHCAKEPYSYDWGQGLTVTVSS (SEQ ID NO: 506)

50 BMS3h-198-6
 EVQLLESGGGLVQPGGSLRLSCAASGSTFAGYEMWWVRQAPGKGLERVS AISGGSTYYADSVKGRFTISRDDSKNTL
 YLQMNSLRPEDTAVYYCVKDPYSFDYWGQGLTVTVSS (SEQ ID NO: 507)

a FR4 region having a sequence X₄-Gly-Y₄-Gly-Thr-Leu-Val-Thr-Val-Ser-Z₄ (SEQ ID NO: 1280), where X₄ is Trp or Arg, Y₄ is Gln or Pro, and Z₄ is Ser or Asn.

Further provided is an antibody polypeptide where the first variable domain comprises the amino acid sequence of BMS3h-56-258 (SEQ ID NO: 10) or BMS3h-56-269 (SEQ ID NO:417).

Further provided is an antibody polypeptide where the antibody polypeptide is selected from the lineage group of BMS3h-37, where the first variable domain comprises the sequence Glu-Val-Gln-Leu-Leu-Glu-Ser-Gly-Gly-Gly-Leu-Val-X₁-Pro-Gly-Gly-Ser-Leu-Arg-Leu-Ser-Cys-Ala-Ala-Ser-Gly-Phe-Thr-Phe-Glu-Trp-Tyr-Glu-Met-Gln-Trp-Val-Arg-Arg-Ala-Pro-Gly-Lys-Gly-Leu-Glu-Trp-Val-Ser-Ala-Ile-Ser-Gly-Asp-Gly-Tyr-Arg-Thr-Tyr-Tyr-Ala-Asp-Ser-Val-Lys-Gly-Arg-Phe-Thr-Ile-Ser-Arg-Asp-Asn-Ser-Lys-Asn-Thr-Leu-Tyr-Leu-Gln-Met-Asn-Ser-Leu-Arg-Ala-Glu-Asp-Thr-Ala-Val-Tyr-Tyr-Cys-Ala-Lys-Y₁-Leu-Z₁-A₁-Phe-Asp-Tyr-B₁-Gly-Arg-Gly-Thr-Leu-Val-Thr-Val-Ser-Ser (SEQ ID NO: 1281); and where X₁ is Gln or Arg; Y₁ is Glu or Gly; Z₁ is Ala, Leu, or Glu; A₁ is Phe or Tyr; and B₁ is Trp or Arg.

Also provided is an antibody polypeptide where the antibody polypeptide is selected from the lineage group of BMS3h-38, where the first variable domain comprises the sequence Glu-Val-Gln-Leu-Leu-Ala-Ser-Gly-Gly-Gly-Leu-Val-Gln-Pro-Gly-Gly-Ser-Leu-Arg-Leu-Ser-Cys-Ala-Ala-Ser-Gly-Phe-X₁-Phe-Glu-Glu-Glu-Glu-Met-Ile-Trp-Val-Arg-Gln-Ala-Pro-Gly-Lys-Gly-Leu-Glu-Trp-Val-Ser-Y₁-Ile-Ser-Z₁-A₁-Gly-B₁-C₁-Thr-Tyr-Tyr-Ala-Asp-Ser-Val-Lys-Gly-Arg-Phe-Thr-Ile-Ser-Arg-Asp-Asn-Ser-Lys-Asn-Thr-Leu-Tyr-Leu-Gln-Met-Asn-Ser-Leu-Arg-Ala-Glu-Asp-Thr-Ala-Val-Tyr-Tyr-Cys-Gly-Lys-Glu-Pro-Phe-D₁-Tyr-Asp-Tyr-Trp-Gly-Gln-Gly-Thr-Leu-Val-Thr-Val-Ser-Ser (SEQ ID NO: 1282); and where X₁ is Thr or Pro; Y₁ is Ala or Ser; Z₁ is Arg or Gly; A₁ is Arg, Ser, Asn, Gln, Gly, His, or Leu; B₁ is Tyr, Phe, Trp, or Gly; C₁ is Ser or Gly; and D₁ is Arg, Met, or Pro.

Also provided is an antibody polypeptide where the antibody polypeptide is selected from the lineage group of BMS3h-198, where the first variable domain comprises the sequence Glu-Val-Gln-Leu-Leu-Glu-Ser-Gly-Gly-Gly-Leu-Val-Gln-Pro-Gly-Gly-Ser-Leu-Arg-Leu-Ser-Cys-Ala-Ala-Ser-Gly-Phe-Thr-Phe-Ala-Gly-Trp-Glu-X₁-Trp-Trp-Y₁-Arg-Gln-Ala-Pro-Gly-Lys-Gly-Leu-Glu-Arg-Val-Ser-Ala-Ile-Ser-Gly-Ser-Gly-Gly-Ser-Thr-Tyr-Tyr-Ala-Asp-Ser-Val-Lys-Gly-Arg-Phe-Thr-Ile-Ser-Arg-Asp-Z₁-A₁-Lys-Asn-Thr-Leu-Tyr-Leu-Gln-Met-Asn-Ser-Leu-Arg-Ala-Glu-Asp-Thr-Ala-Val-Tyr-B₁-Cys-Ala-C₁-D₁-Pro-Tyr-Ser-E₁-Asp-Tyr-F₁-

BMS3h-198-7
 EVQLLES GGG LVQP GGS LRLS CAAS GSTI AGYEMWWVRQAPGKGLERVSAISGSGGSTYYADSVKGRFTISRDDSKNTL
 YLQMNSLRAEDTAVYYCARDPYSFDYWGQGTLPVTSS (SEQ ID NO: 508)

5 BMS3h-198-8
 EVQLMES GGG LVQP GGS LRLS CAAS GSTF AGYEMWWVRQAPGKGLERVSAISGSGRSTYYADSVKGRFTISRDDSKNTL
 YLQMNSLRAEDTAVYYCAKDPYSFDYWGQGTLPVTSS (SEQ ID NO: 509)

10 BMS3h-198-9
 EVQLLES GGG LVQP GGS LRLS CAAS GSTF AGYEMWWVRQAPGKGLERVSAISGSGGSTYYADSVKGRFTISRDDSKNTL
 YLQMNSLRAEDTAVYYCAKEPYSFDYWGQGTLPVTSS (SEQ ID NO: 510)

15 BMS3h-198-10
 EVQLLES GGG LVQP GGS LRLS CAAS GSTI AGYEMWWVRQAPGKGLERVSAISGSGGSTYYADSVKGRFTISRDDSKNTL
 YLQMNSLRAEDTAVYYCAKDPYSFDYWGQGTLPVTSS (SEQ ID NO: 511)

20 BMS3h-198-11
 EVQLLES GGG LVQP GGS LRLS CAAS GSTF AGYEMWWVRQAPGKGLERVSAISGSGGSTYYADSVKGRFTISRDDSKNTL
 YLQMNSLRAEDTAVYYCARDPYSFDYWGQGTLPVSVSS (SEQ ID NO: 512)

25 BMS3h-198-12
 EVQLLES GGG LVQP GGS LRLS CAAS GSTI AGYEMWWVRQAPGKGLERVSAISGSGGSTYYADSVKGRFTISRDDSKNTL
 YLQMNSLRAEDTAVYYCAKDPYSFDYWGQGTLPVTSS (SEQ ID NO: 513)

BMS3h-198-13
 EVQLLES GGG LVQP GGS LRLS CAAS GSTF AGYEMWWVRQAPGKGLERVSAISGSGGSTYYADSVKGRFTITRDDSKNTL
 YLQMNSLRAEDTAVYYCAKEPYSFDYWGQGTLPVTSS (SEQ ID NO: 514)

30 BMS3h-198-14
 EVQLLES GGG LVQP GGS LRLS CAAS GSTF AGYEMWWVRQAPGKGLERVSAISGSGGSTYYADSVKGRFTISRDDTKNTL
 YLQMNSLRAEDTAVYYCAKDPYSFDYWRQGTLPVTSS (SEQ ID NO: 515)

35 BMS3h-198-15
 EVQLLES GGG LVQP GGS LRLS CAAS GSTF AGYEVWWVRQAPGKGLERVSAISGSGGSTYYADSVKGRFTISRDDSKNTL
 YLQMNSLRAEDTAVYYCARDPYSFDYWGQGTLPVTSS (SEQ ID NO: 516)

40 BMS3h-198-16
 EVQLLES GGG LVQP GGS LRLS CAAS GSTF AGYEMWWVRQAPGKGLERISAISGSGGSTYYADSVKGRFTISRDDSKNTL
 YLKMNLSLRAEDTAVYYCAKDPYSFDYWGQGTLPVTSS (SEQ ID NO: 517)

45 BMS3h-198-17
 EVQLLES GGG LVQP GGS LRLS CAAS GSTF AGYEMWWVRQAPGKGLERVSAISGSGGSTYYADSVKGRFTISRDDSKNTL
 YLQMNSLRAEDTAVYYCARDPYSFDYWGQGTLPVTSS (SEQ ID NO: 518)

BMS3h-198-18
 EVQLLES GGG LVQP GGS LRLS CAAS GLTF AGYEMWWVRAPGKGLERVAAISGSGGSTYYADSVKGRFTISRDDSKNTL
 YLQMNSLRAEDTAVYYCARDPYSFDYWGQGTLPVTSS (SEQ ID NO: 519)

50 BMS3h-198-19

EVQLLES GGGGLVQPGGSLRLSCAASGFTFAGYELWWVRQAPGKGLERVSAISGSGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLRAEDTAVYYCARDPYSFDYRGQGLTVTVSS (SEQ ID NO: 520)

5 BMS3h-198-20
EVQLLES GGGGLVQPGGSLRLSCAAPGFTLAGYEMWWVRQAPGKGLERVSAISGSGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLRAEDTAVYYCAKEPYSFDYWGQGLTVTVSS (SEQ ID NO: 521)

10 BMS3h-198-21
EVQLLES GGGGLVQPGGSLRLSCAASGLTFAGYEMWWVRAPGKGLERVSAISGSGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLRAEDTAVYYCARDPYSFDYWGQGLTVTVSS (SEQ ID NO: 522)

15 BMS3h-198-22
EVQLLES GGGGLVQPGGSLRLSCAASGFTFAGYEMWWVRQAPGKGLERVSAISGSGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLRAEDTAVYYCAKEPYSYDYWGHTLVTVSS (SEQ ID NO: 523)

20 BMS3h-198-23
EVQPLESGGGGLVQPGGSLRLSCAASGFTFAGYEMWWVRQAPGKGLERVSAISGSGGNTYYADSVKGRFTISRDDSKNTL
YLQMNSLRAEDTGVYYCARDPYSFDYWGQGLTVTVSS (SEQ ID NO: 524)

25 BMS3h-198-24
EVQLLES GGGGLVQPGGSLRLSCAASGFTFAGYEMWWVRQAPGKGLERVSAISGSGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLRAEDTAVYYCAKEPYSFDSWGQGLTVTVSS (SEQ ID NO: 525)

30 BMS3h-198-25
EAQLLES GGGGLVQPGGSLRLSCAASGLTFAGYEMWWVRQAPGKGLERVSAISGSGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLRAEDTAVYYCARDPYSFDYWGQGLTVTVSS (SEQ ID NO: 526)

35 BMS3h-198-26
EVQLLES GGGGLVQPGGSLRLSCAASGSTFAGYEMWWVRQAPGKGLERVSAISGSGGSTYYADSVKGRFSISRDDSKNTL
YLQMNSLRAEDTAVYYCAKEPYSFDHWGQGLTVTVSS (SEQ ID NO: 527)

40 BMS3h-198-27
EVQLLES GGGGLVQPGGSLRLSCAASGSTFAGYEMWWVRAPGKGLERVSAISGSGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLRAEDTAVYYCARDPYSFDYWGQGLTVTVSS (SEQ ID NO: 528)

45 BMS3h-198-28
EVQLLES GGGGLVQPGGSLRLSCAASGFTFAGYEMWWFRQAPGKGLERVSAISGSGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLRAEDTAVYYCAKDPYSFDNWGQGLTVTVSS (SEQ ID NO: 529)

50 BMS3h-198-29
EVQLLES GGGGLVEPGGSLRLSCAASGFTFAGYEMWWVRQAPGKGLERVSAISGSGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLRAEDTAVYYCAKEPYSFDHRGQGLTVTVSS (SEQ ID NO: 530)

55 BMS3h-198-30
EVQLLES GGGGLVQPGGSLRLSCAASGYTFAGYEMWWVRQAPGKGLERVSAISGSGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLRAEDTAVYYCAKEPYSFDHRGQGLTVTVSS (SEQ ID NO: 531)

60 BMS3h-198-31
EVQLLES GGGGLVQPGGSLRLSCAASGFTFAGYEMWWVRQAPGKGLERVSAISGSGGSTYYADSVKGRFTISRDNKNTL
YLQMNSLRAEDTAVYHCAKEPYSYDYWGQGLTVTVSS (SEQ ID NO: 532)

BMS3h-198-32
EVQLLESGGGLVQPGGSLRLSCAASGFTFAGYEMWWFRQAPGKGLERVSAISGSGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKDPYSFDNWGQGT LVTVSS (SEQ ID NO: 533)

5 BMS3h-198-33
EVQLLESGGGLVQPGGSLRLSCAASGFTFAGYEMWWVRQAPGKGLERVSAISGSGGSTYYADSVKGRFTISRDDS KNTL
YLQMNSLRAEDTAVYYCAKEPYSYDYGQGT LVTVSS (SEQ ID NO: 534)

10 BMS3h-198-34
EVQLLESGGGLVQPGGSLRLSCAASGFTFAGYEMWWVRQAPGKGLERVSAISGSGGSTYYADSVKGRFTISRDDS KNTL
YLQMNSLRAEDTAVYYCAKDPYSFDNWGQGT LVTVSS (SEQ ID NO: 535)

15 BMS3h-198-35
EVQLLESGGGLVQPGGSLRLSCAASGFTFAGYEMWWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDDS KNTL
YLQMNSLRAEDTAVYHCAKEPYSYDYGQGT LVTVSS (SEQ ID NO: 536)

20 BMS3h-198-36
EVQLLESGGGLVQPGGSLRLSCAASGFTFAGYEMWWFRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDDS KNTL
YLQMNSLRAEDTAVYYCAKDPYSFDNWGQGT LVTVSS (SEQ ID NO: 537)

25 BMS3h-198-37
EVQLLESGGGLVQPGGSLRLSCAASGFTFAGYELWWVRQAPGKGLERVSAISGSGGSTYYADSVKGRFTISRDDS KNTL
YLQMNSLRAEDTAVYYCAKDPYSFDYRGQGT LVTVSS (SEQ ID NO: 538)

30 BMS3h-198-38
EVQLLESGGGLVQPGGSLRLSCAASGFTFAGYELWWVRQAPGKGLERVSAISGSGGSTYYADSVKGRFTISRDDS KNTL
YLQMNSLRAEDTAVYYCARDPYSFDYWGQGT LVTVSS (SEQ ID NO: 539)

35 BMS3h-202-1
EVQLLESGGGLVQPGGSLRLSCAASGFTFPTAEMLWVRKAPGKGLEWSSISASGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPVSYVATFDYWGQGT LVTVSS (SEQ ID NO: 540)

40 BMS3h-202-2
EVQLLVSGGGLVQPGGSLRLSCAASGFTFPTAEMLWVRQAPGKGPEWSSISASGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPVSYVATFDYWGQGT LVTVSS (SEQ ID NO: 541)

45 BMS3h-202-3
EVQLLESGGGLVQPGGSLRLSCAASGFTFPTAEMVWVRKAPGMGLEWSSISASGGYTYADSVKGRFTISRDN SKNML
YLQMNSLRAEDTAVYYCAKEPVSYVATFDYWGQGT LVTVTS (SEQ ID NO: 542)

50 BMS3h-202-4
EVQLLVSGGGLVQPGGSLRLSCAASGFTFPTAEMVWVRQAPGKGLEWSSISASGGSTYYADSVKGRFSISRDDS KNTL
YLQMNSLRAEDTAVYYCAKEPVSYVATFDYWGHALVT VSS (SEQ ID NO: 543)

55 BMS3h-202-5
EVQLLESGGGLVQPGGSLRLSCAASGFTFPTAEMLWVRQAPGKGLEWSSISASGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPVSYVATFDYWGQGT LVTVSS (SEQ ID NO: 544)

60 BMS3h-202-6
EAQLLESGGGLVQPGGSLRLSCAASGFTFPTAEMVWVRQAPGKGLEWISSISASGGSTYYADSVKGRFTISRDN SKNTL
YLQLNSLRAEDTAVYYCAKEPVSYVATFDYWGRT LVTVSS (SEQ ID NO: 545)

BMS3h-202-7
 EVQLLES GGG L V Q P G G S L R L S C A A S G F T F P T A E M L W V R Q A P G K G L E W S S I S A S G G S T Y Y A D S V K G R F T I S R D N S K S T L
 Y L Q M N S L R A E D T A V Y Y C A K E P V S Y V A T F D Y W G P G A L V T V S S (SEQ ID NO: 546)

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BMS3h-202-8
 EVQLLES GGG L V Q P G G S L R L S C A A S G F T F P T A E M L W V R K A P G K G L E W S S I S A S G G S T Y Y A D S V K G R F T I S R D N S K N T L
 F L Q M N S L R A E D T A V Y Y C A K E P V S Y V A T F D Y W G Q G T L V T V S S (SEQ ID NO: 547)

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BMS3h-202-9
 EVQLLES GGG L V Q P G G S L R L S C A A S G F T F P T A E M L W V R Q A P G K G L E W S S I S A S G G S T Y Y A D S V K G R F T I S R D N S K N T L
 Y L Q M N S L R A E D T A V Y Y C A K E P V S Y V A T F D Y W G P G A L V T V S S (SEQ ID NO: 548)

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BMS3h-202-10
 EVQLLES GGG L V Q P G G S L R L S C A A S G F T F P T A E M L W V R Q A P G K G L E W S S I S A S G G S T Y Y A D S V K G R F T I S R D N S K N T L
 Y L Q M N S L R A E D T A V Y Y C A K E P V Y Y V A T F D Y W G Q G T L V T V S S (SEQ ID NO: 549)

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BMS3h-202-11
 EVQLLES GGG L V Q P G G S L R L S C A A S G F T F P T A E M L W V R K A P G K G L E W S S I S A S G G S T Y Y A D S V K G R F T I S R D N S K N T L
 Y L Q M N S L R A E D A A V Y Y C A K E P V S Y V A T F D Y W G Q G T L V T V S S (SEQ ID NO: 550)

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BMS3h-217-1
 N I Q M T Q S P S S L S A S V G D R V T I T C R A S H F I G T L L T W Y Q H K P G K A P K L L I T Y G S L L Q S G V P S R F S G S G S G T D F T L T I S S L Q
 P E D F A T Y Y C G Q G V L W P A T F G Q G T K V E I K R (SEQ ID NO: 551)

BMS3h-217-2
 D I Q M T Q S P S S L S A S V G D R V T I T C R A S H F I G T L L S W Y Q Q K P R K A P K L L I T Y G S L L Q S G V P S R F S G S G S G T D F T L T I S S L H
 P E D F A T Y Y C G Q G V L W P P T F G Q G T K V E I K R (SEQ ID NO: 552)

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BMS3h-217-3
 D I Q M T Q S P S S L T A S V G D R V T I T C R A S H F I G T L L S W Y Q Q K P G K A P K L L V T Y G S L L Q S G V P S R F S G S G S G T D F T L T I S N L Q
 P E D F A T Y Y C G Q G V L W P P T F G Q G T K V E N I R (SEQ ID NO: 553)

35

BMS3h-217-4
 D I Q M T Q S P S S L S A S V G D R V T I T C R A S H F I A T L L S W Y Q Q K P G K A P K L L I T Y G S L L Q S G V P S R F S G S G S G T D F T L T I S S L Q
 P E D F A T Y Y C G Q G V L W P P T F G Q G T K V E I K R (SEQ ID NO: 554)

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BMS3h-217-5
 D I Q M T Q S P S F L S A S V G D R V T I T C R A S H F I A T L L S W Y Q Q K P G K A P K L L I T Y G S L L Q S G V P S R F S G S G S G T D F T L T I S S L Q
 P E D F A T Y Y C G Q G V L W P P T F G Q G T K V E I K R (SEQ ID NO: 555)

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BMS3h-217-6
 D I Q M T Q S P S S L S A S V G D R V T I T C R A S H F I G T L L S W Y Q Q K P G K A T K L L I T Y G S L L Q S G V P S R F S G S G S G T D F T L T I S S L Q
 P E D F A T Y Y C G Q G V L W P P T F G Q G T K V E I K R (SEQ ID NO: 556)

BMS3h-217-7
 D I Q M T Q S P S S L S A S V G D R V T I T C R A S H F I G S L L S W Y Q H K P G K A P K L L I T Y G S L L Q S G V P S R F S G S G S G T D F T L T I S S L Q
 P E D F A T Y Y C G Q G V L W P A T F G Q G T K V E I K R (SEQ ID NO: 557)

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BMS3h-217-8

DIQMTQSPSSLSASVGDRVTITCRASHFIGTLLSWYQHKGKAPKLLITYGSLLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCGQGVLPATFGQGTKVEIKR (SEQ ID NO: 558)

BMS3h-217-9

5 DIQMTQSPSSLSASVGDRVTITCRASHFIGTLLSWYQHKGKAPKLLITYGSMLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCGQGVLPATFGQGTKVEIKR (SEQ ID NO: 559)

BMS3h-217-10

10 DIQMTQSPSSLSASVGDRVTITCRASHFIGTLLSWYQHKGKAPKLLITYGSLLQSGVPSRFSGSGSGTEFTLTISLQ
PEDFATYYCGQGVLPATFGQGTKVEIKR (SEQ ID NO: 560)

BMS3h-217-11

15 DIQMTQSPSSLTASVGDRVTITCRASHFIGTLLSWYQHKGKAPKLLITYGSLLQSGVPSRFSGSGSGTEFTLTISLQ
PEDFATYYCGQGVLPATFGQGTKVEIKR (SEQ ID NO: 561)

BMS3h-217-12

NIQMTQSPSSLSASVGDRVTITCRASHFIGTLLSWYQHKGKAPKLLITYGSLLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCGQGVLPATFGQGTKVEIKR (SEQ ID NO: 562)

BMS3h-217-13

20 DIQMTQSPSSLSASVGDRVTINCRASHFIGTLLSWYQHKGKAPKLLITYGSLLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCGQGVLPATFGQGTKVEIKR (SEQ ID NO: 563)

BMS3h-217-14

25 DIQLTQSPSSLSASVGDRVTITCRASHFIGTLLSWYQQKPGKATKLLITYGSLLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCGQGVLPPTFGQGTKVEIKR (SEQ ID NO: 564)

BMS3h-217-15

30 DIQMTQSPSSLYASVGDRVTITCRVSHFIGTLLSWYQQKPGKAPKLLITYGSLLQSGVPSRFSGSGSGTDFTLSISLQ
PEDFATYYCGQGVLPPTFGQGTKVEIKQ (SEQ ID NO: 565)

BMS3h-217-16

35 DIQMTQSPSSLSASVGDRVTITCRASHFIGTLLSWYQQKPRKAPKLLITYGSLLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCGQGVLPPTFGQGTKVEIKR (SEQ ID NO: 566)

BMS3h-217-17

DIQIIQSPSSLSASVGDRVTITCRASHFIGTLLSWYQQKPGKAPKLLITYGSLLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCGQGVLPPTFGQGTKVEIKR (SEQ ID NO: 567)

BMS3h-217-18

40 DIQMTQSPSSLSASVGDRVTITCRASHFIGTLLSWYQLKPGKAPKLLITYGSLLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCGQGVLPATFGQGTKVEIKR (SEQ ID NO: 568)

BMS3h-217-19

45 DIQMTQSPSSLSASVGDRVTITCRASHFIGTLLSWYQLKPGKAPKLLITYGSWLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCGQGVLPATFGQGTKVENKR (SEQ ID NO: 569)

BMS3h-217-20

50 DIQMTQSPSSLSASVGDRVTITCRASHFIGTLLSWYQLKPGKAPKLLITYGSLLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCGQGVLPATFGQGTKVEIKR (SEQ ID NO: 570)

BMS3h-217-21
 DIQMTQAPSSLSASVGDRVTITCRASHFIGTLLSWYQLKPGKAPKLLITYGSLLQSGVPSRFSGSGSGTDFTLTISLQ
 PEDFATYYCGQGVLPATFGQGTKVENKR (SEQ ID NO: 571)

5 BMS3h-217-22
 DIQMTQSPSSLSASVGDRVTITCRASHFIGSLLSWYQQKPGKAPKLLITYGSLLQSGVPSRFSGSGSGTDFALTISSLQ
 PEDFATYYCGQGVLPATFGQGTKVEIKR (SEQ ID NO: 572)

10 BMS3h-217-23
 DIQMTQSPSSLSASVGDRVTITCRASHFIGSLLSWYQVKPGKAPKLLITYGSLLQSGVPSRFSGSGSGTDFTLTISLQ
 PEDFATYYCGQGVLPATFGQGTVEIKR (SEQ ID NO: 573)

15 BMS3h-217-24
 DILMTQSPSSLSASVGDRVTITCRASHFIGSLLSWYQQKPGKAPKLLITYGSLLQSGVPSRFSGSGSGTDFTLTISLQ
 PEDFATYYCGQGVLPATFGQGTKVEIKR (SEQ ID NO: 574)

20 BMS3h-217-25
 DIQMTQSPSSLSASVGDRVTITCRASHFIGTLVSWYQQKPGKAPKLLITYGSLLQSGVPSRFSGSGSGTDFTLTISLQ
 PEDFATYYCGQGVLPATYGQGTKVEIKR (SEQ ID NO: 575)

BMS3h-217-26
 DIQMTQSPSSLSASVGDRVTITCRASHFIGTLVSWYQQKPGKAPKLLITYGSLLQSGVPSRFSGSGSGTDFTLTISLQ
 PEDFATYYCGQGVLPATFGQGTKVENKR (SEQ ID NO: 576)

25 BMS3h-217-27
 DIKMTQSPSSLSASVGDRVTITCRASHFIGTLVSWYQQKPGKAPKLLITYGSMLQSGVPSRFSGSGSGTDFTLTISLQ
 PEDFATYYCGQGVLPATFGQGTKVEIKR (SEQ ID NO: 577)

30 BMS3h-217-28
 DIQMTQSPSSLSASVGDRVTITCASHFIGTLVSWYQQKPGKAPKLLITYGSLLQSGVPSRFSGSGSGTDFTLTISLQ
 PEDFATYYCGQGVLPATFGQGTKVEIKR (SEQ ID NO: 578)

35 BMS3h-217-29
 DIQMTQSPSSLSASVGDRVTITCRASHFIGTLLSWYQQKPGKAPKLLITYGSWLQSGVPSRFSGSGSGTDFTLTISLQ
 PEDFATYYCGQGVLPATFGQGTKVEIKR (SEQ ID NO: 579)

40 BMS3h-217-30
 DIQMTQSPSSLSASVGDRVTITCRASHFIGTLLSWYQLKPGKAPKLLITYGSWLQSGVPSRFSGSGSGTDFTLTISLQ
 PEDFATYYCGQGVLPATFGQGTKVEIKR (SEQ ID NO: 580)

BMS3h-217-31
 DIQMTQSPSSLSASVGDRVTITCRASHFIGTLLSWYQQKPGKAPKLLITYGSLLQSGVPSRFSGSGFGTDFTLTISLQ
 PEDFATYYCGQEVLPATFGQGTKVEIKR (SEQ ID NO: 581)

45 BMS3h-217-32
 DIQMTQSPSSLSASVGDRVSITCRASHFIGTLLSWYQQKPGKAPKLLITYGSLLQSGVPSRFSGSGFGTDFTLTISLQ
 PEDLATYYCGQEVLPATFGQGTKVEIKR (SEQ ID NO: 582)

50 BMS3h-217-33
 DIQMTQSPSSLSASVGDRVTITCASHFIGTLLSWYQQKPGKAPKLLITYGSLLQSGVPSRFSGSGFGTDFTLTISLQ
 PEDFATYYCGQEVLPATFGQGTKVEIKR (SEQ ID NO: 583)

BMS3h-217-34
 DIQMTQSPSSLSASVGDRVTITCRASHFIGTLLSWYQQKPGKAPKLLITYGSLLQSGVPSRFSGSGFGTEFTLTIGSLQ
 PEDFATYYCGQGVLPATFGQGTKVEIKR (SEQ ID NO: 584)

5 BMS3h-217-35
 DIQMTQSPSSLSASVGDRVTITCRASHFIGTLLSWYQQKPGKATKLLITYGSLLQSGVPSRFSGSGSGTDFTLTISLQ
 PEDFATYYCGQGVLPPTFGQGTKVEIKR (SEQ ID NO: 585)

10 BMS3h-217-2301
 DIQMTQSPSSLSASVGDRVTITCRASHFIASLLSWYQVKPGKAPKLLITYGSLLQSGVPSRFSGSGSGTDFTLTISLQ
 PEDFATYYCGQGVLPATFGQGTVEIKR (SEQ ID NO: 586)

15 BMS3h-217-2302
 DIQMTQSPSSLSASVGDRVTITCRASHFIAQLLSWYQVKPGKAPKLLITYGSLLQSGVPSRFSGSGSGTDFTLTISLQ
 PEDFATYYCGQGVLPATFGQGTVEIKR (SEQ ID NO: 587)

20 BMS3h-217-2303
 DIQMTQSPSSLSASVGDRVTITCRASHFIAQLLSWYQVKPGKAPKLLITYGSLLQSGVPSRFSGSGSGTDFTLTISLQ
 PEDFATYYCGQGVLPATFGQGTVEIRR (SEQ ID NO: 588)

25 BMS3h-217-2304
 DIQMTQSPSSLSASVGDRVTITCRASHYIASLLSWYQVKPGKAPKLLITYGSLLQSGAPSRFSGSGSGTDFTLTISLQ
 PEDFATYYCGQGVLPATFGQGTVEIKR (SEQ ID NO: 589)

BMS3h-217-2305
 DIQMTQSPSSLSASVGDRVTITCRASHFIGSLLSWYQVKPGKAPKLLITWASYLQSGVPSRFSGSGSGTDFTLTISLQ
 PEDFATYYCGQGVLPATFGQGTVEIKR (SEQ ID NO: 590)

30 BMS3h-217-2306
 DIQMTQSPSSLSASVGDRVTITCRASHFIGSLLSWYQVKPGKAPKLLITWTSYLQSGVPSRFSGSGSGTDFTLTISLQ
 PEDFATYYCGQGVLPATFGQGTVEIKR (SEQ ID NO: 591)

35 BMS3h-217-2307
 DIQMTQSPSSLSASVGDRVTITCRASHFIGSLLSWYQVKPGKAPKLLITWSSYLQSGVPSRFSGSGSGTDFTLTISLQ
 PEDFATYYCGQGVLPATFGQGTVEIKR (SEQ ID NO: 592)

40 BMS3h-217-2308
 DIQMTQSPSSLSASVGDRVTITCRASHFIGSLLSWYQVKPGKAPKLLITWGSWLQSGVPSRFSGSGSGTDFTLTISLQ
 PEDFATYYCGQGVLPATFGQGTVEIKR (SEQ ID NO: 593)

45 BMS3h-217-2309
 DIQMTQSPSSLSASVGDRVTITCRASHFIGSLLSWYQVKPGKAPKLLITWASWLQSGVPSRFSGSGSGTDFTLTISLQ
 PEDFATYYCGQGVLPATFGQGTVEIKR (SEQ ID NO: 594)

BMS3h-217-2310
 DIQMTQSPSSLSASVGDRVTITCRASHFIGSLLSWYQVKPGKAPKLLITWSSWLQSGVPSRFSGSGSGTDFTLTISLQ
 PEDFATYYCGQGVLPATFGQGTVEIKR (SEQ ID NO: 595)

50 BMS3h-217-2311

DIQMTQSPSSLSASVGDRVTITCRASHWIAQLLSWYQVKPGKAPKLLITYGSLLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCGQGVLPATFGQGTVEIKR (SEQ ID NO: 596)

BMS3h-217-2312

5 DIQMTQSPSSLSASVGDRVTITCRASHFIGSLLRWYQVKPGKAPKLLITYGSLLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCGQGVLPATFGQGTVEIKR (SEQ ID NO: 597)

BMS3h-217-2313

10 DIQMTQSPSSLSASVGDRVTITCRASHRIAQLLSWYQVKPGKAPKLLITYGSLLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCGQGVLPATFGQGTVEIKR (SEQ ID NO: 598)

BMS3h-217-2314

15 DIQMTQSPSSLSASVGDRVTITCRASHYIASLLSWYQVKPGKAPKLLITYGSLLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCGQGVLPATFGQGTVEIKR (SEQ ID NO: 599)

BMS3h-217-2315

DIQMTQSPSSLSASVGDRVTITCRASHFIGSLLSWYQVKPGKAPKLLIRFGSLLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCGQGVLPATFGQGTVEIKR (SEQ ID NO: 600)

BMS3h-217-2316

20 DIQMTQSPSSLSASVGDRVTITCRASHFIGSLLSWYQVKPGKAPKLLITYKSYLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCGQGVLPATFGQGTVEIKR (SEQ ID NO: 601)

BMS3h-217-2317

25 DIQMTQSPSSLSASVGDRVTITCRASHFIGSLLSWYQVKPGKAPKLLITWGSYLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCGQGVLPATFGQGTVEIKR (SEQ ID NO: 602)

BMS3h-217-2318

30 DIQMTQSPSSLSASVGDRVTITCRASHFIWGPLSWYQVKPGKAPKLLITYGSLLQSGVPSRFSGSGSGTDFTLTISLQ
PEDSATYYCGQGVLPATFGQGTVEIKR (SEQ ID NO: 603)

BMS3h-217-2319

35 DIQMTQSPSSLSASVGDRVTITCRASHWIATLLSWYQVKPGKAPKLLITYGSLLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCGQGVLPATFGQGTVEIKR (SEQ ID NO: 604)

BMS3h-217-2320

DIQMTQSPSSLSASVGDRVTITCRASHFIWGPLSWYQVKPGKAPKLLITYGSLLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCGQGVLPATFGQGTVEIKR (SEQ ID NO: 605)

BMS3h-217-2321

40 DIQMTQSPSSLSASVGDRVTITCRASHFIGSLLNWYQVKPGKAPKLLITYGSLLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCGQGVLPATFGQGTVEIKR (SEQ ID NO: 606)

BMS3h-217-2322

45 GIQMTQSPSSLSASVGDRVTITCRASHFIGSLLSWYQVKPGKAPKLLITYGSWLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCGQGVLPATFGQGTVEIKR (SEQ ID NO: 607)

TABLE 4

Human Anti-CD40 Variable Domain Encoding Nucleotide Sequences

- BMS3h-56-201
 5 GAGGTGCAGCTGTTGGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
 GCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGTTTTACTTTCAGGAGT
 GGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 608)
- 10 BMS3h-56-258
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
 GCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
 15 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGTTTTACTTTCAGGAGT
 GGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 609)
- BMS3h-37
 20 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTGAGTGGTATGAGATGCAGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCGATTTCTGG
 TGATGGTTATCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCTTGGGTATTTTGACTACT
 GGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 610)
- BMS3h-38
 25 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGG
 TAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
 TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGAGCCGTTTCGTTTTGACTACT
 GGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 611)
- 30 BMS3h-41
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTACTGAGTATGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTTCGGG
 TAATGGTGCTAATACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
 35 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCCGCTTAGGTTTGACTACT
 GGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 612)
- BMS3h-43
 40 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTACAGCCTCCGGAT
 TCACCTTTAATATGTATGAGATGTCGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTAGTAG
 GCGTGGTTTTACTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
 TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGAGCCGATTACGTATGCTATGA
 GGTATGCGCGTTTTGACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 613)
- 45 BMS3h-56
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
 GCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
 TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTATTTTGACTACT
 50 GGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 614)

BMS3h-106

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTCGACTTATCATATGCAGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTGGAGTGGGTCTCAATGATTGATGC
GGATGGTCTTGGGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
5 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCGGGTCCGCAGTTTGGTCAGT
TTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 615)

BMS3h-107

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCTTCCGGAT
10 TCACCTTTTCGGGGTATGATATGCAGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTAGTGC
GTCGGGTGTTTTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCACCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATATCCTAATCGTTTTGCGCTTA
ATAATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 616)

BMS3h-131

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACATCACTTGCCGGGCAAATA
GTTCTATTTTGTGGGCGTTAGCTTGGTACCAGCAGAAACCAGGGAAAGCCCCCTAAGCTCCTGATCGAGAGTTCTTCCGG
TTTGCAAAGTGGGGTCCCATCACGTTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTGTTTCAAGATGCGGGTGGCCTGGTACGTTTCGGCCAAGGGACCAAGGTGGAAA
20 TCAAACGG (SEQ ID NO: 617)

BMS3h-193

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACATCACTTGCCGGGCAAGTC
AGACGATTGAGCGTCGTTTAAATTGGTATCAGCAGAAACCAGGGAAAGCCCCCTAAGCTCCTGATCTATCTTGCTTCCCG
25 TTTGCAAAGTGGGGTCCCATCACGTTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTGTCAGTATGCGAGTCCACCTTTGACGTTTCGGCCAAGGGACCAAGGTGGAAA
TCAAACGG (SEQ ID NO: 618)

BMS3h-198

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
30 TCACCTTTTGTGGGTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGG
TAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACGATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGATCCTTATAGTTTTGACTACT
GGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 619)

BMS3h-202

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTCCGACTGCTGAGATGGTGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTTCCGC
TAGTGGTGGTTCTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
40 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCCGGTGAGTTATGTGGCGA
CGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 620)

BMS3h-217

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACATCACTTGCCGGGCAAGTC
ATTTTATTGGTACTCTGTTATCTTGGTACCAGCAGAAACCAGGGAAAGCCCCCTAAGCTCCTGATCACTTATGGTTCCTT
GTTGCAAAGTGGGGTCCCATCACGTTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTGGTACGGGGGTGCTGTGGCCTGCGACGTTTCGGCCAAGGGACCAAGGTGGAAA
TCAAACGG (SEQ ID NO: 621)

BMS3h-1

G₁-H₁-Gly-Thr-Leu-Val-Thr-Val-Ser-Ser (SEQ ID NO: 1283); and where X₁ is Met or Leu; Y₁ is Val or Phe; Z₁ is Asp or Asn; A₁ is Ser or Thr; B₁ is Tyr or His; C₁ is Lys or Arg; D₁ is Asp or Glu; E₁ is Tyr or Phe; F₁ is Trp or Arg; G₁ is Gly or Arg; and H₁ is Gln or His.

5 Further provided is an antibody polypeptide where the antibody polypeptide is a domain antibody (dAb).

Further provided is an antibody polypeptide where the variable domain is fused to an Fc domain.

10 Further provided is an antibody polypeptide where the antibody polypeptide further comprises a second variable domain that specifically binds a second antigen, where the second antigen is an antigen other than human CD40.

Also provided is an antibody polypeptide where the second antigen is a cluster of differentiation (CD) molecule or a Major Histocompatibility Complex (MHC) Class II molecule.

15 Also provided is an antibody polypeptide where the second antigen is serum albumin (SA).

Provided is a nucleic acid encoding the antibody polypeptide disclosed herein.

Also provided is a vector comprising the nucleic acid disclosed herein.

Also provided is a host cell comprising the vector disclosed herein.

20 Provided is a pharmaceutical composition comprising a therapeutically-effective amount of the antibody polypeptide disclosed herein and a pharmaceutically acceptable carrier. Also provided is a pharmaceutical composition further comprising an immunosuppressive/immunomodulatory and/or anti-inflammatory agent.

25 Provided is a method of treating an immune disease in a patient in need of such treatment, comprising administering to the patient a therapeutically effective amount of the pharmaceutical composition disclosed herein. Also provided is a method where the pharmaceutical composition is administered in combination with an immunosuppressive/immunomodulatory and/or anti-inflammatory agent.

30 Provided is a method of treating an immune disease where the immune disease is an autoimmune disease or a graft-related disease. Further provided is a method of treating an immune disease where the immune disease is selected from the group consisting of selected

5 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTCCGAAGAATGAGATGACGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCGATTGAGTC
GGATGGTCAGGCTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCTGAGGACACCGCGGTATATTACTGTGCGAAAAATCGGATTCTGATCTTGTGT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 622)

10 BMS3h-2
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGATGCTGGGGCTATGACGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTGATAA
GGAGGGTCTGTCTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGGTAGGATTCTGGGCTGGTTT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 623)

15 BMS3h-3
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGGTGATGCGGCGATGACTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCGATTAGCC
TATGGGTGATGGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCCTCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGCGTATTCTACTCTTCAGT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 624)

20 BMS3h-4
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGAGGATTGCGCTATGACTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTACTTC
GAATGGTTATGAGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
25 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGCGTATTCTACTCTTCATT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 625)

30 BMS3h-5
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGATGAGCATGATATGAGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACGTATTGGTCC
GGATGGTTTTTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGCGTATTCTACTCTTCATT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 626)

35 BMS3h-6
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGGTGAGTATCATATGTCTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGGATTACTCC
TCTTGGTACGTTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
40 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGCGTATTCTTCGTTACGT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 627)

45 BMS3h-7
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGGTACGAATGCGATGAGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTGGAGTGGGTCTCAAGGATTTCCGCC
GGGTGGTGATTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTGTATTACTGTGCGAAAGGGCGTGTTCGGATCTGCTTT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 628)

50 BMS3h-8
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTCCGTCTGAGGAGATGTCTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGGATTTCCGCC

TGATGGTGCTAATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACGCCGCGGTATATTACTGTGCGAAAGGGCGTGTCCGGATCTGCTTT
TTGACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 629)

5 BMS3h-9

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGCTGAGGATGATATGACTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACGTATTGCGGT
TGATGGTGATCGGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTAAGGTTCCGTCTCTTCATT
10 TTGACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 630)

BMS3h-10

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGATCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTAGGACGATGGATATGTCTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACGTATTACGGG
15 TGATGGTATGAATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGGGGACACCGCGGTATATTACTGTGCGAAAGGGGTGACTCCGGATTTGACTT
TTGACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 631)

BMS3h-11

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGAGCGTGATGATATGACGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACGTATTAATGC
20 TGGGGGTGTGCATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGGGGTGACTCCGGATTTGACTT
TTGACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 632)

25

BMS3h-12

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGATGATGATTCTATGACGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACGGATTTGAG
TGATGGTGCGAGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
30 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGGTGACTCCGGATTTGACTT
TTGACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 633)

BMS3h-13

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTACTGAGGAGGATATGACGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACGTATTGATAG
35 TGTTGGTGAGGGGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGGTGACTCCGGATTTGACTT
TTGACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 634)

40 BMS3h-14

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTCTGATTCGGCGATGAGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACGGATTGATAA
TCCTGGTCAGCATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
45 TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGGTACTGTTCTACGCTGGAGT
TTGACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 635)

BMS3h-15

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGGGCAGCATAGTATGACTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACGTATTGATGG
50 TGGGGGTTATAATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG

TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGGAGGTTCTCTGCTTTCATT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 636)

BMS3h-16

5 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGGTCAGGAGCCTATGACTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACGATTGCGTA
TAATGGTGGTGATACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGATTACTCCTAATTTGACTT
10 TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 637)

BMS3h-17

10 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGAGAATTATCCGATGTCTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACGTATTAATGC
TACGGGTTCTATTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
15 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGTTATCCTCATTTGATGT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 638)

BMS3h-18

20 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTCTGATTATGATATGAGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACGTATTACTGG
TACTGGTAATAGTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGCAAGGGGTGGTGCGGTATCTTGCTT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 639)

BMS3h-19

25 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGAGGCTGATGCGATGACGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGGATTAATGT
GGATGGTGATCGGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
30 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTTACTGTTCTACGCTGGAGT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 640)

BMS3h-21

35 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGATCGGGCGGATATGACGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGGATTTGCGG
GGAGGGTAAGTGTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGATGGTTCTAATTTGGTTT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 641)

BMS3h-22

40 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTATTGGGAGCCGATGTCTTGGGTCCGCCAGGCTCCGGGGAAGGGTCTAGAGTGGGTCTCACGTATTAATTC
TTCTGGTTGGGATACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGATGGTTCTAATTTGGTTT
45 TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 642)

BMS3h-24

50 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGCTGATGAGCCGATGACTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACGTATTCCTCC
TGAGGGTGCTCCGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGATTACTCCTAATTTGACTT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 643)

BMS3h-26

5 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTATAATCATGATATGTCTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACGTATTAGTCG
GGGTGGTCTTCAGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGATTGTGCCGGATCTGCATT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 644)

BMS3h-27

10 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTAATGAGTATCCTATGTCTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACGTATTAATGG
GGATGGTGCTAATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGATTATCCGGCTATGCAGT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 645)

BMS3h-28

20 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGGGGATGTGCCTATGTCTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGGATTGATCC
TTATGGTTCTAATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTATTATGCCTAGTCTTACTT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 646)

BMS3h-29

25 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGCGGATTATGATATGTCTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACGTATTTCCGGC
GCTTGGTGCTACTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTGAGCTTCCGGCGTTGGAGT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 647)

BMS3h-30

30 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTAAGCGTTATTATATGACTTGGGTCCGCCAGGCTCCAGGGAAGGATCTAGAGTGGGTCTCAGGTATTGTTCC
TTCTGGTAATAGGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTAGGATTCCGGATCTGCATT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 648)

BMS3h-31

40 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTGCTGATTATGATATGACTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGGATTTCTCC
GACGGGTGGGCAGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTGTTATTCCGTATTGTCTT
TTTCTCCGTTTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 649)

BMS3h-32

45 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTCTAAGTATTGGATGGGTTGGGCCCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTGATTCC
GCATGGTGCTGGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGTCGAGGACACCGCGGTATATTACTGTGCGAAAGGTGCTCCTAAGTTTATGACTA
CGTATACGTTTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 650)

BMS3h-33

5 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTGTCTTATCCGATGCATTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTGATTC
GAGGGGTTTCGGTTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTCATAGTTGGACGTTTGACT
ACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 651)

BMS3h-34
10 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGCGAATAGTAATATGACTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACGTATTAATCC
GGATGGTGGGTCTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAGGGCGTATTCTACTCTTCATT
TTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 652)

BMS3h-35
15 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGGGCCGAGGAGGATGGGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTGATGA
TATTGGTCGTAGGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAGGGGCGCAGGGTGTGTTGTTG
TTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 653)

20 BMS3h-36
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGAGGATTATAGGATGGTTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTTCTAC
TTCTGGTGAGCTGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
25 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAACGGCGGGTCAGTTTTTTGACT
ACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 654)

BMS3h-39
30 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTCCGGAGTATGAGATGGTTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTGGAGTGGGTCTCAGCGATTTTCGCG
TGAGGGTCCGGCTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAACCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGAGCCTGTTCTGTTTTGACTACT
GGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 655)

35 BMS3h-40
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTCGACTTATGAGATGCTTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTTCTTC
TTCTGGTAATTATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCCGCTGATGTTTGACTACT
40 GGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 656)

BMS3h-42
45 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGATACTGAGGAGATGAGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCGATTAGTCC
TAATGGTGCTTTTACATTCTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCCTATTCTGTTTGACTACT
GGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 657)

BMS3h-44
50 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGGTCATTATGATATGGTTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTAATGG

TGCTGGTCTGAATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGCAAAGTGCTAGTCGTATTTTTGACT
ACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 658)

5 BMS3h-45

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTAGGAGTTATGAGATGGCGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTAGTAC
TCTGGGTACGAAGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGCAAATCTTCTACTCATATTTTTGACT
10 ACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 659)

BMS3h-46

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTATTAGGTATGAGATGGCTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTTTCGTC
15 GTCTGGTTGGACGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAAGTGATGCTCATATTTTTGACT
ACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 660)

BMS3h-47

20 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTATGCTTATGAGATGGCTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTTTCGGA
TGATGGTACGCGGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAGATCTGGGGCAGGGGTTTGACT
25 ACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 661)

BMS3h-48

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGCTGATCATGGGATGACGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGGATTGGTCC
GTCTGGTGAGGCGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
30 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAGATCGTATTCCTAATCTTGTGT
TTGACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 662)

BMS3h-49

35 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGAGTCTCAGGATATGCTTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTAGTCC
GAATGGTTGGGATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAAGATAGGTCTGATTTTGACTACT
GGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 663)

40 BMS3h-50

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGGGGATTATGATATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGGATTTCGTCA
TCCGGGTGGTGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAGCTGTTCTAAGGGTTTTGACT
45 ACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 664)

BMS3h-51

50 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTCGGGTTTATTGGATGACTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTGATCC
GCAGGGTGGGATGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCTCGCGACAATTCCAAGAACACGCTG

TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGCGGTATTCTAATTTGGAGT
TTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 665)

BMS3h-52

5 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGAGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTAGTGCTTATGATATGACGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTTGAGTGGGTCTCACGTATTAATCC
GACGGGTTCTTATACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGCTAAGATTCCGAATTTGGTTT
10 TTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 666)

BMS3h-53

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGCGGATAGTGAGATGATGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGCGCA
15 TAATGGTGGGCATACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCTGGTCATCCTCAGCAGACTG
AGGCTTTTACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 667)

BMS3h-54

20 GAGATGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGCTACTTATGATATGATTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAAGATTTCTCC
GAATGGTTGGAGTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATATCAGACGCATTTTACTACT
GGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 668)

BMS3h-55

25 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTAGTGTTTATGATATGAGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTTCTTC
TTCGGGTACGTATACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATATCCTAAGAATTTTACTACT
30 GGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 669)

BMS3h-57

35 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTCTCATGAGGATATGACTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTAGTCC
GAATGGTTGGGATACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACGTACTAGGAGTAAGTTTACT
ACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 670)

BMS3h-58

40 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGAGAAGTATATTATGGGTTGGGCCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTGATTA
TTGGGGTCAGCATACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACGTAGTCATCTTATCCTCTGC
45 AGTTTACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 671)

BMS3h-59

50 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTCTGATTATGCGATGGGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTGGAGTGGGTCTCAACGATTTCTGA
TGTGGGTTATTATACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAAGGCTCTGCGGGGGGAGGCGT
TTACGGAGCGTTTACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 672)

BMS3h-60

5 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTGGTCCGTATATGATGCATTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTGAGGT
 TAATGGTAATAGGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAATTCCAAGAACACGCTG
 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATGGGTGGTTCGAAGACGCTG
 CGGATAAGAGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 673)

BMS3h-61

10 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTGGTACGACGGAGATGGCTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTGGTAG
 TGCTGGTGCTTGGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAATTCCAAGAACACGCTG
 TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAATTTGGTGGGCATCCTCAGGGTC
 AGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 674)

BMS3h-62

20 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTCTAGGGAGTGGATGGCTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTAGCC
 TATGGGTGAGACTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAATTCCAAGAACACGCTG
 TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAATTTCTCGGAATAAGGGGTTTT
 TTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 675)

BMS3h-63

25 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTACGAGTGAGTATATGGGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTCAGAG
 GTATGGTAGTACGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAATTCCAAGAACACGCTG
 TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACATGAGTCTAATTGGGAGACTT
 TTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 676)

BMS3h-70

30 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTTCGGTGTATAGTATGAGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCGATTACTCC
 TAATGGTACTCGGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAATTCCAAGAACACGCTG
 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTCTTGGTCGGGGTTCTTATC
 CTGGTGTGATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 677)

BMS3h-71

40 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTCCGAGTTATGCTATGACGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTGGAGTGGGTCTCAGTATTACGGC
 GGATGGTACTGTTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAATTCCAAGAACACGCTG
 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTTCTATTCCGATGCTTACGT
 TTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 678)

BMS3h-72

45 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTTCGACTTATGATATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTTCTCC
 TAATGGTACTGGTATATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAATTCCAAGAACACGCTG
 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAATCAGAGTGTTTCATCATGCTG
 TTTTGGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 679)

BMS3h-73

5 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGAGAATTATGAGATGACGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACGTATTGCGCC
GCATGGTTCGGCTTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGGTCAGATTCCGATGCTTGATT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 680)

10 BMS3h-74
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTCGATTATATGATGATGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTTCTCA
TTTTGGTGATATTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAAATGATATGGTGATGAAGAATG
GGGGGTTTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 681)

15 BMS3h-75
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGAGAGGTATGATATGAGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACGTATTGATTC
GCGGGGTTGGTCTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGTTGGTGCCGCATCTGAGGT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 682)

20 BMS3h-76
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGCGAATGCGCAGATGACTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGGATTGATGC
TATGGGTGATGCTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
25 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTAAGGTTCCGAGTATTGACT
ACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 683)

30 BMS3h-77
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGCGAATGCGCAGATGACTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGGATTGATGC
TATGGGTGATGCTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGGTGTTATTCCGGCGTTTGACT
ACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 684)

35 BMS3h-78
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTCAAGATGATCGGATGCATTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTTCTGC
TACTGGTGGTGATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACAGACGGGTACGAATCGTTTTG
40 ACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 685)

45 BMS3h-79
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTAATCAGCCTTATATGTCGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTGATGC
TTCGGGTGGTACTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGATCGTATTCTAATCTTGTT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 686)

50 BMS3h-80
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGATAATGAGAATATGACTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACGTATTGATGG

TGGGGGTTATAATACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGCAGGTTCTGAGCTGCTGT
TTGACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 687)

5 BMS3h-81

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGTTTCGTCGAATATGACTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGG
TAGTGGTGGTAGCACATACTATGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTCGGATTCTACGTTGGTGT
10 TTGACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 688)

BMS3h-82

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGTTTCGTCGAATATGACTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGG
15 TAGTGGTGGTAGCACATACTATGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGATCGTATTCTAATCTTGTGT
TTGACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 689)

BMS3h-83

20 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTCTGATGATTGATGAGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGTATTAATGA
TGCTGGTAGTTCTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTACTATTCTTCTTGGAGT
25 TTGACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 690)

BMS3h-84

GAGATGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGTTTCGATACTATGAGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGTATTGATGG
GACTGGTGGTGATACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
30 TATCTGCAAATGAACAGCCTGCGTGCCGGGGACACCGCGGTATATTACTGTGCGAAAGGGCTTATTCTGATCTTCAGT
TTGACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 691)

BMS3h-85

35 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGATGAGGAGGAGATGACGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGTATTATTGG
TGGTGGTCATGAGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTACTATTCTTCTTGGAGT
40 TTGACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 692)

40 BMS3h-86

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGATAATGAGAAATATGACTTGGGTCCGCCAGGCTCCAGGGAAGGATCTAGAGTGGGTCTCAGGATTACTGA
GAGGGGTGATGTGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTACTGTTCTTACGCTGGAGT
45 TTGACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 693)

BMS3h-87

50 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGATGAGGAGGAGATGACGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGTATTATTGG
TGGTGGTCATGAGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG

from the group consisting of Addison's disease, allergies, ankylosing spondylitis, asthma, atherosclerosis, autoimmune diseases of the ear, autoimmune diseases of the eye, autoimmune hepatitis, autoimmune parotitis, colitis, coronary heart disease, Crohn's disease, diabetes, including Type 1 and/or Type 2 diabetes, epididymitis, glomerulonephritis, Graves' disease, Guillain-Barre syndrome, Hashimoto's disease, hemolytic anemia, idiopathic thrombocytopenic purpura, inflammatory bowel disease, immune response to recombinant drug products, systemic lupus erythematosus, male infertility, multiple sclerosis, myasthenia gravis, pemphigus, psoriasis, rheumatic fever, rheumatoid arthritis, sarcoidosis, scleroderma, Sjogren's syndrome, spondyloarthropathies, thyroiditis, transplant rejection, vasculitis, AIDS, atopic allergy, bronchial asthma, eczema, leprosy, schizophrenia, inherited depression, transplantation of tissues and organs, chronic fatigue syndrome, Alzheimer's disease, Parkinson's disease, myocardial infarction, stroke, autism, epilepsy, Arthus's phenomenon, anaphylaxis, alcohol addiction, and drug addiction.

Also provided is a method of targeting CD40 using a first variable domain that specifically binds an epitope of human CD40 comprising the amino acid sequence of SEQ ID NO: 1, where the antibody polypeptide competes with the binding of domain antibody (dAb) BMS3h-56-269 (SEQ ID NO:417).

Provided is the use in medicine of an antibody polypeptide comprising a first variable domain that specifically binds an epitope of human CD40 comprising the amino acid sequence of SEQ ID NO: 1, wherein the antibody polypeptide competes with the binding of domain antibody (dAb) BMS3h-56-201 (SEQ ID NO: 9), or a pharmaceutically acceptable salt thereof.

Provided is the use of an antibody polypeptide comprising a first variable domain that specifically binds an epitope of human CD40 comprising the amino acid sequence of SEQ ID NO: 1, wherein the antibody polypeptide competes with the binding of domain antibody (dAb) BMS3h-56-201 (SEQ ID NO: 9), or a pharmaceutically acceptable salt thereof, in the preparation of a medicament for treatment of an immune disease. In some embodiments, the pharmaceutical composition is administered in combination with an immunosuppressive/immunomodulatory and/or anti-inflammatory agent. In further embodiments, the immune disease is an autoimmune disease or a graft-related disease. In yet further embodiments, the immune disease is selected from the group consisting of selected from the group consisting of Addison's disease, allergies, ankylosing spondylitis, asthma,

TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTAAGTCTTCTACGCTGGAGT
TTGACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 694)

BMS3h-88

5 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTCATGAGACGGAGATGACGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAATCG
GCTGGGTGAGGATACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTAGGATTCTGGGCTGGTTT
10 TTGACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 695)

BMS3h-89

15 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTCTGATGATTGATGAGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAATGA
TGCTGGTAGTTCTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTAAGTCTTCTACGCTGGAGT
TTGACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 696)

BMS3h-90

20 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTGATAATGAGAATATGACTTGGGTCCGCCAGGCTCCAGGGAAGGATCTAGAGTGGGTCTCAGGATTACTGA
GAGGGGTGATGTGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTCGGATTCTACGTTGGTGT
TTGACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 697)

BMS3h-91

25 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTCTGATGATTGATGAGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAATGA
TGCTGGTAGTTCTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGATTACTCTAATTTGACTT
30 TTGACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 698)

BMS3h-92

35 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGCTGATGAGCCGATGACTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGTATTCTCTCC
TGAGGGTGCTCCGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGCTTATTCTGATCTTCAGT
TTGACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 699)

BMS3h-93

40 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTCAGGATAGTGATATGACGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTGCTGC
GCCTGGTGGTAGTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGATCGTATTCTAATCTTAGGT
45 TTGACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 700)

BMS3h-94

50 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGTTTCGATACTATGAGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGTATTGATGG
GACTGGTGGTGATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGCAGGTTCTGAGCTGCTGT
TTGACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 701)

BMS3h-95

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTT CAGGATAGTGATATGACGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTGCTGC
 5 GCCTGGTGGTAGTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
 TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGATCGTATTCTAATCTTGTGT
 TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 702)

BMS3h-96

10 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCGCCGGAT
 TCACCTTTT GATCTGGCGGAGATGACTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTGATGA
 GGATGGTGCTTCTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACGCCGCGGTATATTACTGTGCGGAAGGTGTTATTCGCTCTGACTT
 15 TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 703)

BMS3h-97

20 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTT ACTGATAAGCATATGAGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGATTTCCGCC
 TGATGGTACGTATACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACGCCGCGGTATATTACTGTGCGGAAGGTGTTATTCGCTCTGACTT
 TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 704)

BMS3h-98

25 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTT GCTGAGGATGATATGACTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTGCGGT
 TGATGGTGATCGGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
 TATCTGCAAATGAACAGCCTGCGTACCGAGGACACCGCGGTATATTACTGTGCGAAAGGGAAGACGCCGCATCTTGTGT
 TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 705)

BMS3h-99

30 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCGCCGGAT
 TCACCTTTT GATCTGGCGGAGATGACTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTGATGA
 GGATGGTGCTTCTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTGAGGTTCTGCTTTGGTTT
 35 TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 706)

BMS3h-100

40 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTT GAGGATTTCGATGATGTCGTGGGTCCGCCAGGCGCCAGGGAAGGGTCTAGAGTGGGTCTCAGGATTGATCC
 TGGGGGTGCTCAGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGGTGACTCCGGATTGACTT
 TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 707)

BMS3h-101

45 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTT GAGCATGCGGATATGAGTTGGGTCCGCCAGGCTTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTGATAA
 TAGTGGTCAGTCTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGGTGACTCCGGATTGACGT
 50 TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 708)

BMS3h-102

5 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTAGTGAGGCGGAGATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGTATTACGAC
GGATGGTGATTCTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGCGTATTCTACTCTTCATT
TTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 709)

10 BMS3h-103
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCAGGAT
TCACCTTTGATGATAGTGATATGACTTGGGTCCGCCAGGCTCCAGGGAAGAGTCTAGAGTGGGTCTCATATATTCGGGG
TGATGATGATGAGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAATCGGATTCTGATCTTGTGT
TTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 710)

15 BMS3h-108
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTAATGTGGCGGATATGAGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTAGTCC
GAATGGTTGGGATACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACATGCTTCTACGGAGGGGCCGA
CTGCTTTTACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 711)

20 BMS3h-109
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGGGCCGTATGATATGGGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTGGAGTGGGTCTCATGGATTTCTGC
TCATGGTTCTGTTTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAATTCCAAGAACACGCTG
25 TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAATGGCCTTATAAGTTTACTACT
GGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 712)

30 BMS3h-110
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGGGAGTGGGTCTATGAGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGATTGGTAG
TAATGGTGCGGATACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGATGGTTCCTAATTTGGTTT
TTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 713)

35 BMS3h-111
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTAATCGTTTTGATATGACGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGG
TAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAATTCCAAGAACACGCTG
40 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGATCGTATTCTAATCTTGTGT
TTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 714)

45 BMS3h-112
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGGGGAGAGTGATATGAAGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTAGTCC
GAATGGTTGGGATACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATCTCCTTCTTCTCGTCTTAAGT
TTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 715)

50 BMS3h-139
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGATAGTAGTGAGATGAGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTGAGAA

TCAGGGTGGTGCGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGGGTATATTACTGTGCGAAAGATCGTATTCTAATCTTGTGT
TTGACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 716)

5 BMS3h-140

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCCCTTGATGCGTATCCTATGTATTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATGGATTGCTTC
GGGTGGTGGTGCGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAACGTACGAAGAATTTGACTACT
10 GGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 717)

BMS3h-141

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTATGAGTTATTCTATGGCTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGGATTACTTC
15 TAATGGTAATCGGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGGGTATATTACTGTGCGAAATCGACTGGGGCTAATAGTAGGA
ATTTTACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 718)

BMS3h-142

20 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGAGGGGTATCTGATGTCTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTGCGGC
TAATGGTATGCAGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAAAAGCCGAGGGGTATTTGGGATG
GGGATTTTACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 719)

25

BMS3h-143

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTATGAGTCTACGATGACGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTGCGCA
TCCGGGTGAGTTTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
30 TATCTGCAAATGAACAGCCTGCGTGCCGGGGACACCGGGTATATTACTGTGCGAAAGGGCTTATTCTGATCTTCAGT
TTGACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 720)

BMS3h-144

35 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTGCAGATGTATAGTATGAGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTGCGCC
GCCGGGTGGTAGGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGGGTATATTACTGTGCGAAACAGTCGCTGACGGGGTATAGTA
GGTCTTTTACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 721)

40 BMS3h-145

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTGCAGAATCCGATGTCTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTCTGCGC
GAATGGTCTCTACATCTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGGGTATATTACTGTGCGAAATATAGTCAGCAGCCGGGTCGTC
45 GGTGTTGACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 722)

BMS3h-146

50 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTGCTAATTATCATATGACGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTCTGCA
TAGTGGTAAGCAGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG

TATCTACAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTAGGATTCCGTCTCTTCTTT
TTGACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 723)

BMS3h-147

5 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGCGCAGTATCATATGCGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTAATGA
TATTGGTAGTAATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTTGGGGGGCGGGGAGTTTTT
CTTTTACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 724)

BMS3h-148

10 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTCTTCGTATGATATGAAGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTAGTGC
GTCTGGTGTGTTTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
15 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACGGGAGCATGCGGGTCAGCCGC
CTTTTACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 725)

BMS3h-149

20 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTAATGGTTATGCTATGAGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTAATGC
TAATGGTAAGTATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAGTTGACTCTTGCTTCTAATT
ATTTTACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 726)

BMS3h-150

25 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTATGGATTATGATATGAAGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTACTGC
GCTTGGTAAGAAGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
30 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAGATAGTGTTAAGTATCCTCTTA
ATCTTTTACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 727)

BMS3h-151

35 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTCCGCATTATACGATGGCGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTAGTC
GCCTGGTTGGCGGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAATATGGGGATGGTCTTCCTTTGA
CTTTTACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 728)

BMS3h-167

40 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTAGTGGTACGCCGATGTCTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACGTATTGGGGA
TGAGGGTCAGGAGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGGTGACTCCGGATTTGACTT
45 TTGACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 729)

BMS3h-168

50 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTAGTAGTAGTTCGATGTCTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCGATTGGGTC
TGATGGTCCGAGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGCGTATTCCTACTCTTCATT
TTGACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 730)

BMS3h-169

5 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTAATCCTGGTGGAGATGACGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTGATGG
GTCTGGTTCTTCGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGATGACACCGCGGTATATTACTGTGCGAAAAGGGCGTATTCTACTCTTCATT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 731)

BMS3h-170

10 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTCTGAGTCTATGATGGGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTGGGTA
TCCTGGTGCTACTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAAGGTGGTAGTCGGGATGATAATT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 732)

BMS3h-171

20 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGCCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGGTCAGCATAGTATGCATTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTAGTGT
TCCGGGTCCGAAGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAGTCTTAGGGATTTCGCTCCGG
GTGATAGTAAGAGTTTTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 733)

BMS3h-197

25 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGGTCTGCTGCTATGGATTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTAATGA
TATGGGTTCTAATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAACAGGGTGGTCTTTTACTACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 734)

BMS3h-199

30 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGGTTATGATAGGATGGCTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTGATGG
TCCTGGTGGGGCTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAGGGAGGAGGGTTCCTGATTTTG
35 ACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 735)

BMS3h-200

40 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGGTGAGTATGAGATGACTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGGATTGATCC
GTTTGGTCTGAGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAGGTGTGGTTCCTGATTTGAATT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 736)

BMS3h-201

45 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGATAAGTATGTTATGGGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTGGTAG
TTATGGTGGGGCTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAGGCTTACTCTTAGTGCGACTA
AGTTTACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 737)

BMS3h-203

5 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGAGGATTATGTGATGGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTGCGCA
TCGGGGTGATATTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACGTAGGCGTCTTAGTGATTATC
GGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 738)

BMS3h-204

10 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGGGCAGTTTGATATGTATTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCGATTAGTCC
GGCTGGTACTGGTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCGGGGGATCGGTCTAGTCTTT
TTGACTACAGGGGTGAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 739)

BMS3h-205

15 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTAAGGATACGGGTATGACGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTTCTAG
TTATGGTCGTGATACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATTGAATGCGGCGCTGGGTTTTG
20 ACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 740)

BMS3h-206

25 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGGTCCGTATCCGATGAGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTAATGC
GCCGGGTACGAGGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGCAACAGATGTCTAGTGGGGTTTTTG
ACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 741)

BMS3h-207

30 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTCGAATCAGGATATGACTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTGATAG
TTCTGGTCAGCTTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTTAAGTCTCTTGCGCGGTTTG
ACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 742)

BMS3h-208

35 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGCGCAGCCTCCGGAT
TCACCTTTCTGAGTCTGATATGAAGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTAGTCC
GAATGGTTGGGATACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
40 TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACCGGCTCAGGTTCTGTTGACT
ACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 743)

BMS3h-209

45 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGAGCAGTATGTGATGGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTGGTAC
GTCGGGTAAAGTATACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGCAACGTAGGTCTCTGACTCGGGTTC
ATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 744)

BMS3h-210

5 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGGTGTGGAGCATATGAGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCGATTACGGG
TGATGGTGATCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCGAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAACGGTTTCGTGGAATGGTCGTT
TTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 745)

BMS3h-211

10 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGCGTGGTATAATATGGGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTGGAGTGGGTCTCAAGGATTGCTCC
GTCTGGTATTATTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCGAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGTTGCGTGGAAGTTTGACT
ACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 746)

15 BMS3h-212

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTGAATTATGAGATGAGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTTCTTC
GGCTGGTACTGATACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCGAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACAGTCGCTTAATTTTGACTACT
20 GGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 747)

BMS3h-213

25 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGTAGCCTCCGGAT
TCACCTTTGATGAGGAGCCGATGACTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAATTATTGATCC
GGGTGGTGGGGCGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCGAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATCTAATAGTATGTTTGACTACT
GGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 748)

BMS3h-214

30 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTCTGCGTATCCTATGCATTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTGCTTC
TTCGGGTATTACGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCGAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATTTACTCGGCTGCATTTTCCTG
CGCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 749)

35

BMS3h-215

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGCTGATTATGCGATGGGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGGATTTCTCC
TGAGGGTTCTAGGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCGAAGAACACGCTG
40 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATTGCGGCCGTATGCGTCGAAGT
TTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 750)

BMS3h-230

45 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTAGGCCGTATGATATGGGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTTCTCA
TCAGGGTAATCGGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCGAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTGTCTCATCATTTTGACTACT
GGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 751)

BMS3h-231

5 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTCTGCGTATAATATGTGGTGGGCCCCGCCAGGCTCCAGGGAAGGGTTTAGAGTGGGTCTCATGGATTAATTC
GACTGGTTCTCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAAATTGGCATCGGGGAGGTTTG
ACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 752)

BMS3h-232

10 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGATAGGTATCGGATGGGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTAATCG
GCTGGGTGAGGTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTGAAGAAGCATAAGTTTGACT
ACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 753)

BMS3h-233

15 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGCGCATTATAATATGCGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTACGAA
GACTGGTTTTCTGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGTGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCGGGGCAGTTTGATTTTGACT
20 ACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 754)

BMS3h-234

25 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTAGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTATCCTTATAGTATGCATTGGGTCCGCCAGGCTCCAGGGAAGGGTCTGGAGTGGGTCTCAACTATTGATGG
TAGTGGTATGTTTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAGATTCTCTGAAGGCTTCTTTTG
ACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 755)

BMS3h-235

30 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTCCGCTTTATGGGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATATATTGGGCC
TTATGGTCATACTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAAAGCGGAAGAAGATTGACT
35 ACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 756)

BMS3h-236

40 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTCTAGGTATCGGATGAGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTACTCC
GTATGGTGCTCATACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATATGGTAAGTGGTATTTTGACT
ACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 757)

BMS3h-237

45 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTAATGAGTATGCGATGAGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTGATCG
TCTGGGTCTTCATACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAGTGGGCCTTTTACGTTTGACT
ACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 758)

BMS3h-238

5 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTGAGCGGTATAATATGCGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTGATCG
 GCTGGGTCTTGCTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCGGGTTCGTGGTCTTTTGACT
 ACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 759)

BMS3h-239

10 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTGGTATTTATGATATGAAGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTTCTGC
 GTCGGGTACTCATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATATCCTCAGCCTTATCCTTTTG
 ACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 760)

15 BMS3h-240

20 GAGGTGCAGCTATTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTTGGGTGATGATATGCGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTTCTGC
 GACTGGTGTGCATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATATCCGCTGCTGGTCGGTTTG
 ACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 761)

BMS3h-241

25 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTTCGACTTATGATATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTTCTCC
 TAATGGTACTGGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCTCCGCAGGTGAATACTGAGT
 TTGACTACCGGGGTGAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 762)

BMS3h-243

30 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTGAGAAGGAGGATATGGGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACATATTTCTGCC
 GAATGGTTATGCGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAGTTGGTCTAGTTTTGACTACT
 GGGGTGAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 763)

35 BMS3h-244

40 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTAGTGCTACTCCGATGGAGTGGGCCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTTCTGA
 GAGTGGTTATAGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATGGAATTGACTACTGGTTTTG
 ACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 764)

BMS3h-245

45 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTAATACGGTGGATATGGAGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTAGTCC
 GAATGGTTGGGATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAGCTCCGCATCGGGCGTTTGACT
 ACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 765)

CLAIMS

1. An antibody polypeptide comprising a first variable domain, wherein the first
5 variable domain comprises

(a) a CDR1 region comprising the CDR1 region of BMS3h-56-269 (amino acids 31 to 35
of SEQ ID NO: 417) or differs from the CDR1 region of BMS3h-56-269 by up to two amino
acids,

10 (b) a CDR2 region comprising the CDR2 region of BMS3h-56-269 (amino acids 50 to 66
of SEQ ID NO: 417) or differs from the CDR2 region of BMS3h-56-269 by up to two amino
acids, and

(c) a CDR3 region comprising the CDR3 region of BMS3h-56-269 (amino acids 99 to
105 of SEQ ID NO: 417) or differs from the CDR3 region of BMS3h-56-269 by up to two amino
acids,

15 wherein said antibody polypeptide is a domain antibody that binds CD40 and wherein the
binding of the antibody polypeptide to CD40 antagonizes CD40 activity.

2. The antibody polypeptide of claim 1, wherein the first variable domain comprises
the amino acid sequence of one of the antibody polypeptides of the lineage group of BMS3h-56
20 selected from the group consisting of SEQ ID NO: 317; SEQ ID NO: 318; SEQ ID NO: 320;
SEQ ID NO: 321; SEQ ID NO: 324; SEQ ID NO: 325; SEQ ID NO: 326; SEQ ID NO: 327;
SEQ ID NO: 331; SEQ ID NO: 332; SEQ ID NO: 333; SEQ ID NO: 334; SEQ ID NO: 335;
SEQ ID NO: 336; SEQ ID NO: 337; SEQ ID NO: 341; SEQ ID NO: 342; SEQ ID NO: 343;
SEQ ID NO: 344; SEQ ID NO: 345; SEQ ID NO: 346; SEQ ID NO: 347; SEQ ID NO: 348;
25 SEQ ID NO: 349; SEQ ID NO: 350; SEQ ID NO: 353; SEQ ID NO: 355; SEQ ID NO: 356;
SEQ ID NO: 358; SEQ ID NO: 366; SEQ ID NO: 367; SEQ ID NO: 376; SEQ ID NO: 379;
SEQ ID NO: 381; SEQ ID NO: 386; SEQ ID NO: 394; SEQ ID NO: 403; SEQ ID NO: 405;
SEQ ID NO: 412; SEQ ID NO: 417; and SEQ ID NO: 419.

30 3. The antibody polypeptide of claim 1, wherein:

(a) the CDR1 region comprises the CDR1 region of BMS3h-56-269 (SEQ ID NO: 417),

16. An isolated host cell comprising the nucleic acid of claim 15.

17. A pharmaceutical composition for treating an immune disease comprising a therapeutically-effective amount of the antibody polypeptide of any one of claims 1, 3, 6, 10, and 12 and a pharmaceutically acceptable carrier.

18. The pharmaceutical composition of claim 17, further comprising an immunosuppressive/immunomodulatory and/or anti-inflammatory agent.

19. The pharmaceutical composition of claim 17, wherein the immune disease is selected from the group consisting of ulcerative colitis, Crohn's disease, and inflammatory bowel disease.

20. The pharmaceutical composition of claim 17, wherein the immune disease is systemic lupus erythematosus.

21. The pharmaceutical composition of claim 17, wherein the first variable domain of the antibody polypeptide comprises the amino acid sequence of SEQ ID NO: 417.

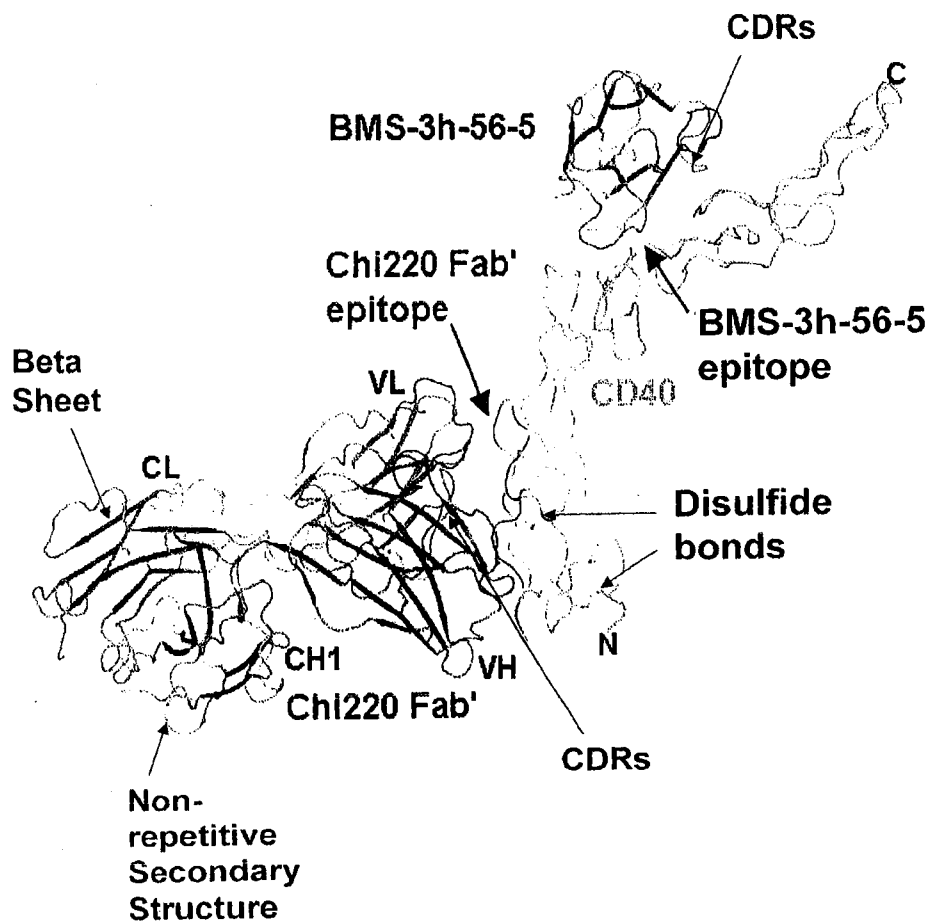
22. The pharmaceutical composition of claim 17, wherein the amino acid sequence of the antibody polypeptide is set forth in SEQ ID NO: 1286.

23. The pharmaceutical composition of claim 17, wherein the amino acid sequence of the antibody polypeptide is set forth in SEQ ID NO: 1287.

24. The antibody polypeptide of any one of claims 1, 3, 6, 10, and 12 for use as a medicament useful in the treatment of an immune disease in a patient in need of such treatment.

25. The antibody polypeptide of claim 24, wherein the immune disease is selected from the group consisting of Addison's disease, allergies, ankylosing spondylitis, asthma, atherosclerosis, autoimmune diseases of the ear, autoimmune diseases of the eye, autoimmune

FIG. 1



BRISTOL-MYERS SQUIBB COMPANY AND
DOMANTIS LIMITED
APPLICANT
SIGUION REYNA MONTECILLO
& ONGSI AKO
BY:

CARLO L. CRUZ

FIG. 7

	CDR1	CDR2	
BMS3h-198-22	EVQLLESGGGLVQPGGSLRLSCAASGFTTFAGYEMWWVRQAPGKGLERVS	AIISGSGGSTYY	60
BMS3h-198-31	EVQLLESGGGLVQPGGSLRLSCAASGFTTFAGYEMWWVRQAPGKGLERVS	AIISGSGGSTYY	60
BMS3h-198-33	EVQLLESGGGLVQPGGSLRLSCAASGFTTFAGYEMWWVRQAPGKGLERVS	AIISGSGGSTYY	60
BMS3h-198-19	EVQLLESGGGLVQPGGSLRLSCAASGFTTFAGYELWWVRQAPGKGLERVS	AIISGSGGSTYY	60
BMS3h-198-38	EVQLLESGGGLVQPGGSLRLSCAASGFTTFAGYELWWVRQAPGKGLERVS	AIISGSGGSTYY	60
BMS3h-198-14	EVQLLESGGGLVQPGGSLRLSCAASGFTTFAGYEMWWVRQAPGKGLERVS	AIISGSGGSTYY	60

	CDR2	CDR3	
BMS3h-198-22	ADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCAKEPYSYDYGWGHGLTVTVSS	116 (SEQ ID NO: 523)	
BMS3h-198-31	ADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYHCAKEPYSYDYGWQGLTVTVSS	116 (SEQ ID NO: 532)	
BMS3h-198-33	ADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCAKEPYSYDYGWQGLTVTVSS	116 (SEQ ID NO: 534)	
BMS3h-198-19	ADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCARDPYSFDYRGQGLTVTVSS	116 (SEQ ID NO: 520)	
BMS3h-198-38	ADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCARDPYSFDYWGQGLTVTVSS	116 (SEQ ID NO: 539)	
BMS3h-198-14	ADSVKGRFTISRDDTKNTLYLQMNSLRAEDTAVYYCAKDPYSFDYWRQGLTVTVSS	116 (SEQ ID NO: 515)	

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 BY:

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