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(54) Title: POLYPEPTIDE CONSTRUCTS BINDING TO CD3

(57) Abstract: The invention relates to a polypeptide or polypeptide construct comprising: a binding domain binding to an extracellular epitope of the human CD3s chain comprising or consisting of a VH region and a VL region, wherein i) the VH region comprises: a CDR-H1 sequence of X_1YAX_2N , where X_1 is K, V, S, G, R, T, or I; and X_2 is M or I; a CDR-H2 sequence of $RIRSKYNNYATYYADX_1VKX_2$, where X_1 is S or Q; and X_2 is D, G, K, S, or E; and a CDR-H3 sequence of $HX_1NFGNSYX_2SX_3X_4AY$, where X_1 is G, R, or A; X_2 is I, L, V, or T; X_3 is Y, W or F; and X_4 is W, F or Y; and ii) wherein the VL region comprises: a CDR-L1 sequence of $X_1SSTGAVTX_2X_3X_4YX_5N$, where X_1 is G, R, or A; X_2 is S or T; X_3 is G or S; X_4 is N or Y; and X_5 is P or A; a CDR-L2 sequence of $X_1TX_2X_3X_4X_5X_6$, where X_1 is G or A; X_2 is K, D, or N; X_3 is F, M or K; X_4 is L or R; X_5 is A, P, or V; and X_6 is P or S; and a CDR-L3 sequence of $X_1LWYSNX_2VW$, where X_1 is V, A, or T; and X_2 is R or L; and iii) wherein one or more of CDR sequences of the VH region of i) and/or of the VL region of ii) comprise one amino acid substitution or a combination thereof selected from X_24V and X_24F in CDR-H1; D15, and X_116A in CDR-H2; H1, X_12E , F4, and N6 in CDR-H3; and X_11L and W3 in CDR-L3. The invention also relates to a polynucleotide encoding the polypeptide or polypeptide construct of the invention, a vector comprising said polynucleotide and a host cell transformed or transfected with said polynucleotide or with said vector. Moreover, the invention also provides for a process for the production of said polypeptide or polypeptide construct and a pharmaceutical composition comprising said polypeptide or polypeptide construct of the invention. Furthermore, the invention relates to medical uses of said polypeptide or polypeptide construct and kits comprising said polypeptide or polypeptide construct.

Polypeptide constructs binding to CD3

[1] The invention relates to a polypeptide or polypeptide construct comprising: a binding domain binding to an extracellular epitope of the human CD3ε chain comprising or consisting of a VH region and a VL region, wherein i) the VH region comprises: a CDR-H1 sequence of X_1YAX_2N , where X_1 is K, V, S, G, R, T, or I; and X_2 is M or I; a CDR-H2 sequence of $RIRSKYNNYATYYADX_1VKX_2$, where X_1 is S or Q; and X_2 is D, G, K, S, or E; and a CDR-H3 sequence of $HX_1NFGNSYX_2SX_3X_4AY$, where X_1 is G, R, or A; X_2 is I, L, V, or T; X_3 is Y, W or F; and X_4 is W, F or Y; and ii) wherein the VL region comprises: a CDR-L1 sequence of $X_1SSTGAVTX_2X_3X_4YX_5N$, where X_1 is G, R, or A; X_2 is S or T; X_3 is G or S; X_4 is N or Y; and X_5 is P or A; a CDR-L2 sequence of $X_1TX_2X_3X_4X_5X_6$; where X_1 is G or A; X_2 is K, D, or N; X_3 is F, M or K; X_4 is L or R; X_5 is A, P, or V; and X_6 is P or S; and a CDR-L3 sequence of $X_1LWYSNX_2WV$, where X_1 is V, A, or T; and X_2 is R or L; and iii) wherein one or more of CDR sequences of the VH region of i) and/or of the VL region of ii) comprise one amino acid substitution or a combination thereof selected from X_24V and X_24F in CDR-H1; D15, and X_116A in CDR-H2; H1, X_12E , F4, and N6 in CDR-H3; and X_11L and W3 in CDR-L3. The invention also relates to a polynucleotide encoding the polypeptide or polypeptide construct of the invention, a vector comprising said polynucleotide and a host cell transformed or transfected with said polynucleotide or with said vector. Moreover, the invention also provides for a process for the production of said polypeptide or polypeptide construct and a pharmaceutical composition comprising said polypeptide or polypeptide construct of the invention. Furthermore, the invention relates to medical uses of said polypeptide or polypeptide construct and kits comprising said polypeptide or polypeptide construct.

[2] T cell engagers (TCEs) make use of T cells' ability to recognize foreign peptides on mutated or infected cells through T cell receptors. T cell recognition is mediated by clonotypically distributed alpha beta and gamma delta T cell receptors (TcR) that interact with the peptide-loaded molecules of the peptide MHC (pMHC) at low affinities. The antigen-specific chains of the TcR do not possess signalling domains but instead are coupled to the conserved multisubunit signaling apparatus CD3. The mechanism by which TcR ligation is directly communicated to the signalling apparatus is a fundamental topic of interest in T cell biology. In brief, CD3 subunits that translate cell surface antigen binding into an intracellular phosphorylation signaling cascade. These phosphorylation events culminate in the activation of transcription factors such as NFAT and NFκB that lead to increased expression of cytokines and effector proteins such as granzymes and perforin. It is this characteristic that is used by TCEs which bind simultaneously a target antigen on a tumor cell and CD3 on T cells

to form an artificial immune synapse eventually leading to the destruction of the cell expressing said target antigen.

[3] From a clinical perspective, TCEs do not only have to show efficient cell killing activity, but at the same time other characteristics like, e.g., a manageable side effect profile are desired. However, these aspects are not the only considerations when it comes to the development of TCEs. Other areas of importance for drug development are pre-patient, i.e. concern characteristics of the TCE outside of the patient's body such as, e.g., shelf life, production scalability, solubility, stability, and ease of formulation. In other terms, an important feature from a pharmaceutical perspective is the developability of a given TCE or parts thereof to address certain needs such as for example in drug production or administration. Bringing together the requirements from clinical and pharmacological perspective is important for TCE platform advancement in relation to commercialization. In view of the biological complexities of having the TCE inducing the formation of the immune synapse, it can be challenging to manipulate the TCE in terms of its other characteristics such as for example shelf life, production scalability, solubility, stability, and ease of formulation while maintaining its effectiveness in mediating the killing of target cells.

[4] Thermal stability of TCEs is an important feature within and outside of the patient's body. A higher thermal stability of TCEs reduces the formation of high molecular weight aggregates caused which in turn provides, e. g., for a TCE that is active for a prolonged time in the body but will also be more stable during storage. Moreover, the reduction of high molecular weight aggregates can also result in a more favourable immunogenetic profile of the TCE upon administration thereby reducing the risk of side effects.

[5] Classically, the VH and VL domains making up the anti-target and anti-CD3 binding domains of TCEs are an area that has been the focus of improving stability. This is in particular true for Fvs that are part of TCEs. The hydrophobic interaction between the VH and the VL is believed to strongly determine the stability of a Fv. The interaction can in many Fvs not be strong enough to be stable for in vitro and/or in vivo applications. This has led to the coupling of the V-domains of an Fv by a linker resulting in single chain Fvs (scFvs). While the linker has shown to be effective in holding the V-domains (variable domains) together, it may not always be effective to keep a scFv active at all or active enough for a given application making it necessary to further improve stability. One approach to increase stability is that by increasing the interaction of the two V-domains, the stability of a biologically active Fv can be increased so that it remains a target binding monomer. Although approaches have been described in the art to improve stability of scFv, there is still a need in the art for improving stability of Fvs that are part of TCEs.

[6] The invention relates to a polypeptide or polypeptide construct comprising:

a binding domain binding to an extracellular epitope of the human CD3ε chain comprising or consisting of a VH region and a VL region, wherein

i) the VH region comprises:

a CDR-H1 sequence of X_1YAX_2N , where X_1 is K, V, S, G, R, T, or I; and X_2 is M or I;

a CDR-H2 sequence of RIRSKYNNYATYYADX₁VKX₂, where X_1 is S or Q; and X_2 is D, G, K, S, or E; and

a CDR-H3 sequence of $HX_1NFGNSYX_2SX_3X_4AY$, where X_1 is G, R, or A; X_2 is I, L, V, or T; X_3 is Y, W or F; and X_4 is W, F or Y; and

ii) wherein the VL region comprises:

a CDR-L1 sequence of $X_1SSTGAVTX_2X_3X_4YX_5N$, where X_1 is G, R, or A; X_2 is S or T; X_3 is G or S; X_4 is N or Y; and X_5 is P or A;

a CDR-L2 sequence of $X_1TX_2X_3X_4X_5X_6$; where X_1 is G or A; X_2 is K, D, or N; X_3 is F, M or K; X_4 is L or R; X_5 is A, P, or V; and X_6 is P or S; and

a CDR-L3 sequence of $X_1LWYSNX_2WV$, where X_1 is V, A, or T; and X_2 is R or L; and

iii) wherein one or more CDR sequences of the VH region of i) and/or of the VL region of ii) comprise one or more amino acid substitutions selected from X_24V and X_24F in CDR-H1;

D15 (preferably E), and X_116A in CDR-H2;

H1 (preferably A or N), X_12E , F4 (preferably I), and N6 (preferably S or T) in CDR-H3; and

X_11L and W3 (preferably Y) in CDR-L3.

[7] The term “polypeptide construct” (alternatively referred to also as “compound” herein) refers to an antigen-binding (or epitope-binding) molecule comprising domains themselves comprising paratopes. In the context of the present invention, a polypeptide construct is understood as an organic polymer which comprises at least one continuous, unbranched amino acid chain that naturally is not existing, but was engineered. An example of a polypeptide construct that is a single polypeptide is a BiTE[®] molecule that comprises a core structure comprising at least one functional target binding domain together with at least one complete functional CD3 binding domain on a single polypeptide chain, wherein these domains are linked directly by flexible peptide (a “linker”) without any further inserted domain unlike, for example, Xmabs that comprise the target binder and the CD3 binder on different polypeptide chains. In the context of the present invention, such a polypeptide construct comprising more than one amino acid chain is likewise envisaged. It is preferred that the term “polypeptide” is used in connection with single chain forms of the compounds of the

present invention, whereas “polypeptide construct” may preferably be more adequate to describe also polypeptides that comprise more than one polypeptide chain, for example two, three or four polypeptide chains. Additionally, the term “polypeptide construct” is also suitable to describe compounds of the invention that comprise one or more non-amino acid-based constituents, e.g. human serum albumin, etc. (HSA). An amino acid chain of a polypeptide typically comprises at least 50 amino acids, preferably at least 100, 200, 300, 400 or 500 amino acids. It is also envisaged in the context of the present invention that an amino acid chain of a polymer is linked to an entity which is not composed of amino acids.

[8] The polypeptides comprise structural and/or functional features based on the structure and/or function of an antibody, e.g., of a full-length immunoglobulin molecule. A polypeptide construct, hence, specifically and, preferably, selectively or immunospecifically binds to its target or antigen, more precisely to an epitope of said target or target antigen, and/or it comprises the heavy chain variable region (VH) and/or the light chain variable region (VL) naturally found in an antibody, or comprises domains derived therefrom. Accordingly, the constructs may alternatively be regarded as comprising paratope-structured and epitope-binding structures, such as those found in natural antibodies or fragments thereof. A polypeptide construct according to the invention comprises the minimum structural requirements of an antibody which allow for immunospecific target binding, i.e., a paratope that recognizes immunospecifically or immunoselectively an epitope on a target antigen unless specified differently. This minimum requirement may e.g. be defined by the presence of at least three light chain CDRs (i.e. CDR1, CDR2 and CDR3 of the VL region, also termed CDR-L1, CDR-L2, and CDR-L3) and/or three heavy chain CDRs (i.e. CDR1, CDR2 and CDR3 of the VH region, also termed CDR-H1, CDR-H2 and CDR-H3), preferably of all six CDRs. A polypeptide construct may hence be characterized by the presence of three or six CDRs in a binding domain, and the skilled person knows where (in which order) those CDRs are located within the paratopic binding structures. In the context of the CD3 binding domain of the polypeptide or polypeptide construct, said paratopic binding structure is specified to be a binding domain characterized by the presence of a VH and VL region comprising CDRs. Hence, a polypeptide/polypeptide construct according to the invention comprises at least a paratopic binding structure being a binding domain binding selectively, immunospecifically and/or immunoselectively to an extracellular epitope of the human CD3ε (also termed CD3epsilon or “CD3 epsilon” herein) chain comprising VH and VL regions with CDRs. Accordingly, a polypeptide/polypeptide construct according to the invention comprises a paratope selectively, immunospecifically and/or immunoselectively binding to an epitope of human CD3 epsilon. The terms “CDR”, and its plural “CDRs”, refer to the complementarity determining region of which three make up the binding character of a light chain variable region (CDR-L1, CDR-L2 and CDR-L3) and three make up the binding character of a heavy

chain variable region (CDR-H1, CDR-H2 and CDR-H3). CDRs contain most of the residues responsible for specific interactions of antibodies (or constructs or binding domain) with an antigen and hence contribute to the functional activity of an antibody molecule: they are the main determinants of antigen specificity. The exact definition of CDR boundaries and lengths is subject to different classification and numbering systems. CDRs may therefore be referred to by Kabat, Chothia, contact or any other boundary definitions, including the numbering system described herein. Despite differing boundaries, each of these systems has some degree of overlap in what constitutes the so called "hypervariable regions" within the variable sequences. CDR definitions according to these systems may therefore differ in length and boundary areas with respect to the adjacent framework region. See for example Kabat (an approach based on cross-species sequence variability), Chothia (an approach based on crystallographic studies of antigen-antibody complexes), and/or MacCallum (Kabat et al., loc. cit.; Chothia et al., J. Mol. Biol, 1987, 196: 901-917; and MacCallum et al., J. Mol. Biol, 1996, 262: 732). Still another standard for characterizing the antigen binding site is the AbM definition used by Oxford Molecular's AbM antibody modeling software. See, e.g., Protein Sequence and Structure Analysis of Antibody Variable Domains. In: Antibody Engineering Lab Manual (Ed.: Duebel, S. and Kontermann, R., Springer-Verlag, Heidelberg). To the extent that two residue identification techniques define regions of overlapping, but not identical regions, they can be combined to define a hybrid CDR. However, the numbering in accordance with the so-called Kabat system is preferred. The term "antigen-binding structure", as used herein, refers to any polypeptide/polypeptide construct that comprises an antigen-binding structure or any molecule that has binding activity to a specified antigen. Said antigen-binding structures or molecules are not limited to those derived from a living organism, and for example, they may be a polypeptide produced from an artificially designed sequence. They may also be any of a naturally occurring polypeptide, synthetic polypeptide, recombinant polypeptide, and such. As the antigen-binding structure in accordance with the present invention bind specifically to parts of an antigen, i.e., they bind specifically to an epitope of CD3epsilon, the antigen (epitope)-binding structure may also be broadly defined as "paratopic structure" herein. Accordingly, the polypeptides/polypeptide constructs according to the invention may also be defined as a domain comprising a paratope that are preferably immunospecifically or immunoselectively binding to a target antigen/target epitope; and in certain embodiments comprising at least a further paratope, preferably immunospecifically or immunoselectively, binding to a further, different or same, target antigen/target epitope. Therefore, whenever the present description refers to a domain of a construct or molecule of the present invention, the construct comprises at least one paratopic structure (or paratope) binding human CD3epsilon as specified herein, particularly according to any one of the appended claims. In certain embodiments, said construct comprises at

least a further paratope binding also to human CD3epsilon or a different target antigen as defined herein.

[9] The term “antibody” as used in accordance with the invention comprises full-length antibodies, also including camelid antibodies and other immunoglobulins generated by biotechnological or protein engineering methods or processes. These full-length antibodies may be for example monoclonal, recombinant, chimeric, deimmunized, humanized and human antibodies, as well as antibodies from other species such as mouse, hamster, rabbit, rat, goat, or non-human primates.

[10] “Polypeptides/polypeptide constructs” of the present invention may also comprise the structure of a full-length immunoglobulin as it occurs naturally. For example, they may comprise (at least) two full-length antibody heavy chains and two full-length antibody light chains. However, given that the polypeptides/polypeptide constructs according to the invention preferably comprise a linker linking the VH and VL region of the CD3 binding domain, preferably resulting in a scFv, and/or, in other embodiments, comprise at least one further binding domain comprising a paratope, they do not occur naturally, and they are markedly different in their function from naturally occurring products. A polypeptide or polypeptide construct of the invention is hence an artificial “hybrid” molecule comprising, preferably, an scFv and/or, in some embodiments, distinct paratopes/binding domains with different specificities and/or selectivities.

[11] As indicated above, the polypeptides of the invention may comprise more than one polypeptide chain, i.e. polypeptides comprising two or more polypeptide chains are also subject to the present invention, particularly polypeptides forming a three-dimensional protein-like structure that allows for the immunospecific binding to CD3epsilon. Therefore, the definition of the term “polypeptide construct” includes molecules consisting of only one polypeptide chain as well as molecules consisting of two, three, four or more polypeptide chains, which chains can be either identical (homodimers, homotrimers or homo oligomers) or different (heterodimer, heterotrimer or heterooligomer). Examples for the above identified antibodies and their fragments, variants, derivatives and constructs derived therefrom are described inter alia in Harlow and Lane, Antibodies: A laboratory manual, CSHL Press (1988); Kontermann and Dübel, Antibody Engineering, Springer, 2nd ed. 2010; and Little, Recombinant Antibodies for Immunotherapy, Cambridge University Press 2009.

[12] “Polypeptides/polypeptide constructs” of the present invention may also comprise fragments of full-length antibodies, such as VH, VHH, VL, (s)dAb, Fv, light chain (VL-CL), Fd (VH-CH1), heavy chain, Fab, Fab', F(ab')₂ or “rlgG” (“half antibody” consisting of a heavy chain and a light chain), whereas not all of the foregoing fragments are applicable for the CD3epsilon binding domain since it is defined to comprise a VH and a VL region, but to the

embodiments regarding the at least one further binding domain. Polypeptides/polypeptide constructs according to the invention may also comprise modified fragments of antibodies, also called antibody variants or antibody derivatives. Examples include, but are not limited to, scFv, di-scFv or bi(s)-scFv, scFv-Fc, scFv-zipper, scFab, Fab2, Fab3, diabodies, single chain
5 diabodies, tandem diabodies (Tandab's), tandem di-scFv, tandem tri-scFv, „minibodies“ exemplified by a structure which is as follows: (VH-VL-CH3)₂, (scFv-CH3)₂, ((scFv)₂-CH3 + CH3), ((scFv)₂-CH3) or (scFv-CH3-scFv)₂, multibodies such as triabodies or tetrabodies, and single domain antibodies such as nanobodies or single variable domain antibodies comprising merely one variable region, which might be VHH, VH or VL, that selectively and,
10 preferably, specifically binds to an antigen or target independently of other variable regions or domains, whereas not all of the foregoing fragments are applicable for the CD3epsilon binding domain since it is defined to comprise a VH and a VL region, but to the embodiments regarding the at least one further binding domain. Further possible formats of the polypeptides/polypeptide constructs according to the invention are cross bodies, maxi
15 bodies, hetero Fc constructs, mono Fc constructs and scFc constructs. Examples for those formats will be described herein below.

[13] Furthermore, the definition of the term “polypeptide construct” includes bivalent and polyvalent / multivalent polypeptides/polypeptide constructs as well as bispecific and polyspecific / multispecific polypeptides/polypeptide constructs, which selectively and,
20 preferably, specifically bind to two, three or more antigenic structures (epitopes), through distinct binding domains. A polypeptide construct can have more binding valences than specificities, e.g. in a case where it has two binding domains for one target (CD3epsilon) and one binding domain for another target, for example those described herein below, or vice versa, in which case the polypeptide construct is trivalent and bispecific. In general, the term
25 “bispecific” includes the meaning that a polypeptide construct binds to at least two different antigens, such as said CD3epsilon and a further target, for example those specified herein below.

[14] The terms “paratope”, “antigen-binding domain”, “epitope-binding domain”, “binding domain” or “domain which binds to...” characterize, in connection with the present invention,
30 a domain of the construct which selectively and, preferably, specifically or immunospecifically binds to / interacts with / recognizes an epitope on the target or antigen (here: CD3). The terms “binding domain” or “domain which binds to...” or “domain” as far as it relates to the herein described “constructs” characterizes in connection with the present invention a domain of the construct which immunospecifically binds to / interacts with / recognizes an
35 epitope on the target or antigen. The structure and function of the CD3epsilon binding domain (also termed as first binding domain in the case of a polypeptide/polypeptide construct comprising a further, consequently second, third, and so on, binding domain), and

preferably also the structure and/or function of any further binding domain (binding to for example to a cell surface antigen such as a tumor antigen), is/are based on the structure and/or function of an antibody, e.g. of a full-length immunoglobulin polypeptide. The "binding domain" or "domain which binds to..." may hence comprise the minimum structural requirements of an antibody which allow for immunospecific target binding. While the structural requirements of the CD3epsilon binding domain is specified to comprise a VH and VL region with corresponding three CDRs per region, said minimum structural requirement in any further binding domain may e.g. be defined by the presence of at least three light chain CDRs (i.e. CDR1, CDR2 and CDR3 of the VL region) and/or of three heavy chain CDRs (i.e. CDR1, CDR2 and CDR3 of the VH region), preferably of all six CDRs. A "domain which binds to" (or a "binding domain") may typically comprise an antibody light chain variable region (VL) and an antibody heavy chain variable region (VH); however, it does not have to comprise both, but may comprise only one of VH or VL. Fd fragments, for example, often retain some antigen-binding function of the intact antigen-binding domain. The terms "paratope", "antigen-binding structure" and "epitope-binding structure, as used herein, refer also to a portion of an antibody (or a molecule according to the invention), which comprises a region that specifically binds and is complementary to the whole or a portion of an antigen or a part thereof, i.e. an antibody can only bind to a particular portion of the antigen. The particular portion is called "epitope". An antigen-binding domain can be provided from one or more antibody variable domains. Preferably, the antigen-binding domains contain antibody variable region that comprising both the antibody light chain variable region (VL) and antibody heavy chain variable region (VH). Such preferable antigen-binding domains include, for example, "single-chain Fv (scFv)", "single-chain antibody", "Fv", "single-chain Fv2 (scFv2)", "Fab", and "F(ab')₂". For the CD3epsilon binding domain it is preferred that it takes the form of an scFv.

[15] Examples for the format of a "domain which binds to", "domain comprising a paratope" (or "binding domain", "antigen-binding structure", "epitope-binding structure") include unless otherwise defined, but are not limited to, full-length antibodies, fragments of full-length antibodies (such as VH, VHH, VL), (s)dAb, Fv, light chain (VL-CL), Fd (VH-CH1), heavy chain, Fab, Fab', F(ab')₂ or "r IgG" ("half antibody")), antibody variants or derivatives such as scFv, di-scFv or bi(s)-scFv, scFv-Fc, scFv-zipper, scFab, Fab2, Fab3, diabodies, single chain diabodies, tandem diabodies (Tandab's), tandem di-scFv, tandem tri-scFv, „minibodies“ (selected from formats such as (VH-VL-CH3)₂, (scFv-CH3)₂, ((scFv)₂-CH3 + CH3)), ((scFv)₂-CH3) or (scFv-CH3-scFv)₂, multibodies such as triabodies or tetrabodies, and single domain antibodies such as nanobodies or single variable domain antibodies comprising merely one variable region, which might be VHH, VH or VL. Further examples for the format of a "domain which binds to" (or a "binding domain") include (1) an antibody

fragment or variant comprising VL, VH, CL and CH1 (such as Fab); (2) an antibody fragment or variant comprising two linked Fab fragments (such as a F(ab')₂); (3) an antibody fragment or variant comprising VH and CH1 (such as Fd); (4) an antibody fragment or variant comprising VL and CL (such as the light chain); (5) an antibody fragment or variant comprising VL and VH (such as Fv); (5) a dAb fragment (Ward et al., (1989) Nature 341 :544-546), which has a VH domain; (6) an antibody variant comprising at least three isolated CDRs of the heavy and/or the light chain; and (7) a single chain Fv (scFv). Examples for embodiments of constructs or binding domains according to the invention are e.g. described in WO 00/006605, WO 2005/040220, WO 2008/119567, WO 2010/037838, WO 2013/026837, WO 2013/026833, US 2014/0308285, US 2014/0302037, WO 2014/144722, WO 2014/151910, and WO 2015/048272. In the context of the present invention, a paratope is understood as an antigen-binding site which is a part of a polypeptide as described herein and which recognizes and binds to an antigen. A paratope is typically a small region of about at least 5 amino acids. A paratope as understood herein typically comprises parts of antibody-derived heavy (VH) and light chain (VL) sequences. Each binding domain of a polypeptide according to the present invention is provided with a paratope comprising a set of 6 complementarity-determining regions (CDR loops) with three of each being comprised within the antibody-derived VH and VL sequence, respectively.

[16] It is envisaged for the compounds, particularly for the constructs of the present invention that a) the construct is a single chain polypeptide or a single chain construct, b) the CD3epsilon binding domain is in the format of an scFv, c) any further, such as a second binding and/or third domain is in the format of an scFv, d) the first and said further, such as said second and/or third domain are connected via a linker, preferably a peptide linker, more preferably a glycine/serine or glycine/glutamine linker, and/or e) the construct comprises a domain providing an extended serum half-life, such as an Fc-based domain, or human serum albumin (HSA). In the latter case, it is a preferred embodiment, wherein the term "polypeptide construct" makes clear that it comprises more than a single peptide chain. A preferred Fc-based domain which extends the serum half-life (also termed "HLE" domain) comprises two polypeptide monomers, each comprising a hinge, a CH2 domain and a CH3 domain, wherein said two polypeptide monomers are fused to each other via a peptide linker (see, e.g., SEQ ID NO: 18 and 19); the format is in N-terminal to C-terminal order: hinge-CH2-CH3-linker-hinge-CH2-CH3.

[17] The constructs of the present invention are preferably "in vitro generated constructs" and/or "recombinant constructs". In the context of the present invention, the term "in vitro generated" refers to a construct according to the above definition where all or part of the binding domain or of a variable region (e.g., at least one CDR) is generated in a non-immune cell selection, e.g., in an in vitro phage display, on a protein chip or in any other method in

which candidate amino acid sequences can be tested for their ability to bind to an antigen. This term thus preferably excludes sequences generated solely by genomic rearrangement in an immune cell in an animal. It is envisaged that the first and/or second domain of the construct is produced by or obtainable by phage display or library screening methods rather than by grafting CDR sequences from a pre-existing (monoclonal) antibody into a scaffold. A
5 "recombinant construct" is a construct generated or produced using (inter alia) recombinant DNA technology or genetic engineering.

[18] The constructs of the present invention are envisaged to be monoclonal. As used herein, polypeptides or constructs that are denominated "monoclonal" (mAb) are obtained
10 from a population of substantially homogeneous antibodies / constructs, i.e., the individual antibodies / constructs comprised in the population are identical (in particular with respect to their amino acid sequence) except for possible naturally occurring mutations and/or post-translational modifications (e.g., isomerizations, amidations) that may be present in minor amounts. Monoclonal antibodies / constructs are highly specific, being directed against a
15 single epitope within the antigen, in contrast to polyclonal antibody preparations which typically include different antibodies directed against different determinants (or epitopes). In addition to their specificity, monoclonal antibodies are advantageous in that they are synthesized by the hybridoma culture, hence uncontaminated by other immunoglobulins. The modifier "monoclonal" indicates the character of the antibody / construct as being obtained
20 from a substantially homogeneous population of antibodies and is not to be construed as requiring production of the antibody by any specific method.

[19] For the preparation of monoclonal antibodies, any technique providing antibodies produced by continuous cell line cultures can be used. For example, monoclonal antibodies to be used may be made by the hybridoma method first described by Koehler et al., Nature,
25 256: 495 (1975), or may be made by recombinant DNA methods (see, e.g., U.S. Patent No. 4,816,567). Examples for further techniques to produce human monoclonal antibodies include the trioma technique, the human B-cell hybridoma technique (Kozbor, Immunology Today 4 (1983), 72) and the EBV-hybridoma technique (Cole et al., Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, Inc. (1985), 77-96).

[20] Hybridomas can then be screened using standard methods, such as enzyme-linked immunosorbent assay (ELISA) and surface plasmon resonance (BIAcore™) analysis, to identify one or more hybridomas that produce an antibody that selectively and, preferably, specifically or immunospecifically binds to a specified antigen. Any form of the relevant antigen may be used as the immunogen, e.g., recombinant antigen, naturally occurring
35 forms, any variants or fragments thereof, as well as an antigenic peptide thereof. Surface plasmon resonance as employed in the BIAcore™ system can be used to increase the

efficiency of phage antibodies / constructs which bind to an epitope of a target antigen (Schier, Human Antibodies Hybridomas 7 (1996), 97-105; Malmborg, J. Immunol. Methods 183 (1995), 7-13).

[21] Another exemplary method of making constructs or binding domains includes screening protein expression libraries, e.g., phage display or ribosome display libraries. Phage display is described, for example, in Ladner et al., U.S. Patent No. 5,223,409; Smith (1985) Science 228:1315-1317, Clackson et al., Nature, 352: 624-628 (1991) and Marks et al., J. Mol. Biol., 222: 581-597 (1991).

[22] In addition to the use of display libraries, the relevant antigen can be used to immunize a non-human animal, e.g., a rodent (such as a mouse, hamster, rabbit or rat). In one embodiment, the non-human animal includes at least a part of a human immunoglobulin gene. For example, it is possible to engineer mouse strains deficient in mouse antibody production with large fragments of the human Ig (immunoglobulin) loci. Using the hybridoma technology, antigen-specific monoclonal antibodies derived from the genes with the desired specificity may be produced and selected. See, e.g., Xenomouse™ mouse, Green et al. (1994) Nature Genetics 7:13-21, US 2003-0070185, WO 96/34096, and WO 96/33735.

[23] A monoclonal antibody can also be obtained from a non-human animal, and then modified, e.g., humanized, deimmunized, rendered chimeric etc., using recombinant DNA techniques known in the art. Examples of modified constructs or binding domains include humanized variants of non-human antibodies / constructs, "affinity matured" constructs or binding domains (see, e.g. Hawkins et al. J. Mol. Biol. 254, 889-896 (1992) and Lowman et al., Biochemistry 30, 10832- 10837 (1991)) and antibody variants or mutants with altered effector function(s) (see, e.g., US Patent 5,648,260, Kontermann and Dübel (2010), loc. cit. and Little (2009), loc. cit.).

[24] In immunology, affinity maturation is the process by which B cells produce antibodies with increased affinity for antigen during the course of an immune response. With repeated exposures to the same antigen, a host will produce antibodies of successively greater affinities. Like the natural prototype, the in vitro affinity maturation is based on the principles of mutation and selection. The in vitro affinity maturation has successfully been used to optimize antibodies, antibody fragments, antibody variants, constructs or binding domains. Random mutations inside the CDRs are introduced using radiation, chemical mutagens or error-prone PCR. In addition, the genetic diversity can be increased by chain shuffling. Two or three rounds of mutation and selection using display methods like phage display usually results in antibodies, antibody fragments, antibody variants, constructs or binding domains with affinities in the low nanomolar range.

[25] A preferred type of an amino acid substitutional variation of the constructs or binding domains of the invention involves substituting one or more residues within the hypervariable region of a parent antibody structure (e.g. a humanized or human antibody structure). Generally, the resulting variant(s) selected for further development will have improved biological properties relative to the parent antibody structure from which they are generated. A convenient way for generating such substitutional variants involves affinity maturation using phage display. Briefly, several sites of the hypervariable region (e. g. 6-7 sites) are mutated to generate all possible amino acid substitutions at each site. The variants thus generated are displayed in a monovalent fashion from filamentous phage particles as fusions to the gene III product of M13 packaged within each particle. The phage-displayed variants are then screened for their biological activity (e.g. binding affinity) as disclosed herein. To identify candidate hypervariable region sites contributing significantly to antigen binding (candidates for modification), alanine scanning mutagenesis can also be performed. Alternatively, or additionally, it may be beneficial to analyze a crystal structure of the complex between the antigen and the construct or the binding domain to identify contact points between the binding domain and its specific antigen. Such contact residues and neighbouring residues are candidates for substitution according to the techniques elaborated herein. Once such variants are generated, the panel of variants is subjected to screening as described herein and antibodies, their antigen-binding fragments, constructs or binding domains with superior properties in one or more relevant assays may be selected for further development.

[26] The constructs and binding domains of the present invention specifically include "chimeric" versions in which a portion of the heavy and/or light chain is identical with or homologous to corresponding sequences in antibodies derived from a particular species or belonging to a particular antibody class or subclass, while the remainder of the chain(s) is/are identical with or homologous to corresponding sequences in antibodies derived from another species or belonging to another antibody class or subclass, as well as fragments or variants of such antibodies, so long as they exhibit the desired biological activity (U.S. Patent No. 4,816,567; Morrison et al., Proc. Natl. Acad. Sci. USA, 81: 6851-6855 (1984)). Chimeric constructs or binding domains of interest herein include "primitized" constructs comprising variable domain antigen-binding sequences derived from a non-human primate (e.g., Old World Monkey, Ape etc.) and human constant region sequences. A variety of approaches for making chimeric antibodies or constructs have been described. See e.g., Morrison et al., Proc. Natl. Acad. Sci. U.S.A. 81:6851, 1985; Takeda et al., Nature 314:452, 1985, Cabilly et al., U.S. Patent No. 4,816,567; Boss et al., U.S. Patent No. 4,816,397; Tanaguchi et al., EP 0171496; EP 0173494; and GB 2177096.

[27] An antibody, polypeptide construct, antibody fragment, antibody variant or binding domain may also be modified by specific deletion of human T cell epitopes (a method called “deimmunization”) using methods disclosed for example in WO 98/52976 or WO 00/34317. Briefly, the heavy and light chain variable regions of an antibody, construct or binding domain can be analyzed for peptides that bind to MHC class II; these peptides represent potential T cell epitopes (as defined e.g. in WO 98/52976 and WO 00/34317). For detection of potential T cell epitopes, a computer modeling approach termed “peptide threading” can be applied, and in addition a database of human MHC class II binding peptides can be searched for motifs present in the VH and VL sequences, as described in WO 98/52976 and WO 00/34317. These motifs bind to any of the 18 major MHC class II DR allotypes, and thus constitute potential T cell epitopes. Potential T cell epitopes detected can be eliminated by substituting small numbers of amino acid residues in the variable domains or variable regions, or preferably, by single amino acid substitutions. Typically, conservative substitutions are made. Often, but not exclusively, an amino acid common to a position in human germline antibody sequences may be used. Human germline sequences are disclosed e.g. in Tomlinson, et al. (1992) J. Mol. Biol. 227:776-798; Cook, G.P. et al. (1995) Immunol. Today Vol. 16 (5): 237-242; and Tomlinson et al. (1995) EMBO J. 14: 14:4628-4638. The V BASE directory (www2.mrc-lmb.cam.ac.uk/vbase/list2.php) provides a comprehensive directory of human immunoglobulin variable region sequences (compiled by Tomlinson, LA. et al. MRC Centre for Protein Engineering, Cambridge, UK). These sequences can be used as a source of human sequence, e.g., for framework regions and CDRs. Consensus human framework regions can also be used, for example as described in US Patent No. 6,300,064.

[28] “Humanized” antibodies, variants or fragments thereof, constructs and binding domains are based on immunoglobulins of mostly human sequences, which contain (a) minimal sequence(s) derived from non-human immunoglobulin. For the most part, humanized antibodies, variants or fragments thereof, constructs and binding domains are based on human immunoglobulins (recipient antibodies) in which residues from a hypervariable region or CDR are replaced by residues from a hypervariable region or CDR of a non-human species (donor antibody) such as a rodent (e.g. mouse, hamster, rat or rabbit) having the desired specificity, affinity, capacity and/or biological activity. In some instances, Fv framework region (FR) residues of the human immunoglobulin are replaced by corresponding non-human residues. Furthermore, “humanized” antibodies, variants or fragments thereof, constructs and binding domains as used herein may also comprise residues which are found neither in the recipient antibody nor the donor antibody. These modifications are made to further refine and optimize antibody performance. The humanized antibodies, variants or fragments thereof, constructs and binding domains may also comprise

at least a portion of an immunoglobulin constant region (such as Fc), typically that of a human immunoglobulin. For further details, see Jones et al., *Nature*, 321: 522-525 (1986); Reichmann et al., *Nature*, 332: 323-329 (1988); and Presta, *Curr. Op. Struct. Biol.*, 2: 593-596 (1992).

5 **[29]** Humanized antibodies, variants or fragments thereof, constructs and binding domains can be generated by replacing sequences of the (Fv) variable region that are not directly involved in antigen binding with equivalent sequences from human (Fv) variable regions. Exemplary methods for generating such molecules are provided by Morrison (1985) *Science* 229:1202-1207; by Oi et al. (1986) *BioTechniques* 4:214; and by US 5,585,089; 10 US 5,693,761; US 5,693,762; US 5,859,205; and US 6,407,213. These methods include isolating, manipulating, and expressing the nucleic acid sequences that encode all or part of immunoglobulin (Fv) variable regions from at least one of a heavy or light chain. Such nucleic acids may be obtained from a hybridoma producing an antibody against a predetermined target, as described above, as well as from other sources. The recombinant DNA encoding 15 the humanized antibody, variant or fragment thereof, construct or binding domain can then be cloned into an appropriate expression vector.

[30] Humanized antibodies, variants or fragments thereof, constructs and binding domains may also be produced using transgenic animals such as mice that express human heavy and light chain genes but are incapable of expressing the endogenous mouse immunoglobulin 20 heavy and light chain genes. Winter describes an exemplary CDR grafting method that may be used to prepare the humanized molecules described herein (U.S. Patent No. 5,225,539). All the CDRs of a given human sequence may be replaced with at least a portion of a non-human CDR, or only some of the CDRs may be replaced with non-human CDRs. It is only necessary to replace the number of CDRs required for binding of the humanized molecule to 25 a predetermined antigen.

[31] A humanized antibody, variant or fragment thereof, construct or binding domain can be optimized by the introduction of conservative substitutions, consensus sequence substitutions, germline substitutions and/or back mutations. Such altered immunoglobulin molecules can be made by any of several techniques known in the art, (e.g., Teng et al., 30 *Proc. Natl. Acad. Sci. U.S.A.*, 80: 7308-7312, 1983; Kozbor et al., *Immunology Today*, 4: 7279, 1983; Olsson et al., *Meth. Enzymol.*, 92: 3-16, 1982, and EP 239 400).

[32] Human anti-mouse antibody (HAMA) responses have led the industry to prepare chimeric or otherwise humanized antibodies / constructs. It is however expected that certain human anti-chimeric antibody (HACA) responses will be observed, particularly in chronic or 35 multi-dose utilizations of an antibody or construct. Thus, it would be desirable to provide

constructs comprising a human binding domain against a target, to vitiate concerns and/or effects of HAMA or HACA response.

[33] Therefore, according to one embodiment, the polypeptide construct having at least one further binding domain, said binding domain(s) are "human". The term "human antibody", "human construct" and "human binding domain" includes antibodies, constructs and binding domains, respectively, having antibody-derived regions such as variable and constant regions or domains which correspond substantially to human germline immunoglobulin sequences known in the art, including, for example, those described by Kabat et al. (1991) (loc. cit.). The human constructs or binding domains of the invention may include amino acid residues not encoded by human germline immunoglobulin sequences (e.g., mutations introduced by random or site-specific mutagenesis in vitro or by somatic mutation in vivo), for example in the CDRs, and particularly in CDR3. The human constructs or binding domains can have at least one, two, three, four, five, or more positions replaced with an amino acid residue that is not encoded by the human germline immunoglobulin sequence. The definition of human antibodies, constructs and binding domains as used herein also contemplates fully human antibodies, constructs and binding domains which include only non-artificially and/or genetically altered human sequences of antibodies as those can be derived by using technologies or systems such as the XenomouseTM mouse.

[34] Polypeptides/polypeptide constructs comprising at least one human binding domain may avoid some of the problems associated with antibodies or constructs that possess non-human such as rodent (e.g. murine, rat, hamster or rabbit) variable and/or constant regions. The presence of such rodent derived proteins can lead to the rapid clearance of the antibodies or constructs or can lead to the generation of an immune response against the antibody or construct by a patient. To avoid the use of rodent-derived constructs, humanized or fully human constructs can be generated through the introduction of human antibody function into a rodent so that the rodent produces fully human antibodies.

[35] The ability to clone and reconstruct megabase-sized human loci in YACs and to introduce them into the mouse germline provides a powerful approach to elucidating the functional components of very large or crudely mapped loci as well as generating useful models of human disease. Furthermore, the use of such technology for substitution of mouse loci with their human equivalents could provide unique insights into the expression and regulation of human gene products during development, their communication with other systems, and their involvement in disease induction and progression.

[36] An important practical application of such a strategy is the "humanization" of the mouse humoral immune system. Introduction of human immunoglobulin (Ig) loci into mice in which the endogenous Ig genes have been inactivated offers the opportunity to study the

mechanisms underlying programmed expression and assembly of antibodies as well as their role in B-cell development. Furthermore, such a strategy could provide an ideal source for production of fully human monoclonal antibodies (mAbs) – an important milestone towards fulfilling the promise of antibody therapy in human disease. Fully human antibodies or constructs derived therefrom are expected to minimize the immunogenic and allergic responses intrinsic to mouse or mouse-derivatized mAbs and thus to increase the efficacy and safety of the administered antibodies / constructs. The use of fully human antibodies or constructs can be expected to provide a substantial advantage in the treatment of chronic and recurring human diseases, such as inflammation, autoimmunity, and cancer, which require repeated compound administrations.

[37] One approach towards this goal was to engineer mouse strains deficient in mouse antibody production with large fragments of the human Ig loci in anticipation that such mice would produce a large repertoire of human antibodies in the absence of mouse antibodies. Large human Ig fragments would preserve the large variable gene diversity as well as the proper regulation of antibody production and expression. By exploiting the mouse machinery for antibody diversification and selection and the lack of immunological tolerance to human proteins, the reproduced human antibody repertoire in these mouse strains should yield high affinity antibodies against any antigen of interest, including human antigens. Using the hybridoma technology, antigen-specific human mAbs with the desired specificity could be readily produced and selected. This general strategy was demonstrated in connection with the generation of the first XenoMouseTM mouse strains (see Green et al. Nature Genetics 7:13-21 (1994)). The XenoMouseTM strains were engineered with yeast artificial chromosomes (YACs) containing 245 kb and 190 kb-sized germline configuration fragments of the human heavy chain locus and kappa light chain locus, respectively, which contained core variable and constant region sequences. The human Ig containing YACs proved to be compatible with the mouse system for both rearrangement and expression of antibodies and were capable of substituting for the inactivated mouse Ig genes. This was demonstrated by their ability to induce B cell development, to produce an adult-like human repertoire of fully human antibodies, and to generate antigen-specific human mAbs. These results also suggested that introduction of larger portions of the human Ig loci containing greater numbers of V genes, additional regulatory elements, and human Ig constant regions might recapitulate substantially the full repertoire that is characteristic of the human humoral response to infection and immunization. The work of Green et al. was extended to the introduction of greater than approximately 80% of the human antibody repertoire through introduction of megabase sized, germline configuration YAC fragments of the human heavy chain loci and kappa light chain loci, respectively. See Mendez et al. Nature Genetics 15:146-156 (1997) and U.S. patent application Ser. No. 08/759,620.

[38] The production of the XenoMouse™ model is further discussed and delineated in U.S. patent applications Ser. No. 07/466,008, Ser. No. 07/610,515, Ser. No. 07/919,297, Ser. No. 07/922,649, Ser. No. 08/031,801, Ser. No. 08/112,848, Ser. No. 08/234,145, Ser. No. 08/376,279, Ser. No. 08/430,938, Ser. No. 08/464,584, Ser. No. 08/464,582, Ser. No. 08/463,191, Ser. No. 08/462,837, Ser. No. 08/486,853, Ser. No. 08/486,857, Ser. No. 08/486,859, Ser. No. 08/462,513, Ser. No. 08/724,752, Ser. No. 08/759,620; and U.S. Pat. Nos. 6,162,963; 6,150,584; 6,114,598; 6,075,181, and 5,939,598 and Japanese Patent Nos. 3 068 180 B2, 3 068 506 B2, and 3 068 507 B2. See also Mendez et al. Nature Genetics 15:146-156 (1997) and Green and Jakobovits J. Exp. Med. 188:483-495 (1998), EP 0 463 151 B1, WO 94/02602, WO 96/34096, WO 98/24893, WO 00/76310, and WO 03/47336.

[39] In an alternative approach, others, including GenPharm International, Inc., have utilized a “minilocus” approach. In the minilocus approach, an exogenous Ig locus is mimicked through the inclusion of pieces (individual genes) from the Ig locus. Thus, one or more VH genes, one or more DH genes, one or more JH genes, a mu constant region, and a second constant region (preferably a gamma constant region) are formed into a construct for insertion into an animal. This approach is described in U.S. Pat. No. 5,545,807 to Surani et al. and U.S. Pat. Nos. 5,545,806; 5,625,825; 5,625,126; 5,633,425; 5,661,016; 5,770,429; 5,789,650; 5,814,318; 5,877,397; 5,874,299; and 6,255,458 each to Lonberg and Kay, U.S. Pat. Nos. 5,591,669 and 6,023,010 to Krimpenfort and Berns, U.S. Pat. Nos. 5,612,205; 5,721,367; and 5,789,215 to Berns et al., and U.S. Pat. No. 5,643,763 to Choi and Dunn, and GenPharm International U.S. patent application Ser. No. 07/574,748, Ser. No. 07/575,962, Ser. No. 07/810,279, Ser. No. 07/853,408, Ser. No. 07/904,068, Ser. No. 07/990,860, Ser. No. 08/053,131, Ser. No. 08/096,762, Ser. No. 08/155,301, Ser. No. 08/161,739, Ser. No. 08/165,699, Ser. No. 08/209,741. See also EP 0 546 073 B1, WO 92/03918, WO 92/22645, WO 92/22647, WO 92/22670, WO 93/12227, WO 94/00569, WO 94/25585, WO 96/14436, WO 97/13852, and WO 98/24884 and U.S. Pat. No. 5,981,175. See further Taylor et al. (1992), Chen et al. (1993), Tuaillon et al. (1993), Choi et al. (1993), Lonberg et al. (1994), Taylor et al. (1994), and Tuaillon et al. (1995), Fishwild et al. (1996).

[40] Kirin has also demonstrated the generation of human antibodies from mice in which, through microcell fusion, large pieces of chromosomes, or entire chromosomes, have been introduced. See European Patent Application Nos. 773 288 and 843 961. Xenerex Biosciences is developing a technology for the potential generation of human antibodies. In this technology, SCID mice are reconstituted with human lymphatic cells, e.g., B and/or T cells. Mice are then immunized with an antigen and can generate an immune response against the antigen. See U.S. Pat. Nos. 5,476,996; 5,698,767; and 5,958,765.

[41] In some embodiments, the constructs of the invention are “isolated” or “substantially pure” constructs. “Isolated” or “substantially pure”, when used to describe the constructs disclosed herein, means a construct that has been identified, separated and/or recovered from a component of its production environment. Preferably, the construct is free or substantially free of association with all other components from its production environment. Contaminant components of its production environment, such as that resulting from recombinant transfected cells, are materials that could interfere with diagnostic or therapeutic uses for the construct, and may include enzymes, hormones, and other proteinaceous or non-proteinaceous compounds. It is understood that the isolated or substantially pure construct may constitute from 5% to 99.9% by weight of the total protein / polypeptide content in a given sample, depending on the circumstances. The desired construct may be produced at a significantly higher concentration using an inducible promoter or high expression promoter. The definition includes the production of a construct in a wide variety of organisms and/or host cells that are known in the art. In certain embodiments, the construct will be purified (1) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (2) to homogeneity by SDS-PAGE under non-reducing or reducing conditions using Coomassie Blue or, preferably, silver staining. Usually, however, an isolated construct will be prepared by at least one purification step.

[42] According to one embodiment, the entire construct and/or the binding domains are in the form of one or more polypeptides or in the form of proteins. In addition to proteinaceous parts, such polypeptides or proteins may include non-proteinaceous parts (e.g. chemical linkers or chemical cross-linking agents such as glutaraldehyde).

[43] Peptides are short chains of amino acid monomers linked by covalent peptide (amide) bonds. Hence, peptides fall under the broad chemical classes of biological oligomers and polymers. Amino acids that are part of a peptide or polypeptide chain are termed “residues” and can be consecutively numbered. All peptides except cyclic peptides have an N-terminal residue at one end and a C-terminal residue at the other end of the peptide. An oligopeptide consists of only a few amino acids (usually between two and twenty). A polypeptide is a longer, continuous, and unbranched peptide chain. Peptides are distinguished from proteins based on size, and as an arbitrary benchmark can be understood to contain approximately 50 or fewer amino acids. Proteins consist of one or more polypeptides, usually arranged in a biologically functional way. While aspects of the lab techniques applied to peptides versus polypeptides and proteins differ (e.g., the specifics of electrophoresis, chromatography, etc.), the size boundaries that distinguish peptides from polypeptides and proteins are not absolute. Therefore, in the context of the present invention,

the terms “peptide”, “polypeptide” and “protein” may be used interchangeably, and the term “polypeptide” is often preferred.

[44] Polypeptides may further form multimers such as dimers, trimers and higher oligomers, which consist of more than one polypeptide molecule, as mentioned above.

Polypeptide molecules forming such dimers, trimers etc. may be identical or non-identical. The corresponding structures of higher order of such multimers are, consequently, termed homo- or heterodimers, homo- or heterotrimers etc. An example for a heteromultimer is an antibody or immunoglobulin molecule, which, in its naturally occurring form, consists of two identical light polypeptide chains and two identical heavy polypeptide chains. The terms “peptide”, “polypeptide” and “protein” also refer to naturally modified peptides / polypeptides / proteins wherein the modification is accomplished e.g. by post-translational modifications like glycosylation, acetylation, phosphorylation and the like. A “peptide”, “polypeptide” or “protein” when referred to herein may also be chemically modified such as pegylated. Such modifications are well known in the art and described herein below.

[45] The terms “selectively” and, “preferably, selectively”, “(specifically or immunospecifically) binds to”, “(specifically or immunospecifically) recognizes”, or “(specifically or immunospecifically) reacts with” mean in accordance with this invention that a construct or a binding domain selectively interacts or (immuno-)specifically interacts with a given epitope on the target molecule (antigen), here: CD3, respectively. This selective interaction or association occurs more frequently, more rapidly, with greater duration, with greater affinity, or with some combination of these parameters, to an epitope on the specific target (here: CD3epsilon) than to alternative substances (non-target molecules, e.g., here CD3gamma, etc.). Because of the sequence similarity between homologous proteins in different species, a construct or a binding domain that selectively and/or immunospecifically binds to its target (such as a human target) may, however, cross-react with homologous target molecules from different species (such as, from non-human primates). The terms “selectively binds to”, “specific / immunospecific binding”, etc. can hence include the binding of a construct or binding domain to epitopes or structurally related epitopes in more than one species. In the context of the present invention, a polypeptide of the present invention binds to its respective target structure in a particular manner. Preferably, a polypeptide according to the present invention comprises one paratope per binding domain which specifically or immunospecifically binds to”, “(specifically or immunospecifically) recognizes”, or “(specifically or immunospecifically) reacts with” its respective target structure. This means in accordance with this invention that a polypeptide or a binding domain thereof interacts or (immuno-)specifically interacts with a given epitope on the target molecule (antigen), namely CD3epsilon, and in certain embodiments with a given epitope on at least one further, such as a second and/or a third target molecule. This interaction or association occurs more

frequently, more rapidly, with greater duration, with greater affinity, or with some combination of these parameters, to an epitope on the specific target than to alternative substances (non-target molecules). Because of the sequence similarity between homologous proteins in different species, an antibody construct or a binding domain that immunospecifically binds to its target (such as a human target) may, however, cross-react with homologous target molecules from different species (such as, from non-human primates). The term “specific / immunospecific binding” can hence include the binding of an antibody construct or binding domain to epitopes and/or structurally related epitopes in more than one species. The term “(immuno-) selectively binds does exclude the binding to structurally related epitopes.

[46] In the context of the present invention, the term “epitope” refers to the part or region of the antigen that is selectively recognized / immunospecifically recognized by the binding structure, i.e. the paratope. An “epitope” is antigenic, and thus the term epitope is sometimes also referred to as “antigenic structure” or “antigenic determinant”. The part of the binding domain that binds to the epitope is called a paratope. Specific binding is believed to be accomplished by specific motifs in the amino acid sequence of the binding domain and the antigen. Thus, binding is achieved because of their primary, secondary and/or tertiary structure as well as the result of potential secondary modifications of said structures. The specific interaction of the paratope with its antigenic determinant may result in a simple binding of said site to the antigen. In some cases, the specific interaction may alternatively or additionally result in the initiation of a signal, e.g. due to the induction of a change of the conformation of the antigen, an oligomerization of the antigen, etc.

[47] The epitopes of protein antigens are divided into two categories, conformational epitopes and linear epitopes, based on their structure and interaction with the paratope. A conformational epitope is composed of discontinuous sections of the antigen's amino acid sequence. These epitopes interact with the paratope based on the three-dimensional surface features and shape or tertiary structure (folding) of the antigen. Methods of determining the conformation of epitopes include, but are not limited to, x-ray crystallography, two-dimensional nuclear magnetic resonance (2D-NMR) spectroscopy and site-directed spin labelling and electron paramagnetic resonance (EPR) spectroscopy. By contrast, linear epitopes interact with the paratope based on their primary structure. A linear epitope is formed by a continuous sequence of amino acids from the antigen and typically includes at least 3 or at least 4, and more usually, at least 5 or at least 6 or at least 7, for example, about 8 to about 10 amino acids in a unique sequence.

[48] A method for epitope mapping for a given human target protein is described in the following: A pre-defined region (a contiguous amino acid stretch) within said given human target protein is exchanged / replaced with a corresponding region of a target protein

paralogue (so long as the binding domain is not cross-reactive with the paralogue used). These human target / paralogue chimeras are expressed on the surface of host cells (such as CHO cells). Binding of the antibody or construct can be tested via FACS analysis. When the binding of the antibody or construct to the chimeric molecule is entirely abolished, or
5 when a significant binding decrease is observed, it can be concluded that the region of human target which was removed from this chimeric molecule is relevant for the immunospecific epitope-paratope recognition. Said decrease in binding is preferably at least 10%, 20%, 30%, 40%, or 50%; more preferably at least 60%, 70%, or 80%, and most preferably 90%, 95% or even 100% in comparison to the binding to human (wild-type) target,
10 whereby binding to the human target is set to be 100%. Alternatively, the above described epitope mapping analysis can be modified by introducing one or several point mutations into the sequence of the human target. These point mutations can e.g. reflect the differences between the human target and its paralogue.

[49] A further method to determine the contribution of a specific residue of a target antigen
15 to the recognition by a construct or binding domain is alanine scanning (see e.g. Morrison KL & Weiss GA. Curr Opin Chem Biol. 2001 Jun;5(3):302-7), where each residue to be analyzed is replaced by alanine, e.g. via site-directed mutagenesis. Alanine is used because of its non-bulky, chemically inert, methyl functional group that nevertheless mimics the secondary structure references that many of the other amino acids possess. Sometimes bulky amino
20 acids such as valine or leucine can be used in cases where conservation of the size of mutated residues is desired.

[50] The interaction between the binding domain and the epitope of the target antigen implies that a binding domain exhibits appreciable or significant affinity for the epitope / the target antigen (here: CD3) and, generally, does not exhibit significant affinity for proteins or
25 antigens other than the target antigen – notwithstanding the above discussed cross-reactivity with homologous targets e.g. from other species. “Significant affinity” includes binding with an affinity (dissociation constant, KD) of $\leq 10^{-6}$ M. Preferably, binding is considered specific when the binding affinity is $\leq 10^{-7}$ M, $\leq 10^{-8}$ M, $\leq 10^{-9}$ M, $\leq 10^{-10}$ M, or even $\leq 10^{-11}$ M, or $\leq 10^{-12}$ M. Whether a binding domain (immuno-)specifically reacts with or binds to a target can be
30 tested readily e.g. by comparing the affinity of said binding domain to its desired target protein or antigen with the affinity of said binding domain to non-target proteins or antigens (here: proteins other than CD3). Preferably, a construct of the invention does not significantly bind to proteins or antigens other than CD3 (i.e., the CD3 binding domain does not bind to proteins other than CD3) – unless any further binding domain(s) directed against a further
35 target is/are deliberately introduced into the construct of the invention, in which case the binding of that binding domain to its specific target is also provided by the present invention.

[51] It is envisaged that the affinity of the first domain for human CD3epsilon is ≤ 100 nM, ≤ 90 nM, ≤ 80 nM, ≤ 70 nM, ≤ 60 nM, ≤ 50 nM, ≤ 40 nM, ≤ 30 nM, or ≤ 20 nM. These values are preferably measured in a cell-based assay, such as a Scatchard assay. Other methods of determining the affinity are also well-known. These values are preferably measured in a surface plasmon resonance assay, such as a Biacore assay.

[52] The term “does not significantly bind” and “does not selectively bind” mean that a construct or binding domain of the present invention does not bind to a protein or antigen other than said CD3, when said protein or antigen is expressed on the surface of a cell. The construct hence shows reactivity of $\leq 30\%$, preferably $\leq 20\%$, more preferably $\leq 10\%$, particularly preferably $\leq 9\%$, $\leq 8\%$, $\leq 7\%$, $\leq 6\%$, $\leq 5\%$, $\leq 4\%$, $\leq 3\%$, $\leq 2\%$, or $\leq 1\%$ with proteins or antigens other than CD3 (when said proteins or antigens are expressed on the surface of a cell), whereby binding to CD3, respectively, is set to be 100%. The “reactivity” can e.g. be expressed in an affinity value (see above).

[53] It is envisaged that the construct of the invention (and more specifically the domain comprising a paratope/binding domain that binds to human CD3epsilon) does not bind or does not significantly bind to CD3epsilon paralogues, more specifically to human CD3epsilon paralogues and/or to macaque / cyno CD3epsilon paralogues. It is also envisaged that the construct does not bind or does not significantly bind to (human or macaque / cyno) CD3epsilon paralogues on the surface of a target cell.

[54] The VH region as part of the binding domain binding to an extracellular epitope of the human CD3ε chain comprises a CDR-H1, a CDR-H2 and CDR-H3 sequence as set out herein above. The CDR sequences contain placeholders denoted as “X” for a given amino acid residue that can take the place of the placeholder as is common practice in the art. The placeholders are consecutively numbered in the format X_1 , X_2 , X_3 , and so forth, per given CDR sequence. The amino acid residues that can take place of the placeholder in the recited CDR sequences are listed according to preference, wherein the first listed amino acid is the most preferred, the second listed is the second most preferred, and so forth, if not otherwise specified, e.g. in other embodiments. If a sequence contains more than one placeholder, the same applies in relation to the preference of the amino acids; namely, it is the combination of the first listed amino acid residue for each of the placeholders that is most preferred, the combination of the second listed amino acid residue for each of the placeholders that is second most preferred, and so forth. This hierarchy of preference does not exclude the combination of amino acid residues for each of the placeholders independent of said preference hierarchy so that amino acid residues of different preference are combined. The same hierarchy is true for all amino acid residues that are listed herein below to take the place of a place holder in an amino acid sequence described herein below. Accordingly, the

above also applies for the placeholders denoted as "X" in the sequences of the VH and VL sequences and any other sequences recited throughout the specification.

[55] The CDR-H1 sequence comprises the amino acid sequence of X_1YAX_2N , where X_1 is K, V, S, G, R, T, or I; and X_2 is M or I. Following the above-explained hierarchy as regards the placeholder amino acids, the amino acids for the placeholders X_1 and X_2 are listed according to their preference, wherein the first listed amino acid is the most preferred, the second listed is the second-most preferred, and so forth. For X_1 , the amino acid K is most preferred, and for X_2 , the amino acid M is most preferred. A preferred combination is M for X_2 in combination with any of the amino acid residues of X_1 , such as the combinations for X_1 and X_2 , respectively, selected from K and M, V and M, S and M, most preferred the combination K and M. Another preferred combination is K and I, for X_1 and X_2 , respectively. Preferred examples of the CDR-H1 sequence are selected from KYAMN, VYAMN, SYAMN, GYAMN, RYAMN, TYAMN, IYAMN, and KYAIN, wherein KYAMN or KYAIN is most preferred.

[56] The CDR-H2 sequence comprises the amino acid sequence of RIRSKYNNYATYYADX₁VK X₂, where X_1 is S or Q; and X_2 is D, G, K, S, or E. For X_1 , the amino acid S is most preferred, and for X_2 , the amino acid D is most preferred. A preferred combination is S for X_1 in combination with any of the amino acid residues of X_2 , such as the combinations for X_1 and X_2 , respectively, selected from S and D, S and G, S and K, S and S, most preferred the combination S and D. Preferred examples of the CDR-H2 sequence are selected from RIRSKYNNYATYYADSVKD, RIRSKYNNYATYYADSVKK, RIRSKYNNYATYYADSVKS, RIRSKYNNYATYYADSVKE, RIRSKYNNYATYYADSVKG, and RIRSKYNNYATYYADQVKD, wherein RIRSKYNNYATYYADSVKD is most preferred.

[57] The CDR-H3 sequence comprises the amino acid sequence of $HX_1NFGNSYX_2SX_3X_4AY$, where X_1 is G, R, or A; X_2 is I, L, V, or T; X_3 is Y, W or F; and X_4 is W, F or Y. For X_1 , the amino acid G is most preferred; for X_2 , the amino acid I is most preferred; for X_3 , the amino acid Y is most preferred; and for X_4 , the amino acid W is most preferred. Preferred examples of the CDR-H3 sequence are selected from HGNFGNSYISYWAY, HGNFGNSYLSWWAY, HGNFGNSYTSYYAY, HRNFGNSYLSWFAY, HGNFGNSYVSFFAY, HGNFGNSYISWWAY, HGNFGNSYVSWWAY, HGNFGNSYLSYFAY, HGNFGNSYLSFWAY, HANFGNSYISYWAY, and HGNFGNSYVSWFAY, wherein HGNFGNSYISYWAY is most preferred.

[58] The CDR-L1 sequence comprises the amino acid sequence of $X_1SSTGAVTX_2X_3X_4YX_5N$, where X_1 is G, R, or A; X_2 is S or T; X_3 is G or S; X_4 is N or Y; and X_5 is P or A. For X_1 , the amino acid G is most preferred; for X_2 , the amino acid S is most preferred; for X_3 , the amino acid G is most preferred; for X_4 , the amino acid N is most preferred; and for X_5 , the amino acid P is most preferred. Preferred examples of the CDR-L1

sequence are selected from GSSTGAVTSGNYPN, RSSTGAVTSGYYPN, GSSTGAVTSGYYPN, ASSTGAVTSGNYPN, and RSSTGAVTTSNYAN, wherein GSSTGAVTSGNYPN is most preferred.

[59] The CDR-L2 sequence comprises the amino acid sequence of $X_1TX_2X_3X_4X_5X_6$; where X_1 is G or A; X_2 is K, D, or N; X_3 is F, M or K; X_4 is L or R; X_5 is A, P, or V; and X_6 is P or S. For X_1 , the amino acid G is most preferred; for X_2 , the amino acid K is most preferred; for X_3 , the amino acid F is most preferred; for X_4 , the amino acid L is most preferred; for X_5 , the amino acid A is most preferred and for X_6 , the amino acid P is most preferred. Preferred examples of the CDR-L2 sequence are selected from GTKFLAP, ATDMRPS, GTKFLVP, and GTNKRAP, wherein GTKFLAP is most preferred.

[60] The CDR-L3 sequence comprises the amino acid sequence of $X_1LWYSNX_2WV$, where X_1 is V, A, or T; and X_2 is R or L. For X_1 , the amino acid V is most preferred, and for X_2 , the amino acid R is most preferred. Preferred combinations are R for X_2 in combination with any of the amino acid residues of X_1 , such as the combinations for X_1 and X_2 , respectively, selected from V and R, A and R, T and R, most preferred the combination V and R. Preferred examples of the CDR-L3 sequence are selected from VLWYSNRWV, ALWYSNRWV, TLWYSNRWV, and ALWYSNLWV, wherein VLWYSNRWV is most preferred.

[61] In a preferred embodiment, said VH region of i) comprises: a CDR-H1 sequence comprising or consisting of the amino acid sequence of X_1YAX_2N , where X_1 is K, V, S, G, R, or I; and X_2 is M or I; a CDR-H2 sequence of RIRSKYNNYATYYADX₁VKX₂, where X_1 is S or Q; and X_2 is D, G, K, S, or E; and a CDR-H3 sequence of $HX_1NFGNSYX_2SX_3X_4AY$, where X_1 is G, R, or A; X_2 is I, L, V, or T; X_3 is Y, W or F; and X_4 is W, F or Y; and said VL region of ii) comprises: a CDR-L1 sequence of $X_1SSTGAVTSGX_2YPN$, where X_1 is G, R, or A; and X_2 is N or Y; a CDR-L2 sequence of $X_1TX_2X_3X_4X_5X_6$; where X_1 is G or A; X_2 is K or D; X_3 is F or M; X_4 is L or R; X_5 is A, P, or V; and X_6 is P or S; and a CDR-L3 sequence of $X_1LWYSNRWV$, where X_1 is V, A, or T; and wherein said one or more CDR sequences of the VH region of i) and/or of the VL region of ii) comprise one or more amino acid substitutions selected from X_24V or X_24F in CDR-H1; D15 (preferably E), X_116A in CDR-H2; H1 (preferably A or N), X_12E , F4 (preferably I), and/or N6 (preferably S or T) in CDR-H3; and W93 (preferably Y) in CDR-L3.

[62] Said CDR-H1 sequence comprises or consists of the amino acid sequence of X_1YAX_2N , where X_1 is K, V, S, G, R, or I; and X_2 is M or I. For X_1 , the amino acid K is most preferred, and for X_2 , the amino acid M is most preferred. A preferred combination is M for X_2 in combination with any of the amino acid residues of X_1 , such as the combinations for X_1 and X_2 , respectively, selected from K and M, V and M, S and M, most preferred the combination K and M. Another preferred combination is K and I, for X_1 and X_2 , respectively.

Preferred examples of the CDR-H1 sequence are selected from KYAMN, VYAMN, SYAMN, GYAMN, RYAMN, IYAMN, and KYAIN, wherein KYAMN or KYAIN is preferred, wherein KYAMN is most preferred.

[63] Said CDR-H2 sequence comprises or consist of the amino acid sequence of RIRSKYNNYATYYADX₁VK X₂, where X₁ is S or Q; and X₂ is D, G, K, S, or E. For X₁, the amino acid S is most preferred, and for X₂, the amino acid D is most preferred. A preferred combination is S for X₁ in combination with any of the amino acid residues of X₂, such as the combinations for X₁ and X₂, respectively, selected from S and D, S and G, S and K, S and S, most preferred the combination S and D. Preferred examples of the CDR-H2 sequence are selected from RIRSKYNNYATYYADSVKD, RIRSKYNNYATYYADSVKK, RIRSKYNNYATYYADSVKS, RIRSKYNNYATYYADSVKE, RIRSKYNNYATYYADSVKG, and RIRSKYNNYATYYADQVKD, wherein RIRSKYNNYATYYADSVKD is most preferred.

[64] The CDR-H3 sequence comprises the amino acid sequence of HX₁NFGNSYX₂SX₃X₄AY, where X₁ is G, R, or A; X₂ is I, L, V, or T; X₃ is Y, W or F; and X₄ is W, F or Y. For X₁, the amino acid G is most preferred; for X₂, the amino acid I is most preferred; for X₃, the amino acid Y is most preferred; and for X₄, the amino acid W is most preferred. Preferred examples of the CDR-H3 sequence are selected from HGNFGNSYISYWAY, HGNFGNSYLSWWAY, HGNFGNSYTSYYAY, HRNFGNSYLSWFAY, HGNFGNSYVSFFAY, HGNFGNSYISWWAY, HGNFGNSYVSWWAY, HGNFGNSYLSYFAY, HGNFGNSYLSFWAY, HANFGNSYISYWAY, and HGNFGNSYVSWFAY, wherein HGNFGNSYISYWAY is most preferred.

[65] The CDR-L1 sequence comprises the amino acid sequence of X₁SSTGAVTSGX₂YPN, where X₁ is G, R, or A; and X₂ is N or Y. For X₁, the amino acid G is most preferred; and for X₂, the amino acid N is preferred. Preferred examples of the CDR-L1 sequence are selected from GSSTGAVTSGNYPN, RSSTGAVTSGYYPN, GSSTGAVTSGYYPN, and ASSTGAVTSGNYPN, wherein GSSTGAVTSGNYPN or ASSTGAVTSGNYPN is preferred, wherein GSSTGAVTSGNYPN is most preferred.

[66] The CDR-L2 sequence comprises the amino acid sequence of X₁TX₂X₃X₄X₅X₆; where X₁ is G or A; X₂ is K or D; X₃ is F or M; X₄ is L or R; X₅ is A, P, or V; and X₆ is P or S. For X₁, the amino acid G is most preferred; for X₂, the amino acid K is most preferred; for X₃, the amino acid F is most preferred; for X₄, the amino acid L is most preferred; for X₅, the amino acid A is most preferred and for X₆, the amino acid P is most preferred. Preferred examples of the CDR-L2 sequence are selected from GTKFLAP, ATDMRPS, and GTKFLVP, wherein GTKFLAP or GTKFLVP is preferred, wherein GTKFLAP is most preferred.

[67] The CDR-L3 sequence comprises the amino acid sequence of X₁LWYSNRWW, where X₁ is V, A, or T, wherein the amino acid V is most preferred. Preferred examples of the CDR-L3 sequence are selected from VLWYSNRWW, ALWYSNRWW, and TLWYSNRWW,

wherein VLWYSNRWV or TLWYSNRWV is more preferred, wherein VLWYSNRWV is most preferred.

[68] In a further preferred embodiment, said VH region of i) comprises: a CDR-H1 sequence comprising or consisting of the amino acid sequence of X_1YAX_2N , where X_1 is K, V, S, R, or I; and X_2 is M or I; a CDR-H2 sequence of $RIRSKYNNYATYYADX_1VKX_2$, where X_1 is S or Q; and X_2 is D, G, K, or S; and a CDR-H3 sequence of $HX_1NFGNSYX_2SX_3X_4AY$, where X_1 is G or A; X_2 is I, L, V, or T; X_3 is Y, W or F; and X_4 is W, F or Y; and said VL region of ii) comprises: a CDR-L1 sequence of $X_1SSTGAVTSGX_2YPN$, where X_1 is G or A; and X_2 is N or Y; a CDR-L2 sequence of $GTKFLX_1P$; where X_1 is A or V; and a CDR-L3 sequence of $X_1LWYSNRWV$, where X_1 is V, A, or T; and wherein said one or more CDR sequences of the VH region of i) and/or of the VL region of ii) comprise one or more amino acid substitutions selected from X_24V or X_24F in CDR-H1; D15 (preferably E), X_116A in CDR-H2; H1 (preferably A or N), X_12E , F4 (preferably I), and/or N6 (preferably S or T) in CDR-H3; and W93 (preferably Y) in CDR-L3.

[69] Said CDR-H1 sequence comprises or consists of the amino acid sequence of X_1YAX_2N , where X_1 is K, V, S, R, or I; and X_2 is M or I. For X_1 , the amino acid K is most preferred, and for X_2 , the amino acid M is most preferred. A preferred combination is M for X_2 in combination with any of the amino acid residues of X_1 , such as the combinations for X_1 and X_2 , respectively, selected from K and M, V and M, S and M, most preferred the combination K and M. Another preferred combination is K and I, for X_1 and X_2 , respectively. Preferred examples of the CDR-H1 sequence are selected from KYAMN, VYAMN, SYAMN, RYAMN, IYAMN, and KYAIN, wherein KYAMN or KYAIN is preferred, wherein KYAMN is most preferred.

[70] Said CDR-H2 sequence comprises or consist of the amino acid sequence of $RIRSKYNNYATYYADX_1VKX_2$, where X_1 is S or Q; and X_2 is D, G, K, or S. For X_1 , the amino acid S is most preferred, and for X_2 , the amino acid D is most preferred. A preferred combination is S for X_1 in combination with any of the amino acid residues of X_2 , such as the combinations for X_1 and X_2 , respectively, selected from S and D, S and G, S and K, S and S, most preferred the combination S and D. Preferred examples of the CDR-H2 sequence are selected from $RIRSKYNNYATYYADSVKD$, $RIRSKYNNYATYYADSVKK$, $RIRSKYNNYATYYADSVKS$, $RIRSKYNNYATYYADSVKG$, and $RIRSKYNNYATYYADQVKD$, wherein $RIRSKYNNYATYYADSVKD$ or $RIRSKYNNYATYYADQVKD$ is preferred, wherein $RIRSKYNNYATYYADSVKD$ is most preferred.

[71] Said CDR-H3 sequence comprises or consist of the amino acid sequence of $HX_1NFGNSYX_2SX_3X_4AY$, where X_1 is G or A; X_2 is I, L, V, or T; X_3 is Y, W or F; and X_4 is W, F or Y. For X_1 , the amino acid G is most preferred; for X_2 , the amino acid I is most preferred; for X_3 , the amino acid Y is most preferred; and for X_4 , the amino acid W is most preferred.

Preferred examples of the CDR-H3 sequence are selected from HGNFGNSYISYWAY, HGNFGNSYLSWWAY, HGNFGNSYTSYYAY, HGNFGNSYVSFFAY, HGNFGNSYISWWAY, HGNFGNSYVSWWAY, HGNFGNSYLSYFAY, HGNFGNSYLSFWAY, and HANFGNSYISYWAY, wherein HGNFGNSYISYWAY or HANFGNSYISYWAY is preferred, wherein HGNFGNSYISYWAY is most preferred.

[72] Said CDR-L1 sequence comprises or consists the amino acid sequence of X_1 SSTGAVTSGX₂YPN, where X_1 is G or A; and X_2 is N or Y. For X_1 , the amino acid G is most preferred; and for X_2 , the amino acid N is preferred. Preferred examples of the CDR-L1 sequence are selected from GSSTGAVTSGNYPN, GSSTGAVTSGYYPN, and ASSTGAVTSGNYPN, wherein GSSTGAVTSGNYPN or ASSTGAVTSGNYPN is preferred, wherein GSSTGAVTSGNYPN is most preferred.

[73] Said CDR-L2 sequence comprises or consists of the amino acid sequence of GTKFLX₁P; where X_1 is A or V. For X_1 , the amino acid A is preferred. Said CDR-L2 sequence is GTKFLAP or GTKFLVP, wherein GTKFLAP is preferred.

[74] The CDR-L3 sequence comprises or consists of the amino acid sequence of X_1 LWYSNRWV, where X_1 is V, A, or T, wherein the amino acid V is most preferred. Preferred examples of the CDR-L3 sequence are selected from VLWYSNRWV, ALWYSNRWV, and TLWYSNRWV, wherein VLWYSNRWV or TLWYSNRWV is more preferred, wherein VLWYSNRWV is most preferred.

[75] In an even more preferred embodiment, said VH region of i) comprises: a CDR-H1 sequence comprising or consisting of the amino acid sequence of X_1 YAMN, where X_1 is K or S; a CDR-H2 sequence of RIRSKYNNYATYYADSVKX₁, where X_1 is D or G; and a CDR-H3 sequence of HGNFGNSYX₁SX₂WAY, where X_1 is I or V; and X_2 is Y or W; and said VL region of ii) comprises: a CDR-L1 sequence of GSSTGAVTSGX₁YPN, where X_1 is N or Y; a CDR-L2 sequence of GTKFLAP; and a CDR-L3 sequence of X_1 LWYSNRWV, where X_1 is V or A; and wherein said one or more CDR sequences of the VH region of i) and/or of the VL region of ii) comprise one or more amino acid substitutions selected from M4V or M4F in CDR-H1; D15 (preferably E), S16A in CDR-H2; H1 (preferably A or N), G2E, F4 (preferably I), and/or N6 (preferably S or T) in CDR-H3; and W93 (preferably Y) in CDR-L3.

[76] Said CDR-H1 sequence comprises or consists of the amino acid sequence of X_1 YAMN, where X_1 is K or S, wherein the amino acid K is preferred. Said CDR-H1 sequence is KYAMN or SYAMN, wherein KYAMN is most preferred.

[77] Said CDR-H2 sequence comprises or consist of the amino acid sequence of RIRSKYNNYATYYADSVKX₁, where X_1 is D or G. For X_1 , the amino acid D is preferred. Said CDR-H2 sequence is RIRSKYNNYATYYADSVKD or RIRSKYNNYATYYADSVKG, wherein RIRSKYNNYATYYADSVKD is preferred.

[78] Said CDR-H3 sequence comprises or consist of the amino acid sequence of HGNFGNSYX₁SX₂WAY, where X₁ is I or V; and X₂ is Y or W. For X₁, the amino acid I is preferred; for X₂, the amino acid Y is preferred. Said CDR-H3 sequence is HGNFGNSYISYWAY or HGNFGNSYVSWWAY, wherein HGNFGNSYISYWAY is preferred.

5 **[79]** Said CDR-L1 sequence comprises or consists the amino acid sequence of GSSTGAVTSGX₁YPN, where X₁ is N or Y. For X₁, the amino acid N is preferred. Said CDR-L1 sequence is GSSTGAVTSGNYPN or GSSTGAVTSGYYPN, wherein GSSTGAVTSGNYPN is preferred.

10 **[80]** Said CDR-L2 sequence comprises or consists of the amino acid sequence of GTKFLAP.

[81] The CDR-L3 sequence comprises or consists of the amino acid sequence of X₁LWYSNRWW, where X₁ is V or A, wherein V is preferred. Said CDR-L3 sequence VLWYSNRWW or ALWYSNRWW, wherein VLWYSNRWW is preferred.

15 **[82]** Each of the CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2 and CDR-L3 sequences be freely combined in the format CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, CDR-L3 (this is the preferred orientation of the VH and the VL region) or CDR-L1, CDR-L2, CDR-L3, CDR-H1, CDR-H2, CDR-H3 and exhibiting the recited binding to an extracellular epitope of the human CD3ε chain.

20 **[83]** Preferred combinations of CDR-L1 to L3 sequences of the VL region and preferred combinations of CDR-H1 to H3 sequences of the VH region are listed in the below Table 1.

CDR-L1	CDR-L2	CDR-L3
GSSTGAVTSGYYPN	GTKFLAP	ALWYSNRWW
RSSTGAVTSGYYPN	ATDMRPS	ALWYSNRWW
GSSTGAVTSGNYPN	GTKFLAP	VLWYSNRWW
ASSTGAVTSGNYPN	GTKFLVP	TLWYSNRWW
RSSTGAVTTSNYAN	GTNKRAP	ALWYSNLWW
CDR-H1	CDR-H2	CDR-H3
IYAMN	RIRSKYNNYATYYADSVKS	HGNFGNSYVSFFAY
KYAMN	RIRSKYNNYATYYADSVKD	HGNFGNSYISYWAY

SYAMN	RIRSKYNNYATYYADSVKG	HGNFGNSYLSFWAY
RYAMN	RIRSKYNNYATYYADSVKG	HGNFGNSYLSYFAY
VYAMN	RIRSKYNNYATYYADSVKK	HGNFGNSYLSWWAY
KYAMN	RIRSKYNNYATYYADSVKS	HGNFGNSYTSYYAY
GYAMN	RIRSKYNNYATYYADSVKE	HRNFGNSYLSWFAY
VYAMN	RIRSKYNNYATYYADSVKK	HGNFGNSYISWWAY
SYAMN	RIRSKYNNYATYYADSVKG	HGNFGNSYVSWWAY
KYAIN	RIRSKYNNYATYYADQVKD	HANFGNSYISYWAY
TYAMN	RIRSKYNNYATYYADSVKD	HGNFGNSYVSWFAY

Table 1

[84] Preferably, any of the above listed combinations of CDR-L1 to L3 combinations is combined with any of the above-listed combinations CDR-H1 to H3 as part of the binding domain binding to an extracellular of the human CD3 ϵ chain. In other words, the VL region comprises or consists of as CDR-L1, CDR-L2, CDR-L3 sequence, in this order,

GSSTGAVTSGYYPN, GTKFLAP, ALWYSNRWW;

RSSTGAVTSGYYPN, ATDMRPS, ALWYSNRWW;

10 GSSTGAVTSGNYPN, GTKFLAP, VLWYSNRWW;

ASSTGAVTSGNYPN, GTKFLVP, TLWYSNRWW; or

RSSTGAVTTSNYAN, GTNKRAP, ALWYSNLWW; and

the VL region comprises or consists of as CDR-H1, CDR-H2, CDR-H3 sequence, in this order,

15 IYAMN, RIRSKYNNYATYYADSVKS, HGNFGNSYVSFFAY;

KYAMN, RIRSKYNNYATYYADSVKD, HGNFGNSYISYWAY;

SYAMN, RIRSKYNNYATYYADSVKG, HGNFGNSYLSFWAY;

RYAMN, RIRSKYNNYATYYADSVKG, HGNFGNSYLSYFAY;

VYAMN, RIRSKYNNYATYYADSVKK, HGNFGNSYLSWWAY;

20 KYAMN, RIRSKYNNYATYYADSVKS, HGNFGNSYTSYYAY;

GYAMN, RIRSKYNNYATYYADSVKE, HRNFGNSYLSWFAY;

VYAMN, RIRSKYNNYATYYADSVKK, HGNFGNSYISWWAY;

SYAMN, RIRSKYNNYATYYADSVKG, HGNFGNSYVSWWAY;

KYAIN, RIRSKYNNYATYYADQVKD, HANFGNSYISYWAY; or

25 TYAMN, RIRSKYNNYATYYADSVKD, HGNFGNSYVSWFAY.

In accordance with the invention, preferred CDR sequence combinations of the VH and the

VL regions, listed in the order CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, CDR-L3, are as defined in SEQ ID NOs: 118 to 123, 166 to 171, 356 to 361, 546 to 551, 724 to 729, 922 to 927, 1100 to 1105, 1290 to 1295, 1468 to 1473, 1658 to 1663, 1848 to 1853.

- 5 Most preferred is that the VL region comprises as CDR-L1, CDR-L2, CDR-L3 sequence, listed in this order,
GSSTGAVTSGNYPN, GTKFLAP, VLWYSNRWW; and
the VL region comprises as CDR-H1, CDR-H2, CDR-H3 sequence, listed in this order,
KYAMN, RIRSKYNNYATYYADSVKD, HGNFGNSYISYWAY; as depicted in SEQ ID NOs:
10 1848 to 1853. Preferably the orientation of the CDRs is VH to VL, i.e. the orientation of the variable regions is from N- to C-terminus VH to VL.

[85] In accordance with the invention, said CDR sequences of the VH and/or the VL region comprise one or more amino acid substitutions. As is common in the art, the position and nature of amino acid substitutions are denoted herein by indicating the original amino acid residue at the position to be substituted and the amino acid used for substitution in the format of, e.g., F4I, wherein "F" denotes the original amino acid residue occurring at position "4" of the given amino acid sequence and "I" denotes the amino acid residue which substituted "F" at position 4. In case substitution is by any amino acid residue (other than the original amino acid residue), no amino acid residue is indicated, but only the originally occurring amino acid residue and its position in the given amino acid sequence, so that the previous example would be denoted as "F4" only. Preferably, only naturally occurring amino acids are used for substitution.

[86] The VH region of i) and/or VL region of ii) comprise one or more amino acid substitutions as specified herein in one or more CDR sequences as recited herein above. Accordingly, at least one of the recited amino acid substitutions of the variable regions is comprised in said binding domain binding to an extracellular epitope of the human CD3ε chain. Said at least one or one or more amino acid substitution, in the case that only one amino acid substitution is present, can be present in a CDR sequence in said VH or said VL region or, in case more than one amino acid substitution is present, in CDRs in both the VH and the VL region or restricted to CDR sequences in only the VH or the VL region. In certain embodiments where there are more than one amino acid substitutions, the substitutions are in the VH and the VL region or, alternatively, only in one variable region. Preferably, the substitutions are in the CDRs of the VH and the VL region.

[87] In case the CDR-H1 is to comprise an amino acid substitution at position 4 it is, preferably, the substitution of the original amino acid with the amino acid V. Preferably, the CDR-H1 sequence is KYAIN or KYAMN, i.e. comprising none of said recited amino acid

substitutions.

[88] In CDR-H2, the amino acid substitution at position 15 is, preferably, D15E, or the amino acid substitution at position 16 with amino acid A. Preferably, CDR-H1 comprises the amino acid residue substitution at position 16 with amino acid A; in this case, a preferred amino acid for the last amino acid of CDR-H2 is D or G, most preferred D. Hence, a preferred CDR-H2 sequence is RIRSKYNNYATYYADAVKD or RIRSKYNNYATYYADAVKG, with RIRSKYNNYATYYADAVKD more preferred. In case CDR-H2 contains two amino acid substitutions, the combination of the amino acid E at position 15 and amino acid A at position 16 are preferred; in this case, a preferred amino acid for the last amino acid of CDR-H2 is G. Hence, a preferred CDR-H2 sequence for the combination of the amino acid E at position 15 and amino acid A at position 16 is RIRSKYNNYATYYAEAVKG.

[89] In CDR-H3, the amino acid substitutions are at position 1, preferably a substitution with amino acid A or N, at position 2 with amino acid E, at position 4, preferably with amino acid I, and at position 6, preferably with amino acid S or T. Preferably, CDR-H3 comprises the amino acid A or N at position 1, the amino acid S or T at position 6; in this case and if placeholders are present in the CDR-H3 sequence at the indicated positions, preferred amino acids for X_1 are G or A, most preferred G; for X_2 is I; for X_3 is Y; and for X_4 are W or Y. In case CDR-H3 comprises two amino acid substitutions, preferred combinations are the amino acid A at position 1 and the amino acid S at position 6; and the amino acid N at position 1 and the amino acid T at position 6; in this case and if placeholders are present in the CDR-H3 sequence at the indicated positions, a preferred amino acid for X_1 is G or A, most preferred G; for X_2 is I, for X_3 is Y, and for X_4 are W and F. In case CDR-H3 comprises three amino acid substitutions, preferred combinations are the amino acid A at position 1, the amino acid I at position 4, and the amino acid S at position 6; and the amino acid N at position 1, the amino acid I at position 4 and the amino acid T at position 6, in this case and if placeholders are present in the CDR-H3 sequence at the indicated positions, a preferred amino acid for X_2 is I, for X_3 is Y, and for X_4 are W and F. In case CDR-H3 comprises four amino acid substitutions, a preferred combination is the amino acid N at position 1, the amino acid E at position 2, the amino acid I at position 4, and the amino acid T at position 6; in this case and if placeholders are present in the CDR-H3 sequence at the indicated positions, a preferred amino acid for X_2 is I, for X_3 is Y, and for X_4 is W. Hence, preferred CDR-H3 sequences are selected from AGNFGSSYISYWAY, NENIGTSYISYWAY, AGNFGTSYISYWAY, NANFGTSYISYFAY, and AGNFGSSYISYFAY, with AGNFGSSYISYWAY and AGNFGSSYISYFAY most preferred.

[90] In CDR-L3, the amino acid substitution at position 1 is with amino acid L or the amino acid substitution is W93, preferably W93Y (which may also be referred to as X_1 93Y), in the sequence of X_1 LWYSN X_2 WV, where X_1 is V, A, or T; and X_2 is R or L. Preferably, the CDR-

L3 sequence is VLYYSNRWW when CDR-L3 comprises only one amino acid substitution. It is preferred, however, that CDR-L3 does not comprise said X₁1L and W93 amino acid substitution, in which case a preferred CDR-L3 sequence is VLYYSNRWW.

[91] Without wishing to be bound by a specific scientific theory, each of the above recited amino acid substitution(s) lead(s) to an increase in thermal stability of the binding domain binding to an extracellular epitope of the human CD3 ϵ chain comprising or consisting of a VH region linked to a VL region as described herein as compared to the binding domain binding to an extracellular epitope of the human CD3 ϵ chain comprising or consisting of a VH region linked to a VL region sequence that is unmodified, i.e. does not contain said amino acid residue substitution(s). Said increase of the temperature stability is, preferably, measured by the well known and also herein described method of Differential Scanning Fluorimetry (DSF). Said method is, e.g., described in Wen et al., "Nano differential scanning fluorimetry for comparability studies of therapeutic proteins", *Analytical Biochemistry*, Volume 593, 2020, 113581, ISSN 0003-2697; or Dart, M. L., et al. (2018). "Homogeneous Assay for Target Engagement Utilizing Bioluminescent Thermal Shift". *ACS medicinal chemistry letters*, 9(6), 546–551). As evident from the example section, it was shown that the amino acid substitutions or combinations thereof as defined herein result in an increased thermal stability (see Example 1, Table 2 and 3) as compared to the unmodified CD3 binding domain defined herein ("I2C") while the cytotoxic activity was maintained which was not the case with a prior art method to improve thermal stability, namely the CC44/100 cys clamp, in which an additional disulfide bond was engineered for stabilizing (Reiter, Y. et al., 1994) by replacing the amino acid residues with cysteine residues at position 44 in the heavy chain variable region and at position 100 in the light chain variable region (numbering scheme according to Kabat et al., 1991) of the unmodified CD3 binding domain defined herein (VH and VL SEQ ID NOs: 1854 and 1855, respectively; see Example 2, Table 5). The VH and VL region combinations of the CD3epsilon binding domain described herein are therefore temperature stabilized as compared to the VH and VL region sequence that does not contain the given substitution(s) that are introduced at the positions defined herein.

[92] In a preferred embodiment of the polypeptide or polypeptide construct of claim 1 of the invention, in addition to said one amino acid substitution or a combination thereof as defined in iii) X₂ is I in said CDR-H1 sequence; X₂ is G in said CDR-H2 sequence; X₁ is A, X₄ is F in said CDR-H3 sequence; and/or X₁ is A in said CDR-L3 sequence. The one amino acid substitution or combination thereof as defined herein is/are in addition combined with specific amino acids at specific positions in the CDRs. Hence, at least one of the recited amino acid substitutions in accordance with iii) is present and at least one of X₂ is G in said CDR-H2 sequence; X₁ is A, X₄ is F in said CDR-H3; and/or X₁ is A in said CDR-L3 sequence is additionally present in the CDRs. As previously stated herein above, a preferred amino acid

for X_2 is I in said CDR-H1 sequence or X_2 is G in said CDR-H2 sequence, if only one additional amino acid is present in the CDRs, wherein it is most preferred that X_2 is I in said CDR-H1 sequence. A preferred combination of two of said additional amino acids is X_2 is I in said CDR-H1 sequence and X_4 is F in said CDR-H3 sequence; or X_2 is G in said CDR-H2 sequence and X_4 is F in said CDR-H3 sequence. A preferred combination of three of said additional amino acids is X_2 is I in said CDR-H1 sequence, X_1 is A, and X_4 is F in said CDR-H3 sequence; or X_2 is I in said CDR-H1 sequence, X_4 is F in said CDR-H3 sequence, and X_1 is A in said CDR-L3 sequence. Since the latter amino acids are to be present additionally, it is understood that those recited additional amino acids that overlap in position with the amino acid substitution of iii) cannot replace the overlapping amino acid substitution. For example, if the only amino acid substitution in accordance with iii) is either X_2 4V or X_2 4F in CDR-H1, said amino acid cannot be replaced by amino acid I in said CDR-H1 sequence, since there would be no amino acid substitution as defined in iii) remaining in the binding domain. In other terms, there must always be at least one of the amino acid substitutions as defined in iii) comprised in the polypeptide or polypeptide construct of the invention.

[93] It is also understood that depending on the actual sequence of the CDRs, one or more of said additional amino acids may already be part of the CDRs as defined herein above or, if this is not the case, those CDRs will be changed to exhibit said additional amino acid(s) in combination with one amino acid substitution or a combination thereof as recited in iii).

[94] In another preferred embodiment, the polypeptide or polypeptide construct of the invention comprises or consists of combinations of said amino acid substitutions as defined in iii) of two, three, four, five, six, seven, eight, nine, ten, eleven, twelve or more amino acid substitutions, or of up to two, three, four, five, six, seven, eight, nine, ten, eleven, twelve amino acid substitutions. Preferably, only the substitution(s) defined herein are introduced in the VH and the VL region sequence. This applies to all embodiments recited herein so that the VH and the VL region sequence consists of the unmodified amino acid sequence with the substitution(s) as defined herein.

[95] More specifically, it is preferred that i) said one amino acid substitution is selected from: a. X_2 4V or X_2 4F in CDR-H1; H1A in CDR-H3; and b. X_1 1L and W3Y in CDR-L3; ii) said combination of two or more amino acid substitutions are selected from X_1 16A in CDR-H2 and N6S in CDR-H3; and X_1 16A in CDR-H2 and N6T in CDR-H3; iii) said combination of three or more amino acid substitutions are selected from X_1 16A in CDR-H2, H1A and N6S in CDR-H3; X_1 16A in CDR-H2, H1A and N6T in CDR-H3; X_1 16A in CDR-H2, H1N and N6T in CDR-H3; iv) said combination of four or more amino acid substitutions are selected from X_1 16A in CDR-H2, H1A, N6S in CDR-H3, and W3Y in CDR-L3; D15E, X_1 16A in CDR-H2, H1A, and N6T in CDR-H3; D15E, X_1 16A in CDR-H2, H1A, and N6S in CDR-H3; X_1 16A in CDR-H2,

H1A, F4I and N6S in CDR-H3; v) said combination of five or six amino acid substitutions are selected from X₁16A in CDR-H2, H1A, X₁2E, F4I, and N6T in CDR-H3; X₁16A in CDR-H2, H1N, X₁2E, F4I, and N6S in CDR-H3; D15E, X₁16A in CDR-H2, H1A, N6S in CDR-H3; and W3Y in CDR-L3; D15E, X₁16A in CDR-H2, H1N, X₁2E, F4I and N6T in CDR-H3; D15E, X₁16A in CDR-H2, H1A, X₁2E, F4I and N6T in CDR-H3; D15E, X₁16A in CDR-H2, X₁2E, F4I and N6T in CDR-H3.

[96] In accordance with the foregoing, the amino acid substitution H1A in CDR-H3 is preferably the amino acid substitution, in case there is only one amino acid substitution in the CD3epsilon binding domain, within the CDR sequences or the VH region sequences as defined herein. Furthermore, in case of combinations of amino acid substitutions as defined in iii) preferably H1A in CDR-H3 is one of the amino acid substitutions of said combination.

[97] In an embodiment, the invention relates to a polypeptide or polypeptide construct comprising: a binding domain binding to an extracellular epitope of the human CD3ε chain comprising or consisting of a VH region and a VL region,, wherein

i) the VH region comprises the sequence of EVX₁LX₂ESGGGLX₃QPX₄GSLKLSCAASGFTFNX₅YAX₆NWVRQAPGKGLEWVA RIRSKYNNYATYYADX₇VKX₈RFTISRDDSX₉X₁₀X₁₁X₁₂YLQMNNLKTEDTAX₁₃YYC VRHX₁₄NFGNSYX₁₅SX₁₆X₁₇AYWGQGLTVTSX₁₈, where X₁ is Q or K; X₂ is V or L; X₃ is V or E; X₄ is G or K; X₅ is K, V, S, G, R, T, or I; X₆ is M or I; X₇ is S or Q; X₈ is D, G, K, S, or E; X₉ is K or Q; X₁₀ is N or S; X₁₁ is T or I; X₁₂ is A or L; X₁₃ is V or M; X₁₄ is G, R or A; X₁₅ is I, L, V, or T; X₁₆ is Y, W or F; X₁₇ is W, F or Y; and X₁₈ is S or A; and

ii) the VL region comprises the sequence of QX₁VVTQEX₂X₃LTX₄SPGX₅TVTLTCX₆SSTGAVTX₇X₈X₉YX₁₀NWVQX₁₁KPX₁₂X₁₃ X₁₄X₁₅X₁₆GLIGX₁₇TX₁₈X₁₉X₂₀X₂₁X₂₂GX₂₃PARFSGSLX₂₄GX₂₅KAALTX₂₆X₂₇GX₂₈QX₂₉EDEAX₃₀YX₃₁CX₃₂LWYSNX₃₃WVFGGGTKLTVL, where X₁ is T or A; X₂ is P or S; X₃ is S or A; X₄ is V or T; X₅ is G or E; X₆ is G, R, or A; X₇ is S or T; X₈ is G or S; X₉ is N or Y; X₁₀ is P or A; X₁₁ is Q or E; X₁₂ is G or D; X₁₃ is Q or H; X₁₄ is A or L; X₁₅ is P or F; X₁₆ is R or T; X₁₇ is G or A; X₁₈ is K or D; X₁₉ is F or M; X₂₀ is L or R; X₂₁ is A, P or V; X₂₂ is P or S; X₂₃ is T or V; X₂₄ is L or I; X₂₅ is G or D; X₂₆ is L or I; X₂₇ is S or T; X₂₈ is V or A; X₂₉ is P or T; X₃₀ is E or I; X₃₁ is Y or F; X₃₂ is V, A, or T; X₃₃ is R or L; and

iii) wherein the VH and/or VL region sequence comprises one or more amino acid substitutions selected from

a. N30 (preferably S), X₆34V, X₆34F, Q39 (E, K, R, D, preferably E), L45 (M or V, preferably M), D64 (preferably E), X₇65A, X₁₂81V, X₁₂81T, X₁₂81I, V99 (A or L,

preferably A), H101 (preferably A or N), X₁₄102E, F104 (preferably I), and N106 (preferably S or T) in the VH region sequence in i); and

- b. L20 (preferably I or M), V38 (preferably I), X₁₁40R, X₁₁40K, X₂₄69 (S or E, preferably S), X₃₂91L, X₃₃93 (preferably Y), and G102 (preferably S) in the VL region sequence in ii).

[98] In this embodiment, preferred VH and VL region sequences comprised in the binding domain and mediating the binding to the human CD3ε chain are described. As evident from the above, the VH and VL region sequences of i) and ii) comprise various placeholders, wherein the same hierarchy and nomenclature applies for the placeholders as recited herein above in the context of the CDRs comprised in said VH and VL region of i) and ii). As is evident from the sequences for the VH and VL region, said CDRs described herein above are part of said VH and VL region sequence. Accordingly, the preferred embodiments of said CDRs of i) and ii) as described herein above also apply to this preferred embodiment.

[99] The VH region of i) comprises or consists of the sequence of EVX₁LX₂ESGGGLX₃QPX₄GSLKLSCAASGFTFNX₅YAX₆NWVRQAPGKGLEWVARIRSKYNNYATYYADX₇VKX₈RFTISRDDX₉X₁₀X₁₁X₁₂YLQMNNLKTEDTAX₁₃YYCVRHX₁₄NFGNSYX₁₅SX₁₆X₁₇AYWGQGLTVTSX₁₈, where X₁ is Q or K; X₂ is V or L; X₃ is V or E; X₄ is G or K; X₅ is K, V, S, G, R, T, or I; X₆ is M or I; X₇ is S or Q; X₈ is D, G, K, S, or E; X₉ is K or Q; X₁₀ is N or S; X₁₁ is T or I; X₁₂ is A or L; X₁₃ is V or M; X₁₄ is G, R or A; X₁₅ is I, L, V, or T; X₁₆ is Y, W or F; X₁₇ is W, F or Y; and X₁₈ is S or A.

[100] The CDR sequences within said VH region are as follows: a CDR-H1 sequence comprising or consisting of X₅YAX₆N; a CDR-H2 sequence comprising or consisting of RIRSKYNNYATYYADX₇VKX₈; and a CDR-H3 sequence comprising or consisting of HX₁₄NFGNSYX₁₅SX₁₆X₁₇AY. Preferred examples of said CDR-H1 sequence X₅YAX₆N are selected from KYAMN, VYAMN, SYAMN, GYAMN, RYAMN, TYAMN, IYAMN, and KYAIN, wherein KYAMN or KYAIN is most preferred. Preferred examples of said CDR-H2 sequence RIRSKYNNYATYYADX₇VKX₈ are selected from RIRSKYNNYATYYADSVKD, RIRSKYNNYATYYADSVKK, RIRSKYNNYATYYADSVKS, RIRSKYNNYATYYADSVKE, RIRSKYNNYATYYADSVKG, and RIRSKYNNYATYYADQVKD, wherein RIRSKYNNYATYYADSVKD is most preferred. Preferred examples of said CDR-H3 sequence HX₁₄NFGNSYX₁₅SX₁₆X₁₇AY are selected from HGNFGNSYISYWAY, HGNFGNSYLSWWAY, HGNFGNSYTSYYAY, HRNFGNSYLSWFAY, HGNFGNSYVSFFAY, HGNFGNSYISWWAY, HGNFGNSYVSWWAY, HGNFGNSYLSYFAY, HGNFGNSYLSFWAY, HANFGNSYISYWAY, and HGNFGNSYVSWFAY, wherein HGNFGNSYISYWAY is most preferred.

[101] For X₁, the amino acid Q is preferred. For X₂, the amino acid V is preferred. For X₃,

the amino acid V is preferred. For X₄, the amino acid G is preferred. For X₅, the amino acid K is most preferred, and for X₆, the amino acid M is most preferred. A preferred combination for X₅ and X₆ is M for X₆ in combination with any of the amino acid residues of X₅, such as the combinations for X₅ and X₆, respectively, selected from K and M, V and M, S and M, most preferred the combination K and M. Another preferred combination is K and I, for X₅ and X₆, respectively. Preferred examples of said CDR-H1 sequence X₅YAX₆N are selected from KYAMN, VYAMN, SYAMN, GYAMN, RYAMN, TYAMN, IYAMN, and KYAIN, wherein KYAMN or KYAIN is most preferred. For X₇, the amino acid S is most preferred, and for X₈, the amino acid D is most preferred. A preferred combination is S for X₇ in combination with any of the amino acid residues of X₈, such as the combinations for X₇ and X₈, respectively, selected from S and D, S and G, S and K, S and S, most preferred the combination S and D. Preferred examples of said CDR-H2 sequence RIRSKYNNYATYYADX₇VKX₈ are selected from RIRSKYNNYATYYADSVKD, RIRSKYNNYATYYADSVKK, RIRSKYNNYATYYADSVKS, RIRSKYNNYATYYADSVKE, RIRSKYNNYATYYADSVKG, and RIRSKYNNYATYYADQVKD, wherein RIRSKYNNYATYYADSVKD is most preferred. For X₉, the amino acid K is preferred. For X₁₀, the amino acid N is preferred. For X₁₁, the amino acid T is preferred. For X₁₂, the amino acid A is preferred. For X₁₃, the amino acid V is preferred. For X₁₄, the amino acid G is most preferred; for X₁₅, the amino acid I is most preferred; for X₁₆, the amino acid Y is most preferred; and for X₁₇, the amino acid W is most preferred. Preferred examples of said CDR-H3 sequence HX₁₄NFGNSYX₁₅SX₁₆X₁₇AY are selected from HGNFGNSYISYWAY, HGNFGNSYLSWWAY, HGNFGNSYTSYYAY, HRNFGNSYLSWFAY, HGNFGNSYVSFFAY, HGNFGNSYISWWAY, HGNFGNSYVSWWAY, HGNFGNSYLSYFAY, HGNFGNSYLSFWAY, HANFGNSYISYWAY, and HGNFGNSYVSWFAY, wherein HGNFGNSYISYWAY is most preferred. For X₁₈, the amino acid sequence S is preferred.

[102] The VL region of ii) comprises or consists of the sequence of QX₁VVTQEX₂X₃LTX₄SPGX₅TVTLTCX₆SSTGAVTX₇X₈X₉YX₁₀NWVQX₁₁KPX₁₂X₁₃X₁₄X₁₅X₁₆GLIGX₁₇TX₁₈X₁₉X₂₀X₂₁X₂₂GX₂₃PARFSGSLX₂₄GX₂₅KAALTX₂₆X₂₇GX₂₈QX₂₉EDEAX₃₀YX₃₁CX₃₂LWYSNX₃₃WVFGGGTKLTVL, where X₁ is T or A; X₂ is P or S; X₃ is S or A; X₄ is V or T; X₅ is G or E; X₆ is G, R, or A; X₇ is S or T; X₈ is G or S; X₉ is N or Y; X₁₀ is P or A; X₁₁ is Q or E; X₁₂ is G or D; X₁₃ is Q or H; X₁₄ is A or L; X₁₅ is P or F; X₁₆ is R or T; X₁₇ is G or A; X₁₈ is K or D; X₁₉ is F or M; X₂₀ is L or R; X₂₁ is A, P or V; X₂₂ is P or S; X₂₃ is T or V; X₂₄ is L or I; X₂₅ is G or D; X₂₆ is L or I; X₂₇ is S or T; X₂₈ is V or A; X₂₉ is P or T; X₃₀ is E or I; X₃₁ is Y or F; X₃₂ is V, A, or T; and X₃₃ is R or L.

[103] The CDR sequences within said VL region are as follows: a CDR-L1 sequence comprising or consisting of X₆SSTGAVTX₇X₈X₉YX₁₀N; a CDR-L2 sequence comprising or consisting of X₁₇TX₁₈X₁₉X₂₀X₂₁X₂₂; and a CDR-L3 sequence comprising or consisting of

X₃₂LWYSNX₃₃WV. Preferred examples of the CDR-L1 sequence are selected from GSSTGAVTSGNYPN, RSSTGAVTSGYYPN, GSSTGAVTSGYYPN, ASSTGAVTSGNYPN, and RSSTGAVTTSNYAN, wherein GSSTGAVTSGNYPN is most preferred. Preferred examples of the CDR-L2 sequence are selected from GTKFLAP, ATDMRPS, GTKFLVP, and GTNKRAP, wherein GTKFLAP is most preferred. Preferred examples of the CDR-L3 sequence are selected from VLWYSNRWW, ALWYSNRWW, TLWYSNRWW, and ALWYSNLWW, wherein VLWYSNRWW is most preferred.

[104] For X₁, the amino acid T is preferred. For X₂, the amino acid P is preferred. For X₃, the amino acid S is preferred. For X₄, the amino acid V is preferred. For X₅, the amino acid G is preferred. For X₆, the amino acid G is most preferred. For X₇, the amino acid S is most preferred. For X₈, the amino acid G is most preferred. For X₉, the amino acid N is most preferred. For X₁₀, the amino acid P is most preferred. X₆ to X₁₀ are part of the CDR-L1 sequence within the VL region. Preferred examples of said CDR-L1 sequence are selected from GSSTGAVTSGNYPN, RSSTGAVTSGYYPN, GSSTGAVTSGYYPN, ASSTGAVTSGNYPN, and RSSTGAVTTSNYAN, wherein GSSTGAVTSGNYPN is most preferred. For X₁₁, the amino acid Q is preferred. For X₁₂, the amino acid G is preferred. For X₁₃, the amino acid Q is preferred. For X₁₄, the amino acid A is preferred. For X₁₅, the amino acid P is preferred. For X₁₆, the amino acid R is preferred. For X₁₇, the amino acid G is preferred. For X₁₈, the amino acid K is preferred. For X₁₉, the amino acid F is preferred. For X₂₀, the amino acid L is preferred. For X₂₁, the amino acid A is preferred. For X₂₂, the amino acid P is preferred. X₁₇ to X₂₂ are part of the CDR-L2 sequence of the VL region. Preferred examples of said CDR-L2 sequence are selected from GTKFLAP, ATDMRPS, GTKFLVP, and GTNKRAP, wherein GTKFLAP is most preferred. For X₂₃, the amino acid T is preferred. For X₂₄, the amino acid L is preferred. For X₂₅, the amino acid G is preferred. For X₂₆, the amino acid L is preferred. For X₂₇, the amino acid S is preferred. For X₂₈, the amino acid V is preferred. For X₂₉, the amino acid P is preferred. For X₃₀, the amino acid E is preferred. For X₃₁, the amino acid Y is preferred. For X₃₂, the amino acid V is preferred. For X₃₃, the amino acid R is preferred. X₃₂ and X₃₃ are part of the CDR-L3 sequence of the VL region. Preferred examples of said CDR-L3 sequence are selected from VLWYSNRWW, ALWYSNRWW, TLWYSNRWW, and ALWYSNLWW, wherein VLWYSNRWW is most preferred.

[105] In a more preferred embodiment, the VH region of i) comprises or consists of the sequence of EVQLVESGGGLX₁QPGGSLKLSAASGFTFNX₂YAX₃NWVRQAPGKGLEWWARIRSKYNNY ATYYADX₄VKX₅RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHX₆NFGNSYX₇SX₈X₉AYWGQGTLLTVSS, where X₁ is V or E; X₂ is K, V, S, G, R, or I; X₃ is M or I; X₄ is S or Q; X₅ is D, G, K, S, or E; X₆ is G, R or A; X₇ is I, L, V, or T; X₈ is Y, W or F; and X₉ is W or F; and the VL region of ii) comprises or consists of the sequence of

QTVVTQEPSLTVSPGGTVTLTCX₁SSTGAVTSGX₂YPNWWQQKPGQAPRGLIGX₃TX₄X₅X₆X₇X₈GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCX₉LWYSNRWWFGGGTKLTVL, where X₁ is G, R, or A; X₂ is N or Y; X₃ is G or A; X₄ is K or D; X₅ is F or M; X₆ is L or R; X₇ is A, P or V; X₈ is P or S; and X₉ is V, A, or T.

- 5 **[106]** The VH region of i) comprises or consists of the sequence of EVQLVESGGGLX₁QPGGSLKLSCAASGFTFNX₂YAX₃NWVRQAPGKGLEWWARIRSKYNNYATYYADX₄VKX₅RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHX₆NFGNSYX₇SX₈X₉AYWGQGTLVTVSS, where X₁ is V or E; X₂ is K, V, S, G, R, or I; X₃ is M or I; X₄ is S or Q; X₅ is D, G, K, S, or E; X₆ is G, R or A; X₇ is I, L, V, or T; X₈ is Y, W or F; and X₉ is W or F.
- 10 **[107]** The CDR sequences within said VH region are as follows: a CDR-H1 sequence comprising or consisting of X₂YAX₃N; a CDR-H2 sequence comprising or consisting of RIRSKYNNYATYYADX₄VKX₅; and a CDR-H3 sequence comprising or consisting of HX₆NFGNSYX₇SX₈X₉AY. Preferred examples of said CDR-H1 sequence X₂YAX₃N are selected from KYAMN, VYAMN, SYAMN, GYAMN, RYAMN, TYAMN, IYAMN, and KYAIN,
- 15 wherein KYAMN or KYAIN is more preferred, wherein KYAMN is most preferred. Preferred examples of said CDR-H2 sequence RIRSKYNNYATYYADX₄VKX₅ are selected from RIRSKYNNYATYYADSVKD, RIRSKYNNYATYYADSVKK, RIRSKYNNYATYYADSVKS, RIRSKYNNYATYYADSVKE, RIRSKYNNYATYYADSVKG, and RIRSKYNNYATYYADQVKD, wherein RIRSKYNNYATYYADSVKD or RIRSKYNNYATYYADQVKD is more preferred,
- 20 wherein RIRSKYNNYATYYADSVKD is most preferred. Preferred examples of said CDR-H3 sequence HX₆NFGNSYX₇SX₈X₉AY are selected from HGNFGNSYISYWAY, HGNFGNSYLSWWAY, HGNFGNSYTSYYAY, HRNFGNSYLSWFAY, HGNFGNSYVSFFAY, HGNFGNSYISWWAY, HGNFGNSYVSWWAY, HGNFGNSYLSYFAY, HGNFGNSYLSFWAY, HANFGNSYISYWAY, and HGNFGNSYVSWFAY, wherein
- 25 HGNFGNSYISYWAY is most preferred.
- [108]** For X₁, the amino acid V is preferred. For X₂, the amino acid K is most preferred, and for X₃, the amino acid M is most preferred. A preferred combination for X₂ and X₃ is M for X₃ in combination with any of the amino acid residues of X₂, such as the combinations for X₂ and X₃, respectively, selected from K and M, V and M, S and M, most preferred the combination K and M. Another preferred combination is K and I, for X₂ and X₃, respectively.
- 30 Preferred examples of said CDR-H1 sequence X₂YAX₃N are selected from KYAMN, VYAMN, SYAMN, GYAMN, RYAMN, TYAMN, IYAMN, and KYAIN, wherein KYAMN or KYAIN is more preferred, wherein KYAMN is most preferred. For X₄, the amino acid S is preferred. For X₅, the amino acid D is most preferred. A preferred combination is S for X₄ in combination with
- 35 any of the amino acid residues of X₅, such as the combinations for X₄ and X₅, respectively, selected from S and D, S and G, S and K, S and S, most preferred the combination S and D. Preferred examples of said CDR-H2 sequence RIRSKYNNYATYYADX₄VKX₅ are selected

from RIRSKYNNYATYYADSVKD, RIRSKYNNYATYYADSVKK, RIRSKYNNYATYYADSVKS, RIRSKYNNYATYYADSVKE, RIRSKYNNYATYYADSVKG, and RIRSKYNNYATYYADQVKD, wherein RIRSKYNNYATYYADSVKD or RIRSKYNNYATYYADQVKD is more preferred, wherein RIRSKYNNYATYYADSVKD is most preferred. For X_6 , the amino acid G is most preferred; for X_7 , the amino acid I is most preferred; for X_8 , the amino acid Y is most preferred; and for X_9 , the amino acid W is most preferred. Preferred examples of said CDR-H3 sequence $HX_6NFGNSYX_7SX_8X_9AY$ are selected from HGNFGNSYISYWAY, HGNFGNSYLSWWAY, HGNFGNSYTSYYAY, HRNFGNSYLSWFAY, HGNFGNSYVSFFAY, HGNFGNSYISWWAY, HGNFGNSYVSWWAY, HGNFGNSYLSYFAY, HGNFGNSYLSFWAY, HANFGNSYISYWAY, and HGNFGNSYVSWFAY, wherein HGNFGNSYISYWAY is most preferred.

[109] The VL region of ii) comprises or consists of the sequence of QTVVTQEPSLTVSPGGTVTLTCX₁SSTGAVTSGX₂YPNWWQQKPGQAPRGLIGX₃TX₄X₅X₆X₇X₈GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCX₉LWYSNRWWFGGGTKLTVL, where X_1 is G, R, or A; X_2 is N or Y; X_3 is G or A; X_4 is K or D; X_5 is F or M; X_6 is L or R; X_7 is A, P or V; X_8 is P or S; and X_9 is V, A, or T.

[110] The CDR sequences within said VL region are as follows: a CDR-L1 sequence comprising or consisting of X_1 SSTGAVTSGX₂YPN; a CDR-L2 sequence comprising or consisting of X_3 TX₄X₅X₆X₇X₈; and a CDR-L3 sequence comprising or consisting of X_9 LWYSNRWW. Preferred examples of the CDR-L1 sequence are selected from GSSTGAVTSGNYPN, RSSTGAVTSGYYPN, GSSTGAVTSGYYPN, ASSTGAVTSGNYPN, and RSSTGAVTTSNYAN, wherein GSSTGAVTSGNYPN is most preferred. Preferred examples of the CDR-L2 sequence are selected from GTKFLAP, ATDMRPS, GTKFLVP, and GTNKRAP, wherein GTKFLAP is most preferred. Preferred examples of the CDR-L3 sequence are selected from VLWYSNRWW, ALWYSNRWW, TLWYSNRWW, and ALWYSNLWW, wherein VLWYSNRWW is most preferred.

[111] For X_1 , the amino acid G is most preferred. For X_2 , the amino acid N is preferred. X_1 and X_2 are part of the CDR-L1 sequence X_1 SSTGAVTSGX₂YPN within the VL region. Preferred examples of said CDR-L1 sequence are selected from GSSTGAVTSGNYPN, RSSTGAVTSGYYPN, GSSTGAVTSGYYPN, ASSTGAVTSGNYPN, and RSSTGAVTTSNYAN, wherein GSSTGAVTSGNYPN is most preferred. For X_3 , the amino acid G is preferred. For X_4 , the amino acid K is preferred. For X_5 , the amino acid F is preferred. For X_6 , the amino acid L is preferred. For X_7 , the amino acid A is most preferred. For X_8 , the amino acid P is preferred. X_3 to X_8 are part of the CDR-L2 sequence X_3 TX₄X₅X₆X₇X₈ of the VL region. Preferred examples of said CDR-L2 sequence are selected from GTKFLAP, ATDMRPS, GTKFLVP, and GTNKRAP, wherein GTKFLAP is most preferred. For X_9 , the amino acid V is most preferred. X_9 is part of the CDR-L3 sequence

X₉LWYSNRWW of the VL region. Preferred examples of said CDR-L3 sequence are selected from VLWYSNRWW, ALWYSNRWW, TLWYSNRWW, and ALWYSNLWW, wherein VLWYSNRWW is most preferred.

[112] In another preferred embodiment, the VH region of ii) comprises or consists of the sequence of

EVQLVESGGGLX₁QPGGSLKLSCAASGFTFNX₂YAX₃NWVRQAPGKGLEWWARIRSKYNNY
ATYYADX₄VKX₅RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHX₆NFGNSYX₇SX₈X₉AYW
GQGTLLTVSS, where X₁ is V or E; X₂ is K, V, S, R, or I; X₃ is M or I; X₄ is S or Q; X₅ is D, G,
K or S; X₆ is G or A; X₇ is I, L, V, or T; X₈ is Y, W or F; and X₉ is W or F; and the VL region of
ii) comprises or consists of the sequence of
QTVVTQEPSLTVSPGGTVTLTCX₁SSTGAVTSGX₂YPNWWQQKPGQAPRGLIGGTKFLX₃PG
TPARFSGSLLGGKAAALTLSGVQPEDEAEYYCX₄LWYSNRWWFGGGTKLTVL, where X₁ is G
or A; X₂ is N or Y; X₃ is A or V; and X₄ is V, A, or T.

[113] The VH region of ii) comprises or consists of the sequence of
EVQLVESGGGLX₁QPGGSLKLSCAASGFTFNX₂YAX₃NWVRQAPGKGLEWWARIRSKYNNY
ATYYADX₄VKX₅RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHX₆NFGNSYX₇SX₈X₉AYW
GQGTLLTVSS, where X₁ is V or E; X₂ is K, V, S, R, or I; X₃ is M or I; X₄ is S or Q; X₅ is D, G,
K or S; X₆ is G or A; X₇ is I, L, V, or T; X₈ is Y, W or F; and X₉ is W or F.

[114] The CDR sequences within said VH region are as follows: a CDR-H1 sequence
comprising or consisting of X₂YAX₃N; a CDR-H2 sequence comprising or consisting of
RIRSKYNNYATYYADX₄VKX₅; and a CDR-H3 sequence comprising or consisting of
HX₆NFGNSYX₇SX₈X₉AY. Preferred examples of said CDR-H1 sequence X₂YAX₃N are
selected from KYAMN, VYAMN, SYAMN, RYAMN, IYAMN, and KYAIN, wherein KYAMN or
KYAIN are more preferred, wherein KYAMN is most preferred. Preferred examples of said

CDR-H2 sequence RIRSKYNNYATYYADX₄VKX₅ are selected from
RIRSKYNNYATYYADSVKD, RIRSKYNNYATYYADSVKK, RIRSKYNNYATYYADSVKS,
RIRSKYNNYATYYADSVKG, and RIRSKYNNYATYYADQVKD, wherein
RIRSKYNNYATYYADSVKD or RIRSKYNNYATYYADQVKD are more preferred, wherein
RIRSKYNNYATYYADSVKD is most preferred. Preferred examples of said CDR-H3
sequence HX₆NFGNSYX₇SX₈X₉AY are selected from HGNFGNSYISYWAY,
HGNFGNSYLSWWAY, HGNFGNSYTSYYAY, HRNFGNSYLSWFAY, HGNFGNSYVSFFAY,
HGNFGNSYISWWAY, HGNFGNSYVSWWAY, HGNFGNSYLSYFAY,
HGNFGNSYLSFWAY, HANFGNSYISYWAY, and HGNFGNSYVSWFAY, wherein
HGNFGNSYISYWAY or HANFGNSYISYWAY are more preferred, wherein
HGNFGNSYISYWAY is most preferred.

[115] For X₁, the amino acid V is preferred. For X₂, the amino acid K is most preferred, and
for X₃, the amino acid M is most preferred. A preferred combination for X₂ and X₃ is M for X₃

in combination with any of the amino acid residues of X_2 , such as the combinations for X_2 and X_3 , respectively, selected from K and M, V and M, S and M, most preferred the combination K and M. Another preferred combination is K and I, for X_2 and X_3 , respectively. Preferred examples of said CDR-H1 sequence X_2YAX_3N are selected from KYAMN, VYAMN, SYAMN, RYAMN, IYAMN, and KYAIN, wherein KYAMN or KYAIN are more preferred, wherein KYAMN is most preferred. For X_4 , the amino acid S is preferred. For X_5 , the amino acid D is most preferred. A preferred combination is S for X_4 in combination with any of the amino acid residues of X_5 , such as the combinations for X_4 and X_5 , respectively, selected from S and D, S and G, S and K, S and S, most preferred the combination S and D.

Preferred examples of said CDR-H2 sequence RIRSKYNNYATYYAD X_4 VK X_5 are selected from RIRSKYNNYATYYADSVKD, RIRSKYNNYATYYADSVKK, RIRSKYNNYATYYADSVKS, RIRSKYNNYATYYADSVKG, and RIRSKYNNYATYYADQVKD, wherein RIRSKYNNYATYYADSVKD or RIRSKYNNYATYYADQVKD are more preferred, wherein RIRSKYNNYATYYADSVKD is most preferred are selected from RIRSKYNNYATYYADSVKD, RIRSKYNNYATYYADSVKK, RIRSKYNNYATYYADSVKS, RIRSKYNNYATYYADSVKE, RIRSKYNNYATYYADSVKG, and RIRSKYNNYATYYADQVKD, wherein RIRSKYNNYATYYADSVKD is most preferred. For X_6 , the amino acid G is most preferred; for X_7 , the amino acid I is most preferred; for X_8 , the amino acid Y is most preferred; and for X_9 , the amino acid W is most preferred. Preferred examples of said CDR-H3 sequence H X_6 NFGNSY X_7 S X_8 X_9 AY are selected from HGNFGNSYISYWAY, HGNFGNSYLSWWAY, HGNFGNSYTSYYAY, HRNFGNSYLSWFAY, HGNFGNSYVSFFAY, HGNFGNSYISWWAY, HGNFGNSYVSWWAY, HGNFGNSYLSYFAY, HGNFGNSYLSFWAY, HANFGNSYISYWAY, and HGNFGNSYVSWFAY, wherein HGNFGNSYISYWAY is most preferred.

[116] The VL region of ii) comprises or consists of the sequence of QTVVTQEPLTVSPGGTVTLTC X_1 SSTGAVTSG X_2 YPNWWQQKPGQAPRGLIGGTKFL X_3 PGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC X_4 LWYSNRWWFGGGTKLTVL, where X_1 is G or A; X_2 is N or Y; X_3 is A or V; and X_4 is V, A, or T.

[117] The CDR sequences within said VL region are as follows: a CDR-L1 sequence comprising or consisting of X_1 SSTGAVTSG X_2 YPN; a CDR-L2 sequence comprising or consisting of GTKFL X_3 P; and a CDR-L3 sequence comprising or consisting of X_4 LWYSNRWW. Preferred examples of the CDR-L1 sequence are selected from GSSTGAVTSGNYPN, RSSTGAVTSGYYPN, GSSTGAVTSGYYPN, ASSTGAVTSGNYPN, and RSSTGAVTTSNYAN, wherein GSSTGAVTSGNYPN is most preferred. Preferred examples of the CDR-L2 sequence are selected from GTKFLAP, ATDMRPS, GTKFLVP, and GTNKRAP, wherein GTKFLAP is most preferred. Preferred examples of the CDR-L3 sequence are selected from VLWYSNRWW, ALWYSNRWW, TLWYSNRWW, and

ALWYSNLWW, wherein VLWYSNRWW is most preferred.

[118] For X_1 , the amino acid G is preferred. For X_2 , the amino acid N is preferred. X_1 and X_2 are part of the CDR-L1 sequence X_1 SSTGAVTSG X_2 YPN within the VL region. Preferred examples of said CDR-L1 sequence are selected from GSSTGAVTSGNYPN, RSSTGAVTSGYYPN, GSSTGAVTSGYYPN, ASSTGAVTSGNYPN, and RSSTGAVTTSNYAN, wherein GSSTGAVTSGNYPN is most preferred. X_3 is part of the CDR-L2 sequence GTKFL X_3 P of the VL region. Said CDR-L2 sequence can either be GTKFLAP or GTKFLVP, wherein GTKFLAP is preferred. For X_3 , the amino acid A is preferred. X_4 is part of the CDR-L3 sequence X_4 LWYSNRWW of the VL region. Preferred examples of said CDR-L3 sequence are selected from VLWYSNRWW, ALWYSNRWW, and TLWYSNRWW, wherein VLWYSNRWW is most preferred. For X_4 , the amino acid V is most preferred.

[119] In a further preferred embodiment, the VH region of i) comprises or consists of the sequence of

EVQLVESGGGLVQPGGSLKLSAASGFTFN X_1 YAMNWVRQAPGKGLEWWARIRSKYNNYA
 TYYADSVK X_2 RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSY X_3 S X_4 WAYWGQ
 GTLVTVSS, where X_1 is K or S; X_2 is D or G; X_3 is I or V; and X_4 is Y or W; and the VL region of ii) comprises or consists of the sequence of
 QTVVTQEPSLTVSPGGTVTLTCSSTGAVTSG X_1 YPNWWQQKPGQAPRGLIGGTKFLAPGT
 PARFSGSLLGGKAALTLSGVQPEDEAEYYC X_2 LWYSNRWWFGGGTKLTVL, where X_1 is N or Y; and X_2 is V or A.

[120] The VH region of i) comprises or consists of the sequence of
 EVQLVESGGGLVQPGGSLKLSAASGFTFN X_1 YAMNWVRQAPGKGLEWWARIRSKYNNYA
 TYYADSVK X_2 RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSY X_3 S X_4 WAYWGQ
 GTLVTVSS, where X_1 is K or S, wherein K is preferred; X_2 is D or G, wherein D is preferred; X_3 is I or V, wherein I is preferred; and X_4 is Y or W, wherein Y is preferred.

[121] The CDR sequences within said VH region are as follows: a CDR-H1 sequence comprising or consisting of X_1 YAMN; a CDR-H2 sequence comprising or consisting of RIRSKYNNYATYYADSVK X_2 ; and a CDR-H3 sequence comprising or consisting of HGNFGNSY X_3 S X_4 WAY. Said CDR-H1 sequence X_1 YAMN is selected from KYAMN or SYAMN, wherein KYAMN is preferred. Preferred examples of said CDR-H2 sequence RIRSKYNNYATYYADSVK X_2 are selected from RIRSKYNNYATYYADSVKD and RIRSKYNNYATYYADSVKG, wherein RIRSKYNNYATYYADSVKD is preferred. Said CDR-H3 sequence HGNFGNSY X_3 S X_4 WAY is HGNFGNSYISYWAY or HGNFGNSYVSWWAY, wherein HGNFGNSYISYWAY is preferred.

[122] The VL region of ii) comprises or consists of the sequence of
 QTVVTQEPSLTVSPGGTVTLTCSSTGAVTSG X_1 YPNWWQQKPGQAPRGLIGGTKFLAPGT

PARFSGSLLGGKAALTLSGVQPEDEAEYYCX₂LWYSNRWWFGGGTKLTVL, where X₁ is N or Y, wherein N preferred; and X₂ is V or A, wherein V preferred.

[123] The CDR sequences within said VL region are as follows: a CDR-L1 sequence comprising or consisting of GSSTGAVTSGX₁YPN; a CDR-L2 sequence comprising or consisting of GTKFLAP; and a CDR-L3 sequence comprising or consisting of X₂LWYSNRWW. The CDR-L1 sequence is GSSTGAVTSGNYPN or GSSTGAVTSGYYPN, wherein GSSTGAVTSGNYPN is preferred. The CDR-L3 sequence is VLWYSNRWW or ALWYSNRWW, wherein VLWYSNRWW is preferred.

[124] In a preferred embodiment, the VH region of i) comprises or consists of the sequence as defined in SEQ ID NOs: 124, 172, 362, 552, 730, 928, 1106, 1296, 1474, 1664 or 1854; and the VL region of ii) comprises or consists of the sequence of as defined in SEQ ID NOs: 125, 173, 363, 553, 731, 929, 1107, 1297, 1475, 1665, or 1855. Preferred combinations of VH and VL regions of i) and ii) are defined in SEQ ID NOs: 124 and 125 (combination of binder termed "2B2"), 172 and 173 ("A2J"), 362 and 363 ("E1L"), 552 and 553 ("E2M"), 730 and 731 ("F12Q"), 928 and 929 ("F6A"), 1106 and 1107 ("F7O"), 1296 and 1297 ("G4H"), 1474 and 1475 ("H1E"), 1664 and 1665 ("H2C"), or 1854 and 1855 ("I2C"). Preferred is that the CD3epsilon binding domain comprises or consists of a combination of VH and VL region of i) and ii) selected from the group consisting of SEQ ID NOs: 124 and 125, 172 and 173, 362 and 363, 552 and 553, 730 and 731, 928 and 929, 1106 and 1107, 1296 and 1297, 1474 and 1475, 1664 and 1665, and 1854 and 1855. More preferred is that the CD3epsilon binding domain comprises or consists of a combination of VH and VL region of i) and ii) selected from the group consisting of SEQ ID NOs: 124 and 125, 362 and 363, 730 and 731, 928 and 929, 1106 and 1107, 1296 and 1297, 1474 and 1475, 1664 and 1665, and 1854 and 1855. Even more preferred is that the CD3epsilon binding domain comprises or consists of a combination of VH and VL region of i) and ii) selected from the group consisting of SEQ ID NOs: 124 and 125, 730 and 731, 1664 and 1665, and 1854 and 1855. In a yet even more preferred embodiment, the CD3epsilon binding domain comprises or consists of a combination of VH and VL region of i) and ii) selected from the group consisting of SEQ ID NOs: 730 and 731, 1664 and 1665, and 1854 and 1855.

[125] In the most preferred embodiment, the VH region of i) comprises or consists of the sequence of

EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWWVRQAPGKGLEWWARIRSKYNNYA
TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT
LVTVSS (SEQ ID NO: 1854); and the VL region of ii) comprises or consists of the sequence

of
QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWWQQKPGQAPRGLIGGTKFLAPGT
PARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWWFGGGTKLTVL (SEQ ID NO:

1855).

[126] As outlined herein above in relation to amino acid substitutions in the CDR sequences and also applying to this embodiment, the VH region of i) and/or VL region of ii) comprise one or more amino acid substitutions as specified herein above. Accordingly, at least one of the recited amino acid substitutions of the variable regions is comprised in said binding domain binding to an extracellular epitope of the human CD3 ϵ chain. Said at least one or one or more amino acid substitution, in the case that only one amino acid substitution is present, can be present in a CDR sequence in said VH or said VL region or, in case more than one amino acid substitution is present, in CDRs in both the VH and the VL region or restricted to CDR sequences in only the VH or the VL region. In certain embodiments where there are more than one amino acid substitutions, the substitutions are in the VH and the VL region or, alternatively, only in one variable region. Preferably, the substitutions are in the VH and the VL region.

[127] Specifically, the VH of i) and/or VL region sequence of ii) comprises one or more amino acid substitutions selected from

- a. N30 (preferably S), X₆34V, X₆34F, Q39 (E, K, R, D, preferably E), L45 (M or V, preferably M), D64 (preferably E), X₇65A, X₁₂81V, X₁₂81T, X₁₂81I, V99 (A or L, preferably A), H101 (preferably A or N), X₁₄102E, F104 (preferably I), N106 (preferably S or T) in the VH region sequence in i); and
- b. L20 (preferably I or M), V38 (I, L, M, F or Y, preferably I), X₁₁40R, X₁₁40K, X₂₄69 (S or E, preferably S), X₃₂91L, X₃₃93 (preferably Y), G102 (preferably S) in the VL region sequence in ii).

[128] In the VH region sequence, the amino acid substitution at position 30 is, preferably, S (hence, can be written as N30S; same is true for the subsequent substitutions given according to their position number). The amino acid substitution at position 34 is V or F. Preferably, position 34 of the VH region sequence comprises an I or M, most preferred an I. The amino acid substitution at position 39 is E, K, R, D, preferably E. The amino acid substitution at position 45 is preferably M or V, more preferred M. The amino acid substitution at position 64 is preferably E. The amino acid substitution at position 65 is A. The amino acid substitution at position 81 is V, T or I, preferably V. The amino acid substitution at position 99 is preferably A or L, more preferred A. The amino acid substitution at position 101 is preferably A or N, more preferred A (H1A). The amino acid substitution at position 102 is E. The amino acid substitution at position 104 is preferably I. The amino acid substitution at position 106 is preferably S or T, more preferred S.

[129] Notwithstanding the above, in the CDR-H2 sequence within the VH region sequence, the amino acid substitution at position 64 is, preferably, D15E, or the amino acid substitution

at position 65 with amino acid A. Preferably, said CDR-H2 comprises the amino acid residue substitution at position 65 with amino acid A; in this case, a preferred amino acid for the last amino acid of CDR-H2 is D or G, preferred D. Hence, a preferred CDR-H2 sequence is RIRSKYNNYATYYADAVKD or RIRSKYNNYATYYADAVKG, with
 5 RIRSKYNNYATYYADAVKD more preferred. In case CDR-H2 contains two amino acid substitutions, the combination of the amino acid E at position 64 and amino acid A at position 64 are preferred; in this case, a preferred amino acid for the last amino acid of CDR-H2 is G. Hence, a preferred CDR-H2 sequence for the combination of the amino acid E at position 64 and amino acid A at position 65 is RIRSKYNNYATYYAEAVKG.

[130] In the CDR-H3 sequence of the VH sequence, the amino acid substitutions are at position 101, preferably a substitution with amino acid A or N, more preferably A, at position 102 with amino acid E, at position 104, preferably with amino acid I, and at position 106, preferably with amino acid S or T. Preferably, CDR-H3 comprises the amino acid A or N at position 101, the amino acid S or T at position 106; in this case and if placeholders are
 15 present in the CDR-H3 sequence at the indicated positions, preferred amino acids for X_{14} are G or A, most preferred G; for X_{15} is I; for X_{16} is Y; and for X_{17} are W or Y. In case CDR-H3 comprises two amino acid substitutions, preferred combinations are the amino acid A at position 101 and the amino acid S at position 106; and the amino acid N at position 101 and the amino acid T at position 106; in this case and if placeholders are present in the CDR-H3
 20 sequence at the indicated positions, a preferred amino acid for X_{14} is G or A, most preferred G; for X_{15} is I, for X_{16} is Y, and for X_{17} are W and F. In case CDR-H3 comprises three amino acid substitutions, preferred combinations are the amino acid A at position 101, the amino acid I at position 104, and the amino acid S at position 106; and the amino acid N at position 101, the amino acid I at position 104 and the amino acid T at position 106, in this case and if
 25 placeholders are present in the CDR-H3 sequence at the indicated positions, a preferred amino acid for X_{15} is I, for X_{16} is Y, and for X_{17} are W and F. In case CDR-H3 comprises four amino acid substitutions, a preferred combination is the amino acid N at position 101, the amino acid E at position 102, the amino acid I at position 104, and the amino acid T at position 106; in this case and if placeholders are present in the CDR-H3 sequence at the
 30 indicated positions, a preferred amino acid for X_{15} is I, for X_{16} is Y, and for X_{17} is W. Hence, preferred CDR-H3 sequences are selected from AGNFGSSYISYWAY, NENIGTSYISYWAY, AGNFGTSYISYWAY, NANFGTSYISYFAY, and AGNFGSSYISYFAY, with AGNFGSSYISYWAY and AGNFGSSYISYFAY most preferred.

[131] In the VL region sequence, the amino acid substitution at position 20 is preferably I or
 35 M, more preferred I. The amino acid substitution at position 38 is preferably I, L, M, F or Y, more preferred with I. The amino acid substitution at position 40 is preferably K or R, more preferred K. The amino acid substitution at position 69 is preferably S or E, more preferred S.

The amino acid substitution at position 91 is L. The amino acid substitution at position 93 is preferably Y. The amino acid substitution at position 102 is preferably S.

[132] Notwithstanding the above, in the CDR-L3 sequence within the VL region sequence, the amino acid substitution at position 1 is with amino acid L or the amino acid substitution is W93, preferably W93Y. Preferably, the CDR-L3 sequence is VLYYSNRWW when CDR-L3 comprises an amino acid substitution. It is preferred, however, that CDR-L3 does not comprise said X₁L and W93 amino acid substitution, in which case a preferred CDR-L3 sequence is VLYYSNRWW.

[133] In accordance with the foregoing, the amino acid substitution H101A in the VH region (part of CDR-H3) is preferably the amino acid substitution, in case there is only one amino acid substitution present in the CD3epsilon binding domain, within the VH and/or VL region sequences as defined herein. Furthermore, in case of combinations of amino acid substitutions as defined in iii) preferably H101A in the VH region sequence is one of the amino acid substitutions of said combination.

[134] In a preferred embodiment of the polypeptide or polypeptide construct of the invention, wherein in addition to said one amino acid substitution or a combination thereof as defined in iii) X₆ is I; X₈ is G; X₁₂ is L, X₁₄ is A, X₁₇ is F in said VH region sequence; and/or X₃₂ is A in said VL region sequence. In a preferred embodiment of the polypeptide or polypeptide construct of claim 1 of the invention, in addition to said one amino acid substitution or a combination thereof as defined in iii) X₆ is I; X₈ is G; X₁₄ is A, X₁₇ is F in said VH region sequence; and/or X₃₂ is A in said VL region sequence. The one amino acid substitution or combination thereof as defined herein is/are in addition combined with specific amino acids at specific positions in the CDRs. Hence, at least one of the recited amino acid substitutions in accordance with iii) is present and at least one of X₈ is G; X₁₄ is A, X₁₇ is F in said VH region sequence; and/or X₃₂ is A in said VL region sequence is additionally present in the CDRs. As previously stated herein above, a preferred amino acid for X₆ is I or X₈ is G in said VH region sequence, if only one additional amino acid is present in the CDRs, wherein it is most preferred that X₅ is I in said VH region sequence. A preferred combination of two of said additional amino acids is X₆ is I and X₁₇ is F in said VH region sequence; or X₈ is G and X₁₇ is F in said VH region sequence. A preferred combination of three of said additional amino acids is X₆ is I, X₁₄ is A, and X₁₇ is F in said VH region sequence; or X₆ is I, X₁₇ is F in said VH region sequence, and X₃₂ is A in said VL region sequence. Since the latter amino acids are to be present additionally, it is understood that those recited additional amino acids that overlap in position with the amino acid substitution of iii) cannot replace the overlapping amino acid substitution. For example, if the only amino acid substitution in accordance with iii) is either X₆34V or X₆34F in CDR-H1, said amino acid cannot be replaced by amino acid I in said CDR-H1 sequence, since there would be no amino acid substitution as defined in iii)

remaining in the binding domain. In other terms, there must always be at least one of the amino acid substitutions as defined in iii) comprised in the polypeptide or polypeptide construct of the invention.

[135] It is also understood that depending on the actual sequence of the VH and/or VL region sequences, one or more of said additional amino acids may already be part of the given variable sequence as defined herein above or, if this is not the case, said given variable region will be changed to exhibit said additional amino acid(s) in combination with one amino acid substitution or a combination thereof as recited in iii).

[136] In a preferred embodiment of the polypeptide or polypeptide construct of the invention, it comprises combinations of said amino acid substitutions as defined in iii) of two, three, four, five, six, seven, eight, nine, ten, eleven, twelve or more amino acid substitutions.

[137] In a preferred embodiment of the polypeptide or polypeptide construct of the invention, i) said one acid substitution is selected from a. X₆34V, Q39E, Q39K, Q39R, Q39D, L45M, L45V, X₁₂81V, X₁₂81T, X₁₂81I, V99A, V99L, H101A, H101N in the VH region; and b. V38I, V38L, V38M, V38F, V38Y, X₁₁40R, X₁₁40K, X₂₄69S, X₂₄69E, X₃₂91L, X₃₃93Y; ii) said combination of two or more amino acid substitutions are selected from X₆34F and A81V (which may also be referred to as X₁₂81V) in the VH region; Q39E in the VH region and X₁₁40K in the VL region; Q39E in the VH region and X₁₁40R in the VL region; Q39D in the VH region and X₁₁40K in the VL region; Q39D in the VH region and X₁₁40R in the VL region; L45V in the VH region and V38F in the VL region; L45V in the VH region and V38Y in the VL region; L45M in the VH region and X₁₁40K in the VL region; L20I and G102S in the VL region; A81V in the VH region and X₁₁40K in the VL region; iii) said combination of three or more amino acid substitutions are selected from Q39E in the VH region, X₁₁40K and G102S in the VL region; Q39E in the VH region, X₁₁40R and G102S in the VL region; Q39D in the VH region, X₁₁40K and G102S in the VL region; Q39D in the VH region, X₁₁40R and G102S in the VL region; L45M in the VH region, X₁₁40K and G102S in the VL region; X₇65A, H101A, and N106S in the VH region; L20I, X₁₁40K, and G102S in the VL region; iv) said combination of four or more amino acid substitutions are selected from Q39E in the VH region, L20I, X₁₁40K and G102S in the VL region; Q39E in the VH region, L20I, X₁₁40R and G102S in the VL region; Q39D in the VH region, L20I, X₁₁40K and G102S in the VL region; Q39D in the VH region, L20I, X₁₁40R and G102S in the VL region; L45M in the VH region, L20I, X₁₁40K and G102S in the VL region; L20I, X₁₁40K, X₂₄69S, and G102S in the VL region; A81V in the VH region, L20I, X₁₁40K, and G102S in the VL region; and/or v) said combination of five, six, seven, eight, nine, ten, or more amino acid substitutions are selected from X₇65A, A81V, V99A, N106S in the VH region, L20I, X₁₁40K, X₂₄69S, and G102S in the VL region; D64E, X₇65A, A81V, X₁₄102E, F104I, N106T in the VH region, L20I, X₂₄69S, and G102S in the VL region; L45M, X₇65A, N106T in the VH region, L20I, X₁₁40K, X₂₄69S, and G102S in the VL

region; X₇65A, A81V, V99A, H101A, F104I, N106S in the VH region, L20I, X₁₁40K, X₂₄69S, and G102S in the VL region; X₇65A, A81V, V99A, H101A, N106S in the VH region; A81V, V99A in the VH region, L20I, X₁₁40K, X₂₄69S, and G102S in the VL region; Q39E, A81V in the VH region, L20I, X₁₁40K, and G102S in the VL region; L45V in the VH region, L20I, V38F, X₁₁40K and G102S in the VL region.

[138] In a more preferred embodiment of the polypeptide or polypeptide construct of the invention, said combination of amino acid substitutions is selected from:

i) in the VH region

- a. X₇65A, A81V, V99A, H101A and N106S;
- b. D64E, X₇65A, A81V, H101N, X₁₄102E, F104I, and N106S;
- c. L45M, X₇65A, H101A, and N106T;
- d. L45M, X₇65A, H101A, and N106S;
- e. Q39E, X₇65A, H101N, and N106T;
- f. D64E, X₇65A, V99A, H101A, and N106T;
- g. X₇65A, A81V, V99A, H101A, X₁₄102E, F104I, and N106T;
- h. X₇65A, A81V, H101N, X₁₄102E, F104I, and N106S;
- i. D64E, X₇65A, A81V, H101A, and N106S;
- j. D64E, X₇65A, H101A, and N106T;
- k. X₇65A, V99A, H101A, and N106T;
- l. D64E, X₇65A, H101A, and N106S;
- m. D64E, X₇65A, A81V, V99A, H101A, and N106S;
- n. X₇65A, H101A and N106S;
- o. N30S, Q39E, D64E, X₇65A, A81V, H101A, X₁₄102E, F104I, and N106T;
- p. L45M, D64E, X₇65A, H101A, and N106T;
- q. N30S, L45M, X₇65A, A81V, H101A, and N106T;
- r. N30S, L45M, D64E, X₇65A, A81V, H101A, and N106S;

ii) in the VL region

- a. L20I, X₁₁40K, X₂₄69S, and G102S;
- b. L20I, X₂₄69S, and G102S;
- c. L20I, V38I, X₁₁40K, X₂₄69E, G102S and W93Y;
- d. X₁₁40K and G102S;
- e. L20I, X₁₁40K, X₂₄69S, G102S and W93Y;
- f. L20M, X₁₁40K and X₂₄69E;
- g. L20I, V38I, X₁₁40K, X₂₄69E and G102S;
- h. X₁₁40K, X₂₄69S and W93Y;
- i. X₁₁40K and X₂₄69S; and

iii) a combination of one amino acid substitution combination of i) and ii).

[139] In yet another preferred embodiment of the polypeptide or polypeptide construct of the invention, said combination of amino acid substitution combinations of iii) is selected from:

- a. X₇65A, A81V, V99A, H101A, N106S in the VH region, L20I, X₁₁40K, X₂₄69S, and G102S in the VL region;
- b. D64E, X₇65A, A81V, H101N, X₁₄102E, F104I, N106S in the VH region, L20I, X₂₄69S, and G102S in the VL region;
- c. L45M, X₇65A, H101A, N106T in the VH region, L20I, X₁₁40K, X₂₄69S, and G102S in the VL region;
- d. L45M, X₇65A, H101A, N106S in the VH region, L20I, V38I, X₁₁40K, X₂₄69E, G102S and W93Y in the VL region;
- e. Q39E, X₇65A, H101N, N106T in the VH region, X₁₁40K and G102S in the VL region;
- f. D64E, X₇65A, V99A, H101A, N106T in the VH region, X₁₁40K and G102S in the VL region;
- g. X₇65A, A81V, V99A, H101A, X₁₄102E, F104I, N106T in the VH region, L20I, X₁₁40K, X₂₄69S, and G102S in the VL region;
- h. X₇65A, A81V, H101N, X₁₄102E, F104I, N106S in the VH region, L20I, X₂₄69S, and G102S in the VL region;
- i. D64E, X₇65A, A81V, H101A, N106S in the VH region, L20I, X₂₄69S, and G102S in the VL region;
- j. D64E, X₇65A, H101A, N106T in the VH region, X₁₁40K and G102S in the VL region;
- k. X₇65A, V99A, H101A, N106T in the VH region, X₁₁40K and G102S in the VL region;
- l. D64E, X₇65A, H101A, N106S in the VH region, X₁₁40K and G102S in the VL region;
- m. D64E, X₇65A, A81V, V99A, H101A, N106S in the VH region, L20I, X₁₁40K, X₂₄69S, G102S and W93Y in the VL region;
- n. X₇65A, H101A N106S in the VH region, X₁₁40K and G102S in the VL region;
- o. N30S, Q39E, D64E, X₇65A, A81V, H101A, X₁₄102E, F104I, N106T in the VH region, L20M, X₁₁40K and X₂₄69E in the VL region;
- p. L45M, D64E, X₇65A, H101A, N106T in the VH region, L20I, V38I, X₁₁40K, X₂₄69E and G102S in the VL region;
- q. N30S, L45M, X₇65A, A81V, H101A, N106T in the VH region, X₁₁40K and X₂₄69S in the VL region; and

- r. N30S, L45M, D64E, X₇65A, A81V, H101A, N106S in the VH region, X₁₁40K and X₂₄69S in the VL region.

[140] In another preferred embodiment of the polypeptide or polypeptide construct of the invention, in said combination of amino acid substitution combinations defined in:

- a. and m. X₆ is I in said VH region sequence;
- b. and r. X₈ is G in said VH region sequence;
- c. X₁₂ is L in said VH region;
- d. X₁₂ is L and X₁₇ is F in said VH region;
- e. X₆ is I, X₁₄ is A and X₁₇ is F in said VH region sequence;
- f. X₆ is I in said VH region sequence; and X₃₂ is A in said VL region sequence;
- g. X₆ is I in said VH region sequence;
- h. and i. X₈ is G in said VH region sequence;
- j., l. and n. X₆ is I and X₁₇ is F in said VH region sequence; and X₃₂ is A in said VL region sequence;
- k. X₆ is I in said VH region sequence; and X₃₂ is A in said VL region sequence;
- p. X₁₂ is L in said VH region; or
- q. X₈ is G and X₁₇ is F in said VH region sequence.

Examples of VH and VL region sequences as defined in this embodiment are defined by SEQ ID NOs: 2012 and 2013; 2020 and 2021; 2028 and 2029; 2036 and 2037; 2044 and 2045; 26 and 27; 34 and 35; 42 and 43; 50 and 51; 58 and 59; 66 and 67; 74 and 75; 82 and 83; 90 and 91; 98 and 99; 100 and 101; 108 and 109; 116 and 117. Table 2 evidences the increase of the aforementioned VH and VL region sequence combinations of the CD3epsilon binding domain in temperature stability over the CD3epsilon binding domain comprising a VH and VL combination defined as "I2C" (SEQ ID NOs: 1854 and 1855, respectively).

[141] In accordance with the invention, the binding domain of the polypeptide or polypeptide construct of the invention that binds to an extracellular epitope of the human CD3ε chain and comprising or consisting of a VH region and a VL region as defined herein comprises at least one of the following CDR sequences or a combination thereof as defined in SEQ ID NOs: 1878, 1908, 1989, and 2003. Said sequences contain one amino acid substitution or a combination thereof as defined in iii), and in some instances also said additional amino acids as defined herein above. Preferred combinations of said CDR sequences are listed in the following in the order of CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, CDR-L3: 1878 to 1883; 1908 to 1913; 1984 to 1989; 1998 to 2003.

[142] Also in accordance with the invention are CDR sequence combinations in the order of CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, CDR-L3 as defined in SEQ ID NOs: 126 to 131; 134 to 139; 142 to 147; 150 to 155; 158 to 163.

[143] Also in accordance with the invention and more preferred are CDR sequence combinations as defined in SEQ ID NOs (listed in the order of CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, CDR-L3): 2006 to 2011; 2014 to 2019; 2022 to 2027; 2030 to 2035; 2038 to 2043; 20 to 25; 36 to 41; 44 to 49; 52 to 57; 60 to 65; 68 to 73; 76 to 81; 84 to 89; 92 to 97; 102 to 107; 110 to 115. Further examples are SEQ ID NOs: 282 to 287; 290 to 295; 298 to 303; 306 to 311; 314 to 319; 472 to 477; 480 to 485; 488 to 493; 496 to 501; 504 to 509; 650 to 655; 658 to 663; 666 to 671; 674 to 679; 682 to 687; 840 to 845; 848 to 853; 856 to 861; 864 to 869; 872 to 877; 1026 to 1031; 1034 to 1039; 1042 to 1047; 1050 to 1055; 1058 to 1063; 1216 to 1221; 1224 to 1229; 1232 to 1237; 1240 to 1245; 1248 to 1253; 1394 to 1399; 1402 to 1407; 1410 to 1415; 1418 to 1423; 1426 to 1431; 1584 to 1589; 1592 to 1597; 1600 to 1605; 1608 to 1613; 1616 to 1621; 1774 to 1779; 1782 to 1787; 1790 to 1795; 1798 to 1803; 1806 to 1811;

[144] In accordance with the invention, the binding domain of the polypeptide or polypeptide construct of the invention that binds to an extracellular epitope of the human CD3 ϵ chain comprises or consists of a VH region sequence as defined in the following SEQ ID NOs: 1856, 1860, 1862, 1864, 1872, 1884, 1894, 1896, 1898, 1900, 1902, 1904, 1906, 1914, 1916, 1918, 1920, 1922, 1924, 1926, 1928, 1930, 1932, 1934, 1936, 1938, 1940, 1942, 1944, 1946, 1948, 1950. Said sequences contain one amino acid substitution or a combination thereof as defined herein above, and in some instances also said additional amino acids as defined herein above. This is also true for the below embodiments characterizing by sequence ID number CD3epsilon binding domains that result from amino acid residue exchanges as specified herein.

[145] In accordance with the invention, the binding domain of the polypeptide or polypeptide construct of the invention that binds to an extracellular epitope of the human CD3 ϵ chain comprises or consists of a VL region sequence as defined in the following SEQ ID NOs: 1867, 1869, 1871, 1875, 1877, 1899, 1901, 1903, 1905, 1907, 1919, 1921, 1923, 1925, 1927, 1929, 1931, 1933, 1935, 1937, 1939, 1941, 1943, 1961, 1963, 1965, 1967, 1969, 1971, 1975, 1991, 1993, 1995, 1997, or 2005.

[146] Preferred combinations of VH and VL region sequences of said binding domain of the polypeptide or polypeptide construct of the invention that binds to an extracellular epitope of the human CD3 ϵ chain are defined in the following SEQ ID NOs: 1856 and 1857; 1860 and 1861; 1862 and 1863; 1864 and 1865; 1866 and 1867; 1868 and 1869; 1870 and 1871; 1872 and 1873; 1874 and 1875; 1876 and 1877; 1884 and 1885; 1894 and 1895; 1896 and 1897; 1898 and 1899; 1900 and 1901; 1902 and 1903; 1904 and 1905; 1906 and 1907; 1914 and 1915; 1916 and 1917; 1918 and 1919; 1920 and 1921; 1922 and 1923; 1924 and 1925; 1926 and 1927; 1928 and 1929; 1930 and 1931; 1932 and 1933; 1934 and 1935; 1936 and 1937; 1938 and 1939; 1940 and 1941; 1942 and 1943; 1944 and 1945; 1946 and 1947; 1948 and

1949; 1950 and 1951; 1960 and 1961; 1962 and 1963; 1964 and 1965; 1966 and 1967; 1968 and 1969; 1970 and 1971; 1974 and 1975; 1990 and 1991; 1992 and 1993; 1994 and 1995; 1996 and 1997; or 2004 and 2005.

[147] Also in accordance with the invention are VH region sequences as defined in SEQ ID NO: 132, 140, 148, 156, and 164.

[148] Also in accordance with the invention are VL region sequences as defined in SEQ ID NO: 133, 141, 149, 157, and 165.

[149] Also in accordance with the invention are any combinations of the foregoing particularly preferred VH and VL region sequences. Preferred are the following VH and VL combinations as defined by SEQ ID NOs: 132 and 133; 140 and 141; 148 and 149; 156 and 157; and 164 and 165.

[150] Also in accordance with the invention and more preferred are VH region sequences as defined in SEQ ID NO: 2012, 2020, 2028, 2036, 2044, 26, 34, 42, 50, 58, 66, 74, 82, 90, 98, 100, 108, and 116. Further examples are SEQ ID NOs: 288, 296, 304, 312, 320, 478, 486, 494, 502, 510, 656, 664, 672, 680, 688, 846, 854, 862, 870, 878, 1032, 1040, 1048, 1056, 1064, 1222, 1230, 1238, 1246, 1254, 1400, 1408, 1416, 1424, 1432, 1590, 1598, 1606, 1614, 1622, 1780, 1788, 1796, 1804, and 1812.

[151] Also in accordance with the invention and more preferred are VL region sequences as defined in SEQ ID NO: 2013, 2021, 2029, 2037, 2045, 27, 35, 43, 51, 59, 67, 75, 83, 91, 99, 101, 109, and 117. Further examples are SEQ ID NOs: 289, 297, 305, 313, 321, 479, 487, 495, 503, 511, 657, 665, 673, 681, 689, 847, 855, 863, 871, 879, 1033, 1041, 1049, 1057, 1065, 1223, 1231, 1239, 1247, 1255, 1401, 1409, 1417, 1425, 1433, 1591, 1599, 1607, 1615, 1623, 1781, 1789, 1797, 1805, and 1813.

[152] Also in accordance with the invention and preferred are any combinations of the foregoing particularly preferred VH and VL region sequences. Preferred are the following VH and VL combinations as defined by SEQ ID NOs: 2012 and 2013; 2020 and 2021; 2028 and 2029; 2036 and 2037; 2044 and 2045; 26 and 27; 34 and 35; 42 and 43; 50 and 51; 58 and 59; 66 and 67; 74 and 75; 82 and 83; 90 and 91; 98 and 99; 100 and 101; 108 and 109; and 116 and 117. Further examples are SEQ ID NOs: 288 and 289; 296 and 297; 304 and 305; 312 and 313; 320 and 321; 478 and 479; 486 and 487; 494 and 495; 502 and 503; 510 and 511; 656 and 657; 664 and 665; 672 and 673; 680 and 681; 688 and 689; 846 and 847; 854 and 855; 862 and 863; 870 and 871; 878 and 879; 1032 and 1033; 1040 and 1041; 1048 and 1049; 1056 and 1057; 1064 and 1065; 1222 and 1223; 1230 and 1231; 1238 and 1239; 1246 and 1247; 1254 and 1255; 1400 and 1401; 1408 and 1409; 1416 and 1417; 1424 and 1425; 1432 and 1433; 1590 and 1591; 1598 and 1599; 1606 and 1607; 1614 and 1615; 1622 and 1623; 1780 and 1781; 1788 and 1789; 1796 and 1797; 1804 and 1805; and 1812 and 1813.

[153] In accordance with the invention, said binding domain of the polypeptide or

polypeptide construct of the invention that binds to an extracellular epitope of the human CD3 ϵ chain comprises or consists of a VH region sequence selected from SEQ ID NOs: 2012, 2020, 2028, 2036, 2044, 26, 34, 42, 50, 58, 66, 74, 82, 90, 98, 100, 108, 116, 288, 296, 304, 312, 320, 478, 486, 494, 502, 510, 656, 664, 672, 680, 688, 846, 854, 862, 870, 878, 1032, 1040, 1048, 1056, 1064, 1222, 1230, 1238, 1246, 1254, 1400, 1408, 1416, 1424, 1432, 1590, 1598, 1606, 1614, 1622, 1780, 1788, 1796, 1804, 1812, 1856, 1860, 1862, 1864, 1872, 1884, 1894, 1896, 1898, 1900, 1902, 1904, 1906, 1914, 1916, 1918, 1920, 1922, 1924, 1926, 1928, 1930, 1932, 1934, 1936, 1938, 1940, 1942, 1944, 1946, 1948, 1950, 132, 140, 148, 156, and 164; and/or a VL region sequence selected from SEQ ID NOs: 2013, 2021, 2029, 2037, 2045, 27, 35, 43, 51, 59, 67, 75, 83, 91, 99, 101, 109, and 117, 289, 297, 305, 313, 321, 479, 487, 495, 503, 511, 657, 665, 673, 681, 689, 847, 855, 863, 871, 879, 1033, 1041, 1049, 1057, 1065, 1223, 1231, 1239, 1247, 1255, 1401, 1409, 1417, 1425, 1433, 1591, 1599, 1607, 1615, 1623, 1781, 1789, 1797, 1805, 1813, 1867, 1869, 1871, 1875, 1877, 1899, 1901, 1903, 1905, 1907, 1919, 1921, 1923, 1925, 1927, 1929, 1931, 1933, 1935, 1937, 1939, 1941, 1943, 1961, 1963, 1965, 1967, 1969, 1971, 1975, 1991, 1993, 1995, 1997, 2005, 133, 141, 149, 157, and 165.

[154] According to the invention, it is preferred that the polypeptide or polypeptide construct comprises: a binding domain binding to an extracellular epitope of the human CD3 ϵ chain comprising or consisting of i) a VH region and ii) a VL region, wherein said VH and VL region of i) and ii) is selected from the VH and VL region combination as defined in SEQ ID NOs: 124 and 125, 172 and 173, 362 and 363, 552 and 553, 730 and 731, 928 and 929, 1106 and 1107, 1296 and 1297, 1474 and 1475, 1664 and 1665, and 1854 and 1855, wherein said one amino acid substitution or a combination thereof in said VH and/or VL region sequence results in a VH and/or a VL region sequence having the amino acid residue:

- i. I at position 34, A at position 65, V at position 81, A at position 99, A at position 101, S at position 106 in the VH region sequence, I at position 20, K at position 40, S at position 69, and S at position 102 in the VL region sequence;
M at position 45, A at position 65, L at position 81, A at position 101, T at position 106 in the VH region sequence, I at position 20, K at position 40, S at position 69 and S at position 102 in the VL region sequence;
M at position 45, A at position 65, L at position 81, A at position 101, S at position 106, F at position 112 in the VH region sequence, I at position 20, I at position 38, K at position 40, E at position 69, S at position 102 and Y at position 93 in the VL region sequence;
- I at position 34, E at position 39, A at position 65, N at position 101, A at position 102, T at position 106, F at position 112 in the VH region sequence, K at position 40 and S at position 102 in the VL region sequence;

I at position 34, E at position 64, A at position 65, A at position 99, A at position 101, T at position 106 in the VH region sequence, K at position 40, A at position 91 and S at position 102 in the VL region sequence;

I at position 34, A at position 65, V at position 81, A at position 99, A at position 101, E at position 102, I at position 104, T at position 106 in the VH region sequence, I at position 20, K at position 40, S at position 69 and S at position 102 in the VL region sequence;

E at position 64, A at position 65, G at position 68, V at position 81, A at position 101, S at position 106 in the VH region sequence, I at position 20, S at position 69 and S at position 102 in the VL region sequence;

I at position 34, E at position 64, A at position 65, A at position 101, T at position 106, F at position 112 in the VH region sequence, K at position 40, A at position 91 and S at position 102 in the VL region sequence;

I at position 34, E at position 64, A at position 65, A at position 101, S at position 106, F at position 112 in the VH region sequence, K at position 40, A at position 91 and S at position 102 in the VL region sequence;

I at position 34, E at position 64, A at position 65, V at position 81, A at position 99, A at position 101, S at position 106 in the VH region sequence, I at position 20, K at position 40, S at position 69, S at position 102 and Y at position 93 in the VL region sequence;

I at position 34, A at position 65, A at position 101, S at position 106, F at position 112 in the VH region sequence, K at position 40, A at position 91 and S at position 102 in the VL region sequence;

M at position 45, E at position 64, A at position 65, L at position 81, A at position 101, T at position 106 in the VH region sequence, I at position 20, I at position 38, K at position 40, E at position 69 and S at position 102 in the VL region sequence;

S at position 30, M at position 45, A at position 65, G at position 68, V at position 81, A at position 101, T at position 106, F at position 112 in the VH region sequence, K at position 40, S at position 69 and Y at position 93 in the VL region sequence; and

S at position 30, M at position 45, E at position 64, A at position 65, G at position 68, V at position 81, A at position 101, S at position 106 in the VH region sequence, K at position 40 and S at position 69 in the VL region sequence;

ii. E at position 64, A at position 65, G at position 68, V at position 81, N at position 101, E at position 102, I at position 104, T at position 106 in the VH region sequence, I at position 20, S at position 69 and S at position 102 in the VL region sequence;

A at position 65, G at position 68, V at position 81, N at position 101, E at position 102, I at position 104, S at position 106 in the VH region sequence, I at position 20, S

at position 69 and S at position 102 in the VL region sequence;

I at position 34, A at position 65, A at position 99, A at position 101, T at position 106 in the VH region sequence, K at position 40, A at position 91 and S at position 102 in the VL region sequence; and

5 S at position 30, E at position 39, E at position 64, A at position 65, V at position 81, A at position 101, E at position 102, I at position 104, T at position 106 in the VH region sequence, M at position 20, K at position 40 and E at position 69 in the VL region sequence;

iii. A at position 101 in the VH region sequence;

10 iv. V at position 81, A at position 99 in the VH region sequence, I at position 20, K at position 40, S at position 69 and S at position 102 in the VL region sequence;

I at position 34, V at position 81 in the VH region sequence, I at position 20, K at position 40 and S at position 102 in the VL region sequence;

15 I at position 34 in the VH region sequence, I at position 20, K at position 40 and S at position 102 in the VL region sequence;

I at position 34, E at position 39, V at position 81 in the VH region sequence, I at position 20, K at position 40 and S at position 102 in the VL region sequence;

v. I at position 34, V at position 81 in the VH region sequence, and K at position 40 in the VL region sequence;

20 M at position 45 in the VH region sequence, I at position 20, K at position 40 and S at position 102 in the VH region sequence;

I at position 34, A at position 65, A at position 101 and S at position 106 in the VH region sequence;

25 I at position 20, K at position 40, S at position 69 and S at position 102 in the VL region sequence;

F at position 34 and V at position 81 in the VH region sequence;

M at position 45 in the VH region sequence, K at position 40 and S at position 102 in the VL region sequence;

30 D at position 39 in the VH region sequence, I at position 20, K at position 40 and S at position 102 in the VL region sequence;

I at position 34 and V at position 81 in the VH region sequence;

E at position 39 in the VH region sequence, I at position 20, K at position 40 and S at position 102 in the VL region sequence;

35 M at position 45 in the VH region sequence and K at position 40 in the VL region sequence;

I at position 34, A at position 65, V at position 81, A at position 99, A at position 101 and S at position 106 in the VH region sequence; or

vi. D at position 39 in the VH region sequence, _I at position 20, _R at position 40 and _S at position 102 in the VL region sequence;

I at position 34 in the VH region sequence;

K at position 40 in the VL region sequence;

5 D at position 39_in the VH region sequence, K at position 40 and _S at position 102 in the VL region sequence;

I at position 20 and _S at position 102 in the VH region sequence;

K at position 39 in the VH region sequence;

10 E at position 39 in the VH region sequence, _K at position 40_and S at position 102 in the VL region sequence;

E at position 39 in the VH region sequence, _I at position 20, _R at position 40_and S at position 102 in the VL region sequence;

D at position 39_in the VH region sequence, _R at position 40_and S at position 102 in the VL region sequence;

15 V at position 81 in the VH region sequence;

D at position 39 in the VH region sequence and _K at position 40 in the VL region sequence;

F at position 112 in the VH region sequence;

20 F at position 112 in the VH region sequence and _I at position 38 in the VL region sequence;

E at position 39 in the VH region sequence and K at position 40 in the VL region sequence;

V at position 34 in the VH region sequence.

25 The above recited amino acid residues are present at the given position(s) in the CD3epsilon binding domain according to the invention. In case one of the VH and/or VL region sequences that are to be changed (the VH region of i) and the VL region of ii)), i.e. the base VH and/or VL region sequence, already contain one of the above recited amino acid residues at a given position, it follows that these cannot be changed since the respective amino acid residue is already present in the VH region and/or VL region of i) and/or ii).

30 More preferred is that the CD3epsilon binding domain comprises or consists of a combination of VH and VL region of i) and ii) selected from the group consisting of SEQ ID NOs: 124 and 125, 362 and 363, 730 and 731, 928 and 929, 1106 and 1107, 1296 and 1297, 1474 and 1475, 1664 and 1665, and 1854 and 1855. Even more preferred is that the CD3epsilon binding domain comprises or consists of a combination of VH and VL region of i) and ii) selected from the group consisting of SEQ ID NOs: 124 and 125, 730 and 731, 1664 and 1665, and 1854 and 1855. In a yet even more preferred embodiment, the CD3epsilon

binding domain comprises or consists of a combination of VH and VL region of i) and ii) selected from the group consisting of SEQ ID NOs: 730 and 731, 1664 and 1665, and 1854 and 1855. Most preferred is that said CD3epsilon binding domain comprises or consists of a combination of VH and VL region of i) and ii) of SEQ ID NOs: 1854 and 1855, respectively.

- 5 As evident from the example section, the above recited amino acid residues at the given position(s) have a favorable effect on an increase of the temperature stability that is measured by the well know and also herein described method of DSF (Differential Scanning Fluorimetry; cf. e.g., Wen et al., "Nano differential scanning fluorimetry for comparability studies of therapeutic proteins", Analytical Biochemistry, Volume 593, 2020, 113581, ISSN 0003-2697; Dart, M. L., et al. (2018). "Homogeneous Assay for Target Engagement Utilizing Bioluminescent Thermal Shift". ACS medicinal chemistry letters, 9(6), 546–551) when introduced in the above recited VH and VL sequences of i) and ii). More specifically, the amino acid residues at the given positions recited in sections i. and iv. exhibit an increase in temperature stability of 6 °C or more as compared to the value measured for the unmodified sequence, i.e. the respective base VH and VL sequence. Section ii. and v. exhibit an increase in temperature stability of 3 °C or more as compared to the value measured for the unmodified sequence, i.e. the respective base VH and VL sequence, whereas sections iii. and vi. exhibit an increase in temperature stability of 1 °C or more as compared to the value measured for the unmodified sequence, i.e. the respective base VH and VL sequence.
- 15
- 20 Preferably, the amino acid residues at the given position(s) in section i. ii., iv., and/or v. are present in the CD3epsilon binding domain according to this embodiment. More preferred is that the amino acid residues at the given position(s) in section i. and/or iv. are present in the CD3epsilon binding domain according to the invention. This preference also applies to the preferred embodiments recited in the following. As outlined herein, it is also preferred that the VH and VL region is linked by a linker, preferably a peptide linker most preferred a G₄S or a G₄Q linker, preferably said G₄S or a G₄Q linker is repeated three times, i.e. it is a (G₄S)₃ or a (G₄Q)₃ linker.
- 25

[155] According to the invention, it relates to a polypeptide or polypeptide construct comprising: a binding domain binding to an extracellular epitope of the human CD3ε chain comprising or consisting of a VH region and a VL region, wherein

30

- a) the VH region comprises or consist of the sequence as defined in SEQ ID NO: 1854 and the VL region comprises or consists of the sequence as defined in SEQ ID NO: 1855; and wherein the VH and/or VL region sequence comprise the amino acid substitution(s) selected from:
- 35
- i. M34I, S65A, A81V, V99A, H101A, N106S in the VH region sequence (resulting VH sequence as defined in SEQ ID NO: 2012), L20I, Q40K, L69S,

and G102S in the VL region sequence (resulting VL sequence as defined in SEQ ID NO: 2013);

L45M, S65A, A81L, H101A, N106T in the VH region sequence (SEQ ID NO: 2036), L20I, Q40K, L69S, and G102S in the VL region sequence (SEQ ID NO: 2037);

L45M, S65A, A81L, H101A, N106S, W112F in the VH region sequence (SEQ ID NO: 2028), L20I, V38I, Q40K, L69E, G102S and W93Y in the VL region sequence (SEQ ID NO: 2029);

M34I, Q39E, S65A, H101N, G102A, N106T, W112F in the VH region sequence (SEQ ID NO: 2044), Q40K and G102S in the VL region sequence (SEQ ID NO: 2045);

M34I, D64E, S65A, V99A, H101A, N106T in the VH region sequence (SEQ ID NO: 34), Q40K, V91A and G102S in the VL region sequence (SEQ ID NO: 35);

M34I, S65A, A81V, V99A, H101A, G102E, F104I, N106T in the VH region sequence (SEQ ID NO: 90), L20I, Q40K, L69S, and G102S in the VL region sequence (SEQ ID NO: 91);

D64E, S65A, D68G, A81V, H101A, N106S in the VH region sequence (SEQ ID NO: 100), L20I, L69S, and G102S in the VL region sequence (SEQ ID NO: 101);

M34I, D64E, S65A, H101A, N106T, W112F in the VH region sequence (SEQ ID NO: 58), Q40K, V91A and G102S in the VL region sequence (SEQ ID NO: 59);

M34I, D64E, S65A, H101A, N106S, W112F in the VH region sequence (SEQ ID NO: 50), Q40K, V91A and G102S in the VL region sequence (SEQ ID NO: 51);

M34I, D64E, S65A, A81V, V99A, H101A, N106S in the VH region sequence (SEQ ID NO: 98), L20I, Q40K, L69S, G102S and W93Y in the VL region sequence (SEQ ID NO: 99);

M34I, S65A, H101A, N106S, W112F in the VH region sequence (SEQ ID NO: 42), Q40K, V91A and G102S in the VL region sequence (SEQ ID NO: 43);

L45M, D64E, S65A, A81L, H101A, N106T in the VH region sequence (SEQ ID NO: 116), L20I, V38I, Q40K, L69E and G102S in the VL region sequence (SEQ ID NO: 117);

N30S, L45M, S65A, D68G, A81V, H101A, N106T, W112F in the VH region sequence (SEQ ID NO: 82), Q40K, L69S and W93Y in the VL region sequence (SEQ ID NO: 83); and

- N30S, L45M, D64E, S65A, D68G, A81V, H101A, N106S in the VH region sequence (SEQ ID NO: 74), Q40K and L69S in the VL region sequence (SEQ ID NO: 75);
- 5 ii. D64E, S65A, D68G, A81V, H101N, G102E, F104I, N106T in the VH region sequence (SEQ ID NO: 2020), L20I, L69S, and G102S in the VL region sequence (SEQ ID NO: 2021);
 S65A, D68G, A81V, H101N, G102E, F104I, N106S in the VH region sequence (SEQ ID NO: 108), L20I, L69S, and G102S in the VL region sequence (SEQ ID NO: 109);
- 10 M34I, S65A, V99A, H101A, N106T in the VH region sequence (SEQ ID NO: 26), Q40K, V91A and G102S in the VL region sequence (SEQ ID NO: 27);
 and
 N30S, Q39E, D64E, S65A, A81V, H101A, G102E, F104I, N106T in the VH region sequence (SEQ ID NO: 66), L20M, Q40K and L69E in the VL region sequence (SEQ ID NO: 67);
- 15 iii. H101A in the VH region sequence (SEQ ID NO: 2560);
 iv. A81V, V99A_in the VH region sequence, L20I, Q40K, L69S and G102S in the VL region sequence;
 M34I,_A81V in the VH region sequence (SEQ ID NO: 1898),_L20I,_Q40K and_G102S in the VL region sequence (SEQ ID NO: 1899);
- 20 M34I in the VH region sequence (SEQ ID NO: 1904), L20I,_Q40K_and G102S in the VL region sequence (1905);
 M34I,_Q39E,_A81V in the VH region sequence (SEQ ID NO: 1906), L20I,_Q40K and_G102S in the VL region sequence (SEQ ID NO: 1907);
- 25 v. M34I,_A81V in the VH region sequence (SEQ ID NO: 1900), and Q40K in the VL region sequence (SEQ ID NO: 1901);
 L45M in the VH region sequence (SEQ ID NO: 1866),_L20I,_Q40K and_G102S in the VH region sequence (SEQ ID NO: 1867);
 M34I,_S65A,_H101A and_N106S in the VH region sequence;
- 30 L20I,_Q40K,_L69S and_G102S in the VL region sequence;
 M34F_and A81V in the VH region sequence (SEQ ID NO: 1884);
 L45M in the VH region sequence (SEQ ID NO: 1870), Q40K and_G102S in the VL region sequence (SEQ ID NO: 1871);
- 35 Q39D in the VH region sequence (SEQ ID NO: 1918), L20I,_Q40K and G102S in the VL region sequence (SEQ ID NO: 1919);
 M34I_and A81V in the VH region sequence (SEQ ID NO: 1869);
 Q39E in the VH region sequence (SEQ ID NO:_1932), L20I,_Q40K

and_G102S in the VL region sequence (SEQ ID NO: 1933);

L45M in the VH region sequence (SEQ ID NO: 1868),_and_Q40K in the VL region sequence (SEQ ID NO: 1869);

M34I,_S65A,_A81V,_V99A,_H101A_and N106S in the VH region sequence;
or

vi. Q39D in the VH region sequence (SEQ ID NO: 1928),_L20I,_Q40R and_G102S in the VL region sequence (SEQ ID NO: 1929);

M34I in the VH region sequence (SEQ ID NO: 1892);

Q40K in the VL region sequence (SEQ ID NO: 1974);

Q39D_in the VH region sequence (SEQ ID NO: 1922), Q40K and_G102S in the VL region sequence (SEQ ID NO: 1923);

L20I and_G102S in the VH region sequence;

Q39K in the VH region sequence (SEQ ID NO: 1944);

Q39E in the VH regions sequence (SEQ ID NO: 1938),_Q40K_and G102S in the VL region sequence (SEQ ID NO: 1939);

Q39E in the VH region sequence (SEQ ID NO: 1934),_L20I,_Q40R_and G102S in the VL region sequence (SEQ ID NO: 1935);

Q39D_in the VH region sequence (SEQ ID NO: 1926),_Q40R_and G102S in the VL region sequence (SEQ ID NO: 1926);

A81V in the VH region sequence (SEQ ID NO: 1862);

Q39D in the VH region sequence (SEQ ID NO: 1920) and_Q40K in the VL region sequence (SEQ ID NO: 1921);

W112F in the VH region sequence (SEQ ID NO: 1958);

W112F in the VH region sequence (SEQ ID NO: 1960) and_V38I in the VL region sequence (SEQ ID NO: 1961);

Q39E in the VH region sequence (SEQ ID NO: 1936)_and_Q40K in the VL region sequence (SEQ ID NO: 1937);

M34V in the VH region sequence (SEQ ID NO: 1914);

b) the VH region comprises or consist of the sequence as defined in SEQ ID NO: 730 and the VL region comprises or consists of the sequence as defined in SEQ ID NO: 731; and wherein the VH and/or VL region sequence comprise the amino acid substitution(s) selected from:

i. M34I, S65A, A81V, V99A, H101A, N106S in the VH region sequence (resulting VH sequence as defined in SEQ ID NO: 846), L20I, Q40K, L69S, and G102S in the VL region sequence (resulting VL sequence as defined in SEQ ID NO: 847);

L45M, S65A, A81L, H101A, N106T in the VH region sequence (SEQ ID NO:

- 870), L20I, Q40K, L69S, and G102S in the VL region sequence (SEQ ID NO: 871);
- L45M, S65A, A81L, H101A, N106S, W112F in the VH region sequence (SEQ ID NO: 862), L20I, V38I, Q40K, L69E, G102S and W93Y in the VL region sequence (SEQ ID NO: 863);
- M34I, Q39E, S65A, H101N, G102A, N106T, W112F in the VH region sequence (SEQ ID NO: 878), Q40K and G102S in the VL region sequence (SEQ ID NO: 879);
- M34I, D64E, S65A, V99A, H101A, N106T in the VH region sequence, Q40K, V91A and G102S in the VL region sequence;
- M34I, S65A, A81V, V99A, H101A, G102E, F104I, N106T in the VH region sequence, L20I, Q40K, L69S, and G102S in the VL region sequence;
- D64E, S65A, A81V, H101A, N106S in the VH region sequence, L20I, L69S, and G102S in the VL region sequence;
- M34I, D64E, S65A, H101A, N106T, W112F in the VH region sequence, Q40K, V91A and G102S in the VL region sequence;
- M34I, D64E, S65A, H101A, N106S, W112F in the VH region sequence, Q40K, V91A and G102S in the VL region sequence;
- M34I, D64E, S65A, A81V, V99A, H101A, N106S in the VH region sequence, L20I, Q40K, L69S, G102S and W93Y in the VL region sequence;
- M34I, S65A, H101A, N106S, W112F in the VH region sequence, Q40K, V91A and G102S in the VL region sequence;
- L45M, D64E, S65A, A81L, H101A, N106T in the VH region sequence, L20I, V38I, Q40K, L69E and G102S in the VL region sequence;
- N30S, L45M, S65A, A81V, H101A, N106T, W112F in the VH region sequence, Q40K, L69S and W93Y in the VL region sequence; and
- N30S, L45M, D64E, S65A, A81V, H101A, N106S in the VH region sequence, Q40K and L69S in the VL region sequence;
- ii. D64E, S65A, A81V, H101N, G102E, F104I, N106T in the VH region sequence (SEQ ID NO: 854), L20I, L69S, and G102S in the VL region sequence (SEQ ID NO: 855);
- S65A, A81V, H101N, G102E, F104I, N106S in the VH region sequence, L20I, L69S, and G102S in the VL region sequence;
- M34I, S65A, V99A, H101A, N106T in the VH region sequence, Q40K, V91A and G102S in the VL region sequence; and
- N30S, Q39E, D64E, S65A, A81V, H101A, G102E, F104I, N106T in the VH region sequence, L20M, Q40K and L69E in the VL region sequence;

- iii. H101A in the VH region sequence;
- iv. A81V, V99A_in the VH region sequence, L20I, Q40K, L69S and G102S in the VL region sequence;
 M34I,_A81V in the VH region sequence (SEQ ID NO: 774),_L20I,_Q40K and_G102S in the VL region sequence (SEQ ID NO: 775);
 M34I in the VH region sequence (SEQ ID NO: 780), L20I,_Q40K_and G102S in the VL region sequence (781);
 M34I,_Q39E,_A81V in the VH region sequence (SEQ ID NO: 782), L20I,_Q40K and_G102S in the VL region sequence (SEQ ID NO: 783);
- 5 v. M34I,_A81V in the VH region sequence (SEQ ID NO: 776), and Q40K in the VL region sequence (SEQ ID NO: 777);
 L45M in the VH region sequence (SEQ ID NO: 742),_L20I,_Q40K and_G102S in the VH region sequence (SEQ ID NO: 743);
 M34I,_S65A,_H101A and_N106S in the VH region sequence;
 15 L20I,_Q40K,_L69S and_G102S in the VL region sequence;
 M34F_and A81V in the VH region sequence (SEQ ID NO: 760);
 L45M in the VH region sequence (SEQ ID NO: 746), Q40K and_G102S in the VL region sequence (SEQ ID NO: 747);
 Q39D in the VH region sequence (SEQ ID NO: 794), L20I,_Q40K and G102S
 20 in the VL region sequence (SEQ ID NO: 795);
 M34I_and A81V in the VH region sequence (SEQ ID NO: 772);
 Q39E in the VH region sequence (SEQ ID NO: 808), L20I,_Q40K and_G102S in the VL region sequence (SEQ ID NO: 809);
 L45M in the VH region sequence (SEQ ID NO: 744)_and_Q40K in the VI
 25 region sequence (SEQ ID NO: 745);
 M34I,_S65A,_A81V,_V99A,_H101A_and N106S in the VH region sequence;
 or
- vi. Q39D in the VH region sequence (SEQ ID NO: 796),_L20I,_Q40R and_G102S in the VL region sequence (SEQ ID NO: 797);
 30 M34I in the VH region sequence (SEQ ID NO: 768);
 Q40K in the VL region sequence (SEQ ID NO: 891);
 Q39D_in the VH region sequence (SEQ ID NO: 800), Q40K and_G102S in the VL region sequence (SEQ ID NO: 801);
 L20I and_G102S in the VH region sequence;
 35 Q39K in the VH region sequence (SEQ ID NO: 820);
 Q39E in the VH region sequence (SEQ ID NO: 814),_Q40K_and G102S in the VL region sequence (SEQ ID NO: 815);

Q39E in the VH region sequence (SEQ ID NO: 810),_L20I,_Q40R_and
G102S in the VL region sequence (SEQ ID NO: 811);

Q39D_in the VH region sequence (SEQ ID NO: 804),_Q40R_and G102S in
the VL region sequence (SEQ ID NO: 805);

5 A81V in the VH region sequence (SEQ ID NO: 738);

Q39D in the VH region sequence (SEQ ID NO: 798) and_Q40K in the VL
region sequence (SEQ ID NO: 799);

W112F in the VH region sequence (SEQ ID NO: 834);

10 W112F in the VH region sequence (SEQ ID NO: 836) and_V38I in the VL
region sequence (SEQ ID NO: 837);

Q39E in the VH region sequence (SEQ ID NO: 812)_and_Q40K in the VL
region sequence (SEQ ID NO: 813);

M34V in the VH region sequence (SEQ ID NO: 790)

15 c) the VH region comprises or consist of the sequence as defined in SEQ ID NO: 1664
and the VL region comprises or consists of the sequence as defined in SEQ ID NO:
1665; and wherein the VH and/or VL region sequence comprise the amino acid
substitution(s) selected from:

20 i. M34I, S65A, A81V, V99A, H101A, N106S in the VH region sequence
(resulting VH sequence as defined in SEQ ID NO: 1780), L20I, Q40K, L69S,
and G102S in the VL region sequence (resulting VL sequence as defined in
SEQ ID NO: 1781);

L45M, S65A, A81L, H101A, N106T in the VH region sequence (SEQ ID NO:
1804), L20I, Q40K, L69S, and G102S in the VL region sequence (SEQ ID NO:
1805);

25 L45M, S65A, A81L, H101A, N106S, W112F in the VH region sequence (SEQ
ID NO: 1796), L20I, V38I, Q40K, L69E, G102S and W93Y in the VL region
sequence (SEQ ID NO: 1797);

M34I, Q39E, S65A, H101N, G102A, N106T, W112F in the VH region
sequence (SEQ ID NO: 1812), Q40K and G102S in the VL region sequence
30 (SEQ ID NO: 1813);

M34I, D64E, S65A, V99A, H101A, N106T in the VH region sequence, Q40K
and G102S in the VL region sequence;

M34I, S65A, A81V, V99A, H101A, G102E, F104I, N106T in the VH region
sequence, L20I, Q40K, L69S, and G102S in the VL region sequence;

35 D64E, S65A, D68G, A81V, H101A, N106S in the VH region sequence, L20I,
L69S, and G102S in the VL region sequence;

M34I, D64E, S65A, H101A, N106T, W112F in the VH region sequence, Q40K

- and G102S in the VL region sequence;
M34I, D64E, S65A, H101A, N106S, W112F in the VH region sequence, Q40K
and G102S in the VL region sequence;
M34I, D64E, S65A, A81V, V99A, H101A, N106S in the VH region sequence,
5 L20I, Q40K, L69S, G102S and W93Y in the VL region sequence;
M34I, S65A, H101A, N106S, W112F in the VH region sequence, Q40K and
G102S in the VL region sequence;
L45M, D64E, S65A, A81L, H101A, N106T in the VH region sequence, L20I,
V38I, Q40K, L69E and G102S in the VL region sequence;
10 N30S, L45M, S65A, D68G, A81V, H101A, N106T, W112F in the VH region
sequence, Q40K, L69S and W93Y in the VL region sequence; and
N30S, L45M, D64E, S65A, D68G, A81V, H101A, N106S in the VH region
sequence, Q40K and L69S in the VL region sequence;
- ii. D64E, S65A, D68G, A81V, H101N, G102E, F104I, N106T in the VH region
15 sequence (SEQ ID NO: 1788), L20I, L69S, and G102S in the VL region
sequence (SEQ ID NO: 1789);
S65A, D68G, A81V, H101N, G102E, F104I, N106S in the VH region
sequence, L20I, L69S, and G102S in the VL region sequence;
M34I, S65A, V99A, H101A, N106T in the VH region sequence, Q40K and
20 G102S in the VL region sequence; and
N30S, Q39E, D64E, S65A, A81V, H101A, G102E, F104I, N106T in the VH
region sequence, L20M, Q40K and L69E in the VL region sequence;
- iii. H101A in the VH region sequence;
- iv. A81V, V99A in the VH region sequence, L20I, Q40K, L69S and G102S in the
25 VL region sequence;
M34I, A81V in the VH region sequence (SEQ ID NO: 1708), L20I, Q40K
and G102S in the VL region sequence (SEQ ID NO: 1709);
M34I in the VH region sequence (SEQ ID NO: 1714), L20I, Q40K and
G102S in the VL region sequence (1715);
- 30 M34I, Q39E, A81V in the VH region sequence (SEQ ID NO: 1716),
L20I, Q40K and G102S in the VL region sequence (SEQ ID NO: 1717);
- v. M34I, A81V in the VH region sequence (SEQ ID NO: 1710), and Q40K in the
VL region sequence (SEQ ID NO: 1711);
L45M in the VH region sequence (SEQ ID NO: 1676), L20I, Q40K
35 and G102S in the VH region sequence (SEQ ID NO: 1677);
M34I, S65A, H101A and N106S in the VH region sequence;
L20I, Q40K, L69S and G102S in the VL region sequence;

- M34F_and A81V in the VH region sequence (SEQ ID NO: 1694);
 L45M in the VH region sequence (SEQ ID NO: 1680), Q40K and_G102S in
 the VL region sequence (SEQ ID NO: 1681);
 Q39D in the VH region sequence (SEQ ID NO: 1728), L20I,_Q40K and
 5 G102S in the VL region sequence (SEQ ID NO: 1729);
 M34I_and A81V in the VH region sequence (SEQ ID NO: 1706);
 Q39E in the VH region sequence (SEQ ID NO:_1742), L20I,_Q40K
 and_G102S in the VL region sequence (SEQ ID NO: 1743);
 L45M in the VH region sequence (SEQ ID NO:_1678)_and_Q40K in the VI
 10 region sequence (SEQ ID NO: 1679);
 M34I,_S65A,_A81V,_V99A,_H101A_and N106S in the VH region sequence;
 or
 vi. Q39D in the VH region sequence (SEQ ID NO: 1730),_L20I,_Q40R
 and_G102S in the VL region sequence (SEQ ID NO: 1731);
 15 M34I in the VH region sequence (SEQ ID NO: 1702);
 Q40K in the VL region sequence (SEQ ID NO: 1755);
 Q39D_in the VH region sequence (SEQ ID NO: 1734), Q40K and_G102S in
 the VL region sequence (SEQ ID NO: 1735);
 L20I and_G102S in the VH region sequence;
 20 Q39K in the VH region sequence (SEQ ID NO: 1754);
 Q39E in the VH regions sequence (SEQ ID NO: 1748),_Q40K_and G102S in
 the VL region sequence (SEQ ID NO: 1749);
 Q39E in the VH region sequence (SEQ ID NO: 1744),_L20I,_Q40R_and
 G102S in the VL region sequence (SEQ ID NO: 1745);
 25 Q39D_in the VH region sequence (SEQ ID NO: 1738),_Q40R_and G102S in
 the VL region sequence (SEQ ID NO: 1739);
 A81V in the VH region sequence (SEQ ID NO: 1672);
 Q39D in the VH region sequence (SEQ ID NO: 1732) and_Q40K in the VL
 region sequence (SEQ ID NO: 1733);
 30 W112F in the VH region sequence (SEQ ID NO: 1768);
 W112F in the VH region sequence (SEQ ID NO: 1770) and_V38I in the VL
 region sequence (SEQ ID NO: 1771);
 Q39E in the VH region sequence (SEQ ID NO: 1746)_and_Q40K in the VL
 region sequence (SEQ ID NO: 1747);
 35 M34V in the VH region sequence (SEQ ID NO: 1724); or
 d) the VH region comprises or consist of the sequence as defined in SEQ ID NO: 124
 and the VL region comprises or consists of the sequence as defined in SEQ ID NO:

125; and wherein the VH and/or VL region sequence comprise the amino acid substitution(s) selected from:

- i. Q65A, A81V, V99A, H101A, N106S in the VH region sequence (resulting VH sequence as defined in SEQ ID NO: 132), L20I, Q40K, L69S, and G102S in the VL region sequence (resulting VL sequence as defined in SEQ ID NO: 133);
 L45M, Q65A, A81L, H101A, N106T in the VH region sequence (SEQ ID NO: 156), L20I, Q40K, L69S, and G102S in the VL region sequence (SEQ ID NO: 157);
 L45M, Q65A, A81L, H101A, N106S, W112F in the VH region sequence (SEQ ID NO: 148), L20I, V38I, Q40K, L69E, G102S and W93Y in the VL region sequence (SEQ ID NO: 149);
 Q39E, Q65A, H101N, N106T, W112F in the VH region sequence (SEQ ID NO: 164), Q40K and G102S in the VL region sequence (SEQ ID NO: 165);
 D64E, Q65A, V99A, H101A, N106T in the VH region sequence, Q40K, T91A and G102S in the VL region sequence;
 Q65A, A81V, V99A, H101A, A102E, F104I, N106T in the VH region sequence, L20I, Q40K, L69S, and G102S in the VL region sequence;
 D64E, Q65A, D68G, A81V, H101A, N106S in the VH region sequence, L20I, L69S, and G102S in the VL region sequence;
 D64E, Q65A, H101A, N106T, W112F in the VH region sequence, Q40K and G102S in the VL region sequence;
 D64E, Q65A, H101A, N106S, W112F in the VH region sequence, Q40K and G102S in the VL region sequence;
 D64E, Q65A, A81V, V99A, H101A, N106S in the VH region sequence, L20I, Q40K, L69S, G102S and W93Y in the VL region sequence;
 Q65A, H101A, N106S, W112F in the VH region sequence, Q40K and G102S in the VL region sequence;
 L45M, D64E, Q65A, A81L, H101A, N106T in the VH region sequence, L20I, V38I, Q40K, L69E and G102S in the VL region sequence;
 N30S, L45M, Q65A, D68G, A81V, H101A, N106T, W112F in the VH region sequence, Q40K, L69S and W93Y in the VL region sequence; and
 N30S, L45M, D64E, Q65A, D68G, A81V, H101A, N106S in the VH region sequence, Q40K and L69S in the VL region sequence;
- ii. D64E, Q65A, D68G, A81V, H101N, A102E, F104I, N106T in the VH region sequence (SEQ ID NO: 140), L20I, L69S, and G102S in the VL region sequence (SEQ ID NO: 141);

- Q65A, D68G, A81V, H101N, A102E, F104I, N106S in the VH region sequence, L20I, L69S, and G102S in the VL region sequence;
 Q65A, V99A, H101A, N106T in the VH region sequence, Q40K and G102S in the VL region sequence; and
- 5 N30S, Q39E, D64E, Q65A, A81V, H101A, A102E, F104I, N106T in the VH region sequence, L20M, Q40K and L69E in the VL region sequence;
- iii. H101A in the VH region sequence;
- iv. A81V, V99A_in the VH region sequence, L20I, Q40K, L69S and G102S in the VL region sequence;
- 10 A81V in the VH region sequence,_L20I,_Q40K and_G102S in the VL region sequence;
 L20I,_Q40K_and G102S in the VL region sequence;
 Q39E,_A81V in the VH region sequence, L20I,_Q40K and_G102S in the VL region sequence;
- 15 v. A81V in the VH region sequence, and Q40K in the VL region sequence;
 L45M in the VH region sequence,_L20I,_Q40K and_G102S in the VH region sequence;
 Q65A,_H101A and_N106S in the VH region sequence;
 L20I,_Q40K,_L69S and_G102S in the VL region sequence;
- 20 I34F_and A81V in the VH region sequence;
 L45M in the VH region sequence, Q40K and_G102S in the VL region sequence;
 Q39D in the VH region sequence, L20I,_Q40K and G102S in the VL region sequence;
- 25 Q39E in the VH region sequence, L20I,_Q40K and_G102S in the VL region sequence;
 L45M in the VH region sequence_and_Q40K in the VL region sequence;
 Q65A,_A81V,_V99A,_H101A_and N106S in the VH region sequence; or
- vi. Q39D in the VH region sequence,_L20I,_Q40R and_G102S in the VL region sequence;
- 30 Q40K in the VL region sequence;
 Q39D_in the VH region sequence, Q40K and_G102S in the VL region sequence;
 L20I and_G102S in the VH region sequence;
- 35 Q39K in the VH region sequence;
 Q39E in the VH region sequence,_Q40K_and G102S in the VL region sequence;

Q39E in the VH region sequence, _L20I, _Q40R_ and G102S in the VL region sequence;

Q39D_ in the VH region sequence, _Q40R_ and G102S in the VL region sequence);

A81V in the VH region sequence;

Q39D in the VH region sequence and _Q40K in the VL region sequence;

W112F in the VH region sequence;

W112F in the VH region sequence and _V38I in the VL region sequence;

Q39E in the VH region sequence_ and _Q40K in the VL region sequence;

M34V in the VH region sequence.

The alternatives a) to c) are preferred, more preferred is the alternative a) as recited above as CD3epsilon binding domain of the polypeptide or polypeptide construct of the invention. The above recited preferred linkers are also preferred for this embodiment, i.e (G₄S)₃ or G₄Q)₃.

[156]

[157] In accordance with the invention, the polypeptide or polypeptide construct the invention may have linkers, half-life extending peptides, and other structural moieties as disclosed in SEQ ID NOs: 1 to 19 and 2551. Details on nature and functions of these structures are found in the sequence table disclosed herein.

[158] The invention provides an embodiment wherein the polypeptide construct is in a format selected from the group consisting of scFv, and to the extent that a further binding domain is present (scFv)₂, diabodies and oligomers of any of the aforementioned formats. The term "is in a format" does not exclude that the construct can be further modified, e.g. by attachment or fusion to other moieties, as described herein. According to one embodiment of the polypeptide construct of the present invention, the domains comprising the herein described paratopes are in the format of an scFv. In an scFv, the VH region and the VL region are arranged in the order VH-VL or VL-VH (from N- to C-terminus). It is envisaged that the VH and the VL regions of the domain(s) are connected via a linker, preferably a peptide linker. In a preferred embodiment, the peptide linker is a G₄S, or G₄Q linker or repetitions thereof, such as preferably (G₄S)₃ (i.e. three repetitions of G₄S), or (G₄Q)₃ (i.e. three repetitions of G₄Q). According to one embodiment of the binding domain(s) comprising the herein described VH and the VL regions, the VH-region is positioned N-terminally of the linker, and the VL-region is positioned C-terminally of the linker. In other words, in one embodiment of the domains comprising the herein described paratopes, the scFv comprises from the N-terminus to the C-terminus: VH-linker-VL. It is furthermore envisaged that binding domain(s) (comprising the herein described paratopes) of the construct, in case the

polypeptide or polypeptide construct comprises at least one further binding domain in addition to said CD3 epsilon binding domain, are connected via a linker, preferably a peptide linker. The construct may e.g. comprise the domains in the order (from N-terminus to C-terminus) CD3 binding domain – linker – further binding domain. The inverse order (further binding domain(s) – linker – CD3 binding domain) is also possible and is the preferred orientation.

[159] The linkers are preferably peptide linkers, more preferably short peptide linkers. In accordance with the present invention, a “peptide linker” comprises an amino acid sequence which connects the amino acid sequences of one domain with another (variable and/or binding) domain (e.g. a variable domain or a binding domain) of the construct. An essential technical feature of such peptide linker is that it does not comprise any polymerization activity. Among the suitable peptide linkers are those described in U.S. Patents 4,751,180 and 4,935,233 or WO 88/09344. The peptide linkers can also be used to attach other domains or modules or regions (such as half-life extending domains) to the construct of the invention. Examples of useful peptide linkers are shown in SEQ ID NOs: 1 to 11 and 2551. In the present context, a “short” linker has between 2 and 50 amino acids, preferably between 3 and 35, between 4 and 30, between 5 and 25, between 6 and 20, or between 6 and 17 amino acids. The linker between two variable regions of one binding domain may have a different length (e.g. may be longer) than the linker between the two binding domains. For example, the linker between two variable regions of one binding domain may have a length between 7 and 15 amino acids, preferably between 9 and 13, and the linker between the two binding domains may have a length between 3 and 10 amino acids, preferably between 4 and 8. It is further envisaged that the peptide linkers are glycine/serine linkers, such as those depicted in SEQ ID NOs: 1 to 11 and 2551. Most of the amino acids in glycine/serine linkers are selected from glycine and serine.

[160] If a linker is used, this linker is preferably of a length and sequence to ensure that each of the first and second domains can, independently from one another, retain their differential binding specificities. For peptide linkers which connect the at least two binding domains (or the two variable regions forming one binding domain) in the construct, those peptide linkers are envisaged which comprise only a few amino acid residues, e.g. 12 amino acid residues or less. Thus, peptide linkers of 12, 11, 10, 9, 8, 7, 6 or 5 amino acid residues are preferred. An envisaged peptide linker with less than 5 amino acids comprises 4, 3, 2 or one amino acid(s), wherein Gly-rich linkers are preferred. A “single amino acid” linker in the context of said “peptide linker” is Gly. Another embodiment of a peptide linker is characterized by the amino acid sequence Gly-Gly-Gly-Gly-Ser, i.e. Gly₄Ser (SEQ ID NO: 15), or polymers thereof, i.e. (Gly₄Ser)_x, where x is an integer of 1 or greater (e.g. 2 or 3), for example SEQ ID NOs: 1 and 2. Preferred linkers are depicted in SEQ ID NOs: 2, 4, 5,

6, 8, 10, 11, and 2551. Another preferred linker comprises or consists of (Gly4Ser)₆. The characteristics of said peptide linkers are known in the art and are described e.g. in Dall'Acqua et al. (Biochem. (1998) 37, 9266-9273), Cheadle et al. (Mol Immunol (1992) 29, 21-30) and Raag and Whitlow (FASEB (1995) 9(1), 73-80). Peptide linkers which do not promote any secondary structures are preferred. The linkage of said domains to each other can be provided, e.g., by genetic engineering. Methods for preparing fused and operatively linked bispecific single chain constructs and expressing them in mammalian cells or bacteria are well-known in the art (e.g. WO 99/54440 or Sambrook et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 2001). More preferred, said peptide linker is a G₄S, or G₄Q linker or repetitions thereof, such as (G₄S)₃ or (G₄Q)₃.

[161] According to one embodiment of the invention, the polypeptide construct of the invention is a "single chain construct" or "single chain polypeptide". In the case of a further binding domain, it is also envisaged that either the CD3 binding or the further (also termed "second") or both binding domains may be in the format of a "single chain Fv" (scFv). Although the two domains of the Fv fragment, VL and VH, are coded for by separate genes, they can be joined, using recombinant methods, by an artificial linker – as described hereinbefore – that enables them to be made as a single protein chain in which the VL and VH regions pair to form a monovalent molecule; see e.g., Huston et al. (1988) Proc. Natl. Acad. Sci USA 85:5879-5883). These antibody fragments are obtained using conventional techniques known to those with skill in the art, and the fragments are evaluated for function in the same manner as are full-length antibodies or IgGs. A single-chain variable fragment (scFv) is hence a fusion protein of the variable region of the heavy chain (VH) and of the light chain (VL) of immunoglobulins, usually connected with a short linker peptide. The linker is usually rich in glycine for flexibility, as well as serine or also threonine for solubility, and can either connect the N-terminus of the VH with the C-terminus of the VL, or vice versa. This protein retains the specificity of the original immunoglobulin, despite removal of the constant regions and introduction of the linker.

[162] Bispecific single chain molecules are known in the art and are described in WO 99/54440, Mack, J. Immunol. (1997), 158, 3965-3970, Mack, PNAS, (1995), 92, 7021-7025, Kufer, Cancer Immunol. Immunother., (1997), 45, 193-197, Löffler, Blood, (2000), 95, 6, 2098-2103, Brühl, Immunol., (2001), 166, 2420-2426, Kipriyanov, J. Mol. Biol., (1999), 293, 41-56. Techniques described for producing single chain constructs (see, inter alia, US Patent 4,946,778, Kontermann and Dübel (2010), loc. cit. and Little (2009), loc. cit.) can be adapted to produce single chain constructs selectively and, preferably, specifically recognizing (an) elected target(s).

[163] Bivalent (also called divalent) or bispecific single-chain variable fragments (bi-scFvs or di-scFvs) having the format (scFv)₂ can be engineered by linking two scFv molecules (e.g. with linkers as described hereinbefore). The linking can be done by producing a single polypeptide chain with two VH regions and two VL regions, yielding tandem scFvs (see e.g. Kufer, P. et al., (2004) Trends in Biotechnology 22(5):238-244). Another possibility is the creation of scFv molecules with linker peptides that are too short for the two variable regions to fold together (e.g. about five amino acids), forcing the scFvs to dimerize. In this case, the VH and the VL of a binding domain (binding either to CD3epsilon or the further target antigen) are not directly connected via a peptide linker. Thus, the VH of the CD3 binding domain may e.g. be fused to the VL of the further target antigen binding domain via a peptide linker, and the VH of the further target antigen binding domain is fused to the VL of the CD3 binding domain via such peptide linker. This type is known as diabodies (see e.g. Hollinger, Philipp et al., (July 1993) Proceedings of the National Academy of Sciences of the United States of America 90 (14): 6444-8.).

[164] In accordance with the invention, the polypeptide or polypeptide construct the invention comprises at least one further binding domain. In other words, the polypeptide or polypeptide construct comprises the CD3epsilon binding domain defined herein above and at least one further binding domain. Said further binding domain can be a further CD3 binding domain, preferably one as defined herein. As such, the polypeptide can comprise two of the same CD3 binding domains as defined herein. Alternatively or additionally (in a construct comprising at least three binding domains), the at least one further binding domain binds to a different target, such as a cell surface antigen.

[165] Preferably, said at least one further binding domain binds to a cell surface antigen. The term "cell surface antigen" as used herein denotes a molecule, which is displayed on the surface of a cell. In most cases, this molecule will be located in or on the plasma membrane of the cell such that at least part of this molecule remains accessible from outside the cell in tertiary form. A non-limiting example of a cell surface molecule, which is located in the plasma membrane is a transmembrane protein comprising, in its tertiary conformation, regions of hydrophilicity and hydrophobicity. Here, at least one hydrophobic region allows the cell surface molecule to be embedded, or inserted in the hydrophobic plasma membrane of the cell while the hydrophilic regions extend on either side of the plasma membrane into the cytoplasm and extracellular space, respectively. It will be appreciated that an extracellular epitope refers to an epitope comprised by a portion of a protein that is disposed in the extracellular space, for example a portion of a cell surface molecule that extends into the extracellular space when that cell surface molecule is a native configuration disposed, embedded, or inserted in the plasma membrane. Non-limiting examples of cell surface molecules which are located on the plasma membrane are proteins which have been

modified at a cysteine residue to bear a palmitoyl group, proteins modified at a C-terminal cysteine residue to bear a farnesyl group or proteins which have been modified at the C-terminus to bear a glycosyl phosphatidyl inositol ("GPI") anchor.

[166] Said cell surface antigen is preferably a tumor antigen. The term "tumor antigen" as used herein may be understood as those antigens that are presented on tumor cells. These antigens can be presented on the cell surface with an extracellular part, which is often combined with a transmembrane and cytoplasmic part of the molecule. These antigens can sometimes be presented only by tumor cells and never by the normal ones. Tumor antigens can be exclusively expressed on tumor cells or might represent a tumor specific mutation compared to normal cells. In this case, they are called tumor-specific antigens. More common are antigens that are presented by tumor cells and normal cells, and they are called tumor-associated antigens. These tumor-associated antigens can be overexpressed compared to normal cells or are accessible for antibody binding in tumor cells due to the less compact structure of the tumor tissue compared to normal tissue.

[167] In a preferred embodiment, the tumor antigen is selected from the group consisting of BCMA (B-cell maturation antigen), CD123 (interleukin-3 receptor alpha chain (IL-3R)), CD19 (B-lymphocyte antigen CD19), CD20 (B-lymphocyte antigen CD20), CD22 (cluster of differentiation-22), CD33 (Siglec-3), CD70 (Cluster of Differentiation 70), CDH19 (Cadherin 19), CDH3 (Cadherin 3), CLL1 (C-type lectin domain family 12 member A), CS1 (CCND3 subset 1), CLDN6 (Claudin-6), CLDN18.2 (Claudin 18.2), DLL3 (Delta-like ligand 3), EGFRvIII (Epidermal growth factor receptor vIII), FLT3 (fms like tyrosine kinase 3), MAGEB2 (Melanoma-associated antigen B2), MART1 (Melanoma Antigen Recognized By T-Cells 1), MSLN (Mesothelin), MUC17 (Mucin-17), PSMA (prostate-specific membrane antigen), and STEAP1 (Metalloreductase STEAP1). These tumor antigens are well known in the art due to their expression on tumor cells.

[168] Preferred CDR sequences and VH/VL region sequences for BCMA binding domains as further binding domains of the polypeptide or polypeptide construct of the invention, and bispecific single chain molecule sequences of a polypeptide or polypeptide construct in accordance with the invention having a BCMA binding domain as further binding domain (with and without half-life extending domain) are defined in SEQ ID NOs: 2072 to 2095.

[169] Preferred CDR sequences and VH/VL region sequences for CD123 binding domains as further binding domains of the polypeptide or polypeptide construct of the invention, and bispecific single chain molecule sequences of a polypeptide or polypeptide construct in accordance with the invention having a CD123 binding domain as further binding domain (with and without half-life extending domain) are defined in SEQ ID NOs: 2096 to 2110.

[170] Preferred CDR sequences and VH/VL region sequences for CD19 binding domains as further binding domains of the polypeptide or polypeptide construct of the invention, and

bispecific single chain molecule sequences of a polypeptide or polypeptide construct in accordance with the invention having a CD19 binding domain as further binding domain (with and without half-life extending domain) are defined in SEQ ID NOs: 2111 to 2125.

[171] Preferred CDR sequences and VH/VL region sequences for CD20 binding domains as further binding domains of the polypeptide or polypeptide construct of the invention, and bispecific single chain molecule sequences of a polypeptide or polypeptide construct in accordance with the invention having a CD20 binding domain as further binding domain (with and without half-life extending domain) are defined in SEQ ID NOs: 2126 to 2140.

[172] Preferred CDR sequences and VH/VL region sequences for CD22 binding domains as further binding domains of the polypeptide or polypeptide construct of the invention, and bispecific single chain molecule sequences of a polypeptide or polypeptide construct in accordance with the invention having a CD22 binding domain as further binding domain (with and without half-life extending domain) are defined in SEQ ID NOs: 2141 to 2154.

[173] Preferred CDR sequences and VH/VL region sequences for CD33 binding domains as further binding domains of the polypeptide or polypeptide construct of the invention, and bispecific single chain molecule sequences of a polypeptide or polypeptide construct in accordance with the invention having a CD33 binding domain as further binding domain (with and without half-life extending domain) are defined in SEQ ID NOs: 2155 to 2178.

[174] Preferred CDR sequences and VH/VL region sequences for CD70 binding domains as further binding domains of the polypeptide or polypeptide construct of the invention, and bispecific single chain molecule sequences of a polypeptide or polypeptide construct in accordance with the invention having a CD70 binding domain as further binding domain (with and without half-life extending domain) are defined in SEQ ID NOs: 2179 to 2192.

[175] Preferred CDR sequences and VH/VL region sequences for CDH19 binding domains as further binding domains of the polypeptide or polypeptide construct of the invention, and bispecific single chain molecule sequences of a polypeptide or polypeptide construct in accordance with the invention having a CDH19 binding domain as further binding domain (with and without half-life extending domain) are defined in SEQ ID NOs: 2193 to 2212.

[176] Preferred CDR sequences and VH/VL region sequences for CDH3 binding domains as further binding domains of the polypeptide or polypeptide construct of the invention, and bispecific single chain molecule sequences of a polypeptide or polypeptide construct in accordance with the invention having a CDH3 binding domain as further binding domain (with and without half-life extending domain) are defined in SEQ ID NOs: 2213 to 2256.

[177] Preferred CDR sequences and VH/VL region sequences for CLL1 binding domains as further binding domains of the polypeptide or polypeptide construct of the invention, and bispecific single chain molecule sequences of a polypeptide or polypeptide construct in accordance with the invention having a CLL1 binding domain as further binding domain (with

and without half-life extending domain) are defined in SEQ ID NOs: 2257 to 2271.

[178] Preferred CDR sequences and VH/VL region sequences for CS1 binding domains as further binding domains of the polypeptide or polypeptide construct of the invention, and bispecific single chain molecule sequences of a polypeptide or polypeptide construct in accordance with the invention having a CS1 binding domain as further binding domain (with and without half-life extending domain) are defined in SEQ ID NOs: 2272 to 2285.

[179] Preferred CDR sequences and VH/VL region sequences for CLDN6 binding domains as further binding domains of the polypeptide or polypeptide construct of the invention, and bispecific single chain molecule sequences of a polypeptide or polypeptide construct in accordance with the invention having a CLDN6 binding domain as further binding domain (with and without half-life extending domain) are defined in SEQ ID NOs: 2286 to 2299.

[180] Preferred CDR sequences and VH/VL region sequences for CLDN18.2 binding domains as further binding domains of the polypeptide or polypeptide construct of the invention, and bispecific single chain molecule sequences of a polypeptide or polypeptide construct in accordance with the invention having a CLDN18.2 binding domain as further binding domain (with and without half-life extending domain) are defined in SEQ ID NOs: 2300 to 2314.

[181] Preferred CDR sequences and VH/VL region sequences for DLL3 binding domains as further binding domains of the polypeptide or polypeptide construct of the invention, and bispecific single chain molecule sequences of a polypeptide or polypeptide construct in accordance with the invention having a DLL3 binding domain as further binding domain (with and without half-life extending domain) are defined in SEQ ID NOs: 2315 to 2328.

[182] Preferred CDR sequences and VH/VL region sequences for EGFRvIII binding domains as further binding domains of the polypeptide or polypeptide construct of the invention, and bispecific single chain molecule sequences of a polypeptide or polypeptide construct in accordance with the invention having a EGFRvIII binding domain as further binding domain (with and without half-life extending domain) are defined in SEQ ID NOs: 2329 to 2342.

[183] Preferred CDR sequences and VH/VL region sequences for FLT3 binding domains as further binding domains of the polypeptide or polypeptide construct of the invention, and bispecific single chain molecule sequences of a polypeptide or polypeptide construct in accordance with the invention having a FLT3 binding domain as further binding domain (with and without half-life extending domain) are defined in SEQ ID NOs: 2343 to 2357.

[184] Preferred CDR sequences and VH/VL region sequences for MAGEB2 binding domains as further binding domains of the polypeptide or polypeptide construct of the invention, and bispecific single chain molecule sequences of a polypeptide or polypeptide construct in accordance with the invention having a MAGEB2 binding domain as further

binding domain (with and without half-life extending domain) are defined in SEQ ID NOs: 2358 to 2378.

[185] Preferred CDR sequences and VH/VL region sequences for MART1 binding domains as further binding domains of the polypeptide or polypeptide construct of the invention are defined in SEQ ID NOs: 2379 to 2387.

[186] Preferred CDR sequences and VH/VL region sequences for MSLN binding domains as further binding domains of the polypeptide or polypeptide construct of the invention, and bispecific single chain molecule sequences of a polypeptide or polypeptide construct in accordance with the invention having a MSLN binding domain as further binding domain (with and without half-life extending domain) are defined in SEQ ID NOs: 2388 to 2431.

[187] Preferred CDR sequences and VH/VL region sequences for MUC17 binding domains as further binding domains of the polypeptide or polypeptide construct of the invention, and bispecific single chain molecule sequences of a polypeptide or polypeptide construct in accordance with the invention having a MUC17 binding domain as further binding domain (with and without half-life extending domain) are defined in SEQ ID NOs: 2432 to 2445.

[188] Preferred CDR sequences and VH/VL region sequences for PSMA binding domains as further binding domains of the polypeptide or polypeptide construct of the invention, and bispecific single chain molecule sequences of a polypeptide or polypeptide construct in accordance with the invention having a PSMA binding domain as further binding domain (with and without half-life extending domain) are defined in SEQ ID NOs: 2446 to 2475.

[189] Preferred bispecific single chain molecule sequences of a polypeptide or polypeptide construct in accordance with the invention having CD20 and CD22 binding domains as further binding domains (with and without a further CD3 binding domain as defined herein) and a half-life extending domain are defined in SEQ ID NOs: 2505 to 2516.

[190] Preferred bispecific single chain molecule sequences of a polypeptide or polypeptide construct in accordance with the invention having CS1 and BCMA binding domains as further binding domains and a half-life extending domain are defined in SEQ ID NOs: 2517 to 2522.

[191] Preferred bispecific single chain molecule sequences of a polypeptide or polypeptide construct in accordance with the invention having MSLN and CDH3 binding domains as further binding domains and a half-life extending domain are defined in SEQ ID NOs: 2529 to 2536.

[192] As laid out herein above, the polypeptide construct of the invention comprises a binding domain which binds to CD3 on the surface of a T cell. "CD3" (cluster of differentiation 3) is a T cell co-receptor composed of four chains. In mammals, the CD3 protein complex contains a CD3 γ (gamma) chain, a CD3 δ (delta) chain, and two CD3 ϵ (epsilon) chains. These four chains associate with the T cell receptor (TCR) and the so-called ζ (zeta) chain to form the "T cell receptor complex" and to generate an activation signal

in T lymphocytes. The CD3 γ (gamma), CD3 δ (delta), and CD3 ϵ (epsilon) chains are highly related cell-surface proteins of the immunoglobulin superfamily and each contain a single extracellular immunoglobulin domain. The intracellular tails of the CD3 molecules contain a single conserved motif known as an immunoreceptor tyrosine-based activation motif (ITAM), which is essential for the signaling capacity of the TCR. The CD3 epsilon molecule is a polypeptide which in humans is encoded by the CD3 epsilon gene which resides on chromosome 11. In the context of the present invention, CD3 is understood as a protein complex and T cell co-receptor that is involved in activating both the cytotoxic T cell (CD8+ naive T cells) and T helper cells (CD4+ naive T cells). It is typically composed of four distinct chains. Especially in mammals, the complex contains a CD3 γ chain, a CD3 δ chain, and two CD3 ϵ chains. These chains associate with the T-cell receptor (TCR) and the ζ -chain (zeta-chain) to generate an activation signal in T lymphocytes. The TCR, ζ -chain, and CD3 molecules together constitute the TCR complex.

[193] The redirected lysis of target cells via the recruitment of T cells by a construct which binds to CD3 on the T cell and to a target protein on the target cell generally involves cytolytic synapse formation and delivery of perforin and granzymes. The engaged T cells are capable of serial target cell lysis and are not affected by immune escape mechanisms interfering with peptide antigen processing and presentation, or clonal T cell differentiation; see e.g. WO 2007/042261.

[194] Cytotoxicity mediated by given tumor antigenxCD3 constructs can be measured in various ways. The "half maximal effective concentration" (EC50) is commonly used as a measure of potency of a biologically active molecule such as a construct of the present invention. It may be expressed in molar units. In the present case of measuring cytotoxicity, the EC50 value refers to the concentration of a construct inducing a cytotoxic response (lysis of target cells) halfway between the baseline and the maximum. Effector cells in a cytotoxicity assay can e.g. be stimulated enriched (human) CD8 positive T cells or unstimulated (human) peripheral blood mononuclear cells (PBMC). An EC50 value may typically be expected to be lower when stimulated / enriched CD8+ T cells are used as effector cells, compared with unstimulated PBMC. If the target cells are of macaque origin or express or are transfected with a given macaque tumor antigen, the effector cells should also be of macaque origin, such as a macaque T cell line, e.g. 4119LnPx. The target cells should express said tumor antigen on the cell surface. Target cells can be a cell line (such as CHO) which is stably or transiently transfected with said tumor antigen. Alternatively, the target cells can be a tumor antigen positive natural expresser cell line, such as the human cancer lines. Usually EC50 values are expected to be lower when using target cells that express higher levels of said tumor antigen on the cell surface compared with target cells having a lower target expression rate.

[195] The effector to target cell (E:T) ratio in a cytotoxicity assay is usually about 10:1, but can also vary. Cytotoxic activity of tumor antigenxCD3 constructs can be measured in a 51-chromium release assay (e.g. with an incubation time of about 18 hours) or in a FACS-based cytotoxicity assay (e.g. with an incubation time of about 48 hours). Modifications of the incubation time (cytotoxic reaction) are also envisaged. Other methods of measuring cytotoxicity are well-known and comprise MTT or MTS assays, ATP-based assays including bioluminescent assays, the sulforhodamine B (SRB) assay, WST assay, clonogenic assay and the ECIS technology.

[196] According to one embodiment, the cytotoxic activity mediated by tumor antigenxCD3 constructs of the present invention is measured in a cell-based cytotoxicity assay. It may also be measured in a 51-chromium release assay. It is envisaged that the EC₅₀ value of the constructs of the invention is ≤300 pM, ≤280 pM, ≤260 pM, ≤250 pM, ≤240 pM, ≤220 pM, ≤200 pM, ≤180 pM, ≤160 pM, ≤150 pM, ≤140 pM, ≤120 pM, ≤100 pM, ≤90 pM, ≤80 pM, ≤70 pM, ≤60 pM, ≤50 pM, ≤40 pM, ≤30 pM, ≤20 pM, ≤15 pM, ≤10 pM, or ≤5 pM.

[197] The above given EC₅₀ values can be measured in different assays and under different conditions. For example, when human PBMCs are used as effector cells and tumor antigen transfected cells such as CHO cells are used as target cells, it is envisaged that the EC₅₀ value of the tumor antigenxCD3 construct is ≤500 pM, ≤400 pM, ≤300 pM, ≤280 pM, ≤260 pM, ≤250 pM, ≤240 pM, ≤220 pM, ≤200 pM, ≤180 pM, ≤160 pM, ≤150 pM, ≤140 pM, ≤120 pM, ≤100 pM, ≤90 pM, ≤80 pM, ≤70 pM, ≤60 pM, ≤50 pM, ≤40 pM, ≤30 pM, ≤20 pM, ≤15 pM, ≤10 pM, or ≤5 pM. When human PBMCs are used as effector cells and when the target cells are a CLDN6 positive cell line such as, it is envisaged that the EC₅₀ value of the CLDN6xCD3 construct is ≤300 pM, ≤280 pM, ≤260 pM, ≤250 pM, ≤240 pM, ≤220 pM, ≤200 pM, ≤180 pM, ≤160 pM, ≤150 pM, ≤140 pM, ≤120 pM, ≤100 pM, ≤90 pM, ≤80 pM, ≤70 pM, ≤60 pM, ≤50 pM, ≤40 pM, ≤30 pM, ≤20 pM, ≤15 pM, ≤10 pM, or ≤5 pM.

[198] According to one embodiment, the tumor antigenxCD3 polypeptides/polypeptide constructs of the present invention do not induce / mediate lysis or do not essentially induce / mediate lysis of cells that do not express said given tumor antigen on their surface (tumor antigen negative cells), such as CHO cells. The term “do not induce lysis”, “do not essentially induce lysis”, “do not mediate lysis” or “do not essentially mediate lysis” means that a construct of the present invention does not induce or mediate lysis of more than 30%, preferably not more than 20%, more preferably not more than 10%, particularly preferably not more than 9%, 8%, 7%, 6% or 5% of tumor antigen negative cells, whereby lysis of tumor antigen expressing target cells (such as cells transformed or transfected with said tumor antigen or a natural expresser cell line such as the human cancer lines) is set to be 100%. This usually applies for concentrations of the construct of up to 500 nM. Cell lysis

measurement is a routine technique. Moreover, the present specification teaches specific instructions how to measure cell lysis.

[199] The difference in cytotoxic activity between the monomeric and the dimeric isoform of individual tumor antigenxCD3 polypeptides/polypeptide constructs is referred to as “potency gap”. This potency gap can e.g. be calculated as ratio between EC50 values of the molecule’s monomeric and dimeric form. In one method to determine this gap, an 18 hour 51-chromium release assay or a 48h FACS-based cytotoxicity assay is carried out as described hereinbelow with purified construct monomer and dimer. Effector cells are stimulated enriched human CD8+ T cells or unstimulated human PBMC. Target cells are hu tumor antigen transfected CHO cells. Effector to target cell (E:T) ratio is 10:1. Potency gaps of the tumor antigenxCD3 constructs of the present invention are preferably ≤ 5 , more preferably ≤ 4 , even more preferably ≤ 3 , even more preferably ≤ 2 and most preferably ≤ 1 .

[200] The binding domain(s) of the polypeptide construct of the invention is/are preferably cross-species specific for members of the mammalian order of primates, such as macaques. According to one embodiment, the further binding domain(s), in addition to binding to a human tumor antigen, will also bind to said tumor antigen of primates including (but not limited to) new world primates (such as *Callithrix jacchus*, *Saguinus Oedipus* or *Saimiri sciureus*), old world primates (such as baboons and macaques), gibbons, orangutans and non-human hominidae. It is envisaged that the domain which binds to human CD3 on the surface of a T cell of the invention also binds at least to macaque CD3. A preferred macaque is *Macaca fascicularis*. *Macaca mulatta* (Rhesus) is also envisaged. The polypeptide or polypeptide construct of the invention comprises a domain which binds to human CD3epsilon on the surface of a T cell and at least macaque CD3.

[201] In one embodiment, the affinity gap of the constructs according to the invention for binding macaque CD3 versus human CD3 [$KD_{ma\ CD3} : KD_{hu\ CD3}$] (as determined e.g. by BiaCore or by Scatchard analysis) is between 0.01 and 100, preferably between 0.1 and 10, more preferably between 0.2 and 5, more preferably between 0.3 and 4, even more preferably between 0.5 and 3 or between 0.5 and 2.5, and most preferably between 0.5 and 1.

[202] As detailed herein above, said binding domain of the polypeptide or polypeptide construct of the invention binds to human CD3 epsilon (or human CD3 epsilon on the surface of a T cell) and, preferably, to *Callithrix jacchus* or *Saimiri sciureus* CD3 epsilon. More specifically, said domain binds to an extracellular epitope of human CD3 epsilon. It is also envisaged that said domain binds to an extracellular epitope of the human and the *Macaca* CD3 epsilon chain. Said extracellular epitope of CD3 epsilon is comprised within amino acid residues 1-27 of the human CD3 epsilon extracellular domain (see SEQ ID NO: 2552; amino

acid residues 1-27 in SEQ ID NO: 2553). Even more particularly, the epitope comprises at least the amino acid sequence Gln-Asp-Gly-Asn-Glu. *Callithrix jacchus* is a new world primate belonging to the family of Callitrichidae, while *Saimiri sciureus* is a new world primate belonging to the family of Cebidae.

5 **[203]** In a preferred embodiment, the polypeptide or polypeptide construct of the invention is a single chain polypeptide that is at least bispecific. It is preferred for this embodiment that the CD3 binding domain according to the invention is present as a scFv in the polypeptide or polypeptide construct.

10 **[204]** It is also envisaged that the polypeptide construct of the invention has, in addition to its function to bind to CD3 and, in certain embodiments to bind to at least a further binding domain, a further function. In this format, the construct may be a trifunctional or multifunctional construct by targeting target cells through, preferably, tumor antigen binding, mediating cytotoxic T cell activity through CD3 binding and providing a further function such as means or domains to enhance or extend serum half-life, a fully functional or modified Fc
15 constant domain mediating cytotoxicity through recruitment of effector cells, a label (fluorescent etc.), a therapeutic agent such as a toxin or radionuclide, etc.

20 **[205]** Examples for means or domains to extend serum half-life of the polypeptides/polypeptide constructs of the invention include peptides, proteins or domains of proteins, which are fused or otherwise attached to the polypeptides/polypeptide constructs. The group of peptides, proteins or protein domains includes peptides binding to other proteins with preferred pharmacokinetic profile in the human body such as serum albumin (see WO 2009/127691). An alternative concept of such half-life extending peptides includes peptides binding to the neonatal Fc receptor (FcRn, see WO 2007/098420), which can also be used in the constructs of the present invention. The concept of attaching larger domains
25 of proteins or complete proteins includes the fusion of human serum albumin, variants or mutants of human serum albumin (see WO 2011/051489, WO 2012/059486, WO 2012/150319, WO 2013/135896, WO 2014/072481, WO 2013/075066) or domains thereof, as well as the fusion of an immunoglobulin constant region (Fc domain) and variants thereof. Such variants of Fc domains are called Fc-based domains and may e.g. be
30 optimized / modified to allow the desired pairing of dimers or multimers, to abolish Fc receptor binding (e.g. to avoid ADCC or CDC) or for other reasons. A further concept known in the art to extend the half-life of substances or molecules in the human body is the pegylation of those molecules (such as the constructs of the present invention).

35 **[206]** In one embodiment, the polypeptides/polypeptide constructs according to the invention are linked (e.g. via peptide bond) with a fusion partner (such as a protein, polypeptide or peptide), e.g. for extending the construct's serum half-life. These fusion

partners can be selected from human serum albumin ("HSA" or "HALB") as well as sequence variants thereof, peptides binding to HSA, peptides binding to FcRn ("FcRn BP"), or constructs comprising an (antibody derived) Fc region. Exemplary sequences of these fusion partners are depicted in SEQ ID NOs: 16, 18 and 19. In general, the fusion partners may be linked to the N-terminus or to the C-terminus of the constructs according to the invention, either directly (e.g. via peptide bond) or through a peptide linker such as (GGGGS)_n or (GGGGQ)_n (wherein "n" is an integer of 2 or greater, e.g. 2 or 3 or 4). Suitable peptide linkers are discussed above and are shown in SEQ ID NOs: 2 and 2551.

[207] It is envisaged that a polypeptide construct according to the present invention comprises a single chain polypeptide that is at least bispecific, wherein said polypeptide comprises or consists of in the following order from N-terminus to C-terminus:

a) VL (comprising part of a cell surface antigen binding domain/paratope) - (G4S)₃ or (G4Q)₃ - VH (comprising part of a cell surface antigen binding domain/paratope) - Peptide linker (SG4S) or (SG4Q) - VH (comprising part of the CD3epsilon binding domain/ paratope) - (G4S)₃ or (G4Q)₃ - VL (comprising part of the CD3epsilon binding domain/paratope);

b) VH (comprising part of a cell surface antigen binding domain/paratope) - (G4S)₃ or (G4Q)₃ - VL (comprising part of a cell surface antigen binding domain/paratope) - Peptide linker (SG4S) or (SG4Q) - VH (comprising part of the CD3epsilon binding domain/ paratope) - (G4S)₃ or (G4Q)₃ - VL (comprising part of the CD3epsilon binding domain/paratope);

c) VL (comprising part of a cell surface antigen binding domain/paratope) - (G4S)₃ or (G4Q)₃ - VH (comprising part of a cell surface antigen binding domain/paratope) - Peptide linker (SG4S) or (SG4Q) - VH (comprising part of the CD3epsilon binding domain/ paratope) - (G4S)₃ or (G4Q)₃ - VL (comprising part of the CD3epsilon binding domain/paratope) - Peptide linker (G4) - Fc monomer (part of the HLE domain) - (G4S)₆ or (G4Q)₆ or - Fc monomer (part of the HLE domain);

d) VH (comprising part of a cell surface antigen binding domain/paratope) - (G4S)₃ or (G4Q)₃ - VL (comprising part of a cell surface antigen binding domain/paratope) - Peptide linker (SG4S) or (SG4Q) - VH (comprising part of the CD3epsilon binding domain/ paratope) - (G4S)₃ or (G4Q)₃ - VL (comprising part of the CD3epsilon binding domain/paratope) - Peptide linker (G4) - Fc monomer (part of the HLE domain) - (G4S)₆ or (G4Q)₆ or - Fc monomer (part of the HLE domain);

e) VH (comprising part of a first cell surface antigen binding domain/paratope) - (G4S)₃ or (G4Q)₃ - VL (comprising part of a first cell surface antigen binding

domain/paratope) – Peptide linker (SG4S) or (SG4Q) – VL (comprising part of a second cell surface antigen binding domain/paratope) - (G4S)3 or (G4Q)3 – VH (comprising part of a second cell surface antigen binding domain/paratope) – Peptide linker (SG4S) or (SG4Q) – VH (comprising part of the CD3epsilon binding domain/ paratope) – (G4S)3 or (G4Q)3 – VL (comprising part of the CD3epsilon binding domain/paratope) – Peptide linker (G4) – Fc monomer (part of the HLE domain) – (G4S)6 or (G4Q)6 or – Fc monomer (part of the HLE domain);

f) VH (comprising part of a first cell surface antigen binding domain/paratope) - (G4S)3 or (G4Q)3 – VL (comprising part of a first cell surface antigen binding domain/paratope) – Peptide linker (SG4S) or (SG4Q) – VH (comprising part of a second cell surface antigen binding domain/paratope) - (G4S)3 or (G4Q)3 – VL (comprising part of a second cell surface antigen binding domain/paratope) – Peptide linker (SG4S) or (SG4Q) – VH (comprising part of the CD3epsilon binding domain/ paratope) – (G4S)3 or (G4Q)3 – VL (comprising part of the CD3epsilon binding domain/paratope) – Peptide linker (G4) – Fc monomer (part of the HLE domain) – (G4S)6 or (G4Q)6 or – Fc monomer (part of the HLE domain);

g) VL (comprising part of a first cell surface antigen binding domain/paratope) - (G4S)3 or (G4Q)3 – VH (comprising part of a first cell surface antigen binding domain/paratope) – Peptide linker (SG4S) or (SG4Q) – VL (comprising part of a second cell surface antigen binding domain/paratope) - (G4S)3 or (G4Q)3 – VH (comprising part of a second cell surface antigen binding domain/paratope) – Peptide linker (SG4S) or (SG4Q) – VH (comprising part of the CD3epsilon binding domain/ paratope) – (G4S)3 or (G4Q)3 – VL (comprising part of the CD3epsilon binding domain/paratope) – Peptide linker (G4) – Fc monomer (part of the HLE domain) – (G4S)6 or (G4Q)6 or – Fc monomer (part of the HLE domain)

h) VL (comprising part of a first cell surface antigen binding domain/paratope) - (G4S)3 or (G4Q)3 – VH (comprising part of a first cell surface antigen binding domain/paratope) – Peptide linker (SG4S) or (SG4Q) – VH (comprising part of a second cell surface antigen binding domain/paratope) - (G4S)3 or (G4Q)3 – VL (comprising part of a second cell surface antigen binding domain/paratope) – Peptide linker (SG4S) or (SG4Q) – VH (comprising part of the CD3epsilon binding domain/ paratope) – (G4S)3 or (G4Q)3 – VL (comprising part of the CD3epsilon binding domain/paratope) – Peptide linker (G4) – Fc monomer (part of the HLE domain) – (G4S)6 or (G4Q)6 or – Fc monomer (part of the HLE domain); or

i) **Binding domain 1** ((VL (comprising part of a first cell surface antigen binding domain/paratope) - (G4S)3 or (G4Q)3 – VH (comprising part of a first cell surface antigen

binding domain/paratope)) or (VH (comprising part of a first cell surface antigen binding domain/paratope) - (G4S)3 or (G4Q)3 – VL (comprising part of a first cell surface antigen binding domain/paratope))) – **Peptide linker (G4S) or (G4Q) – CD3 binding domain 1** (VH (comprising part of a first CD3epsilon binding domain/ paratope) – (G4S)3 or (G4Q)3 – VL (comprising part of a first CD3epsilon binding domain/paratope)) – **Peptide linker (G4) – Fc monomer** (part of the HLE domain) – **(G4S)6 or (G4Q)6 – Fc monomer** (part of the HLE domain) – **Peptide linker (G4) – Binding domain 2** ((VL (comprising part of a second cell surface antigen binding domain/paratope) - (G4S)3 or (G4Q)3 – VH (comprising part of a first cell surface antigen binding domain/paratope)) or (VH (comprising part of a second cell surface antigen binding domain/paratope) - (G4S)3 or (G4Q)3 – VL (comprising part of a second cell surface antigen binding domain/paratope))) – **Peptide linker (G4S) or (G4Q) – CD3 binding domain 2** (VH (comprising part of a second CD3epsilon binding domain/ paratope) – (G4S)3 or (G4Q)3 – VL (comprising part of a second CD3epsilon binding domain/paratope)).

[208] As is evident from the above, the VH and VL region sequence orientation of the binding domain(s) of the cell surface antigen can be VH-VL or VL-VH. Preferably, the cell surface antigen is a tumor antigen as detailed herein above. The HLE domain sequences made up of the Fc monomers and connecting linkers as detailed are preferably selected from the sequences as defined in SEQ ID NOs: 18 and 19. The two CD3 binding domains of the polypeptide construct of item i) are preferably the same CD3 binding domains, such as, preferably, the CD3 binding domain with VH and VL region sequences of SEQ ID NOs: 2028 and 2029. While peptide linkers (SG4S) or (SG4Q) are preferred at the indicated positions, they can also be replaced by (G4S) or (G4Q) linkers.

[209] Covalent modifications of the polypeptides/polypeptide constructs are also included within the scope of this invention, and are generally, but not always, done post-translationally. For example, several types of covalent modifications of the construct are introduced into the molecule by reacting specific amino acid residues of the construct with an organic derivatizing agent that can react with selected side chains or with the N- or C-terminal residues. Derivatization with bifunctional agents is useful for crosslinking the constructs of the present invention to a water-insoluble support matrix or surface for use in a variety of methods. Glutamyl and asparaginyl residues are frequently deamidated to the corresponding glutamyl and aspartyl residues, respectively. Alternatively, these residues are deamidated under mildly acidic conditions. Either form of these residues falls within the scope of this invention. Other modifications include hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, methylation of the α -amino groups of lysine, arginine, and histidine side chains (T. E. Creighton, Proteins: Structure and

Molecular Properties, W. H. Freeman & Co., San Francisco, 1983, pp. 79-86), acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

[210] Another type of covalent modification of the constructs included within the scope of this invention comprises altering the glycosylation pattern of the protein. As is known in the art, glycosylation patterns can depend on both the sequence of the protein (e.g., the presence or absence of specific glycosylation amino acid residues, discussed below), or the host cell or organism in which the protein is produced. Specific expression systems are discussed below. Glycosylation of polypeptides is typically either N-linked or O-linked. N-linked refers to the attachment of the carbohydrate moiety to the side chain of an asparagine residue. The tri-peptide sequences asparagine-X-serine and asparagine-X-threonine, where X is any amino acid except proline, are the recognition sequences for enzymatic attachment of the carbohydrate moiety to the asparagine side chain. Thus, the presence of either of these tri-peptide sequences in a polypeptide creates a potential glycosylation site. O-linked glycosylation refers to the attachment of one of the sugars N-acetylgalactosamine, galactose, or xylose, to a hydroxyamino acid, most commonly serine or threonine, although 5-hydroxyproline or 5-hydroxylysine may also be used.

[211] Addition of glycosylation sites to the construct is conveniently accomplished by altering the amino acid sequence such that it contains one or more of the above-described tri-peptide sequences (for N-linked glycosylation sites). The alteration may also be made by the addition of, or substitution by, one or more serine or threonine residues to the starting sequence (for O-linked glycosylation sites). For ease, the amino acid sequence of a construct may be altered through changes at the DNA level, particularly by mutating the DNA encoding the polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

[212] Another means of increasing the number of carbohydrate moieties on the construct is by chemical or enzymatic coupling of glycosides to the protein. These procedures are advantageous in that they do not require production of the protein in a host cell that has glycosylation capabilities for N- and O-linked glycosylation. Depending on the coupling mode used, the sugar(s) may be attached to (a) arginine and histidine, (b) free carboxyl groups, (c) free sulfhydryl groups such as those of cysteine, (d) free hydroxyl groups such as those of serine, threonine, or hydroxyproline, (e) aromatic residues such as those of phenylalanine, tyrosine, or tryptophan, or (f) the amide group of glutamine. These methods are described in WO 87/05330, and in Aplin and Wriston, 1981, CRC Crit. Rev. Biochem., pp. 259-306.

[213] Removal of carbohydrate moieties present on the starting construct may be accomplished chemically or enzymatically. Chemical deglycosylation requires exposure of the protein to the compound trifluoromethanesulfonic acid, or an equivalent compound. This

treatment results in the cleavage of most or all sugars except the linking sugar (N-acetylglucosamine or N-acetylgalactosamine), while leaving the polypeptide intact. Chemical deglycosylation is described by Hakimuddin et al., 1987, Arch. Biochem. Biophys. 259:52 and by Edge et al., 1981, Anal. Biochem. 118:131. Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved using a variety of endo- and exo-glycosidases as described by Thotakura et al., 1987, Meth. Enzymol. 138:350. Glycosylation at potential glycosylation sites may be prevented using the compound tunicamycin as described by Duskin et al., 1982, J. Biol. Chem. 257:3105. Tunicamycin blocks the formation of protein-N-glycoside linkages.

[214] Other modifications of the construct are also contemplated herein. For example, another type of covalent modification of the construct comprises linking the construct to various non-proteinaceous polymers, including polyols, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337. In addition, as is known in the art, amino acid substitutions may be made in various positions within the construct, e.g. to facilitate the addition of polymers such as polyethylene glycol (PEG).

[215] In some embodiments, the covalent modification of the constructs of the invention comprises the addition of one or more labels. The labelling group may be coupled to the construct via spacer arms of various lengths to reduce potential steric hindrance. Various methods for labelling proteins are known in the art and can be used in performing the present invention. The term "label" or "labelling group" refers to any detectable label. In general, labels fall into a variety of classes, depending on the assay in which they are to be detected – the following examples include, but are not limited to:

- a) isotopic labels, which may be radioactive or heavy isotopes, such as radioisotopes or radionuclides (e.g., ^3H , ^{14}C , ^{15}N , ^{35}S , ^{89}Zr , ^{90}Y , ^{99}Tc , ^{111}In , ^{125}I , ^{131}I)
- b) magnetic labels (e.g., magnetic particles)
- c) redox active moieties
- d) optical dyes (including, but not limited to, chromophores, phosphors and fluorophores) such as fluorescent groups (e.g., FITC, rhodamine, lanthanide phosphors), chemiluminescent groups, and fluorescent labels or fluorophores which can be either "small molecule" fluoeres or proteinaceous fluoeres
- e) enzymatic groups (e.g. horseradish peroxidase, β -galactosidase, luciferase, alkaline phosphatase)
- f) biotinylated groups
- g) predetermined polypeptide epitopes recognized by a secondary reporter (e.g., leucine zipper pair sequences, binding sites for secondary antibodies, metal binding domains, epitope tags, etc.).

[216] By “fluorescent label” is meant any molecule that may be detected via its inherent fluorescent properties. Suitable fluorescent labels include, but are not limited to, fluorescein, rhodamine, tetramethylrhodamine, eosin, erythrosin, coumarin, methyl-coumarins, pyrene, Malacite green, stilbene, Lucifer Yellow, Cascade BlueJ, Texas Red, IAEDANS, EDANS, BODIPY FL, LC Red 640, Cy 5, Cy 5.5, LC Red 705, Oregon green, the Alexa-Fluor dyes (Alexa Fluor 350, Alexa Fluor 430, Alexa Fluor 488, Alexa Fluor 546, Alexa Fluor 568, Alexa Fluor 594, Alexa Fluor 633, Alexa Fluor 660, Alexa Fluor 680), Cascade Blue, Cascade Yellow and R-phycoerythrin (PE) (Molecular Probes, Eugene, OR), FITC, Rhodamine, and Texas Red (Pierce, Rockford, IL), Cy5, Cy5.5, Cy7 (Amersham Life Science, Pittsburgh, PA). Suitable optical dyes, including fluorophores, are described in Molecular Probes Handbook by Richard P. Haugland.

[217] Suitable proteinaceous fluorescent labels also include, but are not limited to, green fluorescent protein, including a Renilla, Ptilosarcus, or Aequorea species of GFP (Chalfie et al., 1994, Science 263:802-805), EGFP (Clontech Laboratories, Inc., Genbank® Accession Number U55762), blue fluorescent protein (BFP, Quantum Biotechnologies, Inc. 1801 de Maisonneuve Blvd. West, 8th Floor, Montreal, Quebec, Canada H3H 1J9; Stauber, 1998, Biotechniques 24:462-471; Heim et al., 1996, Curr. Biol. 6:178-182), enhanced yellow fluorescent protein (EYFP, Clontech Laboratories, Inc.), luciferase (Ichiki et al., 1993, J. Immunol. 150:5408-5417), β galactosidase (Nolan et al., 1988, Proc. Natl. Acad. Sci. U.S.A. 85:2603-2607) and Renilla (WO92/15673, WO95/07463, WO98/14605, WO98/26277, WO99/49019, U.S. Patent Nos. 5,292,658; 5,418,155; 5,683,888; 5,741,668; 5,777,079; 5,804,387; 5,874,304; 5,876,995; 5,925,558).

[218] Leucine zipper domains are peptides that promote oligomerization of the proteins in which they are found. Leucine zippers were originally identified in several DNA-binding proteins (Landschulz et al., 1988, Science 240:1759), and have since been found in a variety of different proteins. Among the known leucine zippers are naturally occurring peptides and derivatives thereof that dimerize or trimerize. Examples of leucine zipper domains suitable for producing soluble oligomeric proteins are described in PCT application WO 94/10308, and the leucine zipper derived from lung surfactant protein D (SPD) described in Hoppe et al., 1994, FEBS Letters 344:191. The use of a modified leucine zipper that allows for stable trimerization of a heterologous protein fused thereto is described in Fanslow et al., 1994, Semin. Immunol. 6:267-78.

[219] The polypeptide construct of the invention may also comprise additional domains, which are e.g. helpful in the isolation of the molecule or relate to an adapted pharmacokinetic profile of the molecule. Domains helpful for the isolation of a construct may be selected from peptide motives or secondarily introduced moieties, which can be captured in an isolation

method, e.g. an isolation column. Non-limiting embodiments of such additional domains comprise peptide motives known as Myc-tag, HAT-tag, HA-tag, TAP-tag, GST-tag, chitin binding domain (CBD-tag), maltose binding protein (MBP-tag), Flag-tag, Strep-tag and variants thereof (e.g. StrepII-tag) and His-tag. All herein disclosed constructs characterized by the identified CDRs may comprise a His-tag domain, which is generally known as a repeat of consecutive His residues in the amino acid sequence of a molecule, e.g. of five His residues, or of six His residues (hexa-histidine). The His-tag may be located e.g. at the N- or C-terminus of the construct. In one embodiment, a hexa-histidine tag (HHHHHH) is linked via peptide bond to the C-terminus of the construct according to the invention. A histidine tag is preferred, especially a 6x His tag.

[220] The invention also relates to a polynucleotide encoding a polypeptide or polypeptide construct of the invention. Nucleic acid molecules are biopolymers composed of nucleotides. A polynucleotide is a biopolymer composed of 13 or more nucleotide monomers covalently bonded in a chain. DNA (such as cDNA) and RNA (such as mRNA) are examples of polynucleotides / nucleic acid molecules with distinct biological function. Nucleotides are organic molecules that serve as the monomers or subunits of nucleic acid molecules like DNA or RNA. The nucleic acid molecule or polynucleotide of the present invention can be double stranded or single stranded, linear or circular. It is envisaged that the nucleic acid molecule or polynucleotide is comprised in a vector. It is furthermore envisaged that such vector is comprised in a host cell. Said host cell is, e.g. after transformation or transfection with the vector or the polynucleotide / nucleic acid molecule of the invention, capable of expressing the construct. For this purpose, the polynucleotide or nucleic acid molecule is operatively linked with control sequences.

[221] The genetic code is the set of rules by which information encoded within genetic material (nucleic acids) is translated into proteins. Biological decoding in living cells is accomplished by the ribosome which links amino acids in an order specified by mRNA, using tRNA molecules to carry amino acids and to read the mRNA three nucleotides at a time. The code defines how sequences of these nucleotide triplets, called codons, specify which amino acid will be added next during protein synthesis. With some exceptions, a three-nucleotide codon in a nucleic acid sequence specifies a single amino acid. Because the vast majority of genes are encoded with exactly the same code, this particular code is often referred to as the canonical or standard genetic code.

[222] Degeneracy of codons is the redundancy of the genetic code, exhibited as the multiplicity of three-base pair codon combinations that specify an amino acid. Degeneracy results because there are more codons than encodable amino acids. The codons encoding one amino acid may differ in any of their three positions; however, often this difference is in

the second or third position. For instance, codons GAA and GAG both specify glutamic acid and exhibit redundancy; but, neither specifies any other amino acid nor thus demonstrate ambiguity. The genetic codes of different organisms can be biased towards using one of the several codons that encode the same amino acid over the others – that is, a greater frequency of one will be found than expected by chance. For example, leucine is specified by six distinct codons, some of which are rarely used. Codon usage tables detailing genomic codon usage frequencies for most organisms are available. Recombinant gene technologies commonly take advantage of this effect by implementing a technique termed codon optimization, in which those codons are used to design a polynucleotide which are preferred by the respective host cell (such as a cell of human hamster origin, an *Escherichia coli* cell, or a *Saccharomyces cerevisiae* cell), e.g. to increase protein expression. It is hence envisaged that the polynucleotides / nucleic acid molecules of the present disclosure are codon optimized. Nevertheless, the polynucleotide / nucleic acid molecule encoding a construct of the invention may be designed using any codon that encodes the desired amino acid.

[223] According to one embodiment, the polynucleotide / nucleic acid molecule of the present invention encoding the polypeptide construct of the invention is in the form of one single molecule or in the form of two or more separate molecules. If the construct of the present invention is a single chain construct, the polynucleotide / nucleic acid molecule encoding such construct will most likely also be in the form of one single molecule. However, it is also envisaged that different components of the polypeptide construct (such as the different domains, e.g. the paratope (antigen-binding (epitope-binding) structure)-comprising domain which binds to a cell surface antigen, the paratope (antigen-binding (epitope-binding) structure)-comprising domain which binds to CD3, and/or further domains such as antibody constant domains) are located on separate polypeptide chains, in which case the polynucleotide / nucleic acid molecule is most likely in the form of two or more separate molecules.

[224] The same applies for the vector comprising a polynucleotide / nucleic acid molecule of the present invention. If the construct of the present invention is a single chain construct, one vector may comprise the polynucleotide which encodes the construct in one single location (as one single open reading frame, ORF). One vector may also comprise two or more polynucleotides / nucleic acid molecules at separate locations (with individual ORFs), each one of them encoding a different component of the construct of the invention. It is envisaged that the vector comprising the polynucleotide / nucleic acid molecule of the present invention is in the form of one single vector or two or more separate vectors. In one embodiment, and for the purpose of expressing the construct in a host cell, the host cell of the invention should comprise the polynucleotide / nucleic acid molecule encoding the

construct or the vector comprising such polynucleotide / nucleic acid molecule in their entirety, meaning that all components of the construct – whether encoded as one single molecule or in separate molecules / locations – will assemble after translation and form together the biologically active construct of the invention.

5 [225] The invention further relates to a vector comprising a polynucleotide / nucleic acid molecule of the invention. A vector is a nucleic acid molecule used as a vehicle to transfer (foreign) genetic material into a cell, usually to ensure the replication and/or expression of the genetic material. The term “vector” encompasses – but is not restricted to – plasmids, viruses, cosmids, and artificial chromosomes. Some vectors are designed specifically for
10 cloning (cloning vectors), others for protein expression (expression vectors). So-called transcription vectors are mainly used to amplify their insert. The manipulation of DNA is normally conducted on *E. coli* vectors, which contain elements necessary for their maintenance in *E. coli*. However, vectors may also have elements that allow them to be maintained in another organism such as yeast, plant or mammalian cells, and these vectors
15 are called shuttle vectors. Insertion of a vector into the target or host cell is usually called transformation for bacterial cells and transfection for eukaryotic cells, while insertion of a viral vector is often called transduction.

[226] In general, engineered vectors comprise an origin of replication, a multicloning site and a selectable marker. The vector itself is generally a nucleotide sequence, commonly a
20 DNA sequence, that comprises an insert (transgene) and a larger sequence that serves as the “backbone” of the vector. While the genetic code determines the polypeptide sequence for a given coding region, other genomic regions can influence when and where these polypeptides are produced. Modern vectors may therefore encompass additional features besides the transgene insert and a backbone: promoter, genetic marker, antibiotic
25 resistance, reporter gene, targeting sequence, protein purification tag. Vectors called expression vectors (expression constructs) specifically are for the expression of the transgene in the target cell, and generally have control sequences.

[227] The term “control sequences” refers to DNA sequences necessary for the expression of an operably linked coding sequence in a specific host organism. The control sequences
30 that are suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, a Kozak sequence and enhancers.

[228] A nucleic acid is “operably linked” when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is
35 operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding

sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned to facilitate translation. Generally, “operably linked” means that the nucleotide sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice.

[229] “Transfection” is the process of deliberately introducing nucleic acid molecules or polynucleotides (including vectors) into target cells. The term is mostly used for non-viral methods in eukaryotic cells. Transduction is often used to describe virus-mediated transfer of nucleic acid molecules or polynucleotides. Transfection of animal cells typically involves opening transient pores or “holes” in the cell membrane, to allow the uptake of material. Transfection can be carried out using biological particles (such as viral transfection, also called viral transduction), chemical-based methods (such as using calcium phosphate, lipofection, Fugene, cationic polymers, nanoparticles) or physical treatment (such as electroporation, microinjection, gene gun, cell squeezing, magnetofection, hydrostatic pressure, impalefection, sonication, optical transfection, heat shock).

[230] The term “transformation” is used to describe non-viral transfer of nucleic acid molecules or polynucleotides (including vectors) into bacteria, and into non-animal eukaryotic cells, including plant cells. Transformation is hence the genetic alteration of a bacterial or non-animal eukaryotic cell resulting from the direct uptake through the cell membrane(s) from its surroundings and subsequent incorporation of exogenous genetic material (nucleic acid molecules). Transformation can be achieved by artificial means. For transformation to happen, cells or bacteria must be in a state of competence, which might occur as a time-limited response to environmental conditions such as starvation and cell density and can also be artificially induced.

[231] Moreover, the invention provides a host cell transformed or transfected with the polynucleotide / nucleic acid molecule of the invention or with the vector of the invention.

[232] As used herein, the terms “host cell” or “recipient cell” are intended to include any individual cell or cell culture that can be or has been recipient of vectors, exogenous nucleic acid molecules and/or polynucleotides encoding the construct of the present invention; and/or recipients of the construct itself. The introduction of the respective material into the cell is carried out by way of transformation, transfection and the like (vide supra). The term “host cell” is also intended to include progeny or potential progeny of a single cell. Because certain modifications may occur in succeeding generations due to either natural, accidental, or deliberate mutation or due to environmental influences, such progeny may not, in fact, be

completely identical (in morphology or in genomic or total DNA complement) to the parent cell but is still included within the scope of the term as used herein. Suitable host cells include prokaryotic or eukaryotic cells and include – but are not limited to – bacteria (such as *E. coli*), yeast cells, fungi cells, plant cells, and animal cells such as insect cells and mammalian cells, e.g., hamster, murine, rat, macaque or human.

[233] In addition to prokaryotes, eukaryotic microbes such as filamentous fungi or yeast are suitable cloning or expression hosts for the construct of the invention. *Saccharomyces cerevisiae*, or common baker's yeast, is the most commonly used among lower eukaryotic host microorganisms. However, a number of other genera, species, and strains are commonly available and useful herein, such as *Schizosaccharomyces pombe*, *Kluyveromyces* hosts such as *K. lactis*, *K. fragilis* (ATCC 12424), *K. bulgaricus* (ATCC 16045), *K. wickerhamii* (ATCC 24178), *K. waltii* (ATCC 56500), *K. drosophilae* (ATCC 36906), *K. thermotolerans*, and *K. marxianus*; *Yarrowia* (EP 402 226); *Pichia pastoris* (EP 183 070); *Candida*; *Trichoderma reesei* (EP 244 234); *Neurospora crassa*; *Schwanniomyces* such as *Schwanniomyces occidentalis*; and filamentous fungi such as *Neurospora*, *Penicillium*, *Tolypocladium*, and *Aspergillus* hosts such as *A. nidulans* and *A. niger*.

[234] Suitable host cells for the expression of a glycosylated construct are derived from multicellular organisms. Examples of invertebrate cells include plant and insect cells. Numerous baculoviral strains and variants and corresponding permissive insect host cells from hosts such as *Spodoptera frugiperda* (caterpillar), *Aedes aegypti* (mosquito), *Aedes albopictus* (mosquito), *Drosophila melanogaster* (fruit fly), and *Bombyx mori* (silkworm) have been identified. A variety of viral strains for transfection are publicly available, e.g., the L-1 variant of *Autographa californica* NPV and the Bm-5 strain of *Bombyx mori* NPV, and such viruses may be used as the virus herein according to the present invention, particularly for transfection of *Spodoptera frugiperda* cells.

[235] Plant cell cultures of cotton, corn, potato, soybean, petunia, tomato, *Arabidopsis* and tobacco can also be used as hosts. Cloning and expression vectors useful in the production of proteins in plant cell culture are known to those of skill in the art. See e.g. Hiatt et al., *Nature* (1989) 342: 76-78, Owen et al. (1992) *Bio/Technology* 10: 790-794, Artsaenko et al. (1995) *The Plant J* 8: 745-750, and Fecker et al. (1996) *Plant Mol Biol* 32: 979-986.

[236] However, interest has been greatest in vertebrate cells, and propagation of vertebrate cells in culture (cell culture) has become a routine procedure. Examples of useful mammalian host cell lines are monkey kidney CV1 line transformed by SV40 (such as COS-7, ATCC CRL 1651); human embryonic kidney line (such as 293 or 293 cells subcloned for growth in suspension culture, Graham et al., *J. Gen Virol.* 36: 59 (1977)); baby hamster kidney cells (such as BHK, ATCC CCL 10); Chinese hamster ovary cells/-DHFR (such as CHO, Urlaub et

al., Proc. Natl. Acad. Sci. USA 77: 4216 (1980)); mouse sertoli cells (such as TM4, Mather, Biol. Reprod. 23: 243-251 (1980)); monkey kidney cells (such as CVI ATCC CCL 70); African green monkey kidney cells (such as VERO-76, ATCC CRL1587); human cervical carcinoma cells (such as HELA, ATCC CCL 2); canine kidney cells (such as MDCK, ATCC CCL 34);
5 buffalo rat liver cells (such as BRL 3A, ATCC CRL 1442); human lung cells (such as W138, ATCC CCL 75); human liver cells (such as Hep G2, 1413 8065); mouse mammary tumor (such as MMT 060562, ATCC CCL-51); TRI cells (Mather et al., Annals N. Y Acad. Sci. (1982) 383: 44-68); MRC 5 cells; FS4 cells; and a human hepatoma line (such as Hep G2).

[237] In a further embodiment, the invention provides a process for the production of a
10 polypeptide or polypeptide construct of the invention, said process comprising culturing a host cell of the invention under conditions allowing the expression of the construct of the invention and recovering the produced construct from the culture.

[238] As used herein, the term “culturing” refers to the in vitro maintenance, differentiation, growth, proliferation and/or propagation of cells under suitable conditions in a medium. Cells
15 are grown and maintained in a cell growth medium at an appropriate temperature and gas mixture. Culture conditions vary widely for each cell type. Typical growth conditions are a temperature of about 37°C, a CO₂ concentration of about 5% and a humidity of about 95%. Recipes for growth media can vary e.g. in pH, concentration of the carbon source (such as glucose), nature and concentration of growth factors, and the presence of other nutrients
20 (such as amino acids or vitamins). The growth factors used to supplement media are often derived from the serum of animal blood, such as fetal bovine serum (FBS), bovine calf serum (FCS), equine serum, and porcine serum. Cells can be grown either in suspension or as adherent cultures. There are also cell lines that have been modified to be able to survive in suspension cultures, so they can be grown to a higher density than adherent conditions
25 would allow.

[239] The term “expression” includes any step involved in the production of a construct of the invention including, but not limited to, transcription, post-transcriptional modification, translation, folding, post-translational modification, targeting to specific subcellular or extracellular locations, and secretion. The term “recovering” refers to a series of processes
30 intended to isolate the construct from the cell culture. The “recovering” or “purification” process may separate the protein and non-protein parts of the cell culture, and finally separate the desired construct from all other polypeptides and proteins. Separation steps usually exploit differences in protein size, physico-chemical properties, binding affinity and biological activity. Preparative purifications aim to produce a relatively large quantity of
35 purified proteins for subsequent use, while analytical purification produces a relatively small amount of a protein for a variety of research or analytical purposes.

[240] When using recombinant techniques, the construct can be produced intracellularly, in the periplasmic space, or directly secreted into the medium. If the construct is produced intracellularly, as a first step, the particulate debris, either host cells or lysed fragments, are removed, for example, by centrifugation or ultrafiltration. The construct of the invention may e.g. be produced in bacteria such as *E. coli*. After expression, the construct is isolated from the bacterial cell paste in a soluble fraction and can be purified e.g. via affinity chromatography and/or size exclusion. Final purification can be carried out in a manner that is like the process for purifying a construct expressed in mammalian cells and secreted into the medium. Carter et al. (Biotechnology (NY) 1992 Feb;10(2):163-7) describe a procedure for isolating antibodies which are secreted to the periplasmic space of *E. coli*.

[241] Where the antibody is secreted into the medium, supernatants from such expression systems are generally first concentrated using a commercially available protein concentration filter, for example, an ultrafiltration unit.

[242] The construct of the invention prepared from the host cells can be recovered or purified using, for example, hydroxylapatite chromatography, gel electrophoresis, dialysis, and affinity chromatography. Other techniques for protein purification such as fractionation on an ion-exchange column, mixed mode ion exchange, HIC, ethanol precipitation, size exclusion chromatography, reverse phase HPLC, chromatography on silica, chromatography on heparin sepharose, chromatography on an anion or cation exchange resin (such as a polyaspartic acid column), immunoaffinity (such as Protein A/G/L) chromatography, chromatofocusing, SDS-PAGE, ultracentrifugation, and ammonium sulfate precipitation are also available depending on the construct to be recovered.

[243] A protease inhibitor may be included in any of the foregoing steps to inhibit proteolysis, and antibiotics may be included to prevent the growth of contaminants.

[244] Moreover, the invention provides a pharmaceutical composition or formulation comprising a polypeptide or polypeptide construct of the invention or a polypeptide or polypeptide construct produced according to the process of the invention.

[245] As used herein, the term "pharmaceutical composition" relates to a composition which is suitable for administration to a patient, preferably a human patient. The particularly preferred pharmaceutical composition of this invention comprises one or a plurality of the construct(s) of the invention, preferably in a therapeutically effective amount. Preferably, the pharmaceutical composition further comprises suitable formulations of one or more (pharmaceutically effective) carriers, stabilizers, excipients, diluents, solubilizers, surfactants, emulsifiers, preservatives and/or adjuvants. Acceptable constituents of the composition are preferably nontoxic to recipients at the dosages and concentrations employed.

Pharmaceutical compositions of the invention include, but are not limited to, liquid, frozen, and lyophilized compositions.

[246] The compositions may comprise a pharmaceutically acceptable carrier. In general, as used herein, "pharmaceutically acceptable carrier" means all aqueous and non-aqueous solutions, sterile solutions, solvents, buffers, e.g. phosphate buffered saline (PBS) solutions, water, suspensions, emulsions, such as oil/water emulsions, various types of wetting agents, liposomes, dispersion media and coatings, which are compatible with pharmaceutical administration, in particular with parenteral administration. The use of such media and agents in pharmaceutical compositions is well known in the art, and the compositions comprising such carriers can be formulated by well-known conventional methods.

[247] Certain embodiments provide pharmaceutical compositions comprising the construct of the invention and further one or more excipients such as those illustratively described in this section and elsewhere herein. Excipients can be used in the invention for a wide variety of purposes, such as adjusting physical, chemical, or biological properties of formulations, such as adjustment of viscosity, and or processes of the invention to improve effectiveness and/or to stabilize such formulations and processes against degradation and spoilage e.g. due to stresses that occur during manufacturing, shipping, storage, pre-use preparation, administration, and thereafter. Excipients should in general be used in their lowest effective concentrations.

[248] In certain embodiments, the pharmaceutical composition may contain formulation materials for modifying, maintaining or preserving certain characteristics of the composition such as the pH, osmolarity, viscosity, clarity, color, isotonicity, odor, sterility, stability, rate of dissolution or release, adsorption or penetration (see, Remington's Pharmaceutical Sciences, 18th Edition, 1990, Mack Publishing Company). In such embodiments, suitable formulation materials may include, but are not limited to:

- amino acids
- antimicrobials such as antibacterial and antifungal agents
- antioxidants
- buffers, buffer systems and buffering agents that are used to maintain the composition at physiological pH or at a slightly lower pH, typically within a range of from about 5 to about 8 or 9
- non-aqueous solvents, vegetable oils, and injectable organic esters
- aqueous carriers including water, alcoholic/aqueous solutions, emulsions or suspensions, including saline and buffered media
- biodegradable polymers such as polyesters
- bulking agents

- chelating agents
- isotonic and absorption delaying agents
- complexing agents
- fillers
- 5 • carbohydrates
- (low molecular weight) proteins, polypeptides or proteinaceous carriers, preferably of human origin
- coloring and flavouring agents
- sulfur containing reducing agents
- 10 • diluting agents
- emulsifying agents
- hydrophilic polymers
- salt-forming counter-ions
- preservatives
- 15 • metal complexes
- solvents and co-solvents
- sugars and sugar alcohols
- suspending agents
- surfactants or wetting agents
- 20 • stability enhancing agents
- tonicity enhancing agents
- parenteral delivery vehicles
- intravenous delivery vehicles

[249] It is common knowledge that the different constituents of the pharmaceutical composition can have different effects, for example, and amino acid can act as a buffer, a stabilizer and/or an antioxidant; mannitol can act as a bulking agent and/or a tonicity enhancing agent; sodium chloride can act as delivery vehicle and/or tonicity enhancing agent; etc.

[250] In the context of the present invention, a pharmaceutical composition may comprise:

- 30 (a) a polypeptide or polypeptide construct as described herein,
- (b) at least one buffer agent,
- (c) at least one saccharide, and
- (d) at least one surfactant;

wherein the pH of the pharmaceutical composition is in the range of 3.5 to 6.

[251] In the composition described above, the first domain preferably has an isoelectric point (pI) in the range of 4 to 9.5; the second domain has a pI in the range of 8 to 10, preferably 8.5 to 9.0; and the construct optionally comprises a third domain comprising two polypeptide monomers, each comprising a hinge, a CH2 domain and a CH3 domain, wherein
5 said two polypeptide monomers are fused to each other via a peptide linker.

[252] In the composition described above, it is further envisaged that the at least one buffer agent is present at a concentration range of 5 to 200 mM, more preferably at a concentration range of 10 to 50 mM. It is also envisaged that the at least one saccharide is selected from the group consisting of monosaccharide, disaccharide, cyclic polysaccharide, sugar alcohol,
10 linear branched dextran or linear non-branched dextran. It is also envisaged that the disaccharide is selected from the group consisting of sucrose, trehalose and mannitol, sorbitol, and combinations thereof. It is further envisaged that the sugar alcohol is sorbitol. It is also envisaged that the at least one saccharide is present at a concentration in the range of 1 to 15% (m/V), preferably in a concentration range of 9 to 12% (m/V). It is further
15 envisaged that the construct is present in a concentration range of 0.1 to 8 mg/ml, preferably of 0.2-2.5 mg/ml, more preferably of 0.25-1.0 mg/ml.

[253] According to one embodiment of the composition described above, the at least one surfactant is selected from the group consisting of polysorbate 20, polysorbate 40, polysorbate 60, polysorbate 80, poloxamer 188, pluronic F68, triton X-100, polyoxyethylen,
20 PEG 3350, PEG 4000 and combinations thereof. It is further envisaged that the at least one surfactant is present at a concentration in the range of 0.004 to 0.5 % (m/V), preferably in the range of 0.001 to 0.01% (m/V). It is envisaged that the pH of the composition is in the range of 4.0 to 5.0, preferably 4.2. It is also envisaged that the pharmaceutical composition has an osmolarity in the range of 150 to 500 mOsm. It is further envisaged that the pharmaceutical
25 composition further comprises an excipient selected from the group consisting of one or more polyol(s) and one or more amino acid(s). It is envisaged in the context of the present invention that said one or more excipient is present in the concentration range of 0.1 to 15 % (w/V).

[254] The present invention also provides a pharmaceutical composition comprising (a) the
30 construct as described herein, preferably in a concentration range of 0.1 to 8 mg/ml, preferably of 0.2-2.5 mg/ml, more preferably of 0.25-1.0 mg/ml; (b) 10 mM glutamate or acetate; (c) 9% (m/V) sucrose or 6% (m/V) sucrose and 6% (m/V) hydroxypropyl- β -cyclodextrin; (d) 0.01% (m/V) polysorbate 80; wherein the pH of the liquid pharmaceutical composition is 4.2.

[255] It is envisaged that the composition of the invention might comprise, in addition to the
35 construct of the invention defined herein, further biologically active agents, depending on the

intended use of the composition. Such agents might be drugs acting on the gastro-intestinal system, drugs acting as cytostatica, drugs preventing hyperurikemia, drugs inhibiting immunoreactions, drugs modulating the inflammatory response, drugs acting on the circulatory system and/or agents such as cytokines known in the art. It is also envisaged that the polypeptide construct of the present invention is applied in a co-therapy, i.e., in combination with another anti-cancer medicament.

[256] In this context, it is envisaged that the pharmaceutical composition of the invention (which comprises a construct comprising a CD3 binding domain and at least a further binding domain which binds to a cell surface target antigen, preferably a tumor antigen on the surface of a target cell, as described in more detail herein above) furthermore comprises an agent, preferably an antibody or construct, which binds to a protein of the immune checkpoint pathway (such as PD-1 or CTLA-4) or to a co-stimulatory immune checkpoint receptor (such as 4-1BB). The present invention also refers to a combination of a polypeptide construct according to the invention (which comprises a construct comprising a CD3 binding domain and at least a further binding domain which binds to a cell surface target antigen, preferably a tumor antigen on the surface of a target cell, as described in more detail herein above) and an agent, preferably an antibody or polypeptide construct, which binds to a protein of the immune checkpoint pathway (such as PD-1 or CTLA-4) or to a co-stimulatory immune checkpoint receptor (such as 4-1BB). Due to the nature of the at least two ingredients of the combination, namely their pharmaceutical activity, the combination can also be referred to as a therapeutic combination. In some embodiments, the combination can be in the form of a pharmaceutical composition or of a kit. According to one embodiment, the pharmaceutical composition or the combination comprises a construct of the invention and an antibody or construct which binds to PD-1. Anti-PD-1 binding proteins useful for this purpose are e.g. described in detail in PCT/US2019/013205 incorporated herein by reference.

[257] In certain embodiments, the optimal pharmaceutical composition is determined depending upon, for example, the intended route of administration, delivery format and desired dosage. See, for example, Remington's Pharmaceutical Sciences, supra. In certain embodiments, such compositions may influence the physical state, stability, rate of in vivo release and rate of in vivo clearance of the construct of the invention. In certain embodiments, the primary vehicle or carrier in a pharmaceutical composition may be either aqueous or non-aqueous in nature. For example, a suitable vehicle or carrier may be water for injection or physiological saline solution, possibly supplemented with other materials common in compositions for parenteral administration. In certain embodiments, the compositions comprising the construct of the invention may be prepared for storage by mixing the selected composition having the desired degree of purity with optional formulation agents (Remington's Pharmaceutical Sciences, supra) in the form of a lyophilized cake or an

aqueous solution. Further, in certain embodiments, the construct of the invention may be formulated as a lyophilizate using appropriate excipients.

[258] When parenteral administration is contemplated, the therapeutic compositions for use in this invention may be provided in the form of a pyrogen-free, parenterally acceptable aqueous solution comprising the desired construct of the invention in a pharmaceutically acceptable vehicle. A particularly suitable vehicle for parenteral injection is sterile distilled water in which the construct of the invention is formulated as a sterile, isotonic solution, properly preserved. In certain embodiments, the preparation can involve the formulation of the desired molecule with an agent that may provide controlled or sustained release of the product which can be delivered via depot injection, or that may promote sustained duration in the circulation. In certain embodiments, implantable drug delivery devices may be used to introduce the desired construct.

[259] Additional pharmaceutical compositions will be evident to those skilled in the art, including formulations involving the construct of the invention in sustained or controlled delivery formulations. Techniques for formulating a variety of sustained- or controlled-delivery means are known to those skilled in the art. The construct may also be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization, in colloidal drug delivery systems, or in macroemulsions. Such techniques are disclosed in Remington's Pharmaceutical Sciences, *supra*.

[260] Pharmaceutical compositions used for *in vivo* administration are typically provided as sterile preparations. Sterilization can be accomplished by filtration through sterile filtration membranes. When the composition is lyophilized, sterilization using this method may be conducted either prior to or following lyophilization and reconstitution. Compositions for parenteral administration can be stored in lyophilized form or in a solution. Parenteral compositions are generally placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

[261] Another aspect of the invention includes self-buffering formulations comprising the construct of the invention, which can be used as pharmaceutical compositions, as described in international patent application WO 2006/138181. A variety of publications are available on protein stabilization and formulation materials and methods useful in this regard, such as Arawaka T. et al., *Pharm Res.* 1991 Mar;8(3):285-91; Kendrick et al., "Physical stabilization of proteins in aqueous solution" in: *Rational Design of Stable Protein Formulations: Theory and Practice*, Carpenter and Manning, eds. *Pharmaceutical Biotechnology*. 13: 61-84 (2002), and Randolph and Jones, *Pharm Biotechnol.* 2002;13:159-75, see particularly the parts

pertinent to excipients and processes for self-buffering protein formulations, especially as to protein pharmaceutical products and processes for veterinary and/or human medical uses.

[262] Salts may be used in accordance with certain embodiments of the invention, e.g. to adjust the ionic strength and/or the isotonicity of a composition or formulation and/or to improve the solubility and/or physical stability of a construct or other ingredient of a composition in accordance with the invention. Ions can stabilize the native state of proteins by binding to charged residues on the protein's surface and by shielding charged and polar groups in the protein and reducing the strength of their electrostatic interactions, attractive, and repulsive interactions. Ions also can stabilize the denatured state of a protein by binding to, particularly the denatured peptide linkages ($--CONH$) of the protein. Furthermore, ionic interaction with charged and polar groups in a protein also can reduce intermolecular electrostatic interactions and, thereby, prevent or reduce protein aggregation and insolubility.

[263] Ionic species differ significantly in their effects on proteins. Several categorical rankings of ions and their effects on proteins have been developed that can be used in formulating pharmaceutical compositions in accordance with the invention. One example is the Hofmeister series, which ranks ionic and polar non-ionic solutes by their effect on the conformational stability of proteins in solution. Stabilizing solutes are referred to as "kosmotropic". Destabilizing solutes are referred to as "chaotropic". Kosmotropes are commonly used at high concentrations to precipitate proteins from solution ("salting-out"). Chaotropes are commonly used to denature and/or to solubilize proteins ("salting-in"). The relative effectiveness of ions to "salt-in" and "salt-out" defines their position in the Hofmeister series.

[264] Free amino acids can be used in formulations or compositions comprising the construct of the invention in accordance with various embodiments of the invention as bulking agents, stabilizers, and antioxidants, as well as for other standard uses. Certain amino acids can be used for stabilizing proteins in a formulation, others are useful during lyophilization to ensure correct cake structure and properties of the active ingredient. Some amino acids may be useful to inhibit protein aggregation in both liquid and lyophilized formulations, and others are useful as antioxidants.

[265] Polyols are kosmotropic and are useful as stabilizing agents in both liquid and lyophilized formulations to protect proteins from physical and chemical degradation processes. Polyols are also useful for adjusting the tonicity of formulations and for protecting against freeze-thaw stresses during transport or the preparation of bulks during the manufacturing process. Polyols can also serve as cryoprotectants in the context of the present invention.

[266] Certain embodiments of the formulation or composition comprising the construct of the invention can comprise surfactants. Proteins may be susceptible to adsorption on surfaces and to denaturation and resulting aggregation at air-liquid, solid-liquid, and liquid-liquid interfaces. These deleterious interactions generally scale inversely with protein concentration and are typically exacerbated by physical agitation, such as that generated during the shipping and handling of a product. Surfactants are routinely used to prevent, minimize, or reduce surface adsorption. Surfactants also are commonly used to control protein conformational stability. The use of surfactants in this regard is protein specific, since one specific surfactant will typically stabilize some proteins and destabilize others.

[267] Certain embodiments of the formulation or composition comprising the construct of the invention can comprise one or more antioxidants. To some extent deleterious oxidation of proteins can be prevented in pharmaceutical formulations by maintaining proper levels of ambient oxygen and temperature and by avoiding exposure to light. Antioxidant excipients can also be used to prevent oxidative degradation of proteins. It is envisaged that antioxidants for use in therapeutic protein formulations in accordance with the present invention can be water-soluble and maintain their activity throughout the shelf life of the product (the composition comprising the construct). Antioxidants can also damage proteins and should hence – among other things – be selected in a way to eliminate or sufficiently reduce the possibility of antioxidants damaging the construct or other proteins in the formulation.

[268] Certain embodiments of the formulation or composition comprising the construct of the invention can comprise one or more preservatives. Preservatives are necessary for example when developing multi-dose parenteral formulations that involve more than one extraction from the same container. Their primary function is to inhibit microbial growth and ensure product sterility throughout the shelf-life or term of use of the drug product. Although preservatives have a long history of use with small-molecule parenterals, the development of protein formulations that include preservatives can be challenging. Preservatives very often have a destabilizing effect (aggregation) on proteins, and this has become a major factor in limiting their use in multi-dose protein formulations. To date, most protein drugs have been formulated for single-use only. However, when multi-dose formulations are possible, they have the added advantage of enabling patient convenience, and increased marketability. A good example is that of human growth hormone (hGH) where the development of preserved formulations has led to commercialization of more convenient, multi-use injection pen presentations. Several aspects need to be considered during the formulation and development of preserved dosage forms. The effective preservative concentration in the drug product must be optimized. This requires testing a given preservative in the dosage form with

concentration ranges that confer anti-microbial effectiveness without compromising protein stability.

[269] As might be expected, development of liquid formulations containing preservatives are more challenging than lyophilized formulations. Freeze-dried products can be lyophilized without the preservative and reconstituted with a preservative containing diluent at the time of use. This shortens the time during which a preservative is in contact with the construct, significantly minimizing the associated stability risks. With liquid formulations, preservative effectiveness and stability should be maintained over the entire product shelf-life. An important point to note is that preservative effectiveness should be demonstrated in the final formulation containing the active drug and all excipient components. Once the pharmaceutical composition has been formulated, it may be stored in sterile vials as a solution, suspension, gel, emulsion, solid, crystal, or as a dehydrated or lyophilized powder. Such formulations may be stored either in a ready-to-use form or in a form (e.g., lyophilized) that is reconstituted prior to administration.

[270] The biological activity of the pharmaceutical composition defined herein can be determined for instance by in vitro cytotoxicity assays, as described in the following examples, in WO 99/54440 or by Schlereth et al. (Cancer Immunol. Immunother. 20 (2005), 1-12). "Efficacy" or "in vivo efficacy" as used herein refers to the response to therapy by the pharmaceutical composition of formulation of the invention, using e.g. standardized NCI response criteria. The success or in vivo efficacy of the therapy using a pharmaceutical composition of the invention refers to the effectiveness of the composition for its intended purpose, i.e. the ability of the composition to cause its desired effect, i.e. depletion of pathologic cells, e.g. tumor cells. The in vivo efficacy may be monitored by established standard methods for the respective disease entities including, but not limited to, white blood cell counts, differentials, fluorescence activated cell sorting, bone marrow aspiration. In addition, various disease specific clinical chemistry parameters and other established standard methods may be used. Furthermore, computer-aided tomography, X-ray, nuclear magnetic resonance tomography, positron-emission tomography scanning, lymph node biopsies/histologies and other established standard methods may be used.

[271] Another major challenge in the development of drugs such as the pharmaceutical composition of the invention is the predictable modulation of pharmacokinetic properties. To this end, a pharmacokinetic profile of the drug candidate, i.e. a profile of the pharmacokinetic parameters that affect the ability of a specific drug to treat a given condition, can be established. Pharmacokinetic parameters of the drug influencing the ability of a drug for treating a certain disease entity include, but are not limited to: half-life, volume of distribution,

hepatic first-pass metabolism and the degree of blood serum binding. The efficacy of a given drug agent can be influenced by each of the parameters mentioned above.

[272] "Half-life" is the time required for a quantity to reduce to half its initial value. The medical sciences refer to the half-life of substances or drugs in the human body. In a medical context, half-life may refer to the time it takes for a substance / drug to lose one-half of its activity, e.g. pharmacologic, physiologic, or radiological activity. The half-life may also describe the time that it takes for the concentration of a drug or substance (e.g., a construct of the invention) in blood plasma / serum to reach one-half of its steady-state value ("serum half-life"). Typically, the elimination or removal of an administered substance / drug refers to the body's cleansing through biological processes such as metabolism, excretion, also involving the function of kidneys and liver. The "first-pass metabolism" is a phenomenon of drug metabolism whereby the concentration of a drug is reduced before it reaches the circulation. It is the fraction of drug lost during the process of absorption. Accordingly, by "hepatic first-pass metabolism" is meant the propensity of a drug to be metabolized upon first contact with the liver, i.e. during its first pass through the liver. "Volume of distribution" (VD) means the degree to which a drug is distributed in body tissue rather than the blood plasma, a higher VD indicating a greater amount of tissue distribution. The retention of a drug can occur throughout the various compartments of the body, such as intracellular and extracellular spaces, tissues and organs, etc. "Degree of blood serum binding" means the propensity of a drug to interact with and bind to blood serum proteins, such as albumin, leading to a reduction or loss of biological activity of the drug.

[273] Pharmacokinetic parameters also include bioavailability, lag time (T lag), T_{max}, absorption rates, and/or C_{max} for a given amount of drug administered. "Bioavailability" refers to the fraction of an administered dose of a drug / substance that reaches the systemic circulation (the blood compartment). When a medication is administered intravenously, its bioavailability is considered to be 100%. However, when a medication is administered via other routes (such as orally), its bioavailability generally decreases. "Lag time" means the time delay between the administration of the drug and its detection and measurability in blood or plasma. C_{max} is the maximum plasma concentration that a drug achieves after its administration (and before the administration of a second dose). T_{max} is the time at which C_{max} is reached. The time to reach a blood or tissue concentration of the drug which is required for its biological effect is influenced by all parameters. Pharmacokinetic parameters of constructs exhibiting cross-species specificity may be determined in preclinical animal testing in non-chimpanzee primates as outlined above and set forth e.g. in Schlereth et al. (supra).

[274] One embodiment provides the construct of the invention (or the construct produced according to the process of the invention), for the use as a medicament, particularly for the use in the prevention, treatment or amelioration (preferably treatment) of a disease, preferably a tumorous disease, more preferred a neoplasm, cancer or tumor. Another embodiment provides the use of the construct of the invention (or of the construct produced according to the process of the invention) in the manufacture of a medicament for the prevention, treatment or amelioration of a disease, preferably a tumorous disease, more preferred a neoplasm, cancer or tumor. It is also envisaged to provide a method for the prevention, treatment or amelioration of a disease, preferably a tumorous disease, more preferred a neoplasm, cancer or tumor, comprising the step of administering to a subject in need thereof the construct of the present invention (or the construct produced according to the process of the present invention). The terms "subject in need", "patient" or those "in need of treatment" include those already with the disease, as well as those in which the disease is to be prevented. The terms also include human and other mammalian subjects that receive either prophylactic or therapeutic treatment.

[275] The polypeptides/polypeptide constructs of the invention and the formulations / pharmaceutical compositions described herein are useful in the treatment, amelioration and/or prevention of the medical condition as described herein in a patient in need thereof. The term "treatment" refers to both therapeutic treatment and prophylactic or preventative measures. Treatment includes the application or administration of the polypeptides/polypeptide constructs / pharmaceutical composition to the body, to an isolated tissue, or to a cell from a patient or a subject in need who has a disease/disorder as described herein, a symptom of such disease/disorder, or a predisposition toward such disease/disorder, with the purpose to cure, heal, alleviate, relieve, alter, remedy, ameliorate, improve, or affect the disease, the symptom of the disease, or the predisposition toward the disease. The term "amelioration" as used herein refers to any improvement of the disease state of a patient, by the administration of a polypeptide construct according to the invention to such patient or subject in need thereof. Such an improvement may be a slowing down or stopping of the progression of the disease of the patient, and/or as a decrease in severity of disease symptoms, an increase in frequency or duration of disease symptom-free periods or a prevention of impairment or disability due to the disease. The term "prevention" as used herein means the avoidance of the occurrence or of the re-occurrence of a disease as specified herein, by the administration of a construct according to the invention to a subject in need thereof.

[276] The term "disease" refers to any condition that would benefit from treatment with the construct or the pharmaceutical composition described herein. This includes chronic and acute disorders or diseases including those pathological conditions that predispose the

mammal to the disease in question. The disease is preferably a tumorous disease, more preferred a neoplasm, cancer or tumor. The disease, neoplasm, cancer or tumor is preferably positive for a tumor antigen, preferably such as those defined herein above, i.e. it is characterized by expression or overexpression of a tumor antigen, preferably such as those defined herein above. An overexpression of a tumor antigen means that there is an increase by at least 10%, in particular at least 25%, at least 50%, at least 100%, at least 250%, at least 500%, at least 750%, at least 1000% or even more. Expression is, preferably, only found in a diseased tissue, while expression in a corresponding healthy tissue is not or significantly not detectable. According to the invention, diseases associated with cells expressing a tumor antigen, preferably such as those defined herein above, include cancer diseases. Furthermore, according to the invention, cancer diseases preferably are those wherein the cancer cells express a tumor antigen. In accordance with the invention, the disease, preferably tumorous disease, more preferred neoplasm, tumor or cancer is preferably characterized by the presence of BCMA-positive, CD123-positive, CD19-positive, CD20-positive, CD22-positive, CD33-positive, CD70-positive, CDH19-positive, CDH3-positive, CLL1-positive, CS1-positive, CLDN6-positive, CLDN18.2-positive, DLL3-positive, EGFRvIII-positive, FLT3-positive, MAGEB2-positive, MART1-positive, MSLN-positive, MUC17-positive, PSMA-positive, or STEAP1-positive cells. In other words, the tumorous disease, more preferred neoplasm, tumor or cancer is preferably associated with the presence of BCMA-positive, CD123-positive, CD19-positive, CD20-positive, CD22-positive, CD33-positive, CD70-positive, CDH19-positive, CDH3-positive, CLL1-positive, CS1-positive, CLDN6-positive, CLDN18.2-positive, DLL3-positive, EGFRvIII-positive, FLT3-positive, MAGEB2-positive, MART1-positive, MSLN-positive, MUC17-positive, PSMA-positive, or STEAP1-positive cells; the tumorous disease, more preferred neoplasm, tumor or cancer can therefore be termed a BCMA-positive, CD123-positive, CD19-positive, CD20-positive, CD22-positive, CD33-positive, CD70-positive, CDH19-positive, CDH3-positive, CLL1-positive, CS1-positive, CLDN6-positive, CLDN18.2-positive, DLL3-positive, EGFRvIII-positive, FLT3-positive, MAGEB2-positive, MART1-positive, MSLN-positive, MUC17-positive, PSMA-positive, or STEAP1-positive neoplasm, tumor or cancer. It is understood herein, that each of said tumor antigen-positive neoplasms, tumors or cancers can be prevented, treated or ameliorated using a polypeptide or polypeptide construct according to the invention that comprises a binding domain against the tumor antigen expressed by the cells with which said neoplasm, tumor or cancer is associated with. A BCMA-positive, CD123-positive, CD19-positive, CD20-positive, CD22-positive, CD33-positive, CD70-positive, CDH19-positive, CDH3-positive, CLL1-positive, CS1-positive, CLDN6-positive, CLDN18.2-positive, DLL3-positive, EGFRvIII-positive, FLT3-positive, MAGEB2-positive, MART1-positive, MSLN-positive, MUC17-positive, PSMA-positive, or STEAP1-positive neoplasm, tumor or cancer

can be prevented, treated or ameliorated using a polypeptide or polypeptide construct according to the invention that comprises a binding domain against BCMA (for a BCMA-positive neoplasm, tumor or cancer), CD123 (for a CD123-positive neoplasm, tumor or cancer), CD19 (for a CD19-positive neoplasm, tumor or cancer), CD20 (for a CD20-positive neoplasm, tumor or cancer), CD22 (for a CD22-positive neoplasm, tumor or cancer), CD33 (for a CD33-positive neoplasm, tumor or cancer), CD70 (for a CD70-positive neoplasm, tumor or cancer), CDH19 (for a CDH19-positive neoplasm, tumor or cancer), CDH3 (for a CDH3-positive neoplasm, tumor or cancer), CLL1 (for a CLL1-positive neoplasm, tumor or cancer), CS1 (for a CS1-positive neoplasm, tumor or cancer), CLDN6 (for a CLDN6-positive neoplasm, tumor or cancer), CLDN18.2 (for a CLDN18.2-positive neoplasm, tumor or cancer), DLL3 (for a DLL3-positive neoplasm, tumor or cancer), EGFRvIII (for a EGFRvIII-positive neoplasm, tumor or cancer), FLT3 (for a FLT3-positive neoplasm, tumor or cancer), MAGEB2 (for a MAGEB2-positive neoplasm, tumor or cancer), MART1 (for a MART1-positive neoplasm, tumor or cancer), MSLN (for a MSLN-positive neoplasm, tumor or cancer), MUC17 (for a MUC17-positive neoplasm, tumor or cancer), PSMA (for a PSMA-positive neoplasm, tumor or cancer), and STEAP1 (for a STEAP1-positive neoplasm, tumor or cancer), respectively.

[277] A “neoplasm” is an abnormal growth of tissue, usually but not always forming a mass. When also forming a mass, it is commonly referred to as a “tumor”. Neoplasms or tumors can be benign, potentially malignant (pre-cancerous), or malignant (cancerous). Malignant neoplasms / tumors are commonly called cancer. They usually invade and destroy the surrounding tissue and may form metastases, i.e., they spread to other parts, tissues or organs of the body. A “primary tumor” is a tumor growing at the anatomical site where tumor progression began and proceeded to yield a cancerous mass. Most cancers develop at their primary site but then go on to metastasize or spread to other parts (e.g. tissues and organs) of the body. These further tumors are “secondary tumors”. Most cancers continue to be called after their primary site, even after they have spread to other parts of the body.

[278] Lymphomas and leukemias are lymphoid neoplasms. For the purposes of the present invention, they are also encompassed by the terms “tumor” and “cancer”. For the purposes of the present invention, the terms “neoplasm”, “tumor” and “cancer” may be used interchangeably, and they comprise both primary tumors / cancers and secondary tumors / cancers (or “metastases”) as well as mass-forming neoplasms (tumors) and lymphoid neoplasms (such as lymphomas and leukemias), and minimal residual disease (MRD).

[279] The term “minimal residual disease” (MRD) refers to the evidence for the presence of small numbers of residual cancer cells that remain in the patient after cancer treatment, e.g. when the patient is in remission (no symptoms or signs of disease). A very small number of

remaining cancer cells usually cannot be detected by routine means because the standard tests used to assess or detect cancer are not sensitive enough to detect MRD. Nowadays, very sensitive molecular biology tests for MRD are available, such as flow cytometry, PCR and next-generation sequencing. These tests can measure minimal levels of cancer cells in tissue samples, sometimes as low as one cancer cell in a million normal cells. In the context of the present invention, the terms "prevention", "treatment" or "amelioration" of a cancer are envisaged to also encompass "prevention, treatment or amelioration of MRD", whether the MRD was detected or not.

[280] The construct of the invention will generally be designed for specific routes and methods of administration, for specific dosages and frequencies of administration, for specific treatments of specific diseases, with ranges of bio-availability and persistence, among other things. The materials of the composition are preferably formulated in concentrations that are acceptable for the site of administration. Formulations and compositions thus may be designed in accordance with the invention for delivery by any suitable route of administration. In the context of the present invention, the routes of administration include, but are not limited to topical routes, enteral routes and parenteral routes.

[281] If the pharmaceutical composition has been lyophilized, the lyophilized material is first reconstituted in an appropriate liquid prior to administration. The lyophilized material may be reconstituted in, e.g., bacteriostatic water for injection (BWFI), physiological saline, phosphate buffered saline (PBS), or the same formulation the protein had been in prior to lyophilization. The pharmaceutical compositions and the construct of this invention are particularly useful for parenteral administration, e.g., intravenous delivery, for example by injection or infusion. Pharmaceutical compositions may be administered using a medical device. Examples of medical devices for administering pharmaceutical compositions are described in U.S. Patent Nos. 4,475,196; 4,439,196; 4,447,224; 4,447,233; 4,486,194; 4,487,603; 4,596,556; 4,790,824; 4,941,880; 5,064,413; 5,312,335; 5,312,335; 5,383,851; and 5,399,163.

[282] The compositions of the present invention can be administered to the subject at a suitable dose which can be determined e.g. in dose escalating studies. As set forth above, the construct of the invention exhibiting cross-species specificity as described herein can also be advantageously used in preclinical testing in non-chimpanzee primates. The dosage regimen will be determined by the attending physician and clinical factors. As is well known in the medical art, dosages for any one patient depend upon many factors, including the patient's size, body surface area, age, the specific compound to be administered, sex, time and route of administration, general health, and other drugs being administered concurrently.

[283] An “effective dose” is an amount of a therapeutic agent that is sufficient to achieve or at least partially achieve a desired effect. A “therapeutically effective dose” is an amount that is sufficient to cure or at least partially arrest the disease and its complications, signs and symptoms in a patient suffering from the disease. Amounts or doses effective for this use will depend on the disease to be treated (the indication), the delivered construct, the therapeutic context and objectives, the severity of the disease, prior therapy, the patient's clinical history and response to the therapeutic agent, the route of administration, the size (body weight, body surface) and/or condition (the age and general health) of the patient, and the general state of the patient's own immune system. The proper dose can be adjusted according to the judgment of the attending physician, to obtain the optimal therapeutic effect.

[284] A therapeutically effective amount of a construct of the invention preferably results in a decrease in severity of disease symptoms, an increase in frequency or duration of disease symptom-free periods or a prevention of impairment or disability due to the disease. In the treatment of tumor antigen-expressing tumors, a therapeutically effective amount of the construct of the invention comprising a binding domain against said tumor antigen preferably inhibits tumor cell growth by at least about 20%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, or at least about 90% relative to untreated patients. The ability of a compound to inhibit tumor growth may also be evaluated in an animal model predictive of efficacy in human tumors.

[285] In a further embodiment, the invention provides a kit comprising a construct of the invention, a construct produced according to the process of the invention, a polynucleotide of the invention, a vector of the invention, and/or a host cell of the invention. In the context of the present invention, the term “kit” means two or more components – one of which corresponding to the construct, the pharmaceutical composition, the polynucleotide, the vector or the host cell of the invention – packaged together in a container, recipient or otherwise. A kit can hence be described as a set of products and/or utensils that are sufficient to achieve a certain goal, which can be marketed as a single unit.

[286] It is envisaged that a further component of the kit of the invention is an agent, preferably an antibody or construct, which binds to a protein of the immune checkpoint pathway (such as PD-1 or CTLA-4) or to a co-stimulatory immune checkpoint receptor (such as 4-1BB). These agents are described in more detail herein above. According to one embodiment, the kit comprises a construct of the invention and an antibody or construct which binds to PD-1. Anti-PD-1 binding proteins useful for this purpose are e.g. described in detail in PCT/US2019/013205. In certain embodiment, the kit allows for the simultaneous and/or sequential administration of the components.

[287] The kit may comprise one or more recipients (such as vials, ampoules, containers, syringes, bottles, bags) of any appropriate shape, size and material (preferably waterproof, e.g. plastic or glass) containing the construct or the pharmaceutical composition of the present invention in an appropriate dosage for administration (see above). The kit may additionally contain directions for use (e.g. in the form of a leaflet or instruction manual), means for administering the construct or the pharmaceutical composition of the present invention such as a syringe, pump, infuser or the like, means for reconstituting the construct of the invention and/or means for diluting the construct of the invention.

[288] The invention also provides kits for a single-dose administration unit. The kit of the invention may also contain a first recipient comprising a dried / lyophilized construct or pharmaceutical composition and a second recipient comprising an aqueous formulation. In certain embodiments of this invention, kits containing single-chambered and multi-chambered pre-filled syringes are provided.

[289] Whenever the term “construct” is used herein, said term refers to the used polypeptide/polypeptide constructs of the invention or controls thereof as indicated.

[290] As used herein, the singular forms “a”, “an”, and “the” include plural references unless the context clearly indicates otherwise. Thus, for example, reference to “a reagent” includes one or more of such different reagents and reference to “the method” includes reference to equivalent steps and methods known to those of ordinary skill in the art that could be modified or substituted for the methods described herein.

[291] Unless otherwise indicated, the term “at least” preceding a series of elements is to be understood to refer to every element in the series. Those skilled in the art will recognize or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the present invention.

[292] The term “and/or” wherever used herein includes the meaning of “and”, “or” and “all or any other combination of the elements connected by said term”.

[293] The term “about” or “approximately” as used herein means within $\pm 20\%$, preferably within $\pm 15\%$, more preferably within $\pm 10\%$, and most preferably within $\pm 5\%$ of a given value or range. It also includes the concrete value, e.g., “about 50” includes the value “50”.

[294] Throughout this specification and the claims, 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

“comprising” can be substituted with the term “containing” or “including” or sometimes when used herein with the term “having”.

[295] 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
5 exclude materials or steps that do not materially affect the basic and novel characteristics of the claim.

[296] In each instance herein, any of the terms “comprising”, “consisting essentially of” and “consisting of” may be replaced with either of the other two terms.

[297] The above description and the below examples provide exemplary arrangements, but
10 the present invention is not limited to the specific methodologies, techniques, protocols, material, reagents, substances, etc., described herein and as such can vary. The terminology used herein serves to describe specific embodiments only. The terminology used herein does not intend to limit the scope of the present invention, which is defined solely by the claims. Aspects of the invention are provided in the independent claims. Some optional
15 features of the invention are provided in the dependent claims.

[298] All publications and patents cited throughout the text of this specification (including all patents, patent applications, scientific publications, manufacturer’s specifications, instructions, etc.), whether supra or infra, are hereby incorporated by reference in their entirety. Nothing herein is to be construed as an admission that the invention is not entitled to
20 antedate such disclosure by virtue of prior invention. To the extent the material incorporated by reference contradicts or is inconsistent with this specification, the specification will supersede any such material.

[299] A better understanding of the present invention and of its advantages will be obtained from the following examples, offered for illustrative purposes only. The examples are not
25 intended and should not be construed as to limit the scope of the present invention in any way.

Brief Description of the Drawings:

[300] Figure 1 A): Effector cells: human unstimulated T cells; Target cells: CHO hu CD70 pEFDHR

Legend:

- 5 I2C: CD70 1-A9D CC x I2C x scFc
- I2CA: CD70 1-A9D CC x I2C H109A x scFc
- 8A8.04: CD70 1-A9D CC x 8A8.04 x scFc
- 5C3.04: CD70 1-A9D CC x 5C3.04 x scFc
- I2E: CD70 1-A9D CC x 5C3.01 x scFc
- 10 I2K: CD70 1-A9D CC x 5G6.05 x scFc
- 5G6.04: CD70 1-A9D CC x 5G6.04 x scFc
- 5G6.03: CD70 1-A9D CC x 5G6.03 x scFc
- 1D5.04: CD70 1-A9D CC x 1D5.04 x scFc
- 8A8.02: CD70 1-A9D CC x 8A8.02 x scFc
- 15 1D5.03: CD70 1-A9D CC x 1D5.03 x scFc

[301] Figure 1 B): Effector cells: human unstimulated T cells; Target cells: hu orl FLT3 v1 co CHO #12

Legend:

- I2C: FL 7-H3 CC x I2C x scFc
- 20 5G6.04: FL 7-H3 CC x 5G6.04 x scFc
- 8A8.04: FL 7-H3 CC x 8A8.04 x scFc
- 5C3.04: FL 7-H3 CC x 5C3.04 x scFc
- I2E: FL 7-H3 CC x 5C3.01 x scFc
- I2K: FL 7-H3 CC x 5G6.05 x scFc
- 25 I2C CC 44/100: FL 7-H3 CC x I2C CC 44/100 x scFc

Examples

[302] Example 1: Thermal stability

[303] Purified monomeric BiTE® protein at 1 mg/ml formulated in screening buffer was analysed. Thermal stability was determined by Dynamic Light Scattering DLS and Differential Scanning Fluorometry DSF.

[304] DLS

100 µl protein solution were transferred in doubles in a multi well plate, overlaid with paraffin oil and placed in a DLS plate reader (DynaPro Plate Reader II with temperature control, Wyatt Technology Europe GmbH, Dernbach – Germany). Thermal stability was determined in a linear increasing temperature scan from 40°C to 70°C while measuring the hydrodynamic radius at the different temperatures in this range. Aggregation temperature was defined at the temperature the radius begins to expand. The mean of both determined aggregation temperatures was calculated and used for candidate ranking.

[305] DSF

Three glass capillaries were filled each with approx. 40 µl protein solution and placed simultaneously into a DSF reader with temperature control (Prometheus nanoDSF, NanoTemper Technologies GmbH, Munich - Germany). Protein internal fluorescence was measured at an excitation wavelength of 280 nm and emission wavelengths 330 and 350 nm in a linear increasing temperature scan from 20°C to 95°C. Changes in the ratio of the two emission wavelength intensities indicate conformational changes in the protein therefore showing the melting temperature(s) of the analyzed BiTE proteins. The first maximum of the first derivate of the ratio 350/330 nm curve was defined as first melting temperature. The mean of all three determined first melting temperatures was calculated and used for candidate ranking.

[306] The incorporation of specific amino acid mutations in the sequence of the anti-CD3 binder I2C (VH and VL defined in SEQ ID NO: 1854 and 1855, respectively, and linked with a peptide linker of SEQ ID NO: 2; CD70 target binder VH and VL defined in SEQ ID NOs: 2185 and 2186, respectively, and linked with a peptide linker of SEQ ID NO: 2; CD70 binding domain linked to CD3 binding domain with linker of SEQ ID NO: 6; HLE domain as specified in SEQ ID NO: 18 linked with a G4 linker to the C-terminus of the VL region of the CD3 binder; CD70 binding domain is at the N-terminus, followed by the CD3 binding domain with the HLE domain at the C-terminus of the BiTE® molecule) in the BiTE-HLE context resulted in aggregation temperature values of 57.5°C to 62.0 °C determined by Dynamic Light Scattering (DLS) and melting temperature values of 62.9 °C to 70.3 °C determined by Differential scanning Fluorometry (DSF). The BiTE-HLE molecules harboring the I2C variants

showed an aggregation temperature increase of 2.3 °C to 6.8 °C in comparison to the unmodified I2C. The same effect was observed in the melting temperature measurements of the I2C variants resulting in an increase of 2.1 °C to 9.5 °C as compared to the unmodified I2C.

- 5 **[307]** Also the BiTE-HLE construct containing the anti-CD3 binder variant I2C CC44/100, in which an additional disulfide bond was engineered for stabilizing (Reiter, Y. et al., 1994) by replacing the amino acid residues with Cysteine residues at position 44 in the heavy chain variable region and at position 100 in the light chain variable region (numbering scheme according to Kabat et al., 1991), showed a thermostability increase of 3.2 °C for DLS and 5.3
- 10 °C for DSF as compared to the unmodified I2C. However, said BiTE®-HLE construct exhibited a significantly decreased cytotoxic activity (see further example) resulting in a construct which is therefore not suitable for further development and use as a part of T cell engagers.

[308]

CD3 binder	Thermostability		
in CD70 BiTE-HLE	DLS aggregation [°C]	DSF melting [°C]	CD3 binding domain SEQ ID NOs: VH, VL, linker
I2E	59,4	68,7	2012, 2013, 2
I2K	58,8	64,6	2020, 2021, 2
I2L	60,4	69,3	2028, 2029, 2
I2M	60,3	67,3	2036, 2037, 2
I2M2	58,9	66,9	2044, 2045, 2
1D5.01	62,0	70,3	42, 43, 2
1D5.03	61,5	70,0	50, 51, 2
1D5.04	61,8	69,7	58, 59, 2
4G10.04	59,4	66,0	66, 67, 2
5B1.05	58,6	67,8	74, 75, 2
5B1.09	58,8	68,2	82, 83, 2
5C3.04	60,6	69,2	90, 91, 2
5C3.05	60,5	69,2	98, 99, 2
5G6.03	60,1	67,4	100, 101, 2
5G6.04	59,3	65,5	108, 109, 2
6H10.03	60,0	67,3	116, 117, 2
8A8.02	59,4	65,9	26, 27, 2
8A8.04	59,3	67,0	34, 35, 2
I2C CC44/100	58,4	66,1	
I2C H109A	57,5	62,9	2560, 2561, 2
I2C	55,2	60,8	1854, 1855, 2

Table 2: Aggregation and melting temperatures of BiTE-HLE molecules harboring various CD3 binding domains determined by Dynamic Light Scattering (DLS) or Differential scanning Fluorometry (DSF), respectively.

[309] The mutation of single or more amino acids in the sequence of the anti-CD3 binder I2C in the BiTE-HLE context resulted in aggregation temperature values of 57.0°C to 62.4°C determined by Dynamic Light Scattering (DLS) and melting temperature values of 62.1°C to 68.8°C determined by Differential scanning Fluorometry (DSF). The BiTE-HLE molecules harboring the I2C mutants showed an aggregation temperature increase of 1.8°C to 7.2°C in comparison to the unmodified I2C. The same effect was observed in the melting temperature measurements of the I2C mutants resulting in an increase of 1.0°C to 7.7°C as compared to the unmodified I2C. The CD3 binder as referenced in the below Table specifies the amino acid residue exchanges and their positions in the first column; for each entry it is shown in brackets the positions as used in reference to the base sequence of the VH region sequence as defined in SEQ ID NO: 1854 and the VL region sequence as defined in SEQ ID NO: 1855 which is the authoritative nomenclature in accordance with the invention.

CD3 binder	Thermostability		
in CD70 BiTE-HLE	DLS aggregation [°C]	DSF melting [°C]	CD3 binding domain SEQ ID NOs: VH, VL, linker
I2C_HC_A89V_V107A_LC_L21I_Q46K_L83S_G141S (I2C_HC_A81V_V99A_LC_L20I_Q40K_L69S_G102S)	61,0	68,8	
I2C_HC_M41I_A89V_LC_L21I_Q46K_G141S (I2C_HC_M34I_A81V_LC_L20I_Q40K_G102S)	62,4	68,6	1898, 1899, 2
I2C_HC_M41I_LC_L21I_Q46K_G141S (I2C_HC_M34I_LC_L20I_Q40K_G102S)	61,9	68,3	1904, 1905, 2
I2C_HC_M41I_Q46E_A89V_LC_L21I_Q46K_G141S (I2C_HC_M34I_Q39E_A81V_LC_L20I_Q40K_G102S)	61,4	68,2	1906, 1907, 2
I2C_HC_M41I_A89V_LC_Q46K (I2C_HC_M34I_A81V_LC_Q40K)	60,5	66,6	1900, 1901, 2
I2C_HC_L52M_LC_L21I_Q46K_G141S (I2C_HC_L45M_LC_L20I_Q40K_G102S)	58,6	65,7	1866, 1867, 2
I2C_HC_M41I_S73A_H109A_N114S (I2C_HC_M34I_S65A_H101A_N106S)	59,0	65,4	
I2C_LC_L21I_Q46K_L83S_G141S (I2C_LC_L20I_Q40K_L69S_G102S)	59,0	65,3	
I2C_HC_M41F_A89V (I2C_HC_M34F_A81V)	59,3	65,0	1884, 1885, 2
I2C_HC_L52M_LC_Q46K_G141S (I2C_HC_L45M_LC_Q40K_G102S)	59,5	65,0	1870, 1871, 2
I2C_HC_Q46D_LC_L21I_Q46K_G141S (I2C_HC_Q39D_LC_L20I_Q40K_G102S)	58,3	64,7	1918, 1919, 2
I2C_HC_M41I_A89V (I2C_HC_M34I_A81V)	59,1	64,3	1896, 1897, 2

			2
I2C_HC_Q46E_LC_L21I_Q46K_G141S (I2C_HC_Q39E_LC_L20I_Q40K_G102S)	58,9	64,3	1932, 1933, 2
I2C_HC_L52M_LC_Q46K (I2C_HC_L45M_LC_Q40K)	58,9	64,3	1868, 1869, 2
I2C_HC_M41I_S73A_A89V_V107A_H109A_N114S (I2C_HC_M34I_S65A_A81V_V99A_H101A_N106S)	58,1	64,2	
I2C_HC_Q46D_LC_L21I_Q46R_G141S (I2C_HC_Q39D_LC_L20I_Q40R_G102S)	58,2	63,7	1928, 1929, 2
I2C_HC_M41I (I2C_HC_M34I)	58,2	63,6	1892, 1893, 2
I2C_LC_Q46K (I2C_LC_Q40K)	58,4	63,5	1974, 1975, 2
I2C_HC_Q46D_LC_Q46K_G141S (I2C_HC_Q39D_LC_Q40K_G102S)	58,2	63,5	1922, 1923, 2
I2C_LC_L21I_G141S (I2C_LC_L20I_G102S)	57,4	63,2	
I2C_HC_Q46K (I2C_HC_Q39K)	57,4	63,2	1944, 1945, 2
I2C_HC_Q46E_LC_Q46K_G141S (I2C_HC_Q39E_LC_Q40K_G102S)	58,0	63,2	1938, 1939, 2
I2C_HC_Q46E_LC_L21I_Q46R_G141S (I2C_HC_Q39E_LC_L20I_Q40R_G102S)	57,9	63,0	1934, 1935, 2
I2C_HC_Q46D_LC_Q46R_G141S (I2C_HC_Q39D_LC_Q40R_G102S)	57,3	62,9	1926, 1927, 2
I2C_HC_A89V (I2C_HC_A81V)	58,2	62,9	1862, 1863, 2
I2C_HC_Q46D_LC_Q46K (I2C_HC_Q39D_LC_Q40K)	57,1	62,8	1920, 1921, 2
I2C_HC_W136F (I2C_HC_W112F)	57,0	62,7	1958, 1959, 2
I2C_HC_W136F_LC_V44I (I2C_HC_W112F _LC_V38I)	57,8	62,4	1960, 1961, 2
I2C_HC_Q46E_LC_Q46K (I2C_HC_Q39E_LC_Q40K)	58,2	62,3	1936, 1937, 2
I2C_HC_M41V (I2C_HC_M34V)	57,6	62,1	1914, 1915, 2
I2C	55,2	60,8	

Table 3: Aggregation and melting temperatures of BiTE-HLE molecules harboring the CD3 binding domain "I2C" (SEQ ID NO: 1854 and 1855, respectively, linked by peptide linker (G₄S)₃ (SEQ ID NO: 2)), respectively) with several amino acid mutations determined by Dynamic Light Scattering (DLS) or Differential scanning Fluorometry (DSF), respectively, as described herein above.

[310]

[311] **Example 2: Cytotoxic activity**

[312] Cytotoxic activity

Human peripheral blood mononuclear cells (PBMC) were prepared by Ficoll density gradient centrifugation from enriched lymphocyte preparations (buffy coats), a side product of blood banks collecting blood for transfusions. Buffy coats were supplied by a local blood bank and PBMC were prepared on the same day of blood collection. After Ficoll density centrifugation and extensive washes with Dulbecco's PBS (Gibco), remaining erythrocytes were removed from PBMC via incubation with erythrocyte lysis buffer (155 mM NH_4Cl , 10 mM KHCO_3 , 100 μM EDTA). Platelets were removed via the supernatant upon centrifugation of PBMC at 100 x g. Remaining lymphocytes mainly encompass B and T lymphocytes, NK cells and monocytes. PBMC were kept in culture at 37°C/5% CO_2 in RPMI medium (Gibco) with 10% FCS (Gibco).

[313] Depletion of CD14⁺ and CD56⁺ cells

For depletion of CD14⁺ cells, human CD14 MicroBeads (Milty Biotec, MACS, #130-050-201) were used, for depletion of NK cells human CD56 MicroBeads (MACS, #130-050-401). PBMC were counted and centrifuged for 10 min at room temperature with 300 x g. The supernatant was discarded and the cell pellet resuspended in MACS isolation buffer [80 μL /10⁷ cells; PBS (Invitrogen, #20012-043), 0.5% (v/v) FBS (Gibco, #10270-106), 2 mM EDTA (Sigma-Aldrich, #E-6511)]. CD14 MicroBeads and CD56 MicroBeads (20 μL /10⁷ cells) were added and incubated for 15 min at 4 - 8°C. The cells were washed with MACS isolation buffer (1 - 2 mL/10⁷ cells). After centrifugation (see above), supernatant was discarded and cells resuspended in MACS isolation buffer (500 μL /10⁸ cells). CD14/CD56 negative cells were then isolated using LS Columns (Milty Biotec, #130-042-401). PBMC w/o CD14⁺/CD56⁺ cells were cultured in RPMI complete medium i.e. RPMI1640 (Biochrom AG, #FG1215) supplemented with 10% FBS (Biochrom AG, #S0115), 1x non-essential amino acids (Biochrom AG, #K0293), 10 mM Hepes buffer (Biochrom AG, #L1613), 1 mM sodium pyruvate (Biochrom AG, #L0473) and 100 U/mL penicillin/streptomycin (Biochrom AG, #A2213) at 37°C in an incubator until needed.

[314] Target cell labeling

For the analysis of cell lysis in flow cytometry assays, the fluorescent membrane dye DiOC₁₈ (DiO) (Molecular Probes, #V22886) was used to label human target-transfected CHO cells as target cells and distinguish them from effector cells. Briefly, cells were harvested, washed once with PBS and adjusted to 10⁶ cell/mL in PBS containing 2 % (v/v) FBS and the membrane dye DiO (5 μL /10⁶ cells). After incubation for 3 min at 37°C, cells were washed twice in complete RPMI medium and the cell number adjusted to 1.25 x 10⁵ cells/mL. The vitality of cells was determined using the NC-250 cell counter (Chemometec).

[315] Flow cytometry based analysis

This assay was designed to quantify the lysis of human target-transfected CHO cells in the presence of serial dilutions of anti-target multi-specific constructs. Equal volumes of DiO-labeled target cells and effector cells (i.e., PBMC w/o CD14⁺ and CD56⁺ cells) were mixed, resulting in an E:T cell ratio of 10:1. 80 µl of this suspension were transferred to each well of a 96-well plate. 20 µL of serial dilutions of the anti-target x anti-CD3 multi-specific constructs and a negative control (a CD3-based multi-specific construct recognizing an irrelevant target antigen) or RPMI complete medium as an additional negative control were added. The multi-specific construct-mediated cytotoxic reaction proceeded for 48 hours in a 7% CO₂ humidified incubator. Then cells were transferred to a new 96-well plate and loss of target cell membrane integrity was monitored by adding propidium iodide (PI) at a final concentration of 1 µg/mL. PI is a membrane impermeable dye that normally is excluded from viable cells, whereas dead cells take it up and become identifiable by fluorescent emission.

[316] Samples were measured by flow cytometry on an iQue Plus instrument and analyzed by Forecyt software (both from Intellicyt). Target cells were identified as DiO-positive cells. PI-negative target cells were classified as living target cells. Percentage of cytotoxicity was calculated according to the following formula:

$$\text{Cytotoxicity}[\%] = \frac{n_{\text{dead target cells}}}{n_{\text{target cells}}} \times 100$$

n = number of events

Using GraphPad Prism 6 software (Graph Pad Software, San Diego), the percentage of cytotoxicity was plotted against the corresponding bispecific construct concentrations. Dose response curves were analyzed with the four parametric logistic regression models for evaluation of sigmoid dose response curves with fixed hill slope and EC50 values were calculated.

[317] Results:

[318] Table 4: EC50 values in pM of T-cell engager with different anti-CD3 scFvs

	EC50 [pM]
I2C	0.2
I2CA	1.2
8A8.04	0.1

5C3.04	0.1
I2E	0.05
I2K	0.1
5G6.04	0.1
5G6.03	0.1
1D5.04	0.4
8A8.02	0.1
1D5.03	0.2

[319] T-cell engager with anti-CD3 scFvs I2C, I2CA, 8A8.04, 5C3.04, I2E, I2K, 5G6.04, 5G6.03, 1D5.04, 8A8.02 and 1D5.03 show similar EC₅₀ values in range from 0.05 pM to 0.4 pM (Fig. 1 A) and Table 4).

5

[320] Table 5: EC₅₀ values in pM of T-cell engager with different anti-CD3 scFvs

[321]

	EC ₅₀ [pM]
I2C	5.3
5G6.04	5.1
8A8.04	7.0
I2E	4.5
I2K	4.5
I2C CC 44/100	1578

[322] T-cell engager with anti-CD3 scFvs I2C, 5G6.04, 8A8.04, I2E and I2K show similar EC₅₀ values in the range from 4.5 pM to 7.0 pM. T-cell engager with anti-CD3 scFv I2C CC 44/100 shows an EC₅₀ value of 1578 pM and is 297-fold less active compared to T-cell engager with anti-CD3 scFv I2C (Fig. 1 B) and Table 5).

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Sequences

[324] The below sequence list is the authoritative list for SEQ ID NOs referred to in the specification text and claims and may contain (a) gap(s) as to consecutive numbering. Any further list, such as the list complying with WIPO Standard ST.25 that contains consecutive numberings has been generated of this list and the difference in Sequence numbers is to be reconciled with the below list. Sequence identity can be identified without further ado by reference to the unique entry in the second column identified as “designation” as well as a sequence alignment.:

[illegible]

17	PD1 (ECM 25-167) - Spacer	artificial	LDSPDRPWNPTFSPALLVTEGDNATFTCSFSNTSESFVLNWRMSPSNQTDKLAAP PEDRSQPGQDCRFRTVQLPNGRDFHMSVVRARRNDSGTYLCGAISLAPKAQIKESLRA ELRVTEERRAEVPTAHFSPSPRPAGQFQ
18	scFc - Spacer	artificial	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGKGGGGS GGGGSGGGGSGGGGSGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIS RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQ DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCV MHEALHNNHYTQKSLSLSPGK
19	scFc_mod_GQ - Spacer	artificial	CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLD SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGKGGGSGGGGQ GGGGSGGGGSGGGGSGGGGQCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYK C KVSNAKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYT QKSLSLSPGK
20	16278-A8.2 - HCDR1	artificial	KYAIN
21	16278-A8.2 - HCDR2	artificial	RIRSKYNNYATYYADAVKD
22	16278-A8.2 - HCDR3	artificial	AGNFGTSYISYWAY
23	16278-A8.2 - LCDR1	artificial	GSSTGAVTSGNYPN
24	16278-A8.2 - LCDR2	artificial	GTKFLAP
25	16278-A8.2 - LCDR3	artificial	ALWYSNRWV
26	16278-A8.2 - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADAVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCARAGNFGTSYISYWAYWG QGTLVTVSS
27	16278-A8.2 - VL	artificial	QTVVTQEPSTLTVSPGGTVTLTCGSSTGAVTSGNYPNWWQKPKGPQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
28	16278-A8.4 - HCDR1	artificial	KYAIN
29	16278-A8.4 - HCDR2	artificial	RIRSKYNNYATYYAEAVKD
30	16278-A8.4 - HCDR3	artificial	AGNFGTSYISYWAY
31	16278-A8.4 - LCDR1	artificial	GSSTGAVTSGNYPN
32	16278-A8.4 - LCDR2	artificial	GTKFLAP
33	16278-A8.4 - LCDR3	artificial	ALWYSNRWV
34	16278-A8.4 - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYAEAVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCARAGNFGTSYISYWAYWG QGTLVTVSS
35	16278-A8.4 - VL	artificial	QTVVTQEPSTLTVSPGGTVTLTCGSSTGAVTSGNYPNWWQKPKGPQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
36	16281-D5.1 - HCDR1	artificial	KYAIN
37	16281-D5.1 - HCDR2	artificial	RIRSKYNNYATYYADAVKD
38	16281-D5.1 - HCDR3	artificial	AGNFGSSYISYFAY
39	16281-D5.1 - LCDR1	artificial	GSSTGAVTSGNYPN
40	16281-D5.1 - LCDR2	artificial	GTKFLAP
41	16281-D5.1 - LCDR3	artificial	ALWYSNRWV
42	16281-D5.1 - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADAVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRAGNFGSSYISYFAYWG QGTLVTVSS
43	16281-D5.1 - VL	artificial	QTVVTQEPSTLTVSPGGTVTLTCGSSTGAVTSGNYPNWWQKPKGPQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
44	16281-D5.3 - HCDR1	artificial	KYAIN
45	16281-D5.3 - HCDR2	artificial	RIRSKYNNYATYYAEAVKD

46	16281-D5.3 - HCDR3	artificial	AGNFGSSYISYFAY
47	16281-D5.3 - LCDR1	artificial	GSSTGAVTSGNYPN
48	16281-D5.3 - LCDR2	artificial	GTKFLAP
49	16281-D5.3 - LCDR3	artificial	ALWYSNRWV
50	16281-D5.3 - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYAEAVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRAGNFGSSYISYFAYWG QGTLVTVSS
51	16281-D5.3 - VL	artificial	QTVVTQEPSTLVSPGGTVTTLTCSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
52	16281-D5.4 - HCDR1	artificial	KYAIN
53	16281-D5.4 - HCDR2	artificial	RIRSKYNNYATYYAEAVKD
54	16281-D5.4 - HCDR3	artificial	AGNFGTSYISYFAY
55	16281-D5.4 - LCDR1	artificial	GSSTGAVTSGNYPN
56	16281-D5.4 - LCDR2	artificial	GTKFLAP
57	16281-D5.4 - LCDR3	artificial	ALWYSNRWV
58	16281-D5.4 - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYAEAVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRAGNFGTSYISYFAYWG QGTLVTVSS
59	16281-D5.4 - VL	artificial	QTVVTQEPSTLVSPGGTVTTLTCSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
60	16334-G10.4 - HCDR1	artificial	KYAMN
61	16334-G10.4 - HCDR2	artificial	RIRSKYNNYATYYAEAVKD
62	16334-G10.4 - HCDR3	artificial	AENIGTSYISYWAY
63	16334-G10.4 - LCDR1	artificial	GSSTGAVTSGNYPN
64	16334-G10.4 - LCDR2	artificial	GTKFLAP
65	16334-G10.4 - LCDR3	artificial	VLWYSNRWV
66	16334-G10.4 - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFSKYAMNWVREAPGKGLEWVARIRSKYNNY ATYYAEAVKDRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRAENIGTSYISYWAYWG QGTLVTVSS
67	16334-G10.4 - VL	artificial	QTVVTQEPSTLVSPGGTVMTCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTKFLAP GTPARFSGSLEGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
68	16335-B1.5 - HCDR1	artificial	KYAMN
69	16335-B1.5 - HCDR2	artificial	RIRSKYNNYATYYAEAVKG
70	16335-B1.5 - HCDR3	artificial	AGNFGSSYISYWAY
71	16335-B1.5 - LCDR1	artificial	GSSTGAVTSGNYPN
72	16335-B1.5 - LCDR2	artificial	GTKFLAP
73	16335-B1.5 - LCDR3	artificial	VLWYSNRWV
74	16335-B1.5 - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFSKYAMNWVRQAPGKGMWVARIRSKYNNY ATYYAEAVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRAGNFGSSYISYWAYWG QGTLVTVSS
75	16335-B1.5 - VL	artificial	QTVVTQEPSTLVSPGGTVTTLTCSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
76	16335-B1.9 - HCDR1	artificial	KYAMN
77	16335-B1.9 - HCDR2	artificial	RIRSKYNNYATYYADAVKG
78	16335-B1.9 - HCDR3	artificial	AGNFGTSYISYFAY
79	16335-B1.9 - LCDR1	artificial	GSSTGAVTSGNYPN
80	16335-B1.9 - LCDR2	artificial	GTKFLAP
81	16335-B1.9 - LCDR3	artificial	VLWYSNRWV

82	16335-B1.9 - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFSKYAMNWVRQAPGKMEWVARIRSKYNNY ATYYADAVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRAGNFGTSYISYFAYWG QGTLVTVSS
83	16335-B1.9 - VL	artificial	QTVVTQEPSTLTVSPGGTIVTITCGSSTGAVTSGNYPNWWQKPGQAPRGLIGGTKFLAP GTPARFSGSLSGGKAALTLSGVQPEDEAEYYCVLYYSNRWVFGSGTKLTVL
84	16335-C3.4 - HCDR1	artificial	KYAIN
85	16335-C3.4 - HCDR2	artificial	RIRSKYNNYATYYADAVKD
86	16335-C3.4 - HCDR3	artificial	AENIGTSYISYWAY
87	16335-C3.4 - LCDR1	artificial	GSSTGAVTSGNYPN
88	16335-C3.4 - LCDR2	artificial	GTKFLAP
89	16335-C3.4 - LCDR3	artificial	VLWYSNRWV
90	16335-C3.4 - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADAVKDRFTISRDDSKNTVYLQMNNLKTEDTAVYYCARAENIGTSYISYWAYWG QGTLVTVSS
91	16335-C3.4 - VL	artificial	QTVVTQEPSTLTVSPGGTIVTITCGSSTGAVTSGNYPNWWQKPGQAPRGLIGGTKFLAP GTPARFSGSLSGGKAALTLSGVQPEDEAEYYCVLYYSNRWVFGSGTKLTVL
92	16335-C3.5 - HCDR1	artificial	KYAIN
93	16335-C3.5 - HCDR2	artificial	RIRSKYNNYATYYAEAVKD
94	16335-C3.5 - HCDR3	artificial	AGNFGSSYISYWAY
95	16335-C3.5 - LCDR1	artificial	GSSTGAVTSGNYPN
96	16335-C3.5 - LCDR2	artificial	GTKFLAP
97	16335-C3.5 - LCDR3	artificial	VLYYSNRWV
98	16335-C3.5 - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYAEAVKDRFTISRDDSKNTVYLQMNNLKTEDTAVYYCARAGNFGSSYISYWAYWG QGTLVTVSS
99	16335-C3.5 - VL	artificial	QTVVTQEPSTLTVSPGGTIVTITCGSSTGAVTSGNYPNWWQKPGQAPRGLIGGTKFLAP GTPARFSGSLSGGKAALTLSGVQPEDEAEYYCVLYYSNRWVFGSGTKLTVL
100	16335-G6.3 - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYAEAVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRAGNFGSSYISYWAYWG QGTLVTVSS
101	16335-G6.3 - VL	artificial	QTVVTQEPSTLTVSPGGTIVTITCGSSTGAVTSGNYPNWWQKPGQAPRGLIGGTKFLAP GTPARFSGSLSGGKAALTLSGVQPEDEAEYYCVLYYSNRWVFGSGTKLTVL
102	16335-G6.4 - HCDR1	artificial	KYAMN
103	16335-G6.4 - HCDR2	artificial	RIRSKYNNYATYYADAVKG
104	16335-G6.4 - HCDR3	artificial	NENIGSSYISYWAY
105	16335-G6.4 - LCDR1	artificial	GSSTGAVTSGNYPN
106	16335-G6.4 - LCDR2	artificial	GTKFLAP
107	16335-G6.4 - LCDR3	artificial	VLWYSNRWV
108	16335-G6.4 - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADAVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRNENIGSSYISYWAYWG QGTLVTVSS
109	16335-G6.4 - VL	artificial	QTVVTQEPSTLTVSPGGTIVTITCGSSTGAVTSGNYPNWWQKPGQAPRGLIGGTKFLAP GTPARFSGSLSGGKAALTLSGVQPEDEAEYYCVLYYSNRWVFGSGTKLTVL
110	16356-H10.3 - HCDR1	artificial	KYAMN
111	16356-H10.3 - HCDR2	artificial	RIRSKYNNYATYYAEAVKD
112	16356-H10.3 - HCDR3	artificial	AGNFGTSYISYWAY
113	16356-H10.3 - LCDR1	artificial	GSSTGAVTSGNYPN
114	16356-H10.3 - LCDR2	artificial	GTKFLAP
115	16356-H10.3 - LCDR3	artificial	VLWYSNRWV
116	16356-H10.3 - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQAPGKMEWVARIRSKYNNY ATYYAEAVKDRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRAGNFGTSYISYWAYWG QGTLVTVSS

117	16356-H10.3 - VL	artificial	QTVVTQEPSTLVSPGGTVTITCGSSTGAVTSGNYPNWIQKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
118	2B2_Compl - HCDR1	artificial	KYAIN
119	2B2_Compl - HCDR2	artificial	RIRSKYNNYATYYADQVKD
120	2B2_Compl - HCDR3	artificial	HANFGNSYISYWAY
121	2B2_Compl - LCDR1	artificial	ASSTGAVTSGNYPN
122	2B2_Compl - LCDR2	artificial	GTKFLVP
123	2B2_Compl - LCDR3	artificial	TLWYSNRWV
124	2B2_Compl - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWG QGTLVTVSS
125	2B2_Compl - VL	artificial	QTVVTQEPSTLVSPGGTVTITCASSTGAVTSGNYPNWWQKPGQAPRGLIGGTFKFLVP GTPARFSGSLGGKAAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL
126	2B2_Compl_I 2E - HCDR1	artificial	KYAIN
127	2B2_Compl_I 2E - HCDR2	artificial	RIRSKYNNYATYYADAVKD
128	2B2_Compl_I 2E - HCDR3	artificial	AANFGSSYISYWAY
129	2B2_Compl_I 2E - LCDR1	artificial	ASSTGAVTSGNYPN
130	2B2_Compl_I 2E - LCDR2	artificial	GTKFLVP
131	2B2_Compl_I 2E - LCDR3	artificial	TLWYSNRWV
132	2B2_Compl_I 2E - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADAVKDRFTISRDDSKNTVYLQMNNLKTEDTAVYYCARAANFGSSYISYWAYWG QGTLVTVSS
133	2B2_Compl_I 2E - VL	artificial	QTVVTQEPSTLVSPGGTVTITCASSTGAVTSGNYPNWWQKPGQAPRGLIGGTFKFLVP GTPARFSGSLGGKAAALTLSGVQPEDEAEYYCTLWYSNRWVFGSGTKLTVL
134	2B2_Compl_I 2K - HCDR1	artificial	KYAMN
135	2B2_Compl_I 2K - HCDR2	artificial	RIRSKYNNYATYYAEAVKG
136	2B2_Compl_I 2K - HCDR3	artificial	NENIGTSYISYWAY
137	2B2_Compl_I 2K - LCDR1	artificial	ASSTGAVTSGNYPN
138	2B2_Compl_I 2K - LCDR2	artificial	GTKFLVP
139	2B2_Compl_I 2K - LCDR3	artificial	TLWYSNRWV
140	2B2_Compl_I 2K - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWWVRQAPGKGLEWVARIRSKYNNY ATYYAEAVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRNENIGTSYISYWAYWG QGTLVTVSS
141	2B2_Compl_I 2K - VL	artificial	QTVVTQEPSTLVSPGGTVTITCASSTGAVTSGNYPNWWQKPGQAPRGLIGGTFKFLVP GTPARFSGSLGGKAAALTLSGVQPEDEAEYYCTLWYSNRWVFGSGTKLTVL
142	2B2_Compl_I 2L - HCDR1	artificial	KYAIN
143	2B2_Compl_I 2L - HCDR2	artificial	RIRSKYNNYATYYADAVKD
144	2B2_Compl_I 2L - HCDR3	artificial	AANFGSSYISYFAY
145	2B2_Compl_I 2L - LCDR1	artificial	ASSTGAVTSGNYPN
146	2B2_Compl_I 2L - LCDR2	artificial	GTKFLVP
147	2B2_Compl_I 2L - LCDR3	artificial	TLYYSNRWV
148	2B2_Compl_I 2L - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKMEWVARIRSKYNNY ATYYADAVKDRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRANFGSSYISYFAYWG QGTLVTVSS
149	2B2_Compl_I 2L - VL	artificial	QTVVTQEPSTLVSPGGTVTITCASSTGAVTSGNYPNWIQKPGQAPRGLIGGTFKFLVP GTPARFSGSLGGKAAALTLSGVQPEDEAEYYCTLYYSNRWVFGSGTKLTVL
150	2B2_Compl_I 2M - HCDR1	artificial	KYAIN
151	2B2_Compl_I 2M - HCDR2	artificial	RIRSKYNNYATYYADAVKD
152	2B2_Compl_I 2M - HCDR3	artificial	AANFGTSYISYWAY

153	2B2_Compl_I 2M - LCDR1	artificial	ASSTGAVTSGNYPN
154	2B2_Compl_I 2M - LCDR2	artificial	GTKFLVP
155	2B2_Compl_I 2M - LCDR3	artificial	TLWYSNRWV
156	2B2_Compl_I 2M - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGMWVARIRSKYNNY ATYYADAVKDRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRAANFGTSYISYWAYWG QGTLVTVSS
157	2B2_Compl_I 2M - VL	artificial	QTVVTQEPSTLTVSPGGTIVTITCASSTGAVTSGNYPNWVQKPKGQAPRGLIGGTGKFLVP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGSGTKLTVL
158	2B2_Compl_I 2M2 - HCDR1	artificial	KYAIN
159	2B2_Compl_I 2M2 - HCDR2	artificial	RIRSKYNNYATYYADAVKD
160	2B2_Compl_I 2M2 - HCDR3	artificial	NANFGTSYISYFAY
161	2B2_Compl_I 2M2 - LCDR1	artificial	ASSTGAVTSGNYPN
162	2B2_Compl_I 2M2 - LCDR2	artificial	GTKFLVP
163	2B2_Compl_I 2M2 - LCDR3	artificial	TLWYSNRWV
164	2B2_Compl_I 2M2 - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVREAPGKGLEWVARIRSKYNNY ATYYADAVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRNANFGTSYISYFAYWG QGTLVTVSS
165	2B2_Compl_I 2M2 - VL	artificial	QTVVTQEPSTLTVSPGGTIVTITCASSTGAVTSGNYPNWVQKPKGQAPRGLIGGTGKFLVP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGSGTKLTVL
166	A2J - HCDR1	artificial	VYAMN
167	A2J - HCDR2	artificial	RIRSKYNNYATYYADSVKK
168	A2J - HCDR3	artificial	HGNFGNSYLSWWAY
169	A2J - LCDR1	artificial	RSSTGAVTSGYYPN
170	A2J - LCDR2	artificial	ATDMRPS
171	A2J - LCDR3	artificial	ALWYSNRWV
172	A2J - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
173	A2J - VL	artificial	QTVVTQEPSTLTVSPGGTIVTITCRSSTGAVTSGYYPNWWQKPKGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
174	A2J_HC_A89I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTIYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
175	A2J_HC_A89I - VL	artificial	QTVVTQEPSTLTVSPGGTIVTITCRSSTGAVTSGYYPNWWQKPKGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
176	A2J_HC_A89L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
177	A2J_HC_A89L - VL	artificial	QTVVTQEPSTLTVSPGGTIVTITCRSSTGAVTSGYYPNWWQKPKGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
178	A2J_HC_A89T - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTTYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
179	A2J_HC_A89T - VL	artificial	QTVVTQEPSTLTVSPGGTIVTITCRSSTGAVTSGYYPNWWQKPKGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
180	A2J_HC_A89V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
181	A2J_HC_A89V - VL	artificial	QTVVTQEPSTLTVSPGGTIVTITCRSSTGAVTSGYYPNWWQKPKGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
182	A2J_HC_L52M - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGMWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
183	A2J_HC_L52M - VL	artificial	QTVVTQEPSTLTVSPGGTIVTITCRSSTGAVTSGYYPNWWQKPKGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
184	A2J_HC_L52M _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGMWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
185	A2J_HC_L52M _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSTLTVSPGGTIVTITCRSSTGAVTSGYYPNWWQKPKGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL

186	A2J_HC_L52M _LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGMWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
187	A2J_HC_L52M _LC_Q46K - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
188	A2J_HC_L52M _LC_Q46K_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGMWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
189	A2J_HC_L52M _LC_Q46K_G1 41S - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
190	A2J_HC_L52V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGVWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
191	A2J_HC_L52V - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
192	A2J_HC_L52V _LC_V44F - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGVWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
193	A2J_HC_L52V _LC_V44F - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
194	A2J_HC_L52V _LC_V44Y - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGVWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
195	A2J_HC_L52V _LC_V44Y - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
196	A2J_HC_M41F _A89V - HCDR1	artificial	VYAFN
197	A2J_HC_M41F _A89V - HCDR2	artificial	RIRSKYNNYATYYADSVKK
198	A2J_HC_M41F _A89V - HCDR3	artificial	HGNFGNSYLSWWAY
199	A2J_HC_M41F _A89V - LCDR1	artificial	RSSTGAVTSGYYPN
200	A2J_HC_M41F _A89V - LCDR2	artificial	ATDMRPS
201	A2J_HC_M41F _A89V - LCDR3	artificial	ALWYSNRWV
202	A2J_HC_M41F _A89V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAFNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
203	A2J_HC_M41F _A89V - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
204	A2J_HC_M41I - HCDR1	artificial	VYAIN
205	A2J_HC_M41I - HCDR2	artificial	RIRSKYNNYATYYADSVKK
206	A2J_HC_M41I - HCDR3	artificial	HGNFGNSYLSWWAY
207	A2J_HC_M41I - LCDR1	artificial	RSSTGAVTSGYYPN
208	A2J_HC_M41I - LCDR2	artificial	ATDMRPS
209	A2J_HC_M41I - LCDR3	artificial	ALWYSNRWV
210	A2J_HC_M41I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
211	A2J_HC_M41I - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
212	A2J_HC_M41I _A89L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
213	A2J_HC_M41I _A89L - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
214	A2J_HC_M41I _A89V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG

			QGTLVTVSS
215	A2J_HC_M41I _A89V - VL	artificial	QTVVTQEPSTLTVSPGGTVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
216	A2J_HC_M41I _A89V_LC_L2 _L1_Q46K_G14 _1S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
217	A2J_HC_M41I _A89V_LC_L2 _L1_Q46K_G14 _1S - VL	artificial	QTVVTQEPSTLTVSPGGTVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
218	A2J_HC_M41I _A89V_LC_Q4 _6K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
219	A2J_HC_M41I _A89V_LC_Q4 _6K - VL	artificial	QTVVTQEPSTLTVSPGGTVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
220	A2J_HC_M41I _L52V_A89V_ _LC_L21I_Q46 _K_G141S_V44 _F - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
221	A2J_HC_M41I _L52V_A89V_ _LC_L21I_Q46 _K_G141S_V44 _F - VL	artificial	QTVVTQEPSTLTVSPGGTVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
222	A2J_HC_M41I _LC_L21I_Q4 _6K_G141S - _VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
223	A2J_HC_M41I _LC_L21I_Q4 _6K_G141S - _VL	artificial	QTVVTQEPSTLTVSPGGTVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
224	A2J_HC_M41I _Q46E_A89V_ _LC_L21I_Q46 _K_G141S - _VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
225	A2J_HC_M41I _Q46E_A89V_ _LC_L21I_Q46 _K_G141S - _VL	artificial	QTVVTQEPSTLTVSPGGTVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
226	A2J_HC_M41V - HCDR1	artificial	VYAVN
227	A2J_HC_M41V - HCDR2	artificial	RIRSKYNNYATYYADSVKK
228	A2J_HC_M41V - HCDR3	artificial	HGNFGNSYLSWWAY
229	A2J_HC_M41V - LCDR1	artificial	RSSTGAVTSGYYPN
230	A2J_HC_M41V - LCDR2	artificial	ATDMRPS
231	A2J_HC_M41V - LCDR3	artificial	ALWYSNRWV
232	A2J_HC_M41V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAVNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
233	A2J_HC_M41V - VL	artificial	QTVVTQEPSTLTVSPGGTVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
234	A2J_HC_Q46D - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
235	A2J_HC_Q46D - VL	artificial	QTVVTQEPSTLTVSPGGTVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
236	A2J_HC_Q46D _LC_L21I_Q4 _6K_G141S - _VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
237	A2J_HC_Q46D _LC_L21I_Q4 _6K_G141S - _VL	artificial	QTVVTQEPSTLTVSPGGTVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL

238	A2J_HC_Q46D _LC_L21I_Q4 6R_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNQYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
239	A2J_HC_Q46D _LC_L21I_Q4 6R_G141S - VL	artificial	QTVVTQEPSTLVSPGGTIVTITCRSSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
240	A2J_HC_Q46D _LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNQYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
241	A2J_HC_Q46D _LC_Q46K - VL	artificial	QTVVTQEPSTLVSPGGTIVTITCRSSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
242	A2J_HC_Q46D _LC_Q46K_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNQYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
243	A2J_HC_Q46D _LC_Q46K_G1 41S - VL	artificial	QTVVTQEPSTLVSPGGTIVTITCRSSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
244	A2J_HC_Q46D _LC_Q46R - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNQYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
245	A2J_HC_Q46D _LC_Q46R - VL	artificial	QTVVTQEPSTLVSPGGTIVTITCRSSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
246	A2J_HC_Q46D _LC_Q46R_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNQYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
247	A2J_HC_Q46D _LC_Q46R_G1 41S - VL	artificial	QTVVTQEPSTLVSPGGTIVTITCRSSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
248	A2J_HC_Q46E - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNQYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
249	A2J_HC_Q46E - VL	artificial	QTVVTQEPSTLVSPGGTIVTITCRSSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
250	A2J_HC_Q46E _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNQYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
251	A2J_HC_Q46E _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSTLVSPGGTIVTITCRSSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
252	A2J_HC_Q46E _LC_L21I_Q4 6R_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNQYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
253	A2J_HC_Q46E _LC_L21I_Q4 6R_G141S - VL	artificial	QTVVTQEPSTLVSPGGTIVTITCRSSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
254	A2J_HC_Q46E _LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNQYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
255	A2J_HC_Q46E _LC_Q46K - VL	artificial	QTVVTQEPSTLVSPGGTIVTITCRSSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
256	A2J_HC_Q46E _LC_Q46K_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNQYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
257	A2J_HC_Q46E _LC_Q46K_G1 41S - VL	artificial	QTVVTQEPSTLVSPGGTIVTITCRSSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
258	A2J_HC_Q46E _LC_Q46R - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNQYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
259	A2J_HC_Q46E _LC_Q46R - VL	artificial	QTVVTQEPSTLVSPGGTIVTITCRSSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
260	A2J_HC_Q46E _LC_Q46R_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNQYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
261	A2J_HC_Q46E _LC_Q46R_G1	artificial	QTVVTQEPSTLVSPGGTIVTITCRSSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL

	41S - VL		
262	A2J_HC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRKAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
263	A2J_HC_Q46K - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
264	A2J_HC_Q46R - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
265	A2J_HC_Q46R - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
266	A2J_HC_V107 A - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCARHGNFGNSYLSWWAYWG QGTLVTVSS
267	A2J_HC_V107 A - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
268	A2J_HC_V107 L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCLRHGNFGNSYLSWWAYWG QGTLVTVSS
269	A2J_HC_V107 L - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
270	A2J_HC_W136 F - HCDR1	artificial	VYAMN
271	A2J_HC_W136 F - HCDR2	artificial	RIRSKYNNYATYYADSVKK
272	A2J_HC_W136 F - HCDR3	artificial	HGNFGNSYLSWFAY
273	A2J_HC_W136 F - LCDR1	artificial	RSSTGAVTSGYYPN
274	A2J_HC_W136 F - LCDR2	artificial	ATDMRPS
275	A2J_HC_W136 F - LCDR3	artificial	ALWYSNRWV
276	A2J_HC_W136 F - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWFAYWG QGTLVTVSS
277	A2J_HC_W136 F - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
278	A2J_HC_W136 F LC_V44I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWFAYWG QGTLVTVSS
279	A2J_HC_W136 F LC_V44I - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
280	A2J_HC_W136 F LC_V44L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWFAYWG QGTLVTVSS
281	A2J_HC_W136 F LC_V44L - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
282	A2J_I2E - HCDR1	artificial	VYAIN
283	A2J_I2E - HCDR2	artificial	RIRSKYNNYATYYADAVKK
284	A2J_I2E - HCDR3	artificial	AGNFGSSYLSWWAY
285	A2J_I2E - LCDR1	artificial	RSSTGAVTSGYYPN
286	A2J_I2E - LCDR2	artificial	ATDMRPS
287	A2J_I2E - LCDR3	artificial	ALWYSNRWV
288	A2J_I2E - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADAVKKRFTISRDDSKNTVYLQMNNLKTEDTAVYYCARAGNFGSSYLSWWAYWG QGTLVTVSS
289	A2J_I2E - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
290	A2J_I2K - HCDR1	artificial	VYAMN
291	A2J_I2K - HCDR2	artificial	RIRSKYNNYATYYAEAVKG
292	A2J_I2K - HCDR3	artificial	NENIGTSYLSWWAY
293	A2J_I2K - LCDR1	artificial	RSSTGAVTSGYYPN

294	A2J_I2K - LCDR2	artificial	ATDMRPS
295	A2J_I2K - LCDR3	artificial	ALWYSNRWV
296	A2J_I2K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYAEAVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRNENIGTSYLSWWAYWG QGTLVTVSS
297	A2J_I2K - VL	artificial	QTVVTQEPSTLVSPGGTVTITCRSSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
298	A2J_I2L - HCDR1	artificial	VYAMN
299	A2J_I2L - HCDR2	artificial	RIRSKYNNYATYYADAVKK
300	A2J_I2L - HCDR3	artificial	AGNFGSSYLSWFAY
301	A2J_I2L - LCDR1	artificial	RSSTGAVTSGYYPN
302	A2J_I2L - LCDR2	artificial	ATDMRPS
303	A2J_I2L - LCDR3	artificial	ALYYSNRWV
304	A2J_I2L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKMEWVARIRSKYNNY ATYYADAVKKRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRAGNFGSSYLSWFAYWG QGTLVTVSS
305	A2J_I2L - VL	artificial	QTVVTQEPSTLVSPGGTVTITCRSSTGAVTSGYYPNWIQKPGQAPRGLIGATDMRPS GTPARFSGSLEGGKAALTLSGVQPEDEAEYYCALYYSNRWVFGSGTKLTVL
306	A2J_I2M - HCDR1	artificial	VYAMN
307	A2J_I2M - HCDR2	artificial	RIRSKYNNYATYYADAVKK
308	A2J_I2M - HCDR3	artificial	AGNFGTSYLSWWAY
309	A2J_I2M - LCDR1	artificial	RSSTGAVTSGYYPN
310	A2J_I2M - LCDR2	artificial	ATDMRPS
311	A2J_I2M - LCDR3	artificial	ALWYSNRWV
312	A2J_I2M - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKMEWVARIRSKYNNY ATYYADAVKKRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRAGNFGTSYLSWWAYWG QGTLVTVSS
313	A2J_I2M - VL	artificial	QTVVTQEPSTLVSPGGTVTITCRSSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
314	A2J_I2M2 - HCDR1	artificial	VYAIN
315	A2J_I2M2 - HCDR2	artificial	RIRSKYNNYATYYADAVKK
316	A2J_I2M2 - HCDR3	artificial	NANFGTSYLSWFAY
317	A2J_I2M2 - LCDR1	artificial	RSSTGAVTSGYYPN
318	A2J_I2M2 - LCDR2	artificial	ATDMRPS
319	A2J_I2M2 - LCDR3	artificial	ALWYSNRWV
320	A2J_I2M2 - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAINWVREAPGKGLEWVARIRSKYNNY ATYYADAVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRNANFGTSYLSWFAYWG QGTLVTVSS
321	A2J_I2M2 - VL	artificial	QTVVTQEPSTLVSPGGTVTITCRSSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
322	A2J_LC_G141 S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
323	A2J_LC_G141 S - VL	artificial	QTVVTQEPSTLVSPGGTVTITCRSSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
324	A2J_LC_G141 S_L21I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
325	A2J_LC_G141 S_L21I - VL	artificial	QTVVTQEPSTLVSPGGTVTITCRSSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
326	A2J_LC_L83E - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
327	A2J_LC_L83E - VL	artificial	QTVVTQEPSTLVSPGGTVTITCRSSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLEGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL

328	A2J_LC_L83S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFN VYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMN NLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
329	A2J_LC_L83S - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCSRSTGAVTSGYYPN WVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYS NRWVFGGGTKLTVL
330	A2J_LC_Q46E - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFN VYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMN NLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
331	A2J_LC_Q46E - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCSRSTGAVTSGYYPN WVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYS NRWVFGGGTKLTVL
332	A2J_LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFN VYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMN NLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
333	A2J_LC_Q46K - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCSRSTGAVTSGYYPN WVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYS NRWVFGGGTKLTVL
334	A2J_LC_A107 L - HCDR1	artificial	VYAMN
335	A2J_LC_A107 L - HCDR2	artificial	RIRSKYNNYATYYADSVKK
336	A2J_LC_A107 L - HCDR3	artificial	HGNFGNSYLSWWAY
337	A2J_LC_A107 L - LCDR1	artificial	RSSTGAVTSGYYPN
338	A2J_LC_A107 L - LCDR2	artificial	ATDMRPS
339	A2J_LC_A107 L - LCDR3	artificial	LLWYSNRWV
340	A2J_LC_A107 L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFN VYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMN NLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
341	A2J_LC_A107 L - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCSRSTGAVTSGYYPN WVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCLWYS NRWVFGGGTKLTVL
342	A2J_LC_V44I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFN VYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMN NLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
343	A2J_LC_V44I - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCSRSTGAVTSGYYPN WVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYS NRWVFGGGTKLTVL
344	A2J_LC_V44L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFN VYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMN NLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
345	A2J_LC_V44L - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCSRSTGAVTSGYYPN WVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYS NRWVFGGGTKLTVL
346	A2J_LC_V44M - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFN VYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMN NLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
347	A2J_LC_V44M - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCSRSTGAVTSGYYPN WVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYS NRWVFGGGTKLTVL
348	A2J_LC_W109 Y - HCDR1	artificial	VYAMN
349	A2J_LC_W109 Y - HCDR2	artificial	RIRSKYNNYATYYADSVKK
350	A2J_LC_W109 Y - HCDR3	artificial	HGNFGNSYLSWWAY
351	A2J_LC_W109 Y - LCDR1	artificial	RSSTGAVTSGYYPN
352	A2J_LC_W109 Y - LCDR2	artificial	ATDMRPS
353	A2J_LC_W109 Y - LCDR3	artificial	ALYYSNRWV
354	A2J_LC_W109 Y - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFN VYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMN NLKTEDTAVYYCVRHGNFGNSYLSWWAYWG QGTLVTVSS
355	A2J_LC_W109 Y - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCSRSTGAVTSGYYPN WVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYS NRWVFGGGTKLTVL
356	E1L - HCDR1	artificial	KYAMN
357	E1L - HCDR2	artificial	RIRSKYNNYATYYADSVKS
358	E1L - HCDR3	artificial	HGNFGNSYTSYYAY
359	E1L - LCDR1	artificial	GSSTGAVTSGYYPN
360	E1L - LCDR2	artificial	GTKFLAP
361	E1L - LCDR3	artificial	ALWYSNRWV
362	E1L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFN KYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMN NLKTEDTAVYYCVRHGNFGNSYTSYYAYWG

			QGTLVTVSS
363	E1L - VL	artificial	QTVVTQEPISLTVSPGGTIVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
364	E1L_HC_A89I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTIYLMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
365	E1L_HC_A89I - VL	artificial	QTVVTQEPISLTVSPGGTIVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
366	E1L_HC_A89L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTLYLMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
367	E1L_HC_A89L - VL	artificial	QTVVTQEPISLTVSPGGTIVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
368	E1L_HC_A89T - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTTYLMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
369	E1L_HC_A89T - VL	artificial	QTVVTQEPISLTVSPGGTIVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
370	E1L_HC_A89V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTVYLMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
371	E1L_HC_A89V - VL	artificial	QTVVTQEPISLTVSPGGTIVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
372	E1L_HC_L52M - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGMWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
373	E1L_HC_L52M - VL	artificial	QTVVTQEPISLTVSPGGTIVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
374	E1L_HC_L52M _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGMWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
375	E1L_HC_L52M _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPISLTVSPGGTIVTITCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
376	E1L_HC_L52M _LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGMWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
377	E1L_HC_L52M _LC_Q46K - VL	artificial	QTVVTQEPISLTVSPGGTIVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
378	E1L_HC_L52M _LC_Q46K_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGMWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
379	E1L_HC_L52M _LC_Q46K_G1 41S - VL	artificial	QTVVTQEPISLTVSPGGTIVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
380	E1L_HC_L52V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGVWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
381	E1L_HC_L52V - VL	artificial	QTVVTQEPISLTVSPGGTIVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
382	E1L_HC_L52V _LC_V44F - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGVWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
383	E1L_HC_L52V _LC_V44F - VL	artificial	QTVVTQEPISLTVSPGGTIVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
384	E1L_HC_L52V _LC_V44Y - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGVWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
385	E1L_HC_L52V _LC_V44Y - VL	artificial	QTVVTQEPISLTVSPGGTIVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
386	E1L_HC_M41F _A89V - HCDR1	artificial	KYAFN
387	E1L_HC_M41F _A89V - HCDR2	artificial	RIRSKYNNYATYYADSVKS
388	E1L_HC_M41F _A89V - HCDR3	artificial	HGNFGNSYTSYYAY
389	E1L_HC_M41F _A89V -	artificial	GSSTGAVTSGYYPN

	LCDR1		
390	E1L_HC_M41F_A89V - LCDR2	artificial	GTKFLAP
391	E1L_HC_M41F_A89V - LCDR3	artificial	ALWYSNRWV
392	E1L_HC_M41F_A89V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAFNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTVYLMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
393	E1L_HC_M41F_A89V - VL	artificial	QTVVTQEPSLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
394	E1L_HC_M41I - HCDR1	artificial	KYAIN
395	E1L_HC_M41I - HCDR2	artificial	RIRSKYNNYATYYADSVKS
396	E1L_HC_M41I - HCDR3	artificial	HGNFGNSYTSYYAY
397	E1L_HC_M41I - LCDR1	artificial	GSSTGAVTSGYYPN
398	E1L_HC_M41I - LCDR2	artificial	GTKFLAP
399	E1L_HC_M41I - LCDR3	artificial	ALWYSNRWV
400	E1L_HC_M41I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
401	E1L_HC_M41I - VL	artificial	QTVVTQEPSLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
402	E1L_HC_M41I_A89L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTLYLMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
403	E1L_HC_M41I_A89L - VL	artificial	QTVVTQEPSLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
404	E1L_HC_M41I_A89V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTVYLMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
405	E1L_HC_M41I_A89V - VL	artificial	QTVVTQEPSLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
406	E1L_HC_M41I_A89V_IC_L2 LI_Q46K_G14 1S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTVYLMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
407	E1L_HC_M41I_A89V_IC_L2 LI_Q46K_G14 1S - VL	artificial	QTVVTQEPSLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
408	E1L_HC_M41I_A89V_IC_Q4 6K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTVYLMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
409	E1L_HC_M41I_A89V_IC_Q4 6K - VL	artificial	QTVVTQEPSLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
410	E1L_HC_M41I_L52V_A89V_IC L2LI_Q46 K_G141S_V44 F - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTVYLMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
411	E1L_HC_M41I_L52V_A89V_IC L2LI_Q46 K_G141S_V44 F - VL	artificial	QTVVTQEPSLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
412	E1L_HC_M41I_IC_L2LI_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
413	E1L_HC_M41I_IC_L2LI_Q4 6K_G141S - VL	artificial	QTVVTQEPSLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
414	E1L_HC_M41I_Q46E_A89V_IC L2LI_Q46 K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTVYLMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS

415	E1L_HC_M41I _Q46E_A89V _LC_L21I_Q46 K_G141S - VL	artificial	QTVVTQEPSTLVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
416	E1L_HC_M41V - HCDR1	artificial	KYAVN
417	E1L_HC_M41V - HCDR2	artificial	RIRSKYNNYATYYADSVKS
418	E1L_HC_M41V - HCDR3	artificial	HGNFGNSYTSYYAY
419	E1L_HC_M41V - LCDR1	artificial	GSSTGAVTSGYYPN
420	E1L_HC_M41V - LCDR2	artificial	GTKFLAP
421	E1L_HC_M41V - LCDR3	artificial	ALWYSNRWV
422	E1L_HC_M41V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAVNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
423	E1L_HC_M41V - VL	artificial	QTVVTQEPSTLVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
424	E1L_HC_Q46D - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
425	E1L_HC_Q46D - VL	artificial	QTVVTQEPSTLVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
426	E1L_HC_Q46D _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
427	E1L_HC_Q46D _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSTLVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
428	E1L_HC_Q46D _LC_L21I_Q4 6R_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
429	E1L_HC_Q46D _LC_L21I_Q4 6R_G141S - VL	artificial	QTVVTQEPSTLVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
430	E1L_HC_Q46D _LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
431	E1L_HC_Q46D _LC_Q46K - VL	artificial	QTVVTQEPSTLVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
432	E1L_HC_Q46D _LC_Q46K_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
433	E1L_HC_Q46D _LC_Q46K_G1 41S - VL	artificial	QTVVTQEPSTLVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
434	E1L_HC_Q46D _LC_Q46R - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
435	E1L_HC_Q46D _LC_Q46R - VL	artificial	QTVVTQEPSTLVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
436	E1L_HC_Q46D _LC_Q46R_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
437	E1L_HC_Q46D _LC_Q46R_G1 41S - VL	artificial	QTVVTQEPSTLVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
438	E1L_HC_Q46E - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
439	E1L_HC_Q46E - VL	artificial	QTVVTQEPSTLVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
440	E1L_HC_Q46E _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS

441	E1L_HC_Q46E _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
442	E1L_HC_Q46E _LC_L21I_Q4 6R_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
443	E1L_HC_Q46E _LC_L21I_Q4 6R_G141S - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
444	E1L_HC_Q46E _LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
445	E1L_HC_Q46E _LC_Q46K - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
446	E1L_HC_Q46E _LC_Q46K_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
447	E1L_HC_Q46E _LC_Q46K_G1 41S - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
448	E1L_HC_Q46E _LC_Q46R - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
449	E1L_HC_Q46E _LC_Q46R - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
450	E1L_HC_Q46E _LC_Q46R_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
451	E1L_HC_Q46E _LC_Q46R_G1 41S - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
452	E1L_HC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRKAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
453	E1L_HC_Q46K - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
454	E1L_HC_Q46R - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
455	E1L_HC_Q46R - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
456	E1L_HC_V107 A - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCARHGNFGNSYTSYYAYWG QGTLVTVSS
457	E1L_HC_V107 A - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
458	E1L_HC_V107 L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCLRHGNFGNSYTSYYAYWG QGTLVTVSS
459	E1L_HC_V107 L - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
460	E1L_HC_Y136 F - HCDR1	artificial	KYAMN
461	E1L_HC_Y136 F - HCDR2	artificial	RIRSKYNNYATYYADSVKS
462	E1L_HC_Y136 F - HCDR3	artificial	HGNFGNSYTSYFAY
463	E1L_HC_Y136 F - LCDR1	artificial	GSSTGAVTSGYYPN
464	E1L_HC_Y136 F - LCDR2	artificial	GTKFLAP
465	E1L_HC_Y136 F - LCDR3	artificial	ALWYSNRWV
466	E1L_HC_Y136 F - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYFAYWG QGTLVTVSS
467	E1L_HC_Y136 F - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
468	E1L_HC_Y136 F_LC_V44I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYFAYWG QGTLVTVSS

469	E1L_HC_Y136 F_LC_V44I - VL	artificial	QTVVTQEPSTLVSPGGTVTITCGSSTGAVTSGYYPNWIQQKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
470	E1L_HC_Y136 F_LC_V44L - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYFAYWG QGTLVTVSS
471	E1L_HC_Y136 F_LC_V44L - VL	artificial	QTVVTQEPSTLVSPGGTVTITCGSSTGAVTSGYYPNWLQKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
472	E1L_I2E - HCDR1	artificial	KYAIN
473	E1L_I2E - HCDR2	artificial	RIRSKYNNYATYYADAVKS
474	E1L_I2E - HCDR3	artificial	AGNFGSSYTSYYAY
475	E1L_I2E - LCDR1	artificial	GSSTGAVTSGYYPN
476	E1L_I2E - LCDR2	artificial	GTKFLAP
477	E1L_I2E - LCDR3	artificial	ALWYSNRWV
478	E1L_I2E - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADAVKSRFTISRDDSKNTVYLQMNNLKTEDTAVYYCARAGNFGSSYTSYYAYWG QGTLVTVSS
479	E1L_I2E - VL	artificial	QTVVTQEPSTLVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
480	E1L_I2K - HCDR1	artificial	KYAMN
481	E1L_I2K - HCDR2	artificial	RIRSKYNNYATYYAEAVKG
482	E1L_I2K - HCDR3	artificial	NENIGTSYTSYYAY
483	E1L_I2K - LCDR1	artificial	GSSTGAVTSGYYPN
484	E1L_I2K - LCDR2	artificial	GTKFLAP
485	E1L_I2K - LCDR3	artificial	ALWYSNRWV
486	E1L_I2K - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYAEAVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRNENIGTSYTSYYAYWG QGTLVTVSS
487	E1L_I2K - VL	artificial	QTVVTQEPSTLVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
488	E1L_I2L - HCDR1	artificial	KYAMN
489	E1L_I2L - HCDR2	artificial	RIRSKYNNYATYYADAVKS
490	E1L_I2L - HCDR3	artificial	AGNFGSSYTSYFAY
491	E1L_I2L - LCDR1	artificial	GSSTGAVTSGYYPN
492	E1L_I2L - LCDR2	artificial	GTKFLAP
493	E1L_I2L - LCDR3	artificial	ALYYSNRWV
494	E1L_I2L - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQAPGKMEWVARIRSKYNNY ATYYADAVKSRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRAGNFGSSYTSYFAYWG QGTLVTVSS
495	E1L_I2L - VL	artificial	QTVVTQEPSTLVSPGGTVTITCGSSTGAVTSGYYPNWIQKPGQAPRGLIGGTFKFLAP GTPARFSGSLEGGKAALTLSGVQPEDEAEYYCALYYSNRWVFGSGTKLTVL
496	E1L_I2M - HCDR1	artificial	KYAMN
497	E1L_I2M - HCDR2	artificial	RIRSKYNNYATYYADAVKS
498	E1L_I2M - HCDR3	artificial	AGNFGTSYTSYYAY
499	E1L_I2M - LCDR1	artificial	GSSTGAVTSGYYPN
500	E1L_I2M - LCDR2	artificial	GTKFLAP
501	E1L_I2M - LCDR3	artificial	ALWYSNRWV
502	E1L_I2M - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQAPGKMEWVARIRSKYNNY ATYYADAVKSRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRAGNFGTSYTSYYAYWG QGTLVTVSS

503	E1L_I2M - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLSGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
504	E1L_I2M2 - HCDR1	artificial	KYAIN
505	E1L_I2M2 - HCDR2	artificial	RIRSKYNNYATYYADAVKS
506	E1L_I2M2 - HCDR3	artificial	NANFGTSYTSYFAY
507	E1L_I2M2 - LCDR1	artificial	GSSTGAVTSGYYPN
508	E1L_I2M2 - LCDR2	artificial	GTKFLAP
509	E1L_I2M2 - LCDR3	artificial	ALWYSNRWV
510	E1L_I2M2 - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVREAPGKGLEWVARIRSKYNNY ATYYADAVKSRTTISRDDSKNTAYLQMNNLKTEDTAVYYCVRNANFGTSYTSYFAYWG QGTLVTVSS
511	E1L_I2M2 - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLSGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
512	E1L_LC_G141 S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRTTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
513	E1L_LC_G141 S - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLSGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
514	E1L_LC_G141 S_L21I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRTTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
515	E1L_LC_G141 S_L21I - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLSGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
516	E1L_LC_L83E - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRTTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
517	E1L_LC_L83E - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLSGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
518	E1L_LC_L83S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRTTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
519	E1L_LC_L83S - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLSGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
520	E1L_LC_Q46E - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRTTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
521	E1L_LC_Q46E - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLSGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
522	E1L_LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRTTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
523	E1L_LC_Q46K - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLSGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
524	E1L_LC_A107 L - HCDR1	artificial	KYAMN
525	E1L_LC_A107 L - HCDR2	artificial	RIRSKYNNYATYYADSVKS
526	E1L_LC_A107 L - HCDR3	artificial	HGNFGNSYTSYYAY
527	E1L_LC_A107 L - LCDR1	artificial	GSSTGAVTSGYYPN
528	E1L_LC_A107 L - LCDR2	artificial	GTKFLAP
529	E1L_LC_A107 L - LCDR3	artificial	LLWYSNRWV
530	E1L_LC_A107 L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRTTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
531	E1L_LC_A107 L - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLSGGKAALTLSGVQPEDEAEYYCLLWYSNRWVFGGGTKLTVL
532	E1L_LC_V44I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRTTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
533	E1L_LC_V44I - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLSGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
534	E1L_LC_V44L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRTTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
535	E1L_LC_V44L - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWLQKPGQAPRGLIGGTKFLAP GTPARFSGSLSGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL

536	E1L_LC_V44M - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
537	E1L_LC_V44M - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
538	E1L_LC_W109 Y - HCDR1	artificial	KYAMN
539	E1L_LC_W109 Y - HCDR2	artificial	RIRSKYNNYATYYADSVKS
540	E1L_LC_W109 Y - HCDR3	artificial	HGNFGNSYTSYYAY
541	E1L_LC_W109 Y - LCDR1	artificial	GSSTGAVTSGYYPN
542	E1L_LC_W109 Y - LCDR2	artificial	GTKFLAP
543	E1L_LC_W109 Y - LCDR3	artificial	ALYYSNRWV
544	E1L_LC_W109 Y - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWG QGTLVTVSS
545	E1L_LC_W109 Y - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALYYSNRWVFGGGTKLTVL
546	E2M - HCDR1	artificial	GYAMN
547	E2M - HCDR2	artificial	RIRSKYNNYATYYADSVKE
548	E2M - HCDR3	artificial	HRNFGNSYLSWFAY
549	E2M - LCDR1	artificial	RSSTGAVTSGYYPN
550	E2M - LCDR2	artificial	ATDMRPS
551	E2M - LCDR3	artificial	ALWYSNRWV
552	E2M - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
553	E2M - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
554	E2M_HC_A89I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTIYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
555	E2M_HC_A89I - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
556	E2M_HC_A89L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
557	E2M_HC_A89L - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
558	E2M_HC_A89T - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTTYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
559	E2M_HC_A89T - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
560	E2M_HC_A89V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
561	E2M_HC_A89V - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
562	E2M_HC_L52M - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVRQAPGKMEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
563	E2M_HC_L52M - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
564	E2M_HC_L52M LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVRQAPGKMEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
565	E2M_HC_L52M LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSTLTVSPGGTIVTITCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
566	E2M_HC_L52M LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVRQAPGKMEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
567	E2M_HC_L52M LC_Q46K - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL

568	E2M_HC_L52M _LC_Q46K_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVRQAPGKGMWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
569	E2M_HC_L52M _LC_Q46K_G1 41S - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGSGTKLTVL
570	E2M_HC_L52V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVRQAPGKGVWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
571	E2M_HC_L52V - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGSGTKLTVL
572	E2M_HC_L52V _LC_V44F - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVRQAPGKGVWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
573	E2M_HC_L52V _LC_V44F - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGSGTKLTVL
574	E2M_HC_L52V _LC_V44Y - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVRQAPGKGVWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
575	E2M_HC_L52V _LC_V44Y - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGSGTKLTVL
576	E2M_HC_M41F _A89V - HCDR1	artificial	GYAFN
577	E2M_HC_M41F _A89V - HCDR2	artificial	RIRSKYNNYATYYADSVKE
578	E2M_HC_M41F _A89V - HCDR3	artificial	HRNFGNSYLSWFAY
579	E2M_HC_M41F _A89V - LCDR1	artificial	RSSTGAVTSGYYPN
580	E2M_HC_M41F _A89V - LCDR2	artificial	ATDMRPS
581	E2M_HC_M41F _A89V - LCDR3	artificial	ALWYSNRWV
582	E2M_HC_M41F _A89V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAFNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
583	E2M_HC_M41F _A89V - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGSGTKLTVL
584	E2M_HC_M41I - HCDR1	artificial	GYAIN
585	E2M_HC_M41I - HCDR2	artificial	RIRSKYNNYATYYADSVKE
586	E2M_HC_M41I - HCDR3	artificial	HRNFGNSYLSWFAY
587	E2M_HC_M41I - LCDR1	artificial	RSSTGAVTSGYYPN
588	E2M_HC_M41I - LCDR2	artificial	ATDMRPS
589	E2M_HC_M41I - LCDR3	artificial	ALWYSNRWV
590	E2M_HC_M41I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
591	E2M_HC_M41I - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGSGTKLTVL
592	E2M_HC_M41I _A89L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
593	E2M_HC_M41I _A89L - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGSGTKLTVL
594	E2M_HC_M41I _A89V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
595	E2M_HC_M41I _A89V - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGSGTKLTVL
596	E2M_HC_M41I _A89V_IC_L2 II_Q46K_G14	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS

	1S - VH		
597	E2M_HC_M41I _A89V_LC_L2 1I_Q46K_G14 1S - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCRSSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
598	E2M_HC_M41I _A89V_LC_Q4 6K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
599	E2M_HC_M41I _A89V_LC_Q4 6K - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCRSSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
600	E2M_HC_M41I _L52V_A89V LC_L21I_Q46 K_G141S_V44 F - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAINWVRQAPGKGVWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
601	E2M_HC_M41I _L52V_A89V LC_L21I_Q46 K_G141S_V44 F - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCRSSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
602	E2M_HC_M41I _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
603	E2M_HC_M41I _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCRSSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
604	E2M_HC_M41I _Q46E_A89V LC_L21I_Q46 K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
605	E2M_HC_M41I _Q46E_A89V LC_L21I_Q46 K_G141S - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCRSSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
606	E2M_HC_M41V - HCDR1	artificial	GYAVN
607	E2M_HC_M41V - HCDR2	artificial	RIRSKYNNYATYYADSVKE
608	E2M_HC_M41V - HCDR3	artificial	HRNFGNSYLSWFAY
609	E2M_HC_M41V - LCDR1	artificial	RSSTGAVTSGYYPN
610	E2M_HC_M41V - LCDR2	artificial	ATDMRPS
611	E2M_HC_M41V - LCDR3	artificial	ALWYSNRWV
612	E2M_HC_M41V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAVNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
613	E2M_HC_M41V - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCRSSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
614	E2M_HC_Q46D - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
615	E2M_HC_Q46D - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCRSSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
616	E2M_HC_Q46D _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
617	E2M_HC_Q46D _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCRSSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
618	E2M_HC_Q46D _LC_L21I_Q4 6R_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
619	E2M_HC_Q46D _LC_L21I_Q4 6R_G141S -	artificial	QTVVTQEPSTLTVSPGGTVTITCRSSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL

	VL		
620	E2M_HC_Q46D _LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
621	E2M_HC_Q46D _LC_Q46K - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSRSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
622	E2M_HC_Q46D _LC_Q46K_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
623	E2M_HC_Q46D _LC_Q46K_G1 41S - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSRSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
624	E2M_HC_Q46D _LC_Q46R - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
625	E2M_HC_Q46D _LC_Q46R - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSRSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
626	E2M_HC_Q46D _LC_Q46R_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
627	E2M_HC_Q46D _LC_Q46R_G1 41S - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSRSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
628	E2M_HC_Q46E - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
629	E2M_HC_Q46E - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSRSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
630	E2M_HC_Q46E _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
631	E2M_HC_Q46E _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSRSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
632	E2M_HC_Q46E _LC_L21I_Q4 6R_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
633	E2M_HC_Q46E _LC_L21I_Q4 6R_G141S - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSRSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
634	E2M_HC_Q46E _LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
635	E2M_HC_Q46E _LC_Q46K - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSRSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
636	E2M_HC_Q46E _LC_Q46K_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
637	E2M_HC_Q46E _LC_Q46K_G1 41S - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSRSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
638	E2M_HC_Q46E _LC_Q46R - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
639	E2M_HC_Q46E _LC_Q46R - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSRSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
640	E2M_HC_Q46E _LC_Q46R_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
641	E2M_HC_Q46E _LC_Q46R_G1 41S - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSRSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
642	E2M_HC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVRKAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
643	E2M_HC_Q46K - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSRSTGAVTSGYYPNWVQKPKGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL

644	E2M_HC_Q46R - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVRRAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
645	E2M_HC_Q46R - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
646	E2M_HC_V107 A - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCARHRNFGNSYLSWFAYWG QGTLVTVSS
647	E2M_HC_V107 A - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
648	E2M_HC_V107 L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCLHRNFGNSYLSWFAYWG QGTLVTVSS
649	E2M_HC_V107 L - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
650	E2M_I2E - HCDR1	artificial	GYAIN
651	E2M_I2E - HCDR2	artificial	RIRSKYNNYATYYADAVKE
652	E2M_I2E - HCDR3	artificial	ARNFGSSYLSWFAY
653	E2M_I2E - LCDR1	artificial	RSSTGAVTSGYYPN
654	E2M_I2E - LCDR2	artificial	ATDMRPS
655	E2M_I2E - LCDR3	artificial	ALWYSNRWV
656	E2M_I2E - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADAVKERFTISRDDSKNTVYLQMNNLKTEDTAVYYCARARNFGSSYLSWFAYWG QGTLVTVSS
657	E2M_I2E - VL	artificial	QTVVTQEPSTLTVSPGGTIVTITCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLSGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
658	E2M_I2K - HCDR1	artificial	GYAMN
659	E2M_I2K - HCDR2	artificial	RIRSKYNNYATYYAEAVKG
660	E2M_I2K - HCDR3	artificial	NENIGTSYLSWFAY
661	E2M_I2K - LCDR1	artificial	RSSTGAVTSGYYPN
662	E2M_I2K - LCDR2	artificial	ATDMRPS
663	E2M_I2K - LCDR3	artificial	ALWYSNRWV
664	E2M_I2K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYAEAVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRNENIGTSYLSWFAYWG QGTLVTVSS
665	E2M_I2K - VL	artificial	QTVVTQEPSTLTVSPGGTIVTITCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLSGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
666	E2M_I2L - HCDR1	artificial	GYAMN
667	E2M_I2L - HCDR2	artificial	RIRSKYNNYATYYAEAVKE
668	E2M_I2L - HCDR3	artificial	ARNFGSSYLSWFAY
669	E2M_I2L - LCDR1	artificial	RSSTGAVTSGYYPN
670	E2M_I2L - LCDR2	artificial	ATDMRPS
671	E2M_I2L - LCDR3	artificial	ALYYSNRWV
672	E2M_I2L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVRQAPGKMEWVARIRSKYNNY ATYYADAVKERFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRARNFGSSYLSWFAYWG QGTLVTVSS
673	E2M_I2L - VL	artificial	QTVVTQEPSTLTVSPGGTIVTITCSRSTGAVTSGYYPNWIQKPGQAPRGLIGATDMRPS GTPARFSGSLEGGAALTLSGVQPEDEAEYYCALYYSNRWVFGSGTKLTVL
674	E2M_I2M - HCDR1	artificial	GYAMN
675	E2M_I2M - HCDR2	artificial	RIRSKYNNYATYYADAVKE
676	E2M_I2M - HCDR3	artificial	ARNFGTSYLSWFAY
677	E2M_I2M - LCDR1	artificial	RSSTGAVTSGYYPN
678	E2M_I2M - LCDR2	artificial	ATDMRPS

679	E2M_I2M - LCDR3	artificial	ALWYSNRWV
680	E2M_I2M - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNGYAMNWVRQAPGKGMWVARIRSKYNNY ATYYADAVKERFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRARNFGTSYLSWFAYWG QGTLVTVSS
681	E2M_I2M - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCRSSTGAVTSGYYPNWVQKPKGPQAPRGLIGATDMRPS GTPARFSGSLSGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
682	E2M_I2M2 - HCDR1	artificial	GYAIN
683	E2M_I2M2 - HCDR2	artificial	RIRSKYNNYATYYADAVKE
684	E2M_I2M2 - HCDR3	artificial	NANFGTSYLSFFAY
685	E2M_I2M2 - LCDR1	artificial	RSSTGAVTSGYYPN
686	E2M_I2M2 - LCDR2	artificial	ATDMRPS
687	E2M_I2M2 - LCDR3	artificial	ALWYSNRWV
688	E2M_I2M2 - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNGYAINWVREAPGKGLEWVARIRSKYNNY ATYYADAVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRNANFGTSYLSYFAYWG QGTLVTVSS
689	E2M_I2M2 - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCRSSTGAVTSGYYPNWVQKPKGPQAPRGLIGATDMRPS GTPARFSGSLSGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
690	E2M_LC_G141 S - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNGYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
691	E2M_LC_G141 S - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCRSSTGAVTSGYYPNWVQKPKGPQAPRGLIGATDMRPS GTPARFSGSLSGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
692	E2M_LC_G141 S_L21I - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNGYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
693	E2M_LC_G141 S_L21I - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCRSSTGAVTSGYYPNWVQKPKGPQAPRGLIGATDMRPS GTPARFSGSLSGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
694	E2M_LC_L83E - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNGYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
695	E2M_LC_L83E - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCRSSTGAVTSGYYPNWVQKPKGPQAPRGLIGATDMRPS GTPARFSGSLEGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
696	E2M_LC_L83S - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNGYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
697	E2M_LC_L83S - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCRSSTGAVTSGYYPNWVQKPKGPQAPRGLIGATDMRPS GTPARFSGSLSGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
698	E2M_LC_Q46E - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNGYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
699	E2M_LC_Q46E - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCRSSTGAVTSGYYPNWVQKPKGPQAPRGLIGATDMRPS GTPARFSGSLSGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
700	E2M_LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNGYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
701	E2M_LC_Q46K - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCRSSTGAVTSGYYPNWVQKPKGPQAPRGLIGATDMRPS GTPARFSGSLSGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
702	E2M_LC_A107 L - HCDR1	artificial	GYAMN
703	E2M_LC_A107 L - HCDR2	artificial	RIRSKYNNYATYYADSVKE
704	E2M_LC_A107 L - HCDR3	artificial	HRNFGNSYLSWFAY
705	E2M_LC_A107 L - LCDR1	artificial	RSSTGAVTSGYYPN
706	E2M_LC_A107 L - LCDR2	artificial	ATDMRPS
707	E2M_LC_A107 L - LCDR3	artificial	LLWYSNRWV
708	E2M_LC_A107 L - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNGYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
709	E2M_LC_A107 L - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCRSSTGAVTSGYYPNWVQKPKGPQAPRGLIGATDMRPS GTPARFSGSLSGGKAALTLSGVQPEDEAEYYCLLWYSNRWVFGGGTKLTVL
710	E2M_LC_V44I - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNGYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
711	E2M_LC_V44I - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCRSSTGAVTSGYYPNWVQKPKGPQAPRGLIGATDMRPS GTPARFSGSLSGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL

712	E2M_LC_V44L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
713	E2M_LC_V44L - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCSRSTGAVTSGYYPNWLQKPGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
714	E2M_LC_V44M - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
715	E2M_LC_V44M - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
716	E2M_LC_W109 Y - HCDR1	artificial	GYAMN
717	E2M_LC_W109 Y - HCDR2	artificial	RIRSKYNNYATYYADSVKE
718	E2M_LC_W109 Y - HCDR3	artificial	HRNFGNSYLSWFAY
719	E2M_LC_W109 Y - LCDR1	artificial	RSSTGAVTSGYYPN
720	E2M_LC_W109 Y - LCDR2	artificial	ATDMRPS
721	E2M_LC_W109 Y - LCDR3	artificial	ALYYSNRWV
722	E2M_LC_W109 Y - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWG QGTLVTVSS
723	E2M_LC_W109 Y - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCSRSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPS GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALYYSNRWVFGGGTKLTVL
724	F12Q - HCDR1	artificial	SYAMN
725	F12Q - HCDR2	artificial	RIRSKYNNYATYYADSVKG
726	F12Q - HCDR3	artificial	HGNFGNSYVSWWAY
727	F12Q - LCDR1	artificial	GSSTGAVTSGNYPN
728	F12Q - LCDR2	artificial	GTKFLAP
729	F12Q - LCDR3	artificial	VLWYSNRWV
730	F12Q - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
731	F12Q - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
732	F12Q_HC_A89 I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTIYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
733	F12Q_HC_A89 I - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
734	F12Q_HC_A89 L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
735	F12Q_HC_A89 L - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
736	F12Q_HC_A89 T - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTTYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
737	F12Q_HC_A89 T - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
738	F12Q_HC_A89 V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
739	F12Q_HC_A89 V - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
740	F12Q_HC_L52 M - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
741	F12Q_HC_L52 M - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
742	F12Q_HC_L52 M_LC_L21I_Q 46K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKMEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
743	F12Q_HC_L52 M_LC_L21I_Q 46K_G141S -	artificial	QTVVTQEPSTLTVSPGGTIVTITCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL

	VL		
744	F12Q_HC_L52 M_LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGMWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
745	F12Q_HC_L52 M_LC_Q46K - VL	artificial	QTVVTQEPISLTVSPGGTIVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
746	F12Q_HC_L52 M_LC_Q46K_G L41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGMWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
747	F12Q_HC_L52 M_LC_Q46K_G L41S - VL	artificial	QTVVTQEPISLTVSPGGTIVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
748	F12Q_HC_L52 V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGMWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
749	F12Q_HC_L52 V - VL	artificial	QTVVTQEPISLTVSPGGTIVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
750	F12Q_HC_L52 V_LC_V44F - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGMWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
751	F12Q_HC_L52 V_LC_V44F - VL	artificial	QTVVTQEPISLTVSPGGTIVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
752	F12Q_HC_L52 V_LC_V44Y - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGMWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
753	F12Q_HC_L52 V_LC_V44Y - VL	artificial	QTVVTQEPISLTVSPGGTIVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
754	F12Q_HC_M41 F_A89V - HCDR1	artificial	SYAFN
755	F12Q_HC_M41 F_A89V - HCDR2	artificial	RIRSKYNNYATYYADSVKG
756	F12Q_HC_M41 F_A89V - HCDR3	artificial	HGNFGNSYVSWWAY
757	F12Q_HC_M41 F_A89V - LCDR1	artificial	GSSTGAVTSGNYPN
758	F12Q_HC_M41 F_A89V - LCDR2	artificial	GTKFLAP
759	F12Q_HC_M41 F_A89V - LCDR3	artificial	VLWYSNRWV
760	F12Q_HC_M41 F_A89V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAFNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
761	F12Q_HC_M41 F_A89V - VL	artificial	QTVVTQEPISLTVSPGGTIVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
762	F12Q_HC_M41 I - HCDR1	artificial	SYAIN
763	F12Q_HC_M41 I - HCDR2	artificial	RIRSKYNNYATYYADSVKG
764	F12Q_HC_M41 I - HCDR3	artificial	HGNFGNSYVSWWAY
765	F12Q_HC_M41 I - LCDR1	artificial	GSSTGAVTSGNYPN
766	F12Q_HC_M41 I - LCDR2	artificial	GTKFLAP
767	F12Q_HC_M41 I - LCDR3	artificial	VLWYSNRWV
768	F12Q_HC_M41 I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
769	F12Q_HC_M41 I - VL	artificial	QTVVTQEPISLTVSPGGTIVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
770	F12Q_HC_M41 I_A89L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
771	F12Q_HC_M41 I_A89L - VL	artificial	QTVVTQEPISLTVSPGGTIVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL

772	F12Q_HC_M41 I_A89V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
773	F12Q_HC_M41 I_A89V - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTSGSSTGAVTSGNYPNWVQKPGQAPRGLIGGKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYCVLWYSNRWVFGGGTKLTVL
774	F12Q_HC_M41 I_A89V_LC_L 21I_Q46K_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
775	F12Q_HC_M41 I_A89V_LC_L 21I_Q46K_G1 41S - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTSGSSTGAVTSGNYPNWVQKPGQAPRGLIGGKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYCVLWYSNRWVFGSGTKLTVL
776	F12Q_HC_M41 I_A89V_LC_Q 46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
777	F12Q_HC_M41 I_A89V_LC_Q 46K - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTSGSSTGAVTSGNYPNWVQKPGQAPRGLIGGKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYCVLWYSNRWVFGGGTKLTVL
778	F12Q_HC_M41 I_L52V_A89V _LC_L21I_Q4 6K_G141S_V4 4F - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
779	F12Q_HC_M41 I_L52V_A89V _LC_L21I_Q4 6K_G141S_V4 4F - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTSGSSTGAVTSGNYPNWVQKPGQAPRGLIGGKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYCVLWYSNRWVFGSGTKLTVL
780	F12Q_HC_M41 I_LC_L21I_Q 46K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
781	F12Q_HC_M41 I_LC_L21I_Q 46K_G141S - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTSGSSTGAVTSGNYPNWVQKPGQAPRGLIGGKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYCVLWYSNRWVFGSGTKLTVL
782	F12Q_HC_M41 I_Q46E_A89V _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
783	F12Q_HC_M41 I_Q46E_A89V _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTSGSSTGAVTSGNYPNWVQKPGQAPRGLIGGKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYCVLWYSNRWVFGSGTKLTVL
784	F12Q_HC_M41 V - HCDR1	artificial	SYAVN
785	F12Q_HC_M41 V - HCDR2	artificial	RIRSKYNNYATYYADSVKG
786	F12Q_HC_M41 V - HCDR3	artificial	HGNFGNSYVSWWAY
787	F12Q_HC_M41 V - LCDR1	artificial	GSSTGAVTSGNYPN
788	F12Q_HC_M41 V - LCDR2	artificial	GTKFLAP
789	F12Q_HC_M41 V - LCDR3	artificial	VLWYSNRWV
790	F12Q_HC_M41 V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAVNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
791	F12Q_HC_M41 V - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTSGSSTGAVTSGNYPNWVQKPGQAPRGLIGGKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYCVLWYSNRWVFGGGTKLTVL
792	F12Q_HC_Q46 D - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
793	F12Q_HC_Q46 D - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTSGSSTGAVTSGNYPNWVQKPGQAPRGLIGGKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYCVLWYSNRWVFGGGTKLTVL
794	F12Q_HC_Q46 D_LC_L21I_Q 46K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
795	F12Q_HC_Q46 D_LC_L21I_Q 46K_G141S -	artificial	QTVVTQEPSTLTVSPGGTIVTLTSGSSTGAVTSGNYPNWVQKPGQAPRGLIGGKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYCVLWYSNRWVFGSGTKLTVL

	VL		
796	F12Q_HC_Q46 D_LC_L21I_Q 46R_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
797	F12Q_HC_Q46 D_LC_L21I_Q 46R_G141S - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGNYPNWWQKPKGPQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
798	F12Q_HC_Q46 D_LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
799	F12Q_HC_Q46 D_LC_Q46K - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGNYPNWWQKPKGPQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
800	F12Q_HC_Q46 D_LC_Q46K_G 141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
801	F12Q_HC_Q46 D_LC_Q46K_G 141S - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGNYPNWWQKPKGPQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
802	F12Q_HC_Q46 D_LC_Q46R - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
803	F12Q_HC_Q46 D_LC_Q46R - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGNYPNWWQKPKGPQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
804	F12Q_HC_Q46 D_LC_Q46R_G 141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
805	F12Q_HC_Q46 D_LC_Q46R_G 141S - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGNYPNWWQKPKGPQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
806	F12Q_HC_Q46 E - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
807	F12Q_HC_Q46 E - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGNYPNWWQKPKGPQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
808	F12Q_HC_Q46 E_LC_L21I_Q 46K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
809	F12Q_HC_Q46 E_LC_L21I_Q 46K_G141S - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGNYPNWWQKPKGPQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
810	F12Q_HC_Q46 E_LC_L21I_Q 46R_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
811	F12Q_HC_Q46 E_LC_L21I_Q 46R_G141S - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGNYPNWWQKPKGPQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
812	F12Q_HC_Q46 E_LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
813	F12Q_HC_Q46 E_LC_Q46K - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGNYPNWWQKPKGPQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
814	F12Q_HC_Q46 E_LC_Q46K_G 141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
815	F12Q_HC_Q46 E_LC_Q46K_G 141S - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGNYPNWWQKPKGPQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
816	F12Q_HC_Q46 E_LC_Q46R - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
817	F12Q_HC_Q46 E_LC_Q46R - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGNYPNWWQKPKGPQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
818	F12Q_HC_Q46 E_LC_Q46R_G 141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS

819	F12Q_HC_Q46 E_LC_Q46R_G 141S - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCGSSTGAVTSGNYPNWWVQRKPGQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
820	F12Q_HC_Q46 K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVRKAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
821	F12Q_HC_Q46 K - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCGSSTGAVTSGNYPNWWVQRKPGQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
822	F12Q_HC_Q46 R - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVRAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
823	F12Q_HC_Q46 R - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCGSSTGAVTSGNYPNWWVQRKPGQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
824	F12Q_HC_V10 7A - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCARHGNFGNSYVSWWAYWG QGTLVTVSS
825	F12Q_HC_V10 7A - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCGSSTGAVTSGNYPNWWVQRKPGQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
826	F12Q_HC_V10 7L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCLRHGNFGNSYVSWWAYWG QGTLVTVSS
827	F12Q_HC_V10 7L - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCGSSTGAVTSGNYPNWWVQRKPGQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
828	F12Q_HC_W13 6F - HCDR1	artificial	SYAMN
829	F12Q_HC_W13 6F - HCDR2	artificial	RIRSKYNNYATYYADSVKG
830	F12Q_HC_W13 6F - HCDR3	artificial	HGNFGNSYVSWFAY
831	F12Q_HC_W13 6F - LCDR1	artificial	GSSTGAVTSGNYPN
832	F12Q_HC_W13 6F - LCDR2	artificial	GTKFLAP
833	F12Q_HC_W13 6F - LCDR3	artificial	VLWYSNRWV
834	F12Q_HC_W13 6F - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWFAYWG QGTLVTVSS
835	F12Q_HC_W13 6F - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCGSSTGAVTSGNYPNWWVQRKPGQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
836	F12Q_HC_W13 6F_LC_V44I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWFAYWG QGTLVTVSS
837	F12Q_HC_W13 6F_LC_V44I - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCGSSTGAVTSGNYPNWIQQKPGQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
838	F12Q_HC_W13 6F_LC_V44L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWFAYWG QGTLVTVSS
839	F12Q_HC_W13 6F_LC_V44L - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCGSSTGAVTSGNYPNWLQKPGQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
840	F12Q_I2E - HCDR1	artificial	SYAIN
841	F12Q_I2E - HCDR2	artificial	RIRSKYNNYATYYADAVKG
842	F12Q_I2E - HCDR3	artificial	AGNFGSSYVSWWAY
843	F12Q_I2E - LCDR1	artificial	GSSTGAVTSGNYPN
844	F12Q_I2E - LCDR2	artificial	GTKFLAP
845	F12Q_I2E - LCDR3	artificial	VLWYSNRWV
846	F12Q_I2E - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADAVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCARAGNFGSSYVSWWAYWG QGTLVTVSS
847	F12Q_I2E - VL	artificial	QTVVTQEPSTLTVSPGGTIVTITCGSSTGAVTSGNYPNWWVQRKPGQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
848	F12Q_I2K - HCDR1	artificial	SYAMN
849	F12Q_I2K - HCDR2	artificial	RIRSKYNNYATYYAEAVKG
850	F12Q_I2K - HCDR3	artificial	NENIGTSYVSWWAY

851	F12Q_I2K - LCDR1	artificial	GSSTGAVTSGNYPN
852	F12Q_I2K - LCDR2	artificial	GTKFLAP
853	F12Q_I2K - LCDR3	artificial	VLWYSNRWV
854	F12Q_I2K - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYAEAVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRNENIGTSYVSWWAYWG QGTLVTVSS
855	F12Q_I2K - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLSGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
856	F12Q_I2L - HCDR1	artificial	SYAMN
857	F12Q_I2L - HCDR2	artificial	RIRSKYNNYATYYADAVKG
858	F12Q_I2L - HCDR3	artificial	AGNFGSSYVSWFAY
859	F12Q_I2L - LCDR1	artificial	GSSTGAVTSGNYPN
860	F12Q_I2L - LCDR2	artificial	GTKFLAP
861	F12Q_I2L - LCDR3	artificial	VLYYSNRWV
862	F12Q_I2L - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNSYAMNWVRQAPGKMEWVARIRSKYNNY ATYYADAVKGRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRAGNFGSSYVSWFAYWG QGTLVTVSS
863	F12Q_I2L - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLSGGKAALTLSGVQPEDEAEYYCVLYYSNRWVFGSGTKLTVL
864	F12Q_I2M - HCDR1	artificial	SYAMN
865	F12Q_I2M - HCDR2	artificial	RIRSKYNNYATYYADAVKG
866	F12Q_I2M - HCDR3	artificial	AGNFGTSYVSWWAY
867	F12Q_I2M - LCDR1	artificial	GSSTGAVTSGNYPN
868	F12Q_I2M - LCDR2	artificial	GTKFLAP
869	F12Q_I2M - LCDR3	artificial	VLWYSNRWV
870	F12Q_I2M - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNSYAMNWVRQAPGKMEWVARIRSKYNNY ATYYADAVKGRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRAGNFGTSYVSWWAYWG QGTLVTVSS
871	F12Q_I2M - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLSGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
872	F12Q_I2M2 - HCDR1	artificial	SYAIN
873	F12Q_I2M2 - HCDR2	artificial	RIRSKYNNYATYYADAVKG
874	F12Q_I2M2 - HCDR3	artificial	NANFGTSYVSWFAY
875	F12Q_I2M2 - LCDR1	artificial	GSSTGAVTSGNYPN
876	F12Q_I2M2 - LCDR2	artificial	GTKFLAP
877	F12Q_I2M2 - LCDR3	artificial	VLWYSNRWV
878	F12Q_I2M2 - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNSYAINWVREAPGKGLEWVARIRSKYNNY ATYYADAVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRNANFGTSYVSWFAYWG QGTLVTVSS
879	F12Q_I2M2 - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLSGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
880	F12Q_LC_G14 1S - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
881	F12Q_LC_G14 1S - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLSGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
882	F12Q_LC_G14 1S_L21I - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
883	F12Q_LC_G14 1S_L21I - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLSGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
884	F12Q_LC_L83 E - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS

885	F12Q_LC_L83 E - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGNYPNWWQKPGQAPRGLIGGTKFLAP GTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
886	F12Q_LC_L83 S - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNSYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
887	F12Q_LC_L83 S - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGNYPNWWQKPGQAPRGLIGGTKFLAP GTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
888	F12Q_LC_Q46 E - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNSYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
889	F12Q_LC_Q46 E - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGNYPNWWQKPGQAPRGLIGGTKFLAP GTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
890	F12Q_LC_Q46 K - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNSYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
891	F12Q_LC_Q46 K - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGNYPNWWQKPGQAPRGLIGGTKFLAP GTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
892	F12Q_LC_V10 7A - HCDR1	artificial	SYAMN
893	F12Q_LC_V10 7A - HCDR2	artificial	RIRSKYNNYATYYADSVKG
894	F12Q_LC_V10 7A - HCDR3	artificial	HGNFGNSYVSWWAY
895	F12Q_LC_V10 7A - LCDR1	artificial	GSSTGAVTSGNYPN
896	F12Q_LC_V10 7A - LCDR2	artificial	GTKFLAP
897	F12Q_LC_V10 7A - LCDR3	artificial	ALWYSNRWV
898	F12Q_LC_V10 7A - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNSYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
899	F12Q_LC_V10 7A - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGNYPNWWQKPGQAPRGLIGGTKFLAP GTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
900	F12Q_LC_V10 7L - HCDR1	artificial	SYAMN
901	F12Q_LC_V10 7L - HCDR2	artificial	RIRSKYNNYATYYADSVKG
902	F12Q_LC_V10 7L - HCDR3	artificial	HGNFGNSYVSWWAY
903	F12Q_LC_V10 7L - LCDR1	artificial	GSSTGAVTSGNYPN
904	F12Q_LC_V10 7L - LCDR2	artificial	GTKFLAP
905	F12Q_LC_V10 7L - LCDR3	artificial	LLWYSNRWV
906	F12Q_LC_V10 7L - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNSYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
907	F12Q_LC_V10 7L - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGNYPNWWQKPGQAPRGLIGGTKFLAP GTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
908	F12Q_LC_V44 I - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNSYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
909	F12Q_LC_V44 I - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGNYPNWWQKPGQAPRGLIGGTKFLAP GTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
910	F12Q_LC_V44 L - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNSYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
911	F12Q_LC_V44 L - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGNYPNWWQKPGQAPRGLIGGTKFLAP GTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
912	F12Q_LC_V44 M - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNSYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWG QGTLVTVSS
913	F12Q_LC_V44 M - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGNYPNWWQKPGQAPRGLIGGTKFLAP GTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
914	F12Q_LC_W10 9Y - HCDR1	artificial	SYAMN
915	F12Q_LC_W10 9Y - HCDR2	artificial	RIRSKYNNYATYYADSVKG
916	F12Q_LC_W10 9Y - HCDR3	artificial	HGNFGNSYVSWWAY
917	F12Q_LC_W10 9Y - LCDR1	artificial	GSSTGAVTSGNYPN
918	F12Q_LC_W10 9Y - LCDR2	artificial	GTKFLAP

919	F12Q_LC_W10 9Y - LCDR3	artificial	VLYYSNRWV
920	F12Q_LC_W10 9Y - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
921	F12Q_LC_W10 9Y - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLYYSNRWVFGGGTKLTVL
922	F6A - HCDR1	artificial	IYAMN
923	F6A - HCDR2	artificial	RIRSKYNNYATYYADSVKS
924	F6A - HCDR3	artificial	HGNFGNSYVSFFAY
925	F6A - LCDR1	artificial	GSSTGAVTSGYYPN
926	F6A - LCDR2	artificial	GTKFLAP
927	F6A - LCDR3	artificial	ALWYSNRWV
928	F6A - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
929	F6A - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCGSSTGAVTSGYYPNWWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
930	F6A_HC_A89I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTIYLMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
931	F6A_HC_A89I - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCGSSTGAVTSGYYPNWWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
932	F6A_HC_A89L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTLYLMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
933	F6A_HC_A89L - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCGSSTGAVTSGYYPNWWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
934	F6A_HC_A89T - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTLYLMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
935	F6A_HC_A89T - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCGSSTGAVTSGYYPNWWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
936	F6A_HC_A89V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
937	F6A_HC_A89V - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCGSSTGAVTSGYYPNWWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
938	F6A_HC_L52M - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAMNWVRQAPGKMEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
939	F6A_HC_L52M - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCGSSTGAVTSGYYPNWWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
940	F6A_HC_L52M _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAMNWVRQAPGKMEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
941	F6A_HC_L52M _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSTLTVSPGGTIVTITCGSSTGAVTSGYYPNWWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
942	F6A_HC_L52M _LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAMNWVRQAPGKMEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
943	F6A_HC_L52M _LC_Q46K - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCGSSTGAVTSGYYPNWWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
944	F6A_HC_L52M _LC_Q46K_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAMNWVRQAPGKMEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
945	F6A_HC_L52M _LC_Q46K_G1 41S - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCGSSTGAVTSGYYPNWWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
946	F6A_HC_L52V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAMNWVRQAPGKGEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
947	F6A_HC_L52V - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCGSSTGAVTSGYYPNWWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
948	F6A_HC_L52V _LC_V44F - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAMNWVRQAPGKGEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
949	F6A_HC_L52V	artificial	QTVVTQEPSTLTVSPGGTIVTLTCGSSTGAVTSGYYPNWWVQKPGQAPRGLIGGTKFLAP

	LC_V44F - VL		GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
950	F6A_HC_L52V LC_V44Y - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAMNWVRQAPGKGVWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
951	F6A_HC_L52V LC_V44Y - VL	artificial	QTVVTQEPSTLVSPGGTIVTLTCGSSTGAVTSGYYPNWYQQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
952	F6A_HC_M41F A89V - HCDR1	artificial	IYAFN
953	F6A_HC_M41F A89V - HCDR2	artificial	RIRSKYNNYATYYADSVKS
954	F6A_HC_M41F A89V - HCDR3	artificial	HGNFGNSYVSFFAY
955	F6A_HC_M41F A89V - LCDR1	artificial	GSSTGAVTSGYYPN
956	F6A_HC_M41F A89V - LCDR2	artificial	GTKFLAP
957	F6A_HC_M41F A89V - LCDR3	artificial	ALWYSNRWV
958	F6A_HC_M41F A89V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAFNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
959	F6A_HC_M41F A89V - VL	artificial	QTVVTQEPSTLVSPGGTIVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
960	F6A_HC_M41I - HCDR1	artificial	IYAIN
961	F6A_HC_M41I - HCDR2	artificial	RIRSKYNNYATYYADSVKS
962	F6A_HC_M41I - HCDR3	artificial	HGNFGNSYVSFFAY
963	F6A_HC_M41I - LCDR1	artificial	GSSTGAVTSGYYPN
964	F6A_HC_M41I - LCDR2	artificial	GTKFLAP
965	F6A_HC_M41I - LCDR3	artificial	ALWYSNRWV
966	F6A_HC_M41I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
967	F6A_HC_M41I - VL	artificial	QTVVTQEPSTLVSPGGTIVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
968	F6A_HC_M41I A89L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
969	F6A_HC_M41I A89L - VL	artificial	QTVVTQEPSTLVSPGGTIVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
970	F6A_HC_M41I A89V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
971	F6A_HC_M41I A89V - VL	artificial	QTVVTQEPSTLVSPGGTIVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
972	F6A_HC_M41I A89V_IC_L2 LI_Q46K_G14 1S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
973	F6A_HC_M41I A89V_IC_L2 LI_Q46K_G14 1S - VL	artificial	QTVVTQEPSTLVSPGGTIVTITCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
974	F6A_HC_M41I A89V_IC_Q4 6K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
975	F6A_HC_M41I A89V_IC_Q4 6K - VL	artificial	QTVVTQEPSTLVSPGGTIVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
976	F6A_HC_M41I L52V_A89V LC_L2LI_Q46 K_G141S_V44	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAINWVRQAPGKGVWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS

	F - VH		
977	F6A_HC_M41I _L52V_A89V _LC_L21I_Q46 K_G141S_V44 F - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
978	F6A_HC_M41I _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
979	F6A_HC_M41I _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
980	F6A_HC_M41I _Q46E_A89V _LC_L21I_Q46 K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAINWVREAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
981	F6A_HC_M41I _Q46E_A89V _LC_L21I_Q46 K_G141S - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
982	F6A_HC_M41V - HCDR1	artificial	IYAVN
983	F6A_HC_M41V - HCDR2	artificial	RIRSKYNNYATYYADSVKS
984	F6A_HC_M41V - HCDR3	artificial	HGNFGNSYVSFFAY
985	F6A_HC_M41V - LCDR1	artificial	GSSTGAVTSGYYPN
986	F6A_HC_M41V - LCDR2	artificial	GTKFLAP
987	F6A_HC_M41V - LCDR3	artificial	ALWYSNRWV
988	F6A_HC_M41V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAVNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
989	F6A_HC_M41V - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
990	F6A_HC_Q46D - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
991	F6A_HC_Q46D - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
992	F6A_HC_Q46D _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
993	F6A_HC_Q46D _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
994	F6A_HC_Q46D _LC_L21I_Q4 6R_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
995	F6A_HC_Q46D _LC_L21I_Q4 6R_G141S - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
996	F6A_HC_Q46D _LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
997	F6A_HC_Q46D _LC_Q46K - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
998	F6A_HC_Q46D _LC_Q46K_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
999	F6A_HC_Q46D _LC_Q46K_G1 41S - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1000	F6A_HC_Q46D _LC_Q46R -	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG

	VH		QGTLVTVSS
1001	F6A_HC_Q46D _LC_Q46R - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQRKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1002	F6A_HC_Q46D _LC_Q46R_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIIYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
1003	F6A_HC_Q46D _LC_Q46R_G1 41S - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQRKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1004	F6A_HC_Q46E - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIIYAMNWWREAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
1005	F6A_HC_Q46E - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1006	F6A_HC_Q46E _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIIYAMNWWREAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
1007	F6A_HC_Q46E _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1008	F6A_HC_Q46E _LC_L21I_Q4 6R_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIIYAMNWWREAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
1009	F6A_HC_Q46E _LC_L21I_Q4 6R_G141S - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQRKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1010	F6A_HC_Q46E _LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIIYAMNWWREAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
1011	F6A_HC_Q46E _LC_Q46K - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1012	F6A_HC_Q46E _LC_Q46K_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIIYAMNWWREAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
1013	F6A_HC_Q46E _LC_Q46K_G1 41S - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1014	F6A_HC_Q46E _LC_Q46R - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIIYAMNWWREAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
1015	F6A_HC_Q46E _LC_Q46R - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQRKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1016	F6A_HC_Q46E _LC_Q46R_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIIYAMNWWREAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
1017	F6A_HC_Q46E _LC_Q46R_G1 41S - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQRKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1018	F6A_HC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIIYAMNWWVRKAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
1019	F6A_HC_Q46K - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1020	F6A_HC_Q46R - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIIYAMNWWVRAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
1021	F6A_HC_Q46R - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1022	F6A_HC_V107 A - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIIYAMNWWVRAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCARHGNFGNSYVSFFAYWG QGTLVTVSS
1023	F6A_HC_V107 A - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1024	F6A_HC_V107 L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIIYAMNWWVRAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCLRHGNFGNSYVSFFAYWG QGTLVTVSS
1025	F6A_HC_V107 L - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL

1026	F6A_I2E - HCDR1	artificial	IYAIN
1027	F6A_I2E - HCDR2	artificial	RIRSKYNNYATYYADAVKS
1028	F6A_I2E - HCDR3	artificial	AGNFGSSYVSFFAY
1029	F6A_I2E - LCDR1	artificial	GSSTGAVTSGYYPN
1030	F6A_I2E - LCDR2	artificial	GTKFLAP
1031	F6A_I2E - LCDR3	artificial	ALWYSNRWV
1032	F6A_I2E - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNIYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADAVKSRFTISRDDSKNTVYLMNNLKTEDTAVYYCARAGNFGSSYVSFFAYWG QGTLVTVSS
1033	F6A_I2E - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPKGPQAPRGLIGGTFKFLAP GTPARFSGSLSGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1034	F6A_I2K - HCDR1	artificial	IYAMN
1035	F6A_I2K - HCDR2	artificial	RIRSKYNNYATYYAEAVKG
1036	F6A_I2K - HCDR3	artificial	NENIGTSYVSFFAY
1037	F6A_I2K - LCDR1	artificial	GSSTGAVTSGYYPN
1038	F6A_I2K - LCDR2	artificial	GTKFLAP
1039	F6A_I2K - LCDR3	artificial	ALWYSNRWV
1040	F6A_I2K - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNIYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYAEAVKGRFTISRDDSKNTVYLMNNLKTEDTAVYYCVRNENIGTSYVSFFAYWG QGTLVTVSS
1041	F6A_I2K - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPKGPQAPRGLIGGTFKFLAP GTPARFSGSLSGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1042	F6A_I2L - HCDR1	artificial	IYAMN
1043	F6A_I2L - HCDR2	artificial	RIRSKYNNYATYYADAVKS
1044	F6A_I2L - HCDR3	artificial	AGNFGSSYVSFFAY
1045	F6A_I2L - LCDR1	artificial	GSSTGAVTSGYYPN
1046	F6A_I2L - LCDR2	artificial	GTKFLAP
1047	F6A_I2L - LCDR3	artificial	ALYYSNRWV
1048	F6A_I2L - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNIYAMNWVRQAPGKMEWVARIRSKYNNY ATYYADAVKSRFTISRDDSKNTLYLMNNLKTEDTAVYYCVRAGNFGSSYVSFFAYWG QGTLVTVSS
1049	F6A_I2L - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWIQKPKGPQAPRGLIGGTFKFLAP GTPARFSGSLSGGKAALTLGSGVQPEDEAEYYCALYYSNRWVFGSGTKLTVL
1050	F6A_I2M - HCDR1	artificial	IYAMN
1051	F6A_I2M - HCDR2	artificial	RIRSKYNNYATYYADAVKS
1052	F6A_I2M - HCDR3	artificial	AGNFGTSYVSFFAY
1053	F6A_I2M - LCDR1	artificial	GSSTGAVTSGYYPN
1054	F6A_I2M - LCDR2	artificial	GTKFLAP
1055	F6A_I2M - LCDR3	artificial	ALWYSNRWV
1056	F6A_I2M - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNIYAMNWVRQAPGKMEWVARIRSKYNNY ATYYADAVKSRFTISRDDSKNTLYLMNNLKTEDTAVYYCVRAGNFGTSYVSFFAYWG QGTLVTVSS
1057	F6A_I2M - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPKGPQAPRGLIGGTFKFLAP GTPARFSGSLSGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1058	F6A_I2M2 - HCDR1	artificial	IYAIN
1059	F6A_I2M2 - HCDR2	artificial	RIRSKYNNYATYYADAVKS
1060	F6A_I2M2 - HCDR3	artificial	NANFGTSYVSFFAY
1061	F6A_I2M2 - LCDR1	artificial	GSSTGAVTSGYYPN

1062	F6A_I2M2 - LCDR2	artificial	GTKFLAP
1063	F6A_I2M2 - LCDR3	artificial	ALWYSNRWV
1064	F6A_I2M2 - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNIYAINWVREAPGKGLEWVARIRSKYNNY ATYYADAVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRNANFGTSYVSFFAYWG QGTLVTVSS
1065	F6A_I2M2 - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTSGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1066	F6A_LC_G141 S - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNIYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
1067	F6A_LC_G141 S - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTSGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1068	F6A_LC_G141 S_L21I - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNIYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
1069	F6A_LC_G141 S_L21I - VL	artificial	QTVVTQEPSTLTVSPGGTIVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1070	F6A_LC_L83E - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNIYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
1071	F6A_LC_L83E - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTSGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLEGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1072	F6A_LC_L83S - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNIYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
1073	F6A_LC_L83S - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTSGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1074	F6A_LC_Q46E - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNIYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
1075	F6A_LC_Q46E - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTSGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1076	F6A_LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNIYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
1077	F6A_LC_Q46K - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTSGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1078	F6A_LC_A107 L - HCDR1	artificial	IYAMN
1079	F6A_LC_A107 L - HCDR2	artificial	RIRSKYNNYATYYADSVKS
1080	F6A_LC_A107 L - HCDR3	artificial	HGNFGNSYVSFFAY
1081	F6A_LC_A107 L - LCDR1	artificial	GSSTGAVTSGYYPN
1082	F6A_LC_A107 L - LCDR2	artificial	GTKFLAP
1083	F6A_LC_A107 L - LCDR3	artificial	LLWYSNRWV
1084	F6A_LC_A107 L - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNIYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
1085	F6A_LC_A107 L - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTSGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCLWYSNRWVFGGGTKLTVL
1086	F6A_LC_V44I - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNIYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
1087	F6A_LC_V44I - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTSGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1088	F6A_LC_V44L - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNIYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
1089	F6A_LC_V44L - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTSGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1090	F6A_LC_V44M - VH	artificial	EVQLVESGGGLVQPGGSLKLSKAASGFTFNIYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
1091	F6A_LC_V44M - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTSGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1092	F6A_LC_W109 Y - HCDR1	artificial	IYAMN
1093	F6A_LC_W109 Y - HCDR2	artificial	RIRSKYNNYATYYADSVKS

1094	F6A_LC_W109 Y - HCDR3	artificial	HGNFGNSYVSFFAY
1095	F6A_LC_W109 Y - LCDR1	artificial	GSSTGAVTSGYYPN
1096	F6A_LC_W109 Y - LCDR2	artificial	GTKFLAP
1097	F6A_LC_W109 Y - LCDR3	artificial	ALYYSNRWV
1098	F6A_LC_W109 Y - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWG QGTLVTVSS
1099	F6A_LC_W109 Y - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALYYSNRWVFGGGTKLTVL
1100	F70 - HCDR1	artificial	VYAMN
1101	F70 - HCDR2	artificial	RIRSKYNNYATYYADSVKK
1102	F70 - HCDR3	artificial	HGNFGNSYISWWAY
1103	F70 - LCDR1	artificial	GSSTGAVTSGYYPN
1104	F70 - LCDR2	artificial	GTKFLAP
1105	F70 - LCDR3	artificial	ALWYSNRWV
1106	F70 - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1107	F70 - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1108	F70_HC_A89I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTIYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1109	F70_HC_A89I - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1110	F70_HC_A89L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1111	F70_HC_A89L - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1112	F70_HC_A89T - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTTYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1113	F70_HC_A89T - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1114	F70_HC_A89V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1115	F70_HC_A89V - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1116	F70_HC_L52M - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAMNWVRQAPGKGMWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1117	F70_HC_L52M - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1118	F70_HC_L52M _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAMNWVRQAPGKGMWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1119	F70_HC_L52M _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1120	F70_HC_L52M _LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAMNWVRQAPGKGMWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1121	F70_HC_L52M _LC_Q46K - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1122	F70_HC_L52M _LC_Q46K_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAMNWVRQAPGKGMWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1123	F70_HC_L52M _LC_Q46K_G1 41S - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1124	F70_HC_L52V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAMNWVRQAPGKGVWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS

1125	F70_HC_L52V - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLGGKAAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1126	F70_HC_L52V _LC_V44F - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNVYAMNWVRQAPGKGVWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1127	F70_HC_L52V _LC_V44F - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLGGKAAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1128	F70_HC_L52V _LC_V44Y - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNVYAMNWVRQAPGKGVWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1129	F70_HC_L52V _LC_V44Y - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLGGKAAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1130	F70_HC_M41F _A89V - HCDR1	artificial	VYAFN
1131	F70_HC_M41F _A89V - HCDR2	artificial	RIRSKYNNYATYYADSVKK
1132	F70_HC_M41F _A89V - HCDR3	artificial	HGNFGNSYISWWAY
1133	F70_HC_M41F _A89V - LCDR1	artificial	GSSTGAVTSGYYPN
1134	F70_HC_M41F _A89V - LCDR2	artificial	GTKFLAP
1135	F70_HC_M41F _A89V - LCDR3	artificial	ALWYSNRWV
1136	F70_HC_M41F _A89V - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNVYAFNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1137	F70_HC_M41F _A89V - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLGGKAAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1138	F70_HC_M41I - HCDR1	artificial	VYAIN
1139	F70_HC_M41I - HCDR2	artificial	RIRSKYNNYATYYADSVKK
1140	F70_HC_M41I - HCDR3	artificial	HGNFGNSYISWWAY
1141	F70_HC_M41I - LCDR1	artificial	GSSTGAVTSGYYPN
1142	F70_HC_M41I - LCDR2	artificial	GTKFLAP
1143	F70_HC_M41I - LCDR3	artificial	ALWYSNRWV
1144	F70_HC_M41I - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNVYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1145	F70_HC_M41I - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLGGKAAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1146	F70_HC_M41I _A89L - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNVYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1147	F70_HC_M41I _A89L - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLGGKAAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1148	F70_HC_M41I _A89V - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNVYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1149	F70_HC_M41I _A89V - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLGGKAAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1150	F70_HC_M41I _A89V_LC_L2 1I_Q46K_G14 1S - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNVYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1151	F70_HC_M41I _A89V_LC_L2 1I_Q46K_G14 1S - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLGGKAAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1152	F70_HC_M41I _A89V_LC_Q4 6K - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNVYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS

1153	F7O_HC_M41I _A89V_IC_Q4 6K - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1154	F7O_HC_M41I _L52V_A89V_ LC_L21I_Q46 K_G141S_V44 F - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAINWVRQAPGKGVLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1155	F7O_HC_M41I _L52V_A89V_ LC_L21I_Q46 K_G141S_V44 F - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1156	F7O_HC_M41I _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAINWVRQAPGKGVLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1157	F7O_HC_M41I _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1158	F7O_HC_M41I _Q46E_A89V_ LC_L21I_Q46 K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAINWVRQAPGKGVLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1159	F7O_HC_M41I _Q46E_A89V_ LC_L21I_Q46 K_G141S - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1160	F7O_HC_M41V - HCDR1	artificial	VYAVN
1161	F7O_HC_M41V - HCDR2	artificial	RIRSKYNNYATYYADSVKK
1162	F7O_HC_M41V - HCDR3	artificial	HGNFGNSYISWWAY
1163	F7O_HC_M41V - LCDR1	artificial	GSSTGAVTSGYYPN
1164	F7O_HC_M41V - LCDR2	artificial	GTKFLAP
1165	F7O_HC_M41V - LCDR3	artificial	ALWYSNRWV
1166	F7O_HC_M41V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAVNWVRQAPGKGVLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1167	F7O_HC_M41V - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1168	F7O_HC_Q46D - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRDAPGKGVLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1169	F7O_HC_Q46D - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1170	F7O_HC_Q46D _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRDAPGKGVLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1171	F7O_HC_Q46D _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1172	F7O_HC_Q46D _LC_L21I_Q4 6R_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRDAPGKGVLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1173	F7O_HC_Q46D _LC_L21I_Q4 6R_G141S - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1174	F7O_HC_Q46D _LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRDAPGKGVLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1175	F7O_HC_Q46D _LC_Q46K - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1176	F7O_HC_Q46D	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRDAPGKGVLEWVARIRSKYNNY

	LC_Q46K_G1 41S - VH		ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1177	F7O_HC_Q46D LC_Q46K_G1 41S - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1178	F7O_HC_Q46D LC_Q46R - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1179	F7O_HC_Q46D LC_Q46R - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1180	F7O_HC_Q46D LC_Q46R_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1181	F7O_HC_Q46D LC_Q46R_G1 41S - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1182	F7O_HC_Q46E - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1183	F7O_HC_Q46E - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1184	F7O_HC_Q46E LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1185	F7O_HC_Q46E LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1186	F7O_HC_Q46E LC_L21I_Q4 6R_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1187	F7O_HC_Q46E LC_L21I_Q4 6R_G141S - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1188	F7O_HC_Q46E LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1189	F7O_HC_Q46E LC_Q46K - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1190	F7O_HC_Q46E LC_Q46K_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1191	F7O_HC_Q46E LC_Q46K_G1 41S - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1192	F7O_HC_Q46E LC_Q46R - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1193	F7O_HC_Q46E LC_Q46R - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1194	F7O_HC_Q46E LC_Q46R_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1195	F7O_HC_Q46E LC_Q46R_G1 41S - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1196	F7O_HC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRKAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1197	F7O_HC_Q46K - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1198	F7O_HC_Q46R - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1199	F7O_HC_Q46R - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1200	F7O_HC_V107 A - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCARHGNFGNSYISWWAYWG QGTLVTVSS
1201	F7O_HC_V107	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP

	A - VL		GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1202	F70_HC_V107 L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCLRHGNFGNSYISWWAYWG QGTLVTVSS
1203	F70_HC_V107 L - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1204	F70_HC_W136 F - HCDR1	artificial	VYAMN
1205	F70_HC_W136 F - HCDR2	artificial	RIRSKYNNYATYYADSVKK
1206	F70_HC_W136 F - HCDR3	artificial	HGNFGNSYISWFAY
1207	F70_HC_W136 F - LCDR1	artificial	GSSTGAVTSGYYPN
1208	F70_HC_W136 F - LCDR2	artificial	GTKFLAP
1209	F70_HC_W136 F - LCDR3	artificial	ALWYSNRWV
1210	F70_HC_W136 F - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWFAYWG QGTLVTVSS
1211	F70_HC_W136 F - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1212	F70_HC_W136 F LC_V44I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWFAYWG QGTLVTVSS
1213	F70_HC_W136 F LC_V44I - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1214	F70_HC_W136 F LC_V44L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWFAYWG QGTLVTVSS
1215	F70_HC_W136 F LC_V44L - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1216	F70_I2E - HCDR1	artificial	VYAIN
1217	F70_I2E - HCDR2	artificial	RIRSKYNNYATYYADAVKK
1218	F70_I2E - HCDR3	artificial	AGNFGSSYISWWAY
1219	F70_I2E - LCDR1	artificial	GSSTGAVTSGYYPN
1220	F70_I2E - LCDR2	artificial	GTKFLAP
1221	F70_I2E - LCDR3	artificial	ALWYSNRWV
1222	F70_I2E - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADAVKKRFTISRDDSKNTVYLQMNNLKTEDTAVYYCARAGNFGSSYISWWAYWG QGTLVTVSS
1223	F70_I2E - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLSGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1224	F70_I2K - HCDR1	artificial	VYAMN
1225	F70_I2K - HCDR2	artificial	RIRSKYNNYATYYAEAVKG
1226	F70_I2K - HCDR3	artificial	NENIGTSYISWWAY
1227	F70_I2K - LCDR1	artificial	GSSTGAVTSGYYPN
1228	F70_I2K - LCDR2	artificial	GTKFLAP
1229	F70_I2K - LCDR3	artificial	ALWYSNRWV
1230	F70_I2K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYAEAVKKRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRNENIGTSYISWWAYWG QGTLVTVSS
1231	F70_I2K - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLSGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1232	F70_I2L - HCDR1	artificial	VYAMN
1233	F70_I2L - HCDR2	artificial	RIRSKYNNYATYYADAVKK
1234	F70_I2L - HCDR3	artificial	AGNFGSSYISWFAY

1235	F70_I2L - LCDR1	artificial	GSSTGAVTSGYYPN
1236	F70_I2L - LCDR2	artificial	GTKFLAP
1237	F70_I2L - LCDR3	artificial	ALYYSNRWV
1238	F70_I2L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKMEWVARIRSKYNNY ATYYADAVKKRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRAGNFGSSYISWFAYWG QGTLVTVSS
1239	F70_I2L - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWIQKKPGQAPRGLIGGTKFLAP GTPARFSGSLEGGKAALTLSGVQPEDEAEYYCALYYSNRWVFGSGTKLTVL
1240	F70_I2M - HCDR1	artificial	VYAMN
1241	F70_I2M - HCDR2	artificial	RIRSKYNNYATYYADAVKK
1242	F70_I2M - HCDR3	artificial	AGNFGTSYISWWAY
1243	F70_I2M - LCDR1	artificial	GSSTGAVTSGYYPN
1244	F70_I2M - LCDR2	artificial	GTKFLAP
1245	F70_I2M - LCDR3	artificial	ALWYSNRWV
1246	F70_I2M - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKMEWVARIRSKYNNY ATYYADAVKKRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRAGNFGTSYISWWAYWG QGTLVTVSS
1247	F70_I2M - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1248	F70_I2M2 - HCDR1	artificial	VYAIN
1249	F70_I2M2 - HCDR2	artificial	RIRSKYNNYATYYADAVKK
1250	F70_I2M2 - HCDR3	artificial	NANFGTSYISWFAY
1251	F70_I2M2 - LCDR1	artificial	GSSTGAVTSGYYPN
1252	F70_I2M2 - LCDR2	artificial	GTKFLAP
1253	F70_I2M2 - LCDR3	artificial	ALWYSNRWV
1254	F70_I2M2 - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAINWVREAPGKGLEWVARIRSKYNNY ATYYADAVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRNANFGTSYISWFAYWG QGTLVTVSS
1255	F70_I2M2 - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1256	F70_LC_G141 S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1257	F70_LC_G141 S - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1258	F70_LC_G141 S_L21I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1259	F70_LC_G141 S_L21I - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1260	F70_LC_L83E - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1261	F70_LC_L83E - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTKFLAP GTPARFSGSLEGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGKTCLTVL
1262	F70_LC_L83S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1263	F70_LC_L83S - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGKTCLTVL
1264	F70_LC_Q46E - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1265	F70_LC_Q46E - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGKTCLTVL
1266	F70_LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1267	F70_LC_Q46K - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGKTCLTVL

1268	F70_LC_A107 L - HCDR1	artificial	VYAMN
1269	F70_LC_A107 L - HCDR2	artificial	RIRSKYNNYATYYADSVKK
1270	F70_LC_A107 L - HCDR3	artificial	HGNFGNSYISWWAY
1271	F70_LC_A107 L - LCDR1	artificial	GSSTGAVTSGYYPN
1272	F70_LC_A107 L - LCDR2	artificial	GTKFLAP
1273	F70_LC_A107 L - LCDR3	artificial	LLWYSNRWV
1274	F70_LC_A107 L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1275	F70_LC_A107 L - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTSGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCLWYSNRWVFGGGTKLTVL
1276	F70_LC_V44I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1277	F70_LC_V44I - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTSGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1278	F70_LC_V44L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1279	F70_LC_V44L - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTSGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1280	F70_LC_V44M - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1281	F70_LC_V44M - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTSGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1282	F70_LC_W109 Y - HCDR1	artificial	VYAMN
1283	F70_LC_W109 Y - HCDR2	artificial	RIRSKYNNYATYYADSVKK
1284	F70_LC_W109 Y - HCDR3	artificial	HGNFGNSYISWWAY
1285	F70_LC_W109 Y - LCDR1	artificial	GSSTGAVTSGYYPN
1286	F70_LC_W109 Y - LCDR2	artificial	GTKFLAP
1287	F70_LC_W109 Y - LCDR3	artificial	ALYYSNRWV
1288	F70_LC_W109 Y - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWG QGTLVTVSS
1289	F70_LC_W109 Y - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTSGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALYYSNRWVFGGGTKLTVL
1290	G4H - HCDR1	artificial	RYAMN
1291	G4H - HCDR2	artificial	RIRSKYNNYATYYADSVKG
1292	G4H - HCDR3	artificial	HGNFGNSYLSYFAY
1293	G4H - LCDR1	artificial	GSSTGAVTSGYYPN
1294	G4H - LCDR2	artificial	GTKFLAP
1295	G4H - LCDR3	artificial	ALWYSNRWV
1296	G4H - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1297	G4H - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTSGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1298	G4H_HC_A89I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTIYLMNMLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1299	G4H_HC_A89I - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTSGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1300	G4H_HC_A89L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTLYLQMNMLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1301	G4H_HC_A89L - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTSGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1302	G4H_HC_A89T - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTIYLMNMLKTEDTAVYYCVRHGNFGNSYLSYFAYWG

			QGTLVTVSS
1303	G4H_HC_A89T - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1304	G4H_HC_A89V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTVYLMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1305	G4H_HC_A89V - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1306	G4H_HC_L52M - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKMEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1307	G4H_HC_L52M - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1308	G4H_HC_L52M _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKMEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1309	G4H_HC_L52M _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1310	G4H_HC_L52M _LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKMEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1311	G4H_HC_L52M _LC_Q46K - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1312	G4H_HC_L52M _LC_Q46K_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKMEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1313	G4H_HC_L52M _LC_Q46K_G1 41S - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1314	G4H_HC_L52V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1315	G4H_HC_L52V - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1316	G4H_HC_L52V _LC_V44F - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1317	G4H_HC_L52V _LC_V44F - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1318	G4H_HC_L52V _LC_V44Y - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1319	G4H_HC_L52V _LC_V44Y - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1320	G4H_HC_M41F _A89V - HCDR1	artificial	RYAFN
1321	G4H_HC_M41F _A89V - HCDR2	artificial	RIRSKYNNYATYYADSVKG
1322	G4H_HC_M41F _A89V - HCDR3	artificial	HGNFGNSYLSYFAY
1323	G4H_HC_M41F _A89V - LCDR1	artificial	GSSTGAVTSGYYPN
1324	G4H_HC_M41F _A89V - LCDR2	artificial	GTKFLAP
1325	G4H_HC_M41F _A89V - LCDR3	artificial	ALWYSNRWV
1326	G4H_HC_M41F _A89V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAFNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTVYLMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1327	G4H_HC_M41F _A89V - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1328	G4H_HC_M41I - HCDR1	artificial	RYAIN

1329	G4H_HC_M41I - HCDR2	artificial	RIRSKYNNYATYYADSVKG
1330	G4H_HC_M41I - HCDR3	artificial	HGNFGNSYLSYFAY
1331	G4H_HC_M41I - LCDRI	artificial	GSSTGAVTSGYYPN
1332	G4H_HC_M41I - LCDR2	artificial	GTKFLAP
1333	G4H_HC_M41I - LCDR3	artificial	ALWYSNRWV
1334	G4H_HC_M41I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1335	G4H_HC_M41I - VL	artificial	QTVVTQEPSTLVSPGGTIVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1336	G4H_HC_M41I _A89L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1337	G4H_HC_M41I _A89L - VL	artificial	QTVVTQEPSTLVSPGGTIVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1338	G4H_HC_M41I _A89V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1339	G4H_HC_M41I _A89V - VL	artificial	QTVVTQEPSTLVSPGGTIVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1340	G4H_HC_M41I _A89V_IC_L2 1I_Q46K_G14 1S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1341	G4H_HC_M41I _A89V_IC_L2 1I_Q46K_G14 1S - VL	artificial	QTVVTQEPSTLVSPGGTIVTITCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1342	G4H_HC_M41I _A89V_IC_Q4 6K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1343	G4H_HC_M41I _A89V_IC_Q4 6K - VL	artificial	QTVVTQEPSTLVSPGGTIVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1344	G4H_HC_M41I _L52V_A89V LC_L21I_Q46 K_G141S_V44 F - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1345	G4H_HC_M41I _L52V_A89V LC_L21I_Q46 K_G141S_V44 F - VL	artificial	QTVVTQEPSTLVSPGGTIVTITCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1346	G4H_HC_M41I _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1347	G4H_HC_M41I _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSTLVSPGGTIVTITCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1348	G4H_HC_M41I _Q46E_A89V LC_L21I_Q46 K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAINWVREAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1349	G4H_HC_M41I _Q46E_A89V LC_L21I_Q46 K_G141S - VL	artificial	QTVVTQEPSTLVSPGGTIVTITCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1350	G4H_HC_M41V - HCDRI	artificial	RYAVN
1351	G4H_HC_M41V - HCDR2	artificial	RIRSKYNNYATYYADSVKG
1352	G4H_HC_M41V - HCDR3	artificial	HGNFGNSYLSYFAY
1353	G4H_HC_M41V - LCDRI	artificial	GSSTGAVTSGYYPN
1354	G4H_HC_M41V	artificial	GTKFLAP

	- LCDR2		
1355	G4H_HC_M41V - LCDR3	artificial	ALWYSNRWV
1356	G4H_HC_M41V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAVNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1357	G4H_HC_M41V - VL	artificial	QTVVTQEPSLTVSPGGTIVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1358	G4H_HC_Q46D - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1359	G4H_HC_Q46D - VL	artificial	QTVVTQEPSLTVSPGGTIVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1360	G4H_HC_Q46D _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1361	G4H_HC_Q46D _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSLTVSPGGTIVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1362	G4H_HC_Q46D _LC_L21I_Q4 6R_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1363	G4H_HC_Q46D _LC_L21I_Q4 6R_G141S - VL	artificial	QTVVTQEPSLTVSPGGTIVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1364	G4H_HC_Q46D _LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1365	G4H_HC_Q46D _LC_Q46K - VL	artificial	QTVVTQEPSLTVSPGGTIVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1366	G4H_HC_Q46D _LC_Q46K_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1367	G4H_HC_Q46D _LC_Q46K_G1 41S - VL	artificial	QTVVTQEPSLTVSPGGTIVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1368	G4H_HC_Q46D _LC_Q46R - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1369	G4H_HC_Q46D _LC_Q46R - VL	artificial	QTVVTQEPSLTVSPGGTIVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1370	G4H_HC_Q46D _LC_Q46R_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1371	G4H_HC_Q46D _LC_Q46R_G1 41S - VL	artificial	QTVVTQEPSLTVSPGGTIVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1372	G4H_HC_Q46E - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1373	G4H_HC_Q46E - VL	artificial	QTVVTQEPSLTVSPGGTIVTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1374	G4H_HC_Q46E _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1375	G4H_HC_Q46E _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSLTVSPGGTIVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1376	G4H_HC_Q46E _LC_L21I_Q4 6R_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1377	G4H_HC_Q46E _LC_L21I_Q4 6R_G141S - VL	artificial	QTVVTQEPSLTVSPGGTIVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1378	G4H_HC_Q46E _LC_Q46K -	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG

	VH		QGTLVTVSS
1379	G4H_HC_Q46E _LC_Q46K - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1380	G4H_HC_Q46E _LC_Q46K_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1381	G4H_HC_Q46E _LC_Q46K_G1 41S - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1382	G4H_HC_Q46E _LC_Q46R - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1383	G4H_HC_Q46E _LC_Q46R - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1384	G4H_HC_Q46E _LC_Q46R_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1385	G4H_HC_Q46E _LC_Q46R_G1 41S - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1386	G4H_HC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRKAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1387	G4H_HC_Q46K - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1388	G4H_HC_Q46R - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1389	G4H_HC_Q46R - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1390	G4H_HC_V107 A - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCARHGNFGNSYLSYFAYWG QGTLVTVSS
1391	G4H_HC_V107 A - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1392	G4H_HC_V107 L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCLRHGNFGNSYLSYFAYWG QGTLVTVSS
1393	G4H_HC_V107 L - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1394	G4H_I2E - HCDR1	artificial	RYAIN
1395	G4H_I2E - HCDR2	artificial	RIRSKYNNYATYYADAVKG
1396	G4H_I2E - HCDR3	artificial	AGNFGSSYLSYFAY
1397	G4H_I2E - LCDR1	artificial	GSSTGAVTSGYYPN
1398	G4H_I2E - LCDR2	artificial	GTKFLAP
1399	G4H_I2E - LCDR3	artificial	ALWYSNRWV
1400	G4H_I2E - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADAVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCARAGNFGSSYLSYFAYWG QGTLVTVSS
1401	G4H_I2E - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLSGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1402	G4H_I2K - HCDR1	artificial	RYAMN
1403	G4H_I2K - HCDR2	artificial	RIRSKYNNYATYYAEAVKG
1404	G4H_I2K - HCDR3	artificial	NENIGTSYLSYFAY
1405	G4H_I2K - LCDR1	artificial	GSSTGAVTSGYYPN
1406	G4H_I2K - LCDR2	artificial	GTKFLAP
1407	G4H_I2K - LCDR3	artificial	ALWYSNRWV
1408	G4H_I2K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYAEAVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRNENIGTSYLSYFAYWG QGTLVTVSS
1409	G4H_I2K -	artificial	QTVVTQEPSTLTVSPGGTVTITCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP

	VL		GTPARFSGSLSGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1410	G4H_I2L - HCDR1	artificial	RYAMN
1411	G4H_I2L - HCDR2	artificial	RIRSKYNNYATYYADAVKG
1412	G4H_I2L - HCDR3	artificial	AGNFGSSYLSYFAY
1413	G4H_I2L - LCDR1	artificial	GSSTGAVTSGYYPN
1414	G4H_I2L - LCDR2	artificial	GTKFLAP
1415	G4H_I2L - LCDR3	artificial	ALYYSNRWV
1416	G4H_I2L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGMWVARIRSKYNNY ATYYADAVKGRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRAGNFGSSYLSYFAYWG QGTLVTVSS
1417	G4H_I2L - VL	artificial	QTVVTQEPSLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALYYSNRWVFGSGTKLTVL
1418	G4H_I2M - HCDR1	artificial	RYAMN
1419	G4H_I2M - HCDR2	artificial	RIRSKYNNYATYYADAVKG
1420	G4H_I2M - HCDR3	artificial	AGNFGTSYLSYFAY
1421	G4H_I2M - LCDR1	artificial	GSSTGAVTSGYYPN
1422	G4H_I2M - LCDR2	artificial	GTKFLAP
1423	G4H_I2M - LCDR3	artificial	ALWYSNRWV
1424	G4H_I2M - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGMWVARIRSKYNNY ATYYADAVKGRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRAGNFGTSYLSYFAYWG QGTLVTVSS
1425	G4H_I2M - VL	artificial	QTVVTQEPSLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTKFLAP GTPARFSGSLSGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1426	G4H_I2M2 - HCDR1	artificial	RYAIN
1427	G4H_I2M2 - HCDR2	artificial	RIRSKYNNYATYYADAVKG
1428	G4H_I2M2 - HCDR3	artificial	NANFGTSYLSYFAY
1429	G4H_I2M2 - LCDR1	artificial	GSSTGAVTSGYYPN
1430	G4H_I2M2 - LCDR2	artificial	GTKFLAP
1431	G4H_I2M2 - LCDR3	artificial	ALWYSNRWV
1432	G4H_I2M2 - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAINWVREAPGKGLEWVARIRSKYNNY ATYYADAVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRNANFGTSYLSYFAYWG QGTLVTVSS
1433	G4H_I2M2 - VL	artificial	QTVVTQEPSLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1434	G4H_LC_G141 S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1435	G4H_LC_G141 S - VL	artificial	QTVVTQEPSLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1436	G4H_LC_G141 S_L21I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1437	G4H_LC_G141 S_L21I - VL	artificial	QTVVTQEPSLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1438	G4H_LC_L83E - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1439	G4H_LC_L83E - VL	artificial	QTVVTQEPSLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGSGTKLTVL
1440	G4H_LC_L83S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1441	G4H_LC_L83S - VL	artificial	QTVVTQEPSLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPKGQAPRGLIGGTKFLAP GTPARFSGSLSGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGSGTKLTVL
1442	G4H_LC_Q46E - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS

1443	G4H_LC_Q46E - VL	artificial	QTVVTQEPSTLVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1444	G4H_LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1445	G4H_LC_Q46K - VL	artificial	QTVVTQEPSTLVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1446	G4H_LC_A107 L - HCDR1	artificial	RYAMN
1447	G4H_LC_A107 L - HCDR2	artificial	RIRSKYNNYATYYADSVKG
1448	G4H_LC_A107 L - HCDR3	artificial	HGNFGNSYLSYFAY
1449	G4H_LC_A107 L - LCDR1	artificial	GSSTGAVTSGYYPN
1450	G4H_LC_A107 L - LCDR2	artificial	GTKFLAP
1451	G4H_LC_A107 L - LCDR3	artificial	LLWYSNRWV
1452	G4H_LC_A107 L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1453	G4H_LC_A107 L - VL	artificial	QTVVTQEPSTLVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCLLWYSNRWVFGGGTKLTVL
1454	G4H_LC_V44I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1455	G4H_LC_V44I - VL	artificial	QTVVTQEPSTLVSPGGTVTTLTCSSTGAVTSGYYPNWIQQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1456	G4H_LC_V44L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1457	G4H_LC_V44L - VL	artificial	QTVVTQEPSTLVSPGGTVTTLTCSSTGAVTSGYYPNWLQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1458	G4H_LC_V44M - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1459	G4H_LC_V44M - VL	artificial	QTVVTQEPSTLVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1460	G4H_LC_W109 Y - HCDR1	artificial	RYAMN
1461	G4H_LC_W109 Y - HCDR2	artificial	RIRSKYNNYATYYADSVKG
1462	G4H_LC_W109 Y - HCDR3	artificial	HGNFGNSYLSYFAY
1463	G4H_LC_W109 Y - LCDR1	artificial	GSSTGAVTSGYYPN
1464	G4H_LC_W109 Y - LCDR2	artificial	GTKFLAP
1465	G4H_LC_W109 Y - LCDR3	artificial	ALYYSNRWV
1466	G4H_LC_W109 Y - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWG QGTLVTVSS
1467	G4H_LC_W109 Y - VL	artificial	QTVVTQEPSTLVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1468	H1E - HCDR1	artificial	SYAMN
1469	H1E - HCDR2	artificial	RIRSKYNNYATYYADSVKG
1470	H1E - HCDR3	artificial	HGNFGNSYLSFWAY
1471	H1E - LCDR1	artificial	GSSTGAVTSGYYPN
1472	H1E - LCDR2	artificial	GTKFLAP
1473	H1E - LCDR3	artificial	ALWYSNRWV
1474	H1E - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1475	H1E - VL	artificial	QTVVTQEPSTLVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1476	H1E_HC_A89I - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTIYQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1477	H1E_HC_A89I - VL	artificial	QTVVTQEPSTLVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL

1478	H1E_HC_A89L - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1479	H1E_HC_A89L - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTSGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1480	H1E_HC_A89T - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTTYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1481	H1E_HC_A89T - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTSGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1482	H1E_HC_A89V - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTVYLYQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1483	H1E_HC_A89V - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTSGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1484	H1E_HC_L52M - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1485	H1E_HC_L52M - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTSGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1486	H1E_HC_L52M _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1487	H1E_HC_L52M _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSTLTVSPGGTIVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1488	H1E_HC_L52M _LC_Q46K - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1489	H1E_HC_L52M _LC_Q46K - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTSGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1490	H1E_HC_L52M _LC_Q46K_G1 41S - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1491	H1E_HC_L52M _LC_Q46K_G1 41S - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTSGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1492	H1E_HC_L52V - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGVWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1493	H1E_HC_L52V - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTSGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1494	H1E_HC_L52V _LC_V44F - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGVWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1495	H1E_HC_L52V _LC_V44F - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTSGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1496	H1E_HC_L52V _LC_V44Y - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGVWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1497	H1E_HC_L52V _LC_V44Y - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTSGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1498	H1E_HC_M41F _A89V - HCDR1	artificial	SYAFN
1499	H1E_HC_M41F _A89V - HCDR2	artificial	RIRSKYNNYATYYADSVKG
1500	H1E_HC_M41F _A89V - HCDR3	artificial	HGNFGNSYLSFWAY
1501	H1E_HC_M41F _A89V - LCDR1	artificial	GSSTGAVTSGYYPN
1502	H1E_HC_M41F _A89V - LCDR2	artificial	GTKFLAP
1503	H1E_HC_M41F _A89V - LCDR3	artificial	ALWYSNRWV
1504	H1E_HC_M41F	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAFNWVRQAPGKGLEWVARIRSKYNNY

	_A89V - VH		ATYYADSVKGRFTISRDDSKNTVYLMQNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1505	H1E_HC_M41F _A89V - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1506	H1E_HC_M41I - HCDR1	artificial	SYAIN
1507	H1E_HC_M41I - HCDR2	artificial	RIRSKYNNYATYYADSVKG
1508	H1E_HC_M41I - HCDR3	artificial	HGNFGNSYLSFWAY
1509	H1E_HC_M41I - LCDR1	artificial	GSSTGAVTSGYYPN
1510	H1E_HC_M41I - LCDR2	artificial	GTKFLAP
1511	H1E_HC_M41I - LCDR3	artificial	ALWYSNRWV
1512	H1E_HC_M41I - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLMQNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1513	H1E_HC_M41I - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1514	H1E_HC_M41I _A89L - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTLYLMQNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1515	H1E_HC_M41I _A89L - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1516	H1E_HC_M41I _A89V - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTVYLMQNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1517	H1E_HC_M41I _A89V - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1518	H1E_HC_M41I _A89V_IC_L2 1I_Q46K_G14 1S - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTVYLMQNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1519	H1E_HC_M41I _A89V_IC_L2 1I_Q46K_G14 1S - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1520	H1E_HC_M41I _A89V_IC_Q4 6K - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTVYLMQNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1521	H1E_HC_M41I _A89V_IC_Q4 6K - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1522	H1E_HC_M41I _L52V_A89V_ LC_L21I_Q46 K_G141S_V44 F - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAINWVRQAPGKGVWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTVYLMQNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1523	H1E_HC_M41I _L52V_A89V_ LC_L21I_Q46 K_G141S_V44 F - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1524	H1E_HC_M41I _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLMQNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1525	H1E_HC_M41I _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1526	H1E_HC_M41I _Q46E_A89V_ LC_L21I_Q46 K_G141S - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAINWVREAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTVYLMQNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1527	H1E_HC_M41I _Q46E_A89V_ LC_L21I_Q46 K_G141S - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1528	H1E_HC_M41V - HCDR1	artificial	SYAVN
1529	H1E_HC_M41V	artificial	RIRSKYNNYATYYADSVKG

	- HCDR2		
1530	H1E_HC_M41V - HCDR3	artificial	HGNFGNSYLSFWAY
1531	H1E_HC_M41V - LCDR1	artificial	GSSTGAVTSGYYPN
1532	H1E_HC_M41V - LCDR2	artificial	GTKFLAP
1533	H1E_HC_M41V - LCDR3	artificial	ALWYSNRWV
1534	H1E_HC_M41V - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAVNWVRQAPGKLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1535	H1E_HC_M41V - VL	artificial	QTVVTQEPISLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1536	H1E_HC_Q46D - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRDAPGKLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1537	H1E_HC_Q46D - VL	artificial	QTVVTQEPISLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1538	H1E_HC_Q46D _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRDAPGKLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1539	H1E_HC_Q46D _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPISLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1540	H1E_HC_Q46D _LC_L21I_Q4 6R_G141S - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRDAPGKLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1541	H1E_HC_Q46D _LC_L21I_Q4 6R_G141S - VL	artificial	QTVVTQEPISLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1542	H1E_HC_Q46D _LC_Q46K - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRDAPGKLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1543	H1E_HC_Q46D _LC_Q46K - VL	artificial	QTVVTQEPISLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1544	H1E_HC_Q46D _LC_Q46K_G1 41S - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRDAPGKLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1545	H1E_HC_Q46D _LC_Q46K_G1 41S - VL	artificial	QTVVTQEPISLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1546	H1E_HC_Q46D _LC_Q46R - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRDAPGKLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1547	H1E_HC_Q46D _LC_Q46R - VL	artificial	QTVVTQEPISLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1548	H1E_HC_Q46D _LC_Q46R_G1 41S - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRDAPGKLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1549	H1E_HC_Q46D _LC_Q46R_G1 41S - VL	artificial	QTVVTQEPISLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1550	H1E_HC_Q46E - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVREAPGKLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1551	H1E_HC_Q46E - VL	artificial	QTVVTQEPISLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1552	H1E_HC_Q46E _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVREAPGKLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1553	H1E_HC_Q46E _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPISLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1554	H1E_HC_Q46E _LC_L21I_Q4 6R_G141S - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVREAPGKLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS

1555	H1E_HC_Q46E _LC_L21I_Q4 6R_G141S - VL	artificial	QTVVTQEPsLTVSPGGTVTLTICGSSTGAVTSGYYPNWVQRKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1556	H1E_HC_Q46E _LC_Q46K - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1557	H1E_HC_Q46E _LC_Q46K - VL	artificial	QTVVTQEPsLTVSPGGTVTLTICGSSTGAVTSGYYPNWVQRKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1558	H1E_HC_Q46E _LC_Q46K_G1 41S - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1559	H1E_HC_Q46E _LC_Q46K_G1 41S - VL	artificial	QTVVTQEPsLTVSPGGTVTLTICGSSTGAVTSGYYPNWVQRKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1560	H1E_HC_Q46E _LC_Q46R - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1561	H1E_HC_Q46E _LC_Q46R - VL	artificial	QTVVTQEPsLTVSPGGTVTLTICGSSTGAVTSGYYPNWVQRKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1562	H1E_HC_Q46E _LC_Q46R_G1 41S - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1563	H1E_HC_Q46E _LC_Q46R_G1 41S - VL	artificial	QTVVTQEPsLTVSPGGTVTLTICGSSTGAVTSGYYPNWVQRKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1564	H1E_HC_Q46K - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRKAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1565	H1E_HC_Q46K - VL	artificial	QTVVTQEPsLTVSPGGTVTLTICGSSTGAVTSGYYPNWVQRKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1566	H1E_HC_Q46R - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1567	H1E_HC_Q46R - VL	artificial	QTVVTQEPsLTVSPGGTVTLTICGSSTGAVTSGYYPNWVQRKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1568	H1E_HC_V107 A - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCARHGNFGNSYLSFWAYWG QGTLVTVSS
1569	H1E_HC_V107 A - VL	artificial	QTVVTQEPsLTVSPGGTVTLTICGSSTGAVTSGYYPNWVQRKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1570	H1E_HC_V107 L - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCLRHGNFGNSYLSFWAYWG QGTLVTVSS
1571	H1E_HC_V107 L - VL	artificial	QTVVTQEPsLTVSPGGTVTLTICGSSTGAVTSGYYPNWVQRKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1572	H1E_HC_W136 F - HCDR1	artificial	SYAMN
1573	H1E_HC_W136 F - HCDR2	artificial	RIRSKYNNYATYYADSVKG
1574	H1E_HC_W136 F - HCDR3	artificial	HGNFGNSYLSFFAY
1575	H1E_HC_W136 F - LCDR1	artificial	GSSTGAVTSGYYPN
1576	H1E_HC_W136 F - LCDR2	artificial	GTKFLAP
1577	H1E_HC_W136 F - LCDR3	artificial	ALWYSNRWV
1578	H1E_HC_W136 F - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFFAYWG QGTLVTVSS
1579	H1E_HC_W136 F - VL	artificial	QTVVTQEPsLTVSPGGTVTLTICGSSTGAVTSGYYPNWVQRKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1580	H1E_HC_W136 F_LC_V44I - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFFAYWG QGTLVTVSS
1581	H1E_HC_W136 F_LC_V44I - VL	artificial	QTVVTQEPsLTVSPGGTVTLTICGSSTGAVTSGYYPNWVQRKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1582	H1E_HC_W136 F_LC_V44L - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFFAYWG QGTLVTVSS
1583	H1E_HC_W136 F_LC_V44L -	artificial	QTVVTQEPsLTVSPGGTVTLTICGSSTGAVTSGYYPNWVQRKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL

	VL		
1584	H1E_I2E - HCDR1	artificial	SYAIN
1585	H1E_I2E - HCDR2	artificial	RIRSKYNNYATYYADAVKG
1586	H1E_I2E - HCDR3	artificial	AGNFGSSYLSFWAY
1587	H1E_I2E - LCDR1	artificial	GSSTGAVTSGYYPN
1588	H1E_I2E - LCDR2	artificial	GTKFLAP
1589	H1E_I2E - LCDR3	artificial	ALWYSNRWV
1590	H1E_I2E - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADAVKGRFTISRDDSKNTVYLMNNLKTEDTAVYYCARAGNFGSSYLSFWAYWG QGTLVTVSS
1591	H1E_I2E - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKKPGQAPRGLIGGTKFLAP GTPARFSGSLSGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1592	H1E_I2K - HCDR1	artificial	SYAMN
1593	H1E_I2K - HCDR2	artificial	RIRSKYNNYATYYAEAVKG
1594	H1E_I2K - HCDR3	artificial	NENIGTSYLSFWAY
1595	H1E_I2K - LCDR1	artificial	GSSTGAVTSGYYPN
1596	H1E_I2K - LCDR2	artificial	GTKFLAP
1597	H1E_I2K - LCDR3	artificial	ALWYSNRWV
1598	H1E_I2K - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYAEAVKGRFTISRDDSKNTVYLMNNLKTEDTAVYYCVRNENIGTSYLSFWAYWG QGTLVTVSS
1599	H1E_I2K - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKKPGQAPRGLIGGTKFLAP GTPARFSGSLSGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1600	H1E_I2L - HCDR1	artificial	SYAMN
1601	H1E_I2L - HCDR2	artificial	RIRSKYNNYATYYADAVKG
1602	H1E_I2L - HCDR3	artificial	AGNFGSSYLSFFAY
1603	H1E_I2L - LCDR1	artificial	GSSTGAVTSGYYPN
1604	H1E_I2L - LCDR2	artificial	GTKFLAP
1605	H1E_I2L - LCDR3	artificial	ALYYSNRWV
1606	H1E_I2L - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGMWVARIRSKYNNY ATYYADAVKGRFTISRDDSKNTLYLMNNLKTEDTAVYYCVRAGNFGSSYLSFFAYWG QGTLVTVSS
1607	H1E_I2L - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWIQKKPGQAPRGLIGGTKFLAP GTPARFSGSLGEGKAALTLSGVQPEDEAEYYCALYYSNRWVFGSGTKLTVL
1608	H1E_I2M - HCDR1	artificial	SYAMN
1609	H1E_I2M - HCDR2	artificial	RIRSKYNNYATYYADAVKG
1610	H1E_I2M - HCDR3	artificial	AGNFGTSYLSFWAY
1611	H1E_I2M - LCDR1	artificial	GSSTGAVTSGYYPN
1612	H1E_I2M - LCDR2	artificial	GTKFLAP
1613	H1E_I2M - LCDR3	artificial	ALWYSNRWV
1614	H1E_I2M - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGMWVARIRSKYNNY ATYYADAVKGRFTISRDDSKNTLYLMNNLKTEDTAVYYCVRAGNFGTSYLSFWAYWG QGTLVTVSS
1615	H1E_I2M - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKKPGQAPRGLIGGTKFLAP GTPARFSGSLSGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1616	H1E_I2M2 - HCDR1	artificial	SYAIN
1617	H1E_I2M2 - HCDR2	artificial	RIRSKYNNYATYYADAVKG
1618	H1E_I2M2 - HCDR3	artificial	NANFGTSYLSFFAY

1619	H1E_I2M2 - LCDR1	artificial	GSSTGAVTSGYYPN
1620	H1E_I2M2 - LCDR2	artificial	GTKFLAP
1621	H1E_I2M2 - LCDR3	artificial	ALWYSNRWV
1622	H1E_I2M2 - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAINWVREAPGKGLEWVARIRSKYNNY ATYYADAVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRNANFGTSYLSFFAYWG QGTLVTVSS
1623	H1E_I2M2 - VL	artificial	QTVVTQEPISLTVPGGTIVTLTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1624	H1E_LC_G141 S - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1625	H1E_LC_G141 S - VL	artificial	QTVVTQEPISLTVPGGTIVTLTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1626	H1E_LC_G141 S_L21I - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1627	H1E_LC_G141 S_L21I - VL	artificial	QTVVTQEPISLTVPGGTIVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1628	H1E_LC_L83E - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1629	H1E_LC_L83E - VL	artificial	QTVVTQEPISLTVPGGTIVTLTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLEGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1630	H1E_LC_L83S - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1631	H1E_LC_L83S - VL	artificial	QTVVTQEPISLTVPGGTIVTLTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLSGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1632	H1E_LC_Q46E - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1633	H1E_LC_Q46E - VL	artificial	QTVVTQEPISLTVPGGTIVTLTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1634	H1E_LC_Q46K - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1635	H1E_LC_Q46K - VL	artificial	QTVVTQEPISLTVPGGTIVTLTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1636	H1E_LC_A107 L - HCDR1	artificial	SYAMN
1637	H1E_LC_A107 L - HCDR2	artificial	RIRSKYNNYATYYADSVKG
1638	H1E_LC_A107 L - HCDR3	artificial	HGNFGNSYLSFWAY
1639	H1E_LC_A107 L - LCDR1	artificial	GSSTGAVTSGYYPN
1640	H1E_LC_A107 L - LCDR2	artificial	GTKFLAP
1641	H1E_LC_A107 L - LCDR3	artificial	LLWYSNRWV
1642	H1E_LC_A107 L - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1643	H1E_LC_A107 L - VL	artificial	QTVVTQEPISLTVPGGTIVTLTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCLLWYSNRWVFGGGTKLTVL
1644	H1E_LC_V44I - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1645	H1E_LC_V44I - VL	artificial	QTVVTQEPISLTVPGGTIVTLTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1646	H1E_LC_V44L - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1647	H1E_LC_V44L - VL	artificial	QTVVTQEPISLTVPGGTIVTLTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1648	H1E_LC_V44M - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1649	H1E_LC_V44M - VL	artificial	QTVVTQEPISLTVPGGTIVTLTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1650	H1E_LC_W109 Y - HCDR1	artificial	SYAMN

1651	H1E_LC_W109 Y - HCDR2	artificial	RIRSKYNNYATYYADSVKG
1652	H1E_LC_W109 Y - HCDR3	artificial	HGNFGNSYLSFWAY
1653	H1E_LC_W109 Y - LCDR1	artificial	GSSTGAVTSGYYPN
1654	H1E_LC_W109 Y - LCDR2	artificial	GTKFLAP
1655	H1E_LC_W109 Y - LCDR3	artificial	ALYYSNRWV
1656	H1E_LC_W109 Y - VH	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNY ATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWG QGTLVTVSS
1657	H1E_LC_W109 Y - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTSGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALYYSNRWVFGGGTKLTVL
1658	H2C - HCDR1	artificial	KYAMN
1659	H2C - HCDR2	artificial	RIRSKYNNYATYYADSVKD
1660	H2C - HCDR3	artificial	HGNFGNSYISYWAY
1661	H2C - LCDR1	artificial	GSSTGAVTSGYYPN
1662	H2C - LCDR2	artificial	GTKFLAP
1663	H2C - LCDR3	artificial	ALWYSNRWV
1664	H2C - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1665	H2C - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTSGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1666	H2C_HC_A89I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTIYLMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1667	H2C_HC_A89I - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTSGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1668	H2C_HC_A89L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTLYLMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1669	H2C_HC_A89L - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTSGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1670	H2C_HC_A89T - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTTYLMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1671	H2C_HC_A89T - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTSGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1672	H2C_HC_A89V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTVYLMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1673	H2C_HC_A89V - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTSGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1674	H2C_HC_L52M - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKMEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1675	H2C_HC_L52M - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTSGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1676	H2C_HC_L52M _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKMEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1677	H2C_HC_L52M _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSTLTVSPGGTIVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1678	H2C_HC_L52M _LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKMEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1679	H2C_HC_L52M _LC_Q46K - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTSGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1680	H2C_HC_L52M _LC_Q46K_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKMEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1681	H2C_HC_L52M _LC_Q46K_G1 41S - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTSGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1682	H2C_HC_L52V	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGEWVARIRSKYNNY

	- VH		ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1683	H2C_HC_L52V - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1684	H2C_HC_L52V _LC_V44F - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQAPGKGVWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1685	H2C_HC_L52V _LC_V44F - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1686	H2C_HC_L52V _LC_V44Y - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQAPGKGVWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1687	H2C_HC_L52V _LC_V44Y - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1688	H2C_HC_M41F _A89V - HCDR1	artificial	KYAFN
1689	H2C_HC_M41F _A89V - HCDR2	artificial	RIRSKYNNYATYYADSVKD
1690	H2C_HC_M41F _A89V - HCDR3	artificial	HGNFGNSYISYWAY
1691	H2C_HC_M41F _A89V - LCDR1	artificial	GSSTGAVTSGYYPN
1692	H2C_HC_M41F _A89V - LCDR2	artificial	GTFKFLAP
1693	H2C_HC_M41F _A89V - LCDR3	artificial	ALWYSNRWV
1694	H2C_HC_M41F _A89V - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAFNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1695	H2C_HC_M41F _A89V - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1696	H2C_HC_M41I - HCDR1	artificial	KYAIN
1697	H2C_HC_M41I - HCDR2	artificial	RIRSKYNNYATYYADSVKD
1698	H2C_HC_M41I - HCDR3	artificial	HGNFGNSYISYWAY
1699	H2C_HC_M41I - LCDR1	artificial	GSSTGAVTSGYYPN
1700	H2C_HC_M41I - LCDR2	artificial	GTFKFLAP
1701	H2C_HC_M41I - LCDR3	artificial	ALWYSNRWV
1702	H2C_HC_M41I - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1703	H2C_HC_M41I - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1704	H2C_HC_M41I _A89L - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1705	H2C_HC_M41I _A89L - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1706	H2C_HC_M41I _A89V - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1707	H2C_HC_M41I _A89V - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1708	H2C_HC_M41I _A89V_IC_L2 1I_Q46K_G14 1S - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1709	H2C_HC_M41I _A89V_IC_L2 1I_Q46K_G14 1S - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1710	H2C_HC_M41I _A89V_IC_Q4	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG

	6K - VH		QGTLVTVSS
1711	H2C_HC_M41I _A89V_LC_Q4 6K - VL	artificial	QTVVTQEPSTLVSPGGTVTTLTCSSTGAVTSGYYPNWVQKKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1712	H2C_HC_M41I _L52V_A89V_ LC_L21I_Q46 K_G141S_V44 F - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGVLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTVYQLQMNLLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1713	H2C_HC_M41I _L52V_A89V_ LC_L21I_Q46 K_G141S_V44 F - VL	artificial	QTVVTQEPSTLVSPGGTVTITCGSSTGAVTSGYYPNWVQKKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1714	H2C_HC_M41I _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGVLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1715	H2C_HC_M41I _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSTLVSPGGTVTITCGSSTGAVTSGYYPNWVQKKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1716	H2C_HC_M41I _Q46E_A89V_ LC_L21I_Q46 K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGVLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTVYQLQMNLLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1717	H2C_HC_M41I _Q46E_A89V_ LC_L21I_Q46 K_G141S - VL	artificial	QTVVTQEPSTLVSPGGTVTITCGSSTGAVTSGYYPNWVQKKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1718	H2C_HC_M41V - HCDR1	artificial	KYAVN
1719	H2C_HC_M41V - HCDR2	artificial	RIRSKYNNYATYYADSVKD
1720	H2C_HC_M41V - HCDR3	artificial	HGNFGNSYISYWAY
1721	H2C_HC_M41V - LCDR1	artificial	GSSTGAVTSGYYPN
1722	H2C_HC_M41V - LCDR2	artificial	GTFKFLAP
1723	H2C_HC_M41V - LCDR3	artificial	ALWYSNRWV
1724	H2C_HC_M41V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAVNWVRQAPGKGVLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1725	H2C_HC_M41V - VL	artificial	QTVVTQEPSTLVSPGGTVTTLTCSSTGAVTSGYYPNWVQKKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1726	H2C_HC_Q46D - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRDAPGKGVLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1727	H2C_HC_Q46D - VL	artificial	QTVVTQEPSTLVSPGGTVTTLTCSSTGAVTSGYYPNWVQKKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1728	H2C_HC_Q46D _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRDAPGKGVLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1729	H2C_HC_Q46D _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSTLVSPGGTVTITCGSSTGAVTSGYYPNWVQKKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1730	H2C_HC_Q46D _LC_L21I_Q4 6R_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRDAPGKGVLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1731	H2C_HC_Q46D _LC_L21I_Q4 6R_G141S - VL	artificial	QTVVTQEPSTLVSPGGTVTITCGSSTGAVTSGYYPNWVQKKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1732	H2C_HC_Q46D _LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRDAPGKGVLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1733	H2C_HC_Q46D _LC_Q46K - VL	artificial	QTVVTQEPSTLVSPGGTVTTLTCSSTGAVTSGYYPNWVQKKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL

1734	H2C_HC_Q46D _LC_Q46K_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1735	H2C_HC_Q46D _LC_Q46K_G1 41S - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCSSTGAVTSGYYPNWVQKPKGPQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1736	H2C_HC_Q46D _LC_Q46R - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1737	H2C_HC_Q46D _LC_Q46R - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCSSTGAVTSGYYPNWVQKPKGPQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1738	H2C_HC_Q46D _LC_Q46R_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRDAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1739	H2C_HC_Q46D _LC_Q46R_G1 41S - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCSSTGAVTSGYYPNWVQKPKGPQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1740	H2C_HC_Q46E - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1741	H2C_HC_Q46E - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCSSTGAVTSGYYPNWVQKPKGPQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1742	H2C_HC_Q46E _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1743	H2C_HC_Q46E _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSTLTVSPGGTIVTITCSSTGAVTSGYYPNWVQKPKGPQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1744	H2C_HC_Q46E _LC_L21I_Q4 6R_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1745	H2C_HC_Q46E _LC_L21I_Q4 6R_G141S - VL	artificial	QTVVTQEPSTLTVSPGGTIVTITCSSTGAVTSGYYPNWVQKPKGPQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1746	H2C_HC_Q46E _LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1747	H2C_HC_Q46E _LC_Q46K - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCSSTGAVTSGYYPNWVQKPKGPQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1748	H2C_HC_Q46E _LC_Q46K_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1749	H2C_HC_Q46E _LC_Q46K_G1 41S - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCSSTGAVTSGYYPNWVQKPKGPQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1750	H2C_HC_Q46E _LC_Q46R - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1751	H2C_HC_Q46E _LC_Q46R - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCSSTGAVTSGYYPNWVQKPKGPQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1752	H2C_HC_Q46E _LC_Q46R_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVREAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1753	H2C_HC_Q46E _LC_Q46R_G1 41S - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCSSTGAVTSGYYPNWVQKPKGPQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1754	H2C_HC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRKAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1755	H2C_HC_Q46K - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCSSTGAVTSGYYPNWVQKPKGPQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1756	H2C_HC_Q46R - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1757	H2C_HC_Q46R - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCSSTGAVTSGYYPNWVQKPKGPQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1758	H2C_HC_V107 A - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCARHGNFGNSYISYWAYWG QGTLVTVSS

1759	H2C_HC_V107 A - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLGGAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1760	H2C_HC_V107 L - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCLRHGNFGNSYISYWAYWG QGTLVTVSS
1761	H2C_HC_V107 L - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLGGAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1762	H2C_HC_W136 F - HCDR1	artificial	KYAMN
1763	H2C_HC_W136 F - HCDR2	artificial	RIRSKYNNYATYYADSVKD
1764	H2C_HC_W136 F - HCDR3	artificial	HGNFGNSYISYFAY
1765	H2C_HC_W136 F - LCDR1	artificial	GSSTGAVTSGYYPN
1766	H2C_HC_W136 F - LCDR2	artificial	GTKFLAP
1767	H2C_HC_W136 F - LCDR3	artificial	ALWYSNRWV
1768	H2C_HC_W136 F - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYFAYWG QGTLVTVSS
1769	H2C_HC_W136 F - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLGGAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1770	H2C_HC_W136 F LC_V44I - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYFAYWG QGTLVTVSS
1771	H2C_HC_W136 F LC_V44I - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCGSSTGAVTSGYYPNWIQQKPGQAPRGLIGGTKFLAP GTPARFSGSLGGAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1772	H2C_HC_W136 F LC_V44L - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYFAYWG QGTLVTVSS
1773	H2C_HC_W136 F LC_V44L - VL	artificial	QTVVTQEPSTLTVSPGGTIVTLTCGSSTGAVTSGYYPNWLQKPGQAPRGLIGGTKFLAP GTPARFSGSLGGAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1774	H2C_I2E - HCDR1	artificial	KYAIN
1775	H2C_I2E - HCDR2	artificial	RIRSKYNNYATYYADAVKD
1776	H2C_I2E - HCDR3	artificial	AGNFGSSYISYWAY
1777	H2C_I2E - LCDR1	artificial	GSSTGAVTSGYYPN
1778	H2C_I2E - LCDR2	artificial	GTKFLAP
1779	H2C_I2E - LCDR3	artificial	ALWYSNRWV
1780	H2C_I2E - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADAVKDRFTISRDDSKNTVYLQMNNLKTEDTAVYYCARAGNFGSSYISYWAYWG QGTLVTVSS
1781	H2C_I2E - VL	artificial	QTVVTQEPSTLTVSPGGTIVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLSGGAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1782	H2C_I2K - HCDR1	artificial	KYAMN
1783	H2C_I2K - HCDR2	artificial	RIRSKYNNYATYYAEAVKG
1784	H2C_I2K - HCDR3	artificial	NENIGTSYISYWAY
1785	H2C_I2K - LCDR1	artificial	GSSTGAVTSGYYPN
1786	H2C_I2K - LCDR2	artificial	GTKFLAP
1787	H2C_I2K - LCDR3	artificial	ALWYSNRWV
1788	H2C_I2K - VH	artificial	EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYAEAVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRNENIGTSYISYWAYWG QGTLVTVSS
1789	H2C_I2K - VL	artificial	QTVVTQEPSTLTVSPGGTIVTITCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLSGGAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1790	H2C_I2L - HCDR1	artificial	KYAMN
1791	H2C_I2L - HCDR2	artificial	RIRSKYNNYATYYADAVKD
1792	H2C_I2L - HCDR3	artificial	AGNFGSSYISYFAY

1793	H2C_I2L - LCDR1	artificial	GSSTGAVTSGYYPN
1794	H2C_I2L - LCDR2	artificial	GTKFLAP
1795	H2C_I2L - LCDR3	artificial	ALYYSNRWV
1796	H2C_I2L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKMEWVARIRSKYNNY ATYYADAVKDRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRAGNFGSSYISYFAYWG QGTLVTVSS
1797	H2C_I2L - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPKGPQAPRGLIGGTKFLAP GTPARFSGSLEGGKAALTLSGVQPEDEAEYYCALYYSNRWVFGSGTKLTVL
1798	H2C_I2M - HCDR1	artificial	KYAMN
1799	H2C_I2M - HCDR2	artificial	RIRSKYNNYATYYADAVKD
1800	H2C_I2M - HCDR3	artificial	AGNFGTSYISYWAY
1801	H2C_I2M - LCDR1	artificial	GSSTGAVTSGYYPN
1802	H2C_I2M - LCDR2	artificial	GTKFLAP
1803	H2C_I2M - LCDR3	artificial	ALWYSNRWV
1804	H2C_I2M - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKMEWVARIRSKYNNY ATYYADAVKDRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRAGNFGTSYISYWAYWG QGTLVTVSS
1805	H2C_I2M - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPKGPQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1806	H2C_I2M2 - HCDR1	artificial	KYAIN
1807	H2C_I2M2 - HCDR2	artificial	RIRSKYNNYATYYADAVKD
1808	H2C_I2M2 - HCDR3	artificial	NANFGTSYISYFAY
1809	H2C_I2M2 - LCDR1	artificial	GSSTGAVTSGYYPN
1810	H2C_I2M2 - LCDR2	artificial	GTKFLAP
1811	H2C_I2M2 - LCDR3	artificial	ALWYSNRWV
1812	H2C_I2M2 - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVREAPGKGLEWVARIRSKYNNY ATYYADAVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRNANFGTSYISYFAYWG QGTLVTVSS
1813	H2C_I2M2 - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPKGPQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1814	H2C_LC_G141 S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1815	H2C_LC_G141 S - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPKGPQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1816	H2C_LC_G141 S_L21I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1817	H2C_LC_G141 S_L21I - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPKGPQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGSGTKLTVL
1818	H2C_LC_L83E - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1819	H2C_LC_L83E - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPKGPQAPRGLIGGTKFLAP GTPARFSGSLEGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGKTCLTVL
1820	H2C_LC_L83S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1821	H2C_LC_L83S - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPKGPQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGKTCLTVL
1822	H2C_LC_Q46E - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1823	H2C_LC_Q46E - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPKGPQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGKTCLTVL
1824	H2C_LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1825	H2C_LC_Q46K - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGYYPNWVQKPKGPQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGKTCLTVL

1826	H2C_LC_A107 L - HCDR1	artificial	KYAMN
1827	H2C_LC_A107 L - HCDR2	artificial	RIRSKYNNYATYYADSVKD
1828	H2C_LC_A107 L - HCDR3	artificial	HGNFGNSYISYWAY
1829	H2C_LC_A107 L - LCDR1	artificial	GSSTGAVTSGYYPN
1830	H2C_LC_A107 L - LCDR2	artificial	GTKFLAP
1831	H2C_LC_A107 L - LCDR3	artificial	LLWYSNRWV
1832	H2C_LC_A107 L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1833	H2C_LC_A107 L - VL	artificial	QTVVTQEPSLTVSPGGTIVTLTSGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCLWYSNRWVFGGGTKLTVL
1834	H2C_LC_V44I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1835	H2C_LC_V44I - VL	artificial	QTVVTQEPSLTVSPGGTIVTLTSGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1836	H2C_LC_V44L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1837	H2C_LC_V44L - VL	artificial	QTVVTQEPSLTVSPGGTIVTLTSGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1838	H2C_LC_V44M - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1839	H2C_LC_V44M - VL	artificial	QTVVTQEPSLTVSPGGTIVTLTSGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
1840	H2C_LC_W109 Y - HCDR1	artificial	KYAMN
1841	H2C_LC_W109 Y - HCDR2	artificial	RIRSKYNNYATYYADSVKD
1842	H2C_LC_W109 Y - HCDR3	artificial	HGNFGNSYISYWAY
1843	H2C_LC_W109 Y - LCDR1	artificial	GSSTGAVTSGYYPN
1844	H2C_LC_W109 Y - LCDR2	artificial	GTKFLAP
1845	H2C_LC_W109 Y - LCDR3	artificial	ALYYSNRWV
1846	H2C_LC_W109 Y - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1847	H2C_LC_W109 Y - VL	artificial	QTVVTQEPSLTVSPGGTIVTLTSGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALYYSNRWVFGGGTKLTVL
1848	I2C - HCDR1	artificial	KYAMN
1849	I2C - HCDR2	artificial	RIRSKYNNYATYYADSVKD
1850	I2C - HCDR3	artificial	HGNFGNSYISYWAY
1851	I2C - LCDR1	artificial	GSSTGAVTSGNYPN
1852	I2C - LCDR2	artificial	GTKFLAP
1853	I2C - LCDR3	artificial	VLWYSNRWV
1854	I2C - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1855	I2C - VL	artificial	QTVVTQEPSLTVSPGGTIVTLTSGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1856	I2C_HC_A89I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTIYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1857	I2C_HC_A89I - VL	artificial	QTVVTQEPSLTVSPGGTIVTLTSGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1858	I2C_HC_A89L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1859	I2C_HC_A89L - VL	artificial	QTVVTQEPSLTVSPGGTIVTLTSGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1860	I2C_HC_A89T - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTIYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG

			QGTLVTVSS
1861	I2C_HC_A89T - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGNYPNWWQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1862	I2C_HC_A89V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1863	I2C_HC_A89V - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGNYPNWWQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1864	I2C_HC_L52M - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKMEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1865	I2C_HC_L52M - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGNYPNWWQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1866	I2C_HC_L52M _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKMEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1867	I2C_HC_L52M _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGNYPNWWQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
1868	I2C_HC_L52M _LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKMEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1869	I2C_HC_L52M _LC_Q46K - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGNYPNWWQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1870	I2C_HC_L52M _LC_Q46K_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKMEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1871	I2C_HC_L52M _LC_Q46K_G1 41S - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGNYPNWWQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
1872	I2C_HC_L52V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGVWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1873	I2C_HC_L52V - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGNYPNWWQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1874	I2C_HC_L52V _LC_V44F - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGVWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1875	I2C_HC_L52V _LC_V44F - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGNYPNWWQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1876	I2C_HC_L52V _LC_V44Y - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGVWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1877	I2C_HC_L52V _LC_V44Y - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGNYPNWWQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1878	I2C_HC_M41F _A89V - HCDR1	artificial	KYAFN
1879	I2C_HC_M41F _A89V - HCDR2	artificial	RIRSKYNNYATYYADSVKD
1880	I2C_HC_M41F _A89V - HCDR3	artificial	HGNFGNSYISYWAY
1881	I2C_HC_M41F _A89V - LCDR1	artificial	GSSTGAVTSGNYPN
1882	I2C_HC_M41F _A89V - LCDR2	artificial	GTKFLAP
1883	I2C_HC_M41F _A89V - LCDR3	artificial	VLWYSNRWV
1884	I2C_HC_M41F _A89V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAFNWRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1885	I2C_HC_M41F _A89V - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGNYPNWWQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1886	I2C_HC_M41I - HCDR1	artificial	KYAIN

1887	I2C_HC_M41I - HCDR2	artificial	RIRSKYNNYATYYADSVKD
1888	I2C_HC_M41I - HCDR3	artificial	HGNFGNSYISYWAY
1889	I2C_HC_M41I - LCDR1	artificial	GSSTGAVTSGNYPN
1890	I2C_HC_M41I - LCDR2	artificial	GTKFLAP
1891	I2C_HC_M41I - LCDR3	artificial	VLWYSNRWV
1892	I2C_HC_M41I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1893	I2C_HC_M41I - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1894	I2C_HC_M41I _A89L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1895	I2C_HC_M41I _A89L - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1896	I2C_HC_M41I _A89V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1897	I2C_HC_M41I _A89V - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1898	I2C_HC_M41I _A89V_IC_L2 1I_Q46K_G14 1S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1899	I2C_HC_M41I _A89V_IC_L2 1I_Q46K_G14 1S - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
1900	I2C_HC_M41I _A89V_IC_Q4 6K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1901	I2C_HC_M41I _A89V_IC_Q4 6K - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1902	I2C_HC_M41I _L52V_A89V LC_L21I_Q46 K_G141S_V44 F - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1903	I2C_HC_M41I _L52V_A89V LC_L21I_Q46 K_G141S_V44 F - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
1904	I2C_HC_M41I _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1905	I2C_HC_M41I _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
1906	I2C_HC_M41I _Q46E_A89V LC_L21I_Q46 K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1907	I2C_HC_M41I _Q46E_A89V LC_L21I_Q46 K_G141S - VL	artificial	QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
1908	I2C_HC_M41V - HCDR1	artificial	KYAVN
1909	I2C_HC_M41V - HCDR2	artificial	RIRSKYNNYATYYADSVKD
1910	I2C_HC_M41V - HCDR3	artificial	HGNFGNSYISYWAY
1911	I2C_HC_M41V - LCDR1	artificial	GSSTGAVTSGNYPN
1912	I2C_HC_M41V	artificial	GTKFLAP

	- LCDR2		
1913	I2C_HC_M41V - LCDR3	artificial	VLWYSNRWV
1914	I2C_HC_M41V - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAVNWVRQAPGKLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1915	I2C_HC_M41V - VL	artificial	QTVVTQEPSLTVSPGGTIVTLTSGSSTGAVTSGNYPNWWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1916	I2C_HC_Q46D - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRDAPGKLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1917	I2C_HC_Q46D - VL	artificial	QTVVTQEPSLTVSPGGTIVTLTSGSSTGAVTSGNYPNWWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1918	I2C_HC_Q46D _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRDAPGKLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1919	I2C_HC_Q46D _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSLTVSPGGTIVTITCGSSTGAVTSGNYPNWWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
1920	I2C_HC_Q46D _LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRDAPGKLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1921	I2C_HC_Q46D _LC_Q46K - VL	artificial	QTVVTQEPSLTVSPGGTIVTLTSGSSTGAVTSGNYPNWWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1922	I2C_HC_Q46D _LC_Q46K_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRDAPGKLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1923	I2C_HC_Q46D _LC_Q46K_G1 41S - VL	artificial	QTVVTQEPSLTVSPGGTIVTLTSGSSTGAVTSGNYPNWWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
1924	I2C_HC_Q46D _LC_Q46R - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRDAPGKLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1925	I2C_HC_Q46D _LC_Q46R - VL	artificial	QTVVTQEPSLTVSPGGTIVTLTSGSSTGAVTSGNYPNWWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1926	I2C_HC_Q46D _LC_Q46R_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRDAPGKLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1927	I2C_HC_Q46D _LC_Q46R_G1 41S - VL	artificial	QTVVTQEPSLTVSPGGTIVTLTSGSSTGAVTSGNYPNWWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
1928	I2C_HC_Q46D _LC_L21I_Q 46R_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRDAPGKLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1929	I2C_HC_Q46D _LC_L21I_Q 46R_G141S - VL	artificial	QTVVTQEPSLTVSPGGTIVTITCGSSTGAVTSGNYPNWWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
1930	I2C_HC_Q46E - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVREAPGKLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1931	I2C_HC_Q46E - VL	artificial	QTVVTQEPSLTVSPGGTIVTLTSGSSTGAVTSGNYPNWWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1932	I2C_HC_Q46E _LC_L21I_Q4 6K_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVREAPGKLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1933	I2C_HC_Q46E _LC_L21I_Q4 6K_G141S - VL	artificial	QTVVTQEPSLTVSPGGTIVTITCGSSTGAVTSGNYPNWWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
1934	I2C_HC_Q46E _LC_L21I_Q4 6R_G141S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVREAPGKLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1935	I2C_HC_Q46E _LC_L21I_Q4 6R_G141S - VL	artificial	QTVVTQEPSLTVSPGGTIVTITCGSSTGAVTSGNYPNWWVQKPGQAPRGLIGGTFKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
1936	I2C_HC_Q46E _LC_Q46K -	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVREAPGKLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG

	VH		QGTLVTVSS
1937	I2C_HC_Q46E _LC_Q46K - VL	artificial	QTVVTQEPISLTVSPGGTIVTLTCSSTGAVTSGNYPNWWQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1938	I2C_HC_Q46E _LC_Q46K_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWWREAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1939	I2C_HC_Q46E _LC_Q46K_G1 41S - VL	artificial	QTVVTQEPISLTVSPGGTIVTLTCSSTGAVTSGNYPNWWQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
1940	I2C_HC_Q46E _LC_Q46R - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWWREAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1941	I2C_HC_Q46E _LC_Q46R - VL	artificial	QTVVTQEPISLTVSPGGTIVTLTCSSTGAVTSGNYPNWWQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1942	I2C_HC_Q46E _LC_Q46R_G1 41S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWWREAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1943	I2C_HC_Q46E _LC_Q46R_G1 41S - VL	artificial	QTVVTQEPISLTVSPGGTIVTLTCSSTGAVTSGNYPNWWQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
1944	I2C_HC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWWREAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1945	I2C_HC_Q46K - VL	artificial	QTVVTQEPISLTVSPGGTIVTLTCSSTGAVTSGNYPNWWQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1946	I2C_HC_Q46R - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWWREAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1947	I2C_HC_Q46R - VL	artificial	QTVVTQEPISLTVSPGGTIVTLTCSSTGAVTSGNYPNWWQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1948	I2C_HC_V107 A - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWWREAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCARHGNFGNSYISYWAYWG QGTLVTVSS
1949	I2C_HC_V107 A - VL	artificial	QTVVTQEPISLTVSPGGTIVTLTCSSTGAVTSGNYPNWWQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1950	I2C_HC_V107 L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWWREAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCLRHGNFGNSYISYWAYWG QGTLVTVSS
1951	I2C_HC_V107 L - VL	artificial	QTVVTQEPISLTVSPGGTIVTLTCSSTGAVTSGNYPNWWQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1952	I2C_HC_W136 F - HCDR1	artificial	KYAMN
1953	I2C_HC_W136 F - HCDR2	artificial	RIRSKYNNYATYYADSVKD
1954	I2C_HC_W136 F - HCDR3	artificial	HGNFGNSYISYFAY
1955	I2C_HC_W136 F - LCDR1	artificial	GSSTGAVTSGNYPN
1956	I2C_HC_W136 F - LCDR2	artificial	GTKFLAP
1957	I2C_HC_W136 F - LCDR3	artificial	VLWYSNRWV
1958	I2C_HC_W136 F - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWWREAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYFAYWG QGTLVTVSS
1959	I2C_HC_W136 F - VL	artificial	QTVVTQEPISLTVSPGGTIVTLTCSSTGAVTSGNYPNWWQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1960	I2C_HC_W136 F_LC_V44I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWWREAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYFAYWG QGTLVTVSS
1961	I2C_HC_W136 F_LC_V44I - VL	artificial	QTVVTQEPISLTVSPGGTIVTLTCSSTGAVTSGNYPNWWQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1962	I2C_HC_W136 F_LC_V44L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWWREAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYFAYWG QGTLVTVSS
1963	I2C_HC_W136 F_LC_V44L - VL	artificial	QTVVTQEPISLTVSPGGTIVTLTCSSTGAVTSGNYPNWWQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1964	I2C_LC_G141 S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWWREAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1965	I2C_LC_G141	artificial	QTVVTQEPISLTVSPGGTIVTLTCSSTGAVTSGNYPNWWQKPGQAPRGLIGGTKFLAP

	S - VL		GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
1966	I2C_LC_G141 S_L21I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1967	I2C_LC_G141 S_L21I - VL	artificial	QTVVTQEPSLTVSPGGTIVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
1968	I2C_LC_L83E - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1969	I2C_LC_L83E - VL	artificial	QTVVTQEPSLTVSPGGTIVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
1970	I2C_LC_L83S - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1971	I2C_LC_L83S - VL	artificial	QTVVTQEPSLTVSPGGTIVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
1972	I2C_LC_Q46E - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1973	I2C_LC_Q46E - VL	artificial	QTVVTQEPSLTVSPGGTIVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
1974	I2C_LC_Q46K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1975	I2C_LC_Q46K - VL	artificial	QTVVTQEPSLTVSPGGTIVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
1976	I2C_LC_V107 A - HCDR1	artificial	KYAMN
1977	I2C_LC_V107 A - HCDR2	artificial	RIRSKYNNYATYYADSVKD
1978	I2C_LC_V107 A - HCDR3	artificial	HGNFGNSYISYWAY
1979	I2C_LC_V107 A - LCDR1	artificial	GSSTGAVTSGNYPN
1980	I2C_LC_V107 A - LCDR2	artificial	GTKFLAP
1981	I2C_LC_V107 A - LCDR3	artificial	ALWYSNRWV
1982	I2C_LC_V107 A - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1983	I2C_LC_V107 A - VL	artificial	QTVVTQEPSLTVSPGGTIVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
1984	I2C_LC_V107 L - HCDR1	artificial	KYAMN
1985	I2C_LC_V107 L - HCDR2	artificial	RIRSKYNNYATYYADSVKD
1986	I2C_LC_V107 L - HCDR3	artificial	HGNFGNSYISYWAY
1987	I2C_LC_V107 L - LCDR1	artificial	GSSTGAVTSGNYPN
1988	I2C_LC_V107 L - LCDR2	artificial	GTKFLAP
1989	I2C_LC_V107 L - LCDR3	artificial	LLWYSNRWV
1990	I2C_LC_V107 L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1991	I2C_LC_V107 L - VL	artificial	QTVVTQEPSLTVSPGGTIVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
1992	I2C_LC_V44I - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1993	I2C_LC_V44I - VL	artificial	QTVVTQEPSLTVSPGGTIVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
1994	I2C_LC_V44L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1995	I2C_LC_V44L - VL	artificial	QTVVTQEPSLTVSPGGTIVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
1996	I2C_LC_V44M - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
1997	I2C_LC_V44M - VL	artificial	QTVVTQEPSLTVSPGGTIVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL

1998	I2C_LC_W109 Y - HCDR1	artificial	KYAMN
1999	I2C_LC_W109 Y - HCDR2	artificial	RIRSKYNNYATYYADSVKD
2000	I2C_LC_W109 Y - HCDR3	artificial	HGNFGNSYISYWAY
2001	I2C_LC_W109 Y - LCDR1	artificial	GSSTGAVTSGNYPN
2002	I2C_LC_W109 Y - LCDR2	artificial	GTKFLAP
2003	I2C_LC_W109 Y - LCDR3	artificial	VLYYSNRWV
2004	I2C_LC_W109 Y - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
2005	I2C_LC_W109 Y - VL	artificial	QTVVTQEPISLTVSPGGTVTITCGSSTGAVTSGNYPNWWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLYYSNRWVFGGSGTKLTVL
2006	I2E - HCDR1	artificial	KYAIN
2007	I2E - HCDR2	artificial	RIRSKYNNYATYYADAVKD
2008	I2E - HCDR3	artificial	AGNFGSSYISYWAY
2009	I2E - LCDR1	artificial	GSSTGAVTSGNYPN
2010	I2E - LCDR2	artificial	GTKFLAP
2011	I2E - LCDR3	artificial	VLWYSNRWV
2012	I2E - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNY ATYYADAVKDRFTISRDDSKNTVYLMNNLKTEDTAVYYCARAGNFGSSYISYWAYWG QGTLVTVSS
2013	I2E - VL	artificial	QTVVTQEPISLTVSPGGTVTITCGSSTGAVTSGNYPNWWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
2014	I2K - HCDR1	artificial	KYAMN
2015	I2K - HCDR2	artificial	RIRSKYNNYATYYAEAVKG
2016	I2K - HCDR3	artificial	NENIGTSYISYWAY
2017	I2K - LCDR1	artificial	GSSTGAVTSGNYPN
2018	I2K - LCDR2	artificial	GTKFLAP
2019	I2K - LCDR3	artificial	VLWYSNRWV
2020	I2K - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYAEAVKGRFTISRDDSKNTVYLMNNLKTEDTAVYYCVRNENIGTSYISYWAYWG QGTLVTVSS
2021	I2K - VL	artificial	QTVVTQEPISLTVSPGGTVTITCGSSTGAVTSGNYPNWWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
2022	I2L - HCDR1	artificial	KYAMN
2023	I2L - HCDR2	artificial	RIRSKYNNYATYYADAVKD
2024	I2L - HCDR3	artificial	AGNFGSSYISYFAY
2025	I2L - LCDR1	artificial	GSSTGAVTSGNYPN
2026	I2L - LCDR2	artificial	GTKFLAP
2027	I2L - LCDR3	artificial	VLYYSNRWV
2028	I2L - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKMEWVARIRSKYNNY ATYYADAVKDRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRAGNFGSSYISYFAYWG QGTLVTVSS
2029	I2L - VL	artificial	QTVVTQEPISLTVSPGGTVTITCGSSTGAVTSGNYPNWIQKPGQAPRGLIGGTKFLAP GTPARFSGSLEGGKAALTLSGVQPEDEAEYYCVLYYSNRWVFGSGTKLTVL
2030	I2M - HCDR1	artificial	KYAMN
2031	I2M - HCDR2	artificial	RIRSKYNNYATYYADAVKD
2032	I2M - HCDR3	artificial	AGNFGTSYISYWAY
2033	I2M - LCDR1	artificial	GSSTGAVTSGNYPN
2034	I2M - LCDR2	artificial	GTKFLAP
2035	I2M - LCDR3	artificial	VLWYSNRWV
2036	I2M - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKMEWVARIRSKYNNY ATYYADAVKDRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRAGNFGTSYISYWAYWG QGTLVTVSS
2037	I2M - VL	artificial	QTVVTQEPISLTVSPGGTVTITCGSSTGAVTSGNYPNWWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL

2038	I2M2 - HCDR1	artificial	KYAIN
2039	I2M2 - HCDR2	artificial	RIRSKYNNYATYYADAVKD
2040	I2M2 - HCDR3	artificial	NANFGTSYISYFAY
2041	I2M2 - LCDR1	artificial	GSSTGAVTSGNYPN
2042	I2M2 - LCDR2	artificial	GTKFLAP
2043	I2M2 - LCDR3	artificial	VLWYSNRWV
2044	I2M2 - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVREAPGKGLEWVARIRSKYNNY ATYYADAVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRNANFGTSYISYFAYWG QGTLVTVSS
2045	I2M2 - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTSGSSTGAVTSGNYPNWWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLGGAALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
2046	consensus_s equence_1 - HCDR1	artificial	KYAMN
2047	consensus_s equence_1 - HCDR2	artificial	RIRSKYNNYATYYADSVKD
2048	consensus_s equence_1 - HCDR3	artificial	HGNFGNSYJSXWAY
2049	consensus_s equence_1 - LCDR1	artificial	GSSTGAVTSGYYPN
2050	consensus_s equence_1 - LCDR2	artificial	GTKFLAP
2051	consensus_s equence_1 - LCDR3	artificial	ALWYSNRWV
2052	consensus_s equence_1 - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYJSXWAYWG QGTLVTVSS
2053	consensus_s equence_1 - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTSGSSTGAVTSGYYPNWWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLGGAALTLGSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
2054	consensus_s equence_2 - HCDR1	artificial	KYAMN
2055	consensus_s equence_2 - HCDR2	artificial	RIRSKYNNYATYYADSVKX
2056	consensus_s equence_2 - HCDR3	artificial	HGNFGNSYJSYWAY
2057	consensus_s equence_2 - LCDR1	artificial	GSSTGAVTSGYYPN
2058	consensus_s equence_2 - LCDR2	artificial	GTKFLAP
2059	consensus_s equence_2 - LCDR3	artificial	ALWYSNRWV
2060	consensus_s equence_2 - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKXRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYJSYWAYWG QGTLVTVSS
2061	consensus_s equence_2 - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTSGSSTGAVTSGYYPNWWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLGGAALTLGSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
2062	consensus_s equence_3 - HCDR1	artificial	KYAMN
2063	consensus_s equence_3 - HCDR2	artificial	RIRSKYNNYATYYADSVKX
2064	consensus_s equence_3 - HCDR3	artificial	HGNFGNSYISYWAY
2065	consensus_s equence_3 -	artificial	GSSTGAVTSGYYPN

	LCDR1		
2066	consensus_s equence_3 - LCDR2	artificial	GTKFLAP
2067	consensus_s equence_3 - LCDR3	artificial	ALWYSNRWV
2068	consensus_s equence_3 - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKXRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
2069	consensus_s equence_3 - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGYYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
2070	consensus_s equence_4 - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNY ATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS
2071	consensus_s equence_4 - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
2072	BC A7 27- C4-G7 - HCDR1	artificial	NHIIH
2073	BC A7 27- C4-G7 - HCDR2	artificial	YINPYPGYHAYNEKFQG
2074	BC A7 27- C4-G7 - HCDR3	artificial	DGYRDTDVLDY
2075	BC A7 27- C4-G7 - LCDR1	artificial	QASQDISNYLN
2076	BC A7 27- C4-G7 - LCDR2	artificial	YTSRLHT
2077	BC A7 27- C4-G7 - LCDR3	artificial	QQGNTLPWT
2078	BC A7 27- C4-G7 - VH	artificial	QVQLVQSGAEVKKPGASVKVSCASGYTFTNHHIHWVRQAPGQGLEWMGYINPYPGYH AYNEKFQGRATMTSDTSTSTVYMESSLRSEDATAVYYCARDGYRDTDVLDYWGQGT LTVTVSS
2079	BC A7 27- C4-G7 - VL	artificial	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYYTSRLHTGV PSRFGSGSGTDFTFTISSLEPEDIATYYCQQGNTLPWTFGQGTKEIK
2080	BC A7 27- C4-G7 CC - VH	artificial	QVQLVQSGAEVKKPGASVKVSCASGYTFTNHHIHWVRQAPGQGLEWMGYINPYPGYH AYNEKFQGRATMTSDTSTSTVYMESSLRSEDATAVYYCARDGYRDTDVLDYWGQGT LTVTVSS
2081	BC A7 27- C4-G7 CC - VL	artificial	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYYTSRLHTGV PSRFGSGSGTDFTFTISSLEPEDIATYYCQQGNTLPWTFGCGTKVEIK
2082	BC A7 27- C4-G7 CC EI GQ - VL	artificial	EIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYYTSRLHTGV PSRFGSGSGTDFTFTISSLEPEDIATYYCQQGNTLPWTFGCGTKVEIK
2083	BC A7 27- C4-G7 EI GQ - VL	artificial	EIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYYTSRLHTGV PSRFGSGSGTDFTFTISSLEPEDIATYYCQQGNTLPWTFGQGTKEIK
2084	BC A7 27- C4-G7X I2C - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCASGYTFTNHHIHWVRQAPGQGLEWMGYINPYPGYH AYNEKFQGRATMTSDTSTSTVYMESSLRSEDATAVYYCARDGYRDTDVLDYWGQGT LTVTVSSGGGGSGGGSGGGSDIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQ KPGKAPKLLIYYTSRLHTGVPSRFGSGSGTDFTFTISSLEPEDIATYYCQQGNTLPW TFGQGTKEIKSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAP GKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCV RHGNFGNSYISYWAYWGQGTLLTVTVSSGGGGSGGGSGGGSGQTVVTQEPSTLTVSPGGT VTITCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAAL TLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
2085	BC A7 27- C4-G7X I2E - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCASGYTFTNHHIHWVRQAPGQGLEWMGYINPYPGYH AYNEKFQGRATMTSDTSTSTVYMESSLRSEDATAVYYCARDGYRDTDVLDYWGQGT LTVTVSSGGGGSGGGSGGGSDIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQ KPGKAPKLLIYYTSRLHTGVPSRFGSGSGTDFTFTISSLEPEDIATYYCQQGNTLPW TFGQGTKEIKSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAP GKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCA RAGNFGSSYISYWAYWGQGTLLTVTVSSGGGGSGGGSGGGSGQTVVTQEPSTLTVSPGGT VTITCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAAL TLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
2086	BC A7 27- C4-G7X I2K - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCASGYTFTNHHIHWVRQAPGQGLEWMGYINPYPGYH AYNEKFQGRATMTSDTSTSTVYMESSLRSEDATAVYYCARDGYRDTDVLDYWGQGT LTVTVSSGGGGSGGGSGGGSDIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQ KPGKAPKLLIYYTSRLHTGVPSRFGSGSGTDFTFTISSLEPEDIATYYCQQGNTLPW

			TFGQGTKEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAP GKGLEWVARIRSKYNNYATYYAAEAVKGRFTISRDDSKNTVYLQMNMLKTEDTAVYYCV RNEIGTSYISYWAYWGQGLTVTVSSGGGGSGGGSGGGGSGQTVVTQEPSTVSPGGT VTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAPGTPARFSGSLSGGKAAL TLSGVQPEDAEYYCVLWYSNRWVFGSGTKLTVL
2087	BC A7 27- C4-G7X I2L - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCASGYTFNTHIIHWVRQAPGQGLEWMGYINPYPGYH AYNEKFQGRATMTSDTSTSTVYMESSLRSRSEDYAVYYCARDGYRDTDVLDYWGQGT LTVTVSSGGGGSGGGSGGGGSDIQMTQSPSSLSASVGDRTITCQASQDISNYLNWYQQ KPGKAPKLLIYYTSRLHTGVPSRFSGSGSGTDFTFTISSLEPEDIATYYCQQGNTLPW TFGQGTKEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAP GKGMWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNMLKTEDTAVYYCV RAGNFGSSYISYFAYWGQGLTVTVSSGGGGSGGGSGGGGSGQTVVTQEPSTVSPGGT VTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAPGTPARFSGSLSGGKAAL TLSGVQPEDAEYYCVLYYSNRWVFGSGTKLTVL
2088	BC A7 27- C4-G7X I2M - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCASGYTFNTHIIHWVRQAPGQGLEWMGYINPYPGYH AYNEKFQGRATMTSDTSTSTVYMESSLRSRSEDYAVYYCARDGYRDTDVLDYWGQGT LTVTVSSGGGGSGGGSGGGGSDIQMTQSPSSLSASVGDRTITCQASQDISNYLNWYQQ KPGKAPKLLIYYTSRLHTGVPSRFSGSGSGTDFTFTISSLEPEDIATYYCQQGNTLPW TFGQGTKEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAP GKGMWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNMLKTEDTAVYYCV RAGNFGTSYISYFAYWGQGLTVTVSSGGGGSGGGSGGGGSGQTVVTQEPSTVSPGGT VTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAPGTPARFSGSLSGGKAAL TLSGVQPEDAEYYCVLWYSNRWVFGSGTKLTVL
2089	BC A7 27- C4-G7X I2M2 - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCASGYTFNTHIIHWVRQAPGQGLEWMGYINPYPGYH AYNEKFQGRATMTSDTSTSTVYMESSLRSRSEDYAVYYCARDGYRDTDVLDYWGQGT LTVTVSSGGGGSGGGSGGGGSDIQMTQSPSSLSASVGDRTITCQASQDISNYLNWYQQ KPGKAPKLLIYYTSRLHTGVPSRFSGSGSGTDFTFTISSLEPEDIATYYCQQGNTLPW TFGQGTKEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYALNWVRQAP GKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTAYLQMNMLKTEDTAVYYCV RNANFGTSYISYFAYWGQGLTVTVSSGGGGSGGGSGGGGSGQTVVTQEPSTVSPGGT VTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAPGTPARFSGSLSGGKAAL TLSGVQPEDAEYYCVLWYSNRWVFGSGTKLTVL
2090	BC A7 27- C4-G7 CC x I2C x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCASGYTFNTHIIHWVRQAPGQCLEWMGYINPYPGYH AYNEKFQGRATMTSDTSTSTVYMESSLRSRSEDYAVYYCARDGYRDTDVLDYWGQGT LTVTVSSGGGGSGGGSGGGGSDIQMTQSPSSLSASVGDRTITCQASQDISNYLNWYQQ KPGKAPKLLIYYTSRLHTGVPSRFSGSGSGTDFTFTISSLEPEDIATYYCQQGNTLPW TFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAP GKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNMLKTEDTAVYYCV RHGNGFNSYISYWAYWGQGLTVTVSSGGGGSGGGSGGGGSGQTVVTQEPSTVSPGGT VTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAPGTPARFSGSLSGGKAAL TLSGVQPEDAEYYCVLWYSNRWVFGGKTCLTVLGGGDKTHTCPPCPAPPELLGGPSV FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGS TYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGGS GGGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAP IEKTIISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
2091	BC A7 27- C4-G7 CC x I2E x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCASGYTFNTHIIHWVRQAPGQCLEWMGYINPYPGYH AYNEKFQGRATMTSDTSTSTVYMESSLRSRSEDYAVYYCARDGYRDTDVLDYWGQGT LTVTVSSGGGGSGGGSGGGGSDIQMTQSPSSLSASVGDRTITCQASQDISNYLNWYQQ KPGKAPKLLIYYTSRLHTGVPSRFSGSGSGTDFTFTISSLEPEDIATYYCQQGNTLPW TFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAP GKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNMLKTEDTAVYYCA RAGNFGSSYISYWAYWGQGLTVTVSSGGGGSGGGSGGGGSGQTVVTQEPSTVSPGGT VTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAPGTPARFSGSLSGGKAAL TLSGVQPEDAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCPPCPAPPELLGGPSV FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGS TYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGGS GGGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAP IEKTIISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
2092	BC A7 27- C4-G7 CC x I2K x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCASGYTFNTHIIHWVRQAPGQCLEWMGYINPYPGYH AYNEKFQGRATMTSDTSTSTVYMESSLRSRSEDYAVYYCARDGYRDTDVLDYWGQGT LTVTVSSGGGGSGGGSGGGGSDIQMTQSPSSLSASVGDRTITCQASQDISNYLNWYQQ KPGKAPKLLIYYTSRLHTGVPSRFSGSGSGTDFTFTISSLEPEDIATYYCQQGNTLPW TFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAP GKGLEWVARIRSKYNNYATYYAAEAVKGRFTISRDDSKNTVYLQMNMLKTEDTAVYYCV RNEIGTSYISYWAYWGQGLTVTVSSGGGGSGGGSGGGGSGQTVVTQEPSTVSPGGT VTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAPGTPARFSGSLSGGKAAL TLSGVQPEDAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCPPCPAPPELLGGPSV FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGS TYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGGS GGGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAP IEKTIISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

[illegible]

	- VH		VSS
2103	CD123 24- B4-f NK CC - VL	artificial	DIVLTQSPSLSPVTPGEPASISCRSSQSLLSHNKYNLYLDWYLQKPGQSPQLLIYLGSN RASGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPPITFGCGTRLEIK
2104	CD123 24- B4-f NK CC EI GQ - VL	artificial	EIVLTQSPSLSPVTPGEPASISCRSSQSLLSHNKYNLYLDWYLQKPGQSPQLLIYLGSN RASGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPPITFGCGTRLEIK
2105	CD123 24- B4-f NK CC x I2C x scFc - Full Sequence	artificial	EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYAMSWVRQAPGKCLEWVSAVSGGGDKT LYADAVKGRFTISRDNKNTLFLQMNSLRAEDTAIYYCARLGRFYYGMDVWGQGTITVT VSSGGGSGGGGSGGGGSDIVLTQSPSLSPVTPGEPASISCRSSQSLLSHNKYNLYLDW YLQKPGQSPQLLIYLGSNRASGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQ TPPITFGCGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWV RQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNKLKTEDTAV YYCVRHGNFGNSYISYWAYWGQGTILVTVSSGGGSGGGGSGGGGSGTQVVTQEPSTLVS PGGTVTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGG KAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKHTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEE QYGYSTYRCVSVLTVLHQLDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLTP PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKL TVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGKGGGSGGGGSGGGGSGGGGSG GGGSGGGGSGDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH DPEVKFNWYVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQLDNLNGKEYCKVSNKA LPAPIEKTISKAKGQPREPQVYTLTPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSL SPGK
2106	CD123 24- B4-f NK CC x I2E x scFc - Full Sequence	artificial	EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYAMSWVRQAPGKCLEWVSAVSGGGDKT LYADAVKGRFTISRDNKNTLFLQMNSLRAEDTAIYYCARLGRFYYGMDVWGQGTITVT VSSGGGSGGGGSGGGGSDIVLTQSPSLSPVTPGEPASISCRSSQSLLSHNKYNLYLDW YLQKPGQSPQLLIYLGSNRASGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQ TPPITFGCGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWV RQAPGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNKLKTEDTAV YYCARAGNFGSSYISYWAYWGQGTILVTVSSGGGSGGGGSGGGGSGTQVVTQEPSTLVS PGGTVTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGG KAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKHTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEE QYGYSTYRCVSVLTVLHQLDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLTP PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKL TVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGKGGGSGGGGSGGGGSGGGGSG GGGSGGGGSGDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH DPEVKFNWYVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQLDNLNGKEYCKVSNKA LPAPIEKTISKAKGQPREPQVYTLTPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSL SPGK
2107	CD123 24- B4-f NK CC x I2K x scFc - Full Sequence	artificial	EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYAMSWVRQAPGKCLEWVSAVSGGGDKT LYADAVKGRFTISRDNKNTLFLQMNSLRAEDTAIYYCARLGRFYYGMDVWGQGTITVT VSSGGGSGGGGSGGGGSDIVLTQSPSLSPVTPGEPASISCRSSQSLLSHNKYNLYLDW YLQKPGQSPQLLIYLGSNRASGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQ TPPITFGCGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWV RQAPGKGLEWVARIRSKYNNYATYYAEAVKGRFTISRDDSKNTVYLQMNKLKTEDTAV YYCVRNENIGTSYISYWAYWGQGTILVTVSSGGGSGGGGSGGGGSGTQVVTQEPSTLVS PGGTVTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGG KAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKHTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEE QYGYSTYRCVSVLTVLHQLDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLTP PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKL TVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGKGGGSGGGGSGGGGSGGGGSG GGGSGGGGSGDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH DPEVKFNWYVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQLDNLNGKEYCKVSNKA LPAPIEKTISKAKGQPREPQVYTLTPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSL SPGK
2108	CD123 24- B4-f NK CC x I2L x scFc - Full Sequence	artificial	EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYAMSWVRQAPGKCLEWVSAVSGGGDKT LYADAVKGRFTISRDNKNTLFLQMNSLRAEDTAIYYCARLGRFYYGMDVWGQGTITVT VSSGGGSGGGGSGGGGSDIVLTQSPSLSPVTPGEPASISCRSSQSLLSHNKYNLYLDW YLQKPGQSPQLLIYLGSNRASGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQ TPPITFGCGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWV RQAPGKMEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTAYLQMNKLKTEDTAV YYCVRAGNFGSSYISYFAYWGQGTILVTVSSGGGSGGGGSGGGGSGTQVVTQEPSTLVS PGGTVTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGG KAALTLSGVQPEDEAEYYCVLYSNRWVFGSGTKLTVLGGGDKHTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEE QYGYSTYRCVSVLTVLHQLDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLTP PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKL TVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGKGGGSGGGGSGGGGSGGGGSG GGGSGGGGSGDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH DPEVKFNWYVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQLDNLNGKEYCKVSNKA LPAPIEKTISKAKGQPREPQVYTLTPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG

			QPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHAEALHNHYTQKSLSL SPGK
2109	CD123 24- B4-f NK CC x I2M x scFc - Full Sequence	artificial	EVQLLESGLLVQPGGSLRLSCAASGFTFSHYAMSWVRQAPGKCLEWVSAVSGGGDKT LYADAVKGRFTISRDNKNTLFLQMNSLRAEDTAIYYCARLRGFFYYGMDVWGQGTITVT VSSGGGSGGGGSGGGGSDIVLTQSPLSLPVTPEGPASISCRSSQSLHNSKYNLYLDW YLQKPGQSPQLLIYLGSNRASGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQ TPPITFGCGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWW RQAPGKGMWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNNLKTEDTAV YYCVRAGNFGTSYISYWAYWGQGTITVTVSSGGGSGGGGSGGGGSGTQVVTQEPSTLVS PGGTVTITCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAPGTPARFSGSLSGG KAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMIISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEE QYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLTP PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKL TVDKSRWQQGNVFSCSVMHAEALHNHYTQKSLSLSPGKGGGSGGGGSGGGGSGGGGSG GGGSGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIISRTPEVTCVVVDVSH DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLTPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHAEALHNHYTQKSLSL SPGK
2110	CD123 24- B4-f NK CC x I2M2 x scFc - Full Sequence	artificial	EVQLLESGLLVQPGGSLRLSCAASGFTFSHYAMSWVRQAPGKCLEWVSAVSGGGDKT LYADAVKGRFTISRDNKNTLFLQMNSLRAEDTAIYYCARLRGFFYYGMDVWGQGTITVT VSSGGGSGGGGSGGGGSDIVLTQSPLSLPVTPEGPASISCRSSQSLHNSKYNLYLDW YLQKPGQSPQLLIYLGSNRASGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQ TPPITFGCGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWV REAPGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTAYLQMNNLKTEDTAV YYCVRNANFGTSYISYFAYWGQGTITVTVSSGGGSGGGGSGGGGSGTQVVTQEPSTLVS PGGTVTITCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAPGTPARFSGSLSGG KAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMIISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEE QYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLTP PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKL TVDKSRWQQGNVFSCSVMHAEALHNHYTQKSLSLSPGKGGGSGGGGSGGGGSGGGGSG GGGSGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIISRTPEVTCVVVDVSH DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLTPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHAEALHNHYTQKSLSL SPGK
2111	CD19 97- G1RE-C2 LH CC - HCDR1	artificial	SYGMH
2112	CD19 97- G1RE-C2 LH CC - HCDR2	artificial	VISYEGSNKYAESVKG
2113	CD19 97- G1RE-C2 LH CC - HCDR3	artificial	DRGTIFGNYGLEV
2114	CD19 97- G1RE-C2 LH CC - LCDR1	artificial	RSSQSLHKNFNYLD
2115	CD19 97- G1RE-C2 LH CC - LCDR2	artificial	LGSNRAS
2116	CD19 97- G1RE-C2 LH CC - LCDR3	artificial	MQALQTPFT
2117	CD19 97- G1RE-C2 LH CC - VH	artificial	QVQLVESGGGVVQPGGSLRLSCAASGFTFSYGMHWVRQAPGKCLEWVAVISYEGSNK YYAESVKGRTISRDNKNTLYLQMNSLRDEDTAVYYCARDRTIFGNYGLEVWGQGT TVTVSS
2118	CD19 97- G1RE-C2 LH CC - VL	artificial	DIVMTQSPLSLPVISGEPASISCRSSQSLHKNFNYLDWYLQKPGQSPQLLIYLGSN RASGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPFTFGCGTKVDIK
2119	CD19 97- G1RE-C2 LH CC EI GQ - VL	artificial	EIVMTQSPLSLPVISGEPASISCRSSQSLHKNFNYLDWYLQKPGQSPQLLIYLGSN RASGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPFTFGCGTKVDIK
2120	CD19 97- G1RE-C2 LH CC x I2C x scFc - Full Sequence	artificial	DIVMTQSPLSLPVISGEPASISCRSSQSLHKNFNYLDWYLQKPGQSPQLLIYLGSN RASGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPFTFGCGTKVDIKGGG SGGGSGGGGSGVQLVESGGGVVQPGGSLRLSCAASGFTFSYGMHWVRQAPGKCLEW VAVISYEGSNKYAESVKGRTISRDNKNTLYLQMNSLRDEDTAVYYCARDRTIFG NYGLEVWGQGTITVTVSSGGGSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMN WVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDT AVYYCVRHGNGFNSYISYWAYWGQGTITVTVSSGGGSGGGGSGGGGSGTQVVTQEPSTL VSPGTVTLTSGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAPGTPARFSGSL GGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMIISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP EEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY

			LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYS KLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGSGGGGSGGGGSGGGG SGGGSGGGGSDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVVS HEDPEVKFNWYVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLS SLSPGK
2121	CD19 97- G1RE-C2 LH CC x I2E x scFc - Full Sequence	artificial	DIVMTQSPSLSPVVISGEPASISCRSSQSLHKNFNYLDWYLQKPGQSPQQLLIYLGSN RASGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPFTFGCGTKVDIKGGGG SGGGSGGGGSGVQVLVESGGGVVQPGRSRLRLSCAASGFTFSSYGMHWVRQAPGKCLEW VAVISYEGSNKYIAESVKGRFTISRDN SKNTLYLQMNSLRDEDTAVYYCARDRGITFG NYGLEWVGQGTITVTVSSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAIN WVRQAPGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNMLKTEDT AVYYCARAGNFGSSYISYWAYWGQGLTIVTVSSGGGSGGGGSGGGGSGTQVVTQEPESLT VSPGGTITTCGSSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAPGTPARFSGSL GGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKHTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPC EEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYS KLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGSGGGGSGGGGSGGGG SGGGSGGGGSDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVVS HEDPEVKFNWYVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLS SLSPGK
2122	CD19 97- G1RE-C2 LH CC x I2K x scFc - Full Sequence	artificial	DIVMTQSPSLSPVVISGEPASISCRSSQSLHKNFNYLDWYLQKPGQSPQQLLIYLGSN RASGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPFTFGCGTKVDIKGGGG SGGGSGGGGSGVQVLVESGGGVVQPGRSRLRLSCAASGFTFSSYGMHWVRQAPGKCLEW VAVISYEGSNKYIAESVKGRFTISRDN SKNTLYLQMNSLRDEDTAVYYCARDRGITFG NYGLEWVGQGTITVTVSSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMN WVRQAPGKGLEWVARIRSKYNNYATYYAEAVKGRFTISRDDSKNTVYLQMNMLKTEDT AVYYCVRNENIGTSYISYWAYWGQGLTIVTVSSGGGSGGGGSGGGGSGTQVVTQEPESLT VSPGGTITTCGSSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAPGTPARFSGSL GGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKHTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPC EEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYS KLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGSGGGGSGGGGSGGGG SGGGSGGGGSDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVVS HEDPEVKFNWYVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLS SLSPGK
2123	CD19 97- G1RE-C2 LH CC x I2L x scFc - Full Sequence	artificial	DIVMTQSPSLSPVVISGEPASISCRSSQSLHKNFNYLDWYLQKPGQSPQQLLIYLGSN RASGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPFTFGCGTKVDIKGGGG SGGGSGGGGSGVQVLVESGGGVVQPGRSRLRLSCAASGFTFSSYGMHWVRQAPGKCLEW VAVISYEGSNKYIAESVKGRFTISRDN SKNTLYLQMNSLRDEDTAVYYCARDRGITFG NYGLEWVGQGTITVTVSSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMN WVRQAPGKMEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNMLKTEDT AVYYCVRAGNFGSSYISYFAYWGQGLTIVTVSSGGGSGGGGSGGGGSGTQVVTQEPESLT VSPGGTITTCGSSSTGAVTSGNYPNWIQKPKGQAPRGLIGGTFKFLAPGTPARFSGSL GGKAALTLSGVQPEDEAEYYCVLYSNRWVFGSGTKLTVLGGGDKHTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPC EEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYS KLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGSGGGGSGGGGSGGGG SGGGSGGGGSDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVVS HEDPEVKFNWYVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLS SLSPGK
2124	CD19 97- G1RE-C2 LH CC x I2M x scFc - Full Sequence	artificial	DIVMTQSPSLSPVVISGEPASISCRSSQSLHKNFNYLDWYLQKPGQSPQQLLIYLGSN RASGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPFTFGCGTKVDIKGGGG SGGGSGGGGSGVQVLVESGGGVVQPGRSRLRLSCAASGFTFSSYGMHWVRQAPGKCLEW VAVISYEGSNKYIAESVKGRFTISRDN SKNTLYLQMNSLRDEDTAVYYCARDRGITFG NYGLEWVGQGTITVTVSSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMN WVRQAPGKMEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNMLKTEDT AVYYCVRAGNFGTSYISYWAYWGQGLTIVTVSSGGGSGGGGSGGGGSGTQVVTQEPESLT VSPGGTITTCGSSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAPGTPARFSGSL GGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKHTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPC EEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYS KLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGSGGGGSGGGGSGGGG SGGGSGGGGSDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVVS HEDPEVKFNWYVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLS SLSPGK

			NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSL SLSPGK
2125	CD19 97- G1RE-C2 LH CC x I2M2 x scFc - Full Sequence	artificial	DIVMTQSPSLSPVISGEPASISCRSSQSLHKNFNYLDWYLQKPGQSPQLLIYLGSN RASGVDPDRFSGSGSGTDFTLKISRVAEDVGVYCYMQLQPTFTFGCGTKVDIKGGGG SGGGSGGGGSQVQLVESGGGVVQPGRSRLSLSCAASGFTFSSYGMHWVRQAPGKCLEW VAVISYEGSNKYAESVKGRFTISRDNKNTLYLQMNSLRDEDTAVYYCARDRTGTFG NYGLEWVGQGTVTVTSSSGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAIN WVREAPGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTAYLQMNLLKTEDT AVYYCVRNANFGTSYISYFAYWGQGTTLVTVSSGGGSGGGSGGGGSQTVTQEPSTLT VSPGGTTLTTCGSSTGAVTSGNYPNWWQKPGQAPRGLIGGTFKFLAPGTPARFSGSLL GGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMI SRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAAKTKPC EEQYGSTYRCVSVLTVLHQLDNLNGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVY LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS KLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGSGGGSGGGSGGGSGG SGGGSGGGGSKTHTCPPCPAPELGGPSVFLFPPKPKDTLMI SRTPEVTCVVDVSH HEDPEVKFNWYVDGVEVHNAAKTKPC EEQYGSTYRCVSVLTVLHQLDNLNGKEYKCKVSN KALPAPI EKTISKAKGQPREPQVY LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSL SLSPGK
2126	CD20 99-E5 CC - HCDR1	artificial	SYWMH
2127	CD20 99-E5 CC - HCDR2	artificial	YITPSTGYTEYNQKFKG
2128	CD20 99-E5 CC - HCDR3	artificial	VHDYDRAMEY
2129	CD20 99-E5 CC - LCDR1	artificial	KASQDINKYIA
2130	CD20 99-E5 CC - LCDR2	artificial	YTSTLQP
2131	CD20 99-E5 CC - LCDR3	artificial	LQYASYPFT
2132	CD20 99-E5 CC - VH	artificial	QVQLVQSGAEVKKPGASVKVSCASGYTFTSYWMHWVRQAPGQCLEWIGYITPSTGYT EYNQKFKGRVTMTDRKSTSTVYMESSLTSED TAVYYCARVHDYDRAMEYWGQGT TVT VSS
2133	CD20 99-E5 CC - VL	artificial	DIQMTQSPSSLSASVGDRTITCKASQDINKYIAWYQQKPKGPKLLIYYTSTLQPGV PSRFSGSGSGTDFTFITISLQPEDIAITYYCLQYASYPFTFGCGTRLEIK
2134	CD20 99-E5 CC EI GQ - VL	artificial	EIQMTQSPSSLSASVGDRTITCKASQDINKYIAWYQQKPKGPKLLIYYTSTLQPGV PSRFSGSGSGTDFTFITISLQPEDIAITYYCLQYASYPFTFGCGTRLEIK
2135	CD20 99-E5 CC x I2C x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCASGYTFTSYWMHWVRQAPGQCLEWIGYITPSTGYT EYNQKFKGRVTMTDRKSTSTVYMESSLTSED TAVYYCARVHDYDRAMEYWGQGT TVT VSSGGGSGGGSGGGGSDIQMTQSPSSLSASVGDRTITCKASQDINKYIAWYQQKPK GKGP KLLIYYTSTLQPGVPSRFSGSGSGTDFTFITISLQPEDIAITYYCLQYASYPFTF GCGTRLEIKSGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNHWVRQAPGK GLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRH GNFGNSYISYWAYWGQGTTLVTVSSGGGSGGGSGGGGSQT VVTQEPSTLT VSPGGT VT LTCGSSTGAVTSGNYPNWWQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGGKAALT SGVQPEDEAEYYCVLWYSNRWVFGGSGTKLTVLGGGDKTHTCPPCPAPELGGPSVFL FPPKPKDTLMI SRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAAKTKPC EEQYGSTY RCVSVLTVLHQLDNLNGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVY LPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGSGGGSGGGSGGGSGGGSGGGSGG GGSDKTHTCPPCPAPELGGPSVFLFPPKPKDTLMI SRTPEVTCVVDVSHEDPEVKF NWWYVDGVEVHNAAKTKPC EEQYGSTYRCVSVLTVLHQLDNLNGKEYKCKVSNKALPAPI E KTISKAKGQPREPQVY LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
2136	CD20 99-E5 CC x I2E x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCASGYTFTSYWMHWVRQAPGQCLEWIGYITPSTGYT EYNQKFKGRVTMTDRKSTSTVYMESSLTSED TAVYYCARVHDYDRAMEYWGQGT TVT VSSGGGSGGGSGGGGSDIQMTQSPSSLSASVGDRTITCKASQDINKYIAWYQQKPK GKGP KLLIYYTSTLQPGVPSRFSGSGSGTDFTFITISLQPEDIAITYYCLQYASYPFTF GCGTRLEIKSGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINHWVRQAPGK GLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNLLKTEDTAVYYCARA GNFGSSYISYWAYWGQGTTLVTVSSGGGSGGGSGGGGSQT VVTQEPSTLT VSPGGT VT ITCGSSTGAVTSGNYPNWWQKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKAALT SGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCPPCPAPELGGPSVFL FPPKPKDTLMI SRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAAKTKPC EEQYGSTY RCVSVLTVLHQLDNLNGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVY LPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGSGGGSGGGSGGGSGGGSGGGSGG GGSDKTHTCPPCPAPELGGPSVFLFPPKPKDTLMI SRTPEVTCVVDVSHEDPEVKF NWWYVDGVEVHNAAKTKPC EEQYGSTYRCVSVLTVLHQLDNLNGKEYKCKVSNKALPAPI E KTISKAKGQPREPQVY LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
2137	CD20 99-E5 CC x I2K x scFc - Full	artificial	QVQLVQSGAEVKKPGASVKVSCASGYTFTSYWMHWVRQAPGQCLEWIGYITPSTGYT EYNQKFKGRVTMTDRKSTSTVYMESSLTSED TAVYYCARVHDYDRAMEYWGQGT TVT VSSGGGSGGGSGGGGSDIQMTQSPSSLSASVGDRTITCKASQDINKYIAWYQQKPK

	Sequence		GKGPKLLIYYTSTLQPGVPSRFSGSGSGTDFTFTISSLQPEDATYYCQYASYPFTF GCGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQAPGK GLEWVARIRSKYNNYATYYAEAVKGRFTISRDDSKNTVYLQMNLLKTEDTAVYYCVRN ENIGTSYISYWAYWQGGLTVTVSSGGGGSGGGSGGGSGTQVVTQEPSTLTVSPGGT ITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKAATL SGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKHTCPCPAPPELLGGPSVFL FPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTY RCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSQSVMEALHNNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGGGSGG GGSDKHTHTCPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKF NWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFPYSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQSVMEALHNNHYTQKSLSLSPGK
2138	CD20 99-E5 CC x I2L x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCASGYTFTSYWMHWVRQAPGQCLEWIGYITPSTGYT EYNQKFKGRVTMTDRKSTSTVYMESSLTSEDVAVYCARVHDYDRAMEYWGQGTITVT VSSGGGGSGGGSGGGSGGSDIQTQSPSSLSASVGDRTITCKASQDINKYIAWYQQKPK GKGPKLLIYYTSTLQPGVPSRFSGSGSGTDFTFTISSLQPEDATYYCQYASYPFTF GCGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQAPGK GMEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNLLKTEDTAVYYCVRN GNFGSSYISYFAYWQGGLTVTVSSGGGGSGGGSGGGSGTQVVTQEPSTLTVSPGGT ITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKAATL SGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKHTCPCPAPPELLGGPSVFL FPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTY RCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSQSVMEALHNNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGGGSGG GGSDKHTHTCPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKF NWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFPYSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQSVMEALHNNHYTQKSLSLSPGK
2139	CD20 99-E5 CC x I2M x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCASGYTFTSYWMHWVRQAPGQCLEWIGYITPSTGYT EYNQKFKGRVTMTDRKSTSTVYMESSLTSEDVAVYCARVHDYDRAMEYWGQGTITVT VSSGGGGSGGGSGGGSGGSDIQTQSPSSLSASVGDRTITCKASQDINKYIAWYQQKPK GKGPKLLIYYTSTLQPGVPSRFSGSGSGTDFTFTISSLQPEDATYYCQYASYPFTF GCGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQAPGK GMEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNLLKTEDTAVYYCVRN GNFGTSYISYFAYWQGGLTVTVSSGGGGSGGGSGGGSGTQVVTQEPSTLTVSPGGT ITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKAATL SGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKHTCPCPAPPELLGGPSVFL FPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTY RCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSQSVMEALHNNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGGGSGG GGSDKHTHTCPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKF NWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFPYSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQSVMEALHNNHYTQKSLSLSPGK
2140	CD20 99-E5 CC x I2M2 x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCASGYTFTSYWMHWVRQAPGQCLEWIGYITPSTGYT EYNQKFKGRVTMTDRKSTSTVYMESSLTSEDVAVYCARVHDYDRAMEYWGQGTITVT VSSGGGGSGGGSGGGSGGSDIQTQSPSSLSASVGDRTITCKASQDINKYIAWYQQKPK GKGPKLLIYYTSTLQPGVPSRFSGSGSGTDFTFTISSLQPEDATYYCQYASYPFTF GCGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGK GLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRN ANFGTSYISYFAYWQGGLTVTVSSGGGGSGGGSGGGSGTQVVTQEPSTLTVSPGGT LTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKAATL SGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKHTCPCPAPPELLGGPSVFL FPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTY RCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSQSVMEALHNNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGGGSGG GGSDKHTHTCPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKF NWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFPYSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQSVMEALHNNHYTQKSLSLSPGK
2141	CD22 28- B7N65S CC - HCDR1	artificial	SYGIS
2142	CD22 28- B7N65S CC - HCDR2	artificial	WISAYSGNAIYAQKLQG
2143	CD22 28- B7N65S CC - HCDR3	artificial	DPDYYGSGSYSDY
2144	CD22 28- B7N65S CC - LCDR1	artificial	RASQSVSSNLA

2145	CD22 28-B7N65S CC - LCDR2	artificial	GASSRAT
2146	CD22 28-B7N65S CC - LCDR3	artificial	QQYHSWPLLT
2147	CD22 28-B7N65S CC - VH	artificial	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQCLEWMGWISAYSAGNA IYAQKLQGRVTMTRDTSTSTAYMELRSLRSDDTAVYYCARDPDYYGSGSYSDYWGQGT LVTVSS
2148	CD22 28-B7N65S CC - VL	artificial	EIVLTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASSRATGI PARFSGSGSGTEFTLTITSSIQSEDAVYYCQQYHSWPLLTFCGCGTKVEIK
2149	CD22 28-B7 N65S CC x I2C x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQCLEWMGWISAYSAGNA IYAQKLQGRVTMTRDTSTSTAYMELRSLRSDDTAVYYCARDPDYYGSGSYSDYWGQGT LVTVSSGGGGSGGGSGGGGSEIVLTQSPATLSVSPGERATLSCRASQSVSSNLAWYQ QKPGQAPRLLIYGASSRATGI PARFSGSGSGTEFTLTITSSIQSEDAVYYCQQYHSWP LLTFCGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYY CVRHGNFNGNSYISYWAYWGQGT LVTVSSGGGGSGGGSGGGGSGTQVVTQEPSTLTVSPG GTVTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKA ALTLTSGVQPEDEAEYCYVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPPELLGGP SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQY GSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTV DKSRWQQGNVFSCSVMEALHNNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGGG GSGGGGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNNHYTQKSLSLSP GK
2150	CD22 28-B7 N65S CC x I2E x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQCLEWMGWISAYSAGNA IYAQKLQGRVTMTRDTSTSTAYMELRSLRSDDTAVYYCARDPDYYGSGSYSDYWGQGT LVTVSSGGGGSGGGSGGGGSEIVLTQSPATLSVSPGERATLSCRASQSVSSNLAWYQ QKPGQAPRLLIYGASSRATGI PARFSGSGSGTEFTLTITSSIQSEDAVYYCQQYHSWP LLTFCGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQ APGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNNLKTEDTAVYY CARAGNFGSSYISYWAYWGQGT LVTVSSGGGGSGGGSGGGGSGTQVVTQEPSTLTVSPG GTVTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKA ALTLTSGVQPEDEAEYCYVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPPELLGGP SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQY GSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTV DKSRWQQGNVFSCSVMEALHNNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGGG GSGGGGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNNHYTQKSLSLSP GK
2151	CD22 28-B7 N65S CC x I2K x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQCLEWMGWISAYSAGNA IYAQKLQGRVTMTRDTSTSTAYMELRSLRSDDTAVYYCARDPDYYGSGSYSDYWGQGT LVTVSSGGGGSGGGSGGGGSEIVLTQSPATLSVSPGERATLSCRASQSVSSNLAWYQ QKPGQAPRLLIYGASSRATGI PARFSGSGSGTEFTLTITSSIQSEDAVYYCQQYHSWP LLTFCGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQ APGKGLEWVARIRSKYNNYATYYAEAVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYY CVRNNENIGTSYISYWAYWGQGT LVTVSSGGGGSGGGSGGGGSGTQVVTQEPSTLTVSPG GTVTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKA ALTLTSGVQPEDEAEYCYVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPPELLGGP SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQY GSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTV DKSRWQQGNVFSCSVMEALHNNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGGG GSGGGGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNNHYTQKSLSLSP GK
2152	CD22 28-B7 N65S CC x I2L x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQCLEWMGWISAYSAGNA IYAQKLQGRVTMTRDTSTSTAYMELRSLRSDDTAVYYCARDPDYYGSGSYSDYWGQGT LVTVSSGGGGSGGGSGGGGSEIVLTQSPATLSVSPGERATLSCRASQSVSSNLAWYQ QKPGQAPRLLIYGASSRATGI PARFSGSGSGTEFTLTITSSIQSEDAVYYCQQYHSWP LLTFCGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQ APGKMEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNNLKTEDTAVYY CVRAGNFGSSYISYFAYWGQGT LVTVSSGGGGSGGGSGGGGSGTQVVTQEPSTLTVSPG GTVTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKA ALTLTSGVQPEDEAEYCYVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPPELLGGP SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQY GSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTV DKSRWQQGNVFSCSVMEALHNNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGGG GSGGGGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNNHYTQKSLSLSP GK

			REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSGGSFFLYSKLTV DKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGG GSGGGGSDKTHTCP PCAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTPPVLDSGGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSP GK
2153	CD22 28-B7 N65S CC x I2M x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCKASGYTFSTSYGISWVRQAPGQCLEWMGWISAYSGNA IYAQKLQGRVTMTTRDTSSTAYMELRSLRSDDTAVVYCARDPDYVYSGSYSDYWGGQT LVTVSSGGGGSGGGSGGGGSEIVLTQSPATLSVSPGERATLSCRASQSVSSNLAWEYQ QKPGQAPRLLIYGASSRATGIPARFSGSGSGTEFTLTITSSLSQSEDFAVYYCQQYHWP LLTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQ APGKMEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNKLKTEDTAVVY CVRAGNFGTSYISYWAYWGQTLVTVSSGGGGSGGGSGGGGSGTQVTVQEPSTLTVSPG GTVTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKA ALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCP PCAPELLGGP SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQY GSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSGGSFFLYSKLTV DKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGG GSGGGGSDKTHTCP PCAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTPPVLDSGGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSP GK
2154	CD22 28-B7 N65S CC x I2M2 x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCKASGYTFSTSYGISWVRQAPGQCLEWMGWISAYSGNA IYAQKLQGRVTMTTRDTSSTAYMELRSLRSDDTAVVYCARDPDYVYSGSYSDYWGGQT LVTVSSGGGGSGGGSGGGGSEIVLTQSPATLSVSPGERATLSCRASQSVSSNLAWEYQ QKPGQAPRLLIYGASSRATGIPARFSGSGSGTEFTLTITSSLSQSEDFAVYYCQQYHWP LLTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRE APGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTAYLQMNKLKTEDTAVVY CVRNANFGTSYISYFAYWGQTLVTVSSGGGGSGGGSGGGGSGTQVTVQEPSTLTVSPG GTVTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKA ALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCP PCAPELLGGP SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQY GSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSGGSFFLYSKLTV DKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGG GSGGGGSDKTHTCP PCAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTPPVLDSGGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSP GK
2155	CD33 E11 - HCDR1	artificial	NYGMN
2156	CD33 E11 - HCDR2	artificial	WINTYTGEPTYADKFQG
2157	CD33 E11 - HCDR3	artificial	WSWSGDGYVYFDY
2158	CD33 E11 - LCDR1	artificial	KSSQSVLDSSTNKNLSA
2159	CD33 E11 - LCDR2	artificial	WASTRES
2160	CD33 E11 - LCDR3	artificial	QQSAHFPIIT
2161	CD33 E11 - VH	artificial	QVQLVQSGAEVKKPGESVKVSCKASGYFTFTNYGMNWKVQAPGQGLEWMGWINTYTGE TYADKFQGRVTMTTDTSTSTAYMEIRNLGGDDTAVVYCARWSWSGDYVYFDYWGQGT SVTVSS
2162	CD33 E11 - VL	artificial	DIVMTQSPDSLTVSLGERTTINCKSSQSVLDSSTNKNLSLAWYQQKPGQPPKLLLSWAS TRESGIPDRFSGSGSGTDFTLTIDSPQPEDSATYYCQQSAHFPIITFGQGTREIK
2163	CD33 E11 CC - VH	artificial	QVQLVQSGAEVKKPGESVKVSCKASGYFTFTNYGMNWKVQAPGQGLEWMGWINTYTGE TYADKFQGRVTMTTDTSTSTAYMEIRNLGGDDTAVVYCARWSWSGDYVYFDYWGQGT SVTVSS
2164	CD33 E11 CC - VL	artificial	DIVMTQSPDSLTVSLGERTTINCKSSQSVLDSSTNKNLSLAWYQQKPGQPPKLLLSWAS TRESGIPDRFSGSGSGTDFTLTIDSPQPEDSATYYCQQSAHFPIITFGQGTREIK
2165	CD33 E11 CC EI GQ - VL	artificial	EIVMTQSPDSLTVSLGERTTINCKSSQSVLDSSTNKNLSLAWYQQKPGQPPKLLLSWAS TRESGIPDRFSGSGSGTDFTLTIDSPQPEDSATYYCQQSAHFPIITFGQGTREIK
2166	CD33 E11 EI GQ - VL	artificial	EIVMTQSPDSLTVSLGERTTINCKSSQSVLDSSTNKNLSLAWYQQKPGQPPKLLLSWAS TRESGIPDRFSGSGSGTDFTLTIDSPQPEDSATYYCQQSAHFPIITFGQGTREIK
2167	E11 x I2C - Full Sequence	artificial	QVQLVQSGAEVKKPGESVKVSCKASGYFTFTNYGMNWKVQAPGQGLEWMGWINTYTGE TYADKFQGRVTMTTDTSTSTAYMEIRNLGGDDTAVVYCARWSWSGDYVYFDYWGQGT SVTVSSGGGGSGGGSGGGGSDIVMTQSPDSLTVSLGERTTINCKSSQSVLDSSTNKN SLAWYQQKPGQPPKLLLSWASTRESGIPDRFSGSGSGTDFTLTIDSPQPEDSATYYCQ QSAHFPIITFGQGTREIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAM NWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNKLKTED TAVVYCVRHGNFGNSYISYWAYWGQTLVTVSSGGGGSGGGSGGGGSGTQVTVQEPST LTVSPGGTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSL

			LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
2168	E11 x I2E - Full Sequence	artificial	QVQLVQSGAEVKKPGESVKVSCASGYTFTNYGMNWKQAPGQGLEWMGWINTYTGEP TYADKFQGRVTMTTDTSTSTAYMEIRNLGGDDTAVYYCARWSWSDGYVYFDYWGGQT SVTVSSGGGGSGGGSGGGGSDIVMTQSPDLSLTVSLGERTTINCKSSQSVLDSSTNKN SLAWYQQKPGQPPKLLLSWASTRESGIPDRFSGSGSGTDFTLTIDSPQPEDSATYYCQ QSAHFPITFGQGRLEIKSGGGGSEVQLVSESGGGLVQPGGSLKLSCAASGFTFNKYAI NWVRQAPGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNKLKTED TAVYYCARAGNFGSSYISYWAYWGQGTTLTVSSGGGGSGGGSGGGGSGTVVTVQEP SLTVSPGGTVTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKLAPGTPARFSGSL SGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
2169	E11 x I2K - Full Sequence	artificial	QVQLVQSGAEVKKPGESVKVSCASGYTFTNYGMNWKQAPGQGLEWMGWINTYTGEP TYADKFQGRVTMTTDTSTSTAYMEIRNLGGDDTAVYYCARWSWSDGYVYFDYWGGQT SVTVSSGGGGSGGGSGGGGSDIVMTQSPDLSLTVSLGERTTINCKSSQSVLDSSTNKN SLAWYQQKPGQPPKLLLSWASTRESGIPDRFSGSGSGTDFTLTIDSPQPEDSATYYCQ QSAHFPITFGQGRLEIKSGGGGSEVQLVSESGGGLVQPGGSLKLSCAASGFTFNKYAM NWVRQAPGKGLEWVARIRSKYNNYATYYAEAVKGRFTISRDDSKNTVYLQMNKLKTED TAVYYCVRNENIGTSYISYWAYWGQGTTLTVSSGGGGSGGGSGGGGSGTVVTVQEP SLTVSPGGTVTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKLAPGTPARFSGSL SGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
2170	E11 x I2L - Full Sequence	artificial	QVQLVQSGAEVKKPGESVKVSCASGYTFTNYGMNWKQAPGQGLEWMGWINTYTGEP TYADKFQGRVTMTTDTSTSTAYMEIRNLGGDDTAVYYCARWSWSDGYVYFDYWGGQT SVTVSSGGGGSGGGSGGGGSDIVMTQSPDLSLTVSLGERTTINCKSSQSVLDSSTNKN SLAWYQQKPGQPPKLLLSWASTRESGIPDRFSGSGSGTDFTLTIDSPQPEDSATYYCQ QSAHFPITFGQGRLEIKSGGGGSEVQLVSESGGGLVQPGGSLKLSCAASGFTFNKYAM NWVRQAPGKMEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNKLKTED TAVYYCVRAGNFGSSYISYFAYWGQGTTLTVSSGGGGSGGGSGGGGSGTVVTVQEP SLTVSPGGTVTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKLAPGTPARFSGSL EGGKAALTLSGVQPEDEAEYYCVLYSNRWVFGSGTKLTVL
2171	E11 x I2M - Full Sequence	artificial	QVQLVQSGAEVKKPGESVKVSCASGYTFTNYGMNWKQAPGQGLEWMGWINTYTGEP TYADKFQGRVTMTTDTSTSTAYMEIRNLGGDDTAVYYCARWSWSDGYVYFDYWGGQT SVTVSSGGGGSGGGSGGGGSDIVMTQSPDLSLTVSLGERTTINCKSSQSVLDSSTNKN SLAWYQQKPGQPPKLLLSWASTRESGIPDRFSGSGSGTDFTLTIDSPQPEDSATYYCQ QSAHFPITFGQGRLEIKSGGGGSEVQLVSESGGGLVQPGGSLKLSCAASGFTFNKYAM NWVRQAPGKMEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNKLKTED TAVYYCVRAGNFGTSYISYWAYWGQGTTLTVSSGGGGSGGGSGGGGSGTVVTVQEP SLTVSPGGTVTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKLAPGTPARFSGSL SGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
2172	E11 x I2M2 - Full Sequence	artificial	QVQLVQSGAEVKKPGESVKVSCASGYTFTNYGMNWKQAPGQGLEWMGWINTYTGEP TYADKFQGRVTMTTDTSTSTAYMEIRNLGGDDTAVYYCARWSWSDGYVYFDYWGGQT SVTVSSGGGGSGGGSGGGGSDIVMTQSPDLSLTVSLGERTTINCKSSQSVLDSSTNKN SLAWYQQKPGQPPKLLLSWASTRESGIPDRFSGSGSGTDFTLTIDSPQPEDSATYYCQ QSAHFPITFGQGRLEIKSGGGGSEVQLVSESGGGLVQPGGSLKLSCAASGFTFNKYAI NWVREAPGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNKLKTED TAVYYCVRNANFGTSYISYFAYWGQGTTLTVSSGGGGSGGGSGGGGSGTVVTVQEP SLTVSPGGTVTLTTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
2173	CD33 E11 CC x I2C x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGESVKVSCASGYTFTNYGMNWKQAPGQGLEWMGWINTYTGEP TYADKFQGRVTMTTDTSTSTAYMEIRNLGGDDTAVYYCARWSWSDGYVYFDYWGGQT SVTVSSGGGGSGGGSGGGGSDIVMTQSPDLSLTVSLGERTTINCKSSQSVLDSSTNKN SLAWYQQKPGQPPKLLLSWASTRESGIPDRFSGSGSGTDFTLTIDSPQPEDSATYYCQ QSAHFPITFGCGTRLEIKSGGGGSEVQLVSESGGGLVQPGGSLKLSCAASGFTFNKYAM NWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNKLKTED TAVYYCVRHGNFGNSYISYWAYWGQGTTLTVSSGGGGSGGGSGGGGSGTVVTVQEP SLTVSPGGTVTLTTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPAPE LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP CEEQYGSTYRCVSVTLVLHQLDNLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPDSIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGKGGGSGGGSGGGSGGGG SGGGGGSGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV SHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVTLVLHQLDNLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPDSIAVEWE SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKS LSLSPGK
2174	CD33 E11 CC x I2E x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGESVKVSCASGYTFTNYGMNWKQAPGQGLEWMGWINTYTGEP TYADKFQGRVTMTTDTSTSTAYMEIRNLGGDDTAVYYCARWSWSDGYVYFDYWGGQT SVTVSSGGGGSGGGSGGGGSDIVMTQSPDLSLTVSLGERTTINCKSSQSVLDSSTNKN SLAWYQQKPGQPPKLLLSWASTRESGIPDRFSGSGSGTDFTLTIDSPQPEDSATYYCQ QSAHFPITFGCGTRLEIKSGGGGSEVQLVSESGGGLVQPGGSLKLSCAASGFTFNKYAI NWVRQAPGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNKLKTED TAVYYCARAGNFGSSYISYWAYWGQGTTLTVSSGGGGSGGGSGGGGSGTVVTVQEP SLTVSPGGTVTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKLAPGTPARFSGSL SGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPE LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP CEEQYGSTYRCVSVTLVLHQLDNLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPDSIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGKGGGSGGGSGGGSGGGG

			GSGGGGSGGGGSDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDV SHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKV NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVSCSMHEALHNNHYTQKS LSLSPGK
2175	CD33 E11 CC x I2K x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGESVKVSKASGYFTFTNYGMNWKQAPGQCLEWMGWINTYTGE TYADKFQGRVTMTTDTSTSTAYMEIRNLGGDDTAVYYCARWSWSDGYVYFDYWGQGT SVTVSSGGGGSGGGSGGGGSDIVMTQSPDLSLTSLGERTTINCKSSQSVLDSSTNKN SLAWYQQKPGQPPKLLLSWASTRESGIPDRFSGSGSGTDFTLTIDSPQPEDSATYYCQ QSAHFPITFGCGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAM NWVRQAPGKGLEWVARIRSKYNNYATYYAEAVKGRFTISRDDSKNTLYLQMNNLKTED TAVYYCVRNENIGTSYISYWAYWGQGTSLTVSSGGGGSGGGSGGGGSGTQVVTQEP TVSPGGTVTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSL SGGKAALTLSGVQPEDEAEYCVLWYSNRWVFGSGTKLTVLGGGGDKHTHTCPPCPAPE LLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKP CEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVSCSMHEALHNNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGG GSGGGGSGGGGSDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDV SHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKV NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVSCSMHEALHNNHYTQKS LSLSPGK
2176	CD33 E11 CC x I2L x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGESVKVSKASGYFTFTNYGMNWKQAPGQCLEWMGWINTYTGE TYADKFQGRVTMTTDTSTSTAYMEIRNLGGDDTAVYYCARWSWSDGYVYFDYWGQGT SVTVSSGGGGSGGGSGGGGSDIVMTQSPDLSLTSLGERTTINCKSSQSVLDSSTNKN SLAWYQQKPGQPPKLLLSWASTRESGIPDRFSGSGSGTDFTLTIDSPQPEDSATYYCQ QSAHFPITFGCGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAM NWVRQAPGKMEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNNLKTED TAVYYCVRAGNFGTSYISYFAYWGQGTSLTVSSGGGGSGGGSGGGGSGTQVVTQEP TVSPGGTVTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSL EGGKAALTLSGVQPEDEAEYCVLYSNRWVFGSGTKLTVLGGGGDKHTHTCPPCPAPE LLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKP CEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVSCSMHEALHNNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGG GSGGGGSGGGGSDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDV SHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKV NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVSCSMHEALHNNHYTQKS LSLSPGK
2177	CD33 E11 CC x I2M x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGESVKVSKASGYFTFTNYGMNWKQAPGQCLEWMGWINTYTGE TYADKFQGRVTMTTDTSTSTAYMEIRNLGGDDTAVYYCARWSWSDGYVYFDYWGQGT SVTVSSGGGGSGGGSGGGGSDIVMTQSPDLSLTSLGERTTINCKSSQSVLDSSTNKN SLAWYQQKPGQPPKLLLSWASTRESGIPDRFSGSGSGTDFTLTIDSPQPEDSATYYCQ QSAHFPITFGCGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAM NWVRQAPGKMEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNNLKTED TAVYYCVRAGNFGTSYISYFAYWGQGTSLTVSSGGGGSGGGSGGGGSGTQVVTQEP TVSPGGTVTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSL SGGKAALTLSGVQPEDEAEYCVLWYSNRWVFGSGTKLTVLGGGGDKHTHTCPPCPAPE LLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKP CEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVSCSMHEALHNNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGG GSGGGGSGGGGSDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDV SHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKV NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVSCSMHEALHNNHYTQKS LSLSPGK
2178	CD33 E11 CC x I2M2 x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGESVKVSKASGYFTFTNYGMNWKQAPGQCLEWMGWINTYTGE TYADKFQGRVTMTTDTSTSTAYMEIRNLGGDDTAVYYCARWSWSDGYVYFDYWGQGT SVTVSSGGGGSGGGSGGGGSDIVMTQSPDLSLTSLGERTTINCKSSQSVLDSSTNKN SLAWYQQKPGQPPKLLLSWASTRESGIPDRFSGSGSGTDFTLTIDSPQPEDSATYYCQ QSAHFPITFGCGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAI NWVREAPGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTAYLQMNNLKTED TAVYYCVRNANFGTSYISYFAYWGQGTSLTVSSGGGGSGGGSGGGGSGTQVVTQEP TVSPGGTVTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYCVLWYSNRWVFGSGTKLTVLGGGGDKHTHTCPPCPAPE LLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKP CEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVSCSMHEALHNNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGG GSGGGGSGGGGSDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDV SHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKV NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVSCSMHEALHNNHYTQKS LSLSPGK

2179	CD70 1 C7D CC - HCDR1	artificial	TYAMS
2180	CD70 1 C7D CC - HCDR2	artificial	AISGSGGRTFYAESVEG
2181	CD70 1 C7D CC - HCDR3	artificial	HDYSNYPYFDY
2182	CD70 1 C7D CC - LCDR1	artificial	RASQSVRSTYLA
2183	CD70 1 C7D CC - LCDR2	artificial	GASSRAT
2184	CD70 1 C7D CC - LCDR3	artificial	QQYGDLPFT
2185	CD70 1 C7D CC - VH	artificial	EVQLLESGGGMVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKCLEWWSAISGSGGRTFYAESVEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGLTVTVSS
2186	CD70 1 C7D CC - VL	artificial	EIVLTQSPGTLTSLSPGERATLSCRASQSVRSTYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYSCQQYGDLPFTFGCGTKLEIK
2187	CD70 1 C7D CC x I2C x scFc - Full Sequence	artificial	EVQLLESGGGMVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKCLEWWSAISGSGGRTFYAESVEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGLTVTVSSGGGGSGGGSGGGSGGGSEIVLTQSPGTLTSLSPGERATLSCRASQSVRSTYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYSCQQYGDLPFTFGCGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGGSGGGSGGGSGGGSQT VVTQEP SLTVSPGGT VTLTCSGSTGAVTSGNYPNWVQKPGQAPRGLIGGT KFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGSKLTVLGGGDKHTHTCPPCPAPELLGGPSVFLFPPPKP KDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGS TYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPPVLDS DGSFFLYSKLTVDKSRWQQGNV FSCSVMH EALHNHYTQKSLSLSPGKGGGSKDKHTHTCPPCPAPELLGGPSVFLFPPPKP KDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGS TYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPPVLDS DGSFFLYSKLTVDKSRWQQGNV FSCSVMH EALHNHYTQKSLSLSPGK
2188	CD70 1 C7D CC x I2E x scFc - Full Sequence	artificial	EVQLLESGGGMVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKCLEWWSAISGSGGRTFYAESVEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGLTVTVSSGGGGSGGGSGGGSGGGSEIVLTQSPGTLTSLSPGERATLSCRASQSVRSTYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYSCQQYGDLPFTFGCGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVY LQMN NLKTEDTAVYYCARAGNFGSSYISYWAYWGQGLTVTVSSGGGGSGGGSGGGSGGGSQT VVTQEP SLTVSPGGT VTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGT KFLAPGTPARFSGSLSGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKHTHTCPPCPAPELLGGPSVFLFPPPKP KDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGS TYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPPVLDS DGSFFLYSKLTVDKSRWQQGNV FSCSVMH EALHNHYTQKSLSLSPGKGGGSKDKHTHTCPPCPAPELLGGPSVFLFPPPKP KDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGS TYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPPVLDS DGSFFLYSKLTVDKSRWQQGNV FSCSVMH EALHNHYTQKSLSLSPGK
2189	CD70 1 C7D CC x I2K x scFc - Full Sequence	artificial	EVQLLESGGGMVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKCLEWWSAISGSGGRTFYAESVEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGLTVTVSSGGGGSGGGSGGGSGGGSEIVLTQSPGTLTSLSPGERATLSCRASQSVRSTYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYSCQQYGDLPFTFGCGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYAEAVKGRFTISRDDSKNTVY LQMN NLKTEDTAVYYCVRNENIGTSYISYWAYWGQGLTVTVSSGGGGSGGGSGGGSGGGSQT VVTQEP SLTVSPGGT VTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGT KFLAPGTPARFSGSLSGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKHTHTCPPCPAPELLGGPSVFLFPPPKP KDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGS TYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPPVLDS DGSFFLYSKLTVDKSRWQQGNV FSCSVMH EALHNHYTQKSLSLSPGKGGGSKDKHTHTCPPCPAPELLGGPSVFLFPPPKP KDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGS TYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPPVLDS DGSFFLYSKLTVDKSRWQQGNV FSCSVMH EALHNHYTQKSLSLSPGK
2190	CD70 1 C7D CC x I2L x scFc - Full Sequence	artificial	EVQLLESGGGMVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKCLEWWSAISGSGGRTFYAESVEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGLTVTVSSGGGGSGGGSGGGSGGGSEIVLTQSPGTLTSLSPGERATLSCRASQSVRSTYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYSCQQYGDLPFTFGCGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGMEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLY LQMN NLKTEDTAVYYCVRAGNFGSSYISYFAYWGQGLTVTVSSGGGGSGGGSGGGSGGGSQT VVTQEP SLTVSPGGT VTITCGSSTGAVTSGNYPNWIQKPGQAPRGLIGGT KFLAPGTPARFSGSLGEGKKAALTLSGVQPEDEAEYYCVLYYSNRWVFGSGTKLTVLGGGDKHTHTCPPCPAPELLGGPSVFLFPPPKP KDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGS TYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPPVLDS DGSFFLYSKLTVDKSRWQQGNV FSCSVMH EALHNHYTQKSLSLSPGK

			FLFPPPKPDKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGS TYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVVFSCVMHEALHNHYTQKSLSLSPGKGGGSGGGSGGGSGGGSGGGSGGG GGGSGDKTHTCPCPAPPELLGGPSVFLFPPPKPDKDTLMI SRTPEVTCVVVDVSHEDPEV KENWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAP IEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVVFSCVMHEALHNHYTQKSLSLSPGK
2191	CD70 1 C7D CC x I2M x scFc - Full Sequence	artificial	EVQLLESGGGMVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKCLEWVSATISGSGGRT FYAESVEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTILV TVSSGGGGSGGGSGGGSGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVRSTYLAWYQQ KPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYSCQQYGDLPF TFGCGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGTFNFKYAINNWREAP GKGMEWVARIRSKYNNYATYYADAVKDRFTISRDDS KNTLYLQMNNLKTEDTAVYYCV RAGNFGTSYISYWAYWGQGTILVTVSSGGGGSGGGSGGGSGGGSGQTVVTQEPSLTVSPGGT VTITCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTKFLAPGTPARFSGSLSGGKAAL TLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPCPAPPELLGGPSV FLFPPPKPDKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGS TYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVVFSCVMHEALHNHYTQKSLSLSPGKGGGSGGGSGGGSGGGSGGGSGGGSG GGGSGDKTHTCPCPAPPELLGGPSVFLFPPPKPDKDTLMI SRTPEVTCVVVDVSHEDPEV KENWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAP IEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVVFSCVMHEALHNHYTQKSLSLSPGK
2192	CD70 1 C7D CC x I2M2 x scFc - Full Sequence	artificial	EVQLLESGGGMVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKCLEWVSATISGSGGRT FYAESVEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTILV TVSSGGGGSGGGSGGGSGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVRSTYLAWYQQ KPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYSCQQYGDLPF TFGCGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGTFNFKYAINNWREAP GKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCV RMANFGTSYISYFAYWGQGTILVTVSSGGGGSGGGSGGGSGGGSGQTVVTQEPSLTVSPGGT VTLTCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTKFLAPGTPARFSGSLGGKAAL TLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPCPAPPELLGGPSV FLFPPPKPDKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGS TYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVVFSCVMHEALHNHYTQKSLSLSPGKGGGSGGGSGGGSGGGSGGGSGGGSG GGGSGDKTHTCPCPAPPELLGGPSVFLFPPPKPDKDTLMI SRTPEVTCVVVDVSHEDPEV KENWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAP IEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVVFSCVMHEALHNHYTQKSLSLSPGK
2193	CH19 2G6.007 CC - HCDR1	artificial	SYGMH
2194	CH19 2G6.007 CC - HCDR2	artificial	FIWYEGSNKYAAESVKD
2195	CH19 2G6.007 CC - HCDR3	artificial	RAGIIGTIGYYYGMDV
2196	CH19 2G6.007 CC - LCDR1	artificial	SGDRLGEKYTS
2197	CH19 2G6.007 CC - LCDR2	artificial	QDTKRPS
2198	CH19 2G6.007 CC - LCDR3	artificial	QAWESSTVV
2199	CH19 2G6.007 CC - VH	artificial	QVQLVESGGGVVQPGGSLRLSCAASGFTSSYGMHWVRQAPGKCLEWVAFIWIYEGSNK YYAESVKDRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWG QGTTVTVSS
2200	CH19 2G6.007 CC - VL	artificial	SYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPQGSPLLVIYQDTKRPSGIP ERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFSGCGTKLTVL
2201	CH19 2G6.007 CCx I2C x scFc - Full Sequence	artificial	QVQLVESGGGVVQPGGSLRLSCAASGFTSSYGMHWVRQAPGKCLEWVAFIWIYEGSNK YYAESVKDRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWG QGTTVTVSSGGGGSGGGSGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSW YQQRPQGSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWES STVVFSGCGTKLTVLSSGGGSEVQLVESGGGLVQPGGSLKLSCAASGTFNFKYAMNWVR QAPGKLEWVARIRSKYNNYATYYADSVKDRFTISRDDS KNTAYLQMNNLKTEDTAVY YCVRHGNFGNSYISYWAYWGQGTILVTVSSGGGGSGGGSGGGSGGGSGGGSGGGSG GGTVTTLTCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTKFLAPGTPARFSGSLGGK AALTLSGVQPEDEAEYYCVLWYSNRWVFGGTKLTVLGGGGDKTHTCPCPAPPELLGG PSVFLFPPPKPDKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQ YGSTYRCVSVLTVLHODWLNNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP

			SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQVMHEALHNNHYTQKSLSLSPGKGGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQVMHEALHNNHYTQKSLSLSPGK
2202	CH19 2G6.007 CCx I2C x scFc delGK - Full Sequence	artificial	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWRQAPGKCLEWVAFIWEYSNKKYYAESVKDRFTISRDNKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYGMDVWGQGTITVTVSSGGGGSGGGSGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPILLVIYQDTRKPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFSGCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFNGSYISYWAYWGQGTITVTVSSGGGGSGGGSGGGSSQTVVTQEPSTLVSPGGTITITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQVMHEALHNNHYTQKSLSLSPGKGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQVMHEALHNNHYTQKSLSLSPGK
2203	CH19 2G6.007 CCx I2E x scFc - Full Sequence	artificial	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWRQAPGKCLEWVAFIWEYSNKKYYAESVKDRFTISRDNKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYGMDVWGQGTITVTVSSGGGGSGGGSGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPILLVIYQDTRKPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFSGCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNNLKTEDTAVYYCARAGNFGSSYISYWAYWGQGTITVTVSSGGGGSGGGSGGGSSQTVVTQEPSTLVSPGGTITITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQVMHEALHNNHYTQKSLSLSPGKGGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQVMHEALHNNHYTQKSLSLSPGK
2204	CH19 2G6.007 CCx I2E x scFc delGK - Full Sequence	artificial	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWRQAPGKCLEWVAFIWEYSNKKYYAESVKDRFTISRDNKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYGMDVWGQGTITVTVSSGGGGSGGGSGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPILLVIYQDTRKPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFSGCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNNLKTEDTAVYYCARAGNFGSSYISYWAYWGQGTITVTVSSGGGGSGGGSGGGSSQTVVTQEPSTLVSPGGTITITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQVMHEALHNNHYTQKSLSLSPGKGGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQVMHEALHNNHYTQKSLSLSPGK
2205	CH19 2G6.007 CCx I2K x scFc - Full Sequence	artificial	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWRQAPGKCLEWVAFIWEYSNKKYYAESVKDRFTISRDNKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYGMDVWGQGTITVTVSSGGGGSGGGSGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPILLVIYQDTRKPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFSGCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYAEAVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRNENIGTSYISYWAYWGQGTITVTVSSGGGGSGGGSGGGSSQTVVTQEPSTLVSPGGTITITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQVMHEALHNNHYTQKSLSLSPGKGGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQVMHEALHNNHYTQKSLSLSPGK

			PENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
2206	CH19 2G6.007 CCx I2K x scFc delGK - Full Sequence	artificial	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWRQAPGKCLEWVAFIWYEGSNK YYAESVKDRFTISRDNKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYGMDVWG QGTITVTVSSGGGSGGGGSGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSW YQQRPGQSPILLVIYQDTRKPSGIPERFSGNSNGTATLTISGTQAMDEADYYCQAWES STVVFSGGCTKLTVLSSGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVR QAPGKGLEWVARIRSKYNNYATYYAEAVKGRFTISRDDSKNTVYLQMNNLKTEDTAVY YCVRNENIGTSYISYWAYWGQGTITVTVSSGGGSGGGGSGGGGSGTQVVTQEPSTLTVSP GGTITITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGGK AALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCPPCPAPPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQ YGSTYRCVSVLTVLHQDWLNGKEYCKKVSNAKALPAPIEKTISKAKGQPREPQVYTLPP SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGGGSGGGGSGGGGSGGGGSGGGG SGGGGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKKVSNAKALPA PIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPG K
2207	CH19 2G6.007 CCx I2L x scFc - Full Sequence	artificial	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWRQAPGKCLEWVAFIWYEGSNK YYAESVKDRFTISRDNKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYGMDVWG QGTITVTVSSGGGSGGGGSGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSW YQQRPGQSPILLVIYQDTRKPSGIPERFSGNSNGTATLTISGTQAMDEADYYCQAWES STVVFSGGCTKLTVLSSGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVR QAPGKGMWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNNLKTEDTAVY YCVRAGNFGSSYISYFAYWGQGTITVTVSSGGGSGGGGSGGGGSGTQVVTQEPSTLTVSP GGTITITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLEGGK AALTLSGVQPEDEAEYYCVLYYSNRWVFGSGTKLTVLGGGDKTHTCPPCPAPPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQ YGSTYRCVSVLTVLHQDWLNGKEYCKKVSNAKALPAPIEKTISKAKGQPREPQVYTLPP SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGSGGGGSGGGGSGGGGSGGGG GGSGGGGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKKVSNAKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPG K
2208	CH19 2G6.007 CCx I2L x scFc delGK - Full Sequence	artificial	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWRQAPGKCLEWVAFIWYEGSNK YYAESVKDRFTISRDNKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYGMDVWG QGTITVTVSSGGGSGGGGSGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSW YQQRPGQSPILLVIYQDTRKPSGIPERFSGNSNGTATLTISGTQAMDEADYYCQAWES STVVFSGGCTKLTVLSSGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVR QAPGKGMWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNNLKTEDTAVY YCVRAGNFGSSYISYFAYWGQGTITVTVSSGGGSGGGGSGGGGSGTQVVTQEPSTLTVSP GGTITITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLEGGK AALTLSGVQPEDEAEYYCVLYYSNRWVFGSGTKLTVLGGGDKTHTCPPCPAPPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQ YGSTYRCVSVLTVLHQDWLNGKEYCKKVSNAKALPAPIEKTISKAKGQPREPQVYTLPP SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGGGSGGGGSGGGGSGGGGSGGGG SGGGGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKKVSNAKALPA PIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPG K
2209	CH19 2G6.007 CCx I2M x scFc - Full Sequence	artificial	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWRQAPGKCLEWVAFIWYEGSNK YYAESVKDRFTISRDNKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYGMDVWG QGTITVTVSSGGGSGGGGSGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSW YQQRPGQSPILLVIYQDTRKPSGIPERFSGNSNGTATLTISGTQAMDEADYYCQAWES STVVFSGGCTKLTVLSSGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVR QAPGKGMWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNNLKTEDTAVY YCVRAGNFGTSYISYWAYWGQGTITVTVSSGGGSGGGGSGGGGSGTQVVTQEPSTLTVSP GGTITITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGGK AALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCPPCPAPPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQ YGSTYRCVSVLTVLHQDWLNGKEYCKKVSNAKALPAPIEKTISKAKGQPREPQVYTLPP SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGSGGGGSGGGGSGGGGSGGGG GGSGGGGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKKVSNAKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPG K
2210	CH19 2G6.007 CCx I2M x scFc	artificial	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWRQAPGKCLEWVAFIWYEGSNK YYAESVKDRFTISRDNKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYGMDVWG QGTITVTVSSGGGSGGGGSGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSW

	delGK - Full Sequence		YQQRPGQSPDLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWES STVVFSGCGTKLTVLSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVR QAPGKMEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNNLKTEDTAVY YCVNRAGNFGTSYISYWAYWQGQTLTVTVSSGGGGSGGGGSGGGGSGTQVVTQEPSTLTVSP GGTITITCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAPGTPARFSGSLSGGK AALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQ YGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLTPP SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLT VDKSRWQQGNVFSQSVMEALHNNHYTQKSLSLSPGGGGSGGGGSGGGGSGGGGSGGGG SGGGGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSQSVMEALHNNHYTQKSLSLSPG K
2211	CH19 2G6.007 CCx I2M2 x scFc - Full Sequence	artificial	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWEYSNK YYAESVKDRFTISRDNKNTLYLQMNLSRAEDTAVYYCARRAGIIGTIGYYGMDVWG QGTITVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYSW YQQRPGQSPDLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWES STVVFSGCGTKLTVLSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVR EAPGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTAYLQMNNLKTEDTAVY YCVNRANFGTSYISYFAYWQGQTLTVTVSSGGGGSGGGGSGGGGSGTQVVTQEPSTLTVSP GGTITITCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAPGTPARFSGSLSGGK AALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQ YGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLTPP SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLT VDKSRWQQGNVFSQSVMEALHNNHYTQKSLSLSPGGGGSGGGGSGGGGSGGGGSGGGG GGGGGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSQSVMEALHNNHYTQKSLSLSPG K
2212	CH19 2G6.007 CCx I2M2 x scFc delGK - Full Sequence	artificial	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWEYSNK YYAESVKDRFTISRDNKNTLYLQMNLSRAEDTAVYYCARRAGIIGTIGYYGMDVWG QGTITVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYSW YQQRPGQSPDLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWES STVVFSGCGTKLTVLSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVR EAPGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTAYLQMNNLKTEDTAVY YCVNRANFGTSYISYFAYWQGQTLTVTVSSGGGGSGGGGSGGGGSGTQVVTQEPSTLTVSP GGTITITCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAPGTPARFSGSLSGGK AALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQ YGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLTPP SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLT VDKSRWQQGNVFSQSVMEALHNNHYTQKSLSLSPGGGGSGGGGSGGGGSGGGGSGGGG SGGGGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSQSVMEALHNNHYTQKSLSLSPG K
2213	CH3 15-E11 CC - HCDR1	artificial	NYWMN
2214	CH3 15-E11 CC - HCDR2	artificial	NIAYGVKGTNYNQKFQG
2215	CH3 15-E11 CC - HCDR3	artificial	RYFYVMDY
2216	CH3 15-E11 CC - LCDR1	artificial	RASQDISNYLN
2217	CH3 15-E11 CC - LCDR2	artificial	YTSRLHS
2218	CH3 15-E11 CC - LCDR3	artificial	VQYAQFPLT
2219	CH3 15-E11 CC - VH	artificial	QVQLVQSGAEVKKPGASVKVSCKASGYTFITNYWMNWVRQAPGQCLEWMGNIAAYGVKGT NYNQKFQGRVTMTVDTSSTAYMELSLRLSDDTAVYYCATRYFYVMDYWGQGTTLTVTS S
2220	CH3 15-E11 CC - VL	artificial	DIQMTQSPSSLSASVGDRVTITCRASQDISNYLNWYQQKPKGKVPKLLIYYTSRLHSGV PSRFGSGSGTDFTLTITSSLPEDVATYYCVQYAQFPLTFGCGTKVEIK
2221	CH3 15-E11 CC EI GQ - VL	artificial	EIQMTQSPSSLSASVGDRVTITCRASQDISNYLNWYQQKPKGKVPKLLIYYTSRLHSGV PSRFGSGSGTDFTLTITSSLPEDVATYYCVQYAQFPLTFGCGTKVEIK
2222	CH3 G8A 6- B12 - HCDR1	artificial	SYPIN
2223	CH3 G8A 6- B12 - HCDR2	artificial	VIWTGGGTNYASSVKG
2224	CH3 G8A 6- B12 - HCDR3	artificial	SRGVYDFDGRGAMDY

2225	CH3 G8A 6-B12 - LCDR1	artificial	KSSQSLLYSSNQKNYFA
2226	CH3 G8A 6-B12 - LCDR2	artificial	WASTRES
2227	CH3 G8A 6-B12 - LCDR3	artificial	QQYYSYPYT
2228	CH3 G8A 6-B12 - VH	artificial	EVQLLESGGGLVQPGGSLRLSCAASGFSFSSYPINWVRQAPGKLEWVGVIWTTGGGTN YASSVKGRFTISRDNKNTVYLQMNLSLRAEDTAVYYCAKSRGVYDFDGRGAMDYWGQG TLTVSS
2229	CH3 G8A 6-B12 - VL	artificial	DIVMTQSPDLSAVSLGERATINCKSSQSLLYSSNQKNYFAWYQQKPGQPPKLLIYWAS TRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSYPYTFGQGTKEIK
2230	CH3 G8A 6-B12 EI GQ - VL	artificial	EIVMTQSPDLSAVSLGERATINCKSSQSLLYSSNQKNYFAWYQQKPGQPPKLLIYWAS TRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSYPYTFGQGTKEIK
2231	CH3 R170R CC - HCDR1	artificial	SYWMH
2232	CH3 R170R CC - HCDR2	artificial	KIDPSDDYTNYNQVKVG
2233	CH3 R170R CC - HCDR3	artificial	WDYSHFDV
2234	CH3 R170R CC - LCDR1	artificial	RASSSVSYMH
2235	CH3 R170R CC - LCDR2	artificial	GTSNLVS
2236	CH3 R170R CC - LCDR3	artificial	QQWSSYPLT
2237	CH3 R170R CC - VH	artificial	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYWMHWVRQTPGKCLEWVSKIDPSDDYT NYNQVKGRFTISIDKSKNTLYLQMNLSLRAEDTAVYYCARWDYSHFDVWGQGTITVTVS S
2238	CH3 R170R CC - VL	artificial	EIVMTQSPATLSVSPGERATLTCRASSSVSYMHWYQQKPGQAPRLLIYGTSNLSVSGVP ARFSGSGSGTEFTLTISSLQSEDFAVYYCQQWSSYPLTFGCGTKVEIK
2239	CH3 15-E11 CC x I2C x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVCSKASGYTFTNYWMNWVRQAPGQCLEWMGNIAYGVKGT NYNQKFQGRVTMTVDTSSTAYMELSRRLSDDTAVYYCATRYFYVMDYWGQGLTVTVS SGGGSGGGSGGGSGGSDIQMTQSPSSLSASVGDRTITCRASQDISNYLNWYQQKPGK VPKLLIYYSRLHSGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCVQYAFPLTFGC GTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQAPGKGL EWVARIISKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGN FGNSYISYWAYWGQGLTVTVSSGGGSGGGSGGGSGGGSGQT VVTQEP SLTVSPGGT VTLT CGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAALTLSG VQPEDEAEYYCVLWYSNRWVFGGSKLTVLGGGDKTHTCPPCPAPPELLGGPSVFLFPP PKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGGGSGGGG SDKTHTCPPCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK
2240	CH3 15-E11 CC x I2E x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVCSKASGYTFTNYWMNWVRQAPGQCLEWMGNIAYGVKGT NYNQKFQGRVTMTVDTSSTAYMELSRRLSDDTAVYYCATRYFYVMDYWGQGLTVTVS SGGGSGGGSGGGSGGSDIQMTQSPSSLSASVGDRTITCRASQDISNYLNWYQQKPGK VPKLLIYYSRLHSGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCVQYAFPLTFGC GTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGL EWVARIISKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNLLKTEDTAVYYCARAGN FGSSYISYWAYWGQGLTVTVSSGGGSGGGSGGGSGGGSGQT VVTQEP SLTVSPGGT VTLT CGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAALTLSG VQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCPPCPAPPELLGGPSVFLFPP PKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGGGSGGGG SDKTHTCPPCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK
2241	CH3 15-E11 CC x I2K x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVCSKASGYTFTNYWMNWVRQAPGQCLEWMGNIAYGVKGT NYNQKFQGRVTMTVDTSSTAYMELSRRLSDDTAVYYCATRYFYVMDYWGQGLTVTVS SGGGSGGGSGGGSGGSDIQMTQSPSSLSASVGDRTITCRASQDISNYLNWYQQKPGK VPKLLIYYSRLHSGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCVQYAFPLTFGC GTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQAPGKGL EWVARIISKYNNYATYYAEAVKGRFTISRDDSKNTVYLQMNLLKTEDTAVYYCVRNEN IGTSYISYWAYWGQGLTVTVSSGGGSGGGSGGGSGGGSGQT VVTQEP SLTVSPGGT VTLT CGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAALTLSG VQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCPPCPAPPELLGGPSVFLFPP PKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQ

[illegible]

	Sequence		NYFAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTITSSSLQAEDVAVYYC QQQYYSYPYTFGQGTLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYA INWVRQAPGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNLLKTE DTAVYYCARAGNFGSSYISYWAYWGQGTTLTVSSGGGGSGGGGSGGGGSGTQVVTQEPS LTVSPGGTVTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGS LSGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKTLTVLGGGDKTHTCPCPAP ELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK PCEEQYGSTYRCVSVTLVLHQQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL YSKLTVDKSRWQQGNVFSCVMHEALHNYTQKSLSLSPGKGGGSGGGGSGGGGSGGGG GSGGGGSGGGGSDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVTLVLHQQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNQGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCVMHEALHNYTQK SLSLSPGK
2247	CH3 G8A 6- B12 x I2K x scFc - Full Sequence	artificial	EVQLLESGGGLVQPGGSLRLSCAASGFSFSSYPINWVRQAPGKGLEWVGVIWTTGGGTN YASSVKGRFTISRDN SKNTVYLQMNSLRAEDTAVYYCAKSRGVYDFDGRGAMDYWGQG TLTVSSGGGGSGGGGSGGGGSDI VMTQSPDSLAVSLGERATINCKSSQSLLYSSNQK NYFAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTITSSSLQAEDVAVYYC QQQYYSYPYTFGQGTLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYA MNWVRQAPGKGLEWVARIRSKYNNYATYYAEAVKGRFTISRDDSKNTVYLQMNLLKTE DTAVYYCVRNENIGTSYISYWAYWGQGTTLTVSSGGGGSGGGGSGGGGSGTQVVTQEPS LTVSPGGTVTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGS LSGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKTLTVLGGGDKTHTCPCPAP ELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK PCEEQYGSTYRCVSVTLVLHQQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL YSKLTVDKSRWQQGNVFSCVMHEALHNYTQKSLSLSPGKGGGSGGGGSGGGGSGGGG GSGGGGSGGGGSDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVTLVLHQQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNQGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCVMHEALHNYTQK SLSLSPGK
2248	CH3 G8A 6- B12 x I2L x scFc - Full Sequence	artificial	EVQLLESGGGLVQPGGSLRLSCAASGFSFSSYPINWVRQAPGKGLEWVGVIWTTGGGTN YASSVKGRFTISRDN SKNTVYLQMNSLRAEDTAVYYCAKSRGVYDFDGRGAMDYWGQG TLTVSSGGGGSGGGGSGGGGSDI VMTQSPDSLAVSLGERATINCKSSQSLLYSSNQK NYFAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTITSSSLQAEDVAVYYC QQQYYSYPYTFGQGTLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYA MNWVRQAPGKGMWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNLLKTE DTAVYYCVRAGNFGSSYISYFAYWGQGTTLTVSSGGGGSGGGGSGGGGSGTQVVTQEPS LTVSPGGTVTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGS LEGGKAALTLSGVQPEDEAEYYCVLYSNRWVFGSGTKTLTVLGGGDKTHTCPCPAP ELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK PCEEQYGSTYRCVSVTLVLHQQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL YSKLTVDKSRWQQGNVFSCVMHEALHNYTQKSLSLSPGKGGGSGGGGSGGGGSGGGG GSGGGGSGGGGSDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVTLVLHQQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNQGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCVMHEALHNYTQK SLSLSPGK
2249	CH3 G8A 6- B12 x I2M x scFc - Full Sequence	artificial	EVQLLESGGGLVQPGGSLRLSCAASGFSFSSYPINWVRQAPGKGLEWVGVIWTTGGGTN YASSVKGRFTISRDN SKNTVYLQMNSLRAEDTAVYYCAKSRGVYDFDGRGAMDYWGQG TLTVSSGGGGSGGGGSGGGGSDI VMTQSPDSLAVSLGERATINCKSSQSLLYSSNQK NYFAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTITSSSLQAEDVAVYYC QQQYYSYPYTFGQGTLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYA MNWVRQAPGKGMWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNLLKTE DTAVYYCVRAGNFGTSYISYWAYWGQGTTLTVSSGGGGSGGGGSGGGGSGTQVVTQEPS LTVSPGGTVTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGS LSGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKTLTVLGGGDKTHTCPCPAP ELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK PCEEQYGSTYRCVSVTLVLHQQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL YSKLTVDKSRWQQGNVFSCVMHEALHNYTQKSLSLSPGKGGGSGGGGSGGGGSGGGG GSGGGGSGGGGSDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVTLVLHQQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNQGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCVMHEALHNYTQK SLSLSPGK
2250	CH3 G8A 6- B12 x I2M2 x scFc - Full Sequence	artificial	EVQLLESGGGLVQPGGSLRLSCAASGFSFSSYPINWVRQAPGKGLEWVGVIWTTGGGTN YASSVKGRFTISRDN SKNTVYLQMNSLRAEDTAVYYCAKSRGVYDFDGRGAMDYWGQG TLTVSSGGGGSGGGGSGGGGSDI VMTQSPDSLAVSLGERATINCKSSQSLLYSSNQK NYFAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTITSSSLQAEDVAVYYC QQQYYSYPYTFGQGTLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYA INWVREAPGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTAYLQMNLLKTE DTAVYYCVRNANFGTSYISYFAYWGQGTTLTVSSGGGGSGGGGSGGGGSGTQVVTQEPS LTVSPGGTVTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGS

			LLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK PCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL YSLKLTVDKSRWQQGNVFCFSVMHEALHNNHYTQKSLSLSPGKGGGSGGGSGGGSGG GGSGGGSGGGSGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTTPVLDSDGSFFLYSLKLTVDKSRWQQGNVFCFSVMHEALHNNHYTQK SLSLSPGK
2251	CH3 R170R CC x I2C x scFc - Full Sequence	artificial	EVQLLESGGGLVQPGGSLRLSCAASGFTSSSYWMHWVRQTTPGKCLEWVSKIDPSDDYT NYNQKVKGRFTTISIDKSKNTLYLQMNLSRAEDTAVVYCARWDYSHFDVWGQGTVTVTS SGGGSGGGSGGGSGGSEIVMTQSPATLSVSPGERATLTCRASSSVSYMHYQQKPGQA PRLLIYGTSNLVSGVPARFSGSGSGTEFTLTITSSLSQSEDFAVVYCCQWSSYPLTFGCG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKDRFTTISRDDS KNTAYLQMNNLKTEDTAVVYCVRHGNE GSSYISYWAYWGQGTTLTVTSVSSGGGSGGGSGGGSGGGSGQTVVTQEPSLTVSPGGTVTITC GSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGGKAAALTLSGV QPEDEAEYYCVLWYSNRWVFGGKTCLTVLGGGGDKTHTCPPCPAPELLGGPSVFLFPP KPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSLKLTVDKSRWQQ GNVFCFSVMHEALHNNHYTQKSLSLSPGKGGGSGGGSGGGSGGGSGGGSGGGSGGGGS DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP PVLDSDGSFFLYSLKLTVDKSRWQQGNVFCFSVMHEALHNNHYTQKSLSLSPGK
2252	CH3 R170R CC x I2E x scFc - Full Sequence	artificial	EVQLLESGGGLVQPGGSLRLSCAASGFTSSSYWMHWVRQTTPGKCLEWVSKIDPSDDYT NYNQKVKGRFTTISIDKSKNTLYLQMNLSRAEDTAVVYCARWDYSHFDVWGQGTVTVTS SGGGSGGGSGGGSGGSEIVMTQSPATLSVSPGERATLTCRASSSVSYMHYQQKPGQA PRLLIYGTSNLVSGVPARFSGSGSGTEFTLTITSSLSQSEDFAVVYCCQWSSYPLTFGCG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLE WVARIRSKYNNYATYYADAVKDRFTTISRDDS KNTVYLQMNNLKTEDTAVVYCARAGNF GSSYISYWAYWGQGTTLTVTSVSSGGGSGGGSGGGSGGGSGQTVVTQEPSLTVSPGGTVTITC GSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAAALTLSGV QPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPELLGGPSVFLFPP KPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSLKLTVDKSRWQQ GNVFCFSVMHEALHNNHYTQKSLSLSPGKGGGSGGGSGGGSGGGSGGGSGGGSGGGGS DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP PVLDSDGSFFLYSLKLTVDKSRWQQGNVFCFSVMHEALHNNHYTQKSLSLSPGK
2253	CH3 R170R CC x I2K x scFc - Full Sequence	artificial	EVQLLESGGGLVQPGGSLRLSCAASGFTSSSYWMHWVRQTTPGKCLEWVSKIDPSDDYT NYNQKVKGRFTTISIDKSKNTLYLQMNLSRAEDTAVVYCARWDYSHFDVWGQGTVTVTS SGGGSGGGSGGGSGGSEIVMTQSPATLSVSPGERATLTCRASSSVSYMHYQQKPGQA PRLLIYGTSNLVSGVPARFSGSGSGTEFTLTITSSLSQSEDFAVVYCCQWSSYPLTFGCG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLE WVARIRSKYNNYATYYAAEAVKGRFTTISRDDS KNTVYLQMNNLKTEDTAVVYCVRNENI GTSYISYWAYWGQGTTLTVTSVSSGGGSGGGSGGGSGGGSGQTVVTQEPSLTVSPGGTVTITC GSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAAALTLSGV QPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPELLGGPSVFLFPP KPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSLKLTVDKSRWQQ GNVFCFSVMHEALHNNHYTQKSLSLSPGKGGGSGGGSGGGSGGGSGGGSGGGSGGGGS DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP PVLDSDGSFFLYSLKLTVDKSRWQQGNVFCFSVMHEALHNNHYTQKSLSLSPGK
2254	CH3 R170R CC x I2L x scFc - Full Sequence	artificial	EVQLLESGGGLVQPGGSLRLSCAASGFTSSSYWMHWVRQTTPGKCLEWVSKIDPSDDYT NYNQKVKGRFTTISIDKSKNTLYLQMNLSRAEDTAVVYCARWDYSHFDVWGQGTVTVTS SGGGSGGGSGGGSGGSEIVMTQSPATLSVSPGERATLTCRASSSVSYMHYQQKPGQA PRLLIYGTSNLVSGVPARFSGSGSGTEFTLTITSSLSQSEDFAVVYCCQWSSYPLTFGCG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGME WVARIRSKYNNYATYYADAVKDRFTTISRDDS KNTLYLQMNNLKTEDTAVVYCVRAGNF GSSYISYFAYWGQGTTLTVTSVSSGGGSGGGSGGGSGGGSGQTVVTQEPSLTVSPGGTVTITC GSSTGAVTSGNYPNWQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAAALTLSGV QPEDEAEYYCVLYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPELLGGPSVFLFPP KPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSLKLTVDKSRWQQ GNVFCFSVMHEALHNNHYTQKSLSLSPGKGGGSGGGSGGGSGGGSGGGSGGGSGGGGS DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP PVLDSDGSFFLYSLKLTVDKSRWQQGNVFCFSVMHEALHNNHYTQKSLSLSPGK

			PPVLDSGSGFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK
2255	CH3 R170R CC x I2M x scFc - Full Sequence	artificial	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYWMHWVRQTPGKCLEWVSKIDPDDYT NYNQVKGRFTISIDKSKNTLYLQMNLSRAEDTAVYYCARWDYSHFDVWGQGTITVTVS SGGGSGGGGSGGGGSEIVMTQSPATLSVSPGERATLTCRASSSVSYMHWWYQQKPGQA PRLLIYGTSLNVSGVPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQWSSYPLTFGCG TKVEIKSGGGGSEVQLVSGGGGLVQPGGSLKLSAASGFTFNKYAMNWRQAPGKGME WVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRAGNF GTSYISYWAYWGQGTILVTVSSGGGSGGGGSGGGGSGTQVTVTQEPSTLTVSPGGTVTITC GSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTKFLAPGTPARFSGSLSGGKAALTLSGV QPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPELLGGPSVFLFPP KPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPCEEQYGYSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKN QVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTTPVLDSGSGFFLYSKLTVDKSRWQQ GNVFSCSVMEALHNHYTQKSLSLSPGKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGG DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWY VDGVEVHNNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTTPVLDSGSGFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK
2256	CH3 R170R CC x I2M2 x scFc - Full Sequence	artificial	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYWMHWVRQTPGKCLEWVSKIDPDDYT NYNQVKGRFTISIDKSKNTLYLQMNLSRAEDTAVYYCARWDYSHFDVWGQGTITVTVS SGGGSGGGGSGGGGSEIVMTQSPATLSVSPGERATLTCRASSSVSYMHWWYQQKPGQA PRLLIYGTSLNVSGVPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQWSSYPLTFGCG TKVEIKSGGGGSEVQLVSGGGGLVQPGGSLKLSAASGFTFNKYAINWVREAPGKGLE WVARIRSKYNNYATYYADAVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRNANF GTSYISYFAYWGQGTILVTVSSGGGSGGGGSGGGGSGTQVTVTQEPSTLTVSPGGTVTITC GSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTKFLAPGTPARFSGSLGGKAALTLSGV QPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPELLGGPSVFLFPP KPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPCEEQYGYSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKN QVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTTPVLDSGSGFFLYSKLTVDKSRWQQ GNVFSCSVMEALHNHYTQKSLSLSPGKGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGG DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWY VDGVEVHNNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTTPVLDSGSGFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK
2257	Cl1 7-D7 CC - HCDR1	artificial	NYMH
2258	Cl1 7-D7 CC - HCDR2	artificial	WINPTSGGANYAQKFQG
2259	Cl1 7-D7 CC - HCDR3	artificial	ESHAIQEGIWFDY
2260	Cl1 7-D7 CC - LCDR1	artificial	RASQISISNYLN
2261	Cl1 7-D7 CC - LCDR2	artificial	DASSLQS
2262	Cl1 7-D7 CC - LCDR3	artificial	QQSYSFPLT
2263	Cl1 7-D7 CC - VH	artificial	QVQLVQSGAEVKKPGASVKVSCASGYTFITNYMHVVRQAPGQCLEWWMWINPTSGG NYAQKFQGRVTMTRDTSISTAYMELSRRLSDDTAVYFCARESHAIQEGIWFDYWGQGT LTVTVSS
2264	Cl1 7-D7 CC - VL	artificial	DIQMTQSPSSLSASVGDRTVISCRAQSISNYLNWYQQKPKGAPKLLIYDASSLQSGV PSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSFPLTFGCGTKVEIK
2265	Cl1 7-D7 CC EI GQ - VL	artificial	EIQMTQSPSSLSASVGDRTVISCRAQSISNYLNWYQQKPKGAPKLLIYDASSLQSGV PSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSFPLTFGCGTKVEIK
2266	Cl1 7-D7 CC x I2Cx scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCASGYTFITNYMHVVRQAPGQCLEWWMWINPTSGG NYAQKFQGRVTMTRDTSISTAYMELSRRLSDDTAVYFCARESHAIQEGIWFDYWGQGT LTVTVSSGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRTVISCRAQSISNYLNWYQ QKPKGAPKLLIYDASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYF LTFGCGTKVEIKSGGGGSEVQLVSGGGGLVQPGGSLKLSAASGFTFNKYAMNWRQA PGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYC VRHGNFGNSYISYWAYWGQGTILVTVSSGGGSGGGGSGGGGSGTQVTVTQEPSTLTVSPG TVTLTCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTKFLAPGTPARFSGSLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPAPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPCEEQY STYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS REEMTKNQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTTPVLDSGSGFFLYSKLTV DKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGKGGGSGGGGSGGGGSGGGGSGGGG SGGGGSGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPE VKFNWYVDGVEVHNNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFPYSDIAVEWESNGQP ENNYKTTTPVLDSGSGFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPG K
2267	Cl1 7-D7 CC x I2Ex scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCASGYTFITNYMHVVRQAPGQCLEWWMWINPTSGG NYAQKFQGRVTMTRDTSISTAYMELSRRLSDDTAVYFCARESHAIQEGIWFDYWGQGT LTVTVSSGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRTVISCRAQSISNYLNWYQ QKPKGAPKLLIYDASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYF

			LTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINNWVRQA PGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNMLKTEDTAVYYC ARAGNFGSSYISYWAYWGQGLTIVTVSSGGGGSGGGSGGGSGGGSGGGSGGGSGGG TVTITCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYG STYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVD KSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGG SGGGGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTTPVLDSDGSEFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPG K
2268	Cl1 7-D7 CC x I2Kx scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVCSKASGYTFNYYMHVVRQAPGQCLEWMGWINPTSGGA NYAQKFQGRVTMTTRDTSISTAYMELSRRLSDDTAVYFCARESHAIQEGIFWFDYWGQGT LVTVSSGGGGSGGGSGGGSGGGSDIQMTQSPSSLSASVGDRTVISCRAQSISNYLNWYQ QKPGKAPKLLIYDASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSEFP LTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQA PGKGLEWVARIRSKYNNYATYYAEAVKGRFTISRDDSKNTVYLQMNMLKTEDTAVYYC VRNENIGTSYISYWAYWGQGLTIVTVSSGGGGSGGGSGGGSGGGSGGGSGGGSGGGG TVTITCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYG STYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVD KSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGG SGGGGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTTPVLDSDGSEFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPG K
2269	Cl1 7-D7 CC x I2Lx scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVCSKASGYTFNYYMHVVRQAPGQCLEWMGWINPTSGGA NYAQKFQGRVTMTTRDTSISTAYMELSRRLSDDTAVYFCARESHAIQEGIFWFDYWGQGT LVTVSSGGGGSGGGSGGGSGGGSDIQMTQSPSSLSASVGDRTVISCRAQSISNYLNWYQ QKPGKAPKLLIYDASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSEFP LTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQA PGKMEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNMLKTEDTAVYYC VRAGNFGSSYISYFAYWGQGLTIVTVSSGGGGSGGGSGGGSGGGSGGGSGGGSGGGG TVTITCGSSTGAVTSGNYPNWIQKKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAA LTLSGVQPEDEAEYYCVLYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYG STYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVD KSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGG SGGGGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTTPVLDSDGSEFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPG K
2270	Cl1 7-D7 CC x I2M2x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVCSKASGYTFNYYMHVVRQAPGQCLEWMGWINPTSGGA NYAQKFQGRVTMTTRDTSISTAYMELSRRLSDDTAVYFCARESHAIQEGIFWFDYWGQGT LVTVSSGGGGSGGGSGGGSGGGSDIQMTQSPSSLSASVGDRTVISCRAQSISNYLNWYQ QKPGKAPKLLIYDASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSEFP LTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINNWREA PGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTAYLQMNMLKTEDTAVYYC VRNANFGTSYISYFAYWGQGLTIVTVSSGGGGSGGGSGGGSGGGSGGGSGGGSGGGG TVTLTCSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYG STYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVD KSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGG SGGGGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTTPVLDSDGSEFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPG K
2271	Cl1 7-D7 CC x I2Mx scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVCSKASGYTFNYYMHVVRQAPGQCLEWMGWINPTSGGA NYAQKFQGRVTMTTRDTSISTAYMELSRRLSDDTAVYFCARESHAIQEGIFWFDYWGQGT LVTVSSGGGGSGGGSGGGSGGGSDIQMTQSPSSLSASVGDRTVISCRAQSISNYLNWYQ QKPGKAPKLLIYDASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSEFP LTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQA PGKMEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNMLKTEDTAVYYC VRAGNFGTSYISYWAYWGQGLTIVTVSSGGGGSGGGSGGGSGGGSGGGSGGGSGGGG TVTITCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPPELLGGPS

[illegible]

	H CC x I2K x scFc - Full Sequence		GGSGGGGSQVQLVQSGAEVKKPGASVKVSCKASGYAFSSSWMNWVRQAPGQCLEWIGR IYPGDADAKYNKFKGKATLTADKSTSTAYMELSSLRSEDATVYYCARSTMIATGAMD YWGQGTTLTVSSSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQA PGKGLEWVARIRSKYNNYATYYAEAVKGRFTISRDDSKNTVYLQMNKLKTEDTAVYYC VRNENIGTSYISYWAYWGQGTTLTVSSSGGGGSGGGGSGGGGSGTQVVTQEPSTLTVSPGG TVTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKAA LTLSGVQPEDEAEYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCTPPCPAPPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYG STYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSGGSFFLYSKLTVD KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGSGGGGSGGGGSGGGGSGGGG SGGGGSDKTHTCTPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTPVLDSGGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG K
2283	CS PDL241.12_L H CC x I2L x scFc - Full Sequence	artificial	DIQMTQSPSSLSASVGDRTITCKASQDVSTAVAWYQQKPGKAPKLLIYSASYRYTGV PDRFTGSGSGTDFTLTITSSLPQEDFATYYCQHHYSTPPYTFGCGTKVEIKRGGGGSGG GGSGGGGSQVQLVQSGAEVKKPGASVKVSCKASGYAFSSSWMNWVRQAPGQCLEWIGR IYPGDADAKYNKFKGKATLTADKSTSTAYMELSSLRSEDATVYYCARSTMIATGAMD YWGQGTTLTVSSSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQA PGKMEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNKLKTEDTAVYYC VRAGNFGSSYISYFAYWGQGTTLTVSSSGGGGSGGGGSGGGGSGTQVVTQEPSTLTVSPGG TVTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKAA LTLSGVQPEDEAEYCVLYSNRWVFGSGTKLTVLGGGDKTHTCTPPCPAPPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYG STYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSGGSFFLYSKLTVD KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGSGGGGSGGGGSGGGGSGGGG SGGGGSDKTHTCTPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTPVLDSGGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG K
2284	CS PDL241.12_L H CC x I2M x scFc - Full Sequence	artificial	DIQMTQSPSSLSASVGDRTITCKASQDVSTAVAWYQQKPGKAPKLLIYSASYRYTGV PDRFTGSGSGTDFTLTITSSLPQEDFATYYCQHHYSTPPYTFGCGTKVEIKRGGGGSGG GGSGGGGSQVQLVQSGAEVKKPGASVKVSCKASGYAFSSSWMNWVRQAPGQCLEWIGR IYPGDADAKYNKFKGKATLTADKSTSTAYMELSSLRSEDATVYYCARSTMIATGAMD YWGQGTTLTVSSSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQA PGKMEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNKLKTEDTAVYYC VRAGNFGTSYISYWAYWGQGTTLTVSSSGGGGSGGGGSGGGGSGTQVVTQEPSTLTVSPGG TVTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKAA LTLSGVQPEDEAEYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCTPPCPAPPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYG STYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSGGSFFLYSKLTVD KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGSGGGGSGGGGSGGGGSGGGG SGGGGSDKTHTCTPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTPVLDSGGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG K
2285	CS PDL241.12_L H CC x I2M2 x scFc - Full Sequence	artificial	DIQMTQSPSSLSASVGDRTITCKASQDVSTAVAWYQQKPGKAPKLLIYSASYRYTGV PDRFTGSGSGTDFTLTITSSLPQEDFATYYCQHHYSTPPYTFGCGTKVEIKRGGGGSGG GGSGGGGSQVQLVQSGAEVKKPGASVKVSCKASGYAFSSSWMNWVRQAPGQCLEWIGR IYPGDADAKYNKFKGKATLTADKSTSTAYMELSSLRSEDATVYYCARSTMIATGAMD YWGQGTTLTVSSSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVREA PGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTAYLQMNKLKTEDTAVYYC VRNANFGTSYISYFAYWGQGTTLTVSSSGGGGSGGGGSGGGGSGTQVVTQEPSTLTVSPGG TVTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKAA LTLSGVQPEDEAEYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCTPPCPAPPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYG STYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSGGSFFLYSKLTVD KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGSGGGGSGGGGSGGGGSGGGG SGGGGSDKTHTCTPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTPVLDSGGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG K
2286	CL6 3D4- 01.G2 LH - HCDR1	artificial	GYMH
2287	CL6 3D4- 01.G2 LH - HCDR2	artificial	WINPNSGETNYAQKFQG
2288	CL6 3D4-	artificial	DALIVVAPVTRDYYYGMDV

	01.G2 LH - HCDR3		
2289	CL6 3D4- 01.G2 LH - LCDR1	artificial	RASQSVSSSYLA
2290	CL6 3D4- 01.G2 LH - LCDR2	artificial	GASSRAT
2291	CL6 3D4- 01.G2 LH - LCDR3	artificial	QQYGSSPLT
2292	CL6 3D4- 01.G2 LH - VH	artificial	QVQLVQSGAEVKKPGASVKVSKASGYTFTGYMHVWRQAPGQCLEWMGWINPNSGET NYAQKFQGRVTMTDRDTSISTAYMELSRRLSDDTAVYYCARDALIVVAPVTRDYVYYGM DVWGQGTITVTVSS
2293	CL6 3D4- 01.G2 LH - VL	artificial	EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATG IPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPLTFGCGTKLEIK
2294	CL6 3D4- 01.G2 LH x I2Cx scFc - Full Sequence	artificial	EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATG IPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPLTFGCGTKLEIKGGGGSGGG GSGGGGSQVQLVQSGAEVKKPGASVKVSKASGYTFTGYMHVWRQAPGQCLEWMGWI NPNSGETNYAQKFQGRVTMTDRDTSISTAYMELSRRLSDDTAVYYCARDALIVVAPVTR DYVYYGMDVWGQGTITVTVSSSGGGGSEVQLVESGGGLVQPGGSLKLSKAASGFTFNKY AMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSNTAYLQMNNLKT EDTAVYYCVRHGNFNSYISYWAYWGQGTITVTVSSGGGGSGGGGSGGGGSGTQVVTQEP SLTVSPGGTVTITCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSG SLSGKAALTLISGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKHTHTCPPCPA PELLGGPSVFLFPPKPKDTLMIISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFF LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSG GGGGSGGGGSGGGGDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKT KPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ KSLSLSPGK
2295	CL6 3D4- 01.G2 LH x I2Ex scFc - Full Sequence	artificial	EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATG IPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPLTFGCGTKLEIKGGGGSGGG GSGGGGSQVQLVQSGAEVKKPGASVKVSKASGYTFTGYMHVWRQAPGQCLEWMGWI NPNSGETNYAQKFQGRVTMTDRDTSISTAYMELSRRLSDDTAVYYCARDALIVVAPVTR DYVYYGMDVWGQGTITVTVSSSGGGGSEVQLVESGGGLVQPGGSLKLSKAASGFTFNKY AINWVRQAPGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSNTAYLQMNNLKT EDTAVYYCARAGNFSSYISYWAYWGQGTITVTVSSGGGGSGGGGSGGGGSGTQVVTQEP SLTVSPGGTVTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSG SLSGKAALTLISGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKHTHTCPPCPA PELLGGPSVFLFPPKPKDTLMIISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFF LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSG GGGGSGGGGSGGGGDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKT KPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ KSLSLSPGK
2296	CL6 3D4- 01.G2 LH x I2Kx scFc - Full Sequence	artificial	EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATG IPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPLTFGCGTKLEIKGGGGSGGG GSGGGGSQVQLVQSGAEVKKPGASVKVSKASGYTFTGYMHVWRQAPGQCLEWMGWI NPNSGETNYAQKFQGRVTMTDRDTSISTAYMELSRRLSDDTAVYYCARDALIVVAPVTR DYVYYGMDVWGQGTITVTVSSSGGGGSEVQLVESGGGLVQPGGSLKLSKAASGFTFNKY AMNWVRQAPGKGLEWVARIRSKYNNYATYYAEAVKGRFTISRDDSNTAYLQMNNLKT EDTAVYYCVRNENIGTSYISYWAYWGQGTITVTVSSGGGGSGGGGSGGGGSGTQVVTQEP SLTVSPGGTVTITCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSG SLSGKAALTLISGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKHTHTCPPCPA PELLGGPSVFLFPPKPKDTLMIISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFF LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSG GGGGSGGGGSGGGGDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKT KPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ KSLSLSPGK
2297	CL6 3D4- 01.G2 LH x I2Lx scFc - Full Sequence	artificial	EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATG IPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPLTFGCGTKLEIKGGGGSGGG GSGGGGSQVQLVQSGAEVKKPGASVKVSKASGYTFTGYMHVWRQAPGQCLEWMGWI NPNSGETNYAQKFQGRVTMTDRDTSISTAYMELSRRLSDDTAVYYCARDALIVVAPVTR DYVYYGMDVWGQGTITVTVSSSGGGGSEVQLVESGGGLVQPGGSLKLSKAASGFTFNKY AMNWVRQAPGKGMWVARIRSKYNNYATYYADAVKDRFTISRDDSNTAYLQMNNLKT

			EDTAVYYCVRAGNFGSSYISYFAYWGQGTTLVTVSSGGGGSGGGGSGGGGSGTQVVTQEP SLTVSPGGTVTITCGSSTGAVTSGNYPNWQKKPGQAPRGLIGGTFKFLAPGTAPARFSG SLEGGKAALTLSGVQPEDEAEYYCVLYYSNRWVFGSGTKLTVLGGGDKHTCPCPCA PELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFF LYSKLTVDKSRWQQGNVFSCVMHEALHNHYTQKSLSLSPGKGGGSGGGGSGGGGSG GGGSGGGSGGGGSGDKHTCPCPCAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKT KPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCVMHEALHNHYTQ KSLSLSPGK
2298	CL6 3D4- 01.G2 LH x I2M2x scFc - Full Sequence	artificial	EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATG IPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSPLTFGCGTKLEIKGGGGSGGG GSGGGGSGVQLVQSGAEVKKPGASVKVSKASGYTFTGYMHVWRQAPGQCLEWMGWI NPNSGETNYAQKFQGRVTMTDRDTSISTAYMELSRRLSDDTAVYYCARDALIVVAPVTR DYIIYGMDVWGQGTITVTVSSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKY AINWVREAPGKLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTAYLQMNNLKT EDTAVYYCVRNANFGTSYISYFAYWGQGTTLVTVSSGGGGSGGGGSGGGGSGTQVVTQEP SLTVSPGGTVTITCGSSTGAVTSGNYPNWQKKPGQAPRGLIGGTFKFLAPGTAPARFSG SLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKHTCPCPCA PELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFF LYSKLTVDKSRWQQGNVFSCVMHEALHNHYTQKSLSLSPGKGGGSGGGGSGGGGSGGGGSG GGGSGGGSGGGGSGDKHTCPCPCAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKT KPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCVMHEALHNHYTQ KSLSLSPGK
2299	CL6 3D4- 01.G2 LH x I2Mx scFc - Full Sequence	artificial	EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATG IPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSPLTFGCGTKLEIKGGGGSGGG GSGGGGSGVQLVQSGAEVKKPGASVKVSKASGYTFTGYMHVWRQAPGQCLEWMGWI NPNSGETNYAQKFQGRVTMTDRDTSISTAYMELSRRLSDDTAVYYCARDALIVVAPVTR DYIIYGMDVWGQGTITVTVSSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKY AMNWRQAPGKMEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNNLKT EDTAVYYCVRAGNFGTSYISYWAYWGQGTTLVTVSSGGGGSGGGGSGGGGSGTQVVTQEP SLTVSPGGTVTITCGSSTGAVTSGNYPNWQKKPGQAPRGLIGGTFKFLAPGTAPARFSG SLSGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKHTCPCPCA PELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFF LYSKLTVDKSRWQQGNVFSCVMHEALHNHYTQKSLSLSPGKGGGSGGGGSGGGGSGGGGSG GGGSGGGSGGGGSGDKHTCPCPCAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKT KPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCVMHEALHNHYTQ KSLSLSPGK
2300	CL 10D8 CC - HCDR1	artificial	GYMH
2301	CL 10D8 CC - HCDR2	artificial	WINPNSGGTKYAQKFQG
2302	CL 10D8 CC - HCDR3	artificial	DRITVAGTYYYYGMDV
2303	CL 10D8 CC - LCDR1	artificial	RASQGVNNWLA
2304	CL 10D8 CC - LCDR2	artificial	TASSLQS
2305	CL 10D8 CC - LCDR3	artificial	QQANSFPIT
2306	CL 10D8 CC - VH	artificial	QVQLVQSGAEVKKPGASVKVSKASGYTFTGYMHVWRQAPGQCLEWMGWINPNSGGT KYAQKFQGRVTMTDRDTSISTAYMELSRRLSDDTAVYYCARDALIVVAPVTR QGTITVTVSS
2307	CL 10D8 CC - VL	artificial	DIQMTQSPSSVSASVGDRTITCRASQGVNNWLAWYQQKPGKAPKLLIYTASSLQSGV PSRFSGSGSGTDFTLTISRLEPEDFAVYYCQQANSFPITFGCGTRLEIK
2308	CL 10D8 CC EI GQ - VL	artificial	EIQMTQSPSSVSASVGDRTITCRASQGVNNWLAWYQQKPGKAPKLLIYTASSLQSGV PSRFSGSGSGTDFTLTISRLEPEDFAVYYCQQANSFPITFGCGTRLEIK
2309	CL 10D8 CC x I2C x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSKASGYTFTGYMHVWRQAPGQCLEWMGWINPNSGGT QGTITVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSVSASVGDRTITCRASQGVNNWLA WYQQKPGKAPKLLIYTASSLQSGVPSRFSGSGSGTDFTLTISRLEPEDFAVYYCQQAN SFPITFGCGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWR QAPGKLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAV YYCVRHGNFGNSYISYWAYWGQGTTLVTVSSGGGGSGGGGSGGGGSGTQVVTQEP SLTVSPGGTVTITCGSSTGAVTSGNYPNWQKKPGQAPRGLIGGTFKFLAPGTAPARFSG SLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGSGTKLTVLGGGDKHTCPCPCAPELLG GPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPCEE

			QYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
2310	CL 10D8 CC x I2E x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHVWRQAPGQCLEWMGWINPNSGGTKYAQKFQGRVTMTTRDTSISTAYMELSRRLSDDTAVYYCARDRITVAGTYYYYGMDVWVGQGTITVTVSSGGGGSGGGSGGGGSDIQMTQSPSSVSASVGRDVTITCRASQGVNNWLA WYQQKPKGAPKLLIYTASSLQSGVPSRFSGSGSGTDFTLTIRSLQPEDFATYYCQQAN SFPITFGCGRTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWV RQAPGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNILKTEDTAV YYCARAGNFGSSYISYWAYWGQGTILVTVSSGGGGSGGGSGGGGSGTQVVTQEPSTLTVS PGGTVTITCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAPGTPARFSGSLSGG KAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKHTHTCPPCPAPELLG GPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEE QYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
2311	CL 10D8 CC x I2K x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHVWRQAPGQCLEWMGWINPNSGGTKYAQKFQGRVTMTTRDTSISTAYMELSRRLSDDTAVYYCARDRITVAGTYYYYGMDVWVGQGTITVTVSSGGGGSGGGSGGGGSDIQMTQSPSSVSASVGRDVTITCRASQGVNNWLA WYQQKPKGAPKLLIYTASSLQSGVPSRFSGSGSGTDFTLTIRSLQPEDFATYYCQQAN SFPITFGCGRTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWV RQAPGKGLEWVARIRSKYNNYATYYAEAVKGRFTISRDDSKNTVYLQMNILKTEDTAV YYCVRNENIGTSYISYWAYWGQGTILVTVSSGGGGSGGGSGGGGSGTQVVTQEPSTLTVS PGGTVTITCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAPGTPARFSGSLSGG KAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKHTHTCPPCPAPELLG GPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEE QYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
2312	CL 10D8 CC x I2L x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHVWRQAPGQCLEWMGWINPNSGGTKYAQKFQGRVTMTTRDTSISTAYMELSRRLSDDTAVYYCARDRITVAGTYYYYGMDVWVGQGTITVTVSSGGGGSGGGSGGGGSDIQMTQSPSSVSASVGRDVTITCRASQGVNNWLA WYQQKPKGAPKLLIYTASSLQSGVPSRFSGSGSGTDFTLTIRSLQPEDFATYYCQQAN SFPITFGCGRTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWV RQAPGKMEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNILKTEDTAV YYCVRAGNFGSSYISYFAYWGQGTILVTVSSGGGGSGGGSGGGGSGTQVVTQEPSTLTVS PGGTVTITCGSSTGAVTSGNYPNWIQKPKGQAPRGLIGGTFKFLAPGTPARFSGSLEGG KAALTLSGVQPEDEAEYYCVLYYSNRWVFGSGTKLTVLGGGGDKHTHTCPPCPAPELLG GPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEE QYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
2313	CL 10D8 CC x I2M x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHVWRQAPGQCLEWMGWINPNSGGTKYAQKFQGRVTMTTRDTSISTAYMELSRRLSDDTAVYYCARDRITVAGTYYYYGMDVWVGQGTITVTVSSGGGGSGGGSGGGGSDIQMTQSPSSVSASVGRDVTITCRASQGVNNWLA WYQQKPKGAPKLLIYTASSLQSGVPSRFSGSGSGTDFTLTIRSLQPEDFATYYCQQAN SFPITFGCGRTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWV RQAPGKMEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNILKTEDTAV YYCVRAGNFGTSYISYWAYWGQGTILVTVSSGGGGSGGGSGGGGSGTQVVTQEPSTLTVS PGGTVTITCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAPGTPARFSGSLSGG KAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKHTHTCPPCPAPELLG GPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEE QYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

			LPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
2314	CL 10D8 CC x I2M2 x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHVWRQAPGQCLEWMGWINPNSGGT KYAQKFQGRVTMTTRDTSISITAYMELSRRLSDDTAVYYCARDRITVAGTYYYGMDVWG QGTITVTVSSGGGGSGGGSGGGSDIQMTQSPSSVSASVGRDVTITCRASQGVNWNLA WYQQKPGKAPKLLIYTASSLQSGVPSRFSGSGSGTDFTLTIRSLQPEDFATYYCQQAN SFPITFGCGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWV REAPGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTAYLQMNNLKTEDTAV YYCVRNANFGTSYISYFAYWGQGTITVTVSSGGGGSGGGSGGGSGGTQTVVTQEPSTLVS PGGTVTLTGSSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTFKFLAPGTPARFSGSLG KAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEE QYGSTYRCVSVLTVLHQLDNLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKL TVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGG GGGGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQLDNLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSL SPGK
2315	DL 8-A7 CC - HCDR1	artificial	SYYS
2316	DL 8-A7 CC - HCDR2	artificial	YVYSGTTNYPNLSKS
2317	DL 8-A7 CC - HCDR3	artificial	IAVTGIFYDY
2318	DL 8-A7 CC - LCDR1	artificial	RASQVRNNNYLA
2319	DL 8-A7 CC - LCDR2	artificial	GASSRAT
2320	DL 8-A7 CC - LCDR3	artificial	QQYDRSPLT
2321	DL 8-A7 CC - VH	artificial	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKCLEWIGYVYSGTTN YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYYCASIATVTFGYFDYWGQGTITVTV SS
2322	DL 8-A7 CC - VL	artificial	EIVLTQSPGTLTSLSPGERVTLSCRASQVRNNNYLAWYQQRPQAPRLLIYGASSRATG IPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYDRSPLTFGCGTKLEIK
2323	DL 8-A7 CC x I2C x scFc - Full Sequence	artificial	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKCLEWIGYVYSGTTN YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYYCASIATVTFGYFDYWGQGTITVTV SSGGGGSGGGSGGGSEIIVLTQSPGTLTSLSPGERVTLSCRASQVRNNNYLAWYQQRP GQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYDRSPLTF GCGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGK GLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRH GNFGNSYISYWAYWGQGTITVTVSSGGGGSGGGSGGGSGGTQTVVTQEPSTLVS PGGTVTITCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTFKFLAPGTPARFSGSLG KAALTLSGVQPEDEAEYYCVLWYSNRWVFGGSGTKLTVLGGGDKTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTY RCVSVLTVLHQLDNLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSR WQQGNVFCFSVMHEALHNHYTQKSLSLSPGGGGSGGGSGGGSGGGSGGGSGGGG SDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQLDNLNGKEYKCKVSNKALPAPIEKT ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
2324	DL 8-A7 CC x I2E x scFc - Full Sequence	artificial	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKCLEWIGYVYSGTTN YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYYCASIATVTFGYFDYWGQGTITVTV SSGGGGSGGGSGGGSEIIVLTQSPGTLTSLSPGERVTLSCRASQVRNNNYLAWYQQRP GQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYDRSPLTF GCGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGK GLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNNLKTEDTAVYYCARA GNFGSSYISYWAYWGQGTITVTVSSGGGGSGGGSGGGSGGTQTVVTQEPSTLVS PGGTVTITCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTFKFLAPGTPARFSGSLG KAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTY RCVSVLTVLHQLDNLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSR WQQGNVFCFSVMHEALHNHYTQKSLSLSPGGGGSGGGSGGGSGGGSGGGSGGGG SDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQLDNLNGKEYKCKVSNKALPAPIEKT ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
2325	DL 8-A7 CC x I2K x scFc - Full Sequence	artificial	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKCLEWIGYVYSGTTN YNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYYCASIATVTFGYFDYWGQGTITVTV SSGGGGSGGGSGGGSEIIVLTQSPGTLTSLSPGERVTLSCRASQVRNNNYLAWYQQRP GQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYDRSPLTF GCGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGK

			GLEWVARIRSKYNNYATYYAEAVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRN ENIGTSYISYWAYWQGGLTVTVSSGGGSGGGGSGGGGSGTQVTVTQEPSSLTVSPGGT ITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAALT SGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKHTHTCPPCPAPPELLGGPSVFL FPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTY RCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGSGGGGSGGGGSGGGGSGGGGSGGGG SDKHTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSLKTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
2326	DL 8-A7 CC x I2L x scFc - Full Sequence	artificial	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKCLEWIGYVYSGTTN YNPSLKSRTVISVDTSKNQFSLKLSSVTAADTAVYYCASIATVTFYFDYWGQGLTVTV SSGGGSGGGGSGGGGSEIVLTQSPGTLSPGERVTLSCRASQVRNNNYLAWYQQRP GQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYDRSPLTF GCGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQAPGK GMEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRA GNFGSSYISYFAYWQGGLTVTVSSGGGSGGGGSGGGGSGTQVTVTQEPSSLTVSPGGT ITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAALT SGVQPEDEAEYYCVLYSNRWVFGSGTKLTVLGGGGDKHTHTCPPCPAPPELLGGPSVFL FPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTY RCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGSGGGGSGGGGSGGGGSGGGGSGGGG SDKHTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSLKTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
2327	DL 8-A7 CC x I2M x scFc - Full Sequence	artificial	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKCLEWIGYVYSGTTN YNPSLKSRTVISVDTSKNQFSLKLSSVTAADTAVYYCASIATVTFYFDYWGQGLTVTV SSGGGSGGGGSGGGGSEIVLTQSPGTLSPGERVTLSCRASQVRNNNYLAWYQQRP GQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYDRSPLTF GCGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQAPGK GMEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRA GNFGTSYISYFAYWQGGLTVTVSSGGGSGGGGSGGGGSGTQVTVTQEPSSLTVSPGGT ITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAALT SGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKHTHTCPPCPAPPELLGGPSVFL FPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTY RCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGSGGGGSGGGGSGGGGSGGGGSGGGG SDKHTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSLKTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
2328	DL 8-A7 CC x I2M2 x scFc - Full Sequence	artificial	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKCLEWIGYVYSGTTN YNPSLKSRTVISVDTSKNQFSLKLSSVTAADTAVYYCASIATVTFYFDYWGQGLTVTV SSGGGSGGGGSGGGGSEIVLTQSPGTLSPGERVTLSCRASQVRNNNYLAWYQQRP GQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYDRSPLTF GCGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVREAPGK GLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRN ANFGTSYISYFAYWQGGLTVTVSSGGGSGGGGSGGGGSGTQVTVTQEPSSLTVSPGGT LTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAALT SGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKHTHTCPPCPAPPELLGGPSVFL FPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTY RCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGSGGGGSGGGGSGGGGSGGGGSGGGG SDKHTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSLKTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
2329	EGFRvIII CC - HCDR1	artificial	NYGMH
2330	EGFRvIII CC - HCDR2	artificial	VIWYDGSCKYADSVRG
2331	EGFRvIII CC - HCDR3	artificial	DGYDILTGNPRDFDY
2332	EGFRvIII CC - LCDR1	artificial	RSSQSLVHSDGNTYLS
2333	EGFRvIII CC - LCDR2	artificial	RISRRFS
2334	EGFRvIII CC - LCDR3	artificial	MQSTHVPRT
2335	EGFRvIII CC - VH	artificial	QVQLVESGGGVVQSGRSLRLSCAASGFTFRNYGMHWVRQAPGKCLEWVAVIWDGSDK YYADSVRGRTISRDNKNTLYLQMNSLRAEDTAVYYCARDGYDILTGNPRDFDYWGQ

			GTLVTVSS
2336	EGFRvIII CC - VL	artificial	DTVMTQTPLSSHVTLGQPASISCRSSQSLVHSDGNTYLSWLQQRPGQPRLLIYRISR RFSGVDPDRFSGSGAGTDFTEISRVEAEDVGVIYCMQSTHVPRTFCGCTKVEIK
2337	EGFRvIII CC x I2C - Full Sequence	artificial	QVQLVESGGGVVQSGRSLRLSCAASGFTFRNYGMHWRQAPGKCLEWVAVIWDGSDK YYADSVRGRTISRDNKNTLYLQMNLSRAEDTAVYYCARDGYDILTGNPRDFDYWGQ GTLVTVSSGGGGSGGGSGGGGSDTVMQTPLSSHVTLGQPASISCRSSQSLVHSDGN TYLSWLQQRPGQPRLLIYRISRFSGVDPDRFSGSGAGTDFTEISRVEAEDVGVIYCMQSTHVPRTFCGCTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYA MNVWRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTE DTAVYYCVRHGNFGNSYISYWAYWGQGTTLVTVSSGGGGSGGGSGGGGSGTAVVTQEPS LTVSPGGTTLTCSGSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAPGTPARFSGS LLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
2338	EGFRvIII CC x I2E - Full Sequence	artificial	QVQLVESGGGVVQSGRSLRLSCAASGFTFRNYGMHWRQAPGKCLEWVAVIWDGSDK YYADSVRGRTISRDNKNTLYLQMNLSRAEDTAVYYCARDGYDILTGNPRDFDYWGQ GTLVTVSSGGGGSGGGSGGGGSDTVMQTPLSSHVTLGQPASISCRSSQSLVHSDGN TYLSWLQQRPGQPRLLIYRISRFSGVDPDRFSGSGAGTDFTEISRVEAEDVGVIYCMQSTHVPRTFCGCTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYA MNVWRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTE DTAVYYCARAGNFGSSYISYWAYWGQGTTLVTVSSGGGGSGGGSGGGGSGTAVVTQEPS LTVSPGGTTLTCSGSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAPGTPARFSGS LSGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
2339	EGFRvIII CC x I2K - Full Sequence	artificial	QVQLVESGGGVVQSGRSLRLSCAASGFTFRNYGMHWRQAPGKCLEWVAVIWDGSDK YYADSVRGRTISRDNKNTLYLQMNLSRAEDTAVYYCARDGYDILTGNPRDFDYWGQ GTLVTVSSGGGGSGGGSGGGGSDTVMQTPLSSHVTLGQPASISCRSSQSLVHSDGN TYLSWLQQRPGQPRLLIYRISRFSGVDPDRFSGSGAGTDFTEISRVEAEDVGVIYCMQSTHVPRTFCGCTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYA MNVWRQAPGKGLEWVARIRSKYNNYATYYAEAVKGRFTISRDDSKNTAYLQMNNLKTE DTAVYYCVRNENIGTSYISYWAYWGQGTTLVTVSSGGGGSGGGSGGGGSGTAVVTQEPS LTVSPGGTTLTCSGSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAPGTPARFSGS LSGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
2340	EGFRvIII CC x I2L - Full Sequence	artificial	QVQLVESGGGVVQSGRSLRLSCAASGFTFRNYGMHWRQAPGKCLEWVAVIWDGSDK YYADSVRGRTISRDNKNTLYLQMNLSRAEDTAVYYCARDGYDILTGNPRDFDYWGQ GTLVTVSSGGGGSGGGSGGGGSDTVMQTPLSSHVTLGQPASISCRSSQSLVHSDGN TYLSWLQQRPGQPRLLIYRISRFSGVDPDRFSGSGAGTDFTEISRVEAEDVGVIYCMQSTHVPRTFCGCTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYA MNVWRQAPGKGMWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNNLKTE DTAVYYCVRAGNFGSSYISYFAYWGQGTTLVTVSSGGGGSGGGSGGGGSGTAVVTQEPS LTVSPGGTTLTCSGSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAPGTPARFSGS LEGGKAALTLSGVQPEDEAEYYCVLYYSNRWVFGSGTKLTVL
2341	EGFRvIII CC x I2M - Full Sequence	artificial	QVQLVESGGGVVQSGRSLRLSCAASGFTFRNYGMHWRQAPGKCLEWVAVIWDGSDK YYADSVRGRTISRDNKNTLYLQMNLSRAEDTAVYYCARDGYDILTGNPRDFDYWGQ GTLVTVSSGGGGSGGGSGGGGSDTVMQTPLSSHVTLGQPASISCRSSQSLVHSDGN TYLSWLQQRPGQPRLLIYRISRFSGVDPDRFSGSGAGTDFTEISRVEAEDVGVIYCMQSTHVPRTFCGCTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYA MNVWRQAPGKGMWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNNLKTE DTAVYYCVRAGNFGTSYISYWAYWGQGTTLVTVSSGGGGSGGGSGGGGSGTAVVTQEPS LTVSPGGTTLTCSGSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAPGTPARFSGS LSGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
2342	EGFRvIII CC x I2M2 - Full Sequence	artificial	QVQLVESGGGVVQSGRSLRLSCAASGFTFRNYGMHWRQAPGKCLEWVAVIWDGSDK YYADSVRGRTISRDNKNTLYLQMNLSRAEDTAVYYCARDGYDILTGNPRDFDYWGQ GTLVTVSSGGGGSGGGSGGGGSDTVMQTPLSSHVTLGQPASISCRSSQSLVHSDGN TYLSWLQQRPGQPRLLIYRISRFSGVDPDRFSGSGAGTDFTEISRVEAEDVGVIYCMQSTHVPRTFCGCTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYA MNVWRQAPGKGMWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTAYLQMNNLKTE DTAVYYCVRNANFGTSYISYFAYWGQGTTLVTVSSGGGGSGGGSGGGGSGTAVVTQEPS LTVSPGGTTLTCSGSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAPGTPARFSGS LLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL
2343	FL 7-A8 CC - HCDR1	artificial	NARMGVS
2344	FL 7-A8 CC - HCDR2	artificial	HIFSNDKSYSTSLKN
2345	FL 7-A8 CC - HCDR3	artificial	IVGYGSGWYGFFDY
2346	FL 7-A8 CC - LCDR1	artificial	RASQGIRNDLG
2347	FL 7-A8 CC - LCDR2	artificial	AASTLQS
2348	FL 7-A8 CC - LCDR3	artificial	LQHNSYPLT
2349	FL 7-A8 CC - VH	artificial	QVTLKESGPTLVKPTETLTCTLSGFSLNNARMGWSWIRQPPGKCLEWLAHIFSNDK KSYSTSLKNRLTISRDDSSKTQVVLMTNVPVDTATYYCARIVGYGSGWYGFFDYWGQ GTLVTVSS
2350	FL 7-A8 CC - VL	artificial	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQKPKGAPKRLIYAASTLQSGV PSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGCGTKVEIK
2351	FL 7-A8 CC EI GQ - VL	artificial	EIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQKPKGAPKRLIYAASTLQSGV PSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGCGTKVEIK

2352	FL 7-A8 CC x I2Cx scFc - Full Sequence	artificial	QVTLKESGPTLVKPTETLTTLCTLSGFSLNNARMGVSWIRQPPGKCLEWLAHIFSNDE KSYSTSLKNRLTISKDSSKTQVVLMTNVDVDTATYYCARIVGYGSGWYFFDYWGQ GTLTVTVSSGGGGSGGGSGGGGSDIQTQSPSSLSASVGDRTTITCRASQGI RNDLGW YQQKPGKAPKRLIYAASLTQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLOHNS YPLTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVR QAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVY YCVRHGNFGNSYISYWAYWGQGTTLTVTVSSGGGGSGGGSGGGGSGTQVVTQEPSTLTVSP GGTTLTTCGSSSTGAVTSGNYPNWVQKPGQAPRGLIGGKFLAPGTPARFSGSLLGGK AALTLSGVQPEDEAEYYCVLWYSNRWVFGGKTTLTVLGGGDKHTHTCPPCPAPELLGG PSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQ YGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFSQSCVMHEALHNNHYTQKSLSLSPGKGGGSGGGSGGGSGGGSGGG GGSGGGGSDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQSCVMHEALHNNHYTQKSLSLSPGK
2353	FL 7-A8 CC x I2Ex scFc - Full Sequence	artificial	QVTLKESGPTLVKPTETLTTLCTLSGFSLNNARMGVSWIRQPPGKCLEWLAHIFSNDE KSYSTSLKNRLTISKDSSKTQVVLMTNVDVDTATYYCARIVGYGSGWYFFDYWGQ GTLTVTVSSGGGGSGGGSGGGGSDIQTQSPSSLSASVGDRTTITCRASQGI RNDLGW YQQKPGKAPKRLIYAASLTQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLOHNS YPLTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVR QAPGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNNLKTEDTAVY YCARAGNFGSSYISYWAYWGQGTTLTVTVSSGGGGSGGGSGGGGSGTQVVTQEPSTLTVSP GGTVTITCGSSSTGAVTSGNYPNWVQKPGQAPRGLIGGKFLAPGTPARFSGSLSGGK AALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKTLTVLGGGDKHTHTCPPCPAPELLGG PSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQ YGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFSQSCVMHEALHNNHYTQKSLSLSPGKGGGSGGGSGGGSGGGSGGG GGSGGGGSDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQSCVMHEALHNNHYTQKSLSLSPGK
2354	FL 7-A8 CC x I2Kx scFc - Full Sequence	artificial	QVTLKESGPTLVKPTETLTTLCTLSGFSLNNARMGVSWIRQPPGKCLEWLAHIFSNDE KSYSTSLKNRLTISKDSSKTQVVLMTNVDVDTATYYCARIVGYGSGWYFFDYWGQ GTLTVTVSSGGGGSGGGSGGGGSDIQTQSPSSLSASVGDRTTITCRASQGI RNDLGW YQQKPGKAPKRLIYAASLTQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLOHNS YPLTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVR QAPGKGLEWVARIRSKYNNYATYYAEAVKGRFTISRDDSKNTVYLQMNNLKTEDTAVY YCVRNENIGTSYISYWAYWGQGTTLTVTVSSGGGGSGGGSGGGGSGTQVVTQEPSTLTVSP GGTVTITCGSSSTGAVTSGNYPNWVQKPGQAPRGLIGGKFLAPGTPARFSGSLSGGK AALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKTLTVLGGGDKHTHTCPPCPAPELLGG PSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQ YGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFSQSCVMHEALHNNHYTQKSLSLSPGKGGGSGGGSGGGSGGGSGGG GGSGGGGSDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQSCVMHEALHNNHYTQKSLSLSPGK
2355	FL 7-A8 CC x I2Lx scFc - Full Sequence	artificial	QVTLKESGPTLVKPTETLTTLCTLSGFSLNNARMGVSWIRQPPGKCLEWLAHIFSNDE KSYSTSLKNRLTISKDSSKTQVVLMTNVDVDTATYYCARIVGYGSGWYFFDYWGQ GTLTVTVSSGGGGSGGGSGGGGSDIQTQSPSSLSASVGDRTTITCRASQGI RNDLGW YQQKPGKAPKRLIYAASLTQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLOHNS YPLTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVR QAPGKMEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNNLKTEDTAVY YCVRAGNFGSSYISYFAYWGQGTTLTVTVSSGGGGSGGGSGGGGSGTQVVTQEPSTLTVSP GGTVTITCGSSSTGAVTSGNYPNWIQKPGQAPRGLIGGKFLAPGTPARFSGSLEGGK AALTLSGVQPEDEAEYYCVLYYSNRWVFGSGTKTLTVLGGGDKHTHTCPPCPAPELLGG PSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQ YGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFSQSCVMHEALHNNHYTQKSLSLSPGKGGGSGGGSGGGSGGGSGGG GGSGGGGSDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQSCVMHEALHNNHYTQKSLSLSPGK
2356	FL 7-A8 CC x I2M2x scFc - Full Sequence	artificial	QVTLKESGPTLVKPTETLTTLCTLSGFSLNNARMGVSWIRQPPGKCLEWLAHIFSNDE KSYSTSLKNRLTISKDSSKTQVVLMTNVDVDTATYYCARIVGYGSGWYFFDYWGQ GTLTVTVSSGGGGSGGGSGGGGSDIQTQSPSSLSASVGDRTTITCRASQGI RNDLGW YQQKPGKAPKRLIYAASLTQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLOHNS YPLTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVR

			EAPGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTAYLQMNNLKTEDTAVY YCVNRANFGTSYISYFAYWGQGLTVTVSSGGGGSGGGGGSGGGGGSGTQVVTQEPSTLTVSP GGTVTLTTCGSSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTKFLAPGTPARFSGSLGGK AALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKHTHTCPCPAPELLGG PSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQ YGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSGDSFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGKGGGGSGGGGGSGGGGGSGGGGGSGG GGSGGGGSDKHTHTCPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGK
2357	FL 7-A8 CC x I2Mx scFc - Full Sequence	artificial	QVTLKESGPTLVKPTETLTTLTCTLSGFSLNNARMGVSWIRQPPGKCLEWLAHIFSNDE KSYSTSLKNRLTISKDSSKTQVVLMTNVDVDTATYYCARIVGYGSGWYGFDFYWGQ GTLTVTVSSGGGGSGGGGGSGGGGGSDIQTQSPSSLSASVGDRTITCRASQGI RNDLGW YQQKPGKAPKRLIYAASLTQSGVPSRFSGSGSGTEFTLTITSSLPEDFATYYCLQHNS YPLTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVR QAPGKMEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNNLKTEDTAVY YCVNRANFGTSYISYWAYWGQGLTVTVSSGGGGSGGGGGSGGGGGSGTQVVTQEPSTLTVSP GGTVTITCGSSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTKFLAPGTPARFSGSLSGGK AALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKHTHTCPCPAPELLGG PSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQ YGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSGDSFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGKGGGGSGGGGGSGGGGGSGGGGGSGG GGSGGGGSDKHTHTCPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGK
2358	MA 10-B5 CC - HCDR1	artificial	NAWMS
2359	MA 10-B5 CC - HCDR2	artificial	RIRRSYSGTTDYAAPVKG
2360	MA 10-B5 CC - HCDR3	artificial	PSYSGSYNYFSVMDV
2361	MA 10-B5 CC - LCDR1	artificial	RTSQSISSYLN
2362	MA 10-B5 CC - LCDR2	artificial	AASSLQG
2363	MA 10-B5 CC - LCDR3	artificial	QQTYSMPFT
2364	MA 10-B5 CC - VH	artificial	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAPGKCLEWVGRIRRSYGG TTDYAAPVKGRTISRDDSKNTLFLQMNLSLKTEDTAVYYCTTPSYSGSYNYFSVMDV WGQGTITVTVSS
2365	MA 10-B5 CC - VL	artificial	DIQMTQSPSSLSASVGDRTITCRTSQSISSYLNWYQQKPGRAPKLLIFAASSLQGGV PSRFSGSGSGTDFTLTITSSLPEDFATYYCQQTYSMPFTFCGCTKVEIK
2366	MA 10-B5 CC EI GQ - VL	artificial	EIQMTQSPSSLSASVGDRTITCRTSQSISSYLNWYQQKPGRAPKLLIFAASSLQGGV PSRFSGSGSGTDFTLTITSSLPEDFATYYCQQTYSMPFTFCGCTKVEIK
2367	MA 10-B5 CC x I2C x scFc - Full Sequence	artificial	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAPGKCLEWVGRIRRSYGG TTDYAAPVKGRTISRDDSKNTLFLQMNLSLKTEDTAVYYCTTPSYSGSYNYFSVMDV WGQGTITVTVSSGGGGSGGGGGSGGGGGSDIQTQSPSSLSASVGDRTITCRTSQSISSY LNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSGSGTDFTLTITSSLPEDFATYYCQQ TYSMPFTFCGCTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMN WVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDT AVYYCVRHNGFNYSYWAYWGQGLTVTVSSGGGGSGGGGGSGGGGGSGTQVVTQEPSTL VSPGGTVTLTTCGSSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTKFLAPGTPARFSGSL GGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKHTHTCPCPAPEL LGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPC EEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSGDSFFLYS KLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGKGGGGSGGGGGSGGGGGSGGGG SGGGGGSGGGGSDKHTHTCPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSL SLSPGK
2368	MA 10-B5 CC x I2E x scFc - Full Sequence	artificial	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAPGKCLEWVGRIRRSYGG TTDYAAPVKGRTISRDDSKNTLFLQMNLSLKTEDTAVYYCTTPSYSGSYNYFSVMDV WGQGTITVTVSSGGGGSGGGGGSGGGGGSDIQTQSPSSLSASVGDRTITCRTSQSISSY LNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSGSGTDFTLTITSSLPEDFATYYCQQ TYSMPFTFCGCTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAIN WVRQAPGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTAYLQMNNLKTEDT AVYYCARAGNFGSSYISYWAYWGQGLTVTVSSGGGGSGGGGGSGGGGGSGTQVVTQEPST VSPGGTVTITCGSSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTKFLAPGTPARFSGSL GGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKHTHTCPCPAPEL

			LGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPC EEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSGDSFFLYS KLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSPGKGGGSGGGGSGGGGSGGGG SGGGSGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDV HEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSL SLSPGK
2369	MA 10-B5 CC x I2K x scFc - Full Sequence	artificial	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAPGKCLEWVGRIRSRSYGG TTDYAAPVKGRFTISRDDSKNTLFLQMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDV WGQGTITVTVSSGGGSGGGGSGGGGSDIQMTQSPSSLSASVGRVITITCRISQSISSY LNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQ TYSMPFTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMN WVRQAPGKGLEWVARIRSKYNNYATYYAEAVKGRFTISRDDSKNTVYLQMNKLKTEDT AVYYCVRNENIGTSYISYWAYWGQGLTVTVSSGGGSGGGGSGGGGSGTQVVTQEP SLTVSPGGTITTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSL GGKAALTLTSGVQPEDEAEYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCPPCPAPEL LGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPC EEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSGDSFFLYS KLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSPGKGGGSGGGGSGGGGSGGGG SGGGSGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDV HEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSL SLSPGK
2370	MA 10-B5 CC x I2L x scFc - Full Sequence	artificial	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAPGKCLEWVGRIRSRSYGG TTDYAAPVKGRFTISRDDSKNTLFLQMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDV WGQGTITVTVSSGGGSGGGGSGGGGSDIQMTQSPSSLSASVGRVITITCRISQSISSY LNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQ TYSMPFTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMN WVRQAPGKMEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNKLKTEDT AVYYCVRAGNFGSSYISYFAYWGQGLTVTVSSGGGSGGGGSGGGGSGTQVVTQEP SLTVSPGGTITTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGS LEGGKAALTLTSGVQPEDEAEYCVLYYSNRWVFGSGTKLTVLGGGDKTHTCPPCPAPEL LGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPC EEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSGDSFFLYS KLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSPGKGGGSGGGGSGGGGSGGGG SGGGSGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDV HEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSL SLSPGK
2371	MA 10-B5 CC x I2M x scFc - Full Sequence	artificial	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAPGKCLEWVGRIRSRSYGG TTDYAAPVKGRFTISRDDSKNTLFLQMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDV WGQGTITVTVSSGGGSGGGGSGGGGSDIQMTQSPSSLSASVGRVITITCRISQSISSY LNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQ TYSMPFTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMN WVRQAPGKMEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNKLKTEDT AVYYCVRAGNFGTSYISYWAYWGQGLTVTVSSGGGSGGGGSGGGGSGTQVVTQEP SLTVSPGGTITTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSL GGKAALTLTSGVQPEDEAEYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCPPCPAPEL LGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPC EEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSGDSFFLYS KLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSPGKGGGSGGGGSGGGGSGGGG SGGGSGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDV HEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSL SLSPGK
2372	MA 10-B5 CC x I2M2 x scFc - Full Sequence	artificial	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAPGKCLEWVGRIRSRSYGG TTDYAAPVKGRFTISRDDSKNTLFLQMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDV WGQGTITVTVSSGGGSGGGGSGGGGSDIQMTQSPSSLSASVGRVITITCRISQSISSY LNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQ TYSMPFTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAIN WVRQAPGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTAYLQMNKLKTEDT AVYYCVRNANFGTSYISYFAYWGQGLTVTVSSGGGSGGGGSGGGGSGTQVVTQEP SLTVSPGGTITTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSL GGKAALTLTSGVQPEDEAEYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCPPCPAPEL LGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPC EEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSGDSFFLYS KLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSPGKGGGSGGGGSGGGGSGGGG SGGGSGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDV

			HEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGK
2373	MA A103 CC x I2C x scFc - Full Sequence	artificial	QVTLKESGPGILQPSQTLSTLCSFSGFSLNTSGMNVGWIRQPSGKCLDWLAHIWNNDD KYYPNPAKLSRLTISKDTSSNNQVFLKIASVVTADTATYYCVRSYFGDYVWYFDVWVWAGT TVTVSSGGGGSGGGSGGGGSDIQMTQTSSLSASLGDRVTISCSASQGIHNYLNWYQ QKPDGTVKLLIYYTSSLHSGVPSRFSGSGSGTDYSLTISNLEPEDATYFCQQYYSKLP RTFGCGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQA PGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNMLKTEDTAVYYC VRHGNFGNSYISYWAYWGQGTTLVTVSSGGGGSGGGSGGGGSGTQVVTQEPSTVSPGG TVTLTCSSTGAVTSGNYPNWWQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGSKLTVLGGGGDKTHTCPCPAPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQY STYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV KSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGG SGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPG K
2374	MA A103 CC x I2E x scFc - Full Sequence	artificial	QVTLKESGPGILQPSQTLSTLCSFSGFSLNTSGMNVGWIRQPSGKCLDWLAHIWNNDD KYYPNPAKLSRLTISKDTSSNNQVFLKIASVVTADTATYYCVRSYFGDYVWYFDVWVWAGT TVTVSSGGGGSGGGSGGGGSDIQMTQTSSLSASLGDRVTISCSASQGIHNYLNWYQ QKPDGTVKLLIYYTSSLHSGVPSRFSGSGSGTDYSLTISNLEPEDATYFCQQYYSKLP RTFGCGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTAYLQMNMLKTEDTAVYYC ARAGNFGSSYISYWAYWGQGTTLVTVSSGGGGSGGGSGGGGSGTQVVTQEPSTVSPGG TVTITCGSSTGAVTSGNYPNWWQKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPCPAPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQY STYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV KSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGG SGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPG K
2375	MA A103 CC x I2K x scFc - Full Sequence	artificial	QVTLKESGPGILQPSQTLSTLCSFSGFSLNTSGMNVGWIRQPSGKCLDWLAHIWNNDD KYYPNPAKLSRLTISKDTSSNNQVFLKIASVVTADTATYYCVRSYFGDYVWYFDVWVWAGT TVTVSSGGGGSGGGSGGGGSDIQMTQTSSLSASLGDRVTISCSASQGIHNYLNWYQ QKPDGTVKLLIYYTSSLHSGVPSRFSGSGSGTDYSLTISNLEPEDATYFCQQYYSKLP RTFGCGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQA PGKGLEWVARIRSKYNNYATYYAEAVKGRFTISRDDSKNTAYLQMNMLKTEDTAVYYC VRNENIGTSYISYWAYWGQGTTLVTVSSGGGGSGGGSGGGGSGTQVVTQEPSTVSPGG TVTITCGSSTGAVTSGNYPNWWQKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPCPAPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQY STYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV KSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGG SGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPG K
2376	MA A103 CC x I2L x scFc - Full Sequence	artificial	QVTLKESGPGILQPSQTLSTLCSFSGFSLNTSGMNVGWIRQPSGKCLDWLAHIWNNDD KYYPNPAKLSRLTISKDTSSNNQVFLKIASVVTADTATYYCVRSYFGDYVWYFDVWVWAGT TVTVSSGGGGSGGGSGGGGSDIQMTQTSSLSASLGDRVTISCSASQGIHNYLNWYQ QKPDGTVKLLIYYTSSLHSGVPSRFSGSGSGTDYSLTISNLEPEDATYFCQQYYSKLP RTFGCGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQA PGKMEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNMLKTEDTAVYYC VRAGNFGSSYISYFAYWGQGTTLVTVSSGGGGSGGGSGGGGSGTQVVTQEPSTVSPGG TVTITCGSSTGAVTSGNYPNWIQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAA LTLSGVQPEDEAEYYCVLYSNRWVFGSGTKLTVLGGGGDKTHTCPCPAPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQY STYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV KSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGG SGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSLSPG K
2377	MA A103 CC	artificial	QVTLKESGPGILQPSQTLSTLCSFSGFSLNTSGMNVGWIRQPSGKCLDWLAHIWNNDD

	x I2M x scFc - Full Sequence		KYYNPALKSRLTISKDTSNQVFLKIASVVTADTATYYCVRSYFGDYVWYFDVWGAGT TVTVSSGGGGSGGGSGGGSGGGSDIQMTQTSSLSASLGDRVTISCSASQGIHNYLNWYQ QKPDGTVKLLIYYTSSLHSGVPSRFSGSGSGTDYSLTISNLEPEDIATYFCQQYSKLP RTFGCGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQA PGKGMWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNKLKTEDTAVYYC VRAGNFGTSYISYWAYWGQGLTVTVSSGGGGSGGGSGGGSGQTVVTPQEPSLTVSPGG TVTITCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYG STYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGGSFFLYSKLTVD KSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGG SGGGGSDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSR EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPG K
2378	MA A103 CC x I2M2 x scFc - Full Sequence	artificial	QVTLKESGPGILQPSQTLSTCSFSGFSLNTSGMNVGWIRQPSGKCLDWLAHIWNDD KYYNPALKSRLTISKDTSNQVFLKIASVVTADTATYYCVRSYFGDYVWYFDVWGAGT TVTVSSGGGGSGGGSGGGSGGGSDIQMTQTSSLSASLGDRVTISCSASQGIHNYLNWYQ QKPDGTVKLLIYYTSSLHSGVPSRFSGSGSGTDYSLTISNLEPEDIATYFCQQYSKLP RTFGCGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVREA PGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTAYLQMNKLKTEDTAVYYC VRANFGTSYISYFAYWGQGLTVTVSSGGGGSGGGSGGGSGGGSGQTVVTPQEPSLTVSPGG TVTITCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYG STYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGGSFFLYSKLTVD KSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGG SGGGGSDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSR EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPG K
2379	MART A103 CC - HCDR1	artificial	TSGMNVG
2380	MART A103 CC - HCDR2	artificial	HIWNDDKYYNPALKS
2381	MART A103 CC - HCDR3	artificial	SYFGDYVWYFDV
2382	MART A103 CC - LCDR1	artificial	SASQGIHNYLN
2383	MART A103 CC - LCDR2	artificial	YTSSLHS
2384	MART A103 CC - LCDR3	artificial	QQYSKLPRT
2385	MART A103 CC - VH	artificial	QVTLKESGPGILQPSQTLSTCSFSGFSLNTSGMNVGWIRQPSGKCLDWLAHIWNDD KYYNPALKSRLTISKDTSNQVFLKIASVVTADTATYYCVRSYFGDYVWYFDVWGAGT TVTVSS
2386	MART A103 CC - VL	artificial	DIQMTQTSSLSASLGDRVTISCSASQGIHNYLNWYQQKPDGTVKLLIYYTSSLHSGV PSRFSGSGSGTDYSLTISNLEPEDIATYFCQQYSKLPRTFGCGTKLEIK
2387	MART A103 CC EI GQ - VL	artificial	EIQMTQTSSLSASLGDRVTISCSASQGIHNYLNWYQQKPDGTVKLLIYYTSSLHSGV PSRFSGSGSGTDYSLTISNLEPEDIATYFCQQYSKLPRTFGCGTKLEIK
2388	MS 15-B12 CC - HCDR1	artificial	SSSYFWG
2389	MS 15-B12 CC - HCDR2	artificial	NIYYSGSSNYNPSLKS
2390	MS 15-B12 CC - HCDR3	artificial	LPRGDRDAFDI
2391	MS 15-B12 CC - LCDR1	artificial	RASQGISNYLA
2392	MS 15-B12 CC - LCDR2	artificial	AASTLQS
2393	MS 15-B12 CC - LCDR3	artificial	QQSYSTPFT
2394	MS 15-B12 CC - VH	artificial	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSSSYFWGWIRQPPGKCLEWIGNIYYSGS SNYNPSLKSRTVISVDTSKNQFSLKLSSVTAADTAVYYCARLPRGDRDAFDIWDGQGT MTVTVSS
2395	MS 15-B12 CC - VL	artificial	DIVMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPKGKVPKLLIYAASTLQSGV PSRFSGSGSGTDFTLTITSLQPEDFATYYCQQSYSTPFTFGCGTKVEIK
2396	MS 15-B12 CC EI GQ - VL	artificial	EIVMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPKGKVPKLLIYAASTLQSGV PSRFSGSGSGTDFTLTITSLQPEDFATYYCQQSYSTPFTFGCGTKVEIK
2397	MS 5-F11 -	artificial	DYYMT

	HCDR1		
2398	MS 5-F11 - HCDR2	artificial	YISSSGSTIYADSVKG
2399	MS 5-F11 - HCDR3	artificial	DRNSHFDY
2400	MS 5-F11 - LCDR1	artificial	RASQGINTWLA
2401	MS 5-F11 - LCDR2	artificial	GASGLQS
2402	MS 5-F11 - LCDR3	artificial	QQAKSFPR
2403	MS 5-F11 - VH	artificial	QVQLVESGGGLVQPGGSLRLSCAASGFTFSDYYMTWIRQAPGKGLEWLSYISSSGSTI YYADSVKGRFTISRDNAKNSLFLQMNSLRAEDTAVYYCARDNRNSHFDYWGQGLTVTVS S
2404	MS 5-F11 - VL	artificial	DIQMTQSPSSVSASVGDRVTITCRASQGINTWLAWYQQKPKGAPKLLIYGASGLQSGV PSRFSGSGSGTDFTLTISLQPEDFATYYCQQAKSFPRTFGQGTKEIK
2405	MS 5-F11 EI GQ - VL	artificial	EIQMTQSPSSVSASVGDRVTITCRASQGINTWLAWYQQKPKGAPKLLIYGASGLQSGV PSRFSGSGSGTDFTLTISLQPEDFATYYCQQAKSFPRTFGQGTKEIK
2406	MS R4L CC - HCDR1	artificial	GYIYH
2407	MS R4L CC - HCDR2	artificial	WINPNSGGTNYAQKFQG
2408	MS R4L CC - HCDR3	artificial	VEAVAGREYYFSGMDV
2409	MS R4L CC - LCDR1	artificial	SGEKLGDKYVY
2410	MS R4L CC - LCDR2	artificial	QSTKRPS
2411	MS R4L CC - LCDR3	artificial	QAYHASTAV
2412	MS R4L CC - VH	artificial	QVQLVQSGAEVKKPGASVKVCKASGYTFTGYYIHWVRQAPGQCLEWMGWINPNSGGT NYAQKFQGRVTMTRDTSISTAYMELSRRLSDDTAVYYCARVEAVAGREYYFSGMDVW GQGTTVTVSS
2413	MS R4L CC - VL	artificial	SYELTQPPSVSVSPGQTASITCSGEKLGDKYVYVYQQKPGQSPVLVIYQSTKRPSGVP ERFSGSNSGNTATLTISGTQAMDEADYYCQAYHASTAVFGCGTKLTVL
2414	MS 15-B12 CC x I2C x scFc - Full Sequence	artificial	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSSSYFWGWIQPPGKCLEWIGNIYYSGS SNYNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYYCARLPRGDRDAFDIWWGQGT MTVTVSSGGGSGGGGSGGGGSDIVMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQ KPGKVPKLLIYAASLTQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPF TFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWRQAP GKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNMLKTEDTAVYYCV RHGNGFNSYISYWAYWGQGLTVTVSSGGGSGGGGSGGGGSGQTVVTQEPSTLVSPGGT VTLTGSSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTAPRFSGSLGGKAAL TLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPAPPELLGGPSV FLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGS TYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDK SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGSGGGGSGGGGSGGGGSGGGG GGGSGDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAP IEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFPYPSDIAVEWESNGQPE NRYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
2415	MS 15-B12 CC x I2E x scFc - Full Sequence	artificial	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSSSYFWGWIQPPGKCLEWIGNIYYSGS SNYNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYYCARLPRGDRDAFDIWWGQGT MTVTVSSGGGSGGGGSGGGGSDIVMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQ KPGKVPKLLIYAASLTQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPF TFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWRQAP GKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNMLKTEDTAVYYCA RAGNFGSSYISYWAYWGQGLTVTVSSGGGSGGGGSGGGGSGQTVVTQEPSTLVSPGGT VTITGSSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTAPRFSGSLGGKAAL TLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPPELLGGPSV FLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGS TYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDK SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGSGGGGSGGGGSGGGGSGGGG GGGSGDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAP IEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFPYPSDIAVEWESNGQPE NRYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
2416	MS 15-B12 CC x I2K x scFc - Full Sequence	artificial	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSSSYFWGWIQPPGKCLEWIGNIYYSGS SNYNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYYCARLPRGDRDAFDIWWGQGT MTVTVSSGGGSGGGGSGGGGSDIVMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQ KPGKVPKLLIYAASLTQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPF TFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWRQAP GKGLEWVARIRSKYNNYATYYAEAVKGRFTISRDDSKNTVYLQMNMLKTEDTAVYYCV RNNENIGTSYISYWAYWGQGLTVTVSSGGGSGGGGSGGGGSGQTVVTQEPSTLVSPGGT

			VTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKAAL TLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPPELLGGPSV FLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGS TYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVSCSVMHEALHNYHTQKSLSLSPGKGGGGSGGGGSGGGGSGGGGSGGGG GGGGSDKHTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAP IEKTIISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVSCSVMHEALHNYHTQKSLSLSPGK
2417	MS 15-B12 CC x I2L x scFc - Full Sequence	artificial	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSSYFWGWIROPFGKCLEWIGNIYYSGS SNYNPSLKSRTVISVDTSKNQFSLKLSSVTAADTAVYYCARLPRGDRDAFDIWGQGT MTVSSGGGGSGGGSGGGGSDIVMTQSPSSLSASVGDRTITCRASQGISNYLAWYQQ KPGKVPKLLIYAASFLQSGVPSRFSGSGSGTDFTLTITSSLPQEDFATYYCQQSYSTPF TFGCGTKVEIKSGGGGSEVQLVSGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQAP GKMEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNNLKTEDTAVYYCV RAGNFGSSYISYFAYWGQGTILVTVSSGGGGSGGGSGGGGSGTQVTVTQEPSTLTVSPGGT VTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKAAL TLSGVQPEDEAEYYCVLYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPPELLGGPSV FLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGS TYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVSCSVMHEALHNYHTQKSLSLSPGKGGGGSGGGGSGGGGSGGGGSGGGG GGGGSDKHTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAP IEKTIISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVSCSVMHEALHNYHTQKSLSLSPGK
2418	MS 15-B12 CC x I2M x scFc - Full Sequence	artificial	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSSYFWGWIROPFGKCLEWIGNIYYSGS SNYNPSLKSRTVISVDTSKNQFSLKLSSVTAADTAVYYCARLPRGDRDAFDIWGQGT MTVSSGGGGSGGGSGGGGSDIVMTQSPSSLSASVGDRTITCRASQGISNYLAWYQQ KPGKVPKLLIYAASFLQSGVPSRFSGSGSGTDFTLTITSSLPQEDFATYYCQQSYSTPF TFGCGTKVEIKSGGGGSEVQLVSGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQAP GKMEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNNLKTEDTAVYYCV RAGNFGTSYISYWAYWGQGTILVTVSSGGGGSGGGSGGGGSGTQVTVTQEPSTLTVSPGGT VTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKAAL TLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPPELLGGPSV FLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGS TYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVSCSVMHEALHNYHTQKSLSLSPGKGGGGSGGGGSGGGGSGGGGSGGGG GGGGSDKHTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAP IEKTIISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVSCSVMHEALHNYHTQKSLSLSPGK
2419	MS 15-B12 CC x I2M2 x scFc - Full Sequence	artificial	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSSYFWGWIROPFGKCLEWIGNIYYSGS SNYNPSLKSRTVISVDTSKNQFSLKLSSVTAADTAVYYCARLPRGDRDAFDIWGQGT MTVSSGGGGSGGGSGGGGSDIVMTQSPSSLSASVGDRTITCRASQGISNYLAWYQQ KPGKVPKLLIYAASFLQSGVPSRFSGSGSGTDFTLTITSSLPQEDFATYYCQQSYSTPF TFGCGTKVEIKSGGGGSEVQLVSGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQAP GKLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCV RNANFGTSYISYFAYWGQGTILVTVSSGGGGSGGGSGGGGSGTQVTVTQEPSTLTVSPGGT VTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKAAL TLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPPELLGGPSV FLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGS TYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVSCSVMHEALHNYHTQKSLSLSPGKGGGGSGGGGSGGGGSGGGGSGGGG GGGGSDKHTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAP IEKTIISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVSCSVMHEALHNYHTQKSLSLSPGK
2420	MS 5-F11 x I2Cx scFc - Full Sequence	artificial	QVQLVSGGGLVKGGLSLRLSCAASGFTFSDYYMTWIRQAPGKLEWLSYISSSSGSTI YYADSVKGRFTISRDNAKNSLFLQMNSLRAEDTAVYYCARDNSHFYWGQGTILTVS SGGGSGGGGSGGGGSDIQTQSPSSVSASVGDRTITCRASQGINWYLAQYQQKPGK APKLLIYAGSLQSGVPSRFSGSGSGTDFTLTITSSLPQEDFATYYCQQAKFPRTFGQ GKVEIKSGGGGSEVQLVSGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQAPGKGL EWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGN FGNSYISYWAYWGQGTILVTVSSGGGGSGGGSGGGGSGTQVTVTQEPSTLTVSPGGT VTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKAAL TLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPPELLGGPSV FLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGS TYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVSCSVMHEALHNYHTQKSLSLSPGKGGGGSGGGGSGGGGSGGGGSGGGG GGGGSDKHTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAP IEKTIISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVSCSVMHEALHNYHTQKSLSLSPGK

			TPPVLDSGGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
2421	MS 5-F11 x I2Ex scFc - Full Sequence	artificial	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMTWIRQAPGKLEWLSYISSSSGSTI YYADSVKGRFTISRDNAKNSLFLQMNSLRAEDTAVYYCARDRNSHFDYWGQGLTLTVS SGGGGSGGGGSGGGGSDIQTQSPSSVSASVGDRTITCRASQGINTWLAWYQQKPGK APKLLIYGASGLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQAKSFPRTFGQ GTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGL EWVARIISKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNKLKTEDTAVYYCARAGN FGSSYISYWAYWGQGLTLTVSSGGGGSGGGGSGGGGSGTQVVTQEPSTLTVSPGGTVTIT CGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGKFLAPGTPARFSGSLSGGKAALTLSG VQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCPPCPAPPELLGGPSVFLFP PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSGGSFFLYSKLTVDKSRWQ QGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSGGGGSGGGGSGGGG SDKTHTCPPCPAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSGGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
2422	MS 5-F11 x I2Kx scFc - Full Sequence	artificial	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMTWIRQAPGKLEWLSYISSSSGSTI YYADSVKGRFTISRDNAKNSLFLQMNSLRAEDTAVYYCARDRNSHFDYWGQGLTLTVS SGGGGSGGGGSGGGGSDIQTQSPSSVSASVGDRTITCRASQGINTWLAWYQQKPGK APKLLIYGASGLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQAKSFPRTFGQ GTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQAPGKGL EWVARIISKYNNYATYYAEAVKGRFTISRDDSKNTVYLQMNKLKTEDTAVYYCVRNEN IGTSYISYWAYWGQGLTLTVSSGGGGSGGGGSGGGGSGTQVVTQEPSTLTVSPGGTVTIT CGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGKFLAPGTPARFSGSLSGGKAALTLSG VQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCPPCPAPPELLGGPSVFLFP PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSGGSFFLYSKLTVDKSRWQ QGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSGGGGSGGGGSGGGG SDKTHTCPPCPAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSGGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
2423	MS 5-F11 x I2Lx scFc - Full Sequence	artificial	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMTWIRQAPGKLEWLSYISSSSGSTI YYADSVKGRFTISRDNAKNSLFLQMNSLRAEDTAVYYCARDRNSHFDYWGQGLTLTVS SGGGGSGGGGSGGGGSDIQTQSPSSVSASVGDRTITCRASQGINTWLAWYQQKPGK APKLLIYGASGLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQAKSFPRTFGQ GTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQAPGKGM EWVARIISKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNKLKTEDTAVYYCVRAGN FGTSYISYFAYWGQGLTLTVSSGGGGSGGGGSGGGGSGTQVVTQEPSTLTVSPGGTVTIT CGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGKFLAPGTPARFSGSLSGGKAALTLSG VQPEDEAEYYCVLYSNRWVFGSGTKLTVLGGGDKTHTCPPCPAPPELLGGPSVFLFP PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSGGSFFLYSKLTVDKSRWQ QGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSGGGGSGGGGSGGGG SDKTHTCPPCPAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSGGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
2424	MS 5-F11 x I2M2x scFc - Full Sequence	artificial	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMTWIRQAPGKLEWLSYISSSSGSTI YYADSVKGRFTISRDNAKNSLFLQMNSLRAEDTAVYYCARDRNSHFDYWGQGLTLTVS SGGGGSGGGGSGGGGSDIQTQSPSSVSASVGDRTITCRASQGINTWLAWYQQKPGK APKLLIYGASGLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQAKSFPRTFGQ GTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGL EWVARIISKYNNYATYYADAVKDRFTISRDDSKNTAYLQMNKLKTEDTAVYYCVRNAN FGTSYISYFAYWGQGLTLTVSSGGGGSGGGGSGGGGSGTQVVTQEPSTLTVSPGGTVTIT CGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGKFLAPGTPARFSGSLSGGKAALTLSG VQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCPPCPAPPELLGGPSVFLFP PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSGGSFFLYSKLTVDKSRWQ QGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSGGGGSGGGGSGGGG SDKTHTCPPCPAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSGGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
2425	MS 5-F11 x I2Mx scFc - Full Sequence	artificial	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMTWIRQAPGKLEWLSYISSSSGSTI YYADSVKGRFTISRDNAKNSLFLQMNSLRAEDTAVYYCARDRNSHFDYWGQGLTLTVS SGGGGSGGGGSGGGGSDIQTQSPSSVSASVGDRTITCRASQGINTWLAWYQQKPGK APKLLIYGASGLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQAKSFPRTFGQ GTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQAPGKGM EWVARIISKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNKLKTEDTAVYYCVRAGN FGTSYISYWAYWGQGLTLTVSSGGGGSGGGGSGGGGSGTQVVTQEPSTLTVSPGGTVTIT CGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGKFLAPGTPARFSGSLSGGKAALTLSG

			VQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPCPAPELLGGPSVFLFP PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRREEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGGGSGGGSG SDKTHTCPCPAPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT ISKAKGQPREPQVYTLPPSRREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
2426	MS R4L CC x I2C x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWRQAPGQCLEWMGWINPNSGGT NYAQKFQGRVTMTTRDTSISTAYMELSRRLSDDTAVYYCARVEAVAGREYYFSGMDVW GQGTITVTVSSGGGGSGGGSGGGSSYELTQPPSVSVSPGQTASITCSGEKLGDKYVY WYQQKPGQSPVLVIYQSTKRPSGVPERFSGSNSGNATLTISGTQAMDEADYYCQAYH ASTAVFGCGTKLTVLSSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWV RQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAV YYCVRHGNFGNSYISYWAYWGQGTILVTVSSGGGGSGGGSGGGSGGGSGGGSGGGSGG PGGTITLTCSSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGG KAALTLSGVQPEDEAEYYCVLWYSNRWVFGGKTCLTVLGGGGDKTHTCPCPAPELLG GPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEE QYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSG GGGGSGGGSDKTHTCPCPAPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSRREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL SPGK
2427	MS R4L CC x I2E x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWRQAPGQCLEWMGWINPNSGGT NYAQKFQGRVTMTTRDTSISTAYMELSRRLSDDTAVYYCARVEAVAGREYYFSGMDVW GQGTITVTVSSGGGGSGGGSGGGSSYELTQPPSVSVSPGQTASITCSGEKLGDKYVY WYQQKPGQSPVLVIYQSTKRPSGVPERFSGSNSGNATLTISGTQAMDEADYYCQAYH ASTAVFGCGTKLTVLSSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINNWV RQAPGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNNLKTEDTAV YYCARAGNFGSSYISYWAYWGQGTILVTVSSGGGGSGGGSGGGSGGGSGGGSGGGSGG PGGTITITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGG KAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPCPAPELLG GPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEE QYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSG GGGGSGGGSDKTHTCPCPAPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSRREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL SPGK
2428	MS R4L CC x I2K x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWRQAPGQCLEWMGWINPNSGGT NYAQKFQGRVTMTTRDTSISTAYMELSRRLSDDTAVYYCARVEAVAGREYYFSGMDVW GQGTITVTVSSGGGGSGGGSGGGSSYELTQPPSVSVSPGQTASITCSGEKLGDKYVY WYQQKPGQSPVLVIYQSTKRPSGVPERFSGSNSGNATLTISGTQAMDEADYYCQAYH ASTAVFGCGTKLTVLSSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWV RQAPGKGLEWVARIRSKYNNYATYYAEAVKGRFTISRDDSKNTVYLQMNNLKTEDTAV YYCVRNENIGTSYISYWAYWGQGTILVTVSSGGGGSGGGSGGGSGGGSGGGSGGGSGG PGGTITITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGG KAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPCPAPELLG GPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEE QYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSG GGGGSGGGSDKTHTCPCPAPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSRREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL SPGK
2429	MS R4L CC x I2L x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWRQAPGQCLEWMGWINPNSGGT NYAQKFQGRVTMTTRDTSISTAYMELSRRLSDDTAVYYCARVEAVAGREYYFSGMDVW GQGTITVTVSSGGGGSGGGSGGGSSYELTQPPSVSVSPGQTASITCSGEKLGDKYVY WYQQKPGQSPVLVIYQSTKRPSGVPERFSGSNSGNATLTISGTQAMDEADYYCQAYH ASTAVFGCGTKLTVLSSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWV RQAPGKMEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNNLKTEDTAV YYCVRAGNFGSSYISYFAYWGQGTILVTVSSGGGGSGGGSGGGSGGGSGGGSGGGSGG PGGTITITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLEGG KAALTLSGVQPEDEAEYYCVLYSNRWVFGSGTKLTVLGGGGDKTHTCPCPAPELLG GPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEE QYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSG GGGGSGGGSDKTHTCPCPAPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSRREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL SPGK

			DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK
2430	MS R4L CC x I2M x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWRQAPGQCLEWMGWIPNSGGTNYAQKFQGRVTMTRDTSISTAYMELSLRLSDDTAVYYCARVEAVAGREYFFYSGMDVWGGGTTVTVSSSGGGSGGGSGGGSSYELTQPPSVSVSPGGQTASITCSGEKLGDKYYVWYQQKPGQSPVLVIYQSTKRPSGVPERFSGSNSGNTATLTISGTQAMDEADYYCQAYHASTAVFGCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGMWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNMLKTEDTAVYYCVNRAGNFGTSYISYWAYWGQGLTVTVSSSGGGSGGGSGGGSSQTVVTVQEPSLTVSPGGTVTITCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK
2431	MS R4L CC x I2M2 x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWRQAPGQCLEWMGWIPNSGGTNYAQKFQGRVTMTRDTSISTAYMELSLRLSDDTAVYYCARVEAVAGREYFFYSGMDVWGGGTTVTVSSSGGGSGGGSGGGSSYELTQPPSVSVSPGGQTASITCSGEKLGDKYYVWYQQKPGQSPVLVIYQSTKRPSGVPERFSGSNSGNTATLTISGTQAMDEADYYCQAYHASTAVFGCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRAPGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTAYLQMNMLKTEDTAVYYCVNRANFGTSYISYFAYWGQGLTVTVSSSGGGSGGGSGGGSSQTVVTVQEPSLTVSPGGTVTITCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK
2432	MU 8-B7 CC - HCDR1	artificial	GYYSWS
2433	MU 8-B7 CC - HCDR2	artificial	DIDASGSTKYNPSSLKS
2434	MU 8-B7 CC - HCDR3	artificial	KKYSTVWSYFDN
2435	MU 8-B7 CC - LCDR1	artificial	SGDKLGDKYAS
2436	MU 8-B7 CC - LCDR2	artificial	QDRKRPS
2437	MU 8-B7 CC - LCDR3	artificial	QAWGSSTAV
2438	MU 8-B7 CC - VH	artificial	QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKCLEWIGDIDASGSTKYNPSSLKSRVTISLDTSKNQFSLKLNSVTAADTAVYFCARKKYSTVWSYFDNWWGQGLTVTVSS
2439	MU 8-B7 CC - VL	artificial	SYELTQPPSVSVPPGQTASITCSGDKLGDKYASWYQQKPGQSPVLVIYQDRKRPSGVPERFSGSNSGNTATLTISGTQAMDEADYYCQAWGSSTAVFGCGTKLTVL
2440	MU 8-B7 CC x I2Cx scFc - Full Sequence	artificial	QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKCLEWIGDIDASGSTKYNPSSLKSRVTISLDTSKNQFSLKLNSVTAADTAVYFCARKKYSTVWSYFDNWWGQGLTVTVSSGGGGSGGGSGGGSSYELTQPPSVSVPPGQTASITCSGDKLGDKYASWYQQKPGQSPVLVIYQDRKRPSGVPERFSGSNSGNTATLTISGTQAMDEADYYCQAWGSSTAVFGCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNMLKTEDTAVYYCVNRHGNFGNSYISYWAYWGQGLTVTVSSGGGGSGGGSGGGSSQTVVTVQEPSLTVSPGGTVTITCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK
2441	MU 8-B7 CC x I2Ex scFc - Full	artificial	QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKCLEWIGDIDASGSTKYNPSSLKSRVTISLDTSKNQFSLKLNSVTAADTAVYFCARKKYSTVWSYFDNWWGQGLTVTVSSGGGGSGGGSGGGSSYELTOPSSSVSVPPGOTASITCSGDKLGDKYASWYQQKPGQSPVLVIYQDRKRPSGVPERFSGSNSGNTATLTISGTQAMDEADYYCQAWGSSTAVFGCGTKLTVL

	Sequence		GQSPVLVIYQDRKRPSGVPERFSGSNSGNTATLTISGTQAMDEADYYCQAWGSSTAVF GCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGK GLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNNLKTEDTAVYYC GNFGSSYISYWAYWQGGLTVTVSSGGGGSGGGSGGGSGTQVVTQEPSTLTVSPGGT ITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPPELLGGPSVFL FPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTY RCVSVLTVLHQDWLNGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGGGSGG GGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKF NWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPI E KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
2442	MU 8-B7 CC x I2Kx scFc - Full Sequence	artificial	QVQLQQWAGALLKPSSETLSLTCAVYGGSFSGYYWSWIRQPPGKCLEWIGDIDASGSK YNPSLKSRTVITSLDTSKNQFSLKLSVTAADTAVYFCARKKYSTVWSYFDNWGQGLTV TVSSGGGGSGGGSGGGSSYELTQPSVSVPPGQTASITCSGDKLGDKYASWYQQKP GQSPVLVIYQDRKRPSGVPERFSGSNSGNTATLTISGTQAMDEADYYCQAWGSSTAVF GCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGK GLEWVARIRSKYNNYATYYAEAVKGRFTISRDDSKNTVYLLQMNNLKTEDTAVYYCVRN ENIGTSYISYWAYWQGGLTVTVSSGGGGSGGGSGGGSGTQVVTQEPSTLTVSPGGT ITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPPELLGGPSVFL FPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTY RCVSVLTVLHQDWLNGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGGGSGG GGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKF NWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPI E KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
2443	MU 8-B7 CC x I2Lx scFc - Full Sequence	artificial	QVQLQQWAGALLKPSSETLSLTCAVYGGSFSGYYWSWIRQPPGKCLEWIGDIDASGSK YNPSLKSRTVITSLDTSKNQFSLKLSVTAADTAVYFCARKKYSTVWSYFDNWGQGLTV TVSSGGGGSGGGSGGGSSYELTQPSVSVPPGQTASITCSGDKLGDKYASWYQQKP GQSPVLVIYQDRKRPSGVPERFSGSNSGNTATLTISGTQAMDEADYYCQAWGSSTAVF GCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGK GMEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRN GNFGSSYISYFAYWQGGLTVTVSSGGGGSGGGSGGGSGTQVVTQEPSTLTVSPGGT ITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKAALTL SGVQPEDEAEYYCVLYYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPPELLGGPSVFL FPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTY RCVSVLTVLHQDWLNGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGGGSGG GGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKF NWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPI E KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
2444	MU 8-B7 CC x I2M2x scFc - Full Sequence	artificial	QVQLQQWAGALLKPSSETLSLTCAVYGGSFSGYYWSWIRQPPGKCLEWIGDIDASGSK YNPSLKSRTVITSLDTSKNQFSLKLSVTAADTAVYFCARKKYSTVWSYFDNWGQGLTV TVSSGGGGSGGGSGGGSSYELTQPSVSVPPGQTASITCSGDKLGDKYASWYQQKP GQSPVLVIYQDRKRPSGVPERFSGSNSGNTATLTISGTQAMDEADYYCQAWGSSTAVF GCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGK GLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRN ANFGTSYISYFAYWQGGLTVTVSSGGGGSGGGSGGGSGTQVVTQEPSTLTVSPGGT LTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPPELLGGPSVFL FPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTY RCVSVLTVLHQDWLNGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGGGSGG GGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKF NWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPI E KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
2445	MU 8-B7 CC x I2Mx scFc - Full Sequence	artificial	QVQLQQWAGALLKPSSETLSLTCAVYGGSFSGYYWSWIRQPPGKCLEWIGDIDASGSK YNPSLKSRTVITSLDTSKNQFSLKLSVTAADTAVYFCARKKYSTVWSYFDNWGQGLTV TVSSGGGGSGGGSGGGSSYELTQPSVSVPPGQTASITCSGDKLGDKYASWYQQKP GQSPVLVIYQDRKRPSGVPERFSGSNSGNTATLTISGTQAMDEADYYCQAWGSSTAVF GCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGK GMEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRN GNFGTSYISYWAYWQGGLTVTVSSGGGGSGGGSGGGSGTQVVTQEPSTLTVSPGGT ITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPPELLGGPSVFL FPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTY RCVSVLTVLHQDWLNGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGGGSGG GGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKF NWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPI E KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

			WQQGNVFSCSVMHEALHNNHYTQKSLSLSPGKGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSDKTHTCPPCPAPELLGGPSVFLFPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWEESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNNHYTQKSLSLSPGK
2446	PM 76-B10 - HCDR1	artificial	DYYMY
2447	PM 76-B10 - HCDR2	artificial	IISDGGYYTYYSDIIKG
2448	PM 76-B10 - HCDR3	artificial	GFPLLRHGAMDY
2449	PM 76-B10 - LCDR1	artificial	KASQNVDTNVA
2450	PM 76-B10 - LCDR2	artificial	SASYRYS
2451	PM 76-B10 - LCDR3	artificial	QQYDSYPYT
2452	PM 76-B10 - VH	artificial	QVQLVESGGGLVKPGESLRLSCAASGFTFSDYYMWVRQAPGKGLEWVAIIISDGGYYTYYSDIIKGRFTISRDNAKNSLYLQMNSLKAEADTAVYYCARGFP LLRHGAMDYW GQGTLVTVSS
2453	PM 76-B10 - VL	artificial	DIQMTQSPSSLSASVGDRVTITCKASQNVDNVAWYQQKPGQAPKSLIYSASYRYSADVPSRFSGSASGTDFTLTISSVQSEDFATYYCCQQYDSYPYTFGGGTKLEIK
2454	PM 76-B10 EI GQ - VL	artificial	EIQMTQSPSSLSASVGDRVTITCKASQNVDNVAWYQQKPGQAPKSLIYSASYRYSADVPSRFSGSASGTDFTLTISSVQSEDFATYYCCQQYDSYPYTFGGGTKLEIK
2455	PM 76-B10.11 CC - HCDR1	artificial	DYYMY
2456	PM 76-B10.11 CC - HCDR2	artificial	IISDGGYYTYYSDIIKG
2457	PM 76-B10.11 CC - HCDR3	artificial	GFPLLRHGAMDY
2458	PM 76-B10.11 CC - LCDR1	artificial	KASQNVDTNVA
2459	PM 76-B10.11 CC - LCDR2	artificial	SASYVYW
2460	PM 76-B10.11 CC - LCDR3	artificial	QQYDQQLIT
2461	PM 76-B10.11 CC - VH	artificial	QVQLVESGGGLVKPGESLRLSCAASGFTFSDYYMWVRQAPGKCLEWVAIIISDGGYYTYYSDIIKGRFTISRDNAKNSLYLQMNSLKAEADTAVYYCARGFP LLRHGAMDYW GQGTLVTVSS
2462	PM 76-B10.11 CC - VL	artificial	DIQMTQSPSSLSASVGDRVTITCKASQNVDNVAWYQQKPGQAPKSLIYSASYVYWDVPSRFSGSASGTDFTLTISSVQSEDFATYYCCQQYDQQLITFGCGTKLEIK
2463	PM 76-B10.11 CC EI GQ - VL	artificial	EIQMTQSPSSLSASVGDRVTITCKASQNVDNVAWYQQKPGQAPKSLIYSASYVYWDVPSRFSGSASGTDFTLTISSVQSEDFATYYCCQQYDQQLITFGCGTKLEIK
2464	PM 76-B10x I2C - Full Sequence	artificial	QVQLVESGGGLVKPGESLRLSCAASGFTFSDYYMWVRQAPGKGLEWVAIIISDGGYYTYYSDIIKGRFTISRDNAKNSLYLQMNSLKAEADTAVYYCARGFP LLRHGAMDYW GQGTLVTVSSGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCKASQNVDNVAWYQQKPGQAPKSLIYSASYRYSADVPSRFSGSASGTDFTLTISSVQSEDFATYYCCQQYDSYPYTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYIISYWAYWGQGLTVTVSSGGGSGGGGSGGGGSGQT VVTQE PSLTVSPGGT VTITCGSSTGAVTSIGNYPNWVQKKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGAAL TL SGVQPEDEAEYYCVLWYSNRWFVGGG TKLTVL
2465	PM 76-B10x I2E - Full Sequence	artificial	QVQLVESGGGLVKPGESLRLSCAASGFTFSDYYMWVRQAPGKGLEWVAIIISDGGYYTYYSDIIKGRFTISRDNAKNSLYLQMNSLKAEADTAVYYCARGFP LLRHGAMDYW GQGTLVTVSSGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCKASQNVDNVAWYQQKPGQAPKSLIYSASYRYSADVPSRFSGSASGTDFTLTISSVQSEDFATYYCCQQYDSYPYTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADA VKDRFTISRDDSKNTVYLQMNNLKTEDTAVYYCARAGNFGSSYIISYWAYWGQGLTVTVSSGGGSGGGGSGGGGSGQT VVTQE PSLTVSPGGT VTITCGSSTGAVTSIGNYPNWVQKKPGQAPRGLIGGTKFLAPGTPARFSGSLSGGKAAL TL SGVQPEDEAEYYCVLWYSNRWFVGS GTKLTVL
2466	PM 76-B10x I2K - Full Sequence	artificial	QVQLVESGGGLVKPGESLRLSCAASGFTFSDYYMWVRQAPGKGLEWVAIIISDGGYYTYYSDIIKGRFTISRDNAKNSLYLQMNSLKAEADTAVYYCARGFP LLRHGAMDYW GQGTLVTVSSGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCKASQNVDNVAWYQQKPGQAPKSLIYSASYRYSADVPSRFSGSASGTDFTLTISSVQSEDFATYYCCQQYDSYPYTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYAAEVKGRFTISRDDSKNTVYLQMNNLKTEDTAVYYCVRNENIGTSYIISYWAYWGQGLTVTVSSGGGSGGGGSGGGGSGQT VVTQE PSLTVSPGGT VTITCGSSTGAVTSIGNYPNWVQKKPGQAPRGLIGGTKFLAPGTPARFSGSLSGGKAAL TL SGVQPEDEAEYYCVLWYSNRWFVGS GTKLTVL

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			KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
2473	PM 76- B10.11 CC x I2L x scFc - Full Sequence	artificial	QVQLVESGGGLVKPAGESLRSLCAASGFTFSDYYMYWVRQAPGKCLEWVAISDGGYYTYSDIIGKRTISRDNAKNSLYLQMNLSLKAEDTAVYYCARGFPLLRHGAMDYWGQGTITVTVSSGGGGSGGGSGGGGSDIQMTQSPSSLSASVGDRTITCKASQNVDTNVAWYQQKPGQAPKSLIYSASVYWDVPSRFSGSASGTDFTLTISVQSEDFATYYCQQYDQQLITFGCGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKMEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRAGNFGSSYISYFAYWGQGTITVTVSSGGGGSGGGSGGGGSGTQVTVTQEPSTLTVSPGGTVTITCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSYRVCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
2474	PM 76- B10.11 CC x I2M x scFc - Full Sequence	artificial	QVQLVESGGGLVKPAGESLRSLCAASGFTFSDYYMYWVRQAPGKCLEWVAISDGGYYTYSDIIGKRTISRDNAKNSLYLQMNLSLKAEDTAVYYCARGFPLLRHGAMDYWGQGTITVTVSSGGGGSGGGSGGGGSDIQMTQSPSSLSASVGDRTITCKASQNVDTNVAWYQQKPGQAPKSLIYSASVYWDVPSRFSGSASGTDFTLTISVQSEDFATYYCQQYDQQLITFGCGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKMEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYLQMNNLKTEDTAVYYCVRAGNFGTSYISYWAYWGQGTITVTVSSGGGGSGGGSGGGGSGTQVTVTQEPSTLTVSPGGTVTITCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSYRVCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
2475	PM 76- B10.11 CC x I2M2 x scFc - Full Sequence	artificial	QVQLVESGGGLVKPAGESLRSLCAASGFTFSDYYMYWVRQAPGKCLEWVAISDGGYYTYSDIIGKRTISRDNAKNSLYLQMNLSLKAEDTAVYYCARGFPLLRHGAMDYWGQGTITVTVSSGGGGSGGGSGGGGSDIQMTQSPSSLSASVGDRTITCKASQNVDTNVAWYQQKPGQAPKSLIYSASVYWDVPSRFSGSASGTDFTLTISVQSEDFATYYCQQYDQQLITFGCGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRNANFGTSYISYFAYWGQGTITVTVSSGGGGSGGGSGGGGSGTQVTVTQEPSTLTVSPGGTVTITCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSYRVCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
2505	CD20 99-E5 CC x CD22 28-B7 N65S CC x I2C x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVCSKASGYTFTSYMMHWVRQAPGQCLEWIGYITPSTGYTEYNQKFKGRVTMTDRKSTSTVYMESSSLTSEDVAVYYCARVHDYDRAMEYWGQGTITVTVSSGGGGSGGGSGGGGSDIQMTQSPSSLSASVGDRTITCKASQDINKYIAWYQQKPGKPKLLIYYTSTLQPGVPSRFSGSGSGTDFTFTISSLQPEDATYYCLQYASYPFTFGCGTRLEIKSGGGGSGVQLVQSGAEVKKPGASVKVCSKASGYTFTSYGISWVRQAPGQCLEWMGWISAYSIGNAIYAQKLQGRVTMTDRDSTSTAYMELRSLRSDDTAVYYCARDPDIYGGSGSYSDYWGQGTITVTVSSGGGGSGGGSGGGGSEIVLTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASSRATGIPARFSGSGSGTEFTLTISLQSEDFAVYYCQQYHSPWLLTFCGCTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAA SGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTITVTVSSGGGGSGGGSGGGGSGTQVTVTQEPSTLTVSPGGTVTITCGSSTGAVTSGNYPNWVQKKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGLVQPGGSLKLSCAAHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSYRVCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
2506	CD20 99-E5	artificial	QVQLVQSGAEVKKPGASVKVCSKASGYTFTSYMMHWVRQAPGQCLEWIGYITPSTGYT

	CC x CD22 28-B7 N65S CC x I2E x scFc - Full Sequence		EYNQKFGRVTMTRDKSTSTVYMESSSLTSED TAVYYCARVHDYDRAMEYWGQGTITVT VSSGGGSGGGGSGGGGSDI QMTQSPSSLSASVGDRTITCKASQDINKYIAWYQQKP GKGPKLLIYYTSTLQPGVPSRFSGSGSGTDFTFTISSLQPEDIAITYYCLQYASYPFTF GCGTRLEIKSGGGGSGVQLVQSGAEVKKPGASVKVSKASGYTFTSYGISWVRQAPGQ CLEWMGWI SAYSGNAIYAQKLQGRVTMTRDTSTSTAYMELRSLRSDDTAVYYCARDPD YYGSGSYSDYWGQGTILVTVSSGGGSGGGGSGGGGSEIVLTQSPATLSVSPGERATLS CRASQSVSSNLAWYQQKPGQAPRLLIYGASSRATGIPARFSGSGSGTEFTLTISLQ EDFAVYYCQQYHSWPLLTFCGCTKVEIKSGGGGSEVQLVSGGGGLVQPGGSLKLSCAA SGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVY LQMNNLKTEDTAVYYCARAGNFGSSYISYWAYWGQGTILVTVSSGGGSGGGGSGGGG QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKLAP GTPARFSGSLSGGKAALTLGSGVQPEDEAEYCVLWYSNRWVFGSGTKLTVLGGGDKT HTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPCEEQYGS TYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV LSDSGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGKGGGSGGG GSGGGSGGGGSGGGGSGGGGSDKHTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRT PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGS TYRCVSVLTVLHQDWL NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSGSGFFLYSKLTVDKSRWQQGNVFCFSVMHE ALHNHYTQKSLSLSPGK
2507	CD20 99-E5 CC x CD22 28-B7 N65S CC x I2K x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSKASGYTFTSYWMHWVRQAPGQCLEWIGYITPSTGYT EYNQKFGRVTMTRDKSTSTVYMESSSLTSED TAVYYCARVHDYDRAMEYWGQGTITVT VSSGGGSGGGGSGGGGSDI QMTQSPSSLSASVGDRTITCKASQDINKYIAWYQQKP GKGPKLLIYYTSTLQPGVPSRFSGSGSGTDFTFTISSLQPEDIAITYYCLQYASYPFTF GCGTRLEIKSGGGGSGVQLVQSGAEVKKPGASVKVSKASGYTFTSYGISWVRQAPGQ CLEWMGWI SAYSGNAIYAQKLQGRVTMTRDTSTSTAYMELRSLRSDDTAVYYCARDPD YYGSGSYSDYWGQGTILVTVSSGGGSGGGGSGGGGSEIVLTQSPATLSVSPGERATLS CRASQSVSSNLAWYQQKPGQAPRLLIYGASSRATGIPARFSGSGSGTEFTLTISLQ EDFAVYYCQQYHSWPLLTFCGCTKVEIKSGGGGSEVQLVSGGGGLVQPGGSLKLSCAA SGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYAEAVKGRFTISRDDSKNTVY LQMNNLKTEDTAVYYCVRNENIGTSYISYWAYWGQGTILVTVSSGGGSGGGGSGGGG QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKLAP GTPARFSGSLSGGKAALTLGSGVQPEDEAEYCVLWYSNRWVFGSGTKLTVLGGGDKT HTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPCEEQYGS TYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV LSDSGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGKGGGSGGG GSGGGSGGGGSGGGGSGGGGSDKHTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRT PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGS TYRCVSVLTVLHQDWL NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSGSGFFLYSKLTVDKSRWQQGNVFCFSVMHE ALHNHYTQKSLSLSPGK
2508	CD20 99-E5 CC x CD22 28-B7 N65S CC x I2L x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSKASGYTFTSYWMHWVRQAPGQCLEWIGYITPSTGYT EYNQKFGRVTMTRDKSTSTVYMESSSLTSED TAVYYCARVHDYDRAMEYWGQGTITVT VSSGGGSGGGGSGGGGSDI QMTQSPSSLSASVGDRTITCKASQDINKYIAWYQQKP GKGPKLLIYYTSTLQPGVPSRFSGSGSGTDFTFTISSLQPEDIAITYYCLQYASYPFTF GCGTRLEIKSGGGGSGVQLVQSGAEVKKPGASVKVSKASGYTFTSYGISWVRQAPGQ CLEWMGWI SAYSGNAIYAQKLQGRVTMTRDTSTSTAYMELRSLRSDDTAVYYCARDPD YYGSGSYSDYWGQGTILVTVSSGGGSGGGGSGGGGSEIVLTQSPATLSVSPGERATLS CRASQSVSSNLAWYQQKPGQAPRLLIYGASSRATGIPARFSGSGSGTEFTLTISLQ EDFAVYYCQQYHSWPLLTFCGCTKVEIKSGGGGSEVQLVSGGGGLVQPGGSLKLSCAA SGFTFNKYAMNWRQAPGKMEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLY LQMNNLKTEDTAVYYCVRAGNFGSSYISYFAYWGQGTILVTVSSGGGSGGGGSGGGG QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKLAP GTPARFSGSLGEGKAALTLGSGVQPEDEAEYCVLYYSNRWVFGSGTKLTVLGGGDKT HTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPCEEQYGS TYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV LSDSGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGKGGGSGGG GSGGGSGGGGSGGGGSGGGGSDKHTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRT PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGS TYRCVSVLTVLHQDWL NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSGSGFFLYSKLTVDKSRWQQGNVFCFSVMHE ALHNHYTQKSLSLSPGK
2509	CD20 99-E5 CC x CD22 28-B7 N65S CC x I2M x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSKASGYTFTSYWMHWVRQAPGQCLEWIGYITPSTGYT EYNQKFGRVTMTRDKSTSTVYMESSSLTSED TAVYYCARVHDYDRAMEYWGQGTITVT VSSGGGSGGGGSGGGGSDI QMTQSPSSLSASVGDRTITCKASQDINKYIAWYQQKP GKGPKLLIYYTSTLQPGVPSRFSGSGSGTDFTFTISSLQPEDIAITYYCLQYASYPFTF GCGTRLEIKSGGGGSGVQLVQSGAEVKKPGASVKVSKASGYTFTSYGISWVRQAPGQ CLEWMGWI SAYSGNAIYAQKLQGRVTMTRDTSTSTAYMELRSLRSDDTAVYYCARDPD YYGSGSYSDYWGQGTILVTVSSGGGSGGGGSGGGGSEIVLTQSPATLSVSPGERATLS CRASQSVSSNLAWYQQKPGQAPRLLIYGASSRATGIPARFSGSGSGTEFTLTISLQ EDFAVYYCQQYHSWPLLTFCGCTKVEIKSGGGGSEVQLVSGGGGLVQPGGSLKLSCAA SGFTFNKYAMNWRQAPGKMEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLY LQMNNLKTEDTAVYYCVRAGNFGTSYISYWAYWGQGTILVTVSSGGGSGGGGSGGGG QTVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKLAP

			GTPARFSGSLSGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKT HTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGSGGG GSGGGSGGGSGGGSGGGSGDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRT PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWL NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHE ALHNHYTQKSLSLSPGK
2510	CD20 99-E5 CC x CD22 28-B7 N65S CC x I2M2 x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCASGYTFTSYWMHWVRQAPGQCLEWIGYITPSTGYT EYNQKFKGRVTMTDRKSTSTVYMESSSLTSEDNAVYICARVHDYDRAMEYWGQGTITV VSSGGGSGGGSGGGSGGGSDIQMTQSPSSLSASVGRVITITCKASQDINKYIAWYQQK GKGPGLLIYYTSTLQPGVPSRFSGSGSGTDFTFTISSLQPEDIAITYYCLQYASYPFTF GCGTRLEIKSGGGGSGVQLVQSGAEVKKPGASVKVSCASGYTFTSYGISWVRQAPGQ CLEWMGWISAYSGNAIYAQKLQGRVTMTDRDSTSTAYMELRSLRSDDTAVYICARDP YYGSGSYSDYWGQGTITVTVSSGGGSGGGSGGGSGGGSEIVLTQSPATLSVSPGERATLS CRASQSVSSNLAWYQQKPGQAPRLIYGASSRATGIPARFSGSGSGTEFTLTISSLSQS EDFAVYYCQQYHSWPLLTFCGCTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAA SGFTFNKYAINWVRAPGKLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTAY LQMNNLKTEDTAVYICVRNANFGTSYISYFAYWGQGTITVTVSSGGGSGGGSGGGSGG QTVVTVQEPSTLTVSPGGTITLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAP GTPARFSGSLSGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKT HTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGSGGG GSGGGSGGGSGGGSGGGSGDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRT PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWL NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHE ALHNHYTQKSLSLSPGK
2511	CD22 28- B7N65S CC x I2C x (G4S)3 x scFc x (G4S)3 x CD20 99E5 CC x I2C - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCASGYTFTSYGISWVRQAPGQCLEWMGWISAYSGNA IYAQKLQGRVTMTDRDSTSTAYMELRSLRSDDTAVYICARDPYYGSGSYSDYWGQGT LVTVSSGGGSGGGSGGGSGGGSEIVLTQSPATLSVSPGERATLSCRASQSVSSNLAWYQ QKPGQAPRLIYGASSRATGIPARFSGSGSGTEFTLTISSLSQSEDFAVYYCQQYHSW PLTFCGCTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQ APGKLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVY CVRHGNFNGSYISYWAYWGQGTITVTVSSGGGSGGGSGGGSGGGSGTQVTVQEPSTLTVSPG GTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAPGTAPARFSGSLSGKA ALTLVSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGSGGGSGGGSGDKTHTCP PCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSD GSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGG GSGGGSGGGSGGGSGGGSGDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHN HYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGVQLVQSGAEVKKPGASVKVSCASGYTFT SYWMHWVRQAPGQCLEWIGYITPSTGYTEYNQKFKGRVTMTDRKSTSTVYMESSSLT SEDNAVYICARVHDYDRAMEYWGQGTITVTVSSGGGSGGGSGGGSGGGSDIQMTQSPSS ASVGRVITITCKASQDINKYIAWYQQKPGKPKLLIYYTSTLQPGVPSRFSGSGSGTD FTFTISSLQPEDIAITYYCLQYASYPFTFCGCTRLEIKSGGGGSEVQLVESGGGLVQPG GSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSVKDRFTISR RDDSKNTAYLQMNNLKTEDTAVYICVRHGNFNGSYISYWAYWGQGTITVTVSSGGGGSG GGGSGGGSGGTQVTVQEPSTLTVSPGGTITLTCGSSTGAVTSGNYPNWVQKPGQAPRGL IGGTKFLAPGTAPARFSGSLSGGKAALTLVSGVQPEDEAEYYCVLWYSNRWVFGGGTKL TVL
2512	CD22 28- B7N65S CC x I2E x (G4S)3 x scFc x (G4S)3 x CD20 99E5 CC x I2E - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCASGYTFTSYGISWVRQAPGQCLEWMGWISAYSGNA IYAQKLQGRVTMTDRDSTSTAYMELRSLRSDDTAVYICARDPYYGSGSYSDYWGQGT LVTVSSGGGSGGGSGGGSGGGSEIVLTQSPATLSVSPGERATLSCRASQSVSSNLAWYQ QKPGQAPRLIYGASSRATGIPARFSGSGSGTEFTLTISSLSQSEDFAVYYCQQYHSW PLTFCGCTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQ APGKLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTAYLQMNNLKTEDTAVY CARAGNFGSSYISYWAYWGQGTITVTVSSGGGSGGGSGGGSGGGSGTQVTVQEPSTLTVSPG GTVITITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAPGTAPARFSGSLSGKA ALTLVSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGSGGGSGGGSGDKTHTCP PCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSD GSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGG GSGGGSGGGSGGGSGGGSGDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHN HYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGVQLVQSGAEVKKPGASVKVSCASGYTFT

			SYWMHWVRQAPGQCLEWIGYITPSTGYTEYNQKFKGRVTMTDRDKSTSTVYMELSSLS EDTAVYYCARVHDYDRAMEYWGQGTTVTVSSGGGGSGGGSGGGGGSDIQMTQSPSSLS ASVGDVRTITCKASQDINKYIAWYQQKPGKPKLLIYYTSTLQPGVPSRFSGSGSGTD FTFTISSLPEDIATYYCLQYASYPFTFGCGTRLEIKSGGGGSEVQLVESGGGLVQPG GSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADAVKDRFTIS RDDS KNTVYLQMNNLKTEDTAVYYCARAGNFGSSYISYWAYWGQGTTLTVTVSSGGGGSG GGGGGGGGSTVVTQEPSTLVSPGGTVTITCGSSTGAVTSGNYPNWVQKPGQAPRGL IGGTKFLAPGTPARFSGSLSGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLT VL
2513	CD22 28- B7N65S CC x I2K x (G4S)3 x scFc x (G4S)3 x CD20 99E5 CC x I2K - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCASGYTFTSYGISWVRQAPGQCLEWMGWISAYSIGNA IYAQKLQGRVTMTTRDTSTSTAYMELRSLRSDDTAVYYCARDPDYSGSGSYSDYWGQGT LTVTVSSGGGGSGGGSGGGGSEIVLTQSPATLSVSPGERATLSCRASQSVSSNLAWYQ QKPGQAPRLLIYGASSRATGIPARFSGSGSGTEFTLTISLQSEDFAVYYCQQYHSWP LLTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQ APGKGLEWVARIRSKYNNYATYYAEAVKGRFTISRDDS KNTVYLQMNNLKTEDTAVYY CVRNENIGTSYISYWAYWGQGTTLTVTVSSGGGGSGGGSGGGGSGTQEPSTLVSPG GTVTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAPGTPARFSGSLSGGKA ALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGSGGGSGGGGSDKTHTCP PCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDS GSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYTQKSLSLSPGKGGGGSGGGSGG GGSGGGSGGGSGGGGSDKTHTCP PCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTTPVLDS DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHN HYTQKSLSLSPGKGGGGSGGGSGGGGSGVQLVQSGAEVKKPGASVKVSCASGYTFT SYWMHWVRQAPGQCLEWIGYITPSTGYTEYNQKFKGRVTMTDRDKSTSTVYMELSSLS EDTAVYYCARVHDYDRAMEYWGQGTTVTVSSGGGGSGGGSGGGGGSDIQMTQSPSSLS ASVGDVRTITCKASQDINKYIAWYQQKPGKPKLLIYYTSTLQPGVPSRFSGSGSGTD FTFTISSLPEDIATYYCLQYASYPFTFGCGTRLEIKSGGGGSEVQLVESGGGLVQPG GSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYAEAVKGRFTISR RDDS KNTVYLQMNNLKTEDTAVYYCVRNENIGTSYISYWAYWGQGTTLTVTVSSGGGGSG GGGGGGGGSTVVTQEPSTLVSPGGTVTITCGSSTGAVTSGNYPNWVQKPGQAPRGL IGGTKFLAPGTPARFSGSLSGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLT VL
2514	CD22 28- B7N65S CC x I2L x (G4S)3 x scFc x (G4S)3 x CD20 99E5 CC x I2L - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCASGYTFTSYGISWVRQAPGQCLEWMGWISAYSIGNA IYAQKLQGRVTMTTRDTSTSTAYMELRSLRSDDTAVYYCARDPDYSGSGSYSDYWGQGT LTVTVSSGGGGSGGGSGGGGSEIVLTQSPATLSVSPGERATLSCRASQSVSSNLAWYQ QKPGQAPRLLIYGASSRATGIPARFSGSGSGTEFTLTISLQSEDFAVYYCQQYHSWP LLTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQ APGKMEWVARIRSKYNNYATYYADAVKDRFTISRDDS KNTLYLQMNNLKTEDTAVYY CVRAGNFGSSYISYFAYWGQGTTLTVTVSSGGGGSGGGSGGGGSGTQEPSTLVSPG GTVTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAPGTPARFSGSLSGGKA ALTLGSGVQPEDEAEYYCVLYSNRWVFGSGTKLTVLGGGGSGGGSGGGGSDKTHTCP PCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDS GSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYTQKSLSLSPGKGGGGSGGGSGG GGSGGGSGGGSGGGGSDKTHTCP PCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTTPVLDS DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHN HYTQKSLSLSPGKGGGGSGGGSGGGGSGVQLVQSGAEVKKPGASVKVSCASGYTFT SYWMHWVRQAPGQCLEWIGYITPSTGYTEYNQKFKGRVTMTDRDKSTSTVYMELSSLS EDTAVYYCARVHDYDRAMEYWGQGTTVTVSSGGGGSGGGSGGGGGSDIQMTQSPSSLS ASVGDVRTITCKASQDINKYIAWYQQKPGKPKLLIYYTSTLQPGVPSRFSGSGSGTD FTFTISSLPEDIATYYCLQYASYPFTFGCGTRLEIKSGGGGSEVQLVESGGGLVQPG GSLKLSCAASGFTFNKYAMNWRQAPGKMEWVARIRSKYNNYATYYADAVKDRFTISR RDDS KNTLYLQMNNLKTEDTAVYYCVRAGNFGSSYISYFAYWGQGTTLTVTVSSGGGGSG GGGGGGGGSTVVTQEPSTLVSPGGTVTITCGSSTGAVTSGNYPNWVQKPGQAPRGL IGGTKFLAPGTPARFSGSLSGGKAALTLGSGVQPEDEAEYYCVLYSNRWVFGSGTKLT VL
2515	CD22 28- B7N65S CC x I2M x (G4S)3 x scFc x (G4S)3 x CD20 99E5 CC x I2M - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCASGYTFTSYGISWVRQAPGQCLEWMGWISAYSIGNA IYAQKLQGRVTMTTRDTSTSTAYMELRSLRSDDTAVYYCARDPDYSGSGSYSDYWGQGT LTVTVSSGGGGSGGGSGGGGSEIVLTQSPATLSVSPGERATLSCRASQSVSSNLAWYQ QKPGQAPRLLIYGASSRATGIPARFSGSGSGTEFTLTISLQSEDFAVYYCQQYHSWP LLTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQ APGKMEWVARIRSKYNNYATYYADAVKDRFTISRDDS KNTLYLQMNNLKTEDTAVYY CVRAGNFGTSYISYWAYWGQGTTLTVTVSSGGGGSGGGSGGGGSGTQEPSTLVSPG GTVTITCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAPGTPARFSGSLSGGKA ALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGSGGGSGGGGSDKTHTCP PCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDS GSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYTQKSLSLSPGKGGGGSGGGSGG GGSGGGSGGGSGGGGSDKTHTCP PCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVT

			CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVSCVMHEALHN HYTQKSLSLSPGKGGGGSGGGSGGGGSQVQLVQSGAEVKKPGASVKVSKASGYTFT SYWMHWVRQAPGQCLEWIGYITPSTGYTEYNQKFKGRVTMTDRKSTSTVYMELSSSLTS EDTAVYYCARVHDYDRAMEYWGQGTITVTVSSGGGGSGGGSGGGGSDIQMTQSPSSLS ASVGDRTVITCKASQDINKYIAWYQQKPGKPKLLIYYTSTLQPGVPSRFSGSGSGTD FTFTISSLPEDIATYYCYLQYASYPFTFGCGTRLEIKSGGGGSEVQLVESGGGLVQPG GSLKLSCAASGFTFNKYAMNWRQAPGKMEWVARIRSKYNNYATYYADAVKDRFTIS RDDSKNTLYLQMNMLKTEDTAVYYCVRAGNFGTSYISYWAYWGQGTITVTVSSGGGGSG GGGSGGGGSQTQVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGNYPNWWQKKPGQAPRGL IGGTKFLAPGTPARFSGSLSGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLT VL
2516	CD22 28- B7N65S CC x I2M2 x (G4S) 3 x scFc x (G4S) 3 x CD20 99E5 CC x I2M2 - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSKASGYTFTSYGISWVRQAPGQCLEWMGWISAYSNGA IYAKQLQGRVTMTDRDSTSTAYMELRSLRSDTAVYYCARDPDYSGSGSYSDYWGQGT LVTVSSGGGGSGGGSGGGSGGGSEIVLTQSPATLSVSPGERATLSCRASQVSSNLAWYQ QKPGQAPRLLIYGASSRATGIPARFSGSGSGTEFTLTITSLQSEDFAVYYCQYHWP LLTFCGCTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRE APGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTAYLQMNMLKTEDTAVYY CVRNANFGTSYISYFAYWGQGTITVTVSSGGGGSGGGSGGGGSQTQVVTQEPSTLTVSPG GTVTLTCSSTGAVTSGNYPNWWQKKPGQAPRGLIGGTKFLAPGTPARFSGSLGGA ALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGSGGGSGGGGSDKTHTCF PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSD GSFFLYSKLTVDKSRWQQGNVSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGG GGGSGGGSGGGSGGGSGGGSDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVSCVMHEALHN HYTQKSLSLSPGKGGGGSGGGSGGGGSQVQLVQSGAEVKKPGASVKVSKASGYTFT SYWMHWVRQAPGQCLEWIGYITPSTGYTEYNQKFKGRVTMTDRKSTSTVYMELSSSLTS EDTAVYYCARVHDYDRAMEYWGQGTITVTVSSGGGGSGGGSGGGGSDIQMTQSPSSLS ASVGDRTVITCKASQDINKYIAWYQQKPGKPKLLIYYTSTLQPGVPSRFSGSGSGTD FTFTISSLPEDIATYYCYLQYASYPFTFGCGTRLEIKSGGGGSEVQLVESGGGLVQPG GSLKLSCAASGFTFNKYAINWVREAPGKGLEWVARIRSKYNNYATYYADAVKDRFTIS RDDSKNTAYLQMNMLKTEDTAVYYCVRNANFGTSYISYFAYWGQGTITVTVSSGGGGSG GGGSGGGGSQTQVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGNYPNWWQKKPGQAPRGL IGGTKFLAPGTPARFSGSLGGAALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLT VL
2517	CS PDL241.12.L H CCx BC A7 27-C4-G7 CC x I2Cx scFc - Full Sequence	artificial	DIQMTQSPSSLSASVGDRTVITCKASQDVSTAVAWYQQKPGKAPKLLIYSASYRYTGV PDRFTGSGSGTDFTLTITSLQPEDFATYYCQHHYSTPPYTFGCGTKVEIKRGGGGSGG GGGGGGSQVQLVQSGAEVKKPGASVKVSKASGYAFSSSWMNWRQAPGQCLEWIGR IYPGDADAKYNAKFKGKATLTADKSTSTAYMELSSLRSEDYAVYYCARSTMIATGAMD YWGQGTITVTVSSGGGGSGQVQLVQSGAEVKKPGASVKVSKASGYTFTNHHIHWVRQA PGQCLEWMGYINPYPGYHAYNEKFQGRATMTSDTSTSTVYMELSSLRSEDYAVYYCAR DGYRYRDTVDLDYWGQGTITVTVSSGGGGSGGGSGGGGSDIQMTQSPSSLSASVGDRTV ITCQASQDISINLWYQQKPGKAPKLLIYYTSSLRHTGVPSRFSGSGSGTDFTFTISSL EPEDIATYYCQGNLTLPWTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSA ASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTA YLQMNMLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTITVTVSSGGGGSGGGSGGGG SQTQVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGNYPNWWQKKPGQAPRGLIGGTKFLA PGTTPARFSGSLGGAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDK THTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP VLDSDGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNHYTQKSLSLSPGKGGGGSGG GGGGGSGGGSGGGSGGGSGGGSDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISR TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDW LNKKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVSCVMH EALHNHYTQKSLSLSPGK
2518	CS PDL241.12.L H CCx BC A7 27-C4-G7 CC x I2Ex scFc - Full Sequence	artificial	DIQMTQSPSSLSASVGDRTVITCKASQDVSTAVAWYQQKPGKAPKLLIYSASYRYTGV PDRFTGSGSGTDFTLTITSLQPEDFATYYCQHHYSTPPYTFGCGTKVEIKRGGGGSGG GGGGGGSQVQLVQSGAEVKKPGASVKVSKASGYAFSSSWMNWRQAPGQCLEWIGR IYPGDADAKYNAKFKGKATLTADKSTSTAYMELSSLRSEDYAVYYCARSTMIATGAMD YWGQGTITVTVSSGGGGSGQVQLVQSGAEVKKPGASVKVSKASGYTFTNHHIHWVRQA PGQCLEWMGYINPYPGYHAYNEKFQGRATMTSDTSTSTVYMELSSLRSEDYAVYYCAR DGYRYRDTVDLDYWGQGTITVTVSSGGGGSGGGSGGGGSDIQMTQSPSSLSASVGDRTV ITCQASQDISINLWYQQKPGKAPKLLIYYTSSLRHTGVPSRFSGSGSGTDFTFTISSL EPEDIATYYCQGNLTLPWTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSA ASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTV YLQMNMLKTEDTAVYYCARAGNFGSSYISYWAYWGQGTITVTVSSGGGGSGGGSGGGG SQTQVVTQEPSTLTVSPGGTVTITCGSSTGAVTSGNYPNWWQKKPGQAPRGLIGGTKFLA PGTTPARFSGSLGGAALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDK THTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK

			AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPP VLDS DGSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPGKGGGSGG GGSGGGGSGGGGSGGGGSGGGGSDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISR TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTTPPVLDS DGSFFLYSKLTVDKSRWQQGNV FSCSVMH EALHNHYTQKSLSLSPGK
2519	CS PDL241.12.L H CCx BC A7 27-C4-G7 CC x I2Kx scFc - Full Sequence	artificial	DIQMTQSPSSLSASVGDRVTITCKASQDVSTAVAWYQQKPGKAPKLLIYSASYRYTGV PDRFTGSGSGTDFTLTITSSLPEDFATYYCQQHYSTPPYTFGCGTKVEIKRGGGGSGG GGSGGGGSGVQLVQSGAEVKKPGASVKVSCASGYAFSSSMNWVRQAPGQCLEWIGR IYPGDADAKYNAKFKGKATLTADKSTSTAYMELSSLRSEDAVYYCARSTMIATGAMD YWGQGTLLTVTSSSGGGGSGVQLVQSGAEVKKPGASVKVSCASGYFTFNHIIHWVRQA PGQCLEWMGYINPYPGYHAYNEKFQGRATMTSDTSTSTVMELSSLRSEDAVYYCAR DGYRDTDLVDLYWGQGTLLTVTSSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVT ITCQASQDISNYLNWYQQKPGKAPKLLIYYTSSLRHTGVPSPRFSGSGSGTDFTFTISSL EPEDIATYYCQQGNTLPWTFGCGTKVEIKSGGGGSEVQLVSEGGGLVQPGGSLKLSA ASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYAEAVKGRFTISRDDSKNTV YLQMNLLKTEDTAVYYCVRNENIGTSYISYWAYWGQGTLLTVTSSSGGGGSGGGGSGGGG SQT VVTQEP SLTVSPGGT VITTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLA PGT PARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPP VLDS DGSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPGKGGGSGG GGSGGGGSGGGGSGGGGSGGGGSDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISR TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTTPPVLDS DGSFFLYSKLTVDKSRWQQGNV FSCSVMH EALHNHYTQKSLSLSPGK
2520	CS PDL241.12.L H CCx BC A7 27-C4-G7 CC x I2Lx scFc - Full Sequence	artificial	DIQMTQSPSSLSASVGDRVTITCKASQDVSTAVAWYQQKPGKAPKLLIYSASYRYTGV PDRFTGSGSGTDFTLTITSSLPEDFATYYCQQHYSTPPYTFGCGTKVEIKRGGGGSGG GGSGGGGSGVQLVQSGAEVKKPGASVKVSCASGYAFSSSMNWVRQAPGQCLEWIGR IYPGDADAKYNAKFKGKATLTADKSTSTAYMELSSLRSEDAVYYCARSTMIATGAMD YWGQGTLLTVTSSSGGGGSGVQLVQSGAEVKKPGASVKVSCASGYFTFNHIIHWVRQA PGQCLEWMGYINPYPGYHAYNEKFQGRATMTSDTSTSTVMELSSLRSEDAVYYCAR DGYRDTDLVDLYWGQGTLLTVTSSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVT ITCQASQDISNYLNWYQQKPGKAPKLLIYYTSSLRHTGVPSPRFSGSGSGTDFTFTISSL EPEDIATYYCQQGNTLPWTFGCGTKVEIKSGGGGSEVQLVSEGGGLVQPGGSLKLSA ASGFTFNKYAMNWVRQAPGKGMWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTL YLQMNLLKTEDTAVYYCVRAGNFGSSYISYFAYWGQGTLLTVTSSSGGGGSGGGGSGGGG SQT VVTQEP SLTVSPGGT VITTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLA PGT PARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPP VLDS DGSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPGKGGGSGG GGSGGGGSGGGGSGGGGSGGGGSDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISR TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTTPPVLDS DGSFFLYSKLTVDKSRWQQGNV FSCSVMH EALHNHYTQKSLSLSPGK
2521	CS PDL241.12.L H CCx BC A7 27-C4-G7 CC x I2M2x scFc - Full Sequence	artificial	DIQMTQSPSSLSASVGDRVTITCKASQDVSTAVAWYQQKPGKAPKLLIYSASYRYTGV PDRFTGSGSGTDFTLTITSSLPEDFATYYCQQHYSTPPYTFGCGTKVEIKRGGGGSGG GGSGGGGSGVQLVQSGAEVKKPGASVKVSCASGYAFSSSMNWVRQAPGQCLEWIGR IYPGDADAKYNAKFKGKATLTADKSTSTAYMELSSLRSEDAVYYCARSTMIATGAMD YWGQGTLLTVTSSSGGGGSGVQLVQSGAEVKKPGASVKVSCASGYFTFNHIIHWVRQA PGQCLEWMGYINPYPGYHAYNEKFQGRATMTSDTSTSTVMELSSLRSEDAVYYCAR DGYRDTDLVDLYWGQGTLLTVTSSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVT ITCQASQDISNYLNWYQQKPGKAPKLLIYYTSSLRHTGVPSPRFSGSGSGTDFTFTISSL EPEDIATYYCQQGNTLPWTFGCGTKVEIKSGGGGSEVQLVSEGGGLVQPGGSLKLSA ASGFTFNKYAINWVREAPGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTA YLQMNLLKTEDTAVYYCVRNANFGTSYISYFAYWGQGTLLTVTSSSGGGGSGGGGSGGGG SQT VVTQEP SLTVSPGGT VITTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLA PGT PARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPP VLDS DGSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPGKGGGSGG GGSGGGGSGGGGSGGGGSGGGGSDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISR TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTTPPVLDS DGSFFLYSKLTVDKSRWQQGNV FSCSVMH EALHNHYTQKSLSLSPGK
2522	CS PDL241.12.L H CCx BC A7 27-C4-G7 CC	artificial	DIQMTQSPSSLSASVGDRVTITCKASQDVSTAVAWYQQKPGKAPKLLIYSASYRYTGV PDRFTGSGSGTDFTLTITSSLPEDFATYYCQQHYSTPPYTFGCGTKVEIKRGGGGSGG GGSGGGGSGVQLVQSGAEVKKPGASVKVSCASGYAFSSSMNWVRQAPGQCLEWIGR IYPGDADAKYNAKFKGKATLTADKSTSTAYMELSSLRSEDAVYYCARSTMIATGAMD

	x I2Mx scFc - Full Sequence		YWGGQTLVTVSSSGGGGSQVQLVQSGAEVKKPGASVKVSCKASGYTFTNHHIHWVRQA PGQCLEWMGYINPYPGYHAYNEKFQGRATMTSDTSTSTVYMESSLSRSEDATVYYCAR DGYRDTDLVDYWGQGTTLTVSSSGGGSGGGSGGGSGGGSDIQMTQSPSSLSASVGDRTV ITCQASQDISNYLNWYQQKPKGAPKLLIYYTSRLHTGVPSPRFSGSGSGTDFTTTSSSL EPEDIATYYCQQGNTLPWTFGCGTKVEIKSGGGGSEVQLVDSGGGLVQPGGSLKLSA ASGFTFNKYAMNWVRQAPGKGMWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTL YLQMNNLKTEDTAVYYCVRAGNFGTSYISYWAYWGQGTTLTVSSSGGGSGGGSGGGG SQT VVTQEP SLTVSPGGT VTI TCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLA PGT PARFSGSLSGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLTPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP VLDSGGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGSGG GGSGGGSGGGSGGGSGGGSGGGSDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISR TPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLTPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTTPVLDSGGSFFLYSKLTVDKSRWQQGNVFCSCVMH EALHNHYTQKSLSLSPGK
2523	FL 7-A8 CC xCD123 24- B4-f NK CC x I2C x scFc - Full Sequence	artificial	QVTLKESGPTLVKPTETLTCTLSGFSLNARMGVSWIRQPPGKCLEWLAHIFSNDE KSYSTSLKNRLTISKDSSKTQVVLMTNVDVDTATYYCARIVGYGSGWYGFDDYWGQ GTLTVTVSSGGGGSGGGSGGGSGGGSDIQMTQSPSSLSASVGDRTVITCRASQGI RNDLGW YQKPKGAPKRLIYAASLTQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNS YPLTFGCGTKVEIKSGGGGSEVQLLES GGGLVQPGGSLRLSCAASGFTFSHYAMSWVR QAPGKCLEWVS AVSGGGDKTLYADAVKGRFTISRDN SKNTLFLQMNLSRAEDTAIYYC ARLRGFFYYGMDVWGQGT TTVTVSSGGGGSGGGSGGGSGGGSDIVLTQSPSLPVT PGPAS ISCRSSQSLHNSKNYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTL KISRVEAEDVGVIYCMQALQTPPITFGCGTRLEIKSGGGGSEVQLVESGGGLVQPGGS LKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADAVKDRFTISR DSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTTLTVTVSSGGGGSGGG SGGGSGSQT VVTQEP SLTVSPGGT VTI TCGSSTGAVTSGNYPNWVQKPKGQAPRGLIG GTKFLAPGT PARFSGSLSGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL GGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVK FNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTLTPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN YKTTTPVLDSGGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK GGGGSGGGSGGGSGGGSGGGSGGGSDKHTHTCPPCPAPELLGGPSVFLFPPKPKD TLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLTPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGGSFFLYSKLTVDKSRWQQGNV FCSCVMHEALHNHYTQKSLSLSPGK
2524	FL 7-A8 CC xCD123 24- B4-f NK CC x I2E x scFc - Full Sequence	artificial	QVTLKESGPTLVKPTETLTCTLSGFSLNARMGVSWIRQPPGKCLEWLAHIFSNDE KSYSTSLKNRLTISKDSSKTQVVLMTNVDVDTATYYCARIVGYGSGWYGFDDYWGQ GTLTVTVSSGGGGSGGGSGGGSGGGSDIQMTQSPSSLSASVGDRTVITCRASQGI RNDLGW YQKPKGAPKRLIYAASLTQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNS YPLTFGCGTKVEIKSGGGGSEVQLLES GGGLVQPGGSLRLSCAASGFTFSHYAMSWVR QAPGKCLEWVS AVSGGGDKTLYADAVKGRFTISRDN SKNTLFLQMNLSRAEDTAIYYC ARLRGFFYYGMDVWGQGT TTVTVSSGGGGSGGGSGGGSGGGSDIVLTQSPSLPVT PGPAS ISCRSSQSLHNSKNYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTL KISRVEAEDVGVIYCMQALQTPPITFGCGTRLEIKSGGGGSEVQLVESGGGLVQPGGS LKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADAVKDRFTISR DSKNTVYLQMNNLKTEDTAVYYCARAGNFGSSYISYWAYWGQGTTLTVTVSSGGGGSGGG SGGGSGSQT VVTQEP SLTVSPGGT VTI TCGSSTGAVTSGNYPNWVQKPKGQAPRGLIG GTKFLAPGT PARFSGSLSGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL GGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVK FNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTLTPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN YKTTTPVLDSGGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK GGGGSGGGSGGGSGGGSGGGSGGGSDKHTHTCPPCPAPELLGGPSVFLFPPKPKD TLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLTPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGGSFFLYSKLTVDKSRWQQGNV FCSCVMHEALHNHYTQKSLSLSPGK
2525	FL 7-A8 CC xCD123 24- B4-f NK CC x I2K x scFc - Full Sequence	artificial	QVTLKESGPTLVKPTETLTCTLSGFSLNARMGVSWIRQPPGKCLEWLAHIFSNDE KSYSTSLKNRLTISKDSSKTQVVLMTNVDVDTATYYCARIVGYGSGWYGFDDYWGQ GTLTVTVSSGGGGSGGGSGGGSGGGSDIQMTQSPSSLSASVGDRTVITCRASQGI RNDLGW YQKPKGAPKRLIYAASLTQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNS YPLTFGCGTKVEIKSGGGGSEVQLLES GGGLVQPGGSLRLSCAASGFTFSHYAMSWVR QAPGKCLEWVS AVSGGGDKTLYADAVKGRFTISRDN SKNTLFLQMNLSRAEDTAIYYC ARLRGFFYYGMDVWGQGT TTVTVSSGGGGSGGGSGGGSGGGSDIVLTQSPSLPVT PGPAS ISCRSSQSLHNSKNYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTL KISRVEAEDVGVIYCMQALQTPPITFGCGTRLEIKSGGGGSEVQLVESGGGLVQPGGS LKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYAEAVKGRFTISR DSKNTVYLQMNNLKTEDTAVYYCVRNENIGTSYISYWAYWGQGTTLTVTVSSGGGGSGGG SGGGSGSQT VVTQEP SLTVSPGGT VTI TCGSSTGAVTSGNYPNWVQKPKGQAPRGLIG GTKFLAPGT PARFSGSLSGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVL GGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVK FNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPI

[illegible]

[illegible]

			TCRASSSVSYMHWYQQKPGQAPRLLIYGTSNLVSGVPAFSGSGSGTEFTLTISSLQS EDFAVYYCQQWSSYPLTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAAS GFTFNKYAINWVRQAPGKLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYL QMNNLKTEDTAVYYCARAGNFGSSYISYWAYWGQGLTIVTSSGGGSGGGGSGGGGSQ TVVTQEPSTLVSPGGTVTITCGSSTGAVTSGNYPNWWQKKPGQAPRGLIGGTFKLAPG TPARFSGSLSGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV EVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSGGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGSGGGG SGGGSGGGSGGGSGGGSGGGSDKHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRT EVTCTVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK
2533	MS R4L CC x CH3 R170R CC x I2K x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCASGYTFTGYYIHVVRQAPGQCLEWMGWINPNSGGT NYAQKFQGRVTMTRDTSISTAYMELSRRLSDDTAVYYCARVEAVAGREYYFYSGMDVW GQGTITVTVSSGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGEKLGDKYVY WYQQKPGQSPVLVIYQSTKRPSGVPERFSGSNSGNTATLTISGTQAMDEADYYCQAYH ASTAVFGCGTKLTVLSSGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSSYWMHWV RQTPGKCLEWVSKIDPDDYTNYNQKVKGRFTISIDKSKNTLYLQMNLSRAEDTAVYY CARWDYSHFDVWGQGTITVTVSSGGGSGGGGSGGGGSEIVMTQSPATLSVSPGERATL TCRASSSVSYMHWYQQKPGQAPRLLIYGTSNLVSGVPAFSGSGSGTEFTLTISSLQS EDFAVYYCQQWSSYPLTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAAS GFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYAEAVKGRFTISRDDSKNTVYL QMNNLKTEDTAVYYCVRNENIGTSYISYWAYWGQGLTIVTSSGGGSGGGGSGGGGSQ TVVTQEPSTLVSPGGTVTITCGSSTGAVTSGNYPNWWQKPGQAPRGLIGGTFKLAPG TPARFSGSLSGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV EVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSGGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGSGGGG SGGGSGGGSGGGSGGGSGGGSDKHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRT EVTCTVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK
2534	MS R4L CC x CH3 R170R CC x I2L x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCASGYTFTGYYIHVVRQAPGQCLEWMGWINPNSGGT NYAQKFQGRVTMTRDTSISTAYMELSRRLSDDTAVYYCARVEAVAGREYYFYSGMDVW GQGTITVTVSSGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGEKLGDKYVY WYQQKPGQSPVLVIYQSTKRPSGVPERFSGSNSGNTATLTISGTQAMDEADYYCQAYH ASTAVFGCGTKLTVLSSGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSSYWMHWV RQTPGKCLEWVSKIDPDDYTNYNQKVKGRFTISIDKSKNTLYLQMNLSRAEDTAVYY CARWDYSHFDVWGQGTITVTVSSGGGSGGGGSGGGGSEIVMTQSPATLSVSPGERATL TCRASSSVSYMHWYQQKPGQAPRLLIYGTSNLVSGVPAFSGSGSGTEFTLTISSLQS EDFAVYYCQQWSSYPLTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAAS GFTFNKYAMNWRQAPGKMEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYL QMNNLKTEDTAVYYCVRAGNFGSSYISYFAYWGQGLTIVTSSGGGSGGGGSGGGGSQ TVVTQEPSTLVSPGGTVTITCGSSTGAVTSGNYPNWIQKKPGQAPRGLIGGTFKLAPG TPARFSGSLSGGKAALTLSGVQPEDEAEYYCVLYYSNRWVFGSGTKLTVLGGGDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV EVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSGGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGSGGGG SGGGSGGGSGGGSGGGSGGGSDKHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRT EVTCTVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK
2535	MS R4L CC x CH3 R170R CC x I2M x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCASGYTFTGYYIHVVRQAPGQCLEWMGWINPNSGGT NYAQKFQGRVTMTRDTSISTAYMELSRRLSDDTAVYYCARVEAVAGREYYFYSGMDVW GQGTITVTVSSGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGEKLGDKYVY WYQQKPGQSPVLVIYQSTKRPSGVPERFSGSNSGNTATLTISGTQAMDEADYYCQAYH ASTAVFGCGTKLTVLSSGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSSYWMHWV RQTPGKCLEWVSKIDPDDYTNYNQKVKGRFTISIDKSKNTLYLQMNLSRAEDTAVYY CARWDYSHFDVWGQGTITVTVSSGGGSGGGGSGGGGSEIVMTQSPATLSVSPGERATL TCRASSSVSYMHWYQQKPGQAPRLLIYGTSNLVSGVPAFSGSGSGTEFTLTISSLQS EDFAVYYCQQWSSYPLTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAAS GFTFNKYAMNWRQAPGKMEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTLYL QMNNLKTEDTAVYYCVRAGNFGTSYISYWAYWGQGLTIVTSSGGGSGGGGSGGGGSQ TVVTQEPSTLVSPGGTVTITCGSSTGAVTSGNYPNWWQKKPGQAPRGLIGGTFKLAPG TPARFSGSLSGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV EVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSGGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGSGGGG SGGGSGGGSGGGSGGGSGGGSDKHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRT

			EVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNLGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
2536	MS R4L CC x CH3 R170R CC x I2M2 x scFc - Full Sequence	artificial	QVQLVQSGAEVKKPGASVKVSCKASGYTFYGGYIHVVRQAPGQCLEWMGWINPNSGGTNYAQKFQGRVTMTTRDTSISTAYMELSRRLSDDTAVYYCARVEAVAGREYFYFSGMDVWGGQTTVTVSSGGGGSGGGGGSGGGSSYELTQPPSVSVSPGQTASITCSGEKLGDKYVYWYQQKPGQSPVLVIYQSTKRPSGVPERFSGSNSGNATLTISGTQAMDEADYYCQAYHASTAVFGCGTKLTVLSSGGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSSYWMHWVRQTPGKCLEWVSKIDPDDYTNYNQKVKGRFTISIDKSKNTLYLQMNLSRAEDTAVYYCARWDYSHFDVWGQTTVTVSSGGGGSGGGGGSGGGSEIVMTQSPATLSVSPGERATLTCRASSSVSYMHVYQQKPGQAPRLLIYGTSNLSVSGVPARFSGSGSGTEFTLTISLQSSEDFAVYYCQWSSYPLTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVREAPGKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRNANFGTSYISYFAYWGQGLVTVSSGGGGSGGGGGSGGGGSGQTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGNYPNWWQKPGQAPRGLIGGKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYCVLWYSNRWVFGSGTKLTVLGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNLGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGGGSGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNLGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
2551	(G4Q)3 - Linker	artificial	GGGGQGGGGQGGGGQ
2552	Human CD3epsilon ECD	artificial	QDGNEEMGGITQTPYKVSISGTTVILTCTPQYPGSEILWQHNDKNIGGEDDKNIGSDE DHLSLKEFSELEQSGYYVCYPRGSKPEDANFYLYLRARVCENCMEMD
2553	Human CD3epsilon ECD / pos. 1-27	artificial	QDGNEEMGGITQTPYKVSISGTTVILT
2554	I2C_HC_H109 A- HCDR1	artificial	KYAMN
2555	I2C_HC_H109 A - HCDR2	artificial	RIRSKYNNYATYYADSVKD
2556	I2C_HC_H109 A - HCDR3	artificial	AGNFGNSYISYWAY
2557	I2C_HC_H109 A - LCDR1	artificial	GSSTGAVTSGNYPN
2558	I2C_HC_H109 A - LCDR2	artificial	GTKFLAP
2559	I2C_HC_H109 A - LCDR3	artificial	VLWYSNRWV
2560	I2C_HC_H109 A - VH	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRAGNFGNSYISYWAYWGQGLTVTVSS
2561	I2C_HC_H109 A - VL	artificial	QTVVTQEPSTLTVSPGGTVTTLTCSSTGAVTSGNYPNWWQKPGQAPRGLIGGKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYCVLWYSNRWVFGGGTKLTVL

Claims

1. A polypeptide or polypeptide construct comprising:
 - 5 a binding domain binding to an extracellular epitope of the human CD3ε chain comprising or consisting of a VH region and a VL region, wherein
 - i) the VH region comprises:
 - a CDR-H1 sequence of X_1YAX_2N , where X_1 is K, V, S, G, R, T, or I; and X_2 is M or I;
 - 10 a CDR-H2 sequence of $RIRSKYNNYATYYADX_1VKX_2$, where X_1 is S or Q; and X_2 is D, G, K, S, or E; and
 - a CDR-H3 sequence of $HX_1NFGNSYX_2SX_3X_4AY$, where X_1 is G, R, or A; X_2 is I, L, V, or T; X_3 is Y, W or F; and X_4 is W, F or Y; and
 - ii) wherein the VL region comprises:
 - 15 a CDR-L1 sequence of $X_1SSTGAVTX_2X_3X_4YX_5N$, where X_1 is G, R, or A; X_2 is S or T; X_3 is G or S; X_4 is N or Y; and X_5 is P or A;
 - a CDR-L2 sequence of $X_1TX_2X_3X_4X_5X_6$; where X_1 is G or A; X_2 is K, D, or N; X_3 is F, M or K; X_4 is L or R; X_5 is A, P, or V; and X_6 is P or S; and
 - a CDR-L3 sequence of $X_1LWYSNX_2WV$, where X_1 is V, A, or T; and X_2 is R or L;
 - 20 and
 - iii) wherein one or more of CDR sequences of the VH region of i) and/or of the VL region of ii) comprise one amino acid substitution or a combination thereof selected from X_24V and X_24F in CDR-H1; D15, and X_116A in CDR-H2; H1, X_12E , F4, and N6 in CDR-H3; and X_11L and W3 in CDR-L3.
2. The polypeptide or polypeptide construct of claim 1, wherein in addition to said one amino acid substitution or a combination thereof as defined in iii) X_2 is I in said CDR-H1 sequence; X_2 is G in said CDR-H2 sequence; X_1 is A, X_4 is F in said CDR-H3 sequence; and/or X_1 is A in said CDR-L3 sequence.
3. The polypeptide or polypeptide construct of claim 1 or 2, comprising combinations of said amino acid substitutions as defined in iii) of two, three, four, five, six, seven, eight, nine, ten, eleven, twelve or more amino acid substitutions.
4. The polypeptide or polypeptide construct of any one of claims 1 to 3, wherein:

- i) said one amino acid substitution is selected from:
 a. X₂4V or X₂4F in CDR-H1; H1A in CDR-H3; and
 b. X₁1L and W3Y in CDR-L3;
- ii) said combination of two or more amino acid substitutions are selected from X₁16A in CDR-H2 and N6S in CDR-H3; and X₁16A in CDR-H2 and N6T in CDR-H3;
- iii) said combination of three or more amino acid substitutions are selected from X₁16A in CDR-H2, H1A and N6S in CDR-H3; X₁16A in CDR-H2, H1A and N6T in CDR-H3; X₁16A in CDR-H2, H1N and N6T in CDR-H3;
- iv) said combination of four or more amino acid substitutions are selected from X₁16A in CDR-H2, H1A, N6S in CDR-H3, and W3Y in CDR-L3; D15E, X₁16A in CDR-H2, H1A, and N6T in CDR-H3; D15E, X₁16A in CDR-H2, H1A, and N6S in CDR-H3; X₁16A in CDR-H2, H1A, F4I and N6S in CDR-H3; or
- v) said combination of five or six amino acid substitutions are selected from X₁16A in CDR-H2, H1A, X₁2E, F4I, and N6T in CDR-H3; X₁16A in CDR-H2, H1N, X₁2E, F4I, and N6S in CDR-H3; D15E, X₁16A in CDR-H2, H1A, N6S in CDR-H3; and W3Y in CDR-L3; D15E, X₁16A in CDR-H2, H1N, X₁2E, F4I and N6T in CDR-H3; D15E, X₁16A in CDR-H2, H1A, X₁2E, F4I and N6T in CDR-H3; D15E, X₁16A in CDR-H2, X₁2E, F4I and N6T in CDR-H3.
5. A polypeptide or polypeptide construct comprising: a binding domain binding to an extracellular epitope of the human CD3ε chain comprising or consisting of a VH region and a VL region, wherein
- i) the VH region comprises the sequence of EVX₁LX₂ESGGGLX₃QPX₄GSLKLSCAASGFTFNX₅YAX₆NWVRQAPGKGLEWWARIRSKYNNYATYYADX₇VKX₈RFTISRDDSX₉X₁₀X₁₁X₁₂YLQMNNLKTEDTAX₁₃YYCV RHX₁₄NFGNSYX₁₅SX₁₆X₁₇AYWGQGTLVTVSX₁₈, where X₁ is Q or K; X₂ is V or L; X₃ is V or E; X₄ is G or K; X₅ is K, V, S, G, R, T, or I; X₆ is M or I; X₇ is S or Q; X₈ is D, G, K, S, or E; X₉ is K or Q; X₁₀ is N or S; X₁₁ is T or I; X₁₂ is A or L; X₁₃ is V or M; X₁₄ is G, R or A; X₁₅ is I, L, V, or T; X₁₆ is Y, W or F; X₁₇ is W, F or Y; and X₁₈ is S or A; and
- ii) the VL region comprises the sequence of QX₁VVTQEX₂X₃LTX₄SPGX₅TVTLTCX₆SSTGAVTX₇X₈X₉YX₁₀NWVQX₁₁KPX₁₂X₁₃X₁₄X₁₅X₁₆GLIGX₁₇TX₁₈X₁₉X₂₀X₂₁X₂₂GX₂₃PARFSGSLX₂₄GX₂₅KAALTX₂₆X₂₇GX₂₈QX₂₉E DEAX₃₀YX₃₁CX₃₂LWYSNX₃₃WVFGGGTKLTVL, where X₁ is T or A; X₂ is P or S; X₃ is S or A; X₄ is V or T; X₅ is G or E; X₆ is G, R, or A; X₇ is S or T; X₈ is G or S; X₉ is N or Y; X₁₀ is P or A; X₁₁ is Q or E; X₁₂ is G or D; X₁₃ is Q or H; X₁₄ is A or L; X₁₅ is P or F; X₁₆ is R or T; X₁₇ is G or A; X₁₈ is K or D; X₁₉ is F or M; X₂₀ is L or R; X₂₁ is

A, P or V; X₂₂ is P or S; X₂₃ is T or V; X₂₄ is L or I; X₂₅ is G or D; X₂₆ is L or I; X₂₇ is S or T; X₂₈ is V or A; X₂₉ is P or T; X₃₀ is E or I; X₃₁ is Y or F; X₃₂ is V, A, or T; X₃₃ is R or L; and

iii) wherein the VH and/or VL region sequence comprises one amino acid substitution or a combination thereof selected from

a. N30, X₆34V, X₆34F, Q39, L45, D64, X₇65A, X₁₂81V, X₁₂81T, X₁₂81I, V99, H101, X₁₄102E, F104, and N106 in the VH region sequence in i); and

b. L20, V38, X₁₁40R, X₁₁40K, X₂₄69, X₃₂91L, X₃₃93, and G102 in the VL region sequence in ii).

6. The polypeptide or polypeptide construct of claim 5, wherein in addition to said one amino acid substitution or a combination thereof as defined in iii) X₆ is I; X₈ is G; X₁₂ is L, X₁₄ is A, X₁₇ is F in said VH region sequence; and/or X₃₂ is A in said VL region sequence.

7. The polypeptide or polypeptide construct of claim 5 or 6, comprising combinations of said amino acid substitutions as defined in iii) of two, three, four, five, six, seven, eight, nine, ten, eleven, twelve or more amino acid substitutions.

8. The polypeptide or polypeptide construct of any one of claims 5 to 7, wherein:

i) said one acid substitution is selected from

a. X₆34V, Q39E, Q39K, Q39R, Q39D, L45M, L45V, X₁₂81V, X₁₂81T, X₁₂81I, V99A, V99L, H101A, H101N in the VH region; and

b. V38I, V38L, V38M, V38F, V38Y, X₁₁40R, X₁₁40K, X₂₄69S, X₂₄69E, X₃₂91L, X₃₃93Y;

ii) said combination of two or more amino acid substitutions are selected from X₆34F and X₁₂81V in the VH region; Q39E in the VH region and X₁₁40K in the VL region; Q39E in the VH region and X₁₁40R in the VL region; Q39D in the VH region and X₁₁40K in the VL region; Q39D in the VH region and X₁₁40R in the VL region; L45V in the VH region and V38F in the VL region; L45V in the VH region and V38Y in the VL region; L45M in the VH region and X₁₁40K in the VL region; L20I and G102S in the VL region; X₁₂81V in the VH region and X₁₁40K in the VL region;

iii) said combination of three or more amino acid substitutions are selected from Q39E in the VH region, X₁₁40K and G102S in the VL region; Q39E in the VH region, X₁₁40R and G102S in the VL region; Q39D in the VH region, X₁₁40K and G102S in the VL region; Q39D in the VH region, X₁₁40R and G102S in the VL region; L45M in the VH region, X₁₁40K and G102S in the VL region; X₇65A, H101A, and N106S in the VH region; L20I, X₁₁40K, and G102S in the VL region;

- iv) said combination of four or more amino acid substitutions are selected from Q39E in the VH region, L20I, X₁₁40K and G102S in the VL region; Q39E in the VH region, L20I, X₁₁40R and G102S in the VL region; Q39D in the VH region, L20I, X₁₁40K and G102S in the VL region; Q39D in the VH region, L20I, X₁₁40R and G102S in the VL region; L45M in the VH region, L20I, X₁₁40K and G102S in the VL region; L20I, X₁₁40K, X₂₄69S, and G102S in the VL region; X₁₂81V in the VH region, L20I, X₁₁40K, and G102S in the VL region;
- 5 v) said combination of five, six, seven, eight, nine, ten, or more amino acid substitutions are selected from X₇65A, X₁₂81V, V99A, N106S in the VH region, L20I, X₁₁40K, X₂₄69S, and G102S in the VL region; D64E, X₇65A, X₁₂81V, X₁₄102E, F104I, N106T in the VH region, L20I, X₂₄69S, and G102S in the VL region; L45M, X₇65A, N106T in the VH region, L20I, X₁₁40K, X₂₄69S, and G102S in the VL region; X₇65A, X₁₂81V, V99A, H101A, F104I, N106S in the VH region, L20I, X₁₁40K, X₂₄69S, and G102S in the VL region; X₇65A, X₁₂81V, V99A, H101A, N106S in the VH region; X₁₂81V, V99A in the VH region, L20I, X₁₁40K, X₂₄69S, and G102S in the VL region; Q39E, X₁₂81V in the VH region, L20I, X₁₁40K, and G102S in the VL region; L45V in the VH region, L20I, V38F, X₁₁40K and G102S in the VL region.
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- 15
- 20 9. The polypeptide or polypeptide construct of any one of claims 5 to 8, wherein said combination of amino acid substitutions is selected from:
- ii) in the VH region
- a. X₇65A, X₁₂81V, V99A, H101A and N106S;
- b. D64E, X₇65A, A81V, H101N, X₁₄102E, F104I, and N106S;
- 25 c. L45M, X₇65A, H101A, and N106T;
- d. L45M, X₇65A, H101A, and N106S;
- e. Q39E, X₇65A, H101N, and N106T;
- f. D64E, X₇65A, V99A, H101A, and N106T;
- g. X₇65A, X₁₂81V, V99A, H101A, X₁₄102E, F104I, and N106T;
- 30 h. X₇65A, X₁₂81V, H101N, X₁₄102E, F104I, and N106S;
- i. D64E, X₇65A, X₁₂81V, H101A, and N106S;
- j. D64E, X₇65A, H101A, and N106T;
- k. X₇65A, V99A, H101A, and N106T;
- l. D64E, X₇65A, H101A, and N106S;
- 35 m. D64E, X₇65A, X₁₂81V, V99A, H101A, and N106S;
- n. X₇65A, H101A and N106S;
- o. N30S, Q39E, D64E, X₇65A, X₁₂81V, H101A, X₁₄102E, F104I, and N106T;

- p. L45M, D64E, X₇65A, H101A, and N106T;
- q. N30S, L45M, X₇65A, X₁₂81V, H101A, and N106T;
- r. N30S, L45M, D64E, X₇65A, X₁₂81V, H101A, and N106S;
- iii) in the VL region
 - a. L20I, X₁₁40K, X₂₄69S, and G102S;
 - b. L20I, X₂₄69S, and G102S;
 - c. L20I, V38I, X₁₁40K, X₂₄69E, G102S and X₃₃93Y;
 - d. X₁₁40K and G102S;
 - e. L20I, X₁₁40K, X₂₄69S, G102S and X₃₃93Y;
 - f. L20M, X₁₁40K and X₂₄69E;
 - g. L20I, V38I, X₁₁40K, X₂₄69E and G102S;
 - h. X₁₁40K, X₂₄69S and X₃₃93Y; or
 - i. X₁₁40K and X₂₄69S; and
- iv) a combination of one amino acid substitution combination of i) and ii).

10. The polypeptide or polypeptide construct of claim 9, wherein said combination of amino acid substitution combinations of iii) is selected from:

- a. X₇65A, X₁₂81V, V99A, H101A, N106S in the VH region, L20I, X₁₁40K, X₂₄69S, and G102S in the VL region;
- b. D64E, X₇65A, X₁₂81V, H101N, X₁₄102E, F104I, N106S in the VH region, L20I, X₂₄69S, and G102S in the VL region;
- c. L45M, X₇65A, H101A, N106T in the VH region, L20I, X₁₁40K, X₂₄69S, and G102S in the VL region;
- d. L45M, X₇65A, H101A, N106S in the VH region, L20I, V38I, X₁₁40K, X₂₄69E, G102S and X₃₃93Y in the VL region;
- e. Q39E, X₇65A, H101N, N106T in the VH region, X₁₁40K and G102S in the VL region;
- f. D64E, X₇65A, V99A, H101A, N106T in the VH region, X₁₁40K and G102S in the VL region;
- g. X₇65A, X₁₂81V, V99A, H101A, X₁₄102E, F104I, N106T in the VH region, L20I, X₁₁40K, X₂₄69S, and G102S in the VL region;
- h. X₇65A, X₁₂81V, H101N, X₁₄102E, F104I, N106S in the VH region, L20I, X₂₄69S, and G102S in the VL region;
- i. D64E, X₇65A, X₁₂81V, H101A, N106S in the VH region, L20I, X₂₄69S, and G102S in the VL region;
- j. D64E, X₇65A, H101A, N106T in the VH region, X₁₁40K and G102S in the VL region;

- k. X₇65A, V99A, H101A, N106T in the VH region, X₁₁40K and G102S in the VL region;
- l. D64E, X₇65A, H101A, N106S in the VH region, X₁₁40K and G102S in the VL region;
- 5 m. D64E, X₇65A, X₁₂81V, V99A, H101A, N106S in the VH region, L20I, X₁₁40K, X₂₄69S, G102S and X₃₃93Y in the VL region;
- n. X₇65A, H101A, N106S in the VH region, X₁₁40K and G102S in the VL region;
- o. N30S, Q39E, D64E, X₇65A, X₁₂81V, H101A, X₁₄102E, F104I, N106T in the VH region, L20M, X₁₁40K and X₂₄69E in the VL region;
- 10 p. L45M, D64E, X₇65A, H101A, N106T in the VH region, L20I, V38I, X₁₁40K, X₂₄69E and G102S in the VL region;
- q. N30S, L45M, X₇65A, X₁₂81V, H101A, N106T in the VH region, X₁₁40K and X₂₄69S in the VL region; and
- r. N30S, L45M, D64E, X₇65A, X₁₂81V, H101A, N106S in the VH region, X₁₁40K and
15 X₂₄69S in the VL region.

11. The polypeptide or polypeptide construct of claim 10, wherein in said combination of amino acid substitution combinations defined in:
- a. and m. X₆ is I in said VH region sequence;
 - 20 b. and r. X₈ is G in said VH region sequence;
 - c. X₁₂ is L in said VH region;
 - d. X₁₂ is L and X₁₇ is F in said VH region;
 - e. X₆ is I, X₁₄ is A and X₁₇ is F in said VH region sequence;
 - f. X₅ is I in said VH region sequence; and X₃₂ is A in said VL region sequence;
 - 25 g. X₅ is I in said VH region sequence;
 - h. and i. X₈ is G in said VH region sequence;
 - j., l. and n. X₆ is I and X₁₇ is F in said VH region sequence; and X₃₂ is A in said VL region sequence;
 - k. X₆ is I in said VH region sequence; and X₃₂ is A in said VL region sequence;
 - 30 p. X₁₂ is L in said VH region; and
 - q. X₈ is G and X₁₇ is F in said VH region sequence.

12. The polypeptide or polypeptide construct of claim 5, or any one of claims 6 to 11, wherein said VH and VL region of i) and ii) is selected from the VH and VL region combinations as defined in SEQ ID NOs: 124 and 125, 172 and 173, 362 and 363, 552 and 553, 730 and 731, 928 and 929, 1106 and 1107, 1296 and 1297, 1474 and 1475, 1664 and 1665, and 1854 and 1855, wherein said one amino acid substitution or a
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combination thereof in said VH and/or VL region sequence results in a VH and/or a VL region sequence having the amino acid residue:

- i. I at position 34, A at position 65, V at position 81, A at position 99, A at position 101, S at position 106 in the VH region sequence, I at position 20, K at position 40, S at position 69, and S at position 102 in the VL region sequence;
M at position 45, A at position 65, L at position 81, A at position 101, T at position 106 in the VH region sequence, I at position 20, K at position 40, S at position 69 and S at position 102 in the VL region sequence;
M at position 45, A at position 65, L at position 81, A at position 101, S at position 106, F at position 112 in the VH region sequence, I at position 20, I at position 38, K at position 40, E at position 69, S at position 102 and Y at position 93 in the VL region sequence;
I at position 34, E at position 39, A at position 65, N at position 101, A at position 102, T at position 106, F at position 112 in the VH region sequence, K at position 40 and S at position 102 in the VL region sequence;
I at position 34, E at position 64, A at position 65, A at position 99, A at position 101, T at position 106 in the VH region sequence, K at position 40, A at position 91 and S at position 102 in the VL region sequence;
I at position 34, A at position 65, V at position 81, A at position 99, A at position 101, E at position 102, I at position 104, T at position 106 in the VH region sequence, I at position 20, K at position 40, S at position 69 and S at position 102 in the VL region sequence;
E at position 64, A at position 65, G at position 68, V at position 81, A at position 101, S at position 106 in the VH region sequence, I at position 20, S at position 69 and S at position 102 in the VL region sequence;
I at position 34, E at position 64, A at position 65, A at position 101, T at position 106, F at position 112 in the VH region sequence, K at position 40, A at position 91 and S at position 102 in the VL region sequence;
I at position 34, E at position 64, A at position 65, A at position 101, S at position 106, F at position 112 in the VH region sequence, K at position 40, A at position 91 and S at position 102 in the VL region sequence;
I at position 34, E at position 64, A at position 65, V at position 81, A at position 99, A at position 101, S at position 106 in the VH region sequence, I at position 20, K at position 40, S at position 69, S at position 102 and Y at position 93 in the VL region sequence;
I at position 34, A at position 65, A at position 101, S at position 106, F at position 112 in the VH region sequence, K at position 40, A at position 91 and S

at position 102 in the VL region sequence;

M at position 45, E at position 64, A at position 65, L at position 81, A at position 101, T at position 106 in the VH region sequence, I at position 20, I at position 38, K at position 40, E at position 69 and S at position 102 in the VL region sequence;

S at position 30, M at position 45, A at position 65, G at position 68, V at position 81, A at position 101, T at position 106, F at position 112 in the VH region sequence, K at position 40, S at position 69 and Y at position 93 in the VL region sequence; and

S at position 30, M at position 45, E at position 64, A at position 65, G at position 68, V at position 81, A at position 101, S at position 106 in the VH region sequence, K at position 40 and S at position 69 in the VL region sequence;

ii. E at position 64, A at position 65, G at position 68, V at position 81, N at position 101, E at position 102, I at position 104, T at position 106 in the VH region sequence, I at position 20, S at position 69 and S at position 102 in the VL region sequence;

A at position 65, G at position 68, V at position 81, N at position 101, E at position 102, I at position 104, S at position 106 in the VH region sequence, I at position 20, S at position 69 and S at position 102 in the VL region sequence;

I at position 34, A at position 65, A at position 99, A at position 101, T at position 106 in the VH region sequence, K at position 40, A at position 91 and S at position 102 in the VL region sequence; and

S at position 30, E at position 39, E at position 64, A at position 65, V at position 81, A at position 101, E at position 102, I at position 104, T at position 106 in the VH region sequence, M at position 20, K at position 40 and E at position 69 in the VL region sequence;

iii. A at position 101 in the VH region sequence;

iv. V at position 81, A at position 99 in the VH region sequence, I at position 20, K at position 40, S at position 69 and S at position 102 in the VL region sequence; I at position 34, V at position 81 in the VH region sequence, I at position 20, K at position 40 and S at position 102 in the VL region sequence;

I at position 34 in the VH region sequence, I at position 20, K at position 40 and S at position 102 in the VL region sequence;

I at position 34, E at position 39, V at position 81 in the VH region sequence, I at position 20, K at position 40 and S at position 102 in the VL region sequence;

- v. I at position 34, V at position 81 in the VH region sequence, and K at position 40 in the VL region sequence;
M at position 45 in the VH region sequence, I at position 20, K at position 40 and S at position 102 in the VH region sequence;
5 I at position 34, A at position 65, A at position 101 and S at position 106 in the VH region sequence;
I at position 20, K at position 40, S at position 69 and S at position 102 in the VL region sequence;
F at position 34 and V at position 81 in the VH region sequence;
10 M at position 45 in the VH region sequence, K at position 40 and S at position 102 in the VL region sequence;
D at position 39 in the VH region sequence, I at position 20, K at position 40 and S at position 102 in the VL region sequence;
I at position 34 and V at position 81 in the VH region sequence;
15 E at position 39 in the VH region sequence, I at position 20, K at position 40 and S at position 102 in the VL region sequence;
M at position 45 in the VH region sequence and K at position 40 in the VL region sequence;
I at position 34, A at position 65, V at position 81, A at position 99, A at position 101 and S at position 106 in the VH region sequence; or
20 vi. D at position 39 in the VH region sequence, I at position 20, R at position 40 and S at position 102 in the VL region sequence;
I at position 34 in the VH region sequence;
K at position 40 in the VL region sequence;
25 D at position 39 in the VH region sequence, K at position 40 and S at position 102 in the VL region sequence;
I at position 20 and S at position 102 in the VH region sequence;
K at position 39 in the VH region sequence;
E at position 39 in the VH region sequence, K at position 40 and S at position 102 in the VL region sequence;
30 E at position 39 in the VH region sequence, I at position 20, R at position 40 and S at position 102 in the VL region sequence;
D at position 39 in the VH region sequence, R at position 40 and S at position 102 in the VL region sequence;
35 V at position 81 in the VH region sequence;
D at position 39 in the VH region sequence and K at position 40 in the VL region sequence;

F at position 112 in the VH region sequence;

F at position 112 in the VH region sequence and_I at position 38 in the VL region sequence;

E at position 39 in the VH region sequence and K at position 40 in the VL region sequence;

V at position 34 in the VH region sequence.

13. The polypeptide or polypeptide construct of any one of claims 1 to 12, wherein the VH and VL region sequence are linked by a linker.

14. The polypeptide or polypeptide construct of claim 13, wherein the linker is a peptide linker.

15. The polypeptide or polypeptide construct of claim 14, wherein said peptide linker comprises or consists of a G₄S linker, or G₄Q linker or repetitions thereof.

16. The polypeptide or polypeptide construct of any one of claims 1 to 15, wherein the polypeptide or polypeptide construct comprises at least one further binding domain.

17. The polypeptide or polypeptide construct of claim 16, wherein said at least one further binding domain binds to a cell surface antigen.

18. The polypeptide or polypeptide construct of claim 17, wherein said cell surface antigen is a tumor antigen.

19. The polypeptide or polypeptide construct of claim 18, wherein the tumor antigen is selected from the group consisting of BCMA, CD123, CD19, CD20, CD22, CD33, CD70, CDH19, CDH3, CLL1, CS1, CLDN6, CLDN18.2, DLL3, EGFRvIII, FLT3, MAGEB2, MART1, MSLN, MUC17, PSMA, and STEAP1.

20. The polypeptide or polypeptide construct of any one of claims 1 to 19, wherein said polypeptide or polypeptide construct is a single chain polypeptide that is at least bispecific.

21. A polynucleotide encoding a polypeptide or polypeptide construct as defined in any one of claims 1 to 20.

22. A vector comprising a polynucleotide as defined in claim 21.

23. A host cell transformed or transfected with the polynucleotide as defined in claim 21 or with the vector as defined in claim 22.

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24. A process for the production of an polypeptide or polypeptide construct according to any one of claims 1 to 20, said process comprising culturing a host cell as defined in claim 23 under conditions allowing the expression of the polypeptide or polypeptide construct as defined in any one of claims 1 to 20 and recovering the produced polypeptide or polypeptide construct from the culture.

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25. A pharmaceutical composition comprising a polypeptide or polypeptide construct according to any one of claims 1 to 20, or produced according to the process of claim 24.

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26. The polypeptide or polypeptide construct of any one of claims 18 to 20, or produced according to the process of claim 24, for use in the prevention, treatment or amelioration of a disease selected from a tumorous disease.

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27. A method for the prevention, treatment or amelioration of a tumorous disease, comprising administering to a subject in need thereof the polypeptide or polypeptide construct according to any one of claims 18 to 20, or produced according to the process of claim 24.

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28. A kit comprising a polypeptide or polypeptide construct according to any one of claims 1 to 20, or produced according to the process of claim 24, a polynucleotide as defined in claim 21, a vector as defined in claim 22, and/or a host cell as defined in claim 23.

Figure 1

A)

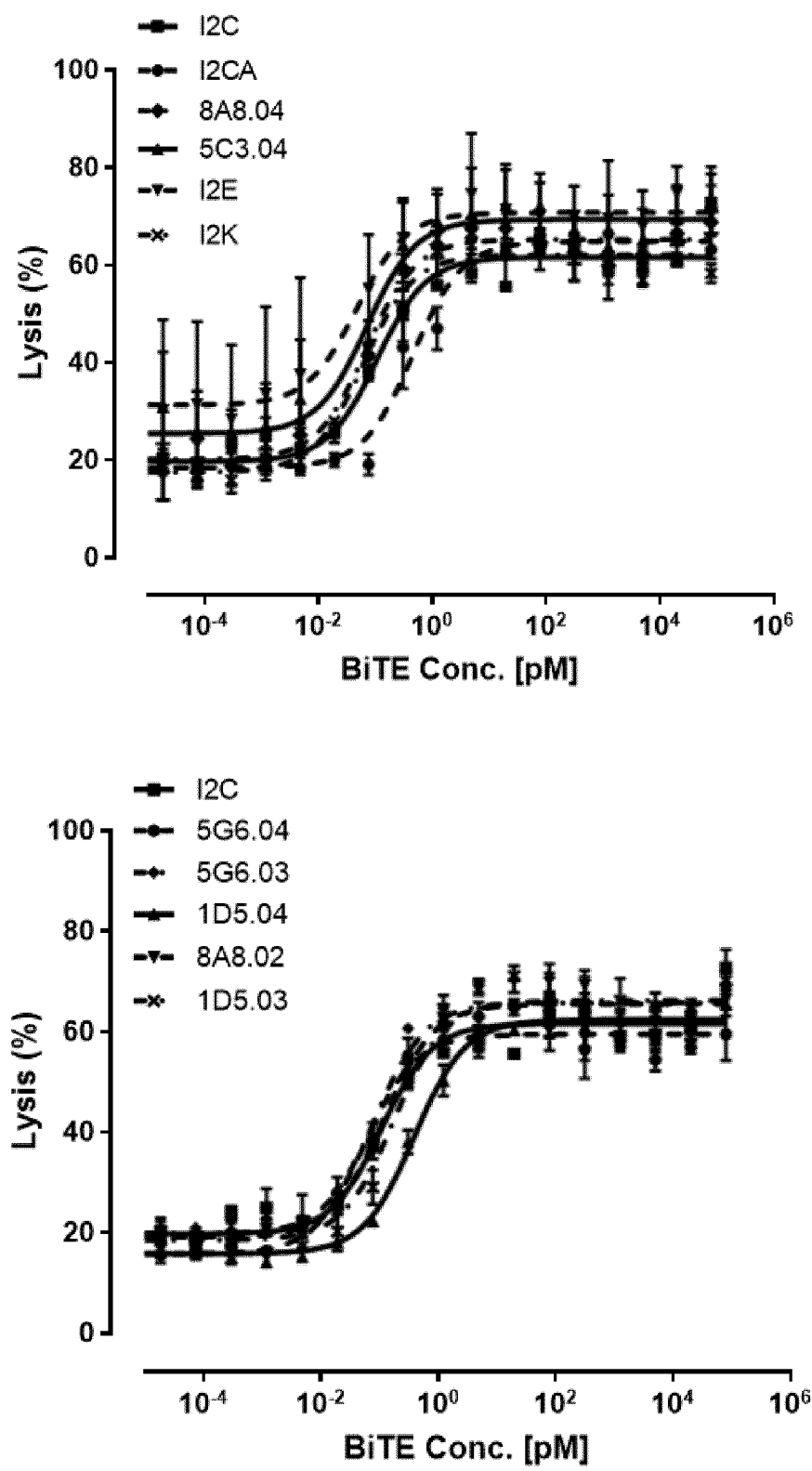
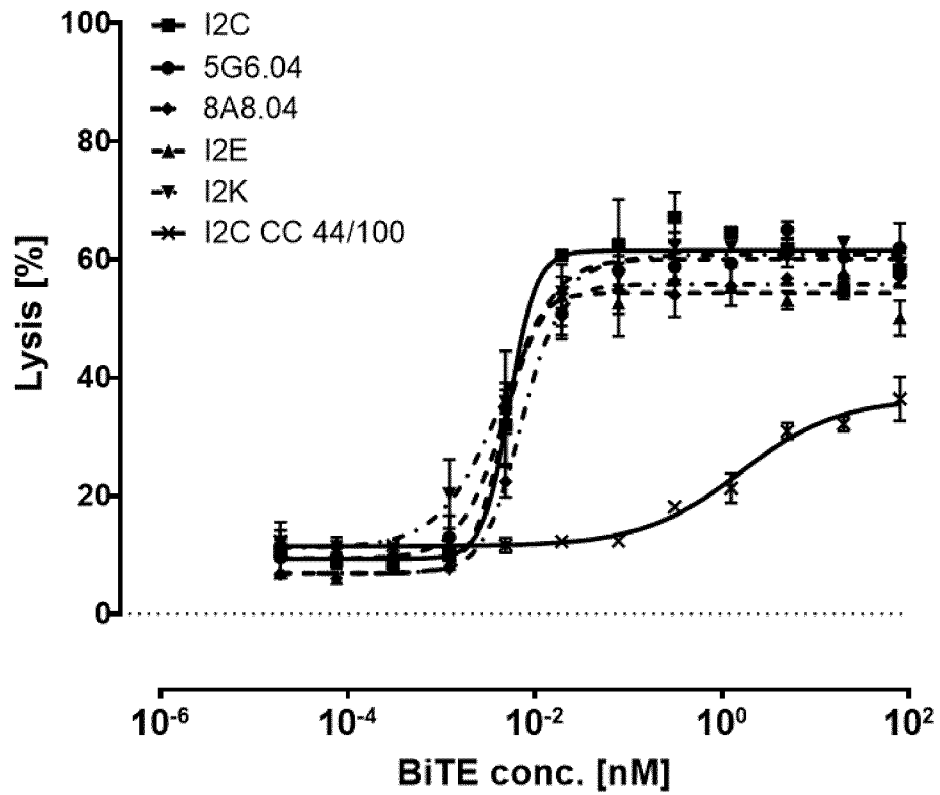


Figure 1 (continued)

B)



INTERNATIONAL SEARCH REPORT

International application No
PCT/EP2021/080859

A. CLASSIFICATION OF SUBJECT MATTER INV. C07K16/28 A61P35/00 ADD.		
According to International Patent Classification (IPC) or to both national classification and IPC		
B. FIELDS SEARCHED Minimum documentation searched (classification system followed by classification symbols) C07K A61P		
Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched		
Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) EPO-Internal, WPI Data		
C. DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 2017/021354 A1 (AMGEN RES GMBH [DE]; AMGEN INC [US]) 9 February 2017 (2017-02-09) [0197], [0361], [0371], [0553], [0764]-[0766] SEQ ID NOs. 842, 844, 878, 914, 916, 906, 907, 915, 918, 919 -----	1-28
X	US 2017/349668 A1 (RATTEL BENNO [DE] ET AL) 7 December 2017 (2017-12-07) Throughout, [0002], [0012], [0142], [0280]-[0324], claims 1, 6 -----	1-28
X	WO 2019/222283 A1 (HARPOON THERAPEUTICS INC [US]) 21 November 2019 (2019-11-21) [0007]-[0009], [0086], [0087], [0095], [0098], [0099], claims 45, 47, 54 ----- -/--	1-28
☒ Further documents are listed in the continuation of Box C. ☒ See patent family annex.		
* Special categories of cited documents : "A" document defining the general state of the art which is not considered to be of particular relevance "E" earlier application or patent but published on or after the international filing date "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) "O" document referring to an oral disclosure, use, exhibition or other means "P" document published prior to the international filing date but later than the priority date claimed "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention "X" document of particular relevance;; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone "Y" document of particular relevance;; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art "&" document member of the same patent family		
Date of the actual completion of the international search 28 February 2022		Date of mailing of the international search report 10/03/2022
Name and mailing address of the ISA/ European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Fax: (+31-70) 340-3016		Authorized officer Wimmer, Georg

INTERNATIONAL SEARCH REPORT

International application No

PCT/EP2021/080859

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 2018/224441 A1 (NUMAB INNOVATION AG [CH]) 13 December 2018 (2018-12-13) [0104]-[0111], [0150], [0151], [00154], [0169], Table 4, SEQ ID 13, 14 -----	1-28
A	ULRICH BRINKMANN ET AL: "The making of bispecific antibodies", MABS, vol. 9, no. 2, 10 January 2017 (2017-01-10), pages 182-212, XP055531122, US ISSN: 1942-0862, DOI: 10.1080/19420862.2016.1268307 the whole document -----	1-28

INTERNATIONAL SEARCH REPORT

International application No.

PCT/EP2021/080859

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

1. With regard to any nucleotide and/or amino acid sequence disclosed in the international application, the international search was carried out on the basis of a sequence listing:
 - a. ☒ forming part of the international application as filed:
 - ☒ in the form of an Annex C/ST.25 text file.
 - ☐ on paper or in the form of an image file.
 - b. ☐ furnished together with the international application under PCT Rule 13ter.1(a) for the purposes of international search only in the form of an Annex C/ST.25 text file.
 - c. ☐ furnished subsequent to the international filing date for the purposes of international search only:
 - ☐ in the form of an Annex C/ST.25 text file (Rule 13ter.1(a)).
 - ☐ on paper or in the form of an image file (Rule 13ter.1(b) and Administrative Instructions, Section 713).
2. ☐ In addition, in the case that more than one version or copy of a sequence listing has been filed or furnished, the required statements that the information in the subsequent or additional copies is identical to that forming part of the application as filed or does not go beyond the application as filed, as appropriate, were furnished.
3. Additional comments:

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No

PCT/EP2021/080859

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
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