

ANTI-TRANSFERRIN RECEPTOR COMPOSITIONS AND METHODS THEREOF**CROSS-REFERENCE TO RELATED APPLICATIONS**

5 This application claims the benefit of priority of US Patent Application No. 63/553,699, filed on February 15, 2024, and US Patent Application No. 63/645,431, filed on May 10, 2024, which are incorporated by reference herein, in their entireties and for all purposes.

FIELD OF THE INVENTION

10 The present invention relates to a blood-brain barrier shuttle that binds to the transferrin receptor (TfR) and methods of using the same.

REFERENCE TO SEQUENCE LISTING SUBMITTED ELECTRONICALLY

15 This application contains a sequence listing, which is submitted electronically. The information contained in the electronic sequence listing (Sequence listing_JBI6864WOPCT_SL.xml; size: 2.127MB; and date of creation: February 11, 2025) is incorporated herein by reference in its entirety.

BACKGROUND

20 While the blood-brain barrier (BBB) prevents harmful substances from entering the brain and is essential for brain homeostasis, it presents a formidable obstacle for efficiently delivering drugs to the brain. Large molecules, such as monoclonal antibodies and other biotherapeutics, have great therapeutic/diagnostic potential for treating/detecting pathology in the central nervous system (CNS). However, their route into the brain is prevented by the BBB. Previous studies
25 have illustrated that only a very small percentage (approximately 0.1%) of an IgG injected in the bloodstream are able to penetrate the BBB into the CNS compartment (Felgenhauer, Klin. Wschr. 52: 1158-1164, 1974)). This will limit any pharmacological effect due to the low concentration within the CNS of the antibody.

30 Numerous approaches have been studied to improve the brain delivery of therapeutic monoclonal antibodies (mAbs), including the use of receptor-mediated transcytosis (RMT). RMT utilizes abundantly expressed receptors on the luminal side of the BBB for transport through brain endothelial cells. Previous efforts to generate a clinically feasible platform for

delivery of therapeutic mAbs into the brain have been focused on antibody engineering to increase the efficiency of transcytosis, with gains made through observations on valency of binding, pH dependency and affinity (reviewed in Goulatis et al., 2017, Curr Opin Struct Biol 45: 109-115). However, translation into NHPs and the clinic has been limited by rapid peripheral
5 clearance from target-mediated drug disposition (TMDD) and safety from acute reticulocyte depletion (Gadkar, 2016, Eur J Pharm Biopharm. 2016 Apr;101:53-61). Transferrin receptor (TfR), particularly TfR1, mediates the transport of iron-loaded transferrin (Tf) from blood to brain and the return of iron-depleted Tf to the blood (Kawabata, Free Radical Biology & Medicine, 133, 46-54, 2019). Anti-TfR1 monoclonal antibodies have been used to deliver drugs
10 to the brain (see, e.g., Burkhart, et al. Progress in neurobiology, 181, 101665, 2019; US 2023/0174646). However, safety liabilities and poor pharmacokinetics (PK) of anti-TfR1 monoclonal antibodies may hamper their clinical development as BBB carriers.

Therefore, there is still a need for an anti-TfR monoclonal antibody or antigen binding
15 fragment thereof that can be used to shuttle drugs into the brain efficiently with improved safety and PK.

SUMMARY OF THE INVENTION

In one general aspect, the application describes an anti-TfR antibody or antigen-binding fragment thereof, comprising a light chain variable region (VL) comprising light chain complementarity determining regions (LCDRs) LCDR1, LCDR2 and LCDR3, and a heavy chain
20 variable region (VH) comprising heavy chain complementarity determining regions (HCDRs) HCDR1, HCDR2 and HCDR3, wherein:

- (1) the LCDR1 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 222-308 and 1456-1485;
- (2) the LCDR2 comprises an amino acid sequence selected from the group consisting of
25 SEQ ID NOs: 309-359 and 1486-1511;
- (3) the LCDR3 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 360-518 and 1512-1561;
- (4) the HCDR1 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 519-645 and 1562-1606;
- (5) the HCDR2 comprises an amino acid sequence selected from the group consisting of
30 SEQ ID NOs: 646-792 and 1607-1661; and

(6) the HCDR3 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 793-980 and 1662-1717.

In certain embodiments, the application relates to an anti-TfR antibody or antigen-binding fragment thereof, wherein the LCDR1, LCDR2 and LCDR3 have the amino acid sequences of the LCDR1, LCDR2 and LCDR3, respectively, of any one of the antigen binding proteins specified in Table 5.

In certain embodiments, the application relates to an anti-TfR antibody or antigen-binding fragment thereof, wherein the VL comprises an amino acid sequence that is at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to an amino acid sequence selected from the group consisting of SEQ ID NOs: 1198-1420 and 1776-1832.

In certain embodiments, the application relates to an anti-TfR antibody or antigen-binding fragment thereof, wherein the VL comprises the amino acid sequence of the light chain variable region of any one of the antigen binding proteins specified in Table 6.

In certain embodiments, the application relates to an anti-TfR antibody or antigen-binding fragment thereof, wherein the HCDR1, HCDR2 and HCDR3 have the amino acid sequences of the HCDR1, HCDR2 and HCDR3, respectively, of any one of the antigen binding proteins specified in Table 5.

In certain embodiments, the application relates to an anti-TfR antibody or antigen-binding fragment thereof, wherein the VH comprises an amino acid sequence that is at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to an amino acid sequence selected from the group consisting of SEQ ID NOs: 981-1197 and 1718-1775.

In certain embodiments, the application relates to an anti-TfR antibody or antigen-binding fragment thereof, wherein the VH comprises the amino acid sequence of the heavy chain variable region of any one of the antigen binding proteins specified in Table 6.

In certain embodiments, the application relates to an anti-TfR antibody or antigen-binding fragment thereof, wherein the LCDR1, LCDR2 LCDR3, HCDR1, HCDR2, and HCDR3 have the amino acid sequences of the LCDR1, LCDR2 LCDR3, HCDR1, HCDR2, and HCDR3, respectively, of any one of the antigen binding proteins specified in Table 5.

In certain embodiments, the application relates to an anti-TfR antibody or antigen-binding fragment thereof, wherein the VL and VH comprise the amino acid sequences of the

light chain variable region and the heavy chain variable region, respectively, of any one of the antigen binding proteins specified in Table 6.

In other embodiments, the application relates to an anti-TfR antibody or antigen-binding fragment thereof, having a single-chain variable fragment (scFv) comprising the VH and VL of the anti-TfR antibody or antigen-binding fragment thereof.

In certain embodiments, the application relates to an anti-TfR antibody or antigen-binding fragment thereof, wherein the scFv further comprises a linker that covalently links the VH and VL, such as a linker having the amino acid sequence selected from the group consisting of SEQ ID NO: 1421 and SEQ ID NOs: 1424-1455.

In certain embodiments, the application relates to an anti-TfR antibody or antigen-binding fragment thereof, wherein the scFv comprises one or more disulfide bonds formed between a cysteine (Cys) in the linker and a surface exposed Cys in VH and/or VL, preferably a surface exposed Cys in a framework region of the VH and/or VL.

In another general aspect, the application describes an anti-TfR antibody or antigen-binding fragment thereof having a single variable domain on a heavy chain (VHH) comprising heavy chain complementarity determining regions (HCDRs) HCDR1, HCDR2 and HCDR3, wherein:

- (1) the HCDR1 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-24;
- (2) the HCDR2 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 25-46; and
- (3) the HCDR3 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 47-70.

In certain embodiments, the application relates to an anti-TfR antibody or antigen-binding fragment thereof, wherein the HCDR1, HCDR2 and HCDR3 have the amino acid sequences of the HCDR1, HCDR2 and HCDR3, respectively, of any one of the VHH antigen binding proteins specified in Table 3.

In certain embodiments, the application relates to an anti-TfR antibody or antigen-binding fragment thereof, comprising an amino acid sequence that is at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to an amino acid sequence selected from the group consisting of SEQ ID NOs: 71-221.

In certain embodiments, the anti-TfR antibody or antigen-binding fragment thereof comprises one or more amino acid modifications that increases its stability. The one or more amino acid modifications can be made using site-directed mutagenesis, for example, as described in Manning, M.C., Chou, D.K., Murphy, B.M. *et al.* Stability of Protein Pharmaceuticals: An Update. *Pharm Res* 27, 544–575 (2010). Forced degradation studies such as described in Nowak C, K Cheung J, M Dellatore S, Katiyar A, Bhat R, Sun J, Ponniah G, Neill A, Mason B, Beck A, Liu H. Forced degradation of recombinant monoclonal antibodies: A practical guide. *MAbs*. 2017 Nov/Dec;9(8):1217-1230 can be used to identify risks (e.g., risks associated with post-translational modifications) that may contribute to lower stability. Site-directed mutagenesis to reduce or eliminate such risks may be employed. The relevant disclosures of all such references are incorporated herein by reference.

In certain embodiments, the application relates to an anti-TfR antibody or antigen-binding fragment thereof, comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 71-221.

In another aspect, the application relates to a conjugate comprising the anti-TfR antibody or antigen-binding fragment thereof of the application coupled to a therapeutic or diagnostic agent, preferably, the conjugate is a multi-specific antibody comprising a first antigen binding region which binds the TfR and comprises the anti-TfR antibody or antigen-binding fragment thereof and a second antigen binding region which binds a brain target. In certain embodiments, the anti-TfR antibody or antigen-binding fragment thereof of the application is coupled to a therapeutic or diagnostic agent, where the therapeutic or diagnostic agent is a polynucleotide.

In certain embodiments, the application relates to a fusion construct comprising the anti-TfR antibody or antigen-binding fragment thereof of the application covalently linked to a second antibody or an antigen binding fragment thereof that binds to a brain target, such as a brain target selected from the group consisting of beta-secretase 1 (BACE1), amyloid beta (A β), epidermal growth factor receptor (EGFR), human epidermal growth factor receptor 2 (HER2), Tau, apolipoprotein E4 (ApoE4), alpha-synuclein, CD20, huntingtin, prion protein (PrP), leucine rich repeat kinase 2 (LRRK2), parkin, presenilin 1, presenilin 2, gamma secretase, death receptor 6 (DR6), amyloid precursor protein (APP), p75 neurotrophin receptor (p75NTR), and caspase 6.

In certain embodiments, the application relates to a fusion construct, wherein the anti-TfR antibody or antigen-binding fragment thereof is covalently linked to the carboxy terminus of only one of the two heavy chains of the second antibody or antigen binding fragment thereof via a linker, preferably the linker has the amino acid sequence of SEQ ID NO: 1422 or SEQ ID NO: 1423.

In certain embodiments, each of the two heavy chains of the second antibody or antigen binding fragment thereof comprises a modified constant heavy chain 3 (CH3) domain as compared to a wild-type CH3 domain to facilitate the formation of a heterodimer between the two heavy chains. Any mutation that facilitates the formation of a heterodimer between the two heavy chains can be used. Preferably, the modified CH3 domain of the first heavy chain comprises amino acid modifications at positions T350, L351, F405, and Y407, and the modified CH3 domain of the second heavy chain comprises amino acid modifications at positions T350, T366, K392 and T394. Preferably, the amino acid modification at position T350 is T350V, T350I, T350L or T350M; the amino acid modification at position L351 is L351Y; the amino acid modification at position F405 is F405A, F405V, F405T or F405S; the amino acid modification at position Y407 is Y407V, Y407A or Y407I; the amino acid modification at position T366 is T366L, T366I, T366V or T366M, the amino acid modification at position K392 is K392F, K392L or K392M, and the amino acid modification at position T394 is T394W. More preferably, the modified heterodimeric CH3 domain of the first heavy chain comprises mutations T350V, L351Y, F405A and Y407V, and the modified heterodimeric CH3 domain of the second heavy chain comprises mutations T350V, T366L, K392L and T394W. The numbering of amino acid residues in the antibody throughout the specification is performed according to the EU index as described in Kabat et al., Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, Md. (1991), unless otherwise explicitly stated.

In certain embodiments, the fragment crystallizable region (Fc region) of the second antibody or antigen binding fragment thereof contains substitutions that alter (increase or diminish), preferably eliminate, effector function, such as antibody dependent cellular cytotoxicity (ADCC) and/or complement dependent cytotoxicity (CDC). Preferably, the Fc region of the second antibody or antigen binding fragment thereof comprises one or more amino acid modifications that decrease or abolish the binding of the second antibody or antigen binding

fragment thereof to Fc gamma receptors (FcγR) and avoid effector function mediated toxicity. For example, the Fc region of the second antibody or antigen binding fragment thereof can comprise one or more amino acid modifications at positions L234, L235, D270, N297, E318, K320, K322, P331, and P329, such as one, two or three mutations of L234A, L235A and P331S, wherein the numbering of amino acid residues is according to the EU index as set forth in Kabat.

In certain embodiments, the Fc region of the second antibody or antigen binding fragment thereof contains substitutions that alter (increase or diminish), preferably increase, the binding of the second antibody or antigen binding fragment thereof to neonatal Fc receptor (FcRn).

Preferably the one or more mutations enhance the binding at an acidic pH, more preferably the Fc has the M252Y/S254T/T256E (YTE) mutations, wherein the numbering of amino acid residues is according to the EU index as set forth in Kabat.

Another general aspect of the application relates to an isolated nucleic acid encoding the antibody or antigen-binding fragment, a conjugate, or a fusion construct of the application. Also provided is a vector comprising the isolated nucleic acid of the application, a host cell

comprising the nucleic acid or the vector of the application.

Another general aspect of the application relates to a method of producing the antibody or antigen-binding fragment, a conjugate, or a fusion construct of the application. The method comprises culturing a cell comprising a nucleic acid of the application under conditions to produce the antibody or antigen-binding fragment, the conjugate, or the fusion construct, and recovering the antibody or antigen-binding fragment, the conjugate or the fusion construct from the cell or cell culture.

Further provided is a pharmaceutical composition comprising a conjugate or a fusion construct of the application and a pharmaceutically acceptable carrier.

Another general aspect of the application relates to a method of treating or detecting a disorder, preferably a neurological disorder, in a subject in need thereof, comprising administering to the subject an antibody or antigen-binding fragment, a conjugate, a fusion construct, or a pharmaceutical composition, preferably, the neurological disorder is selected from the group consisting of neurodegenerative diseases (such as Lewy body disease, postpoliomyelitis syndrome, Shy-Draeger syndrome, olivopontocerebellar atrophy, Parkinson's disease, multiple system atrophy, striatonigral degeneration, spinocerebellar ataxia, spinal muscular atrophy), tauopathies (such as Alzheimer's disease and supranuclear palsy), prion

diseases (such as bovine spongiform encephalopathy, scrapie, Creutzfeldt-Jakob syndrome, kuru, Gerstmann-Straussler-Scheinker disease, chronic wasting disease, and fatal familial insomnia), bulbar palsy, motor neuron disease, and nervous system heterodegenerative disorders (such as Canavan disease, Huntington's disease, neuronal ceroid-lipofuscinosis, Alexander's disease, Tourette's syndrome, Menkes kinky hair syndrome, Cockayne syndrome, Hallervorden-Spatz syndrome, lafora disease, Rett syndrome, hepatolenticular degeneration, Lesch-Nyhan syndrome, and Unverricht-Lundborg syndrome), dementia (such as Pick's disease, and spinocerebellar ataxia), and cancer of the CNS and/or brain (such as brain metastases resulting from cancer elsewhere in the body).

10 Preferably, the antibody or antigen-binding fragment thereof, the conjugate, or the pharmaceutical composition is administered intravenously.

 Also described is a method of delivering a therapeutic or diagnostic agent across the blood-brain barrier (BBB) of a subject in need thereof, comprising administering to the subject a complex comprising the therapeutic or diagnostic agent coupled to, preferably covalently
15 conjugated to, the antibody or antigen-binding fragment thereof of the application. Preferably, the administration of the therapeutic or diagnostic agent coupled to an anti-TfR antibody or antigen-binding fragment thereof of the application to the brain of a subject results in reduced Fc-mediated effector function and/or does not induce rapid reticulocyte depletion, as compared to the administration of the therapeutic or diagnostic agent not coupled to the anti-TfR antibody
20 or antigen-binding fragment thereof.

 Yet another general aspect of the invention relates to a method of inducing antibody-dependent phagocytosis (ADP) without stimulating secretion of a pro-inflammatory cytokine in a subject in need thereof, comprising administering to the subject a complex comprising a therapeutic antibody or antigen binding fragment thereof coupled to, preferably covalently
25 conjugated to, an antigen-binding fragment thereof according to an embodiment of the invention, wherein the therapeutic antibody or antigen binding fragment thereof does not have effector function, for example, the therapeutic antibody or antigen binding fragment thereof comprises one or more amino acid modifications at positions L234, L235, D270, N297, E318, K320, K322, P331, and P329, such as one, two or three mutations of L234A, L235A and P331S, wherein the
30 numbering of amino acid residues is according to the EU index as set forth in Kabat. Preferably, the therapeutic antibody or antigen binding fragment thereof binds specifically to tau aggregates.

Further aspects, features and advantages of the present invention will be better appreciated upon a reading of the following detailed description of the invention and claims.

DETAILED DESCRIPTION OF THE INVENTION

5 Various publications, articles and patents are cited or described in the background and throughout the specification; each of these references is herein incorporated by reference in its entirety. Discussion of documents, acts, materials, devices, articles or the like which has been included in the present specification is for the purpose of providing context for the present invention. Such discussion is not an admission that any or all of these matters form part of the
10 prior art with respect to any inventions disclosed or claimed.

Although any methods and materials similar or equivalent to those described herein can be used in the practice for testing of the present application, exemplary materials and methods are described herein.

15 Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood to one of ordinary skill in the art to which this invention pertains. Otherwise, certain terms used herein have the meanings as set in the specification. All patents, published patent applications, and publications cited herein are incorporated by reference as if set forth fully herein. It must be noted that as used herein and in the appended
20 claims, the singular forms “a,” “an,” and “the” include plural reference unless the context clearly dictates otherwise.

When a list is presented, unless stated otherwise, it is to be understood that each individual element of that list, and every combination of that list, is a separate embodiment. For example, a list of embodiments presented as “A, B, or C” is to be interpreted as including the
25 embodiments, “A,” “B,” “C,” “A or B,” “A or C,” “B or C,” or “A, B, or C.”

Unless otherwise stated, any numerical value, such as a concentration or a concentration range described herein, are to be understood as being modified in all instances by the term “about.” Thus, a numerical value typically includes $\pm 10\%$ of the recited value. For example, a dosage of 10 mg includes 9 mg to 11 mg. As used herein, the use of a numerical range expressly
30 includes all possible subranges, all individual numerical values within that range, including

integers within such ranges and fractions of the values unless the context clearly indicates otherwise.

As used herein, the conjunctive term “and/or” between multiple recited elements is understood as encompassing both individual and combined options. For instance, where two
5 elements are conjoined by “and/or,” a first option refers to the applicability of the first element without the second. A second option refers to the applicability of the second element without the first. A third option refers to the applicability of the first and second elements together. Any one of these options is understood to fall within the meaning, and therefore satisfy the requirement of the term “and/or” as used herein. Concurrent applicability of more than one of the options is also
10 understood to fall within the meaning, and therefore satisfy the requirement of the term “and/or.”

Throughout this specification and the claims which follow, unless the context requires otherwise, the word “comprise,” and variations such as “comprises” and “comprising,” will be understood to imply the inclusion of a stated integer or step or group of integers or steps but not the exclusion of any other integer or step or group of integer or step. When used herein the term
15 “comprising” can be substituted with the term “containing” or “including” or sometimes when used herein with the term “having.”

When used herein “consisting of” excludes any element, step, or ingredient not specified in the claim element. When used herein, “consisting essentially of” does not exclude materials or steps that do not materially affect the basic and novel characteristics of the claim. Any of the
20 aforementioned terms of “comprising,” “containing,” “including,” and “having,” whenever used herein in the context of an aspect or embodiment of the invention can be replaced with the term “consisting of” or “consisting essentially of” to vary scopes of the disclosure.

The term “antibody” herein is used in the broadest sense and specifically includes full-length monoclonal antibodies, polyclonal antibodies, and, unless otherwise stated or contradicted
25 by context, antigen-binding fragments, antibody variants, and multispecific molecules thereof, so long as they exhibit the desired biological activity. Generally, a full-length antibody is a glycoprotein comprising at least two heavy (H) chains and two light (L) chains inter-connected by disulfide bonds, or an antigen binding portion thereof. Each heavy chain is comprised of a heavy chain variable region (abbreviated herein as VH) and a heavy chain constant region. The
30 heavy chain constant region is comprised of three domains, CH1, CH2 and CH3. Each light chain is comprised of a light chain variable region (abbreviated herein as VL) and a light chain

constant region. The light chain constant region is comprised of one domain, CL. The VH and VL regions can be further subdivided into regions of hypervariability, termed complementarily determining regions (CDR), interspersed with regions that are more conserved, termed framework regions (FR). Each VH and VL is composed of three CDRs and four FRs, arranged from amino-terminus to carboxy-terminus in the following order: FR1, CDR1, FR2, CDR2, FR3, CDR3, FR4. The variable regions of the heavy and light chains contain a binding domain that interacts with an antigen. General principles of antibody molecule structure and various techniques relevant to the production of antibodies are provided in, e.g., Harlow and Lane, ANTIBODIES: A LABORATORY MANUAL, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N. Y., (1988).

Depending on the amino acid sequence of the constant domain of their heavy chains, full length antibodies can be assigned to different “classes”. There are five major classes of full-length antibodies: IgA, IgD, IgE, IgG, and IgM, and several of these may be further divided into “subclasses” (isotypes), e.g., IgG1, IgG2, IgG3, IgG4, IgA, and IgA2. The heavy-chain constant domains that correspond to the different classes of antibodies are called alpha, delta, epsilon, gamma, and mu, respectively. The subunit structures and three-dimensional configurations of different classes of immunoglobulins are well known.

An “antibody” can also be a single variable domain on a heavy chain (VHH) antibody, also referred to as a heavy chain only antibody (HcAb), which are devoid of light chains and can be naturally produced by camelids or sharks. The antigen binding portion of the HcAb is comprised of a VHH fragment.

The term “recombinant antibody”, as used herein, refers to an antibody (e.g. a chimeric, humanized, or human antibody or antigen-binding fragment thereof) that is expressed by a recombinant host cell comprising nucleic acid encoding the antibody. Examples of “host cells” for producing recombinant antibodies include: (1) mammalian cells, for example, Chinese Hamster Ovary (CHO), COS, myeloma cells (including YO and NSO cells), baby hamster kidney (BHK), Hela and Vero cells; (2) insect cells, for example, sf9, sf21 and Tn5; (3) plant cells, for example plants belonging to the genus *Nicotiana* (e.g. *Nicotiana tabacum*); (4) yeast cells, for example, those belonging to the genus *Saccharomyces* (e.g. *Saccharomyces cerevisiae*) or the genus *Aspergillus* (e.g. *Aspergillus niger*); (5) bacterial cells, for example *Escherichia coli* cells or *Bacillus subtilis* cells, etc.

“Antibody-dependent phagocytosis” or “ADP” refers to the mechanism of elimination of antibody-coated target cells by internalization by phagocytic cells, such as macrophages or dendritic cells.

“Antigen” refers to any molecule (e.g., protein, peptide, polysaccharide, glycoprotein, glycolipid, nucleic acid, portions thereof, or combinations thereof) capable of being bound by an antigen binding region or a T-cell receptor that is capable of mediating an immune response. Exemplary immune responses include antibody production and activation of immune cells, such as T cells, B cells or NK cells. Antigens may be expressed by genes, synthesized, or purified from biological samples such as a tissue sample, a tumor sample, a cell or a fluid with other biological components, organisms, subunits of proteins/antigens, killed or inactivated whole cells or lysates.

An “antigen binding region” or “antigen binding fragment” or “antigen binding domain” each refers to a portion of a full-length antibody that binds an antigen. An antigen binding region can be synthetic, enzymatically obtainable or genetically engineered polypeptides. An antigen binding region typically comprises one or more portions of at least the VH region. Antigen-binding fragments include multivalent molecules comprising one, two, three, or more antigen-binding portions of an antibody, and single-chain constructs wherein the VL and VH regions, or selected portions thereof, are joined by synthetic linkers or by recombinant methods to form a functional, antigen-binding molecule. Antigen-binding fragments can also be a single-domain antibody (sdAb), also known as a nanobody, which is an antibody fragment consisting of a single monomeric variable antibody domain (VHH). Examples of antigen-binding fragments include Fab, Fab', F(ab)2, F(ab')2, F(ab)3, Fv (typically the VL and VH domains of a single arm of an antibody), single-chain Fv (scFv, see e.g., Bird et al., Science 1988; 242:423-426; and Huston et al. PNAS 1988; 85:5879-5883), dsFv, Fd (typically the VH and CH1 domain), and dAb (typically a VH domain) fragments; VH, VL, VHH, and V-NAR domains; monovalent molecules comprising a single VH and a single VL chain; minibodies, diabodies, triabodies, tetrabodies, and kappa bodies (see, e.g., Ill et al., Protein Eng 1997; 10:949-57); camel IgG; IgNAR; as well as one or more isolated CDRs or a functional paratope, where the isolated CDRs or antigen-binding residues or polypeptides can be associated or linked together so as to form a functional antibody fragment, minimal recognition units consisting of the amino acid residues that mimic the CDRs of an antibody, such as FR3-CDR3-FR4 portions, the HCDR1, the HCDR2

and/or the HCDR3 and the LCDR1, the LCDR2 and/or the LCDR3, alternative scaffolds that bind an antigen, and multispecific antigen-binding constructs comprising the antigen binding regions. Various types of antibody fragments have been described or reviewed in, e.g., Holliger and Hudson, *Nat Biotechnol* 2005; 23:1126-1136; WO2005040219, and published U.S. Patent Applications 20050238646 and 20020161201. Antibody fragments can be obtained using conventional recombinant or protein engineering techniques, and the fragments can be screened for antigen-binding or other function in the same manner as are intact antibodies.

Various techniques have been developed for the production of antibody fragments. Traditionally, these fragments were derived via proteolytic digestion of full-length antibodies (see, e.g., Morimoto et al., *Journal of Biochemical and Biophysical Methods*, 24:107-117 (1992); and Brennan et al., *Science*, 229:81 (1985)). However, these fragments can now be produced directly by recombinant host cells. Alternatively, Fab'-SH fragments can be directly recovered from *E. coli* and chemically coupled to form F(ab')₂ fragments (Carter et al., *Bio/Technology*, 10:163-167 (1992)). According to another approach, F(ab')₂ fragments can be isolated directly from recombinant host cell culture. In other embodiments, the antibody of choice is a single-chain Fv fragment (scFv). See WO 1993/16185; U.S. Pat. No. 5,571,894; and U.S. Pat. No. 5,587,458. The antibody fragment may also be a "linear antibody", e.g., as described in U.S. Pat. No. 5,641,870, for example. Such linear antibody fragments can be monospecific or bispecific.

The term "antibody derivative" as used herein refers to a molecule comprising a full-length antibody or an antigen-binding fragment thereof, wherein one or more amino acids are chemically modified or substituted. Chemical modifications that can be used in antibody derivative includes, e.g., alkylation, PEGylation, acylation, ester formation or amide formation or the like, e.g., for linking the antibody to a second molecule. Exemplary modifications include PEGylation (e.g., cysteine- PEGylation), biotinylation, radiolabeling, and conjugation with a second agent (such as a cytotoxic agent).

Antibodies herein include "amino acid sequence variants" with altered antigen-binding or biological activity. Examples of such amino acid alterations include antibodies with enhanced affinity for antigen (e.g. "affinity matured" antibodies), and antibodies with altered Fc region, if present, e.g. with altered (increased or diminished) antibody dependent cellular cytotoxicity (ADCC) and/or complement dependent cytotoxicity (CDC) (see, for example, WO 00/42072,

Presta, L. and WO 99/51642, Iduosogie et al); and/or increased or diminished serum half-life (see, for example, WO00/42072, Presta, L.).

5 A “multispecific molecule” comprises an antibody, or an antigen-binding fragment thereof, which is associated with or linked to at least one other functional molecule (e.g. another peptide or protein such as another antibody or ligand for a receptor) thereby forming a molecule that binds to at least two different binding sites or target molecules. Exemplary multispecific molecules include bi-specific antibodies and antibodies linked to soluble receptor fragments or ligands.

10 The term “human antibody”, as used herein, is intended to include antibodies having variable regions in which both the framework and CDR regions are derived from (i.e., are identical or essentially identical to) human germline immunoglobulin sequences. Furthermore, if the antibody contains a constant region, the constant region also is “derived from” human germline immunoglobulin sequences. The human antibodies of the invention can include amino acid residues not encoded by human germline immunoglobulin sequences (e.g., mutations
15 introduced by random or site-specific mutagenesis in vitro or by somatic mutation in vivo). However, the term “human antibody”, as used herein, is not intended to include antibodies in which CDR sequences derived from the germline of another mammalian species, such as a mouse, have been grafted onto human framework sequences.

20 A “humanized” antibody is a human/non-human chimeric antibody that contains a minimal sequence derived from non-human immunoglobulin. For the most part, humanized antibodies are human immunoglobulins (recipient antibody) in which residues from a hypervariable region of the recipient are replaced by residues from a hypervariable region of a non-human species (donor antibody) such as mouse, rat, rabbit, or non-human primate having the desired specificity, affinity, and capacity. In some instances, FR residues of the human
25 immunoglobulin are replaced by corresponding non-human residues. Furthermore, humanized antibodies can comprise residues that are not found in the recipient antibody or in the donor antibody. These modifications are made to further refine antibody performance. In general, a humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the hypervariable loops correspond to those of a non-
30 human immunoglobulin and all or substantially all of the FR residues are those of a human immunoglobulin sequence. The humanized antibody can optionally also comprise at least a

portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin. For further details, see, e.g., Jones et al., *Nature* 321:522-525 (1986); Riechmann et al., *Nature* 332:323-329 (1988); and Presta, *Curr. Op. Struct. Biol.* 2:593-596 (1992), WO 92/02190, US Patent Application 20060073137, and U.S. Pat. Nos. 6,750,325, 6,632,927, 6,639,055,
5 6,548,640, 6,407,213, 6,180,370, 6,054,297, 5,929,212, 5,895,205, 5,886,152, 5,877,293, 5,869,619, 5,821,337, 5,821,123, 5,770,196, 5,777,085, 5,766,886, 5,714,350, 5,693,762, 5,693,761, 5,530,101, 5,585,089, and 5,225,539.

The term “hypervariable region” when used herein refers to the amino acid residues of an antibody that are responsible for antigen binding. The hypervariable region generally comprises
10 amino acid residues from a “complementarity-determining region” or “CDR” (residues 24-34 (L1), 50-56 (L2) and 89-97 (L3) in the light-chain variable domain and 31-35 (H1), 50-65 (H2) and 95-102 (H3) in the heavy-chain variable domain; (Kabat et al. (1991) *Sequences of Proteins of Immunological Interest*, Fifth Edition, U.S. Department of Health and Human Services, NIH Publication No. 91-3242) and/or those residues from a “hypervariable loop” (residues 26-32
15 (L1), 50-52 (L2) and 91-96 (L3) in the light-chain variable domain and 26-32 (H1), 53-55 (H2) and 96-101 (H3) in the heavy-chain variable domain; Chothia and Lesk, *J. Mol. Biol.* 1987; 196:901-917). Typically, the numbering of amino acid residues in this region is performed by the method described in Kabat et al., *supra*. Phrases such as “Kabat position”, “variable domain residue numbering as in Kabat” and “according to Kabat” herein refer to this numbering system
20 for heavy chain variable domains or light chain variable domains. Using the Kabat numbering system, the actual linear amino acid sequence of a peptide can contain fewer or additional amino acids corresponding to a shortening of, or insertion into, a FR or CDR of the variable domain. For example, a heavy chain variable domain can include a single amino acid insert (residue 52a according to Kabat) after residue 52 of CDR H2 and inserted residues (e.g. residues 82a, 82b,
25 and 82c, etc. according to Kabat) after heavy chain FR residue 82. The Kabat numbering of residues can be determined for a given antibody by alignment at regions of homology of the sequence of the antibody with a “standard” Kabat numbered sequence.

The term “administering” with respect to the methods of the invention, means a method for therapeutically or prophylactically preventing, treating or ameliorating a syndrome, disorder
30 or disease as described herein by using a conjugate of the invention or a form, composition or medicament thereof. Such methods include administering an effective amount of said antibody,

antigen-binding fragment thereof, or conjugate, or a form, composition or medicament thereof at different times during the course of a therapy or concurrently in a combination form. The methods of the invention are to be understood as embracing all known therapeutic treatment regimens.

5 The ability of a target antibody to “block” the binding of a target molecule to a natural target ligand, means that the antibody, in an assay using soluble or cell-surface associated target and ligand molecules, can detectably reduce the binding of a target molecule to the ligand in a dose-dependent fashion, where the target molecule detectably binds to the ligand in the absence of the antibody.

10 The “blood-brain barrier” or “BBB” refers a physiological barrier between the peripheral circulation and the brain and spinal cord which is formed by tight junctions within the brain capillary endothelial plasma membranes, creating a tight barrier that restricts the transport of molecules into the brain. The BBB can restrict the transport of even very small molecules such as urea (60 Daltons) into the brain. Examples of the BBB include the BBB within the brain, the
15 blood-spinal cord barrier within the spinal cord, and the blood-retinal barrier within the retina, all of which are contiguous capillary barriers within the CNS. The BBB also encompasses the blood-CSF barrier (choroid plexus) where the barrier is comprised of ependymal cells rather than capillary endothelial cells.

A “blood-brain barrier receptor” (abbreviated “R/BBB” herein) is an extracellular
20 membrane-linked receptor protein expressed on brain endothelial cells which is capable of transporting molecules across the BBB or be used to transport exogenous administrated molecules. Examples of R/BBB include, but are not limited to, transferrin receptor (TfR), insulin receptor, insulin-like growth factor receptor (IGF-R), low density lipoprotein receptors including without limitation low density lipoprotein receptor-related protein 1 (LRP1) and low density
25 lipoprotein receptor-related protein 8 (LRP8), and heparin-binding epidermal growth factor-like growth factor (HB-EGF). An exemplary R/BBB herein is transferrin receptor (TfR).

The “central nervous system” or “CNS” refers to the complex of nerve tissues that control bodily function and includes the brain and spinal cord.

“Complementarity determining regions” (CDR) are antibody regions that bind an antigen.
30 There are three CDRs in the VH (HCDR1, HCDR2, HCDR3) and three CDRs in the VL (LCDR1, LCDR2, LCDR3). CDRs may be defined using various delineations such as Kabat

(Wu et al. (1970) J Exp Med 132: 211-50; Kabat et al., Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, Md., 1991), Chothia (Chothia et al. (1987) J Mol Biol 196: 901-17), IMGT (Lefranc et al. (2003) Dev Comp Immunol 27: 55-77), and AbM (Martin and Thornton J Biol Chem 263: 800-15, 1996). The correspondence between the various delineations and variable region numbering is described (see e.g., Lefranc et al. (2003) Dev Comp Immunol 27: 55-77; Honegger and Pluckthun (2001), J Mol Biol 309:657-70; International ImMunoGeneTics (IMGT) database; Web resources, <http://www.imgt.org>). Available programs such as abYsis by UCL Business PLC may be used to delineate CDRs. The terms “CDR”, “HCDR1”, “HCDR2”, “HCDR3”, “LCDR1”, “LCDR2” and “LCDR3” as used herein include CDRs defined by any of the methods described *supra*, Kabat, Chothia, IMGT or AbM, unless otherwise explicitly stated in the specification. Correspondence between the numbering system, including, for example, the Kabat numbering and the IMGT unique numbering system, is well known to one skilled in the art (see, e.g., Kabat, *supra*; Chothia, *supra*; Martin, *supra*; Lefranc et al., *supra*).

Table 1: Relationship Between CDR Numbering Schemes

	IMGT	Kabat	AbM	Chothia
V _H CDR1	27-38	31-35	26-35	26-32
V _H CDR2	56-65	50-65	50-58	53-55
V _H CDR3	105-117	95-102	95-102	96-101
V _L CDR1	27-38	24-34	24-34	26-32
V _L CDR2	56-65	50-56	50-56	50-52
V _L CDR3	105-117	89-97	89-97	91-96

A “conjugate” as used herein refer to an anti-TfR antibody or antigen-binding fragment thereof of the application covalently linked to one or more heterologous molecule(s). Examples of heterologous molecule(s) that can be used in a conjugate of the application include, but are not limited to, a therapeutic peptide or protein, an antibody, a nucleic acid (e.g., DNA or RNA), a label, or a neurological disorder drug. In certain embodiments, an antibody or antigen-binding fragment of the application can be conjugated to one or more heterologous molecule(s) through a non-peptide linker. In certain embodiments, an antibody or antigen-binding fragment of the application can be conjugated to one or more heterologous molecule(s) through a peptide linker. When one protein is conjugated to another protein via a peptide linker, it is also referred to that the two proteins are fused together. By way of a non-limiting example, an antibody or antigen-binding fragment of the application can be conjugated to another polypeptide to form a fusion

protein. In certain embodiments, an antibody or antigen-binding fragment of the application can be conjugated to another polypeptide through a non-peptide linker.

As used herein the term “coupled” refers to the joining or connection of two or more objects together. When referring to chemical or biological compounds, coupled can refer to a covalent connection between the two or more chemical or biological compounds. By way of a non-limiting example, an antibody of the invention can be coupled with a peptide of interest to form an antibody coupled peptide. An antibody coupled peptide can be formed through specific chemical reactions designed to conjugate the antibody to the peptide. In certain embodiments, an antibody of the invention can be covalently coupled with a peptide of the invention through a linker. The linker can, for example, be first covalently connected to the antibody or the peptide, then covalently connected to the peptide or the antibody.

An “effective amount” or “therapeutically effective amount” of an agent, e.g., a pharmaceutical formulation, refers to an amount effective, at dosages and for periods of time necessary, to achieve the desired therapeutic or prophylactic result.

“Encode” or “encoding” refers to the inherent property of specific sequences of nucleotides in a polynucleotide, such as a gene, a cDNA, or an mRNA, to serve as templates for synthesis of other polymers and macromolecules in biological processes having either a defined sequence of nucleotides (*e.g.*, rRNA, tRNA and mRNA) or a defined sequence of amino acids and the biological properties resulting therefrom. Thus, a gene, cDNA, or RNA, encodes a protein if transcription and translation of mRNA corresponding to that gene produces the protein in a cell or other biological system. Both the coding strand, the nucleotide sequence of which is identical to the mRNA sequence, and the non-coding strand, used as the template for transcription of a gene or cDNA, can be referred to as encoding the protein or other product of that gene or cDNA.

“Epitope” refers to a portion of an antigen to which an antibody, or the antigen binding portion thereof, specifically binds. Epitopes typically consist of chemically active (such as polar, non-polar or hydrophobic) surface groupings of moieties such as amino acids or polysaccharide side chains and may have specific three-dimensional structural characteristics, as well as specific charge characteristics. An epitope may be composed of contiguous and/or discontinuous amino acids that form a conformational spatial unit. For a discontinuous epitope, amino acids from differing portions of the linear sequence of the antigen come in close proximity in 3-dimensional

space through the folding of the protein molecule. Antibody “epitope” depends on the methodology used to identify the epitope.

“Expression vector” or “vector” refers to a biotic or abiotic agents that can be utilized in a biological system or in a reconstituted biological system to direct the translation of a polypeptide encoded by a polynucleotide sequence present in the expression vector.

“Fv” or “Fv fragment” refers to an antibody fragment composed of the VH and the VL domains from a single arm of the antibody. Fv fragments lack the constant regions of Fab (CH1 and CL) regions. The VH and VL in Fv fragments are held together by non-covalent interactions.

“Framework region” or “FR” residues are those VH or VL residues other than the CDRs as herein defined.

“Host cell” refers to any cell that contains a heterologous nucleic acid. An exemplary heterologous nucleic acid is a vector (*e.g.*, an expression vector).

A “linker” as used herein refers to a chemical linker or a single chain peptide linker that covalently connects two different entities. A linker can be used to connect any two of an antibody or a fragment thereof, a blood brain barrier shuttle, a fusion protein and a conjugate of the present invention. The linker can connect, for example, the VH and VL in scFv, or the monoclonal antibody or antigen-binding fragment thereof with a therapeutic molecule, such as a second antibody. In some embodiment, if the monovalent binding entity comprises an scFv directed to TfR, preferably huTfR1, and the therapeutic molecule comprises an antibody directed to a CNS target, such as Tau, then the linker can connect the scFv to the antibody directed to Tau. Single chain peptide linkers, comprised of from 1 to 25 amino acids, such as 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 amino acids, joined by peptide bonds, can be used. In certain embodiments, the amino acids are selected from the twenty naturally occurring amino acids. In certain other embodiments, one or more of the amino acids are selected from glycine, alanine, proline, asparagine, glutamine and lysine. Chemical linkers, such as a hydrocarbon linker, a polyethylene glycol (PEG) linker, a polypropylene glycol (PPG) linker, a polysaccharide linker, a polyester linker, a hybrid linker consisting of PEG and an embedded heterocycle, and a hydrocarbon chain can also be used.

A “neurological disorder” as used herein refers to a disease or disorder which affects the CNS and/or which has an etiology in the CNS. Exemplary CNS diseases or disorders include,

but are not limited to, neuropathy, amyloidosis, cancer, an ocular disease or disorder, viral or microbial infection, inflammation, ischemia, neurodegenerative disease, seizure, behavioral disorders, and a lysosomal storage disease. For the purposes of this application, the CNS will be understood to include the eye, which is normally sequestered from the rest of the body by the blood-retina barrier. Specific examples of neurological disorders include, but are not limited to, neurodegenerative diseases (including, but not limited to, Lewy body disease, postpoliomyelitis syndrome, Shy-Draeger syndrome, olivopontocerebellar atrophy, Parkinson's disease, multiple system atrophy, striatonigral degeneration, spinocerebellar ataxia, spinal muscular atrophy), tauopathies (including, but not limited to, Alzheimer's disease and supranuclear palsy), prion diseases (including, but not limited to, bovine spongiform encephalopathy, scrapie, Creutzfeldt-Jakob syndrome, kuru, Gerstmann-Straussler-Scheinker disease, chronic wasting disease, and fatal familial insomnia), bulbar palsy, motor neuron disease, and nervous system heterodegenerative disorders (including, but not limited to, Canavan disease, Huntington's disease, neuronal ceroid-lipofuscinosis, Alexander's disease, Tourette's syndrome, Menkes kinky hair syndrome, Cockayne syndrome, Halervorden-Spatz syndrome, lafora disease, Rett syndrome, hepatolenticular degeneration, Lesch-Nyhan syndrome, and Unverricht-Lundborg syndrome), dementia (including, but not limited to, Pick's disease, and spinocerebellar ataxia), cancer (e.g. of the CNS and/or brain, including brain metastases resulting from cancer elsewhere in the body).

The term "pharmaceutical formulation" or "pharmaceutical composition" refers to a composition comprises an active ingredient and a pharmaceutically acceptable carrier. A "pharmaceutical formulation" or "pharmaceutical composition" is in such form as to permit the biological activity of an active ingredient contained therein to be effective, and which contains no components which are unacceptably toxic to a subject to which the formulation would be administered.

"Pharmaceutically acceptable carrier" or "excipient" refers to an ingredient in a pharmaceutical composition, other than the active ingredient, which is nontoxic to a subject. Exemplary pharmaceutically acceptable carriers include a buffer, stabilizer or preservative.

"Polynucleotide" or "nucleic acid" refers to a synthetic molecule comprising a chain of nucleotides covalently linked by a sugar-phosphate backbone or other equivalent covalent

chemistry. cDNA is a typical example of a polynucleotide. Polynucleotide may be a DNA or a RNA molecule.

“Protein” or “polypeptide” are used interchangeably herein and refers to a molecule that comprises one or more polypeptides each comprised of at least two amino acid residues linked by a peptide bond. Protein may be a monomer, or may be protein complex of two or more subunits, the subunits being identical or distinct. Small polypeptides of less than 50 amino acids may be referred to as “peptides”. Protein may be a heterologous fusion protein, a glycoprotein, or a protein modified by post-translational modifications such as phosphorylation, acetylation, myristoylation, palmitoylation, glycosylation, oxidation, formylation, amidation, citrullination, polyglutamylolation, ADP-ribosylation, pegylation or biotinylation. Protein may be recombinantly expressed.

The phrases “sequence identity” or “percent (%) sequence identity” or “% identity” or “% identical to” when used with reference to an amino acid sequence describe the number of matches (“hits”) of identical amino acids of two or more aligned amino acid sequences as compared to the number of amino acid residues making up the overall length of the amino acid sequences. In other terms, using an alignment, for two or more sequences the percentage of amino acid residues that are the same (e.g. 90%, 91%, 92%, 93%, 94%, 95%, 97%, 98%, 99%, or 100% identity over the full-length of the amino acid sequences) may be determined, when the sequences are compared and aligned for maximum correspondence as measured using a sequence comparison algorithm as known in the art, or when manually aligned and visually inspected. The sequences which are compared to determine sequence identity may thus differ by substitution(s), addition(s) or deletion(s) of amino acids. Suitable programs for aligning protein sequences are known to the skilled person. The percentage sequence identity of protein sequences can, for example, be determined with programs such as CLUSTALW, Clustal Omega, FASTA or BLAST, e.g., using the NCBI BLAST algorithm (Altschul SF, et al (1997), *Nucleic Acids Res.* 25:3389-3402).

The term “substantially identical” in the context of two amino acid sequences means that the sequences, when optimally aligned, such as by the programs GAP or BESTFIT using default gap weights, share at least about 50 percent sequence identity. Typically sequences that are substantially identical will exhibit at least about 60, at least about 70, at least about 80, at least about 90, at least about 95, at least about 98, or at least about 99 percent sequence identity.

"Single chain Fv" or "scFv" refers to a single chain protein comprising a VH, a VL and a linker between the VH and the VL. The scFv may have the VL and VH variable regions in either orientation, e.g., with respect to the N- to C-terminal order of the VH and the VL. The scFv may thus be in the orientation VL-linker-VH or VH-linker-VL. scFv may be engineered to 20

5 comprise disulfide bonds between the VH, the VL and the linker.

"Specific binding" or "specifically binds" or "binds" refer to antibody binding to an antigen or an epitope within the antigen with greater affinity than for other antigens. Typically, the antibody binds to the antigen or the epitope within the antigen with a dissociation constant (K_D) of about 1×10^{-8} M or less, for example about 1×10^{-9} M or less, about 1×10^{-10} M or less, 10 about 1×10^{-11} M or less, or about 1×10^{-12} M or less, typically with a K_D that is at least one hundred fold less than its K_D for binding to a non-specific antigen (e.g., BSA, casein). K_D is the equilibrium dissociation constant, a ratio of k_{off}/k_{on} , between the antibody and its antigen. K_D and affinity are inversely related. The "on-rate" (k_{on}) is a constant used to characterize how quickly the antibody binds to its target. The "off-rate" (k_{off}) is a constant used to characterize 15 how quickly an antibody dissociates from its target. The dissociation constant K_D can be measured using standard procedures. For example, the K_D of an antibody can be determined by using surface plasmon resonance, such as by using a biosensor system, e.g., a Biacore® system, or by using bio-layer interferometry technology, such as an Octet RED96 system. The smaller the value of the K_D of an antibody, the higher affinity that the antibody binds to a target antigen. 20 Antibodies that specifically bind to the antigen or the epitope within the antigen can, however, have cross-reactivity to other related antigens, for example to the same antigen from other species (homologs), such as human or monkey, for example *Macaca fascicularis* (cynomolgus, cyno), *Pan troglodytes* (chimpanzee, chimp) or *Callithrix jacchus* (common marmoset, marmoset). While a monospecific antibody specifically binds one antigen or one epitope, a 25 bispecific antibody specifically binds two distinct antigens or two distinct epitopes.

The term "subject" as used herein refers to a mammal. Mammals include, but are not limited to, domesticated animals (e.g., cows, sheep, cats, dogs, and horses), primates (e.g., humans and non-human primates such as monkeys), rabbits, and rodents (e.g., mice and rats). In certain embodiments, the individual or subject is a human. When the subject is human, they can 30 also be referred to as a "patient".

The term “transferrin receptor” or “TfR,” as used herein, refers to a cell surface receptor necessary for cellular iron uptake by the process of receptor-mediated endocytosis. carrier protein for transferrin. A TfR is involved in iron uptake in vertebrates and is regulated in response to intracellular iron concentration. It imports iron by internalizing the transferrin-iron
5 complex through receptor-mediated endocytosis. Two transferrin receptors in humans, transferrin receptor 1 and transferrin receptor 2, have been characterized. Both these receptors are transmembrane glycoproteins. TfR1 is a high affinity ubiquitously expressed receptor. TfR2 binds to transferrin with a 25-30-fold lower affinity than TfR1. The expression of TfR2 is restricted to certain cell types and is unaffected by intracellular iron concentrations. In one
10 embodiment, the TfR is a human TfR comprising the amino acid sequence as in Schneider et al. Nature 311: 675-678 (1984), for example. It can have a molecular weight of about 180,000 Dalton, having two subunits each of apparent molecular weight of about 90,000 Dalton. Preferably, the TfR is a human TfR1.

A “target antigen” or “brain target,” as used herein, refers to an antigen and/or molecule
15 expressed in the CNS, including the brain, which can be targeted with an antibody or small molecule. Examples of such antigens and/or molecules include, without limitation: beta-secretase 1 (BACE1), amyloid beta (Abeta), epidermal growth factor receptor (EGFR), human epidermal growth factor receptor 2 (HER2), Tau, apolipoprotein E4 (ApoE4), alpha-synuclein, CD20, huntingtin, prion protein (PrP), leucine rich repeat kinase 2 (LRRK2), parkin, presenilin 1,
20 presenilin 2, gamma secretase, death receptor 6 (DR6), amyloid precursor protein (APP), p75 neurotrophin receptor (p75NTR), and caspase 6. In some embodiments, the target antigen is BACE1. In some embodiments, the target antigen is Tau.

As used herein, “treatment” (and grammatical variations thereof such as “treat” or “treating”) refers to clinical intervention in an attempt to alter the natural course of the individual
25 being treated and can be performed either for prophylaxis or during the course of clinical pathology. Desirable effects of treatment include, but are not limited to, preventing occurrence or recurrence of disease, alleviation of symptoms, diminishment of any direct or indirect pathological consequences of the disease, preventing metastasis, decreasing the rate of disease progression, amelioration or palliation of the disease state, and remission or improved prognosis.
30 In some embodiments, antibodies of the invention are used to delay development of a disease or to slow the progression of a disease.

“VHH” refers to a single-domain antibody or nanobody, exclusively composed of the antigen binding region of a heavy chain. A VHH single domain antibody lacks the light chain and the CH1 domain of the heavy chain of conventional Fab region.

5 The numbering of amino acid residues of the antibody constant region throughout the specification is according to the EU index as described in Kabat et al., Sequences of Proteins of 30 Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD. (1991), unless otherwise explicitly stated.

Anti-TfR Antibodies and antigen binding fragments thereof

In one general aspect, the application relates to an anti-TfR antibody or antigen-binding fragment thereof, comprising a light chain variable region (VL) comprising light chain complementarity determining regions (LCDRs) LCDR1, LCDR2 and LCDR3, and a heavy chain variable region (VH) comprising heavy chain complementarity determining regions (HCDRs) HCDR1, HCDR2 and HCDR3, wherein:

- (7) the LCDR1 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 222-308 and 1456-1485;
- (8) the LCDR2 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 308-359 and 1486-1511;
- (9) the LCDR3 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 360-518 and 1512-1561;
- (10) the HCDR1 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 519-645 and 1562-1606;
- (11) the HCDR2 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 646-792 and 1607-1661; and
- (12) the HCDR3 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 793-980 and 1662-1717.

In certain embodiments, the anti-TfR antibody or antigen-binding fragment thereof, comprises a LCDR1, LCDR2 and LCDR3 having the amino acid sequences of the LCDR1, LCDR2 and LCDR3, respectively, of any one of the antigen binding proteins specified in Table 5.

In certain embodiments, the anti-TfR antibody or antigen-binding fragment thereof, comprises a VL having an amino acid sequence that is at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to an amino acid sequence selected from the group consisting of SEQ ID NOs: 1198-1420 and 1776-1832.

In certain embodiments, the anti-TfR antibody or antigen-binding fragment thereof, comprises a VL having the amino acid sequence of the light chain variable region of any one of the antigen binding proteins specified in Table 6.

In certain embodiments, the anti-TfR antibody or antigen-binding fragment thereof, comprises a HCDR1, HCDR2 and HCDR3 having the amino acid sequences of the HCDR1,

HCDR2 and HCDR3, respectively, of any one of the antigen binding proteins specified in Table 5.

In certain embodiments, the anti-TfR antibody or antigen-binding fragment thereof, comprises a VH having an amino acid sequence that is at least 90%, 91%, 92%, 93%, 94%, 95%,
5 96%, 97%, 98%, 99% or 100% identical to an amino acid sequence selected from the group consisting of SEQ ID NOs: 981-1197 and 1718-1775.

In certain embodiments, the anti-TfR antibody or antigen-binding fragment thereof, comprises a VH having the amino acid sequence of the heavy chain variable region of any one of the antigen binding proteins specified in Table 6.

10 In certain embodiments, the anti-TfR antibody or antigen-binding fragment thereof, comprises a LCDR1, LCDR2 LCDR3, HCDR1, HCDR2, and HCDR3 having the amino acid sequences of the LCDR1, LCDR2 LCDR3, HCDR1, HCDR2, and HCDR3, respectively, of any one of the antigen binding proteins specified in Table 5.

In certain embodiments, the anti-TfR antibody or antigen-binding fragment thereof,
15 comprises a VL and a VH having the amino acid sequences of the light chain variable region and the heavy chain variable region, respectively, of any one of the antigen binding proteins specified in Table 6.

In other embodiments, the antibody or antigen-binding fragment thereof is single-chain variable fragment (scFv) comprising the heavy chain variable region (Hv) covalently linked to
20 the light chain variable region (Lv) via a flexible linker. The scFv can retain the specificity of the original immunoglobulin, despite removal of the constant regions and the introduction of the linker. In a scFv, the order of the domains can be either Hv-linker- Lv, or Lv-linker- Hv. The linker can be designed *de novo* or derived from known protein structure to provide a compatible length and conformational in bridging the variable domains of a scFv without serious steric
25 interference. The linker can have 10 to about 25 amino acids in length. Preferably, the linker is a peptide linker spanning about 3.5 nm (35 Å) between the carboxy terminus of the variable domain and the amino terminus of the other domain without affecting the ability of the domains to fold and form an intact antigen-binding site (Huston et al., *Methods in Enzymology*, vol. 203, pp. 46–88, 1991, which is incorporated herein by reference in its entirety). The linker preferably
30 comprises a hydrophilic sequence in order to avoid intercalation of the peptide within or between the variable domains throughout the protein folding (Argos, *Journal of Molecular Biology*, vol.

211, no. 4, pp. 943–958, 1990). For example, the linker can comprise Gly and Ser residues and/or together with the charged residues such as Glu, Thr and Lys interspersed to enhance the solubility. In one embodiment, the linker has the amino acid sequence of SEQ ID NO: 1421 (GTEGKSSGSGSESKST). Any other suitable linker can also be used in view of the present
5 disclosure. For example, the linker can also comprise one or more cysteine (Cys) residues to help stabilize the scFv, such as the linkers described for example in Int. Pat. Publ. No. WO2021/030657.

In certain embodiments, the anti-TfR antibody or antigen-binding fragment thereof of, comprises a scFv further comprises a linker that covalently links the VH and VL, such as a linker
10 having the amino acid sequence selected from the group consisting of SEQ ID NO: 1421 and SEQ ID NOs: 1424-1455.

In certain embodiments, the anti-TfR antibody or antigen-binding fragment thereof of the application, comprises an scFv having one or more disulfide bonds formed between a cysteine (Cys) in the linker and a surface exposed Cys in VH and/or VL, preferably a surface exposed
15 Cys in a framework region of the VH and/or VL.

In some embodiments, the VH Cys is at H105 and the VL Cys is at L42, wherein the residue numbering of the VH and the VL regions are according to Chothia.

In some embodiments, the VH Cys is at H43 and the VL Cys is at a L100, wherein the residue numbering of the VH and the VL regions are according to Chothia.

20 In some embodiments, the VH Cys is at H3 and the VL Cys is at L3, wherein the residue numbering of the VH and the VL regions are according to Chothia.

In some embodiments, the VH Cys is at H3 and the VL Cys is at L5, wherein the residue numbering of the VH and the VL regions are according to Chothia.

25 In some embodiments, the VH Cys is at H3 and the VL Cys is at L39, wherein the residue numbering of the VH and the VL regions are according to Chothia.

In some embodiments, the VH Cys is at H3 and the VL Cys is at L42, wherein the residue numbering of the VH and the VL regions are according to Chothia.

In some embodiments, the VH Cys is at H3 and the VL Cys is at L45, wherein the residue numbering of the VH and the VL regions are according to Chothia.

30 In some embodiments, the VH Cys is at H3 and the VL Cys is at L100, wherein the residue numbering of the VH and the VL regions are according to Chothia.

In some embodiments, the VH Cys is at H3 and the VL Cys is at L102, wherein the residue numbering of the VH and the VL regions are according to Chothia.

In some embodiments, the VH Cys is at H5 and the VL Cys is at L3, wherein the residue numbering of the VH and the VL regions are according to Chothia.

5 In some embodiments, the VH Cys is at H5 and the VL Cys is at L5, wherein the residue numbering of the VH and the VL regions are according to Chothia.

In some embodiments, the VH Cys is at H5 and the VL Cys is at L39, wherein the residue numbering of the VH and the VL regions are according to Chothia.

10 In some embodiments, the VH Cys is at H5 and the VL Cys is at L45, wherein the residue numbering of the VH and the VL regions are according to Chothia.

In some embodiments, the VH Cys is at H5 and the VL Cys is at L100, wherein the residue numbering of the VH and the VL regions are according to Chothia.

In some embodiments, the VH Cys is at H5 and the VL Cys is at L102, wherein the residue numbering of the VH and the VL regions are according to Chothia.

15 In some embodiments, the VH Cys is at H40 and the VL Cys is at L3, wherein the residue numbering of the VH and the VL regions are according to Chothia.

In some embodiments, the VH Cys is at H40 and the VL Cys is at L5, wherein the residue numbering of the VH and the VL regions are according to Chothia.

20 In some embodiments, the VH Cys is at H40 and the VL Cys is at L39, wherein the residue numbering of the VH and the VL regions are according to Chothia.

In some embodiments, the VH Cys is at H40 and the VL Cys is at L42, wherein the residue numbering of the VH and the VL regions are according to Chothia.

In some embodiments, the VH Cys is at H40 and the VL Cys is at L45, wherein the residue numbering of the VH and the VL regions are according to Chothia.

25 In some embodiments, the VH Cys is at H40 and the VL Cys is at L100, wherein the residue numbering of the VH and the VL regions are according to Chothia.

In some embodiments, the VH Cys is at H40 and the VL Cys is at L102, wherein the residue numbering of the VH and the VL regions are according to Chothia.

30 In some embodiments, the VH Cys is at H43 and the VL Cys is at L3, wherein the residue numbering of the VH and the VL regions are according to Chothia.

In some embodiments, the VH Cys is at H43 and the VL Cys is at L5, wherein the residue numbering of the VH and the VL regions are according to Chothia.

In some embodiments, the VH Cys is at H43 and the VL Cys is at L39, wherein the residue numbering of the VH and the VL regions are according to Chothia.

5 In some embodiments, the VH Cys is at H43 and the VL Cys is at L42, wherein the residue numbering of the VH and the VL regions are according to Chothia.

In some embodiments, the VH Cys is at H43 and the VL Cys is at L45, wherein the residue numbering of the VH and the VL regions are according to Chothia.

10 In some embodiments, the VH Cys is at H43 and the VL Cys is at L102, wherein the residue numbering of the VH and the VL regions are according to Chothia.

In some embodiments, the VH Cys is at H46 and the VL Cys is at L3, wherein the residue numbering of the VH and the VL regions are according to Chothia.

In some embodiments, the VH Cys is at H46 and the VL Cys is at L5, wherein the residue numbering of the VH and the VL regions are according to Chothia.

15 In some embodiments, the VH Cys is at H46 and the VL Cys is at L39, wherein the residue numbering of the VH and the VL regions are according to Chothia.

In some embodiments, the VH Cys is at H46 and the VL Cys is at L42, wherein the residue numbering of the VH and the VL regions are according to Chothia.

20 In some embodiments, the VH Cys is at H46 and the VL Cys is at L45, wherein the residue numbering of the VH and the VL regions are according to Chothia.

In some embodiments, the VH Cys is at H46 and the VL Cys is at L100, wherein the residue numbering of the VH and the VL regions are according to Chothia.

In some embodiments, the VH Cys is at H46 and the VL Cys is at L102, wherein the residue numbering of the VH and the VL regions are according to Chothia.

25 In some embodiments, the VH Cys is at H105 and the VL Cys is at L3, wherein the residue numbering of the VH and the VL regions are according to Chothia.

In some embodiments, the VH Cys is at H105 and the VL Cys is at L5, wherein the residue numbering of the VH and the VL regions are according to Chothia.

30 In some embodiments, the VH Cys is at H105 and the VL Cys is at L39, wherein the residue numbering of the VH and the VL regions are according to Chothia.

In some embodiments, the VH Cys is at H105 and the VL Cys is at L45, wherein the residue numbering of the VH and the VL regions are according to Chothia.

In some embodiments, the VH Cys is at H105 and the VL Cys is at L100, wherein the residue numbering of the VH and the VL regions are according to Chothia.

5 In some embodiments, the VH Cys is at H105 and the VL Cys is at L102, wherein the residue numbering of the VH and the VL regions are according to Chothia.

In another general aspect, the application describes an anti-TfR antibody or antigen-binding fragment thereof having a single variable domain on a heavy chain (VHH) comprising heavy chain complementarity determining regions (HCDRs) HCDR1, HCDR2 and HCDR3,

10 wherein:

(4) the HCDR1 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-24;

(5) the HCDR2 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 25-46; and

15 (6) the HCDR3 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 47-70.

In certain embodiments, the anti-TfR antibody or antigen-binding fragment thereof, comprises a HCDR1, HCDR2 and HCDR3 having the amino acid sequences of the HCDR1, HCDR2 and HCDR3, respectively, of any one of the VHH antigen binding proteins specified in

20 Table 3.

Preferably, the anti-TfR antibody or antigen-binding fragment thereof, comprises an amino acid sequence that is at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to an amino acid sequence selected from the group consisting of SEQ ID NOs: 71-221.

25 In certain embodiments, the anti-TfR antibody or antigen-binding fragment thereof, comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 71-221.

An anti-TfR antibody or antigen-binding fragment thereof (such as a VHH or scFv fragment) can be produced using suitable methods in the art in view of the present disclosure.

For example, a VHH or scFv fragment can be recombinantly produced by growing a recombinant host cell (such as a bacterial, yeast or mammalian cell) under suitable conditions for the production of the antibody fragment and recovering the fragment from the cell culture.

30

Brain shuttle construct

An optimized receptor-mediated transcytosis (RMT) brain delivery platform is developed using the transferrin receptor (TfR) by enhancing the intrinsic transcytosis efficiency, extending peripheral pharmacokinetics, and engineering for an acceptable safety profile while maintaining efficacy of the therapeutic mAb.

In one general aspect, the application relates to an antibody-targeted brain delivery system comprising an anti-TfR antibody or antigen binding fragment thereof of the application. The anti-TfR antibody or antigen binding fragment thereof can be used to deliver a therapeutic or diagnostic agent into a cell (e.g., a cancer cell) or a BBB system. Agents that can be delivered include any neurological disorder drug or agent that can be used to detect or analyze a neurological disorder drug. For example, such agent can be neurotrophic factors, including, but not limited to, nerve growth factor (NGF), brain derived neurotrophic factor (BDNF), ciliary neurotrophic factor (CNTF), glial cell-line neurotrophic factor (GDNF) and insulin-like growth factor (IGF); neuropeptides, including, but not limited to, Substance P, neuropeptideY, vasoactive intestinal peptide (VIP), gamma-amino-butyric acid (GABA), dopamine, cholecystokinin (CCK), endorphins, enkephalins and thyrotropin releasing hormone (TRH); cytokines; anxiolytic agents; anticonvulsants; polynucleotides and transgenes, including, for example, small interfering RNAs and/or antisense oligos; or antibodies or antigen binding fragments thereof that bind to a brain target. An anti-TfR antibody or antigen binding fragment thereof of the application can be an effective means to enhance the delivery of an agent of interest from the blood into the brain and function there.

In particular, an agent of interest can be delivered in a combined form or linked to an anti-TfR antibody or antigen binding fragment thereof of the application, parenterally, e.g., intravenously. For example, the agent can be non-covalently attached to the anti-TfR antibody or antigen binding fragment thereof. The agent can also be covalently attached to the anti-TfR antibody or antigen binding fragment thereof to form a conjugate. In certain embodiments, the conjugation is by construction of a protein fusion (i.e., by genetic fusion of the two genes encoding an anti-TfR antibody or antigen binding fragment thereof and a neurological disorder drug and expression as a single protein). Known methods can be used to link an agent to an antibody or antigen binding fragment thereof in view of the present disclosure. See, for example, Wu et al., Nat Biotechnol., 23(9):1137-46, 2005; Trail et al., Cancer Immunol Immunother.,

52(5):328-37, 2003; Saito et al., *Adv Drug Deliv Rev.*, 55(2):199-215, 2003; Jones et al., *Pharmaceutical Research*, 24(9):1759-1771, 2007.

In some embodiments, a therapeutic or diagnostic agent to be delivered to the brain and an anti-TfR antibody or antigen binding fragment thereof can be covalently linked together (or
5 conjugated) via a non-peptide linker or a peptide linker. Examples of non-peptide linkers include, but are not limited to, polyethylene glycol, polypropylene glycol, copolymer of ethylene glycol and propylene glycol, polyoxyethylated polyol, polyvinyl alcohol, polysaccharides, dextran, polyvinyl ether, biodegradable polymer, polymerized lipid, chitins, and hyaluronic acid, or derivatives thereof, or combinations thereof. A peptide linker can be a peptide chain
10 consisting of 1 to 50 amino acids linked by peptide bonds or a derivative thereof, whose N-terminus and C-terminus can be covalently linked to an anti-TfR antibody or an antigen binding fragment thereof.

In certain embodiments, a conjugate of the application is a multi-specific antibody comprising a first antigen binding region which binds a TfR and a second antigen binding region
15 which binds a brain antigen, such as beta-secretase 1 (BACE1), tau, and the other brain antigens disclosed herein. Techniques for making multi-specific antibodies include, but are not limited to, recombinant co-expression of two immunoglobulin heavy chain-light chain pairs having different specificities (see Milstein and Cuello, *Nature* 305: 537, 1983), WO 93/08829, and Traunecker et al, *EMBO J.* 10: 3655, 1991), and “knob-in-hole” engineering (see, e.g., U.S.
20 Patent No. 5,731,168). Multi-specific antibodies can also be made by engineering electrostatic steering effects (WO 2009/089004A1); cross-linking two or more antibodies or fragments (see, e.g., US Patent No. 4,676,980, and Brennan et al, *Science*, 229: 81, 1985); using leucine zippers (see, e.g., Kostelny et al, *J. Immunol.*, 148(5): 1547-1553, 1992)); using “diabody” technology (see, e.g., Hollinger et al, *Proc. Natl. Acad. Sci. USA*, 90:6444-6448, 1993)); using single-chain
25 Fv (sFv) dimers (see, e.g. Gruber et al, *J. Immunol*, 152:5368 (1994)); and preparing trispecific antibodies as described, e.g., in Tutt et al. *J. Immunol.* 147: 60, 1991. A multi-specific antibody of the application also encompasses antibodies having three or more functional antigen binding sites, including “Octopus antibodies” or “dual-variable domain immunoglobulins” (DVDs) (see, e.g., US 2006/0025576A1, and Wu et al. *Nature Biotechnology*, 25(11):1290-7, 2007). A multi-
30 specific antibody of the application also encompasses a “Dual Acting Fab” or “DAF” comprising an antigen binding region that binds to TfR as well as the brain antigen (e.g., BACE1 or Tau)

(see, US 2008/0069820, for example). In one embodiment, the antibody is an antibody fragment, various such fragments being disclosed herein.

In one embodiment, a multi-specific antibody of the application is a fusion construct comprising an anti-TfR antibody or antigen-binding fragment thereof of the application
5 covalently linked (or fused) to a second antibody or antigen binding fragment thereof. Preferably, the second antibody or antigen binding fragment thereof binds to a brain target, such as BACE, tau or other brain antigens, such as those described herein. The anti-TfR antibody or antigen-binding fragment thereof can be fused to the carboxy- and/or amino- terminus of a light and/or heavy chain of the second antibody or antigen binding fragment thereof, directly or via a
10 linker.

In one embodiment, the anti-TfR antibody or antigen-binding fragment thereof is fused to the carboxy-terminus of a light chain of the second antibody or antigen binding fragment thereof, directly or via a linker.

In another embodiment, the anti-TfR antibody or antigen-binding fragment thereof is
15 fused to the amino-terminus of a light chain of the second antibody or antigen binding fragment thereof, directly or via a linker.

In another embodiment, the anti-TfR antibody or antigen-binding fragment thereof is fused to the carboxy-terminus of a heavy chain of the second antibody or antigen binding fragment thereof, directly or via a linker.

In another embodiment, the anti-TfR antibody or antigen-binding fragment thereof is
20 fused to the amino-terminus of a heavy chain of the second antibody or antigen binding fragment thereof, directly or via a linker.

In a preferred embodiment, a fusion construct of the application comprises an anti-TfR antibody or antigen-binding fragment thereof, preferably an anti-huTfR1 VHH or scFv fragment,
25 of the application covalently linked, via a linker, to the carboxy terminus of only one of the two heavy chains of a second antibody or antigen binding fragment thereof that binds to a brain target. Preferably, the linker has the amino acid sequence of SEQ ID NO: 1422 or SEQ ID NO: 1423.

To facilitate the formation of a heterodimer between the two heavy chains, e.g., one with
30 a fusion of the anti-TfR antibody or antigen-binding fragment thereof and one without, or one containing the Fc for the anti-TfR arm and one for the anti-brain target arm, heterodimeric

mutations introduced into the Fc of the two heavy chains. Examples of such Fc mutations include, but are not limited to, the Zymework mutations (see, e.g., US 10,457,742) and the “knob in hole” mutations (see, e.g., Ridgway et al., Protein Eng., 9(7): 617-621, 1996). Other heterodimer mutations can also be used in the invention. In some embodiment, a modified CH3
5 as described herein is used to facilitate the formation of a heterodimer between the two heavy chains.

In addition to the heterodimeric mutations, other mutations can also be introduced. In some embodiment, the Fc region of the fusion construct or bispecific antibody further comprises one or more mutations that alter (increase or diminish), preferably eliminate ADCC/CDC (such
10 as the AAS mutations described herein), and/or one or more mutations that alter (increase or diminish), preferably increase, the binding of the fusion construct or bispecific antibody to FcRn (such as the YTE mutations described herein). In some embodiment, one or more cysteine residues in the fusion construct or bispecific antibody are substituted with other amino acids, such as serine.

15 A conjugate, such as a multi-specific antibody or fusion construct, of the application can be produced by any of a number of techniques known in the art in view of the present disclosure. For example, it can be expressed from a recombinant host cells, wherein expression vector(s) encoding the heavy and light chains of the fusion construct or multi-specific antibody is (are) transfected into a host cell by standard techniques. The host cells can be prokaryotic or
20 eukaryotic host cells.

In an exemplary system, one or more recombinant expression vectors encoding the heterodimeric two heavy chains and the light chains of a fusion construct of the application is/are introduced into host cells by transfection or electroporation. The selected transformant host cells are cultured to allow for expression of the heavy and light chains under conditions sufficient to
25 produce the fusion construct, and the fusion construct is recovered from the culture medium. Standard molecular biology techniques are used to prepare the recombinant expression vector, transfect the host cells, select for transformants, culture the host cells and recover the protein construct from the culture medium.

The application provides an isolated nucleic acid encoding the amino acid sequence of an
30 anti-TfR antibody or antigen binding fragment thereof alone or as part of a fusion construct or

multispecific antibody in any of the embodiments described herein or any of the claims. The isolated nucleic acid can be part of a vector, preferably an expression vector.

In another aspect, the application relates to a host cell transformed with the vector disclosed herein. In an embodiment, the host cell is a prokaryotic cell, for example, *E. coli*. In another embodiment, the host cell is a eukaryotic cell, for example, a protist cell, an animal cell, a plant cell, or a fungal cell. In an embodiment, the host cell is a mammalian cell including, but not limited to, CHO, COS, NS0, SP2, PER.C6, or a fungal cell, such as *Saccharomyces cerevisiae*, or an insect cell, such as Sf9.

Pharmaceutical composition and related methods

The invention also relates to pharmaceutical compositions, methods of preparation and methods for use thereof.

In another general aspect, the invention relates to a pharmaceutical composition, comprising an anti-TfR antibody or antigen binding fragment thereof or a conjugate thereof of the invention and a pharmaceutically acceptable carrier. The anti-TfR antibody or antigen binding fragment thereof or conjugate (such as a multi-specific antibody or fusion construct) of the invention is also useful in the manufacture of a medicament for therapeutic applications mentioned herein. The pharmaceutically acceptable carrier can be any suitable excipient, diluent, filler, salt, buffer, stabilizer, solubilizer, oil, lipid, lipid containing vesicle, microsphere, liposomal encapsulation, or other material well known in the art for use in pharmaceutical formulations. It will be understood that the characteristics of the carrier, excipient or diluent will depend on the route of administration for a particular application.

Accordingly, in one embodiment, the application relates to a method of transporting a therapeutic or diagnostic agent across the blood-brain barrier (BBB) comprising exposing an anti-TfR antibody or antigen binding fragment thereof coupled to the therapeutic or diagnostic agent to the blood- brain barrier such that the antibody or antigen binding fragment thereof transports the agent coupled thereto across the blood- brain barrier. In one embodiment, the agent is a neurological disorder drug. In another embodiment, the agent is an imaging agent or an agent for detecting a neurological disorder. Preferably, the anti-TfR antibody or antigen binding fragment thereof or conjugate thereof does not impair the binding of the TfR to its native ligand transferrin. The antibody specifically binds to TfR in such a manner that it does not inhibit binding of the TfR to transferrin. In some embodiment, the BBB is in a mammal, preferably a

primate, such as a human, more preferably a human having a neurological disorder. In one embodiment, the neurological disorder is selected from the group consisting of Alzheimer's disease (AD), stroke, dementia, muscular dystrophy (MD), multiple sclerosis (MS), amyotrophic lateral sclerosis (ALS), cystic fibrosis, Angelman's syndrome, Liddle syndrome, Parkinson's disease, Pick's disease, Paget's disease, cancer, and traumatic brain injury.

In one embodiment, an anti-TfR antibody or antigen binding fragment thereof, or a conjugate thereof of the application, is used to detect a neurological disorder before the onset of symptoms and/or to assess the severity or duration of the disease or disorder. The antibody, antigen binding fragment or conjugate thereof permits detection and/or imaging of the neurological disorder, including imaging by radiography, tomography, or magnetic resonance imaging (MRI).

In another embodiment, an anti-TfR antibody or antigen binding fragment thereof, or a conjugate thereof, is used in treating a neurological disorder (e.g., Alzheimer's disease), comprising administering to a subject in need of the treatment an effective amount of anti-TfR antibody or antigen binding fragment thereof, or a conjugate thereof. In some embodiments, the method further comprises administering to the subject an effective amount of at least one additional therapeutic agent.

In another embodiment, the application relates to the use of an anti-TfR antibody or antigen binding fragment or conjugate thereof of the application in the manufacture or preparation of a medicament. In one embodiment, the medicament is for treatment of neurological disease or disorder. In a further embodiment, the medicament is for use in a method of treating neurological disease or disorder comprising administering to an individual having neurological disease or disorder an effective amount of the medicament.

Another general aspect of the application relates to a method of inducing antibody dependent phagocytosis (ADP) without stimulating secretion of a pro-inflammatory cytokine in a subject in need thereof, comprising administering to the subject a complex comprising a therapeutic antibody or antigen binding fragment thereof coupled to, preferably covalently conjugated to, the antigen-binding fragment thereof of an anti-TfR antibody binding fragment according to an embodiment of the application, wherein the therapeutic antibody or antigen binding fragment thereof does not have effector function. For example, the therapeutic antibody or antigen binding fragment thereof can comprise one or more amino acid modifications that

reduces or eliminates the effector function, such as the ADCC or CDC, such as mutations that reduce or abolish the binding to Fc gamma receptor. Such mutations can be at positions L234, L235, D270, N297, E318, K320, K322, P331, and P329, such as one, two or three mutations of L234A, L235A and P331S, wherein the numbering of amino acid residues is according to the EU index as set forth in Kabat. In one embodiment, the therapeutic antibody or antigen binding fragment thereof binds specifically to tau aggregates.

In some embodiments, the method further comprises administering to the subject an effective amount of at least one additional therapeutic agent. In certain embodiments, an additional therapeutic agent is a therapeutic agent effective to treat the same or a different neurological disorder as the anti-TfR antibody or antigen binding fragment or conjugate thereof is being employed to treat. Exemplary additional therapeutic agents include, but are not limited to: the various neurological drugs described above, cholinesterase inhibitors (such as donepezil, galantamine, rivastigmine, and tacrine), NMDA receptor antagonists (such as memantine), amyloid beta peptide aggregation inhibitors, antioxidants, γ -secretase modulators, nerve growth factor (NGF) mimics or NGF gene therapy, PPAR γ agonists, HMG-CoA reductase inhibitors (statins), ampa/kines, calcium channel blockers, GABA receptor antagonists, glycogen synthase kinase inhibitors, intravenous immunoglobulin, muscarinic receptor agonists, nicotinic receptor modulators, active or passive amyloid beta peptide immunization, phosphodiesterase inhibitors, serotonin receptor antagonists and anti-amyloid beta peptide antibodies. In certain embodiments, the at least one additional therapeutic agent is selected for its ability to mitigate one or more side effects of the neurological drug. The additional therapeutic agent can be administered in the same or separate formulations and administered together or separately with the anti-TfR antibody or antigen binding fragment or conjugate thereof. The anti-TfR antibody or antigen binding fragment or conjugate of the application can be administered prior to, simultaneously with, and/or following, the administration of the additional therapeutic agent and/or adjuvant. The anti-TfR antibody or antigen binding fragment or conjugate thereof of the application can also be used in combination with other interventional therapies such as, but not limited to, radiation therapy, behavioral therapy, or other therapies known in the art and appropriate for the neurological disorder to be treated or prevented.

The anti-TfR antibody or antigen binding fragment or conjugate thereof of the application (and any additional therapeutic agent) can be administered by any suitable means, including

parenteral, intrapulmonary, and intranasal, and, if desired for local treatment, intralesional administration. Parenteral infusions include intramuscular, intravenous, intraarterial, intraperitoneal, or subcutaneous administration, depending in part on whether the administration is brief or chronic. Various dosing schedules including but not limited to single or multiple
5 administrations over various time- points, bolus administration, and pulse infusion are contemplated herein.

For the prevention or treatment of a disease, the appropriate dosage of an anti-TfR antibody or antigen binding fragment or conjugate thereof of the application (when used alone or in combination with one or more other additional therapeutic agents) will depend on various
10 factors, such as the type of disease to be treated, the type of antibody or conjugate, the severity and course of the disease, whether the antibody, antigen binding fragment or conjugate thereof is administered for preventive or therapeutic purposes, previous therapy, the patient's clinical history and response to the antibody, the physiological state of the subject (including, e.g., age, body weight, health), and the discretion of the attending physician. Treatment dosages are
15 optimally titrated to optimize safety and efficacy. The antibody, antigen binding fragment or conjugate thereof is suitably administered to the patient at one time or over a series of treatments.

According to particular embodiments, a therapeutically effective amount refers to the amount of therapy which is sufficient to achieve one, two, three, four, or more of the following effects: (i) reduce or ameliorate the severity of the disease, disorder or condition to be treated or
20 a symptom associated therewith; (ii) reduce the duration of the disease, disorder or condition to be treated, or a symptom associated therewith; (iii) prevent the progression of the disease, disorder or condition to be treated, or a symptom associated therewith; (iv) cause regression of the disease, disorder or condition to be treated, or a symptom associated therewith; (v) prevent the development or onset of the disease, disorder or condition to be treated, or a symptom
25 associated therewith; (vi) prevent the recurrence of the disease, disorder or condition to be treated, or a symptom associated therewith; (vii) reduce hospitalization of a subject having the disease, disorder or condition to be treated, or a symptom associated therewith; (viii) reduce hospitalization length of a subject having the disease, disorder or condition to be treated, or a symptom associated therewith; (ix) increase the survival of a subject with the disease, disorder or
30 condition to be treated, or a symptom associated therewith; (xi) inhibit or reduce the disease,

disorder or condition to be treated, or a symptom associated therewith in a subject; and/or (xii) enhance or improve the prophylactic or therapeutic effect(s) of another therapy.

In another aspect, the application relates to an article of manufacture (such as a kit) containing materials useful for the treatment, prevention and/or diagnosis of the disorders described above is provided. The article of manufacture comprises a container and a label or package insert on or associated with the container. Suitable containers include, for example, bottles, vials, syringes, IV solution bags, etc. The containers can be formed from a variety of materials such as glass or plastic. The container holds a composition which is by itself or combined with another composition effective for treating, preventing and/or diagnosing the condition and may have a sterile access port (for example the container may be an intravenous solution bag or a vial having a stopper pierceable by a hypodermic injection needle). At least one active agent in the composition is an antibody, antigen binding fragment thereof or a conjugate of the application. The label or package insert indicates that the composition is used for treating the condition of choice. Moreover, the article of manufacture can include (a) a first container with a composition contained therein, wherein the composition comprises an antibody, antigen binding fragment thereof or a conjugate of the application; and (b) a second container with a composition contained therein, wherein the composition comprises a further cytotoxic or otherwise therapeutic agent. The article of manufacture in this embodiment of the invention can further include a package insert indicating that the compositions can be used to treat a particular condition. Optionally, the article of manufacture can further comprise a second (or third) container comprising a pharmaceutically acceptable buffer, such as bacteriostatic water for injection (BWFI), phosphate-buffered saline, Ringer's solution and dextrose solution. It can further include other materials desirable from a commercial and user standpoint, including other buffers, diluents, filters, needles, and syringes.

The following examples of the invention are to further illustrate the nature of the invention. It should be understood that the following examples do not limit the invention and the scope of the invention is to be determined by the appended claims.

EXAMPLES

Example 1. Anti-TfR Antibodies

Anti-TfR antibodies or antigen binding fragments of the invention are illustrated in this Example. Table 3 lists the HCDRs of exemplary anti-TfR VHHs of the invention. Table 4 lists

the VHH sequences of exemplary anti-TfR VHHs of the invention. Table 5 shows the LCDRs and HCDRs of exemplary anti-TfR antibodies or antigen binding fragments of the invention. Table 6 provides the VL and VH sequences of exemplary anti-TfR antibodies or antigen binding fragments of the invention. The CDRs listed in the tables herein are according to IMGT

5 (Lefranc et al. (2003) Dev Comp Immunol 27: 55-77).

The anti-TfR antibodies or antigen binding fragments can be made and tested using methods known in the art in view of the present disclosure.

Example 2: Binding characterization by Surface Plasmon Resonance

The binding interaction of test articles against recombinant human, rat, cynomolgus, and
10 murine transferrin receptor (TfR; TFRW2, TFRW1, TFRW3, TFRW5) are studied by SPR using a Biacore 8k+ instrument at 25°C with pH 7.4 buffer, supplemented with 0.01% BSA, and 0.05% Tween 20. The biosensor surface is prepared by coupling anti-human IgG Fcγ-fragment specific antibody to the surface of a C1 sensor chip using vendor recommended protocol for amine-coupling chemistry (>400 response units (RU)). The coupling buffer is 10 mM sodium
15 acetate, pH 4.5. The test articles are diluted in the running buffer and injected over the anti-human IgG to obtain enough capture to enable detection of antigen binding. Capture of test articles is followed by separate injection of the four recombinant antigens at the same concentration series in single-cycle kinetics mode (200 nM to 7.41 nM series at 3-fold dilutions). The association was monitored for 2 minutes and dissociation for 20 minutes at a 50 µL/min
20 flow rate. Regeneration of the sensor surface is performed with 0.85% H₃PO₄. The binding sensorgrams are fitted using the 1:1 Langmuir binding model to obtain on-rates, off-rates, and affinities.

Example 3: Creation of therapeutic antibody - anti-transferrin receptor (TfR) fusion expression constructs

25 Generation of therapeutic monoclonal antibodies (mAbs) in mammalian expression cell lines incorporates the use of the pEE6.4 and pEE12.4 Chinese hamster ovary (CHO) expression vector system (Lonza). Each vector contains a human cytomegalovirus (huCMV-MIE) promoter to drive the expression of the heavy chain (HC) or light chain (LC) of the mAb and contains the ampicillin resistance gene. The pEE12.4 vector also includes the gene encoding the glutamine
30 synthetase (GS) enzyme. Growth conditions which require glutamine synthetase activity places selective pressure on the cells to maintain the expression vector (GS Gene Expression System

Manual Version 4.0). pEE6.4 is used to clone the HC gene and pEE12.4 to clone the LC gene as single gene vectors.

The DNA encoding the anti-TfR antibody HC and LC or VHH is synthesized and subcloned into the Lonza expression vector backbones pEE6.4 and pEE12.4, respectively, by the In-Fusion Cloning method (Takara Bio) using Type IIS restriction enzyme *AarI*. The open reading frames of subcloned genes are sequence confirmed at Genewiz, Azenta Life Sciences (NJ, USA).

The constructs can be analyzed, e.g., for affinity, binding specificity, internalization, pharmacokinetics and pharmacodynamics, etc., using methods known in the art, such as those described in US 2023/0174646, the relevant content of which is incorporated herein by reference in its entirety.

Example 4: SPR binding analysis method

The anti-transferrin receptor (TfR) antibodies binding to human or cynomolgus transferrin receptor was tested by Surface Plasmon Resonance (SPR) using Carterra LSA instrument at 25°C. The analyses were performed using HBS buffer supplemented with 0.05% Tween-20 and 0.01% BSA as the running buffer. Briefly, the biosensor was prepared by amine coupling of Goat anti-Human IgG Fcγ fragment-specific antibody to the surface of a CMDP sensor chip using vendor recommended protocol for amine-coupling chemistry (~1000 RUs). The Goat anti-Human IgG reagent was prepared in 10 mM sodium acetate, pH 4.5. The anti-TfR antibody solutions and various concentrations of antigens (human or Cyno TfR) were prepared in the running buffer (0.1 nM to 100 nM). The antibodies were captured on the sensor chip with capture levels of ~100 RUs, followed by series of antigen injections in a non-regenerative multi-cycle kinetics mode. The association and dissociation of antigens were measured for 5 and 15 minutes, respectively. The surface of the sensor chip was regenerated using 0.85 % H₃PO₄. The data was evaluated using the Carterra Kinetics software and fitted using 1:1 Langmuir model to obtain binding kinetics (on- and off-rates) and affinities. Table 2 lists the dissociation constant (*K_d*) of the anti-TfR antibodies or antigen binding fragments according to embodiments of the invention.

Table 2: SPR Binding to Human and Cynomolgus Transferrin Receptor (TfR)

CLONE ID	human TfR <i>K_d</i> (M)	Cyno TfR <i>K_d</i> (M)
VR000103638	1.10E-09	7.00E-10
VR000015506	1.80E-09	Low /No Binding

VR000030726	8.10E-12	7.65E-11
VR000103635	5.00E-11	1.95E-10
VR000007193	2.90E-11	1.65E-10
VR000103752	9.00E-10	2.00E-08
VR000017524	4.81E-10	6.65E-10
VR000103741	1.95E-11	1.55E-10
VR000103640	6.50E-11	1.50E-10
VR000103630	2.85E-11	2.70E-10
VR000015801	Low / No Binding	9.05E-10
VR000015806	1.55E-10	4.15E-10
VR000015804	7.60E-11	7.95E-10
VR000015895	5.55E-11	5.75E-10
VR000015789	9.80E-12	1.35E-10
VR000015729	6.40E-11	3.35E-11
VR000103633	1.00E-09	9.10E-09
VR000103720	1.15E-11	1.90E-10
VR000103726	1.15E-11	2.85E-10
VR000103685	3.80E-09	4.25E-10
VR000031164	3.20E-11	4.65E-11
VR000103679	8.45E-11	4.60E-10
VR000103756	4.55E-11	8.35E-10
VR000002423	4.83E-10	9.80E-11
VR000103755	3.94E-10	1.02E-10
VR000103695	3.70E-11	4.50E-12
VR000018327	1.82E-10	5.00E-12
VR000103716	1.40E-09	3.20E-10
VR000103677	3.05E-11	3.15E-11
VR000103732	1.52E-10	2.85E-10
VR000103721	5.75E-11	4.90E-11
VR000103692	1.15E-10	1.35E-10
VR000103678	4.30E-11	1.50E-10
VR000103710	1.10E-09	1.90E-09
VR000004122	5.69E-10	2.10E-11
VR000103687	1.90E-10	1.95E-10
VR000103749	5.05E-11	2.35E-11
VR000103736	1.45E-11	4.20E-11
VR000103672	6.10E-11	8.55E-11
VR000103744	1.75E-11	1.90E-11
VR000103703	7.50E-11	1.20E-11
VR000103681	1.63E-10	4.20E-11
VR000103674	3.05E-10	1.03E-10
VR000103731	7.00E-12	4.80E-11
VR000103702	1.98E-10	3.60E-10

VR000103740	2.82E-10	6.40E-10
VR000103711	5.50E-12	1.12E-11
VR000103739	8.45E-11	4.00E-10
VR000103712	4.90E-11	1.40E-11
VR000103663	7.20E-11	9.85E-11
VR000103680	1.60E-11	2.60E-10
VR000018325	6.15E-11	2.50E-10
VR000103765	6.60E-11	2.75E-11
VR000103698	5.40E-11	1.10E-10
VR000103743	1.83E-10	2.75E-10
VR000103766	5.65E-10	4.80E-10
VR000103700	7.50E-10	1.35E-10
VR000103690	1.21E-10	1.90E-10
VR000103728	1.62E-10	4.60E-10
VR000103763	3.30E-11	9.00E-12
VR000103729	1.04E-10	1.35E-11
VR000103714	1.30E-09	5.15E-10
VR000103691	8.71E-10	6.65E-10
VR000103686	3.47E-10	1.10E-11
VR000103673	9.30E-11	1.20E-10
VR000103754	2.86E-10	7.90E-11
VR000103697	4.78E-10	4.30E-10
VR000103675	4.93E-10	6.90E-10
VR000103725	4.13E-10	1.30E-10
VR000103724	1.20E-09	1.09E-10
VR000103706	2.75E-11	1.05E-11
VR000103676	8.10E-11	1.70E-11
VR000103727	4.15E-10	4.10E-10
VR000017043	5.70E-09	1.70E-09

Example 5: Differential Scanning Fluorimetry (DSF) of Protein Therapeutics

Conformational stability of monovalent Fab-Fc proteins with unique TfR binding arms were measured using advanced differential scanning fluorimetry (nanoDSF) technology, by monitoring the intrinsic fluorescence of tryptophan upon thermal unfolding. The unfolding was measured by loading each sample into 24 well capillary (NanoTemper, Cat# PR-AC002) from a 384 well sample plate (ThermoNunc, Cat# 264573), with a heating ramp of 1°C/minute between 20°C to 95°C using the Prometheus NT.48 instrument (NanoTemper Technologies GmbH). Each sample was measured at 0.5 mg/ml in phosphate buffer saline (PBS) in duplicates. The intrinsic fluorescence of each sample at 330 and 350 nm was used to monitor unfolding during

temperature ramp and recorded as changes in fluorescence intensity over time. Data was collected and saved as projects, processed using the PR.StabilityAnalysis v1.0.2 software. The processed data contained integrated thermal melting profiles, first derivatives for fluorescence at 330nm, 350nm, ratio 330/350, and light scattering data for all the samples. Thermal melting mid-point (T_m) values as well as onset of aggregation (Tagg) were identified and reported.

Various anti-TfR antibodies or antigen binding fragments according to embodiments of the invention were analyzed using the above method, with the determined T_m values ranging from about 50°C to 73°C and Tagg from about 69°C to 79°C.

Example 6: Cell binding

Panels of antibodies were screened for specific TfR binding on 3 cell lines expressing human or cyno TfR and 1 negative control cell line not expressing human or cyno TfR. The 4 cell lines were stained separately with fluorescent cell dyes, to be differentiated through the assay. LIVE/DEAD™ Fixable Near-IR Stain (Thermo Fisher Scientific Cat# L34976) was also added to all the cells to select only live cells for the analysis. Human TfR transfected Canine kidney cells (MDCK huTfR clone 2C5) were stained with CellTrace™ CFSE (Thermo Fisher Scientific Cat# C34554). Cyno TfR transfected cells (MDCK cynoTfR stable pool) were stained with CellTrace™ Violet (Thermo Fisher Scientific Cat# C34557). MDCK parental cells received no stains. Human brain endothelial cells (hCMEC/D3) were stained with CellTrace CFSE and CellTrace Violet.

All four cell lines were mixed 1:1:1:1 together and 50,000 mixed cells were distributed to each well of 96-well assay plates. Fc x Fab-Fc or Fc x VHH-Fc monovalent anti-TfR mAbs were diluted in staining buffer and added to each well. Each antibody was tested in an 11-point dose-response starting at 100nM with 3-fold serial dilutions. Negative control wells received no primary antibody.

After 1 hour incubation at 4°C, cells were washed and stained with Alexa Fluor® 647 F(ab')₂ anti-human Fc (Jackson Immunosciences cat# 109-606-098) for 30min at 4°C. Cells were washed again with staining buffer, and data were acquired by IntelliCyt® iQue Screeners (Sartorius).

Cell lines were identified by fluorescent cell dyes. Live singlets of each cell lines were gated and the associated RL1H Geomean (signal of Alexa Fluor® 647) was measured. Then the signal over Background was calculated using the Forecyt software (S/B = RL1H Geomean for

each cell line in each well / averaged RL1H Geomean for the same cell line from negative control wells). This metric characterizes the antibody binding to each cell line. S/B results were exported and analyzed with Genedata Screener for curve fitting and affinity determination. Max binding activity of each mAb was defined as the highest S/B reached in the tested concentration range.

Various anti-TfR antibodies or antigen binding fragments according to embodiments of the invention were analyzed using the above method. It was shown that apparent binding EC50s ranged from high nM to about 0.7 nM on hCMEC/D3 and MDCK huTfR cells. Apparent binding EC50s ranged from high nM to about 0.8 nM on MDCK cynoTfR cells. No significant binding was detected on MDCK parental cells.

SEQUENCE LIST

Table 3: CDR SEQ ID Nos of VHH clones

CLONE ID	HCDR1	SEQ ID NO	HCDR2	SEQ ID NO	HCDR3	SEQ ID NO
BBB430	GLTFSRYA	1	ISGSGGDT	25	ASDQRAGSWSSGWFSSRSTLY	47
BBB442	GLTFSRYA	1	ISGSGGDT	25	ASDQRAGSWSSGWFSSRSTLY	47
BBB440	GLSFSRYA	2	IGSGGTC	26	ASDQRAESWSSGWFSPSYSLC	48
BBB441	GLSFSRYA	2	IGSGGDEF	27	ASDQRAESWSSGWFSPRSYQSLY	49
BBB437	GLTANRFS	3	INRIPGTT	28	AEHSSLTRWSGSRLVTDYDY	50
BBB903	GFNGDDYA	4	IESGGKP	29	AADYGRCSLWRRTYQY	51
BBB867	GFNGDDYA	4	IESGGKT	30	AADYGRCSLWRRTYQY	51
BBB835	GFNGDDYA	4	IESGGKT	30	AADYGRCSLWRRTYQY	51
BBB790	GFNGDDYA	4	IESGGKT	30	AADYGRCSLWRRTYQY	51
BBB789	GFNGDDYA	4	IESGGKT	30	AADYGRCSLWRRTYQY	51
BBB788	GFNGDDYA	4	IESGGKT	30	AADYGRCSLWRRTYQY	51
BBB834	GFNGDDYA	4	IESGGKT	30	AADYGRCSLWRRTYQY	51
BBB836	GFNGDDYA	4	IESGGKT	30	AADYGRCSLWRRTYQY	51
BBB904	GFNGDDYA	4	IESGGKT	30	AADYGRCSLWRRTYQY	51
BBB913	GFTFDDYA	5	ISWSGGST	31	TKMGVDYSALDLEYDY	52
BBB878	GFTFDDYA	5	ISWSGGST	31	TKMGVDYSALDLEYDY	52
BBB800	GFTFDDYA	5	ISWSGGST	31	TKMGVDYSALDLEYDY	52
BBB845	GFTFDDYA	5	ISWSGGST	31	TKMGVDYSALDLEYDY	52
BBB877	GFTFDDYA	5	ISWSGGST	31	TKMGVDYSALDLEYDY	52
BBB912	GFTFDDYA	5	ISWSGGST	31	TKMGVDYSALDLEYDY	52
BBB807	GFTFDDCA	6	ISWSGGST	31	TKMGVDYSALDLEYDY	52
BBB893	GFTFSSY	7	INTGSRK	32	SGSSLPWCS	53
BBB805	GFTFSSY	7	INTGSRK	32	SGSSLPWCS	53
BBB806	GFTFSSY	7	INTGSRK	32	SGSSLPWCS	53
BBB848	GFTFSSY	7	INTGSRK	32	SGSSLPWCS	53
BBB847	GFTFSSY	8	IDSTGRAP	33	EADVVDGRSN	54
BBB802	GFTFSSY	8	IDSTGRAP	33	EADVVDGRSN	54
BBB803	GFTFSSY	8	IDSTGRAP	33	EADVVDGRSN	54
BBB846	GFTFSSY	8	IDSTGRAP	33	EADVVDGRSN	54
BBB914	GFTFSSY	8	IDSTGRAP	33	EADVVDGRSN	54

BBB804	GFTFSRY	9	INSDGLST	34	ARADKNLYGFDY	55
BBB833	GFTFSSH	10	INPGDRT	35	AKIARGLPPAISD	56
BBB832	GFTFSSH	10	INPGDRT	35	AKIARGLPPAISD	56
BBB928	LRTFDLTG	11	ITGGGGLT	36	AGTAPFRRVVDAYDY	57
BBB895	LRTFDLTG	11	ITGGGGLT	36	AGTAPFRRVVDAYDY	57
BBB791	LRTFDLTG	11	ITGGGGLT	36	AGTAPFRRVVDAYDY	57
BBB827	LRTFDLTG	11	ITGGGGLT	36	AGTAPFRRVVDAYDY	57
BBB862	LRTFDLTG	11	ITGGGGLT	36	AGTAPFRRVVDAYDY	57
BBB896	LRTFDLTG	10	ITGGGGLT	36	AGTAPFRRVVDAYDY	57
BBB798	GRTFDLSP	12	VSSSGSFT	37	AASIRGGLRTVELADY	58
BBB799	GRTFDLSP	12	VSSSGSFT	37	AASIRGGLRTVELADY	58
BBB883	GRTFDLSP	12	VSSSGSFT	37	AASIRGGLRTVELADY	58
BBB801	GFTENTYA	13	IRSKYNNYAT	38	VRHGNFGNSYVSWEAY	59
BBB855	KSIVSINH	14	MTRAGITN	39	RADDEYYDH	60
BBB931	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	61
BBB929	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	61
BBB926	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	61
BBB923	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	61
BBB921	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	61
BBB919	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	61
BBB917	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	61
BBB899	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	61
BBB894	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	61
BBB891	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	61
BBB889	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	61
BBB887	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	61
BBB885	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	61
BBB882	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	61
BBB880	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	61
BBB869	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	61
BBB859	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	61
BBB857	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	61
BBB854	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	61

BBBB850	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	61
BBBB824	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	61
BBBB821	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	61
BBBB817	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	61
BBBB815	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	61
BBBB813	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	61
BBBB811	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	61
BBBB809	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	61
BBBB787	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	61
BBBB796	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	61
BBBB808	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	61
BBBB810	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	61
BBBB812	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	61
BBBB814	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	61
BBBB816	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	61
BBBB820	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	61
BBBB823	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	61
BBBB826	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	61
BBBB853	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	61
BBBB856	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	61
BBBB858	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	61
BBBB860	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	61
BBBB876	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	61
BBBB881	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	61
BBBB884	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	61
BBBB886	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	61
BBBB888	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	61
BBBB890	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	61
BBBB892	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	61
BBBB897	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	61
BBBB915	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	61
BBBB918	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	61
BBBB920	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	61

BBB922	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	61
BBB925	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	61
BBB927	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	61
BBB930	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	61
BBB851	KSIVSIDH	15	MTRAGITN	39	RADDEYYDY	61
BBB825	KSIVSISH	16	MTRAGITN	39	RADDEYYDY	61
BBB898	KSIVSINH	14	MTRACITN	40	RADDEYYDY	61
BBB818	KSIVSINH	14	MTRAGITN	39	RADDEYCDY	62
BBB819	KSIVSINH	14	MTRAGITN	39	RADDEYNDY	63
BBB852	KSIVSIND	17	MTRAGITN	39	RADDEYYDY	61
BBB822	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	64
BBB863	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	64
BBB924	KSIVSINH	14	MTRAGITN	39	RADDEYYDY	64
BBB879	GFTFGSYD	18	MTRAGITN	39	RADEEYYDY	64
BBB861	LRTFDLTG	10	MTRAGITN	39	RADDEYYDY	61
BBB868	GRTFDLSP	18	VSSSGSFT	37	RADDEYYDY	61
BBB866	GFTFSRHW	19	INTDGGST	41	RADDEYYDY	61
BBB795	GSIFSING	20	ITTGRT	42	RADDEYYDY	61
BBB872	EDIFAITY	21	VTYGGTT	43	RADDEYYDY	61
BBB905	GSSFSSAA	22	ITRISRS	44	NTGVT	65
BBB870	GSSFSSAA	22	ITRISRS	44	NTGVT	65
BBB838	GSSFSSAA	22	ITRISRS	44	NTGVT	65
BBB837	GSSFSSAA	22	ITRISRS	44	NTGVT	65
BBB871	GSSFSSAA	22	ITRISRS	44	NTGVT	65
BBB906	GSSFSSAA	22	ITRISRS	44	NTGVT	65
BBB839	GSSFSSAA	22	ITRISRS	44	RADDEYYDC	66
BBB911	GVIVSRTV	23	ITGTGVT	45	NSKLGLRDY	67
BBB875	GVIVSRTV	23	ITGTGVT	45	NSKLGLRDY	67
BBB843	GVIVSRTV	23	ITGTGVT	45	NSKLGLRDY	67
BBB797	GVIVSRTV	23	ITGTGVT	45	NSKLGLRDY	67
BBB910	GVIVSRTV	23	ITGTGVT	45	NSKLGLRDY	67
BBB909	GSIFSING	20	ITTGRT	42	NTNNY	68
BBB874	GSIFSING	20	ITTGRT	42	NTNNY	68

BBB849	GSIFSING	20	ITTGRT	42	NTNNY		68
BBB842	GSIFSING	20	ITTGRT	42	NTNNY		68
BBB841	GSIFSING	20	ITTGRT	42	NTNNY		68
BBB794	GSIFSING	20	ITTGRT	42	NTNNY		68
BBB844	GSIFSING	20	ITTGRT	42	NTNNY		68
BBB873	GSIFSING	20	ITTGRT	42	NTNNY		68
BBB908	GSIFSING	20	ITTGRT	42	NTNNY		68
BBB840	EDIFAITY	21	ITTGRT	42	NSIVRHDY		69
BBB907	EDIFAITY	21	VTYGGTT	43	NSIVRHDY		69
BBB792	EDIFAITY	21	VTYGGTT	43	NSIVRHDY		69
BBB793	EDIFAITY	21	VTYGGTT	43	NSIVRHDY		69
BBB828	EDIFAITY	21	VTYGGTT	43	NSIVRHDY		69
BBB916	EDIFAITY	21	VTYGGTT	43	NSIVRHDY		69
BBB901	GVPGGVFGYNN	24	ISFRGAV	46	NLLHSEELNAQRN		70
BBB865	GVPGGVFGYNN	24	ISFRGAV	46	NLLHSEELNAQRN		70
BBB831	GVPGGVFGYNN	24	ISFRGAV	46	NLLHSEELNAQRN		70
BBB786	GVPGGVFGYNN	24	ISFRGAV	46	NLLHSEELNAQRN		70
BBB829	GVPGGVFGYNN	24	ISFRGAV	46	NLLHSEELNAQRN		70
BBB830	GVPGGVFGYNN	24	ISFRGAV	46	NLLHSEELNAQRN		70
BBB864	GVPGGVFGYNN	24	ISFRGAV	46	NLLHSEELNAQRN		70
BBB900	GVPGGVFGYNN	24	ISFRGAV	46	NLLHSEELNAQRN		70
BBB902	GVPGGVFGYNN	24	ISFRGAV	46	NLLHSEELNAQRN		70

Table 4: VHH SEQ ID NOs							
CLONE ID	VHH						SEQ ID NO
BBB430	QVQLVESGGGLVQAGGSLRLSCAVSGLTFSRYAMGWFRQAPGKEREFVARISGSGGDTTRYADSVKGRFTIARDNARNMV						71
BBB442	QVQLVESGGGLVQAGGSLRLSCAVSGLTFSRYAMGWFRQAPGKEREFVARISGSGGDTTRYADSVKGRFTIARDNARNMV						72
BBB440	QVQLVESGGGLVQAGGSLRLSCAVSGLTFSRYAMGWFRQAPRKREFVARIGSGGTCRYADSVKGRFTISRDNARNMV						73
BBB441	QVQLVESGGGLVQAGGSLRLSCAVSGLTFSRYAMGWFRQAPRKREFVARIGSGGEDFRYADSVKGRFTIARDNARNMV						74
BBB437	QVHLVESGGGLVQAGGSLRLSCAVSGLTANRFSGMGRQYFGKEREFAWINRIPGTTNYVDSVKGRFVFSKDSANNAE						75

BBB903	QVQLVESGGASVQAGESLKLSCERSGFNGDDYAVAWFRQY/PKEREVSCIESGGKPLHEDSVRGRFTISNDNAQSTVYL QMDNLKPEDSALYYCAADYGRCSLWRRITYQYWGGQTLVTYSS	76
BBB867	QLQLVESGGASVQAGESLKLSCERSGFNGDDYAVAWFRQY/PKEREVSCIESGGKTLHEDSVRGRFTISNDNAQSTVYL QMDNLKPEDSALYYCAADYGRCSLWRRITYQYWGGQTLVTYSS	77
BBB835	EVQLVESGGASVQAGESLKLSCERSGFNGDDYAVAWFRQY/PKEREVSCIESGGKTLHEDSVRGRFTISNDNAQSTVYL QMDNLKPEDSALYYCAADYGRCSLWRRITYQYWGGQTLVTYSS	78
BBB790	EVQLVESGGASVQAGESLKLSCERSGFNGDDYAVAWFRQY/PKEREVSCIESGGKTLHEDSVRGRFTISNDNAQSTVYL QMDNLKPEDSALYYCAADYGRCSLWRRITYQYWGGQTLVTYSS	79
BBB789	EVQLVESGGASVQAGESLKLSCERSGFNGDDYAVAWFRQY/PKEREVSCIESGGKTLHEDSVRGRFTISNDNAQSTVYL QMDNLKPEDLALYYCAADYGRCSLWRRITYQYWGGQTLVTYSS	80
BBB788	EVQLVESGGASVQAGESLKLSCERSGFNGDDYAVAWFRQY/PKEREVSCIESGGKTLHEDSVRGRFTISNDNAQRTVYL QMDNLKPEDSALYYCAADYGRCSLWRRITYQYWGGQTLVTYSS	81
BBB834	EVQLVESGGASVQAGESLKLSCERSGFNGDDYAVAWFRQY/PKEREVSCIESGGKTLHEDSVRGRFTISNDNAQSTVYL QMDNLKPEDSALYYCAADYGRCSLWRRITYQYWGGQTLVTYSS	82
BBB836	EVQLVESGGASVQAGESLKLSCERSGFNGDDYAVAWFRQY/PKEREVSCIESGGKTLHEDSVRGRFTISNDNAQSTVY LQMDNLKPEDSALYYCAADYGRCSLWRRITYQYWGGQTLVTYSS	83
BBB904	QVQLVESGGASVQAGESLKLSCERSGFNGDDYAVAWFRQY/PKEREVSCIESGGKTLHEDSVRGRFTISNDNAKSTVYL QMDNLKPEDSALYYCAADYGRCSLWRRITYQYWGGQTLVTYSS	84
BBB913	QVQLVESGGGLVQPGGSLRLSCAASGFTFDDYAMSWVRQAPGKGLEWVSALISWSGGSTYYEESVKGRFTISRDNAKNTL YLQMSLKPEDTAVYYCTKMGGVDYSLDLEIDYDWGGQTLVTYSS	85
BBB878	QLQLVESGGGLVQPGGSLRLSCAASGFTFDDYAMSWVRQAPGKGLEWVSALISWSGGSTYYEESVKGRFTISRDNAKNTL YLQMSLKPEDTAVYYCTKMGGVDYSLDLEIDYDWGGQTLVTYSS	86
BBB800	EVQLVESGGGLVQPGGSLRLSCAASGFTFDDYAMSWVRQAPGKGLEWVSALISWSGGSTYYEESVKGRFTISRDNAKNTL YLQMSLKPEDTAVYYCTKMGGVDYSLDLEIDYDWGGQTLVTYSS	87
BBB845	EVQLVESGGGLVQPGGSLRLSCAASGFTFDDYAMSWVRQAPGKGLEWVSALISWSGGSTYYEESVKGRFTISRDNAKNTL YLQMSLKPEDTAVYYCTKMGGVDYSLDLEIDYDWGGQTLVTYSS	88
BBB877	QLQLVESGGGLVQPGGSLRLSCAASGFTFDDYAMSWVRQAPGKGLEWVSALISWSGGSTYYEESVKGRFTISRDNAKNTL YLQMSLKPEDTAVYYCTKMGGVDYSLDLEIDYDWGGQTLVTYSS	89
BBB912	QVQLVESGGGLVQPGGSLRLSCAASGFTFDDYAMSWVRQAPGKGLEWVSALISWSGGSTYYEESVKGRFTISRDNAKNTL YLQMSLKPEDTAVYYCTKMGGVDYSLDLEIDYDWGGQTLVTYSS	90
BBB807	EVQLVESGGGLVQPGGSPRLSCAASGFTFDDCAMSWMRQAPGKGLEWVSALISWSGGSTYYEESVKGRFTISRDNAKNTL YLQMSLKPEDTAVYYCTKMGGVDYSLDLEIDYDWGGQTLVTYSS	91
BBB893	QLQLVESGGGLVQTGGSLRVSCASGFTFSSYYVSWVPQAPGKMLEWVSGINTGGSRKYYSSDSVKGRFTISRDNAKNTLY LQMSLKPDPDTALYYQSGSLPWCWSWGQGTQVTYSS	92
BBB805	EVQLVESGGGLVQPGSLRVSCASGFTFSSYYVSWVPQAPGKMLEWVSGINTGGSRKYYSSDSVKGRFTISRDNAKNTLY LQMSLKPDPDTALYYQSGSLPWCWSWGQGTQVTYSS	93
BBB806	EVQLVESGGGLVQPGSLRVSCASGFTFSSYYVSWVPQAPGKMLEWVSGINTGGSRKYYSSDSVKGRFTISRDNAKNTLY LQMSLKPDPDTALYYQSGSLPWCWSWGQGTQVTYSS	94
BBB848	EVQLVESGGGLVQPGGSLRVSCASGFTFSSYYVSWVPQAPGKMLEWVSGINTGGSRKYYSSDSVKGRFTISRDNAKNTLY LQMSLKPDPDTALYYQSGSLPWCWSWGQGTQVTYSS	95
BBB847	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYGMWRVRQAPGNDLALYIALIDSTGRAPTYADS VKGRFTISKDNARNTLY LQMSLKPDPDTAVYYCEADVGRSNRGGQGTQVTYSS	96

BBB802	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYGMRWVRQAPGNDLAYIALIDSTGRAPTYADSVKGRFTISKDNARNTLY LQMNSLKPDPTAVYYCEADYDGRSNRGQGLTVSS	97
BBB803	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYGMRWVRQAPGNDLAYIALIDSTGRAPTYADSVKGRFTISKDNARNTLY LQMNSLKPDPTAVYYCEADYDGRSNRGQGLTVSS	98
BBB846	EVQVVESSGGGLVQPGGSLRLSCAASGFTSSYGMRWVRQAPGNDLAYIALIDSTGRAPTYADSVKGRFTISKDNARNTLY LQMNSLKPDPTAVYYCEADYDGRSNRGQGLTVSS	99
BBB914	QVQLVESGGGLVQPGGSLRLSCAASGFTSSYGMRWVRQAPGNDLAYIALIDSTGRAPTYADSVKGRFTISKDNARNTLY LQMNSLKPDPTAVYYCEADYDGRSNRGQGLTVSS	100
BBB804	EVQLVESGGGLVQPGGSLRVSCAASGFTSSRYMNMWVRQAPGKGLEWVAGINSDGLSTYYADSVKGRFISRDNAKNTLY YLQMNSLKPEDTALYYCARADKNLYGFEDYWGKGTQVTVSS	101
BBB833	EVQVVESSGGALVQPGGSLRLSCAASGFTSSHWMHWVRQAPGKGLEWVSAINPGDRITFYADSVKGRFTIARDNAKKT VYLQMDSLKSEDTAVYYCAKIARGRLPPAISDWGQGLTVTVSS	102
BBB832	EVQVVESSGGLVQPGGSLRLSCAASGFTSSHWMHWVRQAPGKGLEWVSAINPGDRITFYADSVKGRFTIARDNAKKT VYLQMDSLKSEDTAVYYCAKIARGRLPPAISDWGQGLTVTVSS	103
BBB928	QVQLVESGGGSVQAGGSLRLSCTASLRITFDLTGMAWFRQAPGKEREFVASITGGGGLTYYADSVKGRFTISRDNNAKNTLY LQMDSLNAEDTATYYCAGTPAFPRRVVDAYDYWGQGLTVTVSS	104
BBB895	QVQLVESGGGSVQAGGSLRLSCTASLRITFDLTGMAWFRQAPGKEREFVASITGGGGLTYYADSVKGRFTISRDNNAKNTLY LQMDSLNAEDTATYYCAGTPAFPRRVVDAYDYWGQGLTVTVSS	105
BBB791	EVQLVESGGGLVQAGESLRLSCTASLRITFDLTGMAWFRQAPGKEREFVASITGGGGLTYYADSVKGRFTISRDNNAKNTLY LQMDSLNAEDTATYYCAGTPAFPRRVVDAYDYWGQGLTVTVSS	106
BBB827	EVQLVESGGGSVQAGGSLRLSCTASLRITFDLTGMAWFRQAPGKEREFVASITGGGGLTYYADSVKGRFTISRDNNAKNTLY LQMDSLNAEDTATYYCAGTPAFPRRVVDAYDYWGQGLTVTVSS	107
BBB862	EVQVVESSGGSVQAGGSLRLSCTASLRITFDLTGMAWFRQAPGKEREFVASITGGGGLTYYADSVKGRFTISRDNNAKNTLY LQMDSLNAEDTATYYCAGTPAFPRRVVDAYDYWGQGLTVTVSS	108
BBB896	QVQLVESGGGSVQAGGSLRLSCTASLRITFDLTGMAWFRQAPGKEREFVASITGGGGLTYYADSVKGRFTISRDNNAKNTLY LQMDSLNAEDTATYYCAGTPAFPRRVVDAYDYWGQGLTVTVSS	109
BBB798	EVQLVESGGGLVQAGGSLRLSCSASGRITFDLSPYGVFRQAPGEEREFVATVSSSGSFTKYADSVKGRFTVSRDNTKNTAY LQMNNLKPEDTALYYSCAASIRGGLRTVELADYWGQGLTVTVSS	110
BBB799	EVQLVESGGGLVQAGGSLRLSCSASGRITFDLSPYGVFRQAPGKEREFVATVSSSGSFTKYADSVKGRFTVSRDNTKNTAY LQMNNLKPEDTALYYSCAASIRGGLRTVELADYWGRTGLTVTVSS	111
BBB883	QVQLVESGGGLVQTGGSLRLSCSASGRITFDLSPYGVFRQAPGKEREFVATVSSSGSFTKYADSVKGRFTVSRDNTKNTAY LQMNNLKPEDTALYYSCAASIRGGLRTVELADYWGQGLTVTVSS	112
BBB801	EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWWVRQAPGKGLEWVARIRSKYNINNYATYYAASVKGRFTISRDDSK NSLYLQMNNLKTEPTAVYYCVRHNGNSYSWFAIYWGGGLTVTVSS	113
BBB855	EVQVVESSGGGLVQTGGSLRLSCVASKSIVSNHMGWVRQAPGKQREAVATMTRAGITNNYYADSVKGRFTMSRDNAKNT VYLQMNRLTPEDTAVYYCRADDEYYDHWGGGLTVTVSS	114
BBB931	QVQVVESSGGGLVQTGGSLRLSCVASKSIVSNHMGWVRQAPGKQREAVATMTRAGITNNYYADSVKGRFTMSRDNAKNT VYLQMNRLTPEDTAVYYCRADDEYYDHWGGGLTVTVSS	115
BBB929	QVQVVESSGGGLVQTGGSLRLSCVASKSIVSNHMGWVRQAPGKQREAVATMTRAGITNNYYADSVKDRFTMSRDNAKNT VYLQMNRLTPEDTAVYYCRADDEYYDHWGGGLTVTVSS	116
BBB926	QVQLVESGGGLVQTGGSLRLSCVASKSIVSNHMGWVRQAPGKQREAVATMTRAGITNNYYADSVKGRFTMSRDNAKNT VYLQMNRLTPEDTAVYYRRADDEYYDHWGGGLTVTVSS	117

BBB923	QVQLVESGGGLVQTGSLRLSCVASKSIVSINHMGWYRQAPGKQREAVATMTRAGITNYYADSVKGRFTMSRDNAKNT VYLQMNRLTPEDAVYYCRADDEYYDYWGQGTQVTVSS	118
BBB921	QLVESGGGLVQTGSLRLSCVASKSIVSINHMGWYRQAPGKQREAVATMTRAGITNYYADSVKGRFTMSRDNAKNTVY LQMNRLTPEDAVYYCRADDEYYDYWGQGTQVTVSS	119
BBB919	QVQLVESGGGLVQTGSLRLSCVASKSIVSINHMGWYRQAPGKQREAVATMTRAGITNYYADSVKGRFTMSRDNAKNT VYLQMNRLTPEDAVYYCRADDEYYDYWGQGTQVTVSS	120
BBB917	QVQLVESGGGLVQTGSLRLSCVASKSIVSINHMGWYRQAPGKQREAVATMTRAGITNYYADSVKGRFTMSRDNAKNT VYLQMNRLTPEDAVYYCRADDEYYDYWGQGTQVTVSS	121
BBB899	QVQLVESAGGLVQTGSLRLSCVASKSIVSINHMGWYRQAPGKQREAVATMTRAGITNYYADSVKGRFTMSRDNAKNT VYLQMNRLTPEDAVYYCRADDEYYDYWGQGTQVTVSS	122
BBB894	QLQLVESGGGLVRTGSLRLSCVASKSIVSINHMGWYRQAPGKQREAVATMTRAGITNYYADSVKGRFTMSRDNAKNT VYLQMNRLTPEDAVYYCRADDEYYDYWGQGTQVTVSS	123
BBB891	QLQLVESGGGLVQTGSLRLSCVASKSIVSINHMGWYRQAPGKQREAVATMTRAGITNYYADSVKGRFTMSRDNAKNT VYLQMNRLTPEDAVYYCRADDEYYDYWGQGTQVTVSS	124
BBB889	QLQLVESGGGLVQTGSLRLSCVASKSIVSINHMGWYRQAPGKQREAVATMTRAGITNYYADSVKGRFTMSRDNAKNT VYPQMNRLTPEDAVYYCRADDEYYDYWGQGTQVTVSS	125
BBB887	QLQLVESGGGLVQTGSLRLSCVASKSIVSINHMGWYRQAPGKQREAVATMTRAGITNYYADSVKGRFTMSRDNAKNT VYLQMNRLTPEDAVYYCRADDEYYDYWGQGTQVTVSS	126
BBB885	QLQLVESGGGLVQTGSLRLSCVASKSIVSINHMGWYRQAPGKQREAVATMTRAGITNYYADSVKGRFTMSRDNAKNT VYLQMNRLTPEDAVYYCRADDEYYDYWGQGTQVTVSS	127
BBB882	QLQLVESGGGLVQTGSLRLSCVASKSIVSINHMGWYRQAPGKQREAVATMTRAGITNYYADSVKGRFTMSRDNAKNT VYLQMNRLTPEDAVYYCRADDEYYDYWGQGTQVTVSS	128
BBB880	QLQLVESGGGLVQPGSLRLSCVASKSIVSINHMGWYRQAPGKQREAVATMTRAGITNYYADSVKGRFTMSRDNAKNT VYLQMNRLTPEDAVYYCRADDEYYDYWGQGTQVTVSS	129
BBB869	QLQLVESGGGLMQTGSLRLSCVASKSIVSINHMGWYRQAPGKQREAVATMTRAGITNYYADSVKGRFTMSRDNAKNT VYLQMNRLTPEDAVYYCRADDEYYDYWGQGTQVTVSS	130
BBB859	EVQLVESGGGLVQTGSLRLSCVASKSIVSINHMGWYRQAPGKQREAVTMTTRAGITNYYADSVKGRFTMSRDNAKNT VYLQMNRLTPEDAVYYCRADDEYYDYWGQGTQVTVSS	131
BBB857	EVQLVESGGGLVQTGSLRLSCVASKSIVSINHMGWYRQAPGKQREAVATMTRAGITNYYADSVKGRFTMSRDNAKNT VYLQMNRLTPEDAVYYCRADDEYYDYWGQGTQVTVSS	132
BBB854	EVQLVESGGGLVQTGSLRLSCVASKSIVSINHMGWYRQAPGKQREAVATMTRAGITNYYADSVKGRFTMSRDNAKNT AYLQMNRLTPEDAVYYCRADDEYYDYWGQGTQVTVSS	133
BBB850	EVQLVESGGGLVQTGSLRLSCVASKSIVSINHMGWYRQAPGKQREAVATMTRAGITNYYADSVKGRFTMSRDNAKNT VYLQMNRLTPEDAVYYCRADDEYYDYWGQGTQVTVSS	134
BBB824	EVQLVESGGGLVQTGSLRLSCVASKSIVSINHMGWYRQAPGKQREAVATMTRAGITNYYADSVKGRFTMSRDNAKNT VYLQMNRLTPEDAVYYCRADDEYYDYWGQGTQVTVSS	135
BBB821	EVQLVESGGGLVQTGSLRLSCVASKSIVSINHMGWYRQAPGKQREAVATMTRAGITNYYADSVKGRFTMSRDNAKNT VYLQMNRLTPEDAVYYCRADDEYYDYWGQGTQVTVSS	136
BBB817	EVQLVESGGGLVQTGSLRLSCVASKSIVSINHMGWYRQAPGKQREAVATMTRAGITNYYADSVKGRFTMSRDNAKNT VYLQMNRLTPEDAVYYCRADDEYYDYWGQGTQVTVSS	137
BBB815	EVQLVESGGGLVQTGSLRLSCVASKSIVSINHMGWYRQAPGKQREAVATMTRAGITNYYADSVKGRFTMSGDNAKNT VYLQMNRLTPEDAVYYCRADDEYYDYWGQGTQVTVSS	138

BBB813	EVQLVESGGGLVQTGSLRLSCVASKSIVSINHMGWYRQAPGKQREAVATMTRAGITNYYADS VKDRFTMSRDNAKNT VYLQMNRLTPEDTAVYYCRADDEYYDYWGQGTLVTVSS	139
BBB811	EVQLVESGGGLVQTGSLRLSCVASKSIVSINHMGWYHQAPEGKQREAVATMTRAGITNYYADS VKGRFTMSRDNAKNT VYLQMNRLTPEDTAVYYCRADDEYYDYWGQGITLVTVSS	140
BBB809	EVQLVESGGGLVQTGSLRLSCAASKSIVSINHMGWYRQAPGKQREAVATMTRAGITNYYADS VKGRFTMSRDNAKNT VYLQMNRLTPEDTAVYYCRADDEYYDYWGQGITLVTVSS	141
BBB787	EVQLVESGGALVQTGSLRLSCAASKSIVSINHMGWYRQAPGKQREAVATMTRAGITNYYADSMKGRFTMSRDNAKNT VYLQMNRLTPEDTAVYYCRADDEYYDYWGQGITLVTVSS	142
BBB796	EVQLVESGGGLVQAGSLRLSCAASKSIVSINHMGWYRQAPGKQREAVATMTRAGITNYYADS VKGRFTMSRDNAKNT VYLQMNRLTPEDTAVYYCRADDEYYDYWGQGITLVTVSS	143
BBB808	EVQLVESGGGLVQTGSLGLSCVASKSIVSINHMGWYRQAPGKQREAVATMTRAGITNYYADS VKGRFTMSRDNAKNT VYLQMNRLTPEDTAAYYCRADDEYYDYWGQGITVTVSS	144
BBB810	EVQLVESGGGLVQTGSLRLSCVAPKSIIVSINHMGWYRQAPGKQREAVATMTRAGITNYYADS VKGRFTMSRDNAKNT VYLQMNRLTPEDTAVYYCRADDEYYDYWGQGITVTVSS	145
BBB812	EVQLVESGGGLVQTGSLRLSCVASKSIVSINHMGWYRLAPGKQREAVATMTRAGITNYYADS VKGRFTMSRDNAKNT VYLQMNRLTPEDTAVYYCRADDEYYDYWGQGITLVTVSS	146
BBB814	EVQLVESGGGLVQTGSLRLSCVASKSIVSINHMGWYRQAPGKQREAVATMTRAGITNYYADS VKDRFTMSRDNAKNT VYLQMNRLTPEDTAVYYCRADDEYYDYWGQGITVTVSS	147
BBB816	EVQLVESGGGLVQTGSLRLSCVASKSIVSINHMGWYRQAPGKQREAVATMTRAGITNYYADS VKGRFTMSRDNAKNT VYLQMNRLAPEDTAVYYCRADDEYYDYWGQGITLVTVSS	148
BBB820	EVQLVESGGGLVQTGSLRLSCVASKSIVSINHMGWYRQAPGKQREAVATMTRAGITNYYADS VKGRFTMSRDNAKNT VYLQMNRLTPEDTAVYYCRADDEYYDYWGQGITLVTVSS	149
BBB823	EVQLVESGGGLVQTGSLRLSCVASKSIVSINHMGWYRQAPGKQREAVATMTRAGITNYYADS VKGRFTMSRDNANNT VYLQMNRLTPEDTAVYYCRADDEYYDYWGQGITLVTVSS	150
BBB826	EVQLVESGGGLVQTGSPRLSCVASKSIVSINHMGWYRQAPGKQREAVATMTRAGITNYYADS VKGRFTMSRDNAKNT VYLQMNRLTPEDTAVYYCRADDEYYDYWGQGITVTVSS	151
BBB853	EVQLVESGGGLVQTGSLRLSCVASKSIVSINHMGWYRQAPGKQREAVATMTRAGITNYHADSVKGRFTMSRDNAKNT VYLQMNRLTPEDTAVYYCRADDEYYDYWGQGITLVTVSS	152
BBB856	EVQLVESGGGLVQTGSLRLSCVASKSIVSINHMGWYRQAPGKQREAVATMTRAGITNYYADSVKGRFTMSRDNAKNT VYLQMNRLTPEDTAVYYCRADDEYYDYWGQGITLVTVSS	153
BBB858	EVQLVESGGGLVQTGSLRLSCVASKSIVSINHMGWYRQAPGKQREAVATMTRAGITNYYADSVKGRFTMSRDNAKNT VYLQMNRLTPEDTVVYYCRADDEYYDYWGQGITLVTVSS	154
BBB860	EVQLVESGGGLVQTGSLRLTCVASKSIVSINHMGWYRQAPGKQREAVATMTRAGITNYYADSVKGRFTMSRDNAKNT VYLQMNRLTPEDTAVYYCRADDEYYDYWGQGITLVTVSS	155
BBB876	QLQLVESGGGLVOHGSRLRLSCVASKSIVSINHMGWYRQAPGKQREAVATMTRAGITNYYADSVKGRFTMSRDNAKNT VYLQMNRLTPEDTAVYYCRADDEYYDYWGQGITLVTVSS	156
BBB881	QLQLVESGGGLVQPGSLRLSCVASKSIVSINHMGWYRQAPGKQREAVATMTRAGITNYYADSVKGRFTMSRDNARNT VYLQMNRLTPEDTAVYYCRADDEYYDYWGQGITVTVSS	157
BBB884	QLQLVESGGGLVQTGSLRLSCVASKSIVSINHMGWYRQAPGKQREAVATMTRAGITNYYADSVKDRFTMSRDNAKNT VYLQMNRLTPEDTAVYYCRADDEYYDYWGQGITLVTVSS	158
BBB886	QLQLVESGGGLVQTGSLRLSCVASKSIVSINHMGWYRQAPGKQREAVATMTRAGITNYYADSVKGRFTMSRDNAKNT VYLHMNRLTPEDTAVYYCRADDEYYDYWGQGITVTVSS	159

BBB888	QLQLVESGGGLVQTGSLRLSCVASKSIVSINHMGWYRQAPGKQREAVATMTRAGITNYYADSVKGRFTMSRDNAKNT VYLQMNRLTPEDTAVYYCRADDEYYDYWGQGTQVTVSS	160
BBB890	QLQLVESGGGLVQTGSLRLSCVASKSIVSINHMGWYRQAPGKQREAVTMTRAGITNYYADSVKGRFTMSRDNAKNT VYLQMNRLTPEDTAVYYCRADDEYYDYWGQGTQVTVSS	161
BBB892	QLQLVESGGGLVQTGSLRLSCVAKSIVSINHMGWYRQAPGKQREAVATMTRAGITNYYADSVKGRFTMSRDNAKNT VYLQMNRLTPEDTAVYYCRADDEYYDYWGQGTQVTVSS	162
BBB897	QLQLVESGGGWQPGSLRLSCVASKSIVSINHVGWYRQAPGKQREAVATMTRAGITNYYADSVKGRFTMSRDNAKNT VYLQMNRLTPEDTAVYYCRADDEYYDYWGQGTQVTVSS	163
BBB915	QVQLVESGGGLVQPGSLRLSCVASKSIVSINHMGWYRQAPGKQREAVATMTRAGITNYYADSVKGRFTMSRDNAKNT VYLQMNRLTPEDTAVYYCRADDEYYDYWGQGTQVTVSS	164
BBB918	QVQLVESGGGLVQTGSLRLSCSASKSIVSINHMGWYRQAPGKQREAVATMTRAGITNYYADSVKGRFTMSRDNAKNT VYLQMNRLTPEDTAVYYCRADDEYYDYWGQGTQVTVSS	165
BBB920	QVQLVESGGGLVQTGSLRLSCVASKSIVSINHMGWYRQAPGEGQREAVATMTRAGITNYYADSVKGRFTMSRDNAKNT VYLQMNRLTPEDTAVYYCRADDEYYDYWGQGTQVTVSS	166
BBB922	QVQLVESGGGLVQTGSLRLSCVASKSIVSINHMGWYRQAPGKQREAVATMTRAGITNYYADSVKGRFTMSRDNAKNT VYLQMNRLTPEDTAVYYCRADDEYYDYWGQGTQVTVSS	167
BBB925	QVQLVESGGGLVQTGSLRLSCVASKSIVSINHMGWYRQAPGKQREAVATMTRAGITNYYADSVKGRFTMSRDNAKNT VYLQMNRLTPEDTAVYYCRADDEYYDYWGQGTQVTVSS	168
BBB927	QVQLVESGGGLVQTGSLRLSCVASKSIVSINHVGWYRQAPGKQREAVATMTRAGITNYYADSVKGRFTMSRDNAKNT VYLQMNRLTPEDTAVYYCRADDEYYDYWGQGTQVTVSS	169
BBB930	QVQVESGGGLVQTGSLRLSCVASKSIVSINHMGWYRQAPGKQREAVATMTRAGITNYYADSVKGRFTMSRDNAKNT VYLQMNRLTPEDTAVYYCRADDEYYDYWGQGTQVTVSS	170
BBB851	EVQLVESGGGLVQTGSLRLSCVASKSIVSIDHMGWYRQAPGKQREAVATMTRAGITNYYADSVKGRFTMSRDNAKNT VYLQMNRLTPEDTAVYYCRADDEYYDYWGQGTQVTVSS	171
BBB825	EVQLVESGGGLVQTGSLRLSCVASKSIVSISHMGWYRQAPGKQREAVATMTRAGITNYYADSVKGRFTMSRDNAKNTV YLQMNRLTPEDTAVYYCRADDEYYDYWGQGTQVTVSS	172
BBB898	QLQLVESRGGLVQTGSLRLSCVASKSIVSINHMGWYRQAPGKQREAVATMTRAGITNYYADSVKGRFTMSRDNAKNT VYLQMNRLTPEDTAVYYCRADDEYYDYWGQGTQVTVSS	173
BBB818	EVQLVESGGGLVQTGSLRLSCVASKSIVSINHMGWYRQAPGKQREAVATMTRAGITNYYADSVKGRFTMSRDNAKNT VYLQMNRLTPEDTAVYYCRADDEYCDYWGGQGTQVTVSS	174
BBB819	EVQLVESGGGLVQTGSLRLSCVASKSIVSINHMGWYRQAPGKQREAVATMTRAGITNYYADSVKGRFTMSRDNAKNT VYLQMNRLTPEDTAVYYCRADDEYNDYWGGQGTQVTVSS	175
BBB852	EVQVVESGGGLVQTGSLRLSCVASKSIVSINDMGWYRQAPGKQREAVATMTRAGITNYYADSVKGRFTMSRDNAKNT VYLQMNRLTPEDTAVYYCRADDEYYDYWGQGTQVTVSS	176
BBB822	EVQLVESGGGLVQTGSLRLSCVASKSIVSINHMGWYRQAPGKQREAVATMTRAGITNYYADSVKGRFTMSRDNAKNT VYLQMNRLTPEDTAVYYCRADDEYYDYWGQGTQVTVSS	177
BBB863	QAQLVESGGGLVQTGSLRLSCVASKSIVSINHMGRYRQAPGKQREAVATMTRAGITNYYADSVKGRFTMSRDNAKNTV YLQMNRLTPEDTAVYYCRADDEYYDYWGQGTQVTVSS	178
BBB924	QVQLVESGGGLVQTGSLRLSCVASKSIVSINHMGWYRQAPGKQREAVATMTRAGITNYYADSVKGRFTMSRDNAKNT VYLQMNRLTPEDTAVYYCRADDEYYDYWGQGTQVTVSS	179
BBB879	QLQLVESGGGLVQPGSLRLSCAASGFTFGSYDMSWVRQAPGKQREAVATMTRAGITNYYADSVKGRFTMSRDNAKNT VYLQMNRLTPEDTAVYYCRADDEYYDYWGQGTQVTVSS	180

BBB861	EVQVVESSGGGLVQAGGSLRLSCTASLRTFDLTGMAWFRQAPGKEREAVATMTRAGITNNYADS VKDRFTMSRDNAKNT VYLQMNRLTPEDTAVYYCRADDEYDYDWGQGTLVTVSS	181
BBB868	QLQLVESGGGLVQAGGSLRLSCSASGRFTDLSPEGWFRQAPGKEREFVATVSSSGSTFKYADSVKGRFTVSRDNTKNTAY LQMNRPTEPTAVYYCRADDEYDYDWGQGTLVTVSS	182
BBB866	QLQLVESGGGLVQPGGSLRLSCASGFTFSRHWMYWRQAPGKGLEWVSLINTDGGSTYYADSVKGRFTMSRDNAKNT VYLQMNRLTPKDTAVYYCRADDEYDYDWGQGTQTVTVSS	183
BBB795	EVQLVESGGGLVQAGGSLRLSCAASGIFSIINGMAWYRQAPGKQRELVALITGTGRTNYADSVKGRFTISRDNAKNTVYL QMNSLKPPDITAVYYCRADDEYDYDWGQGTQTVTVSS	184
BBB872	QLQLVESGGGLVQAGGSLRLSCAASEDIFAITMGWYRQAPGKQRELVARVTYGGTTNYADSVRGRFTISRDNAKNTVY LQMNRLTPEDTAVYYCRADDEYDYDWGQGTLVTVSS	185
BBB905	QVQLVESGGGLVQAGESLRLSCTASGSSFSASAMNWYRQAPGKQREWVAQITRISRSYVATSVKGRFTVSRDNTKNTVY LQMNSLKPEDTAVYYCNTGVTWGQGTLVTVSS	186
BBB870	QLQLVESGGGLVQAGESLRLSCTASGSSFSASAMNWYRQAPGKQREWVAQITRISRSVCATSVKGRFTVSRDNTKNTVYL QMNSLKPEDTAVYYCNTGVTWGQGTLVTVSS	187
BBB838	EVQVVESSGGGLVQAGESLRLSCTASGSSFSASAMNWYRQAPGKQREWVAQITRISRSYVATSVKGRFTVSRDNTKNTVY LQMNSLKPEDTAVYYCNTGVTWGQGTQTVTVSS	188
BBB837	EVQVVESSGGGLVQAGESLRLSCTASGSSFSASAMNWYRQAPGKQREWVAQITRISRSYVATSVKGRFTVSRDNTKNTVY LQMNSLKPEDTAVYYCNTGVTWGQGTLVTVSS	189
BBB871	QLQLVESGGGLVQAGESLRLSCTASGSSFSASAMNWYRQAPGKQREWVAQITRISRSYVATSVKGRFTVSRDNTKNTVY LQMNSLKPEDTAVYYCNTGVTWGQGTQTVTVSS	190
BBB906	QVQLVESGGGLVQAGESLRLSCTASGSSFSASAMNWYRQAPGKQREWVAQITRISRSYVATSVKGRFTVSRDNTKNTVY LQMNSLKPEDTAVYYCNTGVTWGQGTQTVTVSS	191
BBB839	EVQVVESSGGGLVQAGESLRLSCTASGSSFSASAMNWYRQAPGKQREWVAQITRISRSYVATSVKGRFTVSRDNTKNTVY LQMNSLKPEDTAVYYCRADDEYDYDWGQGTQTVTVSS	192
BBB911	QVQLVESGGGLVQAGGSLRLSCAFSGVIVSRITVMGWYRQAPGKQRELVAITITGTGVTNYADS VKGRFNISTDNAKKMAY YLQSDILKPEDTAVYYCNSKLGIRDYWGQGTQTVTVSS	193
BBB875	QLQLVESGGGLVQAGGSLRLSCAFSGVIVSRITVMGWYRQAPGKQRELVAITITGTGVTNYADS VKGRFNISTDNAKKMAY LQSDILKPEDTAVYYCNSKLGIRDYWGQGTLVTVSS	194
BBB843	EVQVVESSGGGLVQAGGSLRLSCAFSGVIVSRITVMGWYRQAPGKQRELVAITITGTGVTNYADS VKGRFNISTDNAKKMAY YLQSDILKPEDTAVYYCNSKLGIRDYWGQGTLVTVSS	195
BBB797	EVQLVESGGGLVQAGGSLRLSCAFSGVIVSRITVMGWYRQAPGKQRELVAITITGTGVTNYADS VKGRFNISTDNAKKMAY LQSDILKPEDTAVYYCNSKLGIRDYWGQGTQTVTVSS	196
BBB910	QVQLVESGGGLVQAGGSLRLSCAFSGVIVSRITVMGWYRQAPGKQRELVAITITGTGVTNYADS VKGRFNISTDNAKKMAY YLQSDILKPEDTAVYYCNSKLGIRDYWGQGTLVTVSS	197
BBB909	QVQLVESGGGLVQAGGSLRLSCAASGIFSIINGMAWYRQAPGKQRELVALITGTGRTNYADSVKGRFTISRDNAKNTVYL QMNSLKPPDITAVYYCNTNNYWGQGTQTVTVSS	198
BBB874	QLQLVESGGGLVQAGGSLRLSCAASGIFSIINGMAWYRQAPGKQRELVALITGTGRTNYADSVKGRFTISRDNAKNTVYL QMNSLKPPDITAVYYCNTNNYWGQGTQTVTVSS	199
BBB849	EVQVVESSGGGLVQTGSLRLSCAASGIFSIINGMAWYRQAPGKQRELVALITGTGRTNYADSVKGRFTISRDNAKNTVYL QMNSLKPPDITAVYYCNTNNYWGQGTQTVTVSS	200
BBB842	EVQVVESSGGGLVQAGGSLRLSCAASGIFSIINGMAWYRQAPGKQRELVALITGTGRTNYADSVKGRFTISRDNAKNTVYL QMNSLKPPDITAVYYCNTNNYWGQGTQTVTVSS	201

BBB841	EVQVVEGGGLVQAGGSLRLSCAASGSIKSIINGMAWYRQAPGRQRELVALITGGRTNYADSVKGRFTISRDNAKNTVYL	202
BBB794	QMNSLKPDDTAVYYCNTNNYWQGTLVTVSS EVQLVESGGGLVQAGGSLRLSCAASGSIKSIINGMAWYRQAPGRQRELVALITGGRTNYADSVKGRFTISRDNAKNTVYL	203
BBB844	QMNSLKPDDTAVYYCNTNNYWQGTLVTVSS EVQVVEGGGLVQAGGSPRLSCAASGSIKSIINGMAWYRQAPGRQRELVALITGGRTNYADSVKGRFTISRDNAKNTVYL	204
BBB873	QMNSLKPDDTAVYYCNTNNYWQGTLVTVSS QMNSLKPDDTAVYYCNTNNYWQGTLVTVSS QMNSLKPDDTAVYYCNTNNYWQGTLVTVSS QMNSLKPDDTAVYYCNTNNYWQGTLVTVSS	205
BBB908	QMNSLKPDDTAVYYCNTNNYWQGTLVTVSS QMNSLKPDDTAVYYCNTNNYWQGTLVTVSS	206
BBB840	QMNSLKPDDTAVYYCNTNNYWQGTLVTVSS QMNSLKPDDTAVYYCNTNNYWQGTLVTVSS	207
BBB907	QMNSLKPDDTAVYYCNTNNYWQGTLVTVSS QMNSLKPDDTAVYYCNTNNYWQGTLVTVSS	208
BBB792	QMNSLKPDDTAVYYCNTNNYWQGTLVTVSS QMNSLKPDDTAVYYCNTNNYWQGTLVTVSS	209
BBB793	QMNSLKPDDTAVYYCNTNNYWQGTLVTVSS QMNSLKPDDTAVYYCNTNNYWQGTLVTVSS	210
BBB828	QMNSLKPDDTAVYYCNTNNYWQGTLVTVSS QMNSLKPDDTAVYYCNTNNYWQGTLVTVSS	211
BBB916	QMNSLKPDDTAVYYCNTNNYWQGTLVTVSS QMNSLKPDDTAVYYCNTNNYWQGTLVTVSS	212
BBB901	QMNSLKPDDTAVYYCNTNNYWQGTLVTVSS QMNSLKPDDTAVYYCNTNNYWQGTLVTVSS	213
BBB865	QMNSLKPDDTAVYYCNTNNYWQGTLVTVSS QMNSLKPDDTAVYYCNTNNYWQGTLVTVSS	214
BBB831	QMNSLKPDDTAVYYCNTNNYWQGTLVTVSS QMNSLKPDDTAVYYCNTNNYWQGTLVTVSS	215
BBB786	QMNSLKPDDTAVYYCNTNNYWQGTLVTVSS QMNSLKPDDTAVYYCNTNNYWQGTLVTVSS	216
BBB829	QMNSLKPDDTAVYYCNTNNYWQGTLVTVSS QMNSLKPDDTAVYYCNTNNYWQGTLVTVSS	217
BBB830	QMNSLKPDDTAVYYCNTNNYWQGTLVTVSS QMNSLKPDDTAVYYCNTNNYWQGTLVTVSS	218
BBB864	QMNSLKPDDTAVYYCNTNNYWQGTLVTVSS QMNSLKPDDTAVYYCNTNNYWQGTLVTVSS	219
BBB900	QMNSLKPDDTAVYYCNTNNYWQGTLVTVSS QMNSLKPDDTAVYYCNTNNYWQGTLVTVSS	220
BBB902	QMNSLKPDDTAVYYCNTNNYWQGTLVTVSS QMNSLKPDDTAVYYCNTNNYWQGTLVTVSS	221

Table 5: CDR SEQ ID NOs of Fv clones

CLONE	LCDR1	SEQ ID NO	LCDR 2	SEQ ID NO	LCDR3	SEQ ID NO	HCDR1	SEQ ID NO	HCDR2	SEQ ID NO	HCDR3	SEQ ID NO
VR0000	SSDVGNYNL	222	EGS	309	CSYAGSTT LV	360	GFTFSGSA	519	VRSKADSS AT	646	TTSGTYFYGFDI	793
VR0000	QGISNY	223	AAS	310	LQHNSTPY T	361	GFTFSGSA	519	VRSKADSS AT	646	TTSGTYFYGFDI	793
VR0000	QGISNY	223	AAS	310	LQHNSTPY T	362	GFTFSGSA	520	IKSKTDGG TL	647	TTTELTVFPDY	794
VR0000	QDIGNY	224	SAS	311	QKYNAPL T	363	GFTFSTS W	521	IKSKIDGGT I	648	TTGGPAFDI	795
VR0000	ESVDRYGNSL	225	LAS	312	HQNNEDPS T	364	GFTFSNY W	522	IRLKSNNY AT	649	TRIDY	796
VR0000	QSLHNGYN C	226	LGS	313	MQALQTP YT	365	GFTFSRY W	523	INNAGNSR	650	SRAGNWDRDTFDI	797
VR0000	ALPKQY	227	KDS	314	QSADSSGT VV	366	GFTFSY W	524	INNIGNSR	651	ARAGNWDRDTFDI	798
VR0000	SSNIGAGYD	228	GNS	315	QSYDSSL S GSGV	367	GFTFSTY W	525	INNAGNSR	650	ARAGNWDRDTFDI	798
VR0000	KLGNKF	229	QDS	316	QAWDSTT VV	368	GFTFSVY Y	526	ISNRGITM	652	ARRTPGEGWFDP	799
VR0000	KLGNKF	229	QDS	316	QAWDSTT VV	368	GFTFSVY Y	526	ISNRGITM	652	ARRTPGEGWFDP	799
VR0000	KLGNKF	229	QDS	316	QAWDSTT VV	368	GFTFSVY Y	526	ISNRGITM	652	ARRTPGEGWFDP	799
VR0000	KLGNKF	229	QDS	316	QAWDSTT VV	368	GFTFSVY Y	526	ISNRGITM	652	ARRTPGEGWFDP	799
VR0000	ELGNKF	230	QDN	317	QAWDSSA VV	369	GFTFSNY Y	527	ISNRATIM	653	ARRTPGEGWFDP	799
VR0000	KLGDY	231	QDN	317	QAWDNST VV	370	GFTFSDY Y	528	ISNRSFTK	654	ARRTPGEGWFDP	799
VR0000	ALPKKY	232	EDS	318	YSTDSSGN HSWV	371	GFTFSDY Y	528	ISNRGSTI	655	ARRMAGTYFDY	800
VR0000	SSNIGSNY	233	SNN	319	AAWDDSL SGPWV	372	GFTFSRYS Y	529	FSTGSSYI	656	ARNWDFDY	801
VR0000	SGINVTYR	234	YKSD	320	MIWHSSA WV	373	GFTFSTY N	530	ISSSSYI	657	ARDKVPGAFDY	802
VR0000	QSLNSENOK NY	235	WAS	321	QNDYGYP LT	374	GGSINSG DYF	531	IYYSGTT	658	ARSNWGFYD	803
VR0000	QISRW	236	KAS	322	QOYNSYS WT	375	GVSISSTY YH	532	IYYGONS	659	ASSHYPEDY	804
VR0000	QSISSW	237	KAS	322	QOYNTYS WT	376	GGSFSGY Y	533	INQSGRT	660	ARAEWELLGFYD	805
VR0000	QDISNY	238	TAS	323	QOYNSYP YT	377	GYIFTKY Y	534	INPSGGST	661	AREGGELYGMDV	806

VR0000 15603	QSVRSRY	239	GAS	324	QOYGSSP T	378	GVSISYY	535	IYSSGST	662	AREFPQSYFPDY	807
VR0000 06496	QSVSSSY	240	GAS	324	QOYGSPPY T	379	GFTFSRYS	529	FSTGSSYI	656	ARNWDFDY	801
VR0000 30726	QSVSSSY	240	VAS	325	QOYGSPP T	380	GGISISNYF	536	ISASGRI	663	ARQWLAFDY	808
VR0000 09731	QSVSSN	241	GAS	324	QQLLWPP RT	381	GYSFTSY W	537	IDPDSYIT	664	ARMYKGRGHLFDY	809
VR0000 34880	QSVAKW	242	YAS	326	QOQFNWPI T	382	GYSFTSY W	537	IYPGDSIT	665	ARVRAGVYGFY	810
VR0000 28040	QSVSKA	243	AAS	310	QOYYRAP YT	383	GGTLGGY G	538	IIPFGTA	666	ARSGGTYGMLDV	811
VR0000 28042	QSVSKA	243	AAS	310	QOYYRAP YT	383	GGTLGGY G	539	IIPGIGTA	667	ARSGGTYGMLDV	811
VR0000 28041	QSVSSN	241	GAS	324	QQLLWPP RT	381	GGTLGGY G	538	IIPFGTA	666	ARSGGTYGMLDV	811
VR0000 49105	QSVSSY	244	DAS	327	QQRSNWP LT	384	GGTFSSY A	540	IRPEYGNA	668	ARGPSWLYGRYYF DY	812
VR0000 30804	QSVSSF	245	DAS	327	QQRSNWP LT	384	GGSISSYC	541	LCYSSGS	669	AAGYSSGWYLDH	813
VR0000 15467	QSVSSY	244	DAS	327	QQRSNWL T	385	GYSISSN W	542	IYFSGIT	670	ARKKGAYDYANAL DI	814
VR0000 29504	QSIGGW	246	EAS	328	QOYNSYS RT	386	GYTLTEL A	543	FDPEDEGET	671	AAGLYYFDY	815
VR0000 29505	ALPKKY	232	EDS	318	YSTDSSGN HRV	387	GYTLTEL A	543	FDPEDEGET	671	AAGLYYFDY	815
VR0000 19738	VLAERY	247	KDS	314	YSAANN LV	388	GYAFTSY A	544	INAGNGNT	672	VRAVEDS	816
VR0000 29862	QSVSSSY	240	GAS	324	QOYGSPP YT	389	GFSLSTSG MS	545	IDWDDDK	673	ALIPGY	817
VR0000 29864	SSDVGGYNY	248	EVS	329	SSYAGSNN VV	390	GFSLSTSG MS	545	IDWRDDK	674	AGIPGY	818
VR0000 15458	SSDVGGYNY	248	EVS	329	SSYAGSNN LV	391	GYSISSSF W	546	IYFSGST	675	ARKRGPYDYGNYGF DY	819
VR0000 15790	SSDVGGYNY	248	EVS	329	SSYAGSNN LV	391	GGSISSSD W	547	IYHSGST	676	ARDSYTSGWYAPLD Y	820
VR0000 31164	SSVDYDGYNY	249	EVN	330	SSYAGSTD VV	392	GGSISSSG FY	548	IYYSGIT	677	ARDRVGSTPDAFDI	821
VR0000 15791	SSDVGNYNL	222	EGS	309	CSYVSGGT FVV	393	GGSISSSD W	547	IYQSGST	678	VRALGGSSWSDWG GFDY	822
VR0000 30727	SSDVGSYNL	250	EGS	309	CSYAGSST VV	394	GGSISSNYF	536	ISASGRI	663	ARQWLAFDY	808

VR0000 13041	SSDVGSYNL	250	EGS	309	CSYAGSST VV	394	GGSISSSS YY	549	IYHSGT	676	ARQPLYNWNPFDY	823
VR0000 15980	SGDVGSYNL	251	EDS	318	CSYAGSST LV	395	GGSISSGA YY	550	IHYSGGI	679	ARGDLYFDY	824
VR0000 11862	SSDVGSYNL	250	EGS	309	CSYSGSTTI	396	GGSIISGT YF	551	FSYCGST	680	ARAWPYFDY	825
VR0000 15665	SSDVGSYNL	250	EGS	309	CSYAGSSR V	397	AGSISSSD W	552	ISHSGT	681	AREGDWLPFDY	826
VR0000 13877	SSDVGSYNL	250	EGS	309	CSYAGSST WV	398	GDSITNSN YY	553	IFHGGNT	682	ARYV/AAPDYFDY	827
VR0000 13880	NSDVGSYNL	252	EGS	309	CSYAGSST WV	398	GGSIISNSN YY	554	IFHGGNT	682	ARYV/AAPDYFDY	827
VR0000 12858	SSDVGGYNY	248	DVS	331	SSYTSSST WV	399	GGSIISNSN YY	554	IFHGGDT	683	ARYIAPDYFDY	828
VR0000 13470	SSDVGGYNY	248	DVS	331	SSYTSSST WV	399	GGSISSSS FY	555	IYFSGS	684	ARREPAADTLDC	829
VR0000 17500	SSDVGGYNY	248	DVS	331	SSYTSSST WV	399	GGSFSDY Y	556	INHGTGT	685	ARGGGWGSDYYFD Y	830
VR0000 17514	SSDVGGYNY	248	DVS	331	SSYTSSST RV	400	GGSFSDY Y	556	INHSGNT	686	AREEWELLGFDF	831
VR0000 17528	SSDIGGYNF	253	DVI	332	SSYTSSST VI	401	GGSFSDY Y	556	IHHSGGT	687	ASTW/AVAGFDY	832
VR0000 17602	SSDIGGYNF	253	DVI	332	SSYTSSST I	402	GGSFSGY Y	553	IHHSGGT	687	ASTW/AVAGFDY	832
VR0000 03047	TSDVGSYNL	254	EGS	309	CSYAGSST V	403	GFTFSSYA	557	VSGSGLTT	688	AKEDYDSTGYYPFD Y	833
VR0000 17983	SSDVGSYNL	250	EGS	309	CSYAGSST LV	395	GFIFSDYQ	558	ISSSGYTT	689	AREDYDSTGYNPF Y	834
VR0000 17618	SSDVGSYNL	250	EGS	309	CSYAGSST WV	398	GGSFSGY Y	553	IDHSGIT	690	ARGRSDSSGYYSFD Y	835
VR0000 06535	SSDVGSYNL	250	EGS	309	CSYAGSST VV	394	GFTFSSYR	559	ISRSSSYI	691	ARHHDYSNSDAF Y	836
VR0000 06523	SSDVGSYNL	250	EGS	309	CSYAGSST VV	394	GFTFSSYK	560	ISRSSITYT	692	ARHHDYSNSDAF Y	837
VR0000 06526	SSDVGSYNL	250	EGS	309	CSYAGSST VV	394	GFTFSSYN	561	IRRSIGNYI	693	ARLHDYSNNDAF Y	838
VR0000 06548	SSDVGSYNL	250	EGS	309	CSYAGSST VV	394	GFTFSSYS	562	ISSSSSYI	657	ARDGGNWGAFDI	839
VR0000 19085	SSDVGNYNL	222	EDS	318	CSYAGSS WV	404	GFTFSTY G	563	ISYDGS Y	694	AKDPGSGTYHHYY Y	840
VR0000 01179	SSDVGSYNR	255	AVS	333	SSYTSSRT WV	405	GFTFSSFA	564	ISGSGGTA	695	AKEDHYHDGTGY Y	841

VR0000 01180	SSDVGGYNY	248	EVS	329	SSYAGSNN LV	391	GFTFSSFV	565	ISGGGGTA	696	AKEDHYDGTGYYP FDY	842
VR0000 18320	SSDVGGYNY	248	EVT	334	SSYAGSNN LV	391	GFTFSSYV	526	ISNRGITM	652	ARRTPGEGWFDP	799
VR0000 02500	SSDVGGYNY	248	DVS	331	CSYAGSFT WV	406	GFTFSSNY A	566	ISGSGYST	697	ALEEWELLGYFDY	843
VR0000 01379	SSDVGGYNY	248	DVS	331	SSYTSSTNT RV	407	GFIHSSYA	567	ISGSGGST	698	ARLDYDITGYPDPEFI	844
VR0000 01346	SSDVGGYNY	248	EVS	329	NSYAGSN NFEV	408	GFTFSSYT	568	ISGGGGST	699	AKLDYDSSGYDYFD D	845
VR0000 05197	SSDVGGYNY	248	EVS	329	SSYAGSNN WV	409	GFTFTSY A	569	ISNTGGNT	700	TKENYDITSGYNPFD Y	846
VR0000 18072	SSDVGGYNY	248	EVS	329	SSYAGSNT RVL	410	GFTFSDY Y	528	ISSSVTI	701	ARESDITSGYDPEFD H	847
VR0000 19015	SSDVGGYNY	248	EVS	329	SSYTSSTL VV	411	GFTFSSYG	570	IWYDGSNK	702	ARVHGYYTRFSDAFDI	848
VR0000 29548	SSDVGNFNF	256	DVG	335	SSYTSGST VL	412	GYTLTHERS	571	GSFDPEDG ET	703	ATVWAVAGFDY	849
VR0000 31043	QSLDSDDDGN	257	TLS	336	QRIIEPPL T	413	GGISIRGV YY	572	IYSSGST	704	ARLSGDYWYFDL	850
VR0000 30733	QSLDSDDDGN	257	MLS	337	QRIIEFPS T	414	GGISINY Y	573	FYPTGRT	705	ARAGSTVTPDYGMD V	851
VR0000 15540	QSLYSDDGKT	258	LVS	338	WQTHFP QT	415	GGISINY Y	574	IFTSGIT	706	ARVEFYDITGYDGFDD I	852
VR0000 06636	QSLDSDDDGN	257	TLS	336	QRIIEPPL T	413	GFTFSSYK	560	ISRSSNYI	707	ARHHDYSNSDAFDI	836
VR0000 06622	QSLHVNNGYN	259	LGS	313	QMALQTP YT	365	GFTFSTY N	530	ISSSSSYI	657	ARDKVPGAFDY	802
VR0000 06525	QSLHNSNGYN	260	LGS	313	QMALQTP YT	365	GFTFSSYN	561	IRRSIGNYI	693	ARLHDYSSNDAFDI	838
VR0000 19197	QSLHNSNGYN	260	LGS	313	QMALQTL T	416	GFTFSSYG	570	IWYDGSNK	702	ARQHGYYTRFSDGFDI	853
VR0000 00693	QSLHNSNGYN	260	LGS	313	QMALQTTT	417	GFTFNKF N	575	ISSGGSYK	708	ARRAPPAWGGFDY	854
VR0000 36146	QSVLFSSNNK	261	WAS	321	QQYYSTPP T	418	GFTFSSYG	570	ISYDGSNK	709	ARAPSHFYFDY	855
VR0000 01378	QSVLYSSNNK	262	WAS	321	QQYYSTPL T	419	GFIHSSYA	567	ISGSGGST	698	ARLDYDITGYPDPEFI	844
VR0000 04017	QIVLYSSSNK	263	WAS	321	QQYYSTPL T	419	GFTFSSYA	557	ISGSGGIT	710	AKQDNYESTGYYPF DY	856
VR0000 11851	QSVLYSSNNK	262	WAS	321	QQYYSTPR T	420	GFTFNSY A	576	IGSGGGST	711	AKALYYDSSSGYYY YYGMDV	857

VR0000 01230	QSVLYSSNNK NY	262	WAS	321	QQYYSTPI T	421	GFTFSNY A	566	ISGSGGNT	712	AKETYYYDSSGYTN YYYVMDY	858
VR0000 15960	QSVLYSSNNK NY	262	WAS	321	QQYYSTPF T	422	GGSIYSTN W	577	IYYSGST	704	ARDGGYSVYDSFDY	859
VR0000 13472	QSVLYSSNNK NY	262	WAS	321	QQYYSTPL T	419	GGSISSSS FY	555	IYFSGST	675	ARREPAADTLDY	860
VR0000 29534	QSVLYSSNNK NY	262	WAS	321	QQYYSTPR T	420	GGSFSGN Y	578	INHSGTT	713	AREDSSWYVGFDY	861
VR0000 29526	QSVLYSSNNK NY	262	WAS	321	QQYYSPPL T	423	GYTLMEI S	579	FDPENGET	714	AAGPSGWYSDAFDF	862
VR0000 07193	QGVSSY	264	YAS	326	QQLISYPR T	424	GFTFSSYD	580	IGSPGDT	715	ARGDFWGGYSYYY YGMDY	863
VR0000 03163	QGIKND	265	AAS	310	LQHNSTYP WT	425	GFTFSSYA	557	IRSRGDVT	716	AKGYFDWLAYYYY ALDY	864
VR0000 19882	QAISHY	266	AAS	310	LQHNSTYPR T	426	GYTFSSY Y	581	INPSGGGT	717	ARSFNWNYVGLSYH GMDY	865
VR0000 06271	QGISSC	267	AAA	339	QQANSFPP T	427	GFTFDDY A	582	ISWNGGSI	718	AKDMGLEAAGPFYY GIDY	866
VR0000 13631	QGISSY	268	AAS	310	QQLNSTYPC S	428	GGSISSSS YY	549	IYYSGNT	719	ARHRLRYFDWPPDS	867
VR0000 13632	QGISSW	269	AAS	310	QQANSFPL T	429	GGSISSSS YY	549	IYYSGNT	719	AREWELFDY	868
VR0000 30711	QGISSY	268	VAS	325	QQLNSTYPL T	430	GGSIDY Y	583	FYASGYT	720	ARERLYNWNYYGGFF DY	869
VR0000 17524	QGIKND	265	AAS	310	LQHNSTYPR T	361	GGSFSDY Y	556	IYHSGST	676	ARVPNSGSYDYFDY	870
VR0000 14697	QGIKND	265	AAS	310	LQHNSTYPR T	361	GGSFSDY Y	556	SDYSGST	721	ARVPDSGSYDYFDF	871
VR0000 17424	QGIKND	265	AAS	310	LQHNSTYPR T	361	GGPFSDY Y	584	INHSGST	722	ARVGDGGSYDPFEF	872
VR0000 17525	QGIKND	265	AAS	310	LQHNSTYPR T	361	GGSFSDY Y	556	INHSGST	722	ARDDSFMAASGPYF DY	873
VR0000 17816	QGIKND	265	AAS	310	LQHNSTYPL T	362	GGSFSTGY Y	585	INHSGST	722	ARNYYDTSGYYSFD Y	874
VR0000 20781	QGIKND	265	AAS	310	LQHNSTYPR T	426	GYTFTSY D	586	MQTNSGN T	723	AREEWELLGFDY	875
VR0000 18817	QGIKND	265	AAS	310	LQHNSTYPR T	426	GFTFSSDA	587	IWYDGSNK	702	ARDRQWLAFDY	876
VR0000 17977	QGISNY	223	AAS	310	QQYNSYPL T	431	GFTFSY Y	526	ISNRGITM	652	ARRTPGEGWFDP	799
VR0000 18329	QGIKND	265	AAS	310	LQHNSTYPP T	432	GFTFSDY Y	528	ISNRGITI	724	ARRLPGTGWFDP	877

VR0000 06547	QGISNY	223	AAS	310	LQHNSTPR T	426	GFTFSSYS	562	ISSSSSYI	657	ARDGGNWGAFDI	839
VR0000 06630	QGVSRW	270	AAS	310	QQADSFPP T	433	GFTFSNY N	588	ITSSSTYI	725	ARRHITPGGVDV	878
VR0000 06534	QGISNY	223	DTS	340	LQHNSTPL T	362	GFTFSSYR	559	ISRSSSYI	691	ARHHDYSNSDAFDI	836
VR0000 08309	QAISHY	266	AAS	310	LQHNSTPR T	426	GFSPSSYS	589	IRRSSTYI	726	ARHHDYSNNDAFDI	879
VR0000 06522	QSVSSSY	240	GAS	324	QQYGGSP WT	434	GFTFSSYK	560	ISRSSTYT	692	ARHHDYSNSDAFDF	837
VR0000 00789	QSISSW	237	KAS	322	QQYDSYS RT	435	GFTFSSYA	557	ISGSAFST	727	AKAPYRSGWEEYFF DY	880
VR0000 17947	QGIRND	265	AAS	310	LQHNSTYP WT	425	GFTFSDY Y	528	VSNSTTI	728	AREDNYESTGYFPFD Y	881
VR0000 18335	QSISSW	237	KAS	322	QQYNSYW T	436	GFTFSDY Y	528	INRSSTIK	729	ARVDNYESTGYHPF DY	882
VR0000 05039	QSVSSN	241	GAS	324	QQYNNWP PLT	437	GFTFTSY A	569	ISGSGGTT	710	AQQGRDTSGYDPFD Y	883
VR0000 17982	QSVSSY	244	DAS	327	QQRNWP LT	384	GFIFSDYQ	558	ISSGYTT	689	AREDYDSTGYNPFD Y	834
VR0000 15801	QGIRND	265	AAS	310	LQHNSTPR T	426	GGSISSN W	590	IYHSGNT	730	AREGGYSVYGSEFY	884
VR0000 15806	QGIRND	265	DAS	327	LQHNSTPR T	426	GGSISSN W	590	IYHSGT	676	AREGGYSVYGSEFY	885
VR0000 15804	QGIRND	265	SAS	311	LQHTTYPF T	438	GGSISSN W	590	IYHSGT	676	AREGGYSVYGSEFY	884
VR0000 15895	QGIRND	265	TAS	323	LQHNSTYP WT	425	GGSISSY W	591	IYHSGT	676	AREGGYSVYDSFDY	886
VR0000 15777	QGIRND	265	AAS	310	LQHNSTYP WT	425	GGSISSNY W	592	IYHSGT	676	AREGWELFFDY	887
VR0000 15789	RGIRND	271	AAS	310	LQHTSYPL T	439	GGSISSD W	547	IYHSGT	676	ARDSYTSGWYAPLD Y	820
VR0000 15654	QDIRND	272	TAS	323	LQDYNNYPF T	440	GGSISSTS W	593	IYHSGT	676	ARKYNNWTTFPDY	888
VR0000 15729	QVIRND	273	VAS	325	LQHNNTYPF T	441	GGSISSNSN W	594	IFHSGT	731	ARDGDYESSGYYG GLDS	889
VR0000 11836	QDIRNA	274	IVS	341	LQDYNNYP YT	442	GFIFNTY W	595	IKQDGSEK	732	AREQQLVPTSHYS GTGTFDI	890
VR0000 07924	SSDVGGYSY	275	DIS	342	SSYTSNT LV	443	GFTFPDY A	582	ISWNRDNI	733	AKDIRWGRSGWYPY YYSGMV	891
VR0000 07925	SLRNNY	276	GKN	343	NSRDSSGN HVV	444	GFTFPDY A	582	ISWNRDNI	733	YYSGMV	891

VR0000 01229	QGISSW	269	AAS	310	QOANSFP T	427	GFTFSNY A	566	ISGSGGNT	712	AKETYYDSSGYTN YYYVMDV	858
VR0000 01228	QGIKND	265	AAS	310	LQHNSTPP T	432	GFTFSNY A	566	ISGSGGNT	712	AKETYYDSSGYTN YYYVMDV	858
VR0000 01231	QSVSSY	244	DAS	327	QQRSNWP LT	384	GFTFSNY A	566	ISGSGGNT	712	AKETYYDSSGYTN YYYVMDV	858
VR0000 01240	KWCYKC	277	QDS	316	QAWDSST VV	445	GFTFSNY A	566	ISGSGGNS	734	AKETYYDSSGYTN YYYVMDV	858
VR0000 01236	KWCYKC	277	QDS	316	QAWDSST VV	445	GFTFSNY A	566	ISGSGGNT	712	AKETYYDSSGYTN YYYVMDV	858
VR0000 01235	KWCYKC	277	QDS	316	QAWDSST VV	445	GFTFSNY A	566	ISGSGGNT	712	AKETYYDSSGYTN YYYVMDV	858
VR0000 01234	SLRSYY	278	GKN	343	NSRDSGNT HVV	444	GFTFSNY A	566	ISGSGGNT	712	AKETYYDSSGYTN YYYVMDV	858
VR0000 01233	SSDVGGYNY	248	EVS	329	SSYAGSNN FVV	446	GFTFSNY A	566	ISGSGGNT	712	AKETYYDSSGYTN YYYVMDV	858
VR0000 01232	SSDVGSYNL	250	EGS	309	CSYAGSST LV	395	GFTFSNY A	566	ISGSGGNT	712	AKETYYDSSGYTN YYYVMDV	858
VR0000 04253	SLRSYY	278	GKN	343	NSRDSGNT HVV	444	GFTFSNY A	557	ISDSGGNT	735	AKEEYDTSGYNPF Y	892
VR0000 03041	NIGSKS	279	DDS	344	QVWDSST DHPV	447	GFTFSNY A	557	ISGSGVST	736	AKEDYDSSGYNPF Y	893
VR0000 04889	ALPKKY	232	EDS	318	YSTDSSGY HVV	448	GFTFSNY A	596	ISGSGGNT	712	AKLNYDSTGYDPP Y	894
VR0000 18073	ALPKKY	232	DDS	344	YSTDSSGN HVV	449	GFTFSNY Y	528	ISSSVTI	701	ARESDTSGYDPP H	847
VR0000 22911	ALPKKY	232	EDS	318	YSTDSSGN HRV	387	GFTFSNY A	557	ISGSGYST	697	AKDLEQWLVRYYY YYAMDV	895
VR0000 02423	ALPKKY	232	EDN	345	YSTDSSGN HRV	387	GFTFSNY A	597	ISGSGDYT	737	AKEGSGSYPPYYY YYGMDV	896
VR0000 01208	ALPNKY	280	EDS	318	YSTDSSGN HRV	387	GFTFSNY A	598	ISGSGGST	698	AKEDYDILTGPPYFY YGMDV	897
VR0000 13875	NIGIKS	281	DDS	344	QVWDSNS DHPV	450	GFTFSNY FY	599	IFHGGNT	682	ARYVAAPDYFDY	827
VR0000 13861	NIASKS	282	DDS	344	QVWDSST DHPV	451	GFTFSNY Y	600	SKHGGNT	738	ARDRVERPYFDY	898
VR0000 15833	NIGSKS	279	DDS	344	QVWDSST DHPV	447	GFTFSNY W	590	IYYSGST	704	ARDGGYSAYGSFDY	899
VR0000 13618	NIGSKS	279	DDS	344	QVWDSST DHPV	452	GFTFSNY YY	549	IYYSGTT	658	ARHDWYGGSYGWF DP	900
VR0000 17522	NIGSKS	279	DDS	344	QVWDSST DHPV	452	GFTFSNY Y	556	ISHSGST	681	ARDDTFMAAAGPFF DY	901

VR0000 15481	NIGSKS	279	DDS	344	QVWDSST DHVV	451	GYSISSN W	542	YFSGST	675	ARKRGPYDYGDYGF DY	902
VR0000 15445	NIGSKS	279	DDT	346	QVWDSST DHVV	451	GYPISSTN W	601	YFSGST	675	ARKRGPYDYGNYG DY	819
VR0000 15444	NIGSKN	283	DDS	344	QVWDSRS DHVI	453	GYPISSTN W	601	YFSGYT	739	ARKPGYSFAYFDY	903
VR0000 17551	NIGSKN	283	DDS	344	QVWDSST DHVI	454	GGSFSGH Y	602	IKHSGLT	740	ARPHSSGWYDRGFG TFDI	904
VR0000 18326	NIGSES	284	GES	347	QVWDSST DYVV	455	GFSSFDY Y	603	ISGTGSAI	741	ARDFGSYAYYYYYG MDV	905
VR0000 18327	NIGSKS	279	GDS	348	QVWDSST DYVL	456	GFSSFDY Y	603	ISGSGSAI	742	ARDFGSYAYYYYYG MDV	905
VR0000 19086	NIGSKN	283	DDS	344	QVWDSST DHV	451	GFTFSTY G	563	ISYDGSBK	694	AKDPGSGTYHHYY GMDV	840
VR0000 18762	NIGSKS	279	DDS	344	QVWDSST DHVV	451	GFTFSNY G	604	ISYDGNK	743	AKPGVINIATIWGH FOH	906
VR0000 04897	RLGDKY	285	QDR	349	QAWDTN VV	457	GFTFTSY A	569	ISGSGTT	710	AKPALDIWQGDYYY YGMDV	907
VR0000 04896	KLGDKF	286	QDR	349	QAWDSST VV	445	GFTFTSY A	569	ISGSGTT	710	AKPALDIWQGDYYY YGMDV	907
VR0000 01274	KLGDQY	287	QDN	317	QAWDSST VV	445	GFTFSYA A	557	ISGSGRT	744	AKSMYYSDSSGSY YYGMDV	908
VR0000 00083	KLGDKY	231	QDH	350	QAWDSNT VV	458	GFTFSYA	557	ISASGGT	745	AKAHFDLTGYANY YYGMDV	909
VR0000 01213	KLGDKY	231	QDR	249	QTWDSST VV	459	GFTFSYA	557	ISGSGST	698	AKAVDYDSTGYPF YYYGMDV	910
VR0000 01212	KLGDKY	231	QDR	249	QTWDSNT VV	460	GFTFSYA	557	ISGSGST	698	AKAVDYDSTGYPF YYYGLDV	911
VR0000 02413	KLGDKY	231	QDR	249	QAWDSST VV	445	GFTFSYS	605	ISGSGTT	710	AKTLDYDSTGYPF YYYGMDV	912
VR0000 11815	KLGDKY	231	QDR	249	QTWDSST VV	459	GFTFSYA	557	MSGGGGS L	746	AKTADFYDSSGYYP YYYGMDV	913
VR0000 19069	KVGDKY	288	QDR	249	QAWDISN VV	461	GFTFSTY G	563	ISYDGSNK	709	AKDLGDSGYHHYY YGMDV	914
VR0000 04994	KLGDKY	231	QDS	316	QAWDSST VV	445	VLTFSSY G	606	ISGRGDST	747	AKDFGHYGSYSY PLFDY	915
VR0000 04122	ELGDKY	289	QDI	351	QAWDSST AV	462	GFTFSYA	557	ISGSGNI	748	AKESSGTIRLLDAF DI	916
VR0000 04019	ELGDKY	289	QDT	352	QAWDSST AV	462	GFTFSYA	557	ISGSGINT	749	AKESSGTIRLLDAF DI	916
VR0000 03201	ELGDKY	289	QDT	352	QAWDSST AV	462	GFTFSYA	557	ISGSGINT	712	AKESSGTIRLLDAF DI	916

VR0000 04023	NLGDRF	290	QDN	317	QTDWDRNT AV	463	GFTFSSYA	557	ISGSGVNT	750	AKESGTYRLDDAF DI	916
VR0000 15290	RLGDKF	291	QDN	317	QTDWDRSLA V	464	GFTFSSNYA	607	ISGSGGST	698	AKEGYDTSGYHPFD Y	917
VR0000 01279	KLGDKF	286	QDN	317	QAWDRRTT AV	465	GFTFTNY D	608	ISGSGGNT	712	ARLDSDTTGYDPFDI	918
VR0000 04727	KLGDKF	286	QDS	316	QTVVANT VV	466	GFTFSSYT	568	ISGSGGAT	751	AKVNYDTTGYPPLD H	919
VR0000 05033	KLGDKF	286	QDS	316	QAWVRRTT VV	467	GFTFSSND	609	ISGSGGST	698	AKLDYDTTGYFPFD H	920
VR0000 01286	KLGDKF	286	QDK	353	QTRVINTV V	468	GFTFSSCD	610	ISGSGGRT	744	AKMEYDSSGYSYFD Y	921
VR0000 01182	KLGDKF	286	QDN	317	QTDWDISTV V	469	GFTFSTY D	611	VSGSGGNT	752	AKFDYDTSGYNYFD Y	922
VR0000 01574	KLGDKF	286	QDT	352	QTWVTNT AV	470	GFTFNNY A	612	ISGSGGNT	712	AKEDADSTGYDPFD Y	923
VR0000 00655	KLGDKF	286	QDT	352	QTDWDETT VV	471	GFTFSSNY A	566	ISGSGGNT	712	AKEDHDLTGYSFPD Y	924
VR0000 03001	KLGDKF	286	QDH	350	QTWVSSST AI	472	GFTFSSYA	557	ISGSGGTP	753	AKEGEDSTGYYPFD H	925
VR0000 04737	KLGDKD	292	QDN	317	QAWDSST VV	445	GFTFSSYV	613	ISGSGGST	698	AKNDYDSSGYDYFD Y	926
VR0000 05036	KLGDKF	286	QDR	249	QAWDSST VV	445	GFTFSSYA	557	ISGSGGWT	754	AKEHSSGWYYPDY	927
VR0000 01203	RLGDKY	285	QDR	249	QTDWSSST VV	473	GFTFSSSA	614	ISGSGGST	698	ARDGDDYGDYDFD Y	928
VR0000 01202	RLGDKY	285	QDR	249	QTDWSSST VV	473	GFTFSSSA	615	ISGSGGST	698	ARDGDDYGDYDFD Y	928
VR0000 03033	KLGDKY	231	QDR	249	QAWDSST AV	474	GFTFSSYA	557	ISGSGGST	698	AKDGSYFDSNGPDY FDY	929
VR0000 18192	KLGDKF	286	QDN	317	QAWASST VV	475	GFTFSDY Y	528	LSSGGSTR	755	ARLDVHESSGYYPF DF	930
VR0000 18171	KLGDKF	286	QDT	352	QAWDRITT VV	476	GFTFSDY Y	528	ISSSGSTI	756	ARLDNYDSTGYYPF DF	931
VR0000 14699	NLGDKF	293	QDN	317	QAWWEYST AI	477	GFTFSDY Y	528	ISSGGSTI	757	ASLDNYESSGYYPFD Y	932
VR0000 14700	KLGDKF	286	QDN	317	QAWDSST VV	445	GFTFSDY Y	528	ISTGGSAL	758	ARQDNYESSGYYPF DS	933
VR0000 18018	KMGDKF	294	QDR	349	QAWDSST VV	445	GFTFSDY D	616	ISTGSSSK	759	ARLDNYESSGYFPFD Y	934
VR0000 18325	RLGEKF	295	QDT	352	QAWDRST VV	478	GFTFNDY Y	617	LSTGCTTT	760	TRADNYESSGYYPF DY	935

VR0000 01139	KLGDKF	286	QDS	316	QARVINTV V	479	GFTFSSYD	580	ISGSGGST	698	AKEDSYESTGYYPF DY	936
VR0000 02972	KLGDKF	286	QDS	316	QTWVSST VL	480	GFTFSSYA	557	ISGSGGIT	761	AKEDNYESTGYYPF DY	937
VR0000 04801	KLGDKF	286	QDS	316	QARDITTV V	481	GFTFSTSD	618	ISGSGGTT	710	AREDHYDSTGYYP FDY	938
VR0000 18183	RLGDKF	291	QDN	317	QTWVRST VL	482	GFTFSDY Y	528	ISSGTYTI	762	ARSEQWLDWYFDL	939
VR0000 18206	KLGDKF	286	QDT	352	QAWVSST VY	483	GFTFSDY Y	528	ITSSAYTI	763	VRVSYDSTGYYPFD Y	940
VR0000 29539	KLGDKF	286	QDN	317	QAWVRST VV	484	GFTFSDY Y	528	ISSSVSSS SVTI	764	ARESDTSGYDPFD H	847
VR0000 18304	KLGDKF	286	QDS	316	QSWDFSTV V	485	GSTFSDYS	619	ISSSTTL	765	ARESDTSGYNYFPD Y	941
VR0000 19296	KLGDKF	286	QDN	317	QTWDRST AV	486	GFTFSDY Y	528	ISGGGSTV	766	ARDHYDSSGYSYFD S	942
VR0000 18029	KLGDKF	286	QDN	317	QTWDRIT VV	487	GFTFSDY H	620	ISSGVSTI	767	ARICYDTSGYDYVD Y	943
VR0000 15340	KLGDKF	286	QDS	316	QAWVSST VV	488	GYTFTDY Y	621	INPNSGGT	768	ARDDSFESTGYYPFD Y	944
VR0000 28861	KLGDKF	286	QDN	317	QAWDSST VV	445	GYTFTGY Y	622	INPNSGGT	768	AREDYDTSGYSPFEY	945
VR0000 31297	RLGDKY	285	QDT	352	QAWDSST VV	445	GASISSGD W	623	IYHSGST	676	ARGTGYDSSGSYS YFDY	946
VR0000 15471	KLGDKY	231	QDS	316	QAWDSST AV	474	GYSISSN W	542	IYFSGST	675	ARKVGGYNYDYQL DY	947
VR0000 15787	KLGYKY	296	QDI	351	QAWDSST VL	489	GGSISSSD W	547	IHQSGST	769	VRGLGGSWSSDWG GFDY	948
VR0000 17797	KLGDKY	231	QDS	316	QAWDSST VV	445	GGSFSSY Y	624	INHSGNT	686	ARGGDYDSSGYYPF FDY	949
VR0000 13862	KLGDKY	231	QDS	316	QTWDSST VV	459	GGSFSGY Y	533	INHSGTT	713	AREGGLYDSSGSEY LOH	950
VR0000 13925	DLGDKY	297	QDT	352	QAWDSGT AV	462	GGSISSS YY	625	IYYSGST	704	ARPYDYDPLGY	951
VR0000 13641	KLGDKY	231	QDS	316	QAWDSST VV	445	GGSISSS YY	549	IYYSGST	704	ARQSLYNNWNPFDY	952
VR0000 16026	KLGDKY	231	QDS	316	QAWDSST VV	445	GGSISSDG YY	626	IHYSGIT	770	AGLVELLRTSDY	953
VR0000 13455	KLGNKD	298	QNS	354	QAWDSRT AV	490	GGSISSSR YY	627	INYSGRT	771	ARHEERGFDY	954
VR0000 12875	KLGDKF	286	QDR	349	QAWDRST VV	478	DDSIITYT YY	628	IHYSGST	772	ARHEVGGGFDY	955

VR0000 13031	KLGDKF	286	QDK	353	QAWDSSV V	491	GGISNSSS HY	629	IYYGGST	773	ARHDSSSDYFDF	956
VR0000 13185	KLGDKF	286	QDR	349	QAWDSSST VV	445	GGSIJFNSD FY	630	IYFSGNT	774	ARRVGAPDYFDY	957
VR0000 12856	KLGDKF	286	QDR	349	QAWDSSA VV	369	GGSIRSSD YY	631	IYFSGRT	775	ARREGPTDYFDY	958
VR0000 13715	KLGDKF	286	QDR	349	QAWDSSST VV	445	GGSISTSN YY	632	VNYSGNT	776	ARRIGDTDYFDY	959
VR0000 13471	KLGDKF	286	QDR	349	QAWDSSST V	492	GGISISSSS FY	555	IYFSGST	675	ARREPAADTLDY	860
VR0000 17649	RLGDF	299	QDN	317	QTWASST VV	493	GGSFSGY Y	533	INHSGGT	777	ARNFYDTSGFYSFDS	960
VR0000 17512	KLGDKF	286	QDN	317	QTWASST VV	493	GGSFSDY Y	556	INHNGGT	778	ARNFYDTSGFYSFDS	960
VR0000 17720	KLGD RF	300	QDN	317	QTWASST VV	493	GGSFSGY Y	533	INHSGST	722	ARSYQDSSGFSFSDY	961
VR0000 17506	KLGDKF	286	QDN	317	QAWASST VV	475	GGSFSDY Y	556	VNHSGST	779	ARGNYDTSGYNWF DP	962
VR0000 17785	KLGDKF	286	QDN	317	QAWDSRIV V	494	GGSFSGY Y	533	INHRGIT	780	ARGHPDTSGFYSFD	963
VR0000 13050	KLGDKF	286	QDN	317	QTWDFST VV	495	GGSISSSS HY	633	FYYSGNT	781	ARGDHDSSGYGYFD V	964
VR0000 13872	TLGDKF	301	QDN	317	QTDWNST VV	496	GGSVSST NYY	634	FFSGGGT	782	ARHSYDASGYDYFD Y	965
VR0000 13395	KLGDKF	286	QDN	317	QTWVFEST VV	497	GGSISSSG YY	635	IYYSGKT	783	ARHGTRHYESSGY QYEGYFDY	966
VR0000 13396	KLGDY	231	QDS	316	QAWDSSN VV	498	GGSISSSG YY	635	IYYSGKT	783	ARHGTRHYESSGY QYEGYFDY	966
VR0000 13186	KLGDY	231	QDN	317	QAWDSSST VV	445	GGSIGSRV YY	636	IYYAGNT	784	ARHVQLERRPYYYY YGMDV	967
VR0000 30698	QGIKND	265	AAS	310	LQHNSTPH T	499	GGSIKSSS HY	637	MYFGGDT	785	ARYNSGGDW/FDP	968
VR0000 30699	ALPKKY	232	EDS	318	YSTDSSGN HVV	449	GGSIKSSS HY	637	MYFGGDT	785	ARYNSGGDW/FDP	968
VR0000 13694	SLRSYY	278	GKN	343	NSRDSSGN HLV	500	GGSISSTS YY	638	IYYSGNT	719	ARHPAVAGTPFDY	969
VR0000 30523	SLRSYY	278	DKN	355	NSRDSSGA HWV	501	GGSISSGD SY	639	IYDSGYT	786	ARELLTGDDAFDI	970
VR0000 13879	SLRSYY	278	GKN	343	NSRDSSGN HLV	500	GGSISSNS YY	554	IFHGGNT	682	ARYV/AAPDYFDY	827
VR0000 13640	SLRRFY	302	GEN	356	NSRDSNV NHL	502	GGSISSSS YY	549	IYYSGST	704	ARQSLYNNWNPFDY	952

VR0000 17365	SLRSYY	278	GRN	357	NSRDISGD YVL	503	GGSFSGY Y	533	INHSGST	722	AREEWELGFDY	875
VR0000 15975	NLRSYF	303	GKN	343	NSRDSGGD HLV	504	GDSISSSG YY	640	IYVSGST	704	ARDRVGSTPDAFDI	821
VR0000 31085	ALPKKY	232	EDS	318	SSTDSSGN HVV	505	GGSISSGG YY	641	IYVSGIT	677	ARDRVGSTPDAFDI	821
VR0000 31175	SLRNNY	276	GKN	343	NSRDSGGD HLL	506	GGSITSGG YY	642	IYVTGTT	787	ATAGYGSWPDAFD I	971
VR0000 13926	ALPSQY	304	KDS	314	QSTVNSVG YVV	507	GGSISSSS YY	625	IYVSGST	704	ARPYVDIPLGY	951
VR0000 13927	ALPNHY	305	KDS	314	QSTDNSVG YVV	508	GGSISSSS YY	549	IYVSGST	704	ARPYVDIPLGS	972
VR0000 13617	ALPSQY	304	KDT	358	QSTVNSVG YVV	507	GGSISSSS YY	549	IYVSGTT	658	ARHDWYGGSYGWF DP	900
VR0000 13080	ALPKQY	227	KDS	314	QSADTSGT YVV	509	DGSISSGR YY	643	IHHSGST	788	ARQSLWFGPEGDY	973
VR0000 13464	ALPKQY	227	KDS	314	QSADSRGI WV	510	GGSISSSS DY	644	MHSSGST	789	ARHEVSGGFDY	974
VR0000 15855	ALPKQY	227	KDS	314	QSADSTGT WV	511	GGSISSSN W	590	IYHSGST	676	ARDGYYDGSYYSS FDR	975
VR0000 17631	ALPKKY	232	EDS	318	YSTDSSGN HRV	387	GGSFSGY Y	533	IKHSGST	790	AKRDYDTSGYDYFD	976
VR0000 17632	KLGDKF	286	QDN	317	QTWDSNT AV	512	GGSFSGY Y	533	IKHSGST	790	AKRDYDTSGYDYFD	976
VR0000 17768	NIGSKS	279	DDS	344	QVWDSSS DHRV	513	GGSFSGY Y	533	FIHSGST	791	ARGSMDSGFYSFDF	977
VR0000 15460	KIASKS	306	DDS	344	QIWDSSSD HVV	514	GYSISSSN W	542	IYFSGIT	670	ARNSKAYSPLYFYFD	978
VR0000 15461	KIASKN	307	DDS	344	QVWDSSS DHVV	451	GYSISSSN W	542	IYFSGST	675	AKNSKAYSPLYFYFD	979
VR0000 15464	NIGSKN	283	DDG	359	QVWDSSS DHVV	451	GYSISSSN W	542	IYFSGST	675	ARNSKAYSPLYFYFD	978
VR0000 15463	ALPKQY	227	KDS	314	QSADSSGT YVV	515	GYSISSSN W	542	IYFSGST	675	ARNSKAYSPLYFYFD	978
VR0000 15462	SSY	308	DVS	331	SSYTSSSTP DVV	516	GYSISSSN W	542	IYFSGST	675	ARNSKAYSPLYFYFD	978
VR0000 15459	QSISSW	237	KAS	322	QOQNSYA LT	517	GYSISSSN W	542	IYFSGIT	670	ARNSKAYSPLYFYFD Y	978
VR0000 17043	SLRNNY	276	GKN	343	NSRDSVVN HLL	518	GDSVSSN NIV	645	TYYRSKW YN	792	VREVLWFGPEPDP	980
VR0001 03638	RASQDIGNYL A	1456	SAST LOS	1486	QKYNSAPL T	1512	GFTFSTS WMN	1562	RIKSKIDG GTID	1607	GGPAFDI	1662

VR0001 03635	RSSQSLHVN GYNLMD	1457	LGSN RAS	1487	MOALQTP YT	1513	GFTFSTY NMN	1563	SISSSSSYIY	1608	DKVPGAFDY	1663
VR0001 03752	RASQGISSWL A	1458	AAAS LOS	1488	QQANSFPP T	1514	GFTFDDY AMH	1564	GISWNGGS ID	1609	DMGLEAAGPFYYGI DV	1664
VR0001 03741	RASQGIKNDL G	1459	AASS LOS	1489	LQHNSTPY T	1515	GGSFSDY YWS	1565	ESDYSGST K	1610	VPDSGSYDYFDF	1665
VR0001 03640	RASQGVSRW LA	1460	AASS LOS	1489	QQADSFPP T	1516	GFTFSNY NMN	1566	TITSSSTYI Y	1611	RHITPGGVDV	1666
VR0001 03630	RASQAISHYL A	1461	AASS LOS	1489	LQHNSTPR T	1517	GFTFSYS MN	1567	SIRRSSTYI Y	1612	HHDYSNNDAFDI	1667
VR0001 03633	RASQDIRNAL G	1462	IVSSL QG	1490	LQDYNYP YT	1518	GFIENY WMS	1568	NIKQDQSE KY	1613	EQQWL VPTSHYSGT GGTFDI	1668
VR0001 03720	SGDKLGKFA S	1463	QDSK RPS	1491	QAWDSTT VV	1519	GFTFSY YMS	1569	EISNRGITM Y	1614	RTPGEGWFDP	1669
VR0001 03726	SGDELGNKFA S	1464	QDNK RPS	1492	QAWDSSA VV	1520	GFTFSNY YMT	1570	DISNRAIT MN	1615	RTPGEGWFDP	1669
VR0001 03685	SGDVLAEKYA R	1465	KDSE RPS	1493	YSAANN LV	1521	GYAFTSY AFH	1571	WINAGNG NTK	1616	AVEDS	1670
VR0001 03679	TGTSSDVGNV NLVS	1466	EDSR RPS	1494	SSYAGSSW V	1522	GFTFSTY GMTY	1572	VISYDGS KY	1617	DPGSGTYHHYYG MDV	1671
VR0001 03756	TGTSSDVGGY SYVS	1467	DISR PS	1495	SSYTSNT LV	1523	GFTFDY AMH	1564	GISWNRDN IG	1618	DIRWGRSGWYPYY YSGMDV	1672
VR0001 03755	GGNNIGSKNV H	1468	DDSD RPS	1496	QVWDSRS DHVI	1524	GYPISSN WWG	1573	YIFESGYT Y	1619	KPGGYSAFYFDY	1673
VR0001 03695	GGNNIGSESV H	1469	GESD RPS	1497	QVWDS DYVV	1525	GFTFSDY YMI	1574	YISGTGSAI Y	1620	DFGSYAYYYYGMD V	1674
VR0001 03716	SGDKLGQY AS	1470	QDNK RPS	1492	QAWDSTT VV	1526	GFTFSYA MS	1575	AISGSGGR TY	1621	SMYYSDSSGSYYY GMDV	1675
VR0001 03677	SGDKLGKY AS	1471	QDHT RPS	1498	QAWDSNT VV	1527	GFTFSYA MS	1575	GISASGGG TY	1622	AHFDLTGYANYYY YGMDV	1676
VR0001 03732	SGDKLGKY VS	1472	QDRK RPS	1499	QTWDSST VV	1528	GFTFSYA MS	1575	AISGSGGS TY	1623	AVDYDSTGYPFY YGMDV	1677
VR0001 03721	SGDKLGKY AS	1471	QDRV RPS	1500	QTWDSNT VV	1529	GFTFSYA MS	1575	AISGSGGS TD	1624	AVDYDSTGYPFY YGLDV	1678
VR0001 03692	SGDKLGKY AS	1471	QDRT RPS	1501	QAWDSTT VV	1526	GFTFSYS LS	1576	AISGSGGT TY	1625	TLDYDSTGYPFY YGMDV	1679
VR0001 03678	SGDKLGKY AS	1471	QDRN RPS	1502	QTWDSST VV	1528	GFTFSYA MN	1577	VMSGGGG SLY	1626	TADFYDSSGYPFY YYGMDV	1680
VR0001 03710	SGDKLGKY AS	1471	QDSR RPS	1503	QAWDSTT VV	1526	VLTFSSY GMS	1578	AISGRGDS TH	1627	DFFGHYGSGYGPLF DY	1681
VR0001 03687	SGDRLGDKFA S	1473	QDNK RPS	1492	QTWDRSIA V	1530	GFIFSNYA IN	1579	SISGSGST S	1628	EGYDTSGYHPFDY	1682

VR0001 03749	SGDKLGDKFA S	1474	QDNK RPS	1492	QAWDRIT AV	1531	GFTFTNY DMT	1580	TISGSGGN TY	1629	LDSDTTGYDPFI	1683
VR0001 03736	SGDKLGDKFA S	1474	QDSK RPS	1491	QTWVANT VV	1532	GFTFSSYT MT	1581	VISGSGGA TS	1630	VNYDTTGYDPLDH	1684
VR0001 03672	SGEKLGDKFA S	1475	QDSK RPS	1491	QAWVRIT VV	1533	GFTFSSND MS	1582	GISGSGGS TD	1631	LDYDTTGYFPFDH	1685
VR0001 03744	SGDKLGDKFA Y	1476	QDKQ QDNK	1504	QTRVINTV V	1534	GFTFSSYD MN	1583	VISGSGGR TY	1632	MEYDSSGYSYFDY	1686
VR0001 03703	SGDKLGDKFA S	1474	QDNK RPS	1492	QTWDISTV V	1535	GFTFSTY DMS	1584	SVSGSGGN TY	1633	FDYDTSGYNYFDY	1687
VR0001 03681	SGDKLGDKFV S	1477	QDTK RPS	1505	QTWVTNT AV	1536	GFTFNNY AMN	1585	SISGSGGN TY	1634	EDADSTGYDPFDY	1688
VR0001 03674	SGDKLGDKFV S	1477	QDTK RPS	1505	QTWDEFTT VV	1537	GFTFSNY AMI	1586	TISGSGGN TD	1635	EDHDLTGYSPFDY	1689
VR0001 03731	SGDKLGDKFV S	1477	QDHS RPS	1506	QTWVSST AI	1538	GFTFSSYA MN	1577	SISGSGGP Y	1636	EGEDSTGYYPFDH	1690
VR0001 03702	SGDRLGDKY AS	1478	QDRN RPS	1502	QTWDSSTT WV	1539	GFTFSSA MS	1587	GISGSGGS TS	1637	DGDDYGDYDFDY	1691
VR0001 03740	SGDRLGDKY AS	1478	QDRN RPS	1502	QTWDSSTT WV	1539	GFTFSRSA MS	1588	GISGSGGS TS	1637	DGDDYGDYDFDY	1691
VR0001 03711	SGDKLGDKY AY	1479	QDRN RPS	1502	QAWDSST AV	1540	GFTFSSYA MN	1577	FISGSGGS Y	1638	DGSYFDSNGPDYFD Y	1692
VR0001 03739	SGDKLGDKFA S	1474	QDNK RPS	1492	QAWASST VV	1541	GFTFSDY YMS	1589	YLSSGGST RH	1639	LDVHESSGYYPFDY	1693
VR0001 03712	SGDKLGDKFA S	1474	QDTK RPS	1505	QAWDRIT VV	1542	GFTFSDY YMS	1589	YISSSGSTI Y	1640	LDNYDSTGYYPFDY	1694
VR0001 03663	SGHNLGDKFT S	1480	QDNK RPS	1492	QAWEST AI	1543	GFTFSDY YMS	1589	YISSGGSTI Y	1641	LDNYESSGYYPFDY	1695
VR0001 03680	SGDKLGDKFA S	1474	QDNK RPS	1492	QAWDSST VV	1526	GFTFSDY YMS	1589	YISTGGSAL Y	1642	QDNYESGFPYFDS	1696
VR0001 03765	SGDKLGDKFA S	1474	QDSK RPS	1491	QARVINTV V	1544	GFTFSSYD MS	1590	TISGSGGS Y	1643	EDSYESTGYYPFDY	1697
VR0001 03698	SGDKLGDKFA S	1474	QDSK RPS	1491	QTWVSST VL	1545	GFTFSSYA MD	1591	AISGSGGIT S	1644	EDNYESTGYYPFDY	1698
VR0001 03743	SGDKLGDKFV S	1477	QDSK RPS	1491	QARDITTV V	1546	GFTFSTSD MN	1592	AISGSGGT TY	1625	EDHYDSTGYYPFDY Y	1699
VR0001 03766	SGDKLGDKFA S	1474	QDTK RPS	1505	QAWVSST VV	1547	GFTFSDY YMS	1589	YITSSAYTI Y	1645	VSYDSTGYYPFDY	1700
VR0001 03700	SGEKLGDKFA S	1475	QDNK RPS	1492	QAWVRST VV	1548	GFTFSDY YMS	1589	YISSSVSS SSVTY	1646	EDSDTSGYDPFDH	1701
VR0001 03690	SGHKLGDKFA S	1481	QDSK RPS	1491	QSWDFSTV V	1549	GSTFSDYS MS	1593	FISSSSTTL Y	1647	EDSDTSGYNYFDY	1702

VR0001	SGDKLGDKFA	1474	QDNK	1492	QTDWRST	1550	GFTFSDY	1589	YISGGGST	1648	DHYDSSGYSFDS	1703
03728	S	RPS	RPS	AV	AV	YMS	YMS	VY	YISGGGST	1648	DHYDSSGYSFDS	1703
VR0001	SGDKLGDKFA	1474	QDNK	1492	QTDWRST	1551	GFTFSDY	1594	YISGGGST	1649	ISYDTSGYDYVDY	1704
03763	S	RPS	RPS	VV	VV	HMS	HMS	Y	YISGGGST	1649	ISYDTSGYDYVDY	1704
VR0001	SGDKLGDKFA	1474	QDSH	1507	QAWVSST	1552	GYTFIDY	1595	RINPNSGG	1650	DDSFESTGYYPFDY	1705
03729	S	RPS	RPS	VV	VV	YLH	YLH	TN	RINPNSGG	1650	DDSFESTGYYPFDY	1705
VR0001	SGDKLGDKY	1478	QDTK	1505	QAWDSST	1526	GASISSGD	1596	EIYHSGST	1651	GTGYDSDGSYSYF	1706
03714	AS	RPS	RPS	VV	VV	WWS	WWS	N	EIYHSGST	1651	GTGYDSDGSYSYF	1706
VR0001	SGDKLGKYK	1482	QDIK	1508	QAWDSST	1553	GGSISSSD	1597	EIHQSGST	1652	GLGGSWSSDWGGFD	1707
03691	AS	RPA	RPA	VL	VL	WWN	WWN		EIHQSGST	1652	GLGGSWSSDWGGFD	1707
VR0001	SGDKLGDKY	1479	QDST	1509	QAWDSST	1526	GGSISSDG	1598	YIHYSGITS	1653	LVELLRTSDY	1708
03686	AY	RPS	RPS	VV	VV	YWS	YWS		YIHYSGITS	1653	LVELLRTSDY	1708
VR0001	SGDKLGDKFV	1477	QDRK	1499	QAWDSSA	1520	GGSIRSSD	1599	DIYFSGRT	1654	REGPTDYFDY	1709
03673	S	RPS	RPS	VV	VV	YWG	YWG	Y	DIYFSGRT	1654	REGPTDYFDY	1709
VR0001	SGDKLGDKFA	1474	QDRR	1510	QAWDSST	1554	GGSISSSS	1600	SIYFSGSTY	1655	REPAADTLDY	1710
03754	S	RPS	RPS	VI	VI	FYWD	FYWD		SIYFSGSTY	1655	REPAADTLDY	1710
VR0001	SGDKLGDKFA	1474	QDNK	1492	QTWASST	1555	GGSFSDY	1565	EINHNGGT	1656	NFYDTSGFYSFDS	1711
03697	S	RPS	RPS	VV	VV	YWS	YWS	N	EINHNGGT	1656	NFYDTSGFYSFDS	1711
VR0001	SGDKLGDKFA	1474	QDNK	1492	QAWDSRIV	1556	GGSFSGY	1601	EINHNGITN	1657	GHPDTSGFYSFDY	1712
03675	S	RPS	RPS	V	V	YWT	YWT		EINHNGITN	1657	GHPDTSGFYSFDY	1712
VR0001	SGHKLGDKFA	1481	QDNK	1492	QTDWFST	1557	GGSISSSS	1602	YFYYSNGT	1658	GDHDSGGYGYFDV	1713
03725	S	RPS	RPS	VV	VV	HYWG	HYWG	Y	YFYYSNGT	1658	GDHDSGGYGYFDV	1713
VR0001	QGDLSRYYA	1483	DKNN	1511	NSRDSSGA	1558	GGSISSGD	1603	YIYDSGYT	1659	ELTGDPAFDI	1714
03724	S	RPS	RPS	HWV	HWV	SYWS	SYWS	D	YIYDSGYT	1659	ELTGDPAFDI	1714
VR0001	SGDALPSQYA	1484	KDSE	1493	QSTVNSVG	1559	GGSISISS	1604	SIYYSGST	1660	PYYDIPLGY	1715
03706	Y	RPS	RPS	YVV	YVV	YYWG	YYWG	Y	SIYYSGST	1660	PYYDIPLGY	1715
VR0001	SGDALPNHYA	1485	KDSE	1493	QSTDNSVG	1560	GGSISSSS	1605	SIYYSGST	1660	PYYDIPLGS	1716
03676	Y	RPS	RPS	YVV	YVV	YYWG	YYWG	Y	SIYYSGST	1660	PYYDIPLGS	1716
VR0001	SGDKLGDKFA	1474	QDNK	1492	QTDWSNT	1561	GGSFSGY	1606	EIKHSGST	1661	RDYDTSGYDYFDY	1717
03727	S	RPS	RPS	AV	AV	YWS	YWS	N	EIKHSGST	1661	RDYDTSGYDYFDY	1717

Table 6: VH/VL SEQ ID NOS of Fv clones

CLONE ID	VH	SEQ ID NO	VL	SEQ ID NO
VR0000	EVQLVESGGGLVOPGSLKLSCAASGFTFSGSAMHWVROASGK GLE	981	QSALTOPASVSGSPGQSITISCTGTSSDVGNVNLVSWYQOHP	1198
06753	WVGRVRSKADSSATAYASAYKGRFAISRDSKNTAYLQMNLSLKTED		GKAPKLMYEGSKRPSGVSNRFSGSKSGNTASLTISGLQAEDE	
	TAVYYCTSGTYFYGFDIWGQGTMTVSS		ADYYCCSYAGSTLVFGGGLTKLTVL	
VR0000	EVQLVESGGGLVOPGSLKLSCAASGFTFSGSAMHWVROASGK GLE	981	DIQMTQSPASMSAVGDIVTITCRASQGISNLYLAWFOOKPGK	1199
06752	WVGRVRSKADSSATAYASAYKGRFAISRDSKNTAYLQMNLSLKTED		VPKRLIYAASSLQSGVPSRFSFGSGSGTEFTLTITSLQPEDFATY	
	TAVYYCTSGTYFYGFDIWGQGTMTVSS		YCLQHNSTPYTFGQGTCKLEIK	

VR0000 06671	EVQLVESGGGLVMPGGSLRLSCAASGFTFSNAWMTWVRQAPGKGL EWMGRKSKTDGGTIYYAAPVKGRFTISRDNKNTLYLRINSLTJEDT AVYYCTTELTVGPFDPYWGGQGLVTYSS	982	DIQMTQSPSAVSASVGDSTVITTCRASQGGISNYLAWFQOKPGK VPRKRLIYAASSLQSGVPSRFSGSGSTIEFTILTISLQPEDFATY YCLQHNSTPLTFGGGTLKVEIK	1200
VR0000 00648	ELQLVESGGDLVKPGGSLRLSCATSGFTFTSWMNMWVRQAPGKGLE WYGRKSKIDGGTIDYAAPVKGRFTISRDNKNTLYLQMNSLKTEDT AVYYCTTGPAFDIWGGQGMVTYSS	983	DIQMTQSPSSLASVGDRAVITTCRASQDIGNYLAWYQOKPGK LPLKLIVSASTLQSGVPSRFSGSGSTIDFTILTISLQPEDVVIY YQCKYNSAPLTFGGGTLKVEIK	1201
VR0000 00718	EVKLEESGGGLVQPGGSMKLSCVASGFTFSNYWMNMWVRQSPKGL EWMVAEIRLKSNNTYATHYAESVKGRFTISRDDSSYYLQMNNLKPE DTGIYYCTRTDYYWGGQGLVTYSS	984	NYLTQSPASLAVSLQORATISCRASESVDRYGNSLMHWYQQ KPGQPKRLIYLAASLESQVPAFRFSGSGRTDFTILTIDPVEVD DAATYYCHQNNEDPSTFGGGTLKLEIK	1202
VR0000 07022	EVQLVESGGGLVQPGGSLRLSCAASGFTFSRYWMHWVRQGPCKGL LWVSRINNAGNSRYSADSVKGRFTISRDNKNTLYLQMNSLRAEDT AVYYCSRAGNWDRTDFDIWGGQGMVTYSS	985	DIVMTQSPSLPVTPEEPASISCRSSQSLHSHNGYNCLGWYLQ KPGQSPQLIYLTGNSRASGVPDFRFSGSGSTIDFTILTISRVEAE DVGIYSCMQALQTPYTFGGQTLQIK	1203
VR0000 07349	EVQLVESGGGLVQPGGSLRLSCAASGFTFSRYWMHWVRQAPGKGL VMVSRINNIGNSRYSADSVKGRFTISRDNKNTLYLQMNSLSAEDTA VYYCARAGNWDRTDFDIWGGQGMVTYSS	986	SYELTQPPSVSVSPGQTARITCSGDALPKQYAYWYQOKPGQ APVLVMYKDSERPSGIPERFSGSNSGTTVTLTISGYQAEDEAD YYCQASADSSGTVVFGGGTKLTVL	1204
VR0000 07442	EVQLVESGGGLVQPGGSLRLSCAASGFTFTSYWMHWVRQAPGKGL VMVSRINNAGNSRYSADSVKGRFTISRDNKNTLYLQMNSLRAEDT AVYYCARAGNWDRTDFDIWGGQGMVTYSS	987	QSVLTQPPSVSGAPGQRAVITISCTGSSSNIGAGYDVHWYQQLP GTAPKRLIYGNNSRPSGYPDFRFSGSGTSASLAIITGLQAEDE ADYYCOSYDSSLSGSGVFGGGTKLTVL	1205
VR0000 18284	QVQLVESGGGLVKPGGSLRLSCAASGFTFSVYYMSWIRQAPGKGLE WVSEISNRGITMYYADSVKGRFTISRDNKAKSLYMQMNSLRAEDTA VYYCARRTPEGEWFDPMWGGQGLVTYSS	988	SYELTQPPSVSVSPGQTANITCSGDKLGNKFACWYQOKPGQS PVVVITYQDSKRPSGTPERLSGNSNGNTATLTISGTQAMDEAD YYCQAWDSTTVVFGGGTKLTVL	1206
VR0000 18285	QVQLVESGGGLVKPGGSLRLSCAASGFTFSVYYMSWIRQAPGKGLE WVSEISNRGITMYYADSVKGRFTISRDNKAKSLYLQMNTLRAEDTA VYYCARRTPEGEWFDPMWGGQGLVTYSS	989	SYELTQPPSVSVSPGQTANITCSGDKLGNKFACWYQOKPGQS PVVVITYQDSKRPSGTPERLSGNSNGNTATLTISGTQAMDEAD YYCQAWDSTTVVFGGGTKLTVL	1206
VR0000 18321	QVQLVESGGGLVKPGGSLRLSCEASGFTFSVYYMTWIRQAPGKGLE WVSEISNRGITMYYADSVKGRFTISRDNKAKSLYLQMNSLRAEDTA VYYCARRTPEGEWFDPMWGGQGLVTYSS	990	SYELTQPPSVSVSPGQTANITCSGDKLGNKFACWYQOKPGQS PVVVITYQDSKRPSGTPERLSGNSNGNTATLTISGTQAMDEAD YYCQAWDSTTVVFGGGTKLTVL	1207
VR0000 18340	QVQLVESGGGLVKPGGSLRLSCTASGFTFSNYMTWIRQAPGKGLE WVSDISNRALTMMYADSVKGRFISRDNKAKSLYLQMNSLRAVEDTA VYYCARRTPEGEWFDPMWGGQGLVTYSS	991	SYELTQPPSVSVSPGQTANITCSGDELGNKFACWYQOKPGQS PVVVITYQDNKRPSGTPERLSGNSNGNTATLTISGTQAMDEAD YYCQAWDSSAVVFGGGTKLTVL	1208
VR0000 18053	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMNMWIRQAPGKGLE WVSYISNRSFTKIFYADSVKGRFTISRDNKAKSLYLQMNSLRAVEDTA VYYCARRTPEGEWFDPMWGGQGLVTYSS	992	SYELTQPPSVSVSPGQTARITCSGDALPKKYAYWYQOKSGQ PVLVIYQDNKRPSGIPERFSGSNSGNTATLTISGTQAMDEADY YCQAWDNSTTVFGGGTKLTVL	1209
VR0000 18067	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMNMWIRQAPGKGL EWMVSSISNRGSTIYYADSVKGRFTISRDNKAKSLYLQMNSLRAEDTA VYYCARMAGTGYEDYWGGQGLVTYSS	993	SYELTQPPSVSVSPGQTARITCSGDALPKKYAYWYQOKSGQ APVLVIYEDSKRPSGIPERFSGSSGTMATLTISGAQVEDEAD YYCYSTIDSSGNHSHWVFGGGTKLTVL	1210
VR0000 06497	EVQLVESGGGLVKPGGSLRLSCAASGFTFSRYSMNMWVRLAPGKGLE WVSSFSTGSSYIYYADSVTGRFTISRDNKAKSLYLQMNSLRAEDTAV YXCARNWDPDYWGQGLVTYSS	994	QSVLTQPPSASGTPGORVTISCSGSSSNIGSNVYVWYQQLPQT APKLAIYNNQRPSPGYPDFRFSGSGTSASLAIISGLRSEDEAD YYCAAWDDSLSGPWVFGGGTKLTVL	1211
VR0000 06623	EVQLVESGGGLVKPGGSLRLSCAASGFTFSTYNNMNVVRQGPCKGLE WVSSISSSSSYIYHADSVKGRFTISRDNKAKNSLYLQMNSLRAEDTAV YXCARDKVPGAFDYWGGQGLVTYSS	995	QAVLTQPPSSLASPGASASLTCTLRSGINVGTYRIYWYQOKP GSPPOYLRLRYKSDSDKQQQSGVPSRFSGSGKASANAGILLISG LQSEDEADYYCMVWHSSAVVFGGGTKLTVL	1212

VR0000 31018	QVQLQESGPGLVKPSQTLSTLCTVSGGSINSGDYFWSWTRQHPGKGL LEWIGHIYSGTTYGNPNPSLKSRAVTISVDTSKNQFSLKLSSTVTADTA VYCARSNWGFDDYWGQGTLLTVYSS	996	DIVMTQSPSSLTVTAGELVTIMCKSSQSLNSENQKNYLTW YQOKPGQPKFLIYWASTRDSGVPRFTGSGSGTDFTLTISSTV QAEELAVYYCONDYGYPLTFGAQTKLEIK	1213
VR0000 15506	QVQLQESGPGLVKPSSETLPLCTVSGVSISSSYHWGWIRQPPGKGL EWIGSIYGGNSHYNPSLKSRAVTMSVDTSKNHFSLLNLSVTAAADTA VYYCASHYPPDYWGQGTLLTVYSS	997	DIQMTQSPSTLSASVGDRAVITTCRASQSIIRWLAWYQOKPGK APNLIIYKASLLEGGVPSRFSGSGSGTEFTLTISLQPDDEFATY YCCQYNYSYWTFGGQTKVEIK	1214
VR0000 17764	QVQLQQWGAAGLLKPSSETLSTCAVYGGSGFYYSWVIRQSPGKGLE WIGELNQSGRTINNPSLKSRAVTISVDTPKNQFSLKLSVTAAADTA VYYCARAEWELLGFDDYWGQGTLLTVYSA	998	DIQMTQSPSTLSASVGDRAVITTCRASQSISSWLAWYQOKPGK APKLIIYKASLLEGGVPSRFSGSGSGTEFTLTISLQPDDEFATY YCCQYNTYSWTFGGQTKVEIK	1215
VR0000 31821	QVQLVQSGAEVKKPGASVKASCASGFIETKYNNHWVRQAPGQGL EWMGINPSGGSSTSSAQKFOGRAVTMTDRDITSTVYMELSSLRSEDTA VYYCAREGGELYGMDVWGQGTITVYSS	999	DIQMTQSPSSLASVGDRAVITTCRASQDISNWLAWYQOKPGK APKSLIYTAASLQSGVPSKFSGSGSGTDFTLTISLQPEDLATY YCCQYNSYPTTFGGQTKLEIK	1216
VR0000 15603	QVQLQESGPGLVKPSSETLSTLCTVSGVSISSYWNWIRQAPGKGLEW IGRIYSSGSTINPNPSLKSRAVTMSADTSKNQFSLKLSVTAAADTA VYYCAREFPGSYPFDYWGQGTLLTVYSS	1000	EIVLTQSPGTLSPGERATLSCRASQSVSRSLAWYQOKPGQ QAPRLIYGASNRATGIPDRFSGSGSGTDFTLTISRLEPEDIAV YVLCQYQYGSPPITLGGQTRLEIK	1217
VR0000 06496	EVQLVESGGGLVKPGGSLRLSCAASGFTFSRYSMNWVRLAPGKGLE WVSSFSTGSSYIYADSVTGRFTISRDNAKNSLYLQMNSLRAEDTA VYYCARNWDFEDYWGQGTLLTVYSS	994	EIVLTQSPGTLSPGERATLSCRASQSVSSSLAWYQOKPGQ APRLIYGASNRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVY YCCQYQYGSPPYTFGGQTKLEIK	1218
VR0000 30726	QVQLQESGPGLVKPSSETLSTLCTVSGGISNFWSWIRQAPGKGLEW IGRIASAGRINPNPSLKSRAVTMSIDTSKNQFSLKLSVTAAADTA VYCARWLAFDYWGQGTLLTVYSS	1001	EIVLTQSPGTLSPGERVILSCRASQSVSSSLAWYQOKPGQ APRLIYVASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVY YCCQYQYGSPPYTFGGQTKVEIK	1219
VR0000 09731	EVQLVQSGAEVKKPGESLKISKSGSYFTSYWIGWVRQMPGKGLE WMGIIIDPSDSYTRYSPSFQGVYTISADKSISTAYLQWSSLKASDTAM VYYCARMYKGRGHLFDYWGQGTLLTVYSS	1002	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQOKPGQ APRLIYGASTRATGIPARFSGSGSGTEFTLTISLQSEDFAVY YCCQQLLWPRRTFGGQTKVEIK	1220
VR0000 34880	EVQLVQSGAEVKKPGESLKISKSGSYFTSYWIGWVRQMPGKGLE WMGIIYPGSDTRYSPSFQGVYTISADKSISTAYLQWSSLKASDTAM VYYCARVRAGVYGFDDYWGQGTLLTVYSS	1003	EIVLTQSPATLSVSPGERATLSCRASQSVAKWLAWYQOKPGQ APRLIYASNRATGIPARFSGSGSGTDFTLTISRLEPEDFAVY YCCQQFKNWPITFGGQTKVEIK	1221
VR0000 28040	QVQLVQSGAEVKKPGSSVKVCSKASGGTLSGYGVSWVRQAPGQGL EWMGNIPGFGTANYAQKFOGRAVTITADESTAYMELSSLRSEDTA VYYCARSGGTKYGMILDVWGQGTIMTVYSS	1004	EIVLTQSPATLSVSPGERATLSCRASQSVSKALAWYQOKPGQ APRLIYASNRATGIPARFSGSGSGTDFTLTISRLEPEDFAVY YCCQYRYRAPYTFGGQTKVEIK	1222
VR0000 28042	QVQLVQSGAEVKKPGSSVKVCSKASGGTLSHYGVSWVRQAPGQGL EWMGNIPGIGTANYAQKFOGRAVTITADESTAYMELSSLRSEDTA VYYCARSGGTKYGMILDVWGQGTIMTVYSS	1005	EIVLTQSPATLSVSPGERATLSCRASQSVSKALAWYQOKPGQ APRLIYASNRATGIPARFSGSGSGTDFTLTISRLEPEDFAVY YCCQYRYRAPYTFGGQTKVEIK	1222
VR0000 28041	QVQLVQSGAEVKKPGSSVKVCSKASGGTLSGYGVSWVRQAPGQGL EWMGNIPGFGTANYAQKFOGRAVTITADESTAYMELSSLRSEDTA VYYCARSGGTKYGMILDVWGQGTIMTVYSS	1004	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQOKPGQ APRLIYGASTRATGIPARFSGSGSGTEFTLTISLQSEDFAVY YCCQQLLWPRRTFGGQTKVEIK	1220
VR0000 49105	QVQLVQSGAEVKKPGSSVKVCSKASGGTFSSYAIHWVRQAPGQGL WMGYRPEYGNANYAQKFOGRAVTITADESTAYMELSSLRSEDTA VYYCARGPSWLLYGRYFDDYWGQGTLLTVYSS	1006	EIVLTQSPATLSVSPGERATLSCRASQSVSSSLAWYQOKPGQ APRLIYDASNRATGIPARFSGSGSGTDFTLTISRLEPEDFAVY YCCQQRSNWPLTFGGQTKVEIK	1223
VR0000 30804	QVQLQESGPGLVKPSSETLSTLCTVSGGISNFWWIRQPPGKGLEW GYLCYSGSSNYPNPSLKSRAVTISVDTSKNQFSLKLSVTAAADTA VYYCC AAGYSSGWYLDHWGQGTLLTVYSS	1007	EIVLTQSPATLSVSPGERATLSCRASQSVSSSLAWYQOKPGQ PRLIYDASNRATGIPARFSGSGSGTDFTLTISRLEPEDFAIYYC QQRSNWPLTFGGQTKVEIK	1224

VR0000 15467	QVQLQESGPGLVKPSDTLSTLCTCAVSGYSISSSNWGWIRQPPGKGLE WIGIYFSGITYNPSLSKSRVTMSVDTSKNQPSLKLNSVTAVDTAVY YCARKKGAYDYANALDIWGOQIMYTVSS	1008	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQ APRLIYDASNRAATGIPARFSGSGGTDFLTITISLEPEDFAVY YCOQRSNWLTFGGGTLKVEIK	1225
VR0000 29504	QVQLVQSGTEVKKPGASVKVSCKVSGYTLTELANHWVRQAPGKGL EWMGFDEPDEGTIYAQKFOQGRVTMTEDTSTDTAYMELSLRSEDT AVVYCAAGLYYEDYWGOQTLVTSS	1009	DIQMTPQSTLSASVGDRAVNTICRASQSISSGWLAWYQQKPGK APKLIVEASLSLESGVPSRFSGSGSGTEFTLTITISLQPPDFAITY YCOQYNYSRTFGQTKVEIK	1226
VR0000 29505	QVQLVQSGTEVKKPGASVKVSCKVSGYTLTELANHWVRQAPGKGL EWMGFDEPDEGTIYAQKFOQGRVTMTEDTSTDTAYMELSLRSEDT AVVYCAAGLYYEDYWGOQTLVTSS	1009	SYELTQPPSVSVSPGQOTARITCSGDALPKKYAYWYQQKSGQ APVLVIYEDSKRPSGIPERFSGSSGTMTATLTISGAQVEDEAD YYCYSTDSSGNHRVYFGGGTKLTVL	1227
VR0000 19738	QVQLVQSGAEVKKPGASVKVSCKASGYAFTSYAFHWVRQAPGQRL EWMGWINAGNGNTEKYSQKFOQGRVTTIRDTASTAYMELSLRSEDT AVVYCVRAVEDSWGOQALVTSS	1010	SYELTQPPSVSVSPGQOTARITCSGDVLAERYARWFOQKPGQA PVLVIYKDSERPSPGIPERFSGSGTGTITLTISGAQVEDEADY YCYSAANNNLVFGGGTKLTVL	1228
VR0000 29862	QVTLRESGPALVKPTQITLTCTFSGFSLSTSGMSVSWIRQPPGKALE WLGLIDWDDDKYYSTLSKTRLTISKDTSKNQVVLTMTNMDPVDTA TYCCALIPGYWGOQTLVTSS	1011	EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQ APRLIYGASSRATGIPDRFSGSGGTDFLTITISLEPEDFAVY YCOQYGSPPYTFGGGTLKLEIK	1229
VR0000 29864	QVTLRESGPALVKPTQITLTCTFSGFSLSTSGMSVSWIRQPPGKAL EWLALIDWRDDKfySTLSKTRLTISQDTSKNQVVLTMTNMDPVDTA TYFCAGIPGYWGOQTLVTSS	1012	QSALETQPPSVASGSPGQSVTISCTGTSSDVGGYNYVSWYQQHP GKAPKLMIYEVSKRPSGVPDRFSGSKSGNTASLTYSGLQAED EADYYCSSYAGSNNNVYFGGGTKLTVL	1230
VR0000 15458	QVQLQESGPGLVKPSDTLSTLCVSGYSISSSNWGWIRQPPGKGLE WIGIYFSGSTYNNPSLESRTVTMSIDTSKNQPSLKLNSVTAVDTAVY YCARKRGPYDGYNGFDYWGOQTLVTSS	1013	QSALETQPPSVASGSPGQSVTISCTGTSSDVGGYNYVSWYQQHP GKAPKLMIYEVSKRPSGVPDRFSGSKSGNTASLTYSGLQAED EADYYCSSYAGSNNNLYFGGGTKLTVL	1231
VR0000 15790	QVQLQESGPGLVKPSGTLSTLCVSGGSISSSDWWSWVRQPPGKGL EWIGEIYHSGSTNNPSLSKSRVTISVDKSKNQPSLKLNSVTAAADTAV YYCARDSTYSGWYAPLDYWGOQTLVTSS	1014	QSALETQPPSVASGSPGQSVTISCTGTSSDVGGYNYVSWYQQHP GKAPKLMIYEVSKRPSGVPDRFSGSKSGNTASLTYSGLQAED EADYYCSSYAGSNNNLYFGGGTKLTVL	1231
VR0000 31164	QVQLQESGPGLVKPSQTLSTLCTVSGGSISSSGFYWGWIROHPGKGL DWIGIYIYSGITTYNPSLSKSRVTISVDTSKNQPSLKLNSVTAAADTAV YFCARDRVGSTPDADFIDWGOQIMYTVSS	1015	QSALETQPPSVASGSPGQSVTISCTGTSSDVGGYNYVSWYQQHP GKAPKLMIYEVNKRPSGVPPDRFSGSESGNTASLTYSGLQAED EADYYCSSYAGSTIDYVYFGGGTKLTVL	1232
VR0000 15791	QVQLQESGPGLVKPSGTLSTLCVSGGSISSSDWWSWVRQPPGKGL EWIGEIYQSGSTTYNPSLSKSRVTISVDKSKNQPSLKLSSVTAAADTAVY YCVRALGGSWSSDWGFDYWGOQTLVTSS	1016	QSALETQPPSVASGSPGQSVTISCTGTSSDVGGYNYVSWYQQHP GKAPKLMIYEGSKRPSGVSNRFSGSKSGNTASLTISGLQAEDE ADYYCCSYVSGSTFYVYFGGGTKLTVL	1233
VR0000 30727	QVQLQESGPGLVKPSSETLSLCTVSGGSISSSYFWSWIRQAPAGKGLEW IGRISASGRINYNPSLSKSRVTMSIDTSKNQPSLKLTSVTAAADTAVFYC ARQWLAFDYWGQGTLTVTSS	1001	QSALETQPPSVASGSPGQSVTISCTGTSSDVGGYNYVSWYQQHPG KAPKLMIYEGSKRPSGVSNRFSGSKSGNTASLTISGLQAEDEA DYCCCSYAGSSTIYVYFGGGTKLTVL	1234
VR0000 13041	QLQLQESGPGLVKPSSETLSLCTSVSGGSISSSYWGWIROPPGKPE WIGSIYHSGSTTYNPSLSKSRVTIFVDTSKNQFSVKLSSVTAAADTAVY YCARQPLYNWNPFDYWGOQTLVTSS	1017	QSALETQPPSVASGSPGQSVTISCTGTSSDVGGYNYVSWYQQHPG KAPKLMIYEGSKRPSGVSNRFSGSKSGNTASLTISGLQAEDEA DYCCCSYAGSSTIYVYFGGGTKLTVL	1234
VR0000 15980	QVQLQESGPGLVKPSQTLSTLNCITYSGGSISSGAYYWTWIRQHPGKGL EWIGFIHYSGGIYTPSLESRTISLDTSKNHFSKLNSLTAAADTAVY YCARGDLYFDYWGOQTLVTSS	1018	QSALETQPPSVASGSPGQSVTISCTGTSSDVGGYNYVSWYQQHPG KAPKLMIYEDSKRPSGVSNRFSGSKSGNTASLTISGLQAEDEA DYCCCSYAGSSTIYVYFGGGTKLTVL	1235
VR0000 11862	HLQLQESGPGLVKPSSETLSLCTVSGGSISSGTIFYWGWIRQPPGKRL WIGSFYCGSTTYNPSLSKSRITISVDTSRNHFSKLTSLTAAADTAVFY CARAWPYFYFDYWGOQTLVTSS	1019	QSALETQPPSVASGSPGQSVTISCTGTSSDVGGYNYVSWYQQHPG EAPKLMIYEGSKRPSGVSNRFSGSKSGNTASLTISGLQAEDEA DYCCCSYSGSTIIFGGGTKLTVL	1236

VR0000 15665	QVQLQESGPGLVKPSGTLSTCAVYSGAISSSDWWVSWVRQPPGKGL EWIGELSHSGTNNPNSLKSRTVISVDKSKNQFLKLSVTAADTAVY YCARREGDWLEPDYWGQGLVTYSS	1020	QSAITQPASVSGSPGQSTITCTGTSSDVGSYNLVSWYQOHPG KAPKLMIEGSKRPSGVSNRFGSGKSGNTASLTISGLQAEDEA DYCCSYAGSSTVYFGGGTLTYL	1237
VR0000 13877	QLQVQESGPGLVKPSSETLSTCTVSGDSITNSNYWGWIRQPPGKGL EWIGSIFHGNTYNNPSLKSRTVISVDTSKNQFSLRLRSVTAADTAV YYCARYVAAPDYFDYWGQGLVTYSS	1021	QSAITQPASVSGSPGQSTITCTGTSSDVGSYNLVSWYQOHPG KAPKLMIEGSKRPSGVSNRFGSGKSGNTASLTISGLQAEDEA DYCCSYAGSSTVYFGGGTLTYL	1238
VR0000 13880	QLQVQESGPGLVKPSSETLSTCTVSGGSISNSNYWGLIRQPPGKGL WIGSIFHGNTYNNPSLKSRTVISVDTSKNQFSLRLRSVTAADTAVY YCARVVAAPDYFDYWGQGLVTYSS	1022	QSAITQPASVSGSPGQSTITCTGTNSDVGSYNLVSWYQOHP GKAPKLMIEGSKRPSGVSNRFGSGKSGNTASLTISGLQAEDE ADYYCCSYAGSSTVYFGGGTLTYL	1239
VR0000 12858	QLLVQESGPGLVKPSSETLSTCTVSGGSISNSNYWGWIRQPPGKGL EWIGSIFHGNTYNNPSLKSRTVISVDTSKNQFSLRLRSVTAADTAV YYCARYVAAPDYFDYWGQGLVTYSS	1023	QSAITQPASVSGSPGQSTITCTGTSSDVGGYNNYVSWYQOHP GKAPKLMIEGSKRPSGVSNRFGSGKSGNTASLTISGLQAEDE EADYYCCSYTSSSTVYFGGGTLTYL	1240
VR0000 13470	QLQVQESGPGLVKPSSETLSTCTVSGGSISSSSFYWDWIRQPPGKGL WIGSIFSGSTISVDTSKNQFSLKLSVTAADTAAAYCARREPAADTL DCWGQGLVTYSS	1024	QSAITQPASVSGSPGQSTITCTGTSSDVGGYNNYVSWYQOHP GKAPKLMIEGSKRPSGVSNRFGSGKSGNTASLTISGLQAEDE EADYYCCSYTSSSTVYFGGGTLTYL	1240
VR0000 17500	QVQLQVWGAGLLKPSSETLSTCAVYGGSFSDYYWNNWIRQPPGKGL EWWGEINHTGSTDYNNPSLKSRTVISVDTSKFQFSLRLSSVTAADTAV YYCARGGGWGSDDYFDYWGQGLVTYSS	1025	QSAITQTPASVSGSPGQSTITCTGTSSDVGGYNNYVSWYQOHP GKAPKLMIEGSKRPSGVSNRFGSGKSGNTASLTISGLQAEDE EADYYCCSYTSSSTVYFGGGTLTYL	1241
VR0000 17514	QVQLQVWGAGLLKPSSETLSTCAVYGGSFSDYYWNNWIRQPPGKGL WIGELNHSNTNYPNSLKSRTVISVDPSKNQFSLKLSVTAADTAVY YCARREWEWLGDFEWGQGLVTYSS	1026	QSAITQPASVSGSPGQSTITCTGTSSDVGGYNNYVSWYQOHP GKAPKLMIEGSKRPSGVSNRFGSGKSGNTASLTISGLQAEDE EADYYCCSYTSSSTVYFGGGTLTYL	1242
VR0000 17528	QVQLQVWGAGLLKPSSETLSTCAVYGGSFSDYYWNNWIRQPPGKGL WIGQIHHSNGTNNPNSLKSRTVISVDTSKNQFSLKLSVTAADTAVY YCASTWAVAGFDYWGQGLVTYSS	1027	QSAITQPASVSGSPGQSTITCTGTSSDYGGINFVSWYQOHPD KAPKLMIEGSKRPSGVSNRFGSGKSGNTASLTISGLQAEDEA DYCCSYTSSSTVYFGGGTLTYL	1243
VR0000 17602	QVQLQVWGAGLLKPSSETLSTCAVYGGSFSDYYWNNWIRQPPGKGL EWIGQIHHSNGTNNPNSLKSRTVISVDTSKNQFSLKLSVTAADTAV YCASTWAVAGFDYWGQGLVTYSS	1028	QSAITQPASVSGSPGQSTITCTGTSSDYGGINFVSWYQOHPD KAPKLMIEGSKRPSGVSNRFGSGKSGNTASLTISGLQAEDES DYCCSYTSSSTVYFGGGTLTYL	1244
VR0000 03047	EVQLLESGGGLVQPGGSLRLSCAASGFTSSYAMNWWVRQAPGKGL WVSGVSGGLTTYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTA YYCAKEDYDSTGYPPDYWGQGLVTYSS	1029	QSAITQPASVSGSPGQSTITCTGTSSDVGSYNLVSWYQOHPG KAPKLMIEGSKRPSGVSNRFGSGKSGNTASLTISGLQAEDEA DYCCSYAGSSTVYFGGGTLTYL	1245
VR0000 17983	QVQLVESGGGLVKPGGSLRLSCAASGFTSSYQMSWIRQAPGKGL CVSYISSSGYTTYADSVKGRFTISRDNAKNSLFLQMNSLRAEDTAV YFCAREDDYDSTGYNPFDDYWGQGLVTYSS	1030	QSAITQPASVSGSPGQSTITCTGTSSDVGSYNLVSWYQOHPG KAPKLMIEGSKRPSGVSNRFGSGKSGNTASLTISGLQAEDEA DYCCSYAGSSTVYFGGGTLTYL	1246
VR0000 17618	QVQLQVWGAGLLKPSSETLSTCAVYGGSFSDYYWNNWIRQPPGKGL WIGELIDHSGITNNYSLMSRVTISVDTSKNQFSLKLSVTAADTAVY YCARGRSDSSGYTFDYWGQGLVTYSS	1031	QSAITQPASVSGSPGQSTITCTGTSSDVGSYNLVSWYQOHPG KAPKLMIEGSKRPSGVSNRFGSGKSGNTASLTISGLQAEDEA DYCCSYAGSSTVYFGGGTLTYL	1238
VR0000 06535	EVQLVESGGGLVKPGGSLRLSCAASGFTSSYKMNWVRQAPGKGL WVSSISRSSSYTYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAV YYCARHHDYNSDAFIDWGGQGLVTYSS	1032	QSAITQPASVSGSPGQSTITCTGTSSDVGSYNLVSWYQOHPG KAPKLMIEGSKRPSGVSNRFGSGKSGNTASLTISGLQAEDEA DYCCSYAGSSTVYFGGGTLTYL	1234
VR0000 06523	EVQLVESGGGLVKPGGSLRLSCAASGFTSSYKMNWVRQAPGKGL WVSSISRSSSYTYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTA YYCARHHDYNSDAFIDWGGQGLVTYSS	1033	QSAITQPASVSGSPGQSTITCTGTSSDVGSYNLVSWYQOHPG KAPKLMIEGSKRPSGVSNRFGSGKSGNTASLTISGLQAEDEA DYCCSYAGSSTVYFGGGTLTYL	1234

VR0000 06526	EVQLVESGGGLVKPGGSLRLSCAASGFTSSYNNMNVVRQAPGKGLE WVSIRSRGNYIYADSVKGRFTISRDNAKNSLFLQMNSLRAEDTAV YYCARLHDYSNNDAFIDWGGQTMVTYSS	1034	Q\$ALTPASVSGSPGQ\$ITICTGTSSDVG\$YNLVS\$WYQOHPG KAPKLMIEG\$KRP\$GV\$SNRFSG\$KSGNTASL\$TISGLQAEDEA DYYCCSYAG\$STYV\$F\$GGGTL\$TVL	1234
VR0000 06548	EVQLVESGGGLVKPGGSLRLSCAASGFTSSY\$MNMNVVRQAPGKGLE WVSSISSSSYIYADSVKGRFTISRDNAKNSLFLQMNSLRAEDTAV YYCARDG\$N\$W\$GAPDIW\$GQGTMYTYSS	1035	Q\$ALTPASVSGSPGQ\$ITICTGTSSDVG\$YNLVS\$WYQOHPG KAPKLMIEG\$KRP\$GV\$SNRFSG\$KSGNTASL\$TISGLQAEDEA DYYCCSYAG\$STYV\$F\$GGGTL\$TVL	1234
VR0000 19085	QVQLVESGGGVVQPGSLRLSCAASGFTSTYGMVYVRQAPGKGL EMVAVISYDGS\$K\$YADSVKGRFTISRDN\$K\$YTLFLQMNSLRAEDT AVYYCAKDPGSGTYHYHYGYMDYWGQGTIVTYSS	1036	Q\$ALTPASVSGSPGQ\$ITICTGTSSDVG\$YNLVS\$WYQOHP GKAPKLMIE\$DRR\$P\$GV\$SDRFSG\$KSGNTASL\$TISGLQAEDE ADYYCCSYAG\$SW\$V\$F\$GGGTL\$TVL	1247
VR0000 01179	EVQLDSGGGLVQPGGSLRLSCAASGFTSS\$F\$AM\$WVRQAPGKGLE WVSAISGSGGTAFYADSVKGRFSISRDNPKNTLFLQLNSLRAEDTAV YYCAKEDHYHDGTGYYPFDYWGQGTIVTYSS	1037	Q\$ALTPPSVSGSPGQ\$VITICTGTSSDVGGYN\$V\$WYQOHP GTAPKLMIYA\$V\$NRP\$GV\$PDRFSG\$KSGNTASL\$TISGLQAEDE ADYYCCSYT\$SR\$TW\$V\$F\$GGGTL\$TVL	1248
VR0000 01180	EVQLDSGGGLVQPGGSLRLSCAASGFTSS\$F\$VNMNVVRQAPGKGLE WVSAISGGG\$GTAFYADSVKGRFTISRDN\$K\$NTLFLQLNSLRAEDTAV YYCAKEDHY\$YDGTGYYPFDYWGQGTIVTYSS	1038	Q\$ALTPPSASG\$PQ\$Q\$VITICTGTSSDVGGYN\$V\$WYQOHP GKAPKLMIE\$V\$TKR\$P\$GV\$PDRFSG\$KSGNTASL\$TV\$SGLQAEDE EADYYCCSYAG\$SN\$NL\$V\$F\$GGGTL\$TVL	1231
VR0000 18320	QVQLVESGGGLVKPGGSLRLSCEASGFTFSY\$Y\$M\$WVRQAPGKGLE WVSEISNRGITMYADSVKGRFTISRDNAKNSLFLQMKSLRAEDTA VYYCARRTPEGWEDPWGQGTIVTYSS	1039	Q\$ALTPPSASG\$PQ\$Q\$VITICTGTSSDVGGYN\$V\$WYQOHP GKAPKLMIE\$V\$TKR\$P\$GV\$PDRFSG\$KSGNTASL\$TV\$SGLQAEDE EADYYCCSYAG\$SN\$NL\$V\$F\$GGGTL\$TVL	1249
VR0000 02500	EVQLLES\$GGGLVQPGGSLRLSCAASGFTFS\$NY\$AM\$WVRQAPGKGLE WVSSISGSGTY\$Y\$ADSVKGRFTISRDN\$K\$NTLFLQMNSLRAEDTA VYYCALEEWELLGYF\$Y\$P\$D\$YWGQGTIVTYSS	1040	Q\$ALTPR\$SVSG\$PQ\$Q\$VITICTGTSSDVGGYN\$V\$WYQOHP QOAPKLMIYD\$V\$Q\$R\$AS\$GV\$PDRF\$G\$K\$SGNTASL\$TISGLQAEDE EADYYCCSYAG\$S\$TW\$V\$F\$GGGTL\$TVL	1250
VR0000 01379	EVQLLES\$GGGLVQPGGSLRLSCAASGFTFS\$Y\$M\$WVRQAPGKGLE WVSTISGSG\$TY\$ADSVKGRFTISRDN\$K\$NTLFLQMNSLRAEDTAL YYCARLDYDITGYD\$P\$FIDW\$GQGTMYTYSS	1041	Q\$ALTPASVSG\$PQ\$Q\$ITICTGTSSDVGGYN\$V\$WYQOHP GKAPKLMIYD\$V\$NRP\$GV\$SNRFSG\$KSGNTASL\$TISGLQAEDE EADYYCCSYT\$SS\$NTR\$V\$F\$GGGTL\$TVL	1251
VR0000 01346	EVQLLES\$GGGLVQPGGSLRLSCAASGFTFS\$Y\$M\$WVRQAPGKGLE WVSGISGGG\$TY\$ADSVKGRFTISRDN\$K\$NMLFLQMNSLRAEDTA VYYCAKLDYDSSGYD\$Y\$FIDW\$GQGTIVTYSS	1042	Q\$ALTPPSASG\$PQ\$Q\$ATICTGTSSDVGGYN\$V\$WYQOHP GKAPKLMIE\$V\$SKR\$P\$GV\$PDRFSG\$KSGNTASL\$TV\$SGLQAEDE EADYYCNSYAG\$SN\$N\$V\$F\$GGGTL\$TVL	1252
VR0000 05197	EVQLGSGGGLIQPGGSLRLSCAASGFTFS\$Y\$AMN\$WVRQAPGKGLE WVSTISNTGNTY\$ADSVKGRFTISRDN\$K\$NTLHLQMNSLRAEDTA VYYCTKENYDTS\$GYN\$P\$D\$YWGQGTIVTYSS	1043	Q\$ALTPPSASG\$PQ\$Q\$VITICTGTSSDVGGYN\$V\$WYQOHP GKAPKLMIE\$V\$SKR\$P\$GV\$PDRFSG\$KSGNTASL\$TV\$SGLQAEDE EADYYCCSYAG\$SN\$N\$W\$V\$F\$GGGTL\$TVL	1253
VR0000 18072	QVQLVESGGGLVKPGGSLRLSCAASGFTFS\$Y\$M\$WVRQAPGKGLE CISYISS\$SVTIYADSVKGRFTISRDNAKNSLFLQMNSLRAEDTAVY YCAR\$ED\$SDTS\$GYD\$P\$FIDW\$GQGTIVTYSS	1044	Q\$ALTPPSASG\$PQ\$Q\$VITICTGTSSDVGGYN\$V\$WYQOHP GKAPKLMIE\$V\$SKR\$P\$GV\$PDRFSG\$KSGNTASL\$TV\$SGLQAEDE EADYYCCSYAG\$SNTR\$V\$F\$GGGTL\$TVL	1254
VR0000 19015	QVQLVESGGGVVQPGSLRLSCAASGFTFS\$Y\$GMH\$WVRQAPGKGL EMVAVIWYDGS\$NK\$YADSVKGRFTISRDN\$K\$NTLFLQMNSLRAED TAVYYCARVHG\$YTR\$F\$DAFIDW\$GQGTIVTYSS	1045	Q\$ALTPASVSG\$PQ\$Q\$ITICTGTSSDVGGYN\$V\$WYQOHP GKAPKLMIE\$V\$SNR\$P\$GV\$SNRFSG\$KSGNTASL\$TISGLQAEDE ADYYCCSYT\$SS\$TL\$V\$F\$GGGTL\$TVL	1255
VR0000 29548	QVQVYQSGAEVKKPGASVK\$V\$CK\$VSGYTLTEFSMH\$WVRQAPGKGL EWMGGGSDPEDGETIYAQK\$Q\$GRVTMTEDT\$TDTA\$Y\$MEL\$SLRSE DTAVYYCATV\$W\$V\$AF\$FDYWGQGTIVTYSS	1046	Q\$ALTOPASVSG\$PQ\$Q\$ITICTGTSSDVGN\$F\$V\$WYQOHPG KAPKLMIYD\$VGNR\$P\$GV\$SNRFSG\$KSGNTASL\$TISGLQAEDE ADY\$C\$SS\$Y\$T\$S\$G\$TVL\$F\$GGGTL\$TVL	1256
VR0000 31043	QVQLQESGPGLVKPSQTL\$LTCTV\$SGSISR\$GVY\$W\$SWIRQHPGKGL EMWIGIY\$SG\$TY\$N\$P\$SL\$K\$R\$VTISVDTSKNQ\$F\$SL\$K\$SSVTAADTAVY YCARLSGDY\$WY\$FDL\$WGRGTLVTYSS	1047	DIVMTOTPL\$LPVTE\$P\$ASICR\$SSQ\$SLD\$SDDGNTYLDWYL QKPGQ\$POLLITLYL\$YR\$AS\$GV\$PDRF\$SG\$G\$GTDFTLKISRVEA EDVGVY\$Y\$CMQRIE\$PFLTFGGG\$TKVEIK	1257

VR0000 30733	QVQLQESGPGLVKPSSETLSLTCTVSGGSISNYYWWSWIRQAPGKGLEW IGRFYPTGRTKYNPSLKSRYVTMSVDTSKNQFSLKLSVTAADTAVVY CARAGSTVTPDYGMDDVMGQGTIVTVSS	1048	DIVAMTQITPLSLPTTPGEPASISCRSSQSLDSDDGNTYLDWYL QKPGQSPQLLIYMLSYRASGVPPDRFSGSGSGTDFTLKISRVEA EDVGVYYCMQRIEFPSTFGQGTLEIK	1258
VR0000 15540	QVQLQESGPGLVKPSSETLSLTCTVSGGSITNYYWIWIRQAPGKGLEW IGHFTSGTTSYNPSLKSRYVTMSVDTSKQFSLKLSVTAADTAIYYC ARVEYDITGYDGFDMWGEGMTVTVSS	1049	DVVMQTQITPLTSLVITIGQPTSLSCKSSQSLYSIDGKTYLSWL QRPQSPKRLIYLVSKLDSGVPPDRFTGSGSGTDFTLKISRVEA EDLGYYICWQGHFPQTFFGGTKLEIK	1259
VR0000 06636	EVQLVESGGGLVQPGGSLRLSCVASGFTFSSYKMNWVRQAPGKGLE WVSSIRSSNYYIYADSVKGRFTISRDNAKNSVELQMNSLRAEDTAV YYCARHHDYNSNDAFDMWGQGTIMTVSS	1050	DIVAMTQITPLSLPTTPGEPASISCRSSQSLDSDDGNTYLDWYL QKPGQSPQLLIYLVSYRASGVPPDRFSGSGSGTDFTLKISRVEA EDGVVYYCMQRIEPLTFGGGTKEIK	1257
VR0000 06622	EVQLVESGGGLVQPGGSLRLSCVASGFTFSTYNNMNWVRQAPGKGLE WVSSISSSSYIYHADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAV YYCARDKVPGAFDYWGQGTLVTVSS	995	DIVAMTQSPSLPVTTPGEPASISCRSSQSLHNGYNYLDWYL QKPGQSPQLLIYLVGSNRSAGVPDRFSGSGSGTDFTLKISRVEA EDGVVYYCMQALQITPYTFGQGTLEIR	1260
VR0000 06525	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYNNMNWVRQAPGKGLE WVSSIRSGNYYIYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAV YYCARLHDYSNDAFDMWGQGTIMTVSS	1034	DIVAMTQSPSLPVTTPGEPASISCRSSQSLHNGYNYLDWYL QKPGQSPQLLIYLVGSNRSAGVPDRFSGSGSGTDFTLKISRVEA DVGYYVCMQALQITPYTFGQGTLEIK	1261
VR0000 19197	QVQLVESGGGVVQPGSLRLSCVASGFTFSSYGIHWVRQAPGKGLE WVTMIVYDGSNKKYYADSVKGRFTISRDNKNTLYLQMYSLRAEDT AVYYCARQHGYYTRFSDGFDMWGQGTIMTVSS	1051	DIVAMTQSPSLPVTTPGEPASISCRSSQSLHNGYNYLDWYL QKPGQSPQLLIYLVGSNRSAGVPDRFSGSGSGTDFTLKISRVEA DVGYYVCMQALQITLTFGGGTKEIK	1262
VR0000 00693	EVHLVESGGSLVQPGGSLRLSCAASGFTFNKNMYWVRQAPRGLE GVSSISGGSGYKRYADSVKGRFTISRDNKNTSLYLQMSLRAEDTAV YYCARRAPPAWGGFDYWGQGTLVTVSS	1052	DIVAMTQSPSLPVTTPGEPASISCRSSQSLHNGYNYLDWFLQ KPGQSPQLLIYLVGSNRSAGVPDRFSGSGSGTDFTLKISRVEA DVGYYVCMQALQITTFGQGTLEIK	1263
VR0000 36146	QVQLVESGGGVVQPGSLRLSCAASGFTFSSYGMHWVRQAPGKGL EWWAIISYDGSNKKHYADSVKGRFTISRDNKNTLYLQMNSLRAEDT AVYYCARAPSHFYFDYWGQGTLVTVSS	1053	DIVAMTQSPDSLAVSLGERATINCKSSQSVLFSSNNKNYLAWY QKPGQPPKLLIYWASTRESGVPPDRFSGSGSGTDFTLTISLQ AEDVAVYYCCQYYSTPLTFGGGTKEIK	1264
VR0000 01378	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLE WVSTISGSGGTTYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAL YYCARLDYDITGYDPEFIWGQGTIMTVSS	1041	DIVAMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWY QKPGQPPKLLIYWASTRESGVPPDRFSGSGSGTDFTLTISLQ AEDVAVYYCCQYYSTPLTFGGGTKEIK	1265
VR0000 04017	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLE WVSAISGSGGTTYADSVKGRFTISRDNKNTLYLQMNSLRAEDTA VYYCAKQDNYESTGYYPFDYWGQGTLVTVSS	1054	DIVAMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWY QKPGQPPKLLIYWASTRESGVPPDRFSGSGSGTDFTLTIRSLQ ADDVAVYYCCQYYSTPLTFGGGTVEIK	1266
VR0000 11851	EVRLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLE WVSAISGSGGTTYADSVKGRFTISRDNKNTLYLQMNSLRAEDTA VYYCAKALYYDDSSGYYYGYGMDYWGQGTIVTVPS	1055	DIVAMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWY QKPGQPPKLLIYWASTRESGVPPDRFSGSGSGTDFTLTISLQ AEDVAVYYCCQYYSTPTFGQGTKEIK	1267
VR0000 01230	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLE WVSAISGSGGNTYYTDSVKGRFTISRDNKNTLYLQMNSLRAEDTA VYYCAKETYYDDSSGYTNYYYVMDYWGQGTIVTVSS	1056	DIVAMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWY QKPGQPPKLLIYWASTRESGVPPDRFSGSGSGTDFTLTISLQ AEDVAVYYCCQYYSTPTFGQGTLEIK	1268
VR0000 15960	QVQLQESGPGLVKPSSETLSLTCTVSGGSISTSNWWSWVROPKGL EWIGELIYSGSTKYNPSLKSRYIISVDSKNQFSLKLSVTAADTAVY YCARDGGYSVYDSFDYWGQGTLVTVSS	1057	DIVAMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWY QKPGQPPKLLIYWASTRESGVPPDRFSGSGSGTDFTLTISLQ AEDVAVYYCCQYYSTPTFGGTKEIK	1269
VR0000 13472	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSSFYWDWIRQAPGKGLE WIGSIYFSGSTYYNPSLKSRYTISVDTSRNQFSLKLSVTAADTAVY CARREPAADTLDYWGQGTLVTVSS	1058	DIVAMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWY QKPGQPPKLLIYWASTRESGVPPDRFSGSGSGTDFTLTISLQ AEDVAVYYCCQYYSTPLTFGGGTKEIK	1265

VR0000 29534	QVQVQWGA GLK PSEITL SLTC A VYGGSFSGNY WSWIRQPGKGL EWIGEINHSGTNNPSLKS RVTIS VDTSKSQFSLRLHS VTAADTAVY YCAREDSSWYVGFDYWGQGLTVTVSS	1059	DI VMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWY QOKPGQPKLLIYWASTRESGV PDRFSGSGGTDFTLTISLQ AEDVAVYYCQOYYSTPRTFGQGTKVEIK	1267
VR0000 29526	QVQVQSGAEVKKPGASVKVSCKVSGYTLMEISHWVRQAPGKGLE WMGGFDPENGETVHAQKFOGRVIMTEDPSTETAHMELSSLSEDTA VYYCAAGPSGWYSDAFDWGGQGMVTVSS	1060	DI VMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWY QORPGQPKLLIYWASTRESGV PDRFSGSGGTDFTLTISLQ AEDVAVYYCQOYYSPPLTFGGGTKVEIK	1270
VR0000 07193	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMHWVRQATGKGLE WYSTIGSPGDTIYPGSGVGRFTISRDNKNTLSLQMNSLRAEDTA YYCARGDFWGGYSYYYYGMDVWGQGITVTVSS	1061	DIQLTQSPFSLASVGD RVTITCRASQGVSSYL VVWYQOKPGK APKLLIYASTLQSGVPSRFSGSGGTFTLTISLQPEDFATY YCOQLISYPTFGQGTKVEIK	1271
VR0000 03163	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLE WVSAIRSRGDTIYYADSVRGRFTISRDNKNTLSLQMNSLRAEDTA VYYCAKG YEDWLAYYYYALDYWGQGITVTVSS	1062	DIQMTQSPFSLASVGD RVTITCRASQOGIRNDL GWDQOKPGK APKRLIYAASSLQSGVPSRFSGSGGTFTLTISLQPEDFATY YCLQHNSYPTFGQGTKVEIK	1272
VR0000 19882	QVQLVQSGAEVKKPGASVKVSCKASGYTFSSTYYIHWVRQAPGQGL EWMGLINPSGGGTYYAQKFOGRVTMNRDITSTYHMESSLRSEDT AVYYCARSEFNWNYVGLSYHGMDVWGQGITVTVSS	1063	DIQMTQSPSAMISASVGD RVTITCRASQAISHYLAWFQORPGK VPKRLIYAASSLQSGVPSRFSGSGGTFTLTISLQPEDFATY YCLQHNSYPTFGQGTKVEIK	1273
VR0000 06271	EVQLVESGGGLEQPGKSLRLSCAASGFTFDYAMHWVRQPGKGL EWWSGISWNGGSDYADSVKGRFTMSRDNAKNSLYLQMNSLRAED TALYYCAKDMGLEAAGPFYYGIDVWGQGITVTVSS	1064	DIQMTQSPSSVASVGD RVTITCRASQGISCLAWYQOKPGK APKLLIYAAASLQSGVPSRFSGSGGTDFTLTISLQPEDFATY YCOQANSFPPTFGQGTKVEIK	1274
VR0000 13631	QQLQESGPGLVKPSSETLSLCTVSGSGSISSSYWGWIRQPPGKGLE WIGTIYSGNTYYNLSLKS RVTISDTSKNQFSLKLSVTAADTGVVY CARHRLRYFDWPDSDSWGQGLTVTVSS	1065	DIQLTQSPFSLASVGD RVTITCRASQGISSYLAWYQOKPGKA PKLLIYAASTLQSGVPSRFSGSGGTFTLTISLQPEDFATY CQQLNSYPCSFQGGTKLEIK	1275
VR0000 13632	QLQLQESGPGLVKPSSETLSLCTVSGSGSISSSYWGWIRQPPGKGLE WIGTIYSGNTYYNPSLKS RVTISVDTSKNQFSLKLSVTAADTAVY YCAREWELLDYWGQGLTVTVSS	1066	DIQMTQSPSSVASVGD RVTITCRASQGISSWLAWYQOKPGK APKLLIYAAASLQSGVPSRFSGSGGTDFTLTISLQPEDFATY YCOQANSFPLTFGGGTKVEIK	1276
VR0000 30711	QVQLQESGPGLVKPSSETLSLCTVSGSGSISSSYWSWIRQPAKGLEW IGRFYASGYTNNPSLKS RVTMSVDTSKNQFSLKLSVTAADTAVYF CARERLYNNWNYGGFFDYWGQGLTVTVSS	1067	DIQLTQSPFSLASVGD RVTITCRASQGISSYLAWYQOKPGKA PKLLIYVASTLQSGVPSRFSGSGGTFTLTISLQPEDFATY CQQLNSYPLTFGGGTKVEIK	1277
VR0000 17524	QVQLQWGA GLK PSEITL SLTC A VYGGSFSDYYWSWIRQPPGKGLE WIGEIYHSGSTTYNPSLTS RVTISVDTSKNQFSLKLSVTAADTAVVY CARVPNSGSYDYFDYWGGQGLTVTVSS	1068	DIQMTQSPSLASVGD RVTITCRASQOGIRNDL GWWYQOKPGK APKRLIYAAASLQSGVPSRFSGSGGTFTLTISLQPEDFATY YCLQHNSYPTFGQGTKLEIK	1278
VR0000 14697	QVHLQWGA GLK PSEITL SLTC A VYGGSFSDYYWSWIRQPPGKGLE WIGESDYSGSTKYNPSLES RVTISADTSKNQFSLKLSVTAADTAVY YCARVPDSGSYDYFDYWGGQGLTVTVSS	1069	DIQMTQSPSLASVGD RVTITCRASQOGIRNDL GWWYQOKPGK APKRLIYAAASLQSGVPSRFSGSGGTFTLTISLQPEDFATY YCLQHNSYPTFGQGTKLEIK	1278
VR0000 17424	QVQLQWGA GLK PSEITL SLTC A VYGGSFSDYYWSWIRQPPGKGLE WIGEINHSGSTYNPSLKS RVTMSVETSKNQFSLKLSMTAADTGVY YCARVGDGGSYDPFEFWGGQGLTVTVSS	1070	DIQMTQSPSLASVGD RVTITCRASQOGIRNDL GWWYQOKPGK APKRLIYAAASLQSGVPSRFSGSGGTFTLTISLQPEDFATY YCLQHNSYPTFGQGTKLEIK	1279
VR0000 17525	QVQLQWGA GLK PSEITL SLTC A VYGGSFSDYYWSWIRQPPGKGLE WMGEINHSGSTQYNPSLKS RVTISVDTSKNQFSLKLSVTAADTAMY YCARDDSFMAASGRPYDYWGQGLTVTVSS	1071	DIQMTQSPSLASVGD RVTITCRASQOGIRNDL NWYQOKPGK APKRLIYAAASLQSGVPSRFSGSGGTFTLTISLQPEDFATY YCLQHNSYPTFGQGTKLEIK	1280
VR0000 17816	QVQLQWGA GLK PSEITL SLTC A VYGGSFSTGYWWSWIRQPPGKGLE WIGEINHSGSTYNPSLKS RVTISVDTSKNQFSLKLSVTAADTAVVY CARNY YDTSGYYSFDYFGQGLTVTVSS	1072	DIQMTQSPSLASVGD RVTITCRASQOGIRNDL GWWYQOKPGK APKRLIYAAASLQSGVPSRFSGSGGTFTLTISLQPEDFATY YCLQHNSYPLTFGGGTKVEIK	1281

VR0000 20781	QVQLVQSGAEVKKPKPGASVKYSCKASGYTFTSYDINWVRQATGQGL EWMGMQNTNSGNTDYAQKFGQGRVTMTRNTSISTAYMELSSLRSED TAVYYCAREWELLGFDYWGGQGLVTYSS	1073	DIQMTQSPSSLASVGDRAVTTTCRASQGIKNDLAWYQOKPGK APKRLIYAASLQSGVPSRFGSGSGTEFTLTISLQPEDFATY YCLQHNSTPRTFGGQTKVEIK	1282
VR0000 18817	QVQLVESGGGVVQPGKSLRLSCAASGFTFSSDAMHWVRQAPGKGL EWVAIVWYDGSNKYSADSVKGRFTISRDNKNTLYLQMNSLRAEDT AVYYCARDROWLAFDYWGGQGLVTYSS	1074	DIQMTQSPSSLASVGDRAVTTTCRASQGIKNDLAWYQOKPGK APKRLIYAASLQSGVPSRFGSGSGTEFTLTISLQPEDFATY YCLQHNSTPRTFGGQTKVEIK	1283
VR0000 17977	QVQLVESGGGLVKPGGSLRLCCAASGFTFSYVYMSWIRQTPGKGLE WVSEISNRGITMYADSVKGRFTISRDNKNSLYLQMNSLRAEDTA VYYCARRIPEGWEDPWGQGLVTYSS	1075	DIQMTQSPSSLASVGDRAVTTTCRASQGISNYLAWFQOKPGK APKSLIYAASLQSGVPSRFGSGSGTDFTLTISLQPEDFATY YCOQYNSYPLTFGGGQTKVEIK	1284
VR0000 18329	QVQLVESGGGLVKPGGSLRLSCTASGFTFSDYVYMIWIRQAPGKGLE WVSSISNRGITIYYAVSVKGRFTISRDNARNSLYLQMNSLRAEDTAV YYCARLPGTWEDPWGQGLVTYSS	1076	DIQMTQSPSSLASVGDRAVTTTCRASQGIKNDLAWYQOKPGK APKRLIYAASLQSGVPSRFGSGSGTEFTLTISLQPEDFATY YCLQHNSTPRTFGGQTKVEIK	1285
VR0000 06547	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLE WVSSISSSSYIYYADSVKGRFTISRDNKNSLYLQMNSLRAEDTAV YYCARDGGNWGAFDIWWGQGTMYTVSS	1035	DIQMTQSPSAMISASVGDRAVTTTCRASQGISNYLAWFQOKPGK VPKRLIYAASLQSGVPSRFGSGSGTEFTLTISLQPEDFATY YCLQHNSTPRTFGGQTKVEIK	1286
VR0000 06630	EVQLVESGGGLVKPGGSLRLSCTASGFTFSYNMNWVRQAPGKGLE WVSTTSSSTIYYADSVKGRFTISRDNKNSLYLQMNSLRAEDTAIY YCARHITPGVDYWGGQGTIVTVSS	1077	DIQMTQSPSSTVASYGDRVTTTCRASQGVSRWLAWYQOKPG KAPKRLIYAASLQSGVPSRFGSGSGTAFTLTISLQPEDFAT YYCQQADSEPFTEGPGTVDYK	1287
VR0000 06534	EVQLVESGGGLVKPGGSLRLSCAASGFTFSYRNMWVRQAPGKGLE WVSSISRSSYIYYADSVKGRFTISRDNKNSLYLQMNSLRAEDTAV YYCARHHDYNSNDAFDIWWGQGTMYTVSS	1032	DIQMTQSPSAMISASVGDRAVTTTCRASQGISNYLAWFQOKPGK VPKRLIYDTSLSQGVPSRFGSGSGAEFTLTISLQPEDFATY YCLQHNSTPLTFGGGQTKVEIK	1288
VR0000 08309	EVQLVESGGGVKPGGSLRLSCAASGFSSSYSMNWVRQAPGKGLE WVSSIRASSTIYYADSVKGRFTISRDNKNSLYLQMNSLRAEDTAV YYCARHHDYNSNDAFDIWWGQGTIVTVSS	1078	DIQMTQSPSAMISASVGDRAVTTTCRASQAIASHYLAWFQORPGK VPKRLIYAASLQSGVPSRFGSGSGTEFTLTISLQPEDFATY YCLQHNSTPRTFGGQTKVEIK	1273
VR0000 06522	EVQLVESGGGLVKPGGSLRLSCAASGFTFSYKMNWVRQAPGKGLE WVSSISRSTIYYADSVKGRFTISRDNKNSLYLQMNSLRAEDTA VYYCARHHDYNSNDAFDIWWGQGTMYTVSS	1033	EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQOKPGQ APRLIYGASSRATGIPDRFSGSGGTDFTLTISLQPEDFAVY YCOQYGSPPWTFGGQTKVEIK	1289
VR0000 00789	EVKLLESGGGLVOPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLE WVSAISGSAFTIYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAV YYCAKAPYRSGWEEYFPDYWGQGLVTYSS	1079	DIQMTQSPSTLASVGDRAVTTTCRASQSISSWLAWYQOSP GK APKLIYKASSLQSGVPSRFGSGSGTEFTLTISLQPEDFATY YCOQYDYSRTEGQGTKEIK	1290
VR0000 17947	QVQLVESGGDLVKPGGSLRLSCTASGFTFSDYVYMSWIRQAPGKGLE WVSYVNSGTIYYADSVKGRFTISRDNKNSLYLQMNSLRAEDTA VYYCAREDNVESTGYFPEDYWGGQGLVTYSS	1080	DIQMTQSPSSLASVGDRAVTTTCRASQSISSWLAWYQOKPGK APKRLIYAASLQSGVPSRFGSGSGTEFTLTISLQPEDFATY YCLQHNSTPRTFGGQTKVEIK	1291
VR0000 18335	QVQLVESGGGLVKPGGSLRLSCTASGFTFSSYAMSWVRQAPGKGLE WVSYINRSGSTKYHADSVKGRFTISRDNKNSLYLQMNSLRAEDTA VYSCARVDNVESTGYHFPEDYWGGQGLVTYSS	1081	DIQMTQSPSTLASVGDRAVTTTCRASQSISSWLAWYQOKPGK APKLIYKASSLESGVPSRFGSGSGTEFTLTISLQPEDFATY YCOQYNSYWTFGGQTKVEIK	1292
VR0000 05039	EVQLLESGGGLVOPGGSLRLSCGASGFTFTSYAMDWVRQAPGKGLE WVSGISGSGGTIYYADSVKGRFAISRDNKNTLYLQMNSLRAEDTA AYYCAQQGRDTSGYDPFDYWGGQGLVTYSS	1082	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQOKPGQ APRLIYGASTRATGIPARFSGSGSGTEFTLTISLQSEDFAVY YCOQYNNWPLTFGGGQTKVEIK	1293
VR0000 17982	QVQLVESGGGLVKPGGSLRLSCAASGFESDYQMSWIRQAPGKGLE CVSYISSSGYTTIYYADSVKGRFTISRDNKNSLYLQMNSLRAEDTAV YFCAREDDYDSTGYNFDYWGGQGLVTYSS	1030	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQOKPGQ APRLIYDASNRAATGIPARFSGSGSGTDFTLTISLQPEDFAVY YCOQRSNWPLTFGGGQTKVEIK	1294

VR0000 15801	QVQLQESGPGLVKPSGTLSLTCAVSGGSISSSNWVWVVRQPPGKGLE WIGELIYHSGNTNPNPSLKSRYVTITMDKSKNQFSLNLSVTAADTAVY YCARREGGYSVYGSPDYWGQGLVTYSS	1083	DIQMTQSPSSLSASYGDRVTITTCRASQGIRNDLGWYQQEPPGK APKRLIYAASLSQSGVPSRFSGSGSTEFTLTISSLQPEDFATY YCLQHNSTYPTFGGQTKVEIK	1295
VR0000 15806	QVQLQESGPGLVKPSGTLSLTCAVSGGSISSSNWVWVVRQPPGKGL EWIGELIYHSGTHYNPNSLKSRYVTISLDESKNQFSLKLSVTAADTAVY YCARREGGYSVYGSPDYWGQGLVTYSS	1084	DIQMTQSPSSLSASYGDRVTITTCRASQGIRNDLGWYQQKPGK APKRLIYDASLSQSGVPSRFSGSGSTEFTLTISSLQPEDFATY YCLQHNSTYPTFGGQTKVEIK	1296
VR0000 15804	QVQLQESGPGLVKPSGTLSLTCAVSGGSISSSNWVWVVRQPPGKGL EWIGDIYHSGSTNPNPSLKSRYVTISVDTSKNQFSLKLSVTAADTAV YCARREGGYSVYGSPDYWGQGLVTYSS	1085	DIQMTQSPSSLSASYGDRVTITTCRASQGIRNDLGWYQQKPGK APNRLIYASLTQSGVPSRFSGSGSTEFTLTISSLQPEDFATY YCLQHNSTYPTFGGQTKVDIK	1297
VR0000 15895	QVQLQESGPGLVKPSGTLSLTCAVSGGSISSSNWVWVVRQPPGKGL EWIGDIYHSGSTNPNPSLKSRYVTISVDTSKNQFSLKLSVTAADTAVY YCARREGGYSVYDSPDYWGQGLVTYSS	1086	DIQMTQSPSSLSASYGDRVTITTCRASQGIRNDLGWYQQKPGK APKRLIYTAASLSQSGVPSRFSGSGSTEFTLTISSLQPEDFATY YCLQHNSTYPTFGGQTKVEIK	1298
VR0000 15777	QVQLQESGPGLVKPSGTLSLTCAVSGGSISSSNWVWVVRQPPGKGL EWIGELIYHSGSTNPNPSLKSRYVTISVDTSKNQFSLKLSVTAADTAIY YCARREGWELLFPDYWGQGLVTYSS	1087	DIQMTQSPSSLSASYGDRVTITTCRASQGIRNDLGWYQQKPGK APKRLIYAASLSQSGVPSRFSGSGSTEFTLTISSLQPEDFATY YCLQHNSTYPTFGGQTKVEIK	1291
VR0000 15789	QVQLQESGPGLVKPSGTLSLTCAVSGGSISSSNWVWVVRQPPGKGL EWIGELIYHSGSTNPNPSLKSRYVTISVDKSKNQFSLKLSVTAADTAV YCARDSYTSIGWYAPLDYWGQGLVTYSS	1014	DIQMTQSPSSLSASYGDRVTITTCRASRGIRNDLGWYQQKPGK APKRLIYAASLSQSGVPSRFSGSGSTEFTLTISSLQPEDFATY YCLQHTSYPLTFGGGQTKVEIK	1299
VR0000 15654	QVQLQESGPGLVKPSGTLSLICAVSGGSISSSTWWSVVRQPPGKGLE WIGELIYHSGSTNPNPSLKSRYVTISVDKSKNQFSLKLSVTAADTAVY YCARKNYWTTPEDYWGQGLVTYSS	1088	AIQMTQSPSSLSASYGDRVTITTCRASQDQIRNDLGWYQQKPGK APKRLIYTAASLSQSGVPSRFSGSGTDFTLTISSLQPEDFATY YCLQDYNYPFTFGPQTKVDIK	1300
VR0000 15729	QVQLQESGPGLVKPSGTLSLTCAVSGGSISSSNWWSVVRQPPGKGL EWIGELIYHSGSTNPNPSLKSRYVTISLTKSKNHFSCLKTSVTAADTAVY YCARDGDYESSGGYGLDWSGQGLVTYSS	1089	DIQMTQSPSSLSASYGDRVTITTCRASQVIRNDLGWYQQKPGK APKRLIYVASRLQSGVPSRFSGSGSTEFTLTISSLQPEDFATY YCLQHNSTYPTFGPQTKVDIK	1301
VR0000 11836	EVQVVESGGGLVQPGGSLRLSCAASGFTFDDYAMHWVRQAPGKGL EWWANIKQDQSEKYYVDSYKGRFTISRDNAKNLLYLQMNSLRAEDT AFYTCAREQQLWVPTSHYSGTGTFDIWGQGLVTYSS	1090	AIQMTQSPSSLSASYGDRVTITTCRASQDQIRNDLGWYQQKPGK APKRLIYVSSLQGGVPSRFSGSGTDFTLTISSLQPEDFATY YCLQDYNYPYTFGGQTKLEIK	1302
VR0000 07924	EVQLVESGGGLVQPGSLRLSCAASGFTFDDYAMHWVRQAPGKGL EWWSGISWNRDNIGYADSVKGRFTISRDNAKNSLFLQMDSLRAEDT AFYYCAKDIRWGRSGWYPYYYSQGMVWGQGTITVYSS	1091	QSALTQPASVSGSPGQSLAISCTGTSSDVGGYSYVSWYQQHP GKAPKLTIIDISSRPSGVSNRFSGKSGNTASLTITGQAQAEDEA DYCCSYTSSNTLVFGGQTRLTVL	1303
VR0000 07925	EVQLVESGGGLVQPGSLRLSCAASGFTFDDYAMHWVRQAPGKGL EWWSGISWNRDNIGYADSVKGRFTISRDNAKNSLFLQMDSLRAEDT AFYYCAKDIRWGRSGWYPYYYSQGMVWGQGTITVYSS	1091	SSELTQDPAAVSVALQGTVRITCQGDRLRNYASWYQQKPGQ APVLVIYCKNNRPSGIPDRFSGSSGNTASLTITGQAQAEDEAD YFCNSRDSGGNHVYFGGGQTKLTVL	1304
VR0000 01229	EVQLLESQGGLEQPGGSLRLSCAASGFTFSNAMSVMVRQAPGKGLE WVSAISGSGGNTYYTDSVKGRFTISRDNKNTLYLQMNSLRVEDTA VYYCAKETIYYDSSGYTNYVMVWGQGTITVYSS	1056	DIQMTQSPSSVSASYGDRVTITTCRASQGISWLAWYQQKPGR APKRLIYAASLTQSGVPSRFSGSGTDFTLTISSLQPEDFATY YCOQANSFPTFGGQTKVENK	1305
VR0000 01228	EVQLLESQGGLEQPGGSLRLSCAASGFTFSNAMSVMVRQAPGKGLE WVSAISGSGGNTYYTDSVKGRFTISRDNKNTLYLQMNSLRVEDTA VYYCAKETIYYDSSGYTNYVMVWGQGTITVYSS	1056	DIQMTQSPSSLSASYGDRVTITTCRASQGIRNDLGWYQQKPGK APKRLIYAASLSQSGVPSRFSGSGSTEFTLTISSLQPEDFATY YCLQHNSTYPTFGPQTKVDIK	1306
VR0000 01231	EVQLLESQGGLEQPGGSLRLSCAASGFTFSNAMSVMVRQAPGKGLE WVSAISGSGGNTYYTDSVKGRFTISRDNKNTLYLQMNSLRVEDTA VYYCAKETIYYDSSGYTNYVMVWGQGTITVYSS	1056	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQ APRLIYDASNRAATGIPARFSGSGGTDFTLTISLPEDEFAVY YCOQQRSNWPLTFGGGQTKVEIK	1294

VR0000 01240	EVQLESGGGLEQOPGGSLRLSCAASGFTFSSYAMTWVRQAPGKGLE WVS/SAISGSGNYYTDSVKGRFTISRDNKNTL.YLQMNSLRAEDTA YYYCAKETIYYDSSGYTNYYYVMDVWGQGITVTVSS	1092	SYELTOPPSVSVSPGOTASITCSGDKWCYKCYCWYQOKPGQ SPVPVIYQDSKRPSGIPERFSGSNSGNTATLTISGTOAMDEAD YYCQAWDSSTVVFGGTKL.TVL	1307
VR0000 01236	EVQLESGGGLEQOPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLE WVS/SAISGSGNYYTDSVKGRFTISRDNKNTL.YLQMNSLRAEDTA YYYCAKETIYYDSSGYTNYYYVMDVWGQGITVTVSS	1056	SYELTOPPSVSVSPGOTASITCSGDKWCYKCYCWYQOKPGQ SPVPVIYQDSKRPSGIPERFSGSNSGNTATLTISGTOAMDEAD YYCQAWDSSTVVFGGTKL.TVL	1307
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VR0000 01234	EVQLESGGGLEQOPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLE WVS/SAISGSGNYYTDSVKGRFTISRDNKNTL.YLQMNSLRAEDTA YYYCAKETIYYDSSGYTNYYYVMDVWGQGITVTVSS	1056	SSELTOPPAVSVALGQTVRITCQGDLSRYYASWYQOKPGQ APVL.VIYCKNNRPSGIPDRFSGSSGNTASLTITGAQAEDEAD FYCNSRSDSSGNHVVFEGGTKL.TVL	1309
VR0000 01233	EVQLESGGGLEQOPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLE WVS/SAISGSGNYYTDSVKGRFTISRDNKNTL.YLQMNSLRAEDTA YYYCAKETIYYDSSGYTNYYYVMDVWGQGITVTVSS	1056	QSALETQPPASVSGSPGQSTITCTGTSSDVGGYNVSWYQOHPG KAPKLMIYEGSKRPSGVNDRFSGSKSGNTASLTISGLQAEDEA EADYYCCSYAGSNNEVFEGGTKL.TVL	1310
VR0000 01232	EVQLESGGGLEQOPGGSLRLSCAASGFTFSSYAMTWVRQAPGKGLE WVS/SAISGSGNYYTDSVKGRFTISRDNKNTL.YLQMNSLRAEDTA YYYCAKETIYYDSSGYTNYYYVMDVWGQGITVTVSS	1056	QSALETQPPASVVALGQTVRITCQGDLSRYYASWYQOKAGQ KAPKLMIYEGSKRPSGVNDRFSGSSGNTASLTITGAQAEDEAD DYYCCSYAGSSTLVFEGGTKL.TVL	1246
VR0000 04253	EVQLESGGGLEQOPGGSLRLSCAASGFTFSSYAMTWVRQAPGKGLE WVS/GISGSGNYYTDSVKGRFTISRDNKNTL.YLQMNSLRAEDTA YYYCAKEEYDTSGYNPDPYWGQGITLVSS	1093	SSELTOPPAVSVALGQTVRITCQGDLSRYYASWYQOKAGQ APVL.VIYCKNNRPSGIPDRFSGSSGNTASLTITGAQAEDEAD YYCNSRSDSSGNHVVFEGGTKL.TVL	1311
VR0000 03041	EVQLESGGGLEQOPGGSLRLSCAASGFTFSSYAMTWVRQAPGKGLE WVS/GISGSGNYYTDSVKGRFTISRDNKNTL.YLQMNSLRAEDTA YYYCAKEDYDSSGYNPDPYWGQGITLVSS	1094	SYVLTOPPSVSVAPGQOTARITCGNNGISKSVHWYQOKPGQ APVL.VVYDDSDRSPGIPERFSGSNSGNTATLTISRVEAGDEAD YYCQVWDSSDHPVFGGTKL.TVL	1312
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VR0000 18073	QVQLESVSGGLEQOPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLE CISYISSSVTIIYADSVKGRFTISRDNKNTL.YLQMNSLRAEDTAVY YCAREDSDTSGYDFPDHWGQGITLVSS	1044	SYELTOPPSVSVSPGOTARITCSGDALPKKYAYWYQOKSGQ APVVICDDSKRPSGIPERFSGSSGTMATLTISGAQVEDEAD YYCYSTDSSGNHVVFEGGTKL.TVL	1314
VR0000 29911	RVQLESVSGGLEQOPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLE WVS/SAISGSGNYYTDSVGRFTISRDNKNTL.YLQMNSLRAEDTA YYYCAKDLQOWL.VRIYIYAMDVWGQGITVTVSS	1096	SYELTOPPSVSVSPGOTARITCSGDALPKKYGYWYQOKSGQ APVL.VIYEDSKRPSGIPERFSGSSGTMATLTISGAQVEDEAD YYCYSTDSSGNHRVFGGTKL.TVL	1315
VR0000 02423	EVQLESVSGGLEQOPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLE WVS/SAISGSGNYYTDSVKGRFTISRDNKNTL.YLQMNSLRAEDTAV YYCAKEGSGSYPIYIYGMVWGQGITVTVSS	1097	SYELTOPPSVSVSPGOTARITCSGDALPKKYAYWYQOKSGQ PVL.VIYEDNKRPSGIPERFSGSSGTMATLTISGAQVEDEADY YCYSTDSSGNHRVFGGTKL.TVL	1316
VR0000 01208	EVQLESVSGGLEQOPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLE WVS/SAISGSGNYYTDSVKGRFTISRDNKNTL.YLQMNSLRAEDTAV YYCAKEDYDIL.TGPPYFYGMVWGQGITVTVSS	1098	SYELTOPPSVSVSPGOTARITCSGDALPKKYAYWYQOKSGQ APVL.VIYEDSKRPSGIPERFSGSSGTMATLTISGAQVEDEAD YYCYSTDSSGNHRVFGGTKL.TVL	1317
VR0000 13875	QLOVESGPGLEQPKSETL.SLTCTVSGDSTISNFWYWGWRQAPGKGLE EWIGSIFHGNTYYNPSLSKRVITISVDTSKNQFSLRLRSVTAADTAV YYCARYVAAPDYFDYWGQGITLVSS	1099	SYVLTOPPSVSVAPGQOTARISCGNNGISKSVWYQORPGQA PVL.VVYDDSDRSPGIPDRFSGSKSGNTATLTISRVEAGDEADY YQVWDSNSDHRVFGGTKL.TVL	1318

VR0000 13861	QLOQWAGALKPSETL.SLTCGVYGGSFSGFYWTWLRQPPGKLE WIGESKHGNTNPNPSLKSRTVITSVDTSKNQLSLKLSNVTAAADTAV YYCARDVERPYFDYWGOGLTVTVSS	1100	SYVLTOPPSVS/APGQATARITCGENNIGSKSVHWYQOKPGQA PVLVVYDDSDRPSGIPERFSGSNSGNTATLISRVEAGDEADY YQCWWDSSSDHVVFGGTKLTVL	1319
VR0000 15833	QVOLQESGPGLVKPSGTL.SLTCVAVSGGSISSSNWWSWVRQPPGKGL EWIGDIYSGSTNPNPSLKSRAVALDPSKNQFSLKLSVTAAADTAV YYCARDGGYSAYGSPFDYWGOGLTVTVSS	1101	SYVLTOPPSVS/APGQATARITCGENNIGSKSVHWYQOKPQG APVLVVYDDSDRPSGIPERFSGSNSGNTATLISRVEAGDEAD YQCWWDSSSDHPVFGGTKLTVL	1312
VR0000 13618	QLOQESGPGLVKPSETL.SLTCVSGSGSISSSSYYWGWRQPPGKLE WIGSIYSGTTHNPNPSLKSRTVITSVDTSKNQFSLKLSVTAAADTVVY CARHDWYGGSYGWFDPWGQGLTVTVSS	1102	SYVLTOPPSVS/APGQATARITCGENNIGSKSVHWYQOKPQG APVLVVYDDSDRPSGIPERFSGSNSGNTATLISRVEAGDEAD YQCWWDSSSDHWVFGGTKLTVL	1320
VR0000 17522	QVOLQOWGAGALKPSETL.SLTCVAVGGSFSDYYWSWIRQPPGKLE WIGEISHSGSTYNPSLESRTVITSVTSRNQFSLNLTSTVTAADTAVVY CARDITFMAAAGPFEDYWGOGLTVTVSS	1103	SYVLTOPPSVS/APGQATARITCGENNIGSKSVHWYQOKPQG APVLVVYDDSDRPSGIPERFSGSNSGNTATLISRVEAGDEAD YQCWWDSSSDHWVFGGTKLTVL	1320
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VR0000 15445	QVOLQESGPGLVKPSDTL.SLTCVAVSGYPISSSNWGWWSRQPPGKGL EWIGIYFSGSTYNPNPSLTSRVTMSVDTSKNQFSLKLSVTAVDTAV YYCARKRGPYDYGDFDYWGQGLTVTVSS	1105	SYVLTOPPSVS/APGQATARITCGENNIGSKSVHWYQOKPQG APVLVVYDDTDTRPSGIPERFSGSNSGNTATLISRVEAGDEAD YQCQVWDSSSDHVVFGGTKLTVL	1322
VR0000 15444	QVOLQESGPGLVKPSDTL.SLTCVAVSGYPISSSNWGWWRQPPGKLE WIGIYFSGTYTYPNPSLKSRTVMTSVDTSKNQFSLNLSVTAVDTAVY FCARKPGYSFAYEDYWGOGLTVTVSS	1106	SYVLTOPPSVS/APGQATARITCGENNIGSKNVHWYQOKPQG APVLVVYDDSDRPSGIPERFSGSNSGNTATLISRVEAGDEAD YQCQVWDSDRSDHVIFGGTKLTVL	1323
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VR0000 18327	QVOLVESGGGLVKPGGSLRLSCTASGFSFSDYYMIWIRQAPGKGLD WISYISGTGSAITYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAV YYCARDFGSYAYYYYGMDVWGQGLTVTVSS	1109	SYVLTOPPSVS/APGQATARITCGENNIGSKSVHWYQOKPQG APVLVVYGDSDRPSGIPERFSGSKSGNTATLISRVEAGDEAD YQCQVWDSSSDYVLFGGTKLTVL	1326
VR0000 19086	QVOLVESGGGVVQPGSLRLSCAASGTFSTYGMYYWVRQAPGKGL EMVAVISYDGDKEYADSVKGRFTISRDNASKNTLFLQMNSLRAEDT AYYYCAKDPGSGTYHYHYGMDVWGQGLTVTVSS	1036	SYVLTOPPSVS/APGQATARITCGENNIGSKNVHWYQOKPQG APLVVYDDSDRPSGIPERFSGSNSGNTATLISRVEAGDEAV YYSQVWDSSSDHVVFGGTKLTVL	1327
VR0000 18762	QVOLVESGGGVVQPGSLRLSCAASGTFSTYGMHWWVRQAPGKGL EMVALISYDGNKKYADSVKGRFTISRDNASKNTLFLQMNSLRAEDT AYYYCAKPGVNIVATIWHFHQHWGOGLTVTVSS	1110	SYVLTOPPSVS/APGQATARITCGENNIGSKSVHWYQOKPQG APVLVVYDDSDRPSGIPERFSGSNSGNTATLISRVEAGDEAD YQCQVWDSSSDHVVFGGTKLTVL	1328
VR0000 04897	EVOLLESGGGLVOPGSLRLSCAASGTFSTYAMSWVRQAPGKGLE WVSGISGSGGTTYAEFVKGRFTISRDNASKNTLQMNSLRAEDTAV YYCAKPALDIWQGDYYYGMDVWGQGLTVTVSS	1111	SYELTOPPSVS/APGQATARITCGENNIGSKSVHWYQOKPQGS PVLVIYQDRKRPSGIPERFSGSNSGNTATLTISGTQAMDEADY YQCAWDITSNVVFEGGTKLTVL	1329
VR0000 04896	EVOLLESGGGLVOPGSLRLSCAASGTFSTYAMSWVRQAPGKGLE WVSGISGSGGTTYAEFVKGRFTISRDNASKNTLQMNSLRAEDTAV YYCAKPALDIWQGDYYYGMDVWGQGLTVTVSS	1111	SYELTOPPSVS/APGQATARITCGENNIGSKSVHWYQOKPQGS PVLVIYQDRKRPSGIPERFSGSNSGNTATLTISGTQAMDEADY YQCAWDSSTVVFEGGTKLTVL	1330

VR0000 01274	EVQLESGGGLIOPGGSRLSCAASGFTFSSYAMSWVRQAPGKGLE WVSAISGSGRTYYADSVKGRFTISRDNKNTLYLQMNSPRAEDTA YYYCAKSMYYSDSSGSYYYGMDVWGQGTIVTSS	1112	SYELTOPPSVSVSPGOTASITCSGDKLGDQYACWYQOLKPGQS PVLVIYQDNKRSPSGIPARFSGSNSGNTATLTISGTQAMDEAD YQCQAWDSSTVVFGGGTKLTYL	1331
VR0000 00083	DVQLESGGGLVOPGGSRLSCAASGFTFSSYAMSWVRQAPGKGLE WVSGISASGGTTYVDSVKGRFTISRDNKNTLYLQMNSLRAEDTAI YYCAKAFHFDLTGYANYYYYGMDVWGQGTIVTSS	1113	SYELTOPPSVSVSPGOTASITCSGDKLGDKYACWYQOKPGQS PVLVIYQDHTRPSGIPERFSGSNSGNTATLTISGTQAMDEADY YQCQAWDSNTVVFGGGTKLTYL	1332
VR0000 01213	EVQLESGGDLVOPGGSRLSCAASGFTFSSYAMSWVRQAPGKGLE WVSAISGSGTTYADSVKGRFTISRDNKNTLYLQMNSLRAEDTA YYYCAKAVDYDSTGYPEYYYGMDVWGQGTIVTSS	1114	SYELTOPPSVSVSPGOTASITCSGDKLGDKYVVCWYQOKPGQS PVLVIWQDRKRSPGIPERFSGSNSGNTATLTISGTQAMDEADF YQCQWDSSTVVFGGGTKLTYL	1333
VR0000 01212	EVQLESGGDLVOPGGSRLSCAASGFTFSSYAMSWVRQAPGKGLE WVSAISGSGSTDYADSVKGRFTISRDNKNTLYLQMNSLRAEDTA YYYCAKAVDYDSTGYPEYYYGLDVWGQGTIVTSS	1115	SYELTOPPSVSVSPGOTASITCSGDKLGDKYACWYQOKPGQS PVLVIYQDRVRPSGIPERFSGSNSGNTATLTISGTQAMDEADF YQCQWDSNTVVFGGGTKLTYL	1334
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VR0000 11815	EVQLESGGGLVOPGGSRLSCAASGFTFSSYAMNWVRQAPGKGLE WVSVMSGGGSLYYADSVKGRFTISRDNKNTLYLQMNSLRAEDT AVYYCAKTADFYDSSGYPPYYYGMDVWGQGTIVTSS	1117	SYELTOPPLVSVSPGOTASITCSGDKLGDKYACWYQOKPGQS PVLVIYQDRNRSSGIPERFSGSNSGNTATLTISRTQAMDEADY YQCQWDSSTVVFGGGTKLTYL	1336
VR0000 19069	QVQLESVSGGGLVOPGRSLRLSCAASGFTFSTYGMHWVRQAPGKGL EMVAVISYDGSNKYYADSVRGPITISRDNKNTLYLQMNSLRAEDT AVYYCAKDLGDSGSHYYYYYGMDVWGQGTIVTSS	1118	SYELTOPPSVSVSPGOTASITCSGDKVGDKYVCWYQOKPGQS PALVIYQDRKRPSGIPERFSGSNSGNTATLTIGGTQAMDEADY YQCQAWDISNVVFGGGTKLTYL	1337
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VR0000 04122	EVQLESGGGLVOPGGSRLSCAASGFTFSSYAMSWVRQAPGKGLE WVSGISGSGNTYEDSVKGRFTISRDNKNTLYLQMNSLRAEDTAV YYYCAKESGTYRLDAFDIWGQGTIVTSS	1120	SYELTOPPSVSVSPGOTASITCSGDELGDKYASWYQOKPGQS PVLVIYQDISRSPSGIPERFSGSNSRNTATLTISGTQAMDEADY YQCQAWDSGTAVFGGGTKLTYL	1339
VR0000 04019	EVQLESGGGLVOPGGSRLSCAASGFTFSSYAMSWVRQAPGKGLE WVSAISGSGINTYEDSVKGRFTISRDNKNTLYLQMNSLRAEDTAV YYYCAKESGTYRLDAFDIWGQGTIVTSS	1121	SYELTOPPSVSVSPGOTASITCSGDELGDKYASWYQOKPGQS PVLVIYQDTERPSGIPERFSGSNSGNTATLTISGTQAMDEADY YQCQAWDSGTAVFGGGTKLTYL	1340
VR0000 03201	EVQLESGGGLVOPGGSRLSCAASGFTFSSYAMSWVRQAPGKGLE WVSAISGSGNTYEDSVKGRFTISRDNKNTLYLQMNSLRAEDTA YYYCAKESGTYRLDAFDIWGQGTIVTSS	1122	SYELTOPPSVSVSPGOTASITCSGDELGDKYASWYQOKPGQS PVLVIYQDTERPSGIPERFSGSNSGNTATLTISGTQAMDEADY YQCQAWDSGTAVFGGGTKLTYL	1341
VR0000 04023	EVQLESGGGLVOPGGSRLSCAASGFTFSSYAMSWVRQAPGKGLE WVSAISGSGVNTYEDSVKGRFTISRDNKNTLYLQMNSLRAEDTA YYYCAKESGTYRLDAFDIWGQGTIVTSS	1123	SYELAOPPSVSVSPGOTASIACSGDNLGDRFACWYQOKPGQS PVLVIYQDNKRPSGIPERFSGSNSGNTATLTISGTQAMDEADF YQCQWDRNTAVFGGGTKLTYL	1342
VR0000 15290	QVQLESGGGLVOPGGSRLSCAASGFSSYAINWVRQAPGKGLE WVSSISGSGSTSYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAV YYCAKEGYDTSYHPDYWGQGTIVTSS	1124	SYELTOPPSVSVSPGOTASITCSGDLGDKFACWYQOKPGQS PVLVIYQDNKRPSGIPERFSGSNSGNTATLTISGTQAMDEADY YQCQWDRSIAVLGGGTKLTYL	1343
VR0000 01279	EVQLESGGGLIOPGGSRLSCAASGFTFNTYDMTWVRQAPGKGLE WVSTISGSGNTYYADSVKGQFTISRDNKNTLYLQMNSLRPEDTAL YYCARLDSPTTGYDPEFDIWGQGTIVTSS	1125	SYELTOPPSVSVSPGOTASITCSGDKLGDKFACWYQOKPGQS PVLVIYQDNKRPSGIPERFSGSNSGNTATLTISGTQAMDEADY YQCQAWDRTTAVFGGGTKLTYL	1344

VR0000 04727	EVQLES GGGL VOPGGS LRLSCAASGFTFSS YTMITWVRQTPGKGLE WVSVISGSGATS Y ADS VKGRFTVSRGDSNN TL YLQMNSLRAEDTA IYYCAKVN YDITGVDPLDHWGQGT LVTYSS	1126	SYELIQPVS VSPGQTASITCSGDKLGDKFACWYQORPGQS VLVIYQDSKRPSGIPERFSGSNSGNTATLTIRGTQAMDEGDY CQIWVANTVVEGGGTQLTVL	1345
VR0000 05033	EVQLES GGGL VOPGGS LRLSCAASGFTFSSNDMSWVRQAPGKGLE WVSIGSGGSTDY ADS VKGRFTISRDN SKNTL YLQMNSLRAEDTA VYYCAKL DYDTIGYFPDHWGQGT LVTYSS	1127	SYELTOPPVS VSPGOTASITCSGEKLGDKFACWYQOKPGQS PVLVIYQDSKRPSGIPERFSGSNSGNTATLTISGTQAMDEADY YCOAWVRTVVEGGGTKLTVL	1346
VR0000 01286	EVQLES GGGL VOPGGS LRLSCAASGFTFSSCDMNWVRQAPGKGLE WVSVISGSGRTY Y ADS VKGRFTISRDN SKNTL YLQMNSLRAEDTA VYYCAKMEYDSSGYSPFDYWGOGT LVTYSS	1128	SYELTOPPVS VSPGOTATITCSGDKLGDKFAYWYQOKPGQS PVLVIYQDKQRPSGIPERFSGSNSGNTATLTISGTQAMDEAVY YCQIRVINTVVEGGGTKLTVL	1347
VR0000 01182	EVQLDS GGGL VOPGGS LRLSCAASGFTFSTYDMSWVRQAPGKGLE WVSSVSGSGNTY YTDS VKGRFTISRDN SKNTL YLQMHSLRAEDTA VYYCAKEDYDITSGYNYFDYWGOGT LVTYSS	1129	SYELTOPPVS VSPGOTASITCSGDKLGDKFACWYQOKPGQS PVLVIYQDNKRPSGIPERFSGSNSGNTATLTISGTQAVDEADY YCQIWDISTVVEGGGTKLTVL	1348
VR0000 01574	EVQLES GGGL VOPGGS LRLSCAASGFTFNNYAMNWVRQAPGKGL EWSVISGSGNTY Y ADS VKGRFTISRDN SKNTL YLQMNSLRAEDTA VYYCAKEDADSTGYDPFDYWGOGT LVTYSS	1130	SYELTOPPVS VSPGOTASITCSGDKLGDKFVCWYQOKPGQS PVLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADF YCQIWTNTAVFEGGTRLTVP	1349
VR0000 00655	EMQLES GGGL VOPGGS LRLSCAASGFTFSNYAMIWVRQTPGKGLE WVSTISGSGNTDHDADS VKGRFTISRDN SKNTL YLQMNSLRATEDTA VYYCAKEDHDLTGYSPFDYWGOGT LVTYSS	1131	SYELTOPPVS VSPGOTASITCSGDKLGDKFVCWYQOKPGQS PVLVIYQDTKRPSGIPERFSGSNSGNTATLTISGPQAMDEADY YCQIWDFTTVVEGGGTKLTVL	1350
VR0000 03001	EVQLES GGGL VOPGGS LRLSCAASGFTFSSYAMNWVRQAPGKGLE WISSISGSGTPLY Y ADS VKGRFTISRDN SKNTL YLQINSLRAEDTAVY YCAKEGEDSTGYYPDHWGOGT LVTYSS	1132	SYELTOPPVS VSPGOTASITCSGDKLGDKFVCWYQOKPGRS PVLVIYQDHSRPSGIPERFSGSNSGNTATLTISGPQAMDEADY YCQIWTVSTAFEGGTKLTVL	1351
VR0000 04737	EVQLES GGGL VOPGGS LRLSCAASGFTFSSYAMTWVRQAPGKGLE WVSGISGSGSTY Y ADS VKGRFTISRDN SKNTL YLQMNSLRAEDTA VYYCAKNDYDSSGYDYFDYWGOGT LVTYSS	1133	SYELTOPPVS VSPGOTASITCSGDKLGDKDYCWYQOKPGQS PVLVIYQDNKRPSGIPERFSGSNSGNTATLTISGTQAMDEADY YCQAWDSSTVVEGGGTKLTVL	1352
VR0000 05036	EVQLES GGGL VOPGGS LRLSCEASGFTFSSYAMTWVRQAPGKGLE WISISGSGWTNHADS VKGRFTISRDN SKNTLNLQMNSLRAEDTAV YYYCAKEHSSGWYFYFDYWGOGT LVTYSS	1134	SYELTOPPVS VSPGOTASITCSGDKLGDKFVCWYQOKPGQS PVLVIYQDNKRPSGIPERFSGSNSGNTATLTISGTQAMDEADY YCQAWDSSTVVEGGGTKLTVL	1330
VR0000 01203	EVQLES GGDLQOPGGS LRLSCAASGFTFSSYAMSWVRQAPGKGLE WVSGISGSGGSTCADSVKGRFTISRDN SKNTL YLQMNSLRAEDTAI YYCARDGDDYGDYDFD YWGOGT LVTYSS	1135	SYELTOPPVS VSPGOTASITCSGDRLGDKYACWYQOKPGQS PVLVIYQDNKRPSGIPERFSGSNSGNTATLTISGTQAMDEADY YCQIWDSSSTVVEGGGTKLTVL	1353
VR0000 01202	EVQLES GGDLQOPGGS LRLSCAASGFTFSSYAMNWVRQAPGKGLE WVSGISGSGGSTCADSVKGRFTISRDN SKNTL YLQMNSLRAEDTAI YYCARDGDDYGDYDFD YWGOGT LVTYSS	1136	SYELTOPPVS VSPGOTASITCSGDRLGDKYACWYQOKPGQS PVLVIYQDNKRPSGIPERFSGSNSGNTATLTISGTQAMDEADY YCQIWDSSSTVVEGGGTKLTVL	1353
VR0000 03033	EVQLES GGGL VOPGGS LRLSCAASGFTFSSYAMNWVRQAPGKGLE WVSFISGSGGSTYNADSVKGRFTISRDN SKNTL YLQMNSLSAEDTAV YYCAKDGSYFDSNGPYFDYWGOGT LVTYSS	1137	SFELTOPPVS VSPGOTASITCSGDKLGDKYAYWYQOKPGQS PVLVIYQDNKRPSGIPERFSGSNSGNTATLTISGTQWMEADF YCQAWDSSTAVFEGGTKLTVL	1354
VR0000 18192	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYMSWVRQAPGKGLE WVSYLSGGSTRHYADSVKGRFTISRDN SKNTL YLQMNSLSAEDTA VYYCARLDVHSSGYYPFDYWGOGT LVTYSS	1138	SYDLTOPPVS VSPGOTASITCSGDKLGDKFACWYQOKPGQS PVLVIYQDNKRPSGIPERFSGSNSGNTATLTISGTQAMDEADY YCQAWASSTVVEGGGTKLTVL	1355
VR0000 18171	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYMSWVRQAPGKGLE WVSYISSSGSTIYHADSVKGRFTMSRDNAKNSL YLQMNSLRAEDTA VYYCARLDNYDSTGYYPFDYWGOGT LVTYSS	1139	SYDLTOPPVS VSPGOTASITCSGDKLGDKFACWYQOTPGQS PVLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADY YCQAWDRITTVVEGGGTKLTVL	1356

VR0000 14699	QVHLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLE WVSYISSGGSTIYYTDSVKGRFTMSRDNAKNSLYLQMDSLTAEDTA VYYCASLDNYESGGYYPEDYWGOGTLVTYSS	1140	SFELTQPPSVSVSPGQTASITCSGHNLDGKFTSWYQOKPGQSP VLVIFQDNKRPSGIPERFSGSNSGNTATLTISGTQALDAADYY QOAWESTAIFFGGTKLTVL	1357
VR0000 14700	QVHLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLE WVSYISTGGSAIYYADSVKGRFTISRDNAKNSLFLQVNSLRAEDTAM YFCARQDNYESGGYYPEDSWGQGTLYTVSS	1141	SYELTQPPSVSVSPGQTASIACSGDKLDGKFACWYQOKPGQS PVLVIFQDNKRPSGIPERFSGSNSGNTATLTISGTQAMDEADY YCOAWDSSTVVFGGTKLTVL	1358
VR0000 18018	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYDMSWIRQAPGRGPE WVSHISTGGSSKYYADSMKGRFTISRDNAKNSLYLQMNSLRAEDTA VYYCARLDNYESGGYYPEDYWGOGTLVTYSS	1142	SYEVTQPPSVSVSPGQTASITCSGDKMGDKFYCWYQOKPGQ SPVLVIYQDNRKPSGIPERFAGSKSGNTATLTISGTQAMDEAD YNCQAWDSSTVVFGGTKLTVL	1359
VR0000 18325	QVQLVESGGGLVKPGGSLRLSCASGFTFENDYYMSWIRQAPGKGLE WVSHLSTGGTTIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTA VYYCTRADNYESGGYYPEDYWGOGTLVTYSS	1143	SYELTQPPSVSVSPGQTASITCSGDRLGEKFAWYQOKPGQSP LLVIYQDTRKPSGIPERFSGSNSGDTATLTISGTQAMDEADFY COAWDRSTVVFGGTKLTVL	1360
VR0000 01139	EVLLLESGGGLVQPGGSLRLSCAASGFTFSSYDMSWVRQAPGKGLE WVSTISGGSGSTIYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTA VYYCAKEDSYESTGYYPEDYWGOGTLVTYSS	1144	SYELTQPPSVSVSPGQTASITCSGDKLDGKFACWYQOKPGQS PVLVIYQDSKRPSGIPERFSGSNSGNTATLTISGTQAMDEADY YCOARVINIVVFGGTKLTVL	1361
VR0000 02972	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMDWVRQAPGKGLE WVSAISGGSGITTSADSVKGRFTISRDNKNTLYLQMNSLRAEDTAV VYYCAKEDNYESTGYYPEDYWGOGTLVTYSS	1145	SYELTQPPSVSVSPGQTASITCSGDKLDGKFACWYQOKPGQS PVLVIYQDSKRPSGIPARFSGSNSGNTATLTISGTQAMDEADY YCOITWVRSITVVFGGTKLTVL	1362
VR0000 04801	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTSDMNWVRQAPGKGLE WVSAISGGSGTTIYYADSVTGRFTISRDNKNTLYLQMNSLRAEDTA VYYCAREDHYDSTGYYPEDYWGOGTLVTYSS	1146	SYELTQPPSVSVSPGQTASITCSGDKLDGKFVWCWYQOKAGQS PVLVIYQDSKRPSGIPERFSGSNSGNTATLTISGTQAMDEADY FCQARDITTVFVGGLTKLTVL	1363
VR0000 18183	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLE WVSYISSSGYTTIYYADSVKGRFTISRDNAKNSLSLQMNSLAEDTAV VYYCARSEQWLWDWYEDLWGRGTLVTYSS	1147	SYELTQPPSVSVSPGQTASITCSGERLDGKFACWYQOKPGQS PVVVIYQDNKRPSGIPERFSGSNSGNTATLTISGTQAMDEADY YCOITWVRSITVVFGGTKLTVL	1364
VR0000 18206	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGRGLE WVSYITSSAYTTIYYADSVKGRFTISRDNAKNSLFLQMNSLRAEDTAV VYYCVRVSYDSTGYYPEDYWGOGTLVTYSS	1148	SYELTQPPSVSVSPGQTASITCSGDKLDGKFACWYQOKPGQS PVLVIYQDTRKPSGIPERFSGSNSGNTATLTISGTQAMDEADY YCOAWVRSITVVFGGTKLTVL	1365
VR0000 29539	QVQVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQTPGKGLE CISYISSSVSSSVTTIYYADSVKGRFTISRDNAKNSLFLQMNSLRAED TAVYYCARSDSDTSGYYPEDYWGOGTLVTYSS	1149	SYELTQPPSVSVSPGQTASITCSGEKLDGKFAWYQOKPGQS PVLVIFQDNKRPSGIPERFSGSNSGNTATLTISGTQAMDEADY YCOAWVRSITVVFGGTKLTVL	1366
VR0000 18304	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLE WVSYFISSSTLTYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAV VYYCAREDSDTSGYYPEDYWGOGTLVTYSS	1150	SYEMTQPPSVSVSPGQTATITCSGHKLDGKFACWYQOKPGQ SPVLVIYQDSKRPSGIPERFSGSNSGNTATLTISGTQAMDEAD YCCQSWDESTVVFGGTRLLTVL	1367
VR0000 19296	QVQLVGSGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRRAPGKGLE WVSYNISGGGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTA VYYCARDDHYDSGSYFDSWGQGTLYTVSS	1151	SYELTQPPSVSVSPGQTASITCSGDKLDGKFACWYQOKPGQS PVLVIYQDNKRPSGIPERFSGSNSGNTATLTISGTQAMDEADY YCOITWDRSTAVFGGTKLTVL	1368
VR0000 18029	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYHMSWIRQAPGKGOE WVSYIISGYSITYYADSVKGRFTISRDNAKNSLDLQMNSLRAEDTAV VYYCARICVDISTGYDYDYWGQGTLYTVSS	1152	SYELTQPPSLVSPGQTASITCSGDKLDGKFACWYQOKPGQS PELVIFQDNKRPSGIPERFSGSNSGNTATLTISGTQAMDEADY YCOITWDRITTVVFGGTKLTVL	1369
VR0000 15340	QVQLMOSGAEEVKKPGASVSKASGATFTDYLYLHWVRQAPGQG LDWMGRINPNNSGNTIYAQKFOGRVTIMTRDTISISTAYMELSLRSDD TAVYFCARDDSFESTGYYPEDYWGOGTLVTYSS	1153	SYELTQPPSVSVSPGQTASITCSGDKLDGKFACWYQOKPGQS PVLVIYQDSHRPSGIPERFSGSNSGNTATLTISGTQAMDEADY YCOAWVRSITVVFGGTKLTVL	1370

VR0000 28861	QVQLVQSGAEVKKPQGSVKVSCKASGYTFTGYMHVVRQAPGQG LDWMGRINPNSGNTNYAQKFGQGRVTMTTRDTSISTAYMDLSRLTSDSD TAVYYCAREDDYDTSYGSPFEYWGQGTLVTYSS	1154	SYELTQSPSVSVSPGQTASITCSGDKLGDKFACWYHQKPGQS PVLVIYQDNKRPSGIPERFSGSNSGNTATLTISGTQAMDEADY YCOAWDSSIVVFGGGTKLTVL	1371
VR0000 31297	QVQLQSGSPGLVKRBSGTLSLTCAVSGASISSGDWWSVWRQPPGKGL EWIGELIYHSGSTNYPNLSKSRVTISVDTSKNQFSLKLGSVTAADTAV YYCARGTGYDSSGSYSYFYDWGQGLVTYSS	1155	SYELTQPPSVSVSPGQTATITCSGDRLGDKYACWYQOKPAGQ SPVMVHQDTRKPSGIPERFSGSNSGNTATLTISGTQAMDEAE YHCQAWDSSIVVFGGGTKLTVL	1372
VR0000 15471	QVQLQESGPGLVKPSDTLSLTCTVSGSISNNWVGWIRQPPGKGLE WIGYIFSGSTYNNPSLKSRTVMSVDTSKNQFSLKLSVTAVDTAVY YCARVGGYNYDYQLDYWGQGLVTYSS	1156	SYELTQPPSVSVSPGQTASITCSGDKLGDKYACWYQOKPQGS PVLVIYQDSKRPSGIPERFSGSNSGNTATLTISGTQAMDEADY YCOAWDSSIVVFGGGTKLTVL	1373
VR0000 15787	QVQLQESGPGLVKPSGTLSLTCAVSGGISSSDWVNWVRQPPGKGL EWIGELHQSGSTYNNPSLKSRTVSLDKSKNQFSLKLSVTAVDTAVY YCVRGLGGWSWDWGFDYWGQGLVTYSS	1157	SSELTQPPSVSVSPGQTVMICSGDKLGKYACWYQOKPQGS VLVIYQDIKRPAGIPERFSGSGNTAALTISGTQAMDEADY CQAWDSSIVLFGGTKLTVL	1374
VR0000 17797	QVQLQQWGAGLLKPSGTLSLTCAVYGGSFSSYVWSWIRQPPGKGLE WIGELNHSNTTYNNPSLKSRTVTSVDTSKNQFSLNLSVTAAADTAVY CARGGDYDSSGYYPFEDYWGQGLVTYSS	1158	SYELTQPPSVSVSPGQTASITCSGDKLGDKYACWYQOKPQGS PVLVIYQDSKRPSGIPERFSGSNSGNTATLTISGTQAMDEADY YCOAWDSSIVVFGGGTKLTVL	1375
VR0000 13862	QVQLQQWGAGLLKPSGTLSLTCAVSGGSFSGYVWTWIRQPPGKGLE WIGELNHSGTTKYNNPSLKSRTVTSVGTSKNQFSLKLSVTAAADTAVY YCAREGGLYDSSGSEYLOHWGQGLVTYSS	1159	SYELTQPPSVSVSPGQTASITCSGDKLGDKYAYWYQOKPQGS PVLVIYQDSKRPSGIPERFSGSNSGNTATLTISGTQAMDEADY YCOIWDSSIVVFGGGTKLTVL	1376
VR0000 13925	QPOLQESGPGLVKPSETLSLRTCTVPGGSISISYVWAWIRQPPGKGLE WIGSIYSGSTYNNPSLKSRTVTSVDTSKNQFSLKLSVTAAADTAVYF CARPYIDIPLGYYWGQGLVTYSS	1160	SYELTQPPSVSVSPGQTASITCSGDDLGDKYASWYQOKPQGS PVLVIYQDTERPSGIPERFSGSNSGNTATLTISGTQAMDEADY YCOAWDSSIVVFGGGTKLTVL	1377
VR0000 13641	QVQLQESGPGLVKPSETLSLTCTVSGGSISSSYVWGWIRQPPGKGLE WIGTIYSGSTYNNPSLKSRTVMSVDTSKNHFSKLKLSVTAAADTAVY YCARQSLYNNWNPEDYWGQGLVTYSS	1161	SYELTQPPSVSVSPGQTASITCSGDKLGDKYACWYQOKPQGS PVLVIYQDSKRPSGIPERFSGSNSGNTATLTISGTQAMDEADY YCOAWDSSIVVFGGGTKLTVL	1378
VR0000 16026	QVQLQESGPGLVKPSQTLSLTCAVSGGISSSDGYVWSWIRQPPGKGL EWIGYIHYSGITSYNNPSLKSRTVMSVDTSKNQFSLKLSVTAAADTAVY CAGLVELLRTSDYWGQGLVTYSSP	1162	SYELTQPPSVSVSPGETASITCSGDKLGDKYAYWYQOKPQGS PVLVIYQDSTRPSGIPERFSGSNSGNTAALTISGTQAMDEADY CQAWDSSIVVFGGGTKLTVL	1379
VR0000 13455	QVQLQESGPGLVKPSETLSLTCTVSGGSISSSRYVWGWIRQPPGKGLE WIGSINYSGRTYNNPSLKSRTVTSVDTSENQFSLNLSVTAAADTAVY YCARHEERGFDPYWGQGLVTYSS	1163	SYELTQPPSVSVSPGQTASITCSGDKLGDKFVACWYQOKPQGS PVLVIYQNSKRPSGIPERFSGSNSGNTAALTISGTQAMDEADY YCOAWDSRTAVFGGTKLTVL	1380
VR0000 12875	QVQLQASGPGLVKPSETLSLTCTVSDSITSYTYVWGWIRQPPGKGL EWIGTIHYSGSTYYSPLSKSRVTMPDSSKNQFSLRLTSVTAAADTALY YCARHEVGGGFDYWGQGLVTYSS	1164	SYELTQPPSVSVSPGQTASITCSGDKLGDKFVACWYQOKPQGS PVLVIYQDRWRPSGIPERFSGSNSGNTAALTISGTQAMDEADY YCOAWDRSTVVFGGGTKLTVL	1381
VR0000 13031	QVQLQESGPGLVKPSETLSLTCTSVSGGSISNSSHYVWGWIRQPPGKGLE WIGSIYGGSTYNNPSLKSRTVTSVDTSKNQFSLKLSVTAAADTALY CARHDSDDYFDFWGGQGLVTYSS	1165	SYELTQPPSVSVSPGQTASITCSGDKLGDKFASWYQOKPQGS PVLVIYQDKRKRPSGIPERFSGSNSGNTAALTISGTQAMDEADY YCOAWDSSVVFEGGTKLTVL	1382
VR0000 13185	QVQLQESGPGLVKPSETLSLTCTVSGGSISNSDFVWGWIRQPPGKGL EWIGDIYFSGNTYNNPSLKSRTVTSVDTSKNQFSLKLSVTAAADTAVY YCARVVGAPDYFDYWGQGLTVSVSS	1166	SYELTQPPSVSVSPGQTAIITCSGDKLGDKFASWYQOKPQGS PVLVIYQDKRKRPSGIPERFSGSNSGNTAALTISGTQPTDEADY YCOAWDSSIVVFGGGTKLTVL	1383
VR0000 12856	QVQLQESGPGLVKPSETLSLTCTVSGGSIRSSDYVWGWIRQPPGKGL EWIGDIYFSGRTYNNPSLKSRTVTSVDTSKNQFSLKLSVTAAADTAV YVCAREGPTDYFDYWGQGLVTYSS	1167	SYDLTOPPSVSVSPGQTANITCSGDKLGDKFVACWYQOKPQGS PVLVIYQDKRKRPSGIPERFSGSNSGNTAALTISGTQAMDEADY YCOAWDSSAVVFEGGTKLTVL	1384

VR0000 13715	QLOQESGPGLVKPSETLSLCTVSGSGSISTSNYYWGWIROPKGL EWIGDVNYSGNTYNNPSLKSRTVITSVDTSKNQLSLSSVTAADTAV YSCARIGDIDYFDYWGQGLTVTSS	1168	SYDLTOPPSVSVSPGOTASITCSGDKLGDKFACWYQOLKSGQS PVLVIYQDNRKRPSPGIPERFSGSNSGNTATLTISGTQAMDEADY YCOAWDSSTVVFGGGTKLTVL	1385
VR0000 13471	QLOQESGPGLVKPSETLSLCTVSGSGSISSEFYWDWIRQPPKGLE WIGSIYFSGSTYNNPSLKSRTVITSVDTSRNOFSELSVNAADTAAY CARREPAADLTLDYWGQGLTVTSS	1169	SYELAQPPSVSVSPGOTANITCSGDKLGDKFACWYQOKPGQS PVLVIYQDNRKRPSPGIPERFSGSNSGNTATLTISGTQAMDEADY YCOAWDSSTVVFGGGTKLTVL	1386
VR0000 17649	QVQLQOWGAGLLKPSETLSLTCVAVYGGSFSGYYWSWIRQPPKGLE WIGENHSGTNNPSLKSRTVITSVDTSKNQFSLKSSVTAADTAVYF CARNFYDTSGFYSFDSWGQGLTVTSS	1170	SYELTOPPSVSVSPGOTASITCSGDKLGDKFASWYQOKPGQS PVLVIYQDNRKRPSPGIPERFSGSNSGNTATLTISGTQAMDEADY YCQIWASSTVVFGGGTKLTVL	1387
VR0000 17512	QVQLQOWGAGLLKPSETLSLTCVAVYGGSFSDYYWSWIRQPPKGLE WIGENHNGTNNPSLKSRTVITSVDTSKNQFSLKSSVTTADTAVY FCARNFYDTSGFYSFDSWGQGLTVTSS	1171	SYELTOPPSVSVSPGOTASITCSGDKLGDKFASWYQORPGQS PVLVIYQDNRKRPSPGIPERFSGSNSGNTATLTISGTQAVDGADF YCQIWASSTVVFGGGTRLTVL	1388
VR0000 17720	QVQLQOWGAGLLKPSETLSLTCVAVYGGSFSGYYWSWIRQPPKGLE WIGENHSGSTNNPSLKSRTVITSVDTSKNQFSLKSSVTAADTAVY YCARSYQDSSGFSFSDYWGQGLTVTSS	1172	SYDLTOPPSVSVSPGOTASITCSGDKLGDKFASWYQOKPGQS PMLVIYQDNRKRPSPGIPERFSGSNSGNTATLTISGTQAVDEADY CCQIWASSTVVFGGGTKLTVL	1389
VR0000 17506	QVQLQOWGAGLLKPSETLSLTCVAVYGGSFSDYYWSWIRQPPKGLE WIGDVNHSGSTDYNNPSLKSRTVITSVDTSKNQFSLKSSVTAADTAV YYCARGNYDTSGYNWDPPWGQGLTVTSS	1173	SYDLTOPPSVSVSPGOTASITCSGDKLGDKFVCMWYQOKPGQS PVLVIYQDNRKRPSPGIPERFSGSNSGNTATLTISGTQALDEADY COAWASSTVVFGGGTKLTVL	1390
VR0000 17785	QVQLQOWGAGLLKPSETLSLTCVAVYGGSFSGYYWTWVROPPKGL EWIGENHRTGNTNNPSLTSRTVITSVDTSNNQFSLRLSSVTAADTAVY FCARGHPDTSGFYSFSDYWGQGLTVTSS	1174	SYELTOPPSVSVSPGOKASITCSGDKLGDKFACWYQOKPGQS PVLVIYQDNRKRPSPGIPERFSGSNSGNTATLTISGTQAMDE ADYYCOAWDSRIVVFGGGTKLTVL	1391
VR0000 13050	QLOQESGPGLVKPSETLSLCTVSGSGSISSESHYWGWIROPKGLE LIGFYYSGNTYNNPSLKSRTVITSVDTSKNQFSLKLSVTAADTAVY YCARGDHDSGYYGYFDVWGRGTLTVTSS	1175	SYELTOPPSVSVSPGOTASITCSGDKLGDKFACWYQOKPGQS PVLVIYQDNRKRPSPGIPERFSGSNSGNTATLTISGTQAVDEADY YCQIWDEFSTVVFGGGTKLTVL	1392
VR0000 13872	QLOQESGPGLVKPSESLSLCTVSGSVSSSTNNYWGWIROPKGL EWIGSFFSGGTTYSPSLKSRLIIPVDTSKTQFSLKLSVTAADTAVY YCARHSYDASGYDYFDYWGQGLTVTSS	1176	SYELTOPPSVSVSPGOTASFSCSGHTLGDKFACWYQOKSGQS PVLVIYQDNRKRPSPGIPDRFSGSNSGNTATLTISGTQAMDEADY YCQIWDNSTVVFGGGTKLTVL	1393
VR0000 13395	QLOQESGPGLVKPSETLSLCTVSGSGSISSEGYWGWIRQPPKGL EWIGNIYYSKTTYKPSLKSRTVITSLDTSKNQFSLKLSVTAADTAV YYCARHGTRHYYESGYYEGYFDYWGQGLTVTSS	1177	SYELTOPPSVSVSPGOTASITCSGDKLGDKFACWYQOKPGQS PVLVIYQDNRKRPSPGIPERFSGSNSGNTATLTISGTQAMDEADY YCQIWEFSTVVFGGGTKLTVL	1394
VR0000 13396	QLOQESGPGLVKPSETLSLCTVSGSGSISSEGYWGWIRQPPKGL EWIGNIYYSKTTYKPSLKSRTVITSLDTSKNQFSLKLSVTAADTAV YYCARHGTRHYYESGYYEGYFDYWGQGLTVTSS	1177	SYELTOPPSVSVSPGOTASITCSGDKLGDKYACWYQOKPGQS PVLVIYQDNRKRPSPGIPERFSGSNSGNTATLTISGTQAMDEADY YCQAWDSSNVVFGGGTKLTVL	1395
VR0000 13186	QLOQESGPGLVKPSETLSLCTVSGSGSISSESHYWGWIROPKGL EWIGITIYAGNTYNNPSLKSRTVITSVDTSKNQFSLKLSVTAADTAV YYCARHVQLERPPYYYYYGMDVWGQGLTVTSS	1178	SYELTOPPSVSVSPGOTASITCSGDKLGDKYACWYQOKPGQS PVLVIYQDNRKRPSPGIPERFSGSNSGNTATLTISGTQAMDEADY YCQAWDSSSTVVFGGGTKLTVL	1396
VR0000 30698	QVQLQESGPGLVKPSETLSLCTVSGSGSISSESHYWGWIROPKGL EYIGNMYFGDITYNNPSLKSRTVITSVDTSKNQSLKLSVTAADTAV YYCARYNSGGDWEDPWGOGLTVTSS	1179	DIOMTQPSLSASVGDREYITTCRASOGIRNDLGWYQOKPGK APKRLIYAASSLQSGVPSRFSGSGTEFTILTISLQPEDFATY YCLQHNSYPHTEGOGKLEIK	1397
VR0000 30699	QVQLQESGPGLVKPSETLSLCTVSGSGSISSESHYWGWIROPKGL EYIGNMYFGDITYNNPSLKSRTVITSVDTSKNQSLKLSVTAADTAV YYCARYNSGGDWEDPWGOGLTVTSS	1179	SYELTOPPSVSVSPGOTARITCSGDALPKKYAYWYQOKSGQ APVLVIYEDSKRPSGIPERFSGSNSGNTATLTISGAQVEDEAD YHCYSTIDSSGNHYVFGGGTKLTV	1398

VR0000 13694	QQLQESGPGLVKPSETLSLCTVSGGSISSTSYWGWIRQPPGKGL KMWISIIYSGNTYYNPISLKSRTVISVDTSKNQFSLKLSSTLAADTAVY YCARHPAVAGTIPEDYWGOGLVTYSS	1180	SSELTDPPAVSVVALGQTVRITTCQGDLSRSTYASWYQOKPGQ APVLVIYGNRNRPSGIPDRFSGSSSGNTASLTITGAQAEDEAD YYCNSRDSGHNHVFEGGTKLTVL	1399
VR0000 30523	QVQLQESGPGLVKPSETLSLTCNVSGGSISGDSYWSWIRQHPGKGL EWIGIYDSGYTDYNPISLKSRLTISVDTSKNQFSLKLSRTAADTAIY YCARRELTGDAFEDIWGQGMVTYSS	1181	SSELTQDPAVSVALGQTVRITTCQGDLSRSTYASWYQOKPGQ APVLVFIYDKNNRPSGIPDRISGSSSGNTASLTITGAQAEDEAAY YYCNSRDSGAMHVFEGGTKLTVL	1400
VR0000 13879	QLQVQESGPGLVKPSETLSLCTVSGGSISNSNYWGLIRQPPGKGLE WIGSIFHGNTYFNPSLKSRTVISVDTSKNQFSLRLRSVTAADTAVY CARYVAAPDYFDYWGOGLVTYSS	1182	SSELTQDPAVSVALGQTVRITTCQGDLSRSTYASWYQOKPGQ APVLVIYGNRNRPSGIPDRFSGSSSGNTASLTITGAQAEDEAD YYCNSRDSGHNHVFEGGTKLTVL	1399
VR0000 13640	QLQVQESGPGLVKPSETLSLCTVSGGSISSSSYWGWIRQPPGKGLE WIGTIYSGSTYYNPISLKSRTVMSVDTSKNHFSLKLSSTAADTAVY YCARQSLYNWNPFDYWGOGLVTYSS	1161	SSELTQDPAVSVALGQTVRITTCQGDLSRSTYASWYQOKAGQ APGLVHGENNRPSGIPDRFSGSSSGNTASLTITGAQAEDEAD YYCNSRDSNVNHLFEGGTKLTVL	1401
VR0000 17365	QVQLQWDAGLLKPSETLSLTCVYGGSFSGYWSWIRQPPGKGLE WIGEINHSGSTKNPISLKSRTVISVDTSKNQFSLKLSRTAADTAIY CAREWELLGFDYWGOGLVTYSS	1183	SSELTQDPAVSVALGQTVRITTCQGDLSRSTYASWYQOKPGQ APVLVIYGRNSRPSGIPDRFSGSSSGNTASLTITGAQAEDEAD YYCNSRDISGDYVLFEGGTKLTVL	1402
VR0000 15975	QVQLQESGPGLVKPSQTLFLCTVSGDSISSGYYWSWIRQHPGKGL EWIGIYISGSTYYNPISLKSRTVISIDTSKNQFSLKLSSTAADTAVY FCARDRVGSTDPAFDIWGOGIMVTYSS	1184	SSELTQDPAVSVALGQTVRITTCQGDNLRSYFASWYQOKPGQ APVLVIYGNRNRPSGIPDRFSGSSSGNTASLTITGAQAEDEAD YYCNSRDSGDNHVFEGGTKLTVL	1403
VR0000 31085	QVQLQESGPGLVKPSQTLSLCTVSGGSISGGYYWGWIRQHPGKGL DWIGIYISGITYYNPISLKSRTVISVDTSKNQFSLKLSSTAADTAVY FCARDRVGSTDPAFDIWGOGIMVTYSS	1185	SYELTOPPSVSPGQOTARITCSGDALPKKYAYWYQOKSGQ APVLVIYEDSKRPSGIPERFSGSSSGTMTATLTISGAQVEDEAD YYCSDTDSGHNHVFEGGTKLTVL	1404
VR0000 31175	QVQLQESGPGLVKPSQTLSLCTVSGGSISGGYYWGWIRQHPGKGL LEWIGIYITGTTYNPISLKSRTVISVDTSKNQFSLKLSSTAADTAVY YYCATAGYGSWPDPAFDIWGOGIMVTYSS	1186	SSELTQDPAVSVALGQTVRITTCQGDLSRNYVYWYQOKPGQ APVLVIYGNKRRPSGIPDRFSGSSSGNTASLTITGAQAEDEAD YYCNSRDSGDNHVFEGGTKLTVL	1405
VR0000 13926	QPOLQESGPGLVKPSETLSLCTVSGGSISISSYWGWIRQPPGKGLE WIGSIYSGSTYYNPISLKSRTVISVDTSKNQFSLKLSSTAADTAVY CARPYIDIPLGYWGOGLVTYSS	1187	SYELTOPPSVSPGQOTARITCSGDALPSQYAYWYQOKPGQA PVMVIYKDSERPSGIPERFSGSSSGTTVTLTISGVQAEDEADY YCOQSTVNSVGYVVFEGGTTLTVL	1406
VR0000 13927	QPOLQESGPGLVKPSETLSLCTVSGGSISSSSYWGWIRQPPGKGLE WIGSIYSGSTYYNPISLKSRTVISVDTSKNQFSLKLSSTAADTAVY CARPYIDIPLGSWGOGLVTYSS	1188	SYELTOPPSVSPGQOTARITCSGDALPNHYAYWYQOKPGQ APVLVIYKDSERPSGIPERFSGSSSGTTVTLTINGVQAEDEAD YCCQSTDNSVGYVVFEGGTTLTVL	1407
VR0000 13617	QLQLQESGPGLVKPSETLSLCTVSGGSISSSSYWGWIRQPPGKGLE WIGSIYSGTTHYNPISLKSRTVISVDTSKNQFSLKLSSTAADTAVY CARHDWYGGSYGWFDPWGOGLVTYSS	1102	SYELTOPPSVSPGQOTARITCSGDALPSQYAYWFKQOKPGQA PVMVIYKDSERPSGIPDRFSGSSSGTTVTLTISGVQAEDEADY YCOQSTVNSVGYVVFEGGTTLTVL	1408
VR0000 13080	QLQLQESGPGLVKPSETLSLCTVSDGSISGRYYWGWIRQPPGKGL EWIAITHHSGSTYYNPISLKSRTVISVDTSKNQFSLKLSSTAADTALY YCARQSLWFEPEGDYWGOGLVTYSS	1189	SYELTOPPSVSPGQOTARITCSGDALPKQYAYWNOQRPGQA PVLMLFKDSERPSGTPERFSGSSSGTTVTLTISGVQAEDEADY YCOQADTSGTYWVFEGGTKLTVL	1409
VR0000 13464	QLQLQESGPGLVKPSETLSLCTVSGGSISSSSYWGWIRQPPGKGLE WIGTMHSSGSTYYNPISLKSRTVISIDTPKNQSLKLSSTVTAADTAVY YCARHEVSGGFDYWGOGLVTYSS	1190	SYELTOPPSVSPGQOTARITCSGDALPKQYAYWNOQRPGQA PVMVIYKDSERPSGIPERFSGSSSGTTVTLTISGVQAEDEADY YCOQADSGIWWVFEGGTKLTVL	1410
VR0000 15855	QVQLQESGPGLVKPSGTLSLTCVYSGGSISSNWWSWIRQPPGKGL EWIGEIYHSGSTYNPISLKSRTVISIDSKTNOFSLKLSSTVTAADTAMY YCARDGYDDGSYYSSFDRWGOGLVTYSS	1191	SYELTOPPSVSPGQOTARITCSGDALPKQYACWHQOKPGQA PVLVIYKDSERPSGIPARFSGSSSGTTVTLTISGVQAEDEADYS COQADSTGTWVFEGGTKLTVL	1411

VR0000 17631	QVQLQQWGAELLPSEITLSTCAVYGGSFSGYYWSWIRQPPGKLE WIGELKHSSTNPNPSLKSRTVITISVDTSKNQFSLKLSSTVAADTAVYY CAKRDYDTSGYDFDYWGQGTLVTYSS	1192	SYELTQPPSVSVSPGQTARITCSGDALPKKYAYWYQOKSGQ APVLVIYEDSKRPSGIPERFSGSSGTMATLTISGAQVEDEAD YYCYSTDSSGNHRVYFGGTKLTVL	1227
VR0000 17632	QVQLQQWGAELLPSEITLSTCAVYGGSFSGYYWSWIRQPPGKLE WIGELKHSSTNPNPSLKSRTVITISVDTSKNQFSLKLSSTVAADTAVYY CAKRDYDTSGYDFDYWGQGTLVTYSS	1192	SYELTQPPSVSVSPGQTASITCSGDKLGDKFACWYQOKPGQS PVLVIYQDNKRPSGIPERFSGSNSGNTATLTISGTQAMDEAGY YCOITWDSNTAVFGGTKLTVL	1412
VR0000 17768	QVQLQQWGAELLPSEITLSTCAVYGGSFSGYYWTWIRQPPGKLE WIGEFHSGSTNPNPSLKSRTVITISVDTSKNQFSLKLSSTVAADTAVYF CARGMDSGFSYDFDWGQGTLVTYSS	1193	SYVLTPPSVSVAPGQTARITCGGNIGSKSVHWYQOKPQG APVLVVYDDSDRPSGIPERFSGSNSGNTATLTISRVEAGDEAD YYCQVWDSDDHVVFGGTKLTVL	1413
VR0000 15460	QVQLQESGPGLVKPSDTLSTCAVSGYSISSNWWGWIRQPPGKLE WIGNIFYSGITYNPNSLKSRTVMTSVDTSKDQFSLKLSSTVAVDTAVY YCARNSKAYSPLYFYFDYWGGQTLVTYSS	1194	SYVLTPPSVSVAPGQPARITCGGNKIASKSVHWYQOKPQQA PVLVVYDDSDRPSGIPERFSGSNSGNTATLTISRVEAGDEADY HCQIWDSSSDHVVYFGGTKLTVL	1414
VR0000 15461	QVQLQESGPGLVKPSDTLSTCAVSGYSISSNWWGWIRQPPGKLE WIGNIFYSGITYNPNSLKSRTVMTSVDTSKDQFSLKLSSTVAVDTAVY YCAKNSKAYSPLYFYFDYWGGQTLVTYSS	1195	SYVLTPPSVSVAPGQPARITCGGNIGSKNVHWYQOKPQG APVLVVYDDSDRPSGIPERFSGSNSGNTATLTISRVEAGDEAD YYCQVWDSDDHVVFGGTKLTVL	1415
VR0000 15464	QVQLQESGPGLVKPSDTLSTCAVSGYSISSNWWGWIRQPPGKLE WIGSIYFSGSTYNNPSLKSRTVMTSVDTSKDQFSLKLSSTVAVDTAVY YCARNSKAYSPLYFYFDYWGGQTLVTYSS	1196	SYVLTPPSVSVAPGQTARITCGGNIGSKNVHWYQOKPQG APVLVVYDDGDRPSGIPERFSGSNSGNTATLTISRVEAGDEA DYSCQVWDSDDHVVFGGTKLTVL	1416
VR0000 15463	QVQLQESGPGLVKPSDTLSTCAVSGYSISSNWWGWIRQPPGKLE WIGSIYFSGSTYNNPSLKSRTVMTSVDTSKDQFSLKLSSTVAVDTAVY YCARNSKAYSPLYFYFDYWGGQTLVTYSS	1196	SYELTQPPSVSVSPGQTARITCSGDALPKQYAWYQOKPQG APVLVIYKDSERPSPGIPERFSGSSGTTVTLTISGYQAEDEADY YCOQADSSGTYVYFGGTKLTVL	1417
VR0000 15462	QVQLQESGPGLVKPSDTLSTCAVSGYSISSNWWGWIRQPPGKLE WIGSIYFSGSTYNNPSLKSRTVMTSVDTSKDQFSLKLSSTVAVDTAVY YCARNSKAYSPLYFYFDYWGGQTLVTYSS	1196	QSAITQPASVSGSPGQSTITCTGTSSYVSWYQOHPGKAPKL MIVDVSNRPSGVSNRFSGSGSGNTASLTISGLQAEDEADYYC SSYTSSTPDPVYFGGTKLTVL	1418
VR0000 15459	QVQLQESGPGLVKPSDTLSTCAVSGYSISSNWWGWIRQPPGKLE WIGNIFYSGITYNPNSLKSRTVMTSVDTSKDQFSLKLSSTVAVDTAVY YCARNSKAYSPLYFYFDYWGGQTLVTYSS	1194	DIQMTQSPSTLSASYGDRVTITCRASQSISSWLAWYQOKPGK APKLITYKASSLESQVPSRFSGSGTEFTLTITSSLQPPDFATY YCOQYNSYALTFGGGTKVEIK	1419
VR0000 17043	QVQLQQSGPGLVKPSQTLSTLCAISGDSVSSNNIVWNWIRQSPSRGL EWLGRITYYRSKWNNDYAVSVKSRISINPDTSKNQFSLQLNSVTPEDT AYYYCVREVLWGEFEPDPWGQGTLVTYSS	1197	SSELTQDPVAVSVALGQTVRITCQGDLSLRNYASWYQOKPGQ APVLVIYGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEAD YYCNSRDSSTVNHLLFGGGTKLTVL	1420
VR0001 03638	EVQLVESGGDLVKPGSLRLSCATISGFTFTFSWMNWRQAPGKGLE WVGRKISKIDGGTIDYAAPYKGRFTISRDKNTLYLQMNLSLKTEDT AIYYCTTGGPAFDIWGQGTMTVSS	1718	DIQMTQSPSLSASYGDRVSIITCRASQIDIGNYLAWYQOKPGK LPKLITYSASTLQSGVPSPRFSGSGGTDFTLTITSSLQPEDVVIY YCQKYNSAPLTFGGGTKVEIK	1776
VR0001 03635	EVQLVESGGGLVKPGSLRLSCAVSGFTFTSYNNMNWVRQPGKGLE WVSSISSSSSYIYHADSVKGRFTISRDNAKNSLYLQMNLSRAEDTAV YYCARDKVPGAFDYWGGQTLVTYSS	1719	DIVMTQSPSLPTPGEPAISICRSSQSLHVNNGYNLMDWYL QKPQSPQLLITLGSNKRASGVPRFSGSGGTDFTLKISRVEA EDVGVYYCMAQLQTPYTFGQGTKEIK	1777
VR0001 03752	EVQLVESGGGLEQPGSLRLSCAASGFTFDYAMHWVRQPGKGL EWWSGISWNGGSDYADSVKGRFTISRDNAKNSLYLQMNLSRAED TALYYCAKDMGLEAAAGFYGYGIDYWGGQTLVTYSS	1720	DIQMTQSPSSVASYGDRVTITCRASQIGISSWLAWYQOKPGK APKLITYAASLSQGYPSRFSGSGGTDFTLTITSSLQPEDFATY YCOQANSFPFTFGQGTKEIK	1778
VR0001 03741	QVQLQQWGAELLPSEITLSTCAVYGGSFSDYYWSWIRQPPGKGLE WIGESDYSGSTKYNPISLESRTVITISADTSKNQFSLKLTSTVAADTAVY YCARVPDSGSYDFDFWGGQTLVTYSS	1721	DIQMTQSPSLSASYGDRVTITCRASQIGIRNDLGWYQOKPGK APKRLITYAASSLSQGYPSRFSGSGGTEFTLTITSSLQPEDFATY YCLQHNSYPTFTFGQGTKEIK	1779

VR0001 03640	EVQLVESGGGLVKPGGSLRLSCTASGFTFSNYNMNVVRQAPGKGLE WVSTITSSSTIYYADSVKGRFTISRDNAKNSLFLQMNSLRAEDTAIY YCARHITPGGVNDVWGQGDTITVSS	1722	DIQMTQSPSSVTASVIGDRVTITCRASQGVSRWLAWYQQKPG KAPKLIIYAASLQSQGVPSRFSGSGGTAFITLTISLQPEDFAT YQCQADSPFTFGPGTKVDIK	1780
VR0001 03630	EVQLVESGGGQVKPGGSLRLSCAASGTFSSYSMTNVVRQAPGKGLE WVSSIRRSSTIYYADSVKGRFTISRDNAKNSLFLQMNSLRAEDTAV YYCARHHDYSNDAFIDWVGQGLITVSS	1723	DIQMTQSPSAMISASVIGDRVITITCRASQAISHYLAWFQQRPK VPKRLIYAASLQSQGVPSRFSGSGGTFTLTISLQPEDFATY YCLQHNSTPRTFGQGTKVEIK	1781
VR0001 03633	EVQLVESGGGLVOPGGSLRLSCAASGTFITFYWMMSVVRQAPGKGLE WVANIKQDGESEKYYVDSVKGRFTISRDNAKNLLYLQMNSLRAEDT AVFYCARQQQWLVPISHYSGTGTFIDWVGQGLITVSS	1724	AIQMTQSPSSLASVIGDRVITITCRASQDIRNALGWYQQKPGK APKLIIYVSSLQGGVPSRFSGSGGTDFITLTISLQPEDFATY YCLQDYNYPYTFGQGTKLEIK	1782
VR0001 03720	QVQLVESGGGLVKPGGSLRLSCEASGFTFSVYYMMSVIRQAPGKGLE WVSEISNRGITMYYADSVKGRFTISRDNAKNSLFLQMNSLRAEDTA VYYCARRTPEGWEDPWGQGLITVSS	1725	SYELTQPPSVSVSPGQTASITCSGDKLGDKYVSWYQQKPGQS PVVVYYQDSKRPSGTPERLSGSNSGNTATLTISGTQAMDEAD YYCQAWDSTTVVFGGGTKLITVL	1783
VR0001 03726	QVQLVESGGGLVKPGGSLRLSCTASGFTFSNYMTWIRQAPGKGLE WVSDISNRALTMMYADSVKGRFISRDNAKNSLFLQMNSLRAVEDTA VYYCARRTPEGWEDPWGQGLITVSS	1726	SYELTQPPSVSVSPGQTASITCSGDELGNKFASWYQQKPGQS PVVVYYQDNKRPSGTPERLSGSNSGNTATLTISGTQAMDEAD YYCQAWDSSAVVFGGGTKLITVL	1784
VR0001 03685	QVQLVQSGAEVKKPGASVKYSCKASGYAFTSYAFHWVRQAPGQRL EWMGWINAGNGNTKYSQKFGQGRVTITRDTASTAYMELISLRS EDT AVYYCVRAVEDSWGQGLITVSS	1727	SYELTQPPSVSVSPGQTARITCSGDVLAERYARWFQOKPGQA PVLVIYKDSERPISGIPERFSGSGTITVLTISGAQVEDEADY YCYSAAANNL VFGGGTKLITVL	1785
VR0001 03679	QVQLVESGGGVOPGRSLRLSCAASGFTFSTYGMYYVRQAPGKGL EMVAVISYDGSdkYYADSVKGRFTISRDNskyTLFLQMNSLRAEDT AVYYCAKDPGSGTYHYHYYGMDVWGQGTITVSS	1728	QSAITQPASVSGSPQSTITICTGTSSDVGNYNLVSWYQQHP GKAPKLMIYEDSRPSGVSDRFSGSGSGNTASLTISGLQAEDE ADYYCSSYAGSSWVFGGGTKLITVL	1786
VR0001 03756	EVQLVESGGGLVOPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGL EMVSGISWNRDNIGYADSVKGRFTISRDNAKNSLFLQMNSLRAEDT AFYYCAKDIRWGRSGWYPYYHYYSGMDVWGQGTITVSS	1729	QSAITQPASVSGSPQSTIAISCTGTSSDVGGYSVSWYQQHP GKAPKLTIYDISRPSGSVSNRFSGFKSGNTASLTISGLQAEDEA DYYCSSYTSNTLVFGGGTKLITVL	1787
VR0001 03755	QVQLQESGPGLVKPSDITLSTCAVSGYPISSNWGWIRQPPGKGLE WGIYIFSGYTYYNPSLKSRYTMSVDTSKNQFSLKSSVTAVDTA VY FCARKPGGYSEAFYFDYWGQGLITVSS	1730	SYVLITQPPSVSVAPGQTARITCGNNIGSKNVHWYQQKPGQ APVLVYYDDSDRPSGIPERFSGSGNSGNTATLTISRVEAGDEAD YYCQVWDSRSDHVFEGGGTKLITVL	1788
VR0001 03695	QVQLVESGGGLVKPGGSLRLSCTASGFSFSYYMIIWIRQAPGGLD WISYISGTGSAIYYADSVKGRFTISRDNAKNSLFLQMNSLRAEDTAV YYCARDFGSYAYYYHYYGMDVWGQGTITVSS	1731	SYVLITQPPSVSVAPGQTARITCGNNIGSESVHWYQQKPGQA PVLVYYGESDRPSGIPERFSGSGNSGNTATLTISRVEAGDEADY YQVWWDSSSDYVVFEGGGTKLITVL	1789
VR0001 03716	EVQLLESGGGLQPGGSLRLSCAASGTFSSYAMSWVRQAPGKGLE WVSAISGGGRITYYADSVKGRFTISRDNskyNTLFLQMNSPRAEDTA VYYCAKSMYYSDSSGSYYYGMDVWGQGTITVSS	1732	SYELTQPPSVSVSPGQTASITCSGDKLGDKYASWYQOLKPGQS PVVVYYQDNKRPSGIPARFSGSGNSGNTATLTISGTQAMDEAD YYCQAWDSSTVVFGGGTKLITVL	1790
VR0001 03677	EVQLLESGGGLVOPGGSLRLSCAASGTFSSYAMSWVRQAPGKGLE WVSGISASGGGITYYVDSVKGRFTISRDNskyNTLFLQMDSLRAEDTAI YYCAKAHFDELITGYANYYYYGMDVWGQGTITVSS	1733	SYELTQPPSVSVSPGQTASITCSGDKLGDKYASWYQQKPGQS PVLVIYQDHTRPSGIPERFSGSGNSGNTATLTISGTQAMDEADY YQCAWDSNTVVFEGGGTKLITVL	1791
VR0001 03732	EVQLLESGGDLVOPGGSLRLSCAASGTFSSYAMSWVRQAPGKGLE WVSAISGGGSTYYADSVKGRFTISRDNskyNTLFLQMNSLRAEDTA VYYCAKAVDYDSTGYPFYYHYYGMDVWGQGTITVSS	1734	SYELTQPPSVSVSPGQTASITCSGDKLGDKYVSWYQQKPGQS PVLVIWQDRKRPSGIPERFSGSGNSGNTATLTISGTQAMDEADF YQQTWDSSTVVFEGGGTKLITVL	1792
VR0001 03721	EVQLLESGGDLVOPGGSLRLSCAASGTFSSYAMSWVRQAPGKGLE WVSAISGGGSTDYADSVKGRFTISRDNskyNTLFLQMNSLRAEDTA VYYCAKAVDYDSTGYPFYYHYYGLDVWGQGTITVSS	1735	SYELTQPPSVSVSPGQTASITCSGDKLGDKYASWYQQKPGQS PVLVIYQDRVRRPSGIPERFSGSGNSGNTATLTISGTQAMDEADF YQQTWDSNTVVFEGGGTKLITVL	1793

VR0001 03692	EVQLES GGGL VOPGGS LRLSCAASGFTFSSYLSWVRQAPGKGLEW VSAISGGTTYTDSVKGRFTISRDN SKNTL YLQMSLRAEDTAVY YCAKTLDDYDSTGYPPYY GMDVWGQGTIVTVSS	1736	SYELTOPPSVSVSPGOTASITCSGDKLGDKYASWYQOKPGQS PVLVIYQDRTRPSGIPDRFSGSNSGNTATLTISGTQAMDEADY YCOAWDSSTVVFGGGTKLTVL	1794
VR0001 03678	EVQLES GGGL VOPGGS LRLSCAASGFTFSSYAMNWVRQAPGKGLE WVSVMGGGGS LYYADSVKGRFTISRDN SKNTL YLQMSLRAEDT AVVYCAKTADIFYDSSGYPPYY GMDVWGQGTIVTVSS	1737	SYELTOPPLVSVSPGOTASITCSGDKLGDKYASWYQOKPGQS PVLVIYQDRNRKPSGIPERFSGSNSGNTATLTISRQAMDEADY YCOIWDSTTVVFGGGTKLTVL	1795
VR0001 03710	EVQLES GGGL VOPGGS LRLSCAASVLTFSYGMWVRQAPGKGLE WVSAISGRGDS THYADSVKGRFTISRDN SKNTL YLMLNSLRAEDTA VYYCAKDEF GHYGS GYPLDYWGQGTIVTVSS	1738	SYELTOPPSVSVSPGOTASITCSGDKLGDKYASWYQOKPGQS PVLVIYQDRSRPSGIPERFSGSNSGNTATLTISGTQAMDEADY YCOAWDSSTVVFGGGTKLTVL	1796
VR0001 03687	EVQLES GGGL VOPGGS LRLSCAASGFTFSSYAINWVRQAPGKGLE WVSSISGGGS TYADSVKGRFTISRDN SKNTL YLQMSLRAEDTAV YYCAKEGYDTS GYHPDYWGQGTIVTVSS	1739	SYELTOPPSVSVSPGOTASITCSGDKLGDKFASWYQOKPGQS PVLVIYQDNKRPSGIPERFSGSNSGNTATLTISGTQTMDEADY YCOIWDRSIAYLGGGTKLTVL	1797
VR0001 03749	EVQLES GGGL IOPGGS LRLSCAASGFTTNYDMTWVRQAPGKGLE WVSTISGGGNTYYADSVKQGF TISRDN SKNTL FLQMSLRAEDTAL YYCARLDS DITGYDPEDIWGQGTMYTVSS	1740	SYELTOPPSVSVSPGOTASITCSGDKLGDKFASWYQOKPGQS PVLVIYQDNKRPSGIPERFSGSNSGNTATLTISGTQAMDEADY YCOAWDRITTA VFGG GTKLTVL	1798
VR0001 03736	EVQLES GGGL VOPGGS LRLSCAASGFTFSSYTMTWVRQTPGKGLE WVSVISGGGATSYADSVKGRFTVSRGDSKNTL YLQMSLKAEDTA IYYCAKVN YDITGYDPLDHWGQGTIVTVSS	1741	SYELTOPPSVSVSPGOTASITCSGDKLGDKFASWYQORPGQS PVLVIYQDSKRPSGIPERFSGSNSGNTATLTIRGTQAMDEGDY YCOIWWANTVVFGGGTOLTVL	1799
VR0001 03672	EVQLES GGGL VOPGGS LRLSCEASGFTFSSYDMNWVRQAPGKGLE WVSGISGGSDTYADSVKGRFTISRDN SKNTL YLQMSLRAEDTA VYYCAKLDYDITGYFPEDHWGQGTIVTVSS	1742	SYELTOPPSVSVSPGOTASITCSGEKLGDKFASWYQOKPGQS PVLVIYQDSKRPSGIPERFSGSNSGNTATLTISGTQAMDEADY YCOAWVRITTVVFGGGTKLTVL	1800
VR0001 03744	EVQLES GGGL IOPGGS LRLSCAASGFTFSSYDMNWVRQAPGKGLE WVSVISGGGRITYADSVKGRFTISRDN SKNTL YLQMSLRAEDTA VYYCAKMEYDSS GSYFDYWGQGTIVTVSS	1743	SYELTOPPSVSVSPGOTASITCSGDKLGDKFASWYQOKPGQS PVLVIYQDNKRPSGIPDRFSGSNSGNTATLTISGTQAMDEAVY YCOIWININTVVFGGGTKLTVL	1801
VR0001 03703	EVQLES GGGL VOPGGS LRLSCAASGFTFSSYAMNWVRQAPGKGLE WVSSVSGSGNTYYADSVKGRFTISRDN SKNTL YLQMSLRAEDTA VYYCAKEDYDTS GYNYPDYWGQGTIVTVSS	1744	SYELTOPPSVSVSPGOTASITCSGDKLGDKFASWYQOKPGQS PVLVIYQDNKRPSGIPERFSGSNSGNTATLTISGTQAVDEADY YCOIWDISTTVVFGGGTKLTVL	1802
VR0001 03681	EVQLES GGGL VOPGGS LRLSCAASGFTFSSYAMNWVRQAPGKGL EWWSSISGGNTYYADSVKGRFTISRDN SKNTL YLQMSLRAEDTA VYYCAKEDADSTGYDPEDYWGQGTIVTVSS	1745	SYELTOPPSVSVSPGOTASITCSGDKLGDKFVSWYQOKPGQS PVLVIYQDITKRPSGIPERFSGSNSGNTATLTISGTQAMDEADF YCOIWWINTAVFGGGTKLTVL	1803
VR0001 03674	EVQLES GGGL VOPGGS LRLSCAASGFTFSSYAMNWVRQAPGKGLE WVSTISGGGNTDHADSVKGRFTISRDN SKNTL YLQMSLRTEDTA VYYCAKEDHDLTGYSPEDYWGQGTIVTVSS	1746	SYELTOPPSVSVSPGOTASITCSGDKLGDKFVSWYQOKPGQS PVLVIFQDITKRPSGIPERFSGSNSGNTATLTISGPQAMDEADY YCOIWDFTTVVFGGGTKLTVL	1804
VR0001 03731	EVQLES GGGL VOPGGS LRLSCAASGFTFSSYAMNWVRQAPGKGLE WISSISGGGTPYYADSVKGRFTISRDN SKNTL YLQINSLRAEDTAVY YCAKEGEDSTGYPPEDHWGQGTIVSVSS	1747	SYELTOPPSVSVSPGOTASITCSGDKLGDKFVSWYQOKPGRS PVLVIYQDHSRPSGIPERFSGSNSGNTATLTISGPQAMDEADY YCOIWWSSITAFGGGTKLTVL	1805
VR0001 03702	EVQLES GGGL IOPGGS LRLSCAASGFTFSSYAMNWVRQAPGKGLE WVSGISGGGS TYADSVKGRFTISRDN SKNTL YLQMSLRAEDTAI YYCARDGDDYGDYDFDYWGQGTIVTVSS	1748	SYELTOPPSVSVSPGOTASITCSGDKLGDKYASWYQOKPGQS PVLVIYQDRNRKPSGIPERFSGSNSGNTATLTISGTQAMDEADY YCOIWDSSSTTVVFGGGTKLTVL	1806
VR0001 03740	EVQLES GGGL IOPGGS LRLSCAASGFTFSSYAMSWVRQAPGKGLE WVSGISGGGS TYADSVKGRFTISRDN SKNTL YLQMSLRAEDTAI YYCARDGDDYGDYDFDYWGQGTIVTVSS	1749	SYELTOPPSVSVSPGOTASITCSGDKLGDKYASWYQOKPGQS PVLVIYQDRNRKPSGIPERFSGSNSGNTATLTISGTQAMDEADY YCOIWDSSSTTVVFGGGTKLTVL	1806

VR0001 03711	EVQLESGGGLVOPGGSRLRLSCAASGFTFSSYAMNWRQAPGKGLE WVSFISSGGSTYNADSVKGRFTISRDNKSNLTLQMNLSLAEDTAV YYCAKDGSYFDSNGPDYFDYWGOGLTVYSS	1750	SYELTOPPSVSVSPGOTASITCSGDKLGDKYAYWYQOKPGQS PVLVIFQDRNRPSGVPDRFSGSNSGNTATLTISGTQTMDEADF YCOAWDSTAVFGGGTKLTVL	1807
VR0001 03739	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMMSWIRQAPGKGLE WVSYLSSGGSTRHYADSVKGRFTISRDNAKNSLYLQMNLSLAEDTA VYYCARLDVHESSGYYPDFWGOGLTVYSS	1751	SYELTOPPSVSVSPGOTASITCSGDKLGDKFASWYQOKPGQS PVLVIYQDNKRPSGIPERFSGSNSGNTATLTISGTQAMDEADY YCOAWASSIVVFGGGTKLTVL	1808
VR0001 03712	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMMSWIRQAPGKGLE WVSYSSGGSTIYHADS VKGRFTISRDNAKNSLYLQMNLSLAEDTA VYYCARLDNYDSTGYYPDFWGOGLTVYSS	1752	SYELTOPPSVSVSPGOTASITCSGDKLGDKFASWYQOTPGQS PVLVIYQDNKRPSGIPERFSGSNSGNTATLTISGTQAMDEADY YCOAWDRITTVFVGGLTKLTVL	1809
VR0001 03663	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMMSWIRQAPGKGLE WVSYISSGGSTIYTDYSVKGRFTMSRDNAKNSLYLQMDSLTAEDTA VYYCASLDNYESSGYYPEDYWGOGLTVYSS	1753	SFELTOPPSVSVSPGOTASITCSGHNLGDKFTSWYQOKPGQSP VLVIFQDNKRPSGIPERFSGSNSGNTATLTISGTQALDAADY COAWEYSTAIFGGGTKLTVL	1810
VR0001 03680	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMMSWIRQAPGKGLE WVSYISTGGSAIYVADSVKGRFTISRDNAKNSLFLQVNSLRAEDTAM YFCARODNYESSGYYPFDSWGOGLTVYSS	1754	SYELTOPPSVSVSPGOTASITCSGDKLGDKFASWYQOKPGQS PVLVIFQDNKRPSGIPERFSGSNSGNTATLTISGTQAMDEADY YCOAWDSTTVFVGGLTKLTVL	1811
VR0001 03765	EVQLESGGGLVOPGGSRLRLSCAASGFTFSSYDMSWVRQAPGKGLE WVSTISGGSTIYADSVKGRFTISRDNKSNLTLQMNLSLAEDTA VYYCAKEDSYESTGYYPEDYWGOGLTVYSS	1755	SYELTOPPSVSVSPGOTASITCSGDKLGDKFASWYQOKPGQS PVLVIYQDNKRPSGIPERFSGSNSGNTATLTISGTQAMDEADY YCOARVINTVFVGGLTKLTVL	1812
VR0001 03698	EVQLESGGGLVOPGGSRLRLSCAASGFTFSSYAMDWVRQAPGKGLE WVSAISGGGITSADSVKGRFTISRDNKSNLTLQMNLSLAEDTAV VYYCAKEDNYESTGYYPEDYWGOGLTVYSS	1756	SYELTOPPSVSVSPGOTASITCSGDKLGDKFASWYQOKPGQS PVLVIYQDNKRPSGIPARFSGSNSGNTATLTISGTQAMDEADY YCOQWVSTTVFVGGLTKLTVL	1813
VR0001 03743	EVQLESGGGLVOPGGSRLRLSCAASGFTFSDYMDMNVRQAPGKGLE WVSAISGGGTTIYADSVTGRFTISRDNKSNLTLQMNLSLAEDTA VYYCAREDHYDSTGYYPEDYWGOGLTVYSS	1757	SYELTOPPSVSVSPGOTASITCSGDKLGDKFVSWYQOKAGQS PVLVIYQDNKRPSGIPERFSGSNSGNTATLTISGTQAMDEADY FCQARDITTVFVGGLTKLTVL	1814
VR0001 03766	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMMSWIRQAPGKGLE WVSYITSSAYTIYADSVKGRFTISRDNAKNSLFLQMNLSLAEDTAV YYCVRVSYDSTGYYPEDYWGOGLTVYSS	1758	SYELTOPPSVSVSPGOTASITCSGDKLGDKFASWYQOKPGQS PVLVIYQDNKRPSGIPERFSGSNSGNTATLTISGTQAMDEADY YCOAWVSTTVFVGGLTKLTVL	1815
VR0001 03700	QVQVESGGGLVKPGGSLRLSCAASGFTFSDYYMMSWIRQAPGKGLE WISYISSSSVSSSVTIYADSVKGRFTISRDNAKNSLFLQMNLSRAE DTAVYYCAREDSDTSGYDPFDHWGOGLTVYSS	1759	SYELTOPPSVSVSPGOTASITCSGEKLGDKFASWYQOKPGQS PVLVIFQDNKRPSGIPERFSGSNSGNTATLTISGTQAMDEADY YCOAWVRSITVFGGGLTKLTVL	1816
VR0001 03690	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYSMSWIRQAPGKGLE WVSFISSSSTLLYADSVKGRFTISRDNAKNSLYLQMNLSLAEDTAV YYCAREDSDTSGYNYFDYWGOGLTVYSS	1760	SYELTOPPSVSVSPGOTATITCSGHKLGDKFASWYQOKPGQS PVLVIYQDNKRPSGIPERFSGSNSGNTATLTISGTQAMDEADY YCOQWDESTVVFVGGLTKLTVL	1817
VR0001 03728	QVQLVGSGGGLVKPGGSLRLSCAASGFTFSDYYMMSWIRQAPGKGLE WVSYISGGGTVIYADSVKGRFTISRDNAKNSLYLQMNLSLAEDTA VYYCARDHYDSSGYSYFDSWGOGLTVYSS	1761	SYELTOPPSVSVSPGOTASITCSGDKLGDKFASWYRQOKPGQS PVLVIYQDNKRPSGIPERFSGSNSGNTATLTISGTQAMDEADY YCOQWDRSTAVFVGGLTKLTVL	1818
VR0001 03763	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYHMSWIRQAPGKGOE WVSYISSGVSTIYADSVKGRFTISRDNAKNSLDLQMNLSLAEDTAV YYCARISYDTSGYVDYVWGOGLTVYSS	1762	SYELTOPPSLVSPGOTASITCSGDKLGDKFASWYQOKPGQS PELVIFQDNKRPSGIPERFSGSNSGNTATLTISGTQAMDEADY YCOQWDRITTVFVGGLTKLTVL	1819
VR0001 03729	QVQLVQSGAEVKKPGASVKVCKASGYTFTDYYLHWVRQAPGOGL DWMGRINPNSGGTINYAQKFOGRVTMTTRDTISITAYMELSLRSDDT AVYFCARDDSFESTGYYPFDYWGOGLTVYSS	1763	SYELTOPPSVSVSPGOTASITCSGDKLGDKFASWYQOKPGQS PVLVIYQDNKRPSGIPERFSGSNSGNTATLTISGTQAMDEADY YCOAWVSTTVFVGGLTKLTVL	1820

VR0001 03714	QVQLQESGPGLVKPSGTLSTCAVSGASISSGDWWSWVRQPPGKGL EWIGELIYHSGSTNNPNSLKSRVTISVDKSKNQFSLKLGSVTAADTAV YYCARGTGYDYSGSYSYFDYWGOGTLVTYSS	1764	SYELTOPPSVSVSPGQTATITTCSGDRLGDKYASWYQOKPGQS PVMVVIHQDTRKRPSPGPERFSGSNSGNTATLTISGTQAMDEAEY HCQAWDSSTVVFGGGTLTYL	1821
VR0001 03691	QVQLQESGPGLVKPSGTLSTCAVSGGSISSDWWNNVRQPPGKGL EWIGELHQSGSTNNPNSLKSRVTISLDKSKNQFSLKLSVTVAADTAVY YCVRLGGSWSDWGFDYWGOGTLVTYSS	1765	SYELTOPPSVSVSPGQTVIIICSGDKLGKYASWYQOKPGQSP VLVIYQDIKRPAGIPERFSGSKSGNTAILTISGTQAMDEADYY CQAWDSSTVLFGGGTLTYL	1822
VR0001 03686	QVQLQESGPGLVKPSQTLSTCAVSGGSISSDGYWWSWIRQHPGKGL EWIGYIHYSGITSYNPNSLKSRVTISIDTSKNQFSLKLSVTAAADTAVYY CAGVELLRISDYWGQGLVTYSS	1766	SYELTOPPSVSVSPGETASITCSGDKLGDKYAYWYQOKPGQS PVLVIYQDSTRSPGIPERFSGSNSGNTAILTISGTQIMDEADYY CQAWDSSTVVFGGGTLTYL	1823
VR0001 03673	QVQLQESGPGLVKPSETLSTCTVSGGSISSSFYWDWIRQPPGKGL EWIGDIYFSGRTYNPNPSLKSRVTISVDTSKNQFSLKLSVTAAADTAV YYCARREGPTIDYFDYWGOGTLVTYSS	1767	SYELTOPPSVSVSPGQTASITCSGDKLGDKFVSWYQOKPGQS PVLVIYQDNRKRPSPGIPERFSGSNSGNTATLTISGTQAMDEADY YCQAWDSSAVVFEGGTLTYL	1824
VR0001 03754	QVQLQESGPGLVKPSETLSTCTVSGGSISSSFYWDWIRQPPGKGL WIGSIYFSGSTYNNPNSLKSRVTISVDTSRNNQFSLKLSVTAADTAVY CARREPAADTLIDYWGOGTLVTYSS	1768	SYELTOPPSVSVSPGQTASITCSGDKLGDKFASWYQOKPGQS PVVVVIYQDRRRPSPGIPERFSGSNSGNTATLTISGTQAMDEADY YCQAWDSSTVIFGGGTLTYL	1825
VR0001 03697	QVQLQWGAAGLLKPSSETLSTCAVYGGSFSDYWSWIRQPPGKGL WIGELNHNGGTNNPNSLKSRVTISVDTSKNQFSLKLSVTTADTAVY FCARNFYDITSGFYSFDSWGQGLVTYSS	1769	SYELTOPPSVSVSPGQTASITCSGDKLGDKFASWYQOKRPGQS PVLVIYQDNKRPSRIPARFSGSNSGNTATLTISGTQAVDEADF YCQITWASSSTVVFGGGTLTYL	1826
VR0001 03675	QVQLQWGAAGLLKPSSETLSTCAVYGGSFSGYWTWVRQPPGKGL EWIGELNHNGGTNNPNSLKSRVTISVDTSNNQFSLRLSVTAADTAVY FCARGHPDITSGFYSFDYWGOGTLVTYSS	1770	SYELTOPPSVSVSPGORASITCSGDKLGDKFASWYQOKRPGQS PVLVIYQDNKRPSGIPERFSGSNSGNTATLTISGTQAMDE ADYYCQAWDSRLVVFGGGTLTYL	1827
VR0001 03725	QVQLQESGPGLVKPSETLSTCTGSGGSISSSHYWGWIROPKGL LIGFYYSNGTYNPNPSLKSRVTSISVDTSKNQFSLKLSVTAAADTAVY YCARGDHDSGYYGFDVWGRGTLVTYSS	1771	SYELTOPPSVSVSPGQTASITCSGHLGDKFASWYQOKRPGQS PVLVIYQDNKRPSGIPERFSGSNSGNTATLTISGTQAVDEADY YCQITWDESTVVFGGGTLTYL	1828
VR0001 03724	QVQLQESGPGLVKPSETLSTCTVSGGSISSGDYSWWSWIRQHPKGL EWIGYIYDSGYTDYNNPNSLKSRLTISVDTSKNQFSLKLSVTAAADTAIY YCARLLTGDDAFDIWGOGTMTYSS	1772	SSELTDPAVSVALGQTVIRITCQGDLSRYSYASWYQOKRPGQ APLVIFYDKNNRPSGIPDRISGSSGNTASLTITGQAQAEDEAA YCNRSDDSSGAHWVFEGGTLTYL	1829
VR0001 03706	QVQLQESGPGLVKPSETLSTCTVPGGSISSSYWGWIROPKGL WIGSIYSGSTYNNPNSLKSRVTISVDTSKNQFSLKLSVTAAADTAVYY CARPYIDIPLGYWGQGLVTYSS	1773	SYELTOPPSVSVSPGQTARITCSGDALPSQYAYWYQOKRPGQA PVMVVIYKDSERPSGIPERFSGSSGTTVTLTISGVQAEDEADY YCQSTVNSVGYVVFEGGTLTYL	1830
VR0001 03676	QLQLQESGPGLVKPSETLSLCTVSGGSISSSYWGWIROPKGL WIGSIYSGSTYNNPNSLKSRVTISVDTSKNQFSLKLSVTAAADTAVYY CARPYIDIPLGSWGQGLVTYSS	1774	SYELTOPPSVSVSPGQTARITCSGDALPNHYAYWYQOKRPGQ APVLVIYKDSERPSGIPERFSGSSGTTVTLTISGVQAEDEADY YCQSTDNSVGYVVFEGGTLTYL	1831
VR0001 03727	QVQLQWGAAGLLKPSSETLSTCAVYGGSFSGYWSWIRQPPKGL WIGELKHSGSTNNPNSLKSRVTISVDTSKNQFSLKLSVTAAADTAVYY CAKRDYDITSGYDYFDYWGOGTLVTYSS	1775	SYELTOPPSVSVSPGQTASITCSGDKLGDKFASWYQOKRPGQS PVLVIYQDNKRPSGIPERFSGSNSGNTATLTISGTQAMDEAGY YCQITWDSNTAVFEGGTLTYL	1832

Table 7: Linker SEQ ID NOs

Linker Sequence	SEQ ID NO
GTEGKSSGSGSESKST	1421
GGSGGS	1422
GGAGGA	1423
GGGSGGGGSGGGGSGGGGS	1424
GGGSGGSGGCPPCGSGG	1425
GGGSGGCPPCGGSGG	1426
GGSGGSGGCPPCGSGG	1427
GGGSGGSGGCPPCGSGG	1428
GGGSGGGSGCPPCGGGG	1429
CPPC	1430
CGPC	1431
CPGC	1432
CGGC	1433
CSPG	1434
CPSC	1435
CSSC	1436
CGSC	1437
CSGC	1438
CPPPC	1439
CGPPC	1440
CPGPC	1441
CPPGC	1442
CGGPC	1443
CPGGC	1444
CGGGC	1445
CSPPC	1446
CPSPC	1447
CPPSC	1448
CSSPC	1449
CPSSC	1450
CSSSC	1451
CGSPC	1452
CPGSC	1453
CSGPC	1454
CPSGC	1455

CLAIMS

We claim:

1. An anti-TfR antibody or antigen-binding fragment thereof, comprising a light chain variable region (VL) comprising light chain complementarity determining regions (LCDRs) LCDR1, LCDR2 and LCDR3, and a heavy chain variable region (VH) comprising heavy chain complementarity determining regions (HCDRs) HCDR1, HCDR2 and HCDR3, wherein:
 - (i) the LCDR1 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 222-308 and 1456-1485;
 - (ii) the LCDR2 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 309-359 and 1486-1511;
 - (iii) the LCDR3 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 360-518 and 1512-1561;
 - (iv) the HCDR1 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 519-645 and 1562-1606;
 - (v) the HCDR2 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 646-792 and 1607-1661; and
 - (vi) the HCDR3 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 793-980 and 1662-1717.
2. The anti-TfR antibody or antigen-binding fragment thereof of claim 1, wherein the LCDR1, LCDR2 and LCDR3 have the amino acid sequences of the LCDR1, LCDR2 and LCDR3, respectively, of any one of the antigen binding proteins specified in Table 5.
3. The anti-TfR antibody or antigen-binding fragment thereof of claim 1 or 2, wherein the VL comprises an amino acid sequence that is at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to an amino acid sequence selected from the group consisting of SEQ ID NOs: 1198-1420 and 1776-1832.
4. The anti-TfR antibody or antigen-binding fragment thereof of claim 3, wherein the VL comprises the amino acid sequence of the light chain variable region of any one of the antigen binding proteins specified in Table 6.
5. The anti-TfR antibody or antigen-binding fragment thereof of any one of the previous claims, wherein the HCDR1, HCDR2 and HCDR3 have the amino acid sequences of the

HCDR1, HCDR2 and HCDR3, respectively, of any one of the antigen binding proteins specified in Table 5.

6. The anti-TfR antibody or antigen-binding fragment thereof of claim 5, wherein the VH comprises an amino acid sequence that is at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to an amino acid sequence selected from the group consisting of SEQ ID NOs: 981-1197 and 1718-1775.

7. The anti-TfR antibody or antigen-binding fragment thereof of claim 6, wherein the VH comprises the amino acid sequence of the heavy chain variable region of any one of the antigen binding proteins specified in Table 6.

8. The anti-TfR antibody or antigen-binding fragment thereof of any one of the previous claims, wherein the LCDR1, LCDR2 LCDR3, HCDR1, HCDR2, and HCDR3 have the amino acid sequences of the LCDR1, LCDR2 LCDR3, HCDR1, HCDR2, and HCDR3, respectively, of any one of the antigen binding proteins specified in Table 3.

9. The anti-TfR antibody or antigen-binding fragment thereof of claim 8, wherein the VL and VH comprise the amino acid sequences of the light chain variable region and the heavy chain variable region, respectively, of any one of the antigen binding proteins specified in Table 4.

10. The anti-TfR antibody or antigen-binding fragment thereof of any of the previous claims, having a single-chain variable fragment (scFv) comprising the VH and VL of the anti-TfR antibody or antigen-binding fragment thereof.

11. The anti-TfR antibody or antigen-binding fragment thereof of claim 10, wherein the scFv further comprises a linker that covalently links the VH and VL, such as a linker having the amino acid sequence selected from the group consisting of SEQ ID NO: 1421 and SEQ ID NOs: 1424-1455.

12. The anti-TfR antibody or antigen-binding fragment thereof of claim 11, wherein the scFv comprises one or more disulfide bonds formed between a cysteine (Cys) in the linker and a surface exposed Cys in VH and/or VL, preferably a surface exposed Cys in a framework region of the VH and/or VL.

13. An anti-TfR antibody or antigen-binding fragment thereof having a single variable domain on a heavy chain (VHH) comprising heavy chain complementarity determining regions (HCDRs) HCDR1, HCDR2 and HCDR3, wherein:

- (i) the HCDR1 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-24;
 - (ii) the HCDR2 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 25-46; and
 - (iii) the HCDR3 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 47-70.
14. The anti-TfR antibody or antigen-binding fragment thereof of claim 13, wherein the HCDR1, HCDR2 and HCDR3 have the amino acid sequences of the HCDR1, HCDR2 and HCDR3, respectively, of any one of the VHH antigen binding proteins specified in Table 3.
15. The anti-TfR antibody or antigen-binding fragment thereof of claim 13 or 14, comprising an amino acid sequence that is at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to an amino acid sequence selected from the group consisting of SEQ ID NOs: 71-221.
16. The anti-TfR antibody or antigen-binding fragment thereof of claim 15, comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 71-221.
17. A conjugate comprising the anti-TfR antibody or antigen-binding fragment thereof of any one of claims 1-16 coupled to a therapeutic or diagnostic agent, preferably, the conjugate is a multi-specific antibody comprising a first antigen binding region which binds the TfR and comprises the anti-TfR antibody or antigen-binding fragment thereof of any one of claims 1-16 and a second antigen binding region which binds a brain target, such as a brain target selected from the group consisting of beta-secretase 1 (BACE1), amyloid beta (Abeta), epidermal growth factor receptor (EGFR), human epidermal growth factor receptor 2 (HER2), Tau, apolipoprotein E4 (ApoE4), alpha-synuclein, CD20, huntingtin, prion protein (PrP), leucine rich repeat kinase 2 (LRRK2), parkin, presenilin 1, presenilin 2, gamma secretase, death receptor 6 (DR6), amyloid precursor protein (APP), p75 neurotrophin receptor (p75NTR), and caspase 6.
18. A fusion construct comprising the anti-TfR antibody or antigen-binding fragment thereof of any one of claims 1 to 16 covalently linked to a second antibody or an antigen binding fragment thereof that binds to a brain target, such as a brain target selected from the group consisting of beta-secretase 1 (BACE1), amyloid beta (Abeta), epidermal growth factor receptor (EGFR), human epidermal growth factor receptor 2 (HER2), Tau, apolipoprotein E4 (ApoE4), alpha-synuclein, CD20, huntingtin, prion protein (PrP), leucine rich repeat kinase 2 (LRRK2),

parkin, presenilin 1, presenilin 2, gamma secretase, death receptor 6 (DR6), amyloid precursor protein (APP), p75 neurotrophin receptor (p75NTR), and caspase 6.

19. The fusion construct of claim 18, wherein the anti-TfR antibody or antigen-binding fragment thereof is covalently linked to the carboxy terminus of only one of the two heavy chains of the second antibody or antigen binding fragment thereof via a linker, preferably the linker has the amino acid sequence of SEQ ID NO: 1422 or SEQ ID NO: 1423.
20. The fusion construct of claim 19, wherein each of the two heavy chains of the second antibody or antigen binding fragment thereof comprises one or more heterodimeric mutations, such as a modified heterodimeric CH3 domain, or one or more knob and hole mutations, as compared to a wild-type CH3 domain polypeptide.
21. The fusion construct of claim 20, wherein the heterodimeric mutations comprise the modified heterodimeric CH3 domain of the first heavy chain comprises amino acid modifications at positions T350, L351, F405, and Y407, and the modified heterodimeric CH3 domain of the second heavy chain comprises amino acid modifications at positions T350, T366, K392 and T394, wherein the amino acid modification at position T350 is T350V, T350I, T350L or T350M; the amino acid modification at position L351 is L351Y; the amino acid modification at position F405 is F405A, F405V, F405T or F405S; the amino acid modification at position Y407 is Y407V, Y407A or Y407I; the amino acid modification at position T366 is T366L, T366I, T366V or T366M, the amino acid modification at position K392 is K392F, K392L or K392M, and the amino acid modification at position T394 is T394W, and wherein the numbering of amino acid residues is according to the EU index as set forth in Kabat.
22. The fusion construct of claim 20, wherein the modified heterodimeric CH3 domain of the first heavy chain comprises mutations T350V, L351Y, F405A and Y407V, and the modified heterodimeric CH3 domain of the second heavy chain comprises mutations T350V, T366L, K392L and T394W.
23. The fusion of any one of claims 18-22, wherein the second antibody or antigen binding fragment thereof comprises one or more mutations in the Fc domain that enhance binding of the fusion to the neonatal Fc receptor (FcRn), preferably the one or more mutations enhance the binding at an acidic pH, more preferably the Fc has the M252Y/S254T/T256E (YTE) mutations, wherein the numbering of amino acid residues is according to the EU index as set forth in Kabat.

24. The fusion of any one of claims 18-23, wherein the second antibody or antigen binding fragment thereof comprises one or more mutations in the Fc domain that reduce or eliminate the effector function, preferably the Fc has one or more amino acid modifications at positions L234, L235, D270, N297, E318, K320, K322, P331, and P329, such as one, two or three mutations of L234A, L235A and P331S, wherein the numbering of amino acid residues is according to the EU index as set forth in Kabat.
25. An isolated nucleic acid encoding the antibody or antigen-binding fragment of any one of claims 1-16, the conjugate of claim 17 or the fusion construct of any one of claims 18-24.
26. A vector comprising the isolated nucleic acid of claim 25.
27. A host cell comprising the nucleic acid of claim 25 or the vector of claim 26.
28. A method of producing the antibody or antigen-binding fragment of any one of claims 1-16, the conjugate of claim 17, or the fusion construct of any one of claims 18-24, comprising culturing a cell comprising a nucleic acid encoding the antibody or antigen-binding fragment, the conjugate or the fusion construct under conditions to produce the antibody or antigen-binding fragment, the conjugate or the fusion construct, and recovering the antibody or antigen-binding fragment, the conjugate or the fusion construct from the cell or cell culture.
29. A pharmaceutical composition comprising the antibody or antigen-binding fragment of any one of claims 1-16, the conjugate of claim 17, or the fusion construct of any one of claims 18-24, and a pharmaceutically acceptable carrier.
30. A method of treating or detecting a disorder, preferably a neurological disorder, in a subject in need thereof, comprising administering to the subject the antibody or antigen-binding fragment of any one of claims 1-16, the conjugate of claim 17, or the fusion construct of any one of claims 18-24, or the pharmaceutical composition of claim 29, preferably, the neurological disorder is selected from the group consisting of neurodegenerative diseases (such as Lewy body disease, postpoliomyelitis syndrome, Shy-Draeger syndrome, olivopontocerebellar atrophy, Parkinson's disease, multiple system atrophy, striatonigral degeneration, spinocerebellar ataxia, spinal muscular atrophy), tauopathies (such as Alzheimer's disease and supranuclear palsy), prion diseases (such as bovine spongiform encephalopathy, scrapie, Creutzfeldt-Jakob syndrome, kuru, Gerstmann-Straussler-Scheinker disease, chronic wasting disease, and fatal familial insomnia), bulbar palsy, motor neuron disease, and nervous system heterodegenerative disorders (such as Canavan disease, Huntington's disease, neuronal ceroid-lipofuscinosis,

Alexander's disease, Tourette's syndrome, Menkes kinky hair syndrome, Cockayne syndrome, Hallervorden-Spatz syndrome, lafora disease, Rett syndrome, hepatolenticular degeneration, Lesch-Nyhan syndrome, and Unverricht-Lundborg syndrome), dementia (such as Pick's disease, and spinocerebellar ataxia), and cancer of the CNS and/or brain (such as brain metastases resulting from cancer elsewhere in the body).

31. The method of claim 30, wherein the antibody or antigen-binding fragment thereof, the conjugate, or the pharmaceutical composition is administered intravenously.

32. A method of delivering a therapeutic or diagnostic agent across the blood-brain barrier (BBB) of a subject in need thereof, comprising administering to the subject a complex comprising the therapeutic or diagnostic agent coupled to, preferably covalently conjugated to, the antibody or antigen-binding fragment thereof of any one of claims 1 to 16.

33. The method of any one of claims 30 to 32, wherein the administration reduces Fc-mediated effector function and/or does not induce rapid reticulocyte depletion.