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(54) Title: IMPROVED IMMUNOGLOBULIN VARIABLE DOMAINS

(57) Abstract: VH domain, in which: (i) the amino acid residue at position 1 12 is one of K or Q; and/or (ii) the amino acid residue at position 89 is T; and/or (iii) the amino acid residue at position 89 is L and the amino acid residue at position 1 10 is one of K or Q; and (iv) in each of cases (i) to (hi), the amino acid at position 1 1 is preferably V; and in which said VH domain contains a C-terminal extension (X)n, in which n is 1 to 10, preferably 1 to 5, such as 1, 2, 3, 4 or 5 (and preferably 1 or 2, such as 1); and each X is an (preferably naturally occurring) amino acid residue that is independently chosen, and preferably independently chosen from the group consisting of alanine (A), glycine (G), valine (V), leucine (L) or isoleucine (I).

Improved immunoglobulin variable domains

The present invention relates to improved heavy-chain immunoglobulin variable domains.

The invention in particular refers to improved heavy-chain immunoglobulin variable domains that either have an exposed C-terminal region or end (as further described herein; see also WO 12/175741) or that are used in (or intended for use in) applications where they have an exposed C-terminal region or end (again, as further described herein). Some preferred but non-limiting examples of the former are immunoglobulin single variable domains (also referred to herein as “ISV’s” or “ISVD’s”) such as Nanobodies (including VHH’s, humanized VHH’s and camelized VH’s such as camelized human VH’s), (single domain) antibodies that are VH domains or derived from VH domains, and dAb’s that are VH domains or derived from VH domains. Some preferred but non-limiting examples of the latter are VH domains that are used in (or intended for use in) single chain FV’s (ScFv’s) or diabodies.

The invention also relates to proteins, polypeptides and other constructs, molecules or chemical entities that comprise or essentially consist of (one or more of) the improved heavy-chain immunoglobulin variable domains of the invention as described herein; to methods for expressing/producing the improved heavy-chain immunoglobulin variable domains of the invention and/or for expressing/producing proteins, polypeptides and other constructs, molecules or chemical entities comprising the same; to compositions and products (such as pharmaceutical compositions and products) that comprise the improved heavy-chain immunoglobulin variable domains of the invention and/or proteins, polypeptides and other constructs, molecules or chemical entities comprising the same; to nucleotide sequence and nucleic acids that encode the improved heavy-chain immunoglobulin variable domains of the invention and/or that encode proteins or polypeptides comprising the same; and to uses (and in particular therapeutic, prophylactic and diagnostic uses) of the improved heavy-chain immunoglobulin variable domains of the invention and of proteins, polypeptides and other constructs, molecules or chemical entities comprising the same.

Further aspects, embodiments, advantages, applications and uses of the invention will become clear from the further description herein.

In the present application, the amino acid residues/positions in an immunoglobulin heavy-chain variable domain will be indicated with the numbering according to Kabat. For the sake of convenience, Figure 1 gives a table listing some of the amino acid positions that will be specifically referred to herein and their numbering according to some alternative

numbering systems (such as Aho and IMGT. Note: for the present description and claims, Kabat numbering is decisive; other numbering systems are given for reference only).

Also, in the invention, an immunoglobulin variable domain is said to have “an exposed C-terminal end or region” when it is not associated with or linked to a constant domain (such as a C_H1 domain). Reference is made to the relevant prior art cited herein.

In particular, as described in WO 12/175741, the C-terminal region (as this term is also used herein) is part of a putative epitope on the ISV that also includes, among other residues, the amino acid residue at position 14 (and the amino acid residues next/close to the same in the amino acid sequence, such as positions 11, 13 and 15) and may also comprise the

10 amino acid residue at position 83 (and the amino acid residues next/close to the same in the amino acid sequence, such as positions 82, 82a, 82b and 84) and/or the amino acid residue at position 108 (and the amino acid residues next/close to the same in the amino acid sequence, such as positions 107. As in WO 12/17574, this putative epitope is also collectively referred to herein as the “C-terminal region”, it being understood that this C-terminal region at least comprises the C terminal sequence VTVSS (i.e. each of positions 109, 110, 111, 112 and 113) and the amino acid residue at position 14, and may also comprise the amino acid residues at positions 83 and 108, and possibly also the amino acid residues at positions 13, 15, 82b, 83, 84 and 107.

As a result of research into single chain Fv's or "ScFv's" (which are constructs that 20 contain immunoglobulin variable domains that, similar to ISVD's, are not associated with constant domains), it has been described in the art that the C-terminus of an immunoglobulin variable domain contains a hydrophobic patch that in a conventional full-sized antibody is buried in the interface between the variable domain and the constant domain but that becomes solvent-exposed when the variable domain is not associated with a constant domain (see for example Nieba et al., Protein Engineering, 10, 435-444 (1997) and Harmsen et al., Molecular Immunology (2000), 579-590).

It is also well known that epitopes that are usually buried within the structure of a protein (also referred to as “neo-epitopes” or “cryptic epitopes”) may trigger the immune system once they become solvent-exposed, for example due to degradation, misfolding or 30 aggregation of the protein involved. For example, in the case of buried hydrophobic portions of biomolecules (so-called “hypos”), it has been suggested that these form part of a general damage-associated molecular pattern that leads to innate immune responses once the hypos become solvent-exposed (see for example Seong and Matzinger, Nature Reviews 2004, 469), and various examples of previously-buried hydrophobic patches triggering immune responses

have been described in the art (see for example David et al., JBC, 2001, 6370-6377; Matsuura et al., International Immunology, 2000, 1183-1192; Rasheed et al., Life Sciences 79 (2000), 2320-2328). More generally, it is also known in the art that hydrophobic amino acids are prone to be part of B-cell epitopes (see for example WO 11/07586, page 10; and Kolaskar, FEBS 276, 172-174 (1990)). Similarly, it has been described that the hydrophobic patch at the C-terminus of a heavy-chain variable domain (as described by Nieba et al. and Harmsen et al., *supra*) may form B-cell epitopes which can give rise to and/or interact with (emerging and/or pre-existing) anti-drug antibodies (WO 11/07586). For this reason, it has been proposed to make mutations to some of the amino acid residues that form part of the C-terminus of the 10 variable domains to reduce hydrophobicity and/or to remove B-cell epitopes. For example, Nieba et al. suggest to mutate positions 11, 14, 41, 84, 87 and/or 89 of a VH region (numbering according to Kabat), whereas in WO 11/07586 it is suggested to mutate positions 99, 101 and/or 148 (AHo numbering) of a VL domain or positions 12, 97, 98, 99, 103 and/or 144 of a VH domain (again AHo numbering - these positions correspond to positions 11, 83, 84, 85, 89 and 103 according to Kabat). Similarly, Harmsen et al. suggest to mutate positions 12 and 101 (IMGT numbering; these are positions 11 and 89 according to Kabat) to compensate for the absence of a C_{H1} domain; and they also identify a specific subfamily of VHH's (called "VHH4's") that contain amino acids that are suitable candidates for substitutions at these positions.

20 It has also been described in the art (see for example WO 12/175741 and the references cited in the next paragraphs) that biological samples obtained from human subjects may contain (pre-existing) proteins or factors that are capable of binding to the exposed C-terminal region or end of an immunoglobulin variable domain (for example, the C-terminal region or end of an ISVD or of a VH or VL domain in an ScFv or diobody).

For example, WO 2013/024059 states that "*in sera from some healthy naive human subjects, pre-existing anti-VH autoantibodies are present that can bind both VH domain antibodies and VHH molecules, as well as anti-VL (eg V kappa (VK)) autoantibodies that can bind VL molecules.*"", and that "*the pre-existing ADAs that bind VH dAbs are similar to anti-hinge antibodies in that they bind IgG fragments but not those same sequences found in situ on intact IgG.*"

Holland et al., J. Clin. Immunol. 2013, 33(7):1192-203 describe that the blood of around half of normal healthy humans contain varying levels of a new class of anti-IgG autoantibodies that can bind to the framework sequences of fully human V_H domain antibodies (which Holland et al. also refer to as "*HAVH auto-antibodies*"). Holland et al.

further mention that these auto-antibodies appear to be predominantly of the IgG isotype, display a relatively high affinity (about 10^{-10} M) affinity for V_H sequences, and that a free C-terminus appears to be important for the binding of these HAVH autoantibodies to V_H domains.

The issues relating to pre-existing biotherapeutic-reactive antibodies against biotherapeutic molecules and their regulatory impact are also generally discussed by Xue et al., AAPS J. 2013; 15(3):852-5.

The aforementioned prior art has also focused on ways in which the sequence of an immunoglobulin variable domain may be modified so as to prevent or reduce binding of such pre-existing antibodies/factor(s) to the variable domains. In this respect, WO 2011/07586 suggests to make one or more mutations in the amino acid sequence of the variable domain at some specific positions of the domain (which positions are surface-exposed). WO 12/175741 describes that the binding of such pre-existing antibodies/factors may be reduced by adding a few amino acid residues (and as little as one alanine residue) to the C-terminal end of the VH-domain and/or by making one or more specific substitutions or deletions within the C-terminal region of the variable domain, which is described in WO 12/175741 as at least comprising the C-terminal amino acid sequence VTVSS and the amino acid residue at position 14 (for which position WO 12/175741 teaches that the presence of an alanine residue provides for reduced binding of pre-existing antibodies as compared to the presence of the “human” amino acid residue proline), and possibly also the amino acid residues at positions 108 and 83 and amino acid residues close to said positions (WO 2013/024059 provides essentially the same teaching as WO 12/175741).

For example, in research performed by applicant/assignee leading up to the filing of WO 12/175741, it has been found that adding a single alanine residue to the C-terminal region or end of an exposed VH domain will usually prevent/remove (essentially all of) the binding of pre-existing antibodies/factors that are present in samples obtained from most human subjects (see for example page 62, lines 20-25 and page 57, line 30 to page 58, lines 3 of WO 12/175741) ; and these findings have been confirmed by additional results that were obtained by applicant/assignee after the filing of WO 12/175741 when the C-terminal alanine substitution of WO 12/175741 was applied to other Nanobodies (data not shown).

Also, in WO 12/175741 as well as in WO 12/175400 by applicant/assignee, the C-terminal extensions described in WO 12/175741 are applied to certain serum-albumin-binding Nanobodies (see for example WO 12/175741: SEQ ID NO's: 37, 51-53 and 55-64 and the

constructs shown in SEQ ID NO's: 41, 43 and 44; and WO 12/175400; SEQ ID NO's: 6 to 11).

Figure 9 of WO 12/175741 also describes two albumin-binding sequences that are used as reference sequences in the Experimental Part below. These are SEQ ID NO:37 from Figure 9 of WO 12/175741 (also referred to herein as "*Reference B*"; its sequence is given herein as SEQ ID NO: 45) and "*SEQ ID NO:37 without the added C-terminal amino acid residues*" from Figure 9 of WO 12/175741 (also referred to herein as "*Reference A*"; its sequence is given in SEQ ID NO:44). Reference A and Reference B are both derived from the sequence of the humanized anti-albumin Nanobody "*Alb-8*" that is given as SEQ ID NO:62 in WO 06/122787 (and that is also referred to herein as "*Alb-11*"); but, compared to the sequence of Alb-11, Reference A comprises an N-terminal His tag; and Reference B comprises an N-terminal His tag and a C-terminal alanine residue. Reference A, Reference B and Alb-8/Alb-11 all contain the CDRs given in SEQ ID NO's: 41 to 43, respectively.

Other examples of Nanobodies and other immunoglobulin single variable domains that have C-terminal extensions and/or mutations in the C-terminal region can for example be found in the following prior art: WO 06/129843 (see for example SEQ ID NO's: 4, 6, 8 and 10); WO 03/035695 (see for example some of the sequences listed on pages 61-64); Vu et al., Molecular Immunology, 1121-1131, 1997 (see for example some of the sequences listed in Figure 2); WO 11/003622 (see for example the sequences given as SEQ ID NO's: 10 to 27); WO 09/058383 (see for example the sequence TAR2h-10-27 mentioned on page 51); WO 10/042815 (see for example the sequences of SEQ ID NO's: 15, 17, 27 and 30); and WO 04/044204 (see for example the sequences of SEQ ID NO's: 31, 35, 37, 47 and 49).

Some of the references cited herein also give examples of ISVD sequences in which the last C-terminal amino acid of the ISVD is an amino acid other than serine (S), for example because the serine at position 113 has been replaced by another amino acid and/or because the serine at position 113 has been deleted and a C-terminal amino acid has been added (in practice, the end-result in terms of the C-terminal amino acid sequence will be the same).

Some of the references cited herein also give examples of Nanobodies and other immunoglobulin single variable domains in which position 112 is an amino acid other than serine. For example, WO 12/175741 describes Nanobodies in which position 112 is glycine (G); Vu et al. (supra) describes Nanobodies in which position 112 is alanine (A) or isoleucine (I); WO 13/024059 exemplifies a S112A substitution; and WO 08/020079 cited below exemplifies an S112F substitution and also generally states that the Nanobodies described

therein can contain a limited number of amino acid residues added at the carboxy-terminal end of the amino acid sequence of the Nanobody.

In the research leading up to the present invention, after having established that adding C-terminal extension (which may be as simple as a single C-terminal alanine residue, see again WO 12/175741, Example 3) to the C-terminal region or end of a nanobody essentially prevents/removes binding of pre-existing antibodies/factors in most samples of human subjects/patients, it was investigated whether samples obtained from human subjects (healthy volunteers and/or subjects suffering from a disease or disorder) possibly contain (other) pre-existing antibodies or factors that can bind to the exposed C-terminal region of a nanobody

10 (or other VH domain) even when a C-terminal extension is present. In doing so, the present inventors have found that, although essentially no such pre-existing antibodies binding to a C-terminally extended VH domain can be found in the blood or serum of healthy volunteers or in blood or serum obtained from human patients suffering from one of a number of different diseases (including some inflammatory diseases or auto-immune disorders – data not shown), some blood or serum samples that have been obtained from certain (but not all) human subjects suffering from certain severe (auto-)immune disorders (such as systemic lupus erythematosus; also abbreviated herein as “SLE”) appear to contain some pre-existing antibodies/factors that can bind to nanobodies even when said nanobodies comprise a C-terminal extension.

20 Thus, generally, the purpose of the present invention is to provide improved heavy-chain immunoglobulin variable domains (and in particular improved heavy-chain ISVD's and more in particular improved nanobodies) that, when they have an exposed C-terminal region or end, are less prone to be bound by pre-existing antibodies/factors, such as those found in blood or serum samples obtained from human subjects.

In particular, the purpose of the present invention is to provide improved heavy-chain immunoglobulin variable domains that, when they have an exposed C-terminal region or end, are less prone to binding by pre-existing antibodies/factors (again, such as those found in blood or serum samples obtained from human subjects) that can still bind to the exposed C-terminal region or end of the heavy-chain variable domain when said domain comprises a C-terminal extension (for example, as described in WO 12/175741, WO 13/024059 and the further prior art cited herein).

As mentioned herein, such pre-existing antibodies that can bind to a heavy-chain variable domain with a C-terminal extension have been found, by the present inventors, to be present in blood or serum samples obtained from human subjects suffering from certain

(auto-) immune diseases or disorders that severely impact/activate the immune system (such as SLE).

Thus, more in particular, the purpose of the present invention is to provide improved heavy-chain immunoglobulin variable domains (and in particular improved heavy-chain ISVD's and more in particular improved nanobodies) that, when they have an exposed C-terminal region or end, are less prone to binding by pre-existing antibodies/factors, such as those that are found in blood or serum samples obtained from human subjects suffering from certain (auto-) immune diseases or disorders that severely impact/activate the immune system (such as SLE).

Even more in particular, the purpose of the present invention is to provide improved heavy-chain immunoglobulin variable domains (and in particular improved heavy-chain ISVD's and more in particular improved nanobodies) that, when they have an exposed C-terminal region or end, are less prone to binding by those pre-existing antibodies/factors that are found in blood or serum samples obtained from human subjects suffering from certain (auto-) immune diseases or disorders and that can still bind to the exposed C-terminal region or end of the VH domain when the VH domain comprises a C-terminal extension.

It has now been found that the binding of pre-existing antibodies/factors to a heavy-chain variable domain with an exposed C-terminal end can be (further) reduced by a mutation of the serine at position 112 (Kabat numbering) to either lysine (K) or glutamine (Q). In particular, it has been found that such an S112K or S112Q mutation can (further) reduce or essentially prevent/remove binding of pre-existing antibodies/factors that can bind to a heavy-chain variable domain that comprises a C-terminal extension (but no S112K or S112Q mutation), such as those pre-existing antibodies/factors that are found in the blood or serum of human subjects suffering from severe auto-immune disorders such as SLE.

It has also been found that introducing the specific mutations disclosed herein (and in particular the following mutations L11V in combination with V89L, and optionally further in combination with T110K) may improve, or contribute to a (further) improvement of, the solubility of immunoglobulin single variable domains, such as the ISVD's generally and specifically disclosed herein (data not shown).

Any discussion of the prior art throughout the specification should in no way be considered as an admission that such prior art is widely known or forms part of common general knowledge in the field.

Unless the context clearly requires otherwise, throughout the description and the claims, the words "comprise", "comprising", and the like are to be construed in an inclusive sense as opposed to an exclusive or exhaustive sense; that is to say, in the sense of "including, but not limited to".

According to a first aspect, the present invention provides a heavy-chain immunoglobulin single variable domain (ISVD), in which the amino acid residue at position 89 is L and the amino acid residue at position 11 is V, wherein the amino acid residues/positions are indicated with the numbering according to Kabat.

5 According to a second aspect, the present invention provides a heavy-chain ISVD, in which:

- the amino acid residue at position 11 is V; and
- the amino acid residue at position 14 is one of A or P; and
- the amino acid residue at position 41 is one of A or P; and
- the amino acid residue at position 89 is L; and
- the amino acid residue at position 108 is one of Q or L; and
- the amino acid residue at position 110 is one of T, K or Q; and
- the amino acid residue at position 112 is one of S, K or Q;

and in which said VH domain optionally contains a C-terminal extension (X)ⁿ , in which

5 n is 1 to 10, preferably 1 to 5, such as 1, 2, 3, 4 or 5 (and preferably 1 or 2, such as 1); and each X is an (preferably naturally occurring) amino acid residue that is independently chosen, and preferably independently chosen from the group consisting of alanine (A), glycine (G), valine (V), leucine (L) or isoleucine (I),

wherein the amino acid residues/positions are indicated with the numbering according to

0 Kabat.

According to a third aspect, the present invention provides a library of heavy-chain ISVDs according to the invention.

According to a fourth aspect, the present invention provides a polypeptide, construct or compound that comprises at least one heavy-chain immunoglobulin single variable domain 25 according to the invention.

According to a fifth aspect, the present invention provides a nucleic acid that encodes the heavy-chain immunoglobulin single variable domain according to the invention or the polypeptide, construct or compound according to the invention.

According to a sixth aspect, the present invention provides a method for producing the 30 heavy-chain immunoglobulin single variable domain according to the invention or the polypeptide, construct or compound according to the invention, optionally comprising expressing the nucleic acid according to the invention in a suitable host organism.

According to a seventh aspect, the present invention provides a composition comprising the heavy-chain immunoglobulin single variable domain according to the invention, the

polypeptide, construct or compound according to the invention or the nucleic acid according to the invention, wherein the composition is optionally a pharmaceutical composition.

According to an eighth aspect, the present invention provides the heavy-chain immunoglobulin single variable domain according to the invention or the polypeptide, construct or compound according to the invention for use in medicine.

Thus, in another aspect, the invention relates to an immunoglobulin heavy-chain variable domain (VH domain) in which the amino acid residue at position 112 (Kabat numbering) is either a lysine (K) residue or a glutamine (Q) residue. Such an immunoglobulin heavy-chain variable domain is also referred to herein as a “*VH domain of the invention*”. When a VH domain of the invention is an immunoglobulin single variable domain (as is

preferred), it will also be referred to herein as an “*ISVD of the invention*”. Similarly, when the VH domain of the invention is a Nanobody (as is even more preferred), it will also be referred to herein as a “*Nanobody of the invention*”.

Generally, the VH domains of the invention either have an exposed C-terminal end or region, and/or are present in a protein, polypeptide, compound, entity or construct in which they have an exposed C-terminal end or region, and/or are intended for a use in which they have an exposed C-terminal region (for example, for use in in a protein, polypeptide, compound, entity or construct in which they are intended to form the C-terminal end or region).

10 In one aspect of the invention, the VH domain of the invention is an (heavy-chain) immunoglobulin single variable domain, meaning a heavy-chain variable domain that can form a functional antigen binding site without interaction with a VL domain. For example, the VH domain of the invention can be a Nanobody (including a VHH, a humanized VHH and/or a camelized VHs such as camelized human VH’s), a (single) domain antibody that is a VH domain or that is derived from a VH domain, or a dAb that is a VH domain or that is derived from a VH domain. The VH domain of the invention is preferably a nanobody (e.g. a VHH domain, a humanized VHH domain or a camelized VH domain such as a camelized human VH domain).

20 According to another aspect of the invention, the VH domain of the invention can be a heavy-chain variable domain that, in the protein, polypeptide, protein or construct in which is it present, does require an interaction with a VL domain in order to form an antigen binding site and that does have or form an exposed C-terminal end or region. For example, a VH domain according to this aspect of the invention can be a VH domain that is present in and/or used in an ScFv and or a diabody.

According to a more specific aspect of the invention, the VH domain of the invention has a C-terminal sequence (positions 109 to 113 according to Kabat) that is VTVKS (SEQ ID NO:1) or VTVQS (SEQ ID NO:2), or a sequence that has one amino acid difference (i.e. at one of the positions 109, 110, 111 or 113) with either the sequence VTVKS and/or VTVQS and that still has either a lysine (K) or glutamine (Q) at position 112.

30 Also, as further described herein, in one particularly preferred aspect of the invention, the VH domain of the invention also contains a C-terminal extension (e.g. as described in WO 12/175741 and/or in WO 13/024059) at its C-terminal end (i.e. linked to the serine residue at the end of the VTVKS-, VTVQS- or similar motif), in particular a C-terminal extension that is as further defined herein. However, as also further described herein, it is also possible that

the VTVKS-, VTVQS- or similar motif forms the C-terminal end of the VH domain (although this will usually be less preferred) or that the VH domain of the invention is linked at its C-terminal end (optionally via a suitable linker) to another amino acid sequence, moiety, domain or binding unit. For example, when the VH domain of the invention is an ISVD, the VH domain may be linked at its C-terminal end to another ISVD, optionally via a linker (and said other ISVD may then also be a VH domain of the invention).

Overall, as is well known for immunoglobulin variable domains generally, the VH domains of the invention will comprise 4 framework regions (FW1, FW2, FW3 and FW4) and 3 CDR's (CDR1, CDR2 and CDR3). As with immunoglobulin variable domains

10 generally, the sequence of the CDR's will depend on the antigen/target(s) to which the VH domains of the invention have been raised and/or are intended to bind. The framework regions can generally be any suitable framework regions for VH domains (albeit that position 112 and/or position 89 will be as further described herein). If the VH domain of the invention is an ISVD, the VH domain will have framework sequences that are suitable for an ISVD (optionally in association with one or more of the CDR's). For example, if the VH domain of the invention is a Nanobody, the framework regions will generally contain a suitable number of VHH hallmark residues (for which reference is for example made to WO 08/020079 and to some of the other patent applications of applicant/assignee cited herein).

Thus, for example, when the VH domains of the invention are Nanobodies, said

20 Nanobodies of the invention can contain one or more of the "Hallmark residues" that are characteristic of VHH's/Nanobodies (e.g. at positions 11, 37, 44, 45, 47, 83, 84, 103, 104 and/or 108; see for example Tables A-3 and A-5 to A-8 of WO 08/020079); one or more other amino acid residues that can be present in VHH's/Nanobodies (such as one or more humanizing substitutions that are known per se for VHH's and Nanobodies; reference is for example made to the teaching in WO 08/020079; see again the previously mentioned Tables A-3 and A-5 to A-8) and/or one or more other suitable amino acid residues or substitutions for VHH's/Nanobodies; or any suitable combination of such amino acid residues/substitutions.

Nanobodies of the invention in which position 112 is K or Q (i.e. with or without a C-terminal extension) preferably contain an amino acid at position 11 that is chosen from

30 L (the most often occurring amino acid residue in VHH's), E, K, M, S, V, W or Y; more preferably from L, E, K, V or Y, and even more preferably from L, K or V (with V being most preferred). For example and without limitation, compared to the leucine residue that most often occurs in VHH's, they can contain an L11K or L11V mutation. They can also, but without limitation, for example contain a Q108L mutation (a well-known humanizing

substitution for VHH's/Nanobodies). Other amino acid residues that can be present (again, without limitation, and for example other amino acid residues that naturally occur at this position in human VH's or VHH's may also be present at these positions) are for example one or more of an alanine (A) at position 14 (which is a very frequently occurring amino acid residue at this position in naturally occurring VHH's), a proline at position 14 (which is the most common amino acid at this position in human VH domains), as well as the mutations suggested by Harmsen et al. (in particular, those that Harmsen et al suggest based on the sequence of VHH4-class VHH's, such as V89M or V89T) and/or (other) mutations at the positions suggested by Nieba (for example, at one or more of positions 11, 87 and/or 89, see

10 Nieba, page 437, right hand column). Another suitable mutation is for example T110K or T110Q. Also: (i) position 41 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 41 and may in particular be (or be chosen from) proline (P), serine (S), threonine (T), alanine (A) or leucine (L), which are some of the amino acid residues that most frequently occur at this position in either humans or llamas, and may more in particular be either proline (P) or alanine (A); and/or (ii) Also, position 42 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 42 and may in particular be (or be chosen from) glycine (G) or glutamic acid (E); and/or (iii) position 87 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-7 of WO 20

20 08/020079 for position 87 and may in particular be (or be chosen from) threonine (T) or alanine (A)

According to a more specific aspect of the invention, a VH domain of the invention (which is as further described herein) has a framework 4 (FW4 sequence) that is either:

a) is one of the FW4 sequences of SEQ ID NO's: 3 to 20 mentioned in Table 1 below

Table 1: FW4 sequences

WGQGTQTVKS (SEQ ID NO:3)
WGKGTLTVKS (SEQ ID NO:4)
RGQGTRTVKS (SEQ ID NO:5)
WGLGTQVTIIS (SEQ ID NO:6)
GSQGTQTVKS (SEQ ID NO:7)
LRGGTQTVKS (SEQ ID NO:8)
RGQGTLTVKS (SEQ ID NO:9)
RSRGIQTVKS (SEQ ID NO:10)
WGKGTVKS (SEQ ID NO:11)
WGQGTQTVQS (SEQ ID NO:12)
WGKGTLTVQS (SEQ ID NO:13)
RGQGTRTVQS (SEQ ID NO:14)
WGLGTQVTIIS (SEQ ID NO:15)
GSQGTQTVQS (SEQ ID NO:16)
LRGGTQTVQS (SEQ ID NO:17)
RGQGTLTVQS (SEQ ID NO:18)
RSRGIQTVQS (SEQ ID NO:19)
WGKGTVQS (SEQ ID NO:20)

or:

b) is a sequence that has no more than three, preferably no more than two amino acid differences with at least one of the FW4 sequences of SEQ ID NO's 3 to 20, in which (i) the amino acid residue at the position corresponding to position 112 of the Kabat numbering is either K or Q; and in which (ii) the amino acid residue at the position corresponding to position 103 of the Kabat numbering is preferably W or R; (iii) the amino acid residue at the position corresponding to position 104 of the Kabat numbering is preferably G; (iv) the amino acid residue at the position corresponding to position 106 of the Kabat numbering is preferably G; (v) the amino acid residue at the position corresponding to position 107 of the Kabat numbering is preferably T; (vi) the amino acid residue at the position corresponding to position 108 of the Kabat numbering is preferably Q or L (and in humanized nanobodies preferably L); (vii) the amino acid residue at the position corresponding to position 109 of the Kabat numbering is preferably V; (viii) the

amino acid residue at the position corresponding to position 110 of the Kabat numbering is preferably T (or alternatively may be K or Q); (ix) the amino acid residue at the position corresponding to position 111 of the Kabat numbering is preferably V. Table 2 below gives some non-limiting examples of amino acid residues that can be present at the different positions (numbered according to Kabat) of such FW4 sequences.

Table 2: Examples of amino acid residues that can be present in the FW4 sequences of the VH domains of the invention.

Pos.	Amino acid residue(s):
103	W, R, G, S, K, A, M, Y, L, F, T, N, V, Q, P, E, C; preferably W
104	G, A, S, T, D, P, N, E, C, L; preferably G
105	Q, K, H, R, P, E, L, T, N, S, V, A, M, G
106	G, R, E
107	T, Q, I, A, S, N, R, V, D
108	Q, L, R, P, E, K, S, T, M, A, H; preferably Q or L
109	V, I, L
110	T, S, N, A, I, F, K, Q
111	V, I, A
112	<u>K or Q (invention)</u>
113	S, T, A, L, P, F, E, V

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Preferably, the VH domain of the invention has a framework 4 (FW4 sequence) that is either:

- WGQGTQVTVK (SEQ ID NO:3) or WGQGTQVTVQS (SEQ ID NO:12); or
- a sequence that has no more than three, preferably no more than two amino acid differences (such as only one amino acid difference) with SEQ ID NO:3 and/or SEQ ID NO: 12, in which (i) the amino acid residue at the position corresponding to position 112 of the Kabat numbering is either K or Q; and in which (ii) the amino acid residue at the position corresponding to position 103 of the Kabat numbering is preferably W or R; (iii) the amino acid residue at the position corresponding to position 104 of the Kabat numbering is preferably G; (iv) the amino acid residue at the position corresponding to

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position 106 of the Kabat numbering is preferably G; (v) the amino acid residue at the position corresponding to position 107 of the Kabat numbering is preferably T; (vi) the amino acid residue at the position corresponding to position 108 of the Kabat numbering is preferably Q or L (and in humanized nanobodies preferably L); (vii) the amino acid residue at the position corresponding to position 109 of the Kabat numbering is preferably V; (viii) the amino acid residue at the position corresponding to position 110 of the Kabat numbering is preferably T (or alternatively may be K or Q); (ix) the amino acid residue at the position corresponding to position 111 of the Kabat numbering is preferably V. Again, Table 2 gives some non-limiting examples of amino acid residues that can be present at the different positions (numbered according to Kabat) of such FW4 sequences.

As described further herein, according to a preferred aspect of the invention, VH domains of the invention that comprise a FW4 sequence as described above preferably also contains a C-terminal extension (as further described herein). However, as also further described herein, it is also possible that the FW4 sequence forms the C-terminal end of the VH domain (although this will usually be less preferred) or that the VH domain of the invention is linked at its C-terminal end (optionally via a suitable linker) to another amino acid sequence, moiety, domain or binding unit. For example, when the VH domain of the invention is an ISVD, the VH domain may be linked at its C-terminal end to another ISVD, optionally via a linker (and said other ISVD may then also be a VH domain of the invention).

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As indicated herein, according to a preferred but non-limiting aspect of the invention, the VH domains of the invention contain a C-terminal extension, such as a C-terminal extension that is as described in WO 12/175741 and/or in WO 13/024059, and in particular as described in WO 12/175741

Thus, according to this aspect, the VH domain of the invention is an immunoglobulin heavy-chain variable domain (VH domain) in which: (i) the amino acid residue at position 112 (Kabat numbering) is not a serine residue, and is preferably either a lysine (K) residue or a glutamine (Q) residue; and that (ii) at its C-terminal end (i.e. linked to the amino acid residue at position that is or corresponds to position 113 according to the Kabat numbering) is linked to a further amino acid sequence (i.e. the “C-terminal extension”) that comprises between 1 and 5 (such as 1, 2, 3, 4 or 5, and preferably 1, 2 or 3, and most preferably only 1 or 2 such as only 1) amino acid residues that are each independently chosen from suitable amino acid residues, and preferably each independently chosen from naturally occurring amino acids, and more preferably each independently chosen from the group consisting of

alanine (A), glycine (G), valine (V), leucine (L) or isoleucine (I) (however, as can be seen from the data presented in WO 12/17574, other amino acid residues such as serine, proline, threonine and/or lysine can also be used as part of the C-terminal extension).

In particular, according to this aspect of the invention, the VH domain of the invention preferably has a C-terminal sequence that is VTVKS(X)_n (SEQ ID NO:21) or VTVQS(X)_n (SEQ ID NO:22) (or that is an amino acid sequence that, at the positions of the VTVKS motif or the VTVQS-motif, has one amino acid difference with either the sequence VTVKS and/or VTVQS and that still has either a lysine (K) or glutamine (Q) at position 112), in which (i) the amino acid residues of the VTVKS- or VTVQS-motif (or VTVKS- or VTVQS-like motif)

10 correspond to positions 109 to 113 of the VH domain according to the Kabat numbering; (ii) n is 1 to 10, preferably 1 to 5, such as 1, 2, 3, 4 or 5 (and preferably 1 or 2, such as 1); and (iii) each X is an (preferably naturally occurring) amino acid residue that is independently chosen, and preferably independently chosen from the group consisting of alanine (A), glycine (G), valine (V), leucine (L) or isoleucine (I).

More in particular, according to this aspect of the invention, the VH domain of the invention may have, as its FW4 sequence, one of the FW4 sequences of SEQ ID NO's 3 to 20 (or an amino sequence that has no more than three, preferably no more than two amino acid differences with at least one of the FW4 sequences of SEQ ID NO's 3 to 20, in which the amino acid residue at the position corresponding to position 112 of the Kabat numbering is either K or Q), in which said FW 4 sequence is linked, at its C-terminal end, to a C-terminal extension (X)_n, in which n is 1 to 10, preferably 1 to 5, such as 1, 2, 3, 4 or 5 (and preferably 1 or 2, such as 1); and each X is an (preferably naturally occurring) amino acid residue that is independently chosen, and preferably independently chosen from the group consisting of alanine (A), glycine (G), valine (V), leucine (L) or isoleucine (I).

Accordingly, in this aspect of the invention, a VH domain of the invention may have, at its C-terminal end, either:

a) one of the amino acid sequences given as SEQ ID NO's: 23 to 40 in Table 3;

Table 3: FW4 sequences with C-terminal extension

WGQGTQVTVK(S(X) _n) (SEQ ID NO:23)
WGKGTLVTVK(S(X) _n) (SEQ ID NO:24)
RGQGTRVTVK(S(X) _n) (SEQ ID NO:25)
WGLGTQVTIIS(X) _n (SEQ ID NO:26)
GSQGTQVTVK(S(X) _n) (SEQ ID NO:27)
LRGGTQVTVK(S(X) _n) (SEQ ID NO:28)
RGQGTLVTVK(S(X) _n) (SEQ ID NO:29)
RSRGIQVTVK(S(X) _n) (SEQ ID NO:30)
WGKGTVQTVKS(X) _n (SEQ ID NO:31)
WGQGTQVTVQS(X) _n (SEQ ID NO:32)
WGKGTLVTVQS(X) _n (SEQ ID NO:33)
RGQGTRVTVQS(X) _n (SEQ ID NO:34)
WGLGTQVTIIS(X) _n (SEQ ID NO:35)
GSQGTQVTVQS(X) _n (SEQ ID NO:36)
LRGGTQVTVQS(X) _n (SEQ ID NO:37)
RGKGTLVTVQS(X) _n (SEQ ID NO:38)
RSRGIQVTVQS(X) _n (SEQ ID NO:39)
WGKGTVQTVQS(X) _n (SEQ ID NO:40)

in which (i) the amino acid residues of the FW4 sequences that precede the (X)_n C-terminal extension in SEQ ID NO's: 23 to 40 correspond to the amino acid positions of FW4 of a VH domain (i.e. positions 103 to 113 according to the Kabat numbering); (ii) n is 1 to 10, preferably 1 to 5, such as 1, 2, 3, 4 or 5 (and preferably 1 or 2, such as 1); and (iii) each X is an (preferably naturally occurring) amino acid residue that is independently chosen, and preferably independently chosen from the group consisting of alanine (A), glycine (G), valine (V), leucine (L) or isoleucine (I); or

10 b) an amino acid sequence that has no more than three, preferably no more than two, amino acid differences with at least one of the amino acid sequences SEQ ID NO's 23 to 40 (in which said amino acid differences are at the positions that correspond to the amino acid positions of FW4 of a VH domain, i.e. at positions 103 to 113 according to the Kabat numbering, with any amino acid differences within the C-terminal extension (X)_n being disregarded), in which: (i) the amino acid residue at the position corresponding to position

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112 of the Kabat numbering is either K or Q; (ii) n is 1 to 10, preferably 1 to 5, such as 1, 2, 3, 4 or 5 (and preferably 1 or 2, such as 1); and (iii) each X is an (preferably naturally occurring) amino acid residue that is independently chosen, and preferably independently chosen from the group consisting of alanine (A), glycine (G), valine (V), leucine (L) or isoleucine (I). Again, further to features (i) to (iii) as mentioned in the previous sentence, in such an amino acid sequence: (iv) the amino acid residue at the position corresponding to position 103 of the Kabat numbering is preferably W or R; (v) the amino acid residue at the position corresponding to position 104 of the Kabat numbering is preferably G; (vi) the amino acid residue at the position corresponding to position 106 of the Kabat numbering is preferably G; (vii) the amino acid residue at the position corresponding to position 107 of the Kabat numbering is preferably T; (viii) the amino acid residue at the position corresponding to position 108 of the Kabat numbering is preferably Q or L (and in humanized nanobodies preferably L); (ix) the amino acid residue at the position corresponding to position 109 of the Kabat numbering is preferably V; (x) the amino acid residue at the position corresponding to position 110 of the Kabat numbering is preferably T (or alternatively may be K or Q); (xi) the amino acid residue at the position corresponding to position 111 of the Kabat numbering is preferably V; and reference is again made to the Table 2 for possible amino acid residues that can be present at each position.

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Preferably, according to this aspect of the invention, a VH domain of the invention has, at its C-terminal end, either:

- a) an amino acid sequence that is WGQGTQVTVKS(X)_n (SEQ ID NO:23) or WGQGTQVTVQS(X)_n (SEQ ID NO:32), in which (ii) n is 1 to 10, preferably 1 to 5, such as 1, 2, 3, 4 or 5 (and preferably 1 or 2, such as 1); and (iii) each X is an (preferably naturally occurring) amino acid residue that is independently chosen, and preferably independently chosen from the group consisting of alanine (A), glycine (G), valine (V), leucine (L) or isoleucine (I); or
- b) an amino acid sequence that has no more than three, preferably no more than two, amino acid differences with at least one of the amino acid sequences WGQGTQVTVKS(X)_n (SEQ ID NO:23) or WGQGTQVTVQS(X)_n (SEQ ID NO:32) (in which said amino acid differences are at the positions that correspond to the amino acid positions of FW4 of a VH domain, i.e. at positions 103 to 113 according to the Kabat numbering, with any amino acid differences within the C-terminal extension (X)_n being disregarded), in which:

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(i) the amino acid residue at the position corresponding to position 112 of the Kabat numbering is either K or Q; (ii) n is 1 to 10, preferably 1 to 5, such as 1, 2, 3, 4 or 5 (and preferably 1 or 2, such as 1); and (iii) each X is an (preferably naturally occurring) amino acid residue that is independently chosen, and preferably independently chosen from the group consisting of alanine (A), glycine (G), valine (V), leucine (L) or isoleucine (I). Again, for such amino acid sequences, features (vi) to (xi) as described in the preceding paragraphs preferably also apply.

Also, as mentioned herein, the VH domains of the invention can also contain other amino acid residues or substitutions that are known per se in the art for VH domains and in particular for ISVD's (and more in particular for Nanobodies) at the relevant positions. Some non-limiting examples may be as mentioned herein and for example include one or more of the "Hallmark residues" that are characteristic of VHH's/Nanobodies (including for example a leucine (L) at position 11), other amino acid residues that naturally occur in VHH's (such as an alanine (A) at position 14), humanizing substitutions known per se for VHH's/Nanobodies (such as Q108L and A14P), one or more of the mutations suggested by Harmsen (such as V89M or V89T) and/or at the positions suggested by Nieba (e.g. 11, 87 or 89); or any suitable combination thereof; and/or for example a T110K, T110Q or V89L mutation.

When a VH domain of the invention contains a C-terminal extension (X)_n, according to some preferred, but non-limiting examples of such extensions, X and n can be as follows:

- 20 (a) n = 1 and X = Ala;
- (b) n = 2 and each X = Ala;
- (c) n = 3 and each X = Ala;
- (d) n = 2 and at least one X = Ala (with the remaining amino acid residue(s) X being independently chosen from any naturally occurring amino acid but preferably being independently chosen from Val, Leu and/or Ile);
- (e) n = 3 and at least one X = Ala (with the remaining amino acid residue(s) X being independently chosen from any naturally occurring amino acid but preferably being independently chosen from Val, Leu and/or Ile);
- (f) n = 3 and at least two X = Ala (with the remaining amino acid residue(s) X being independently chosen from any naturally occurring amino acid but preferably being independently chosen from Val, Leu and/or Ile);
- 30 (g) n = 1 and X = Gly;
- (h) n = 2 and each X = Gly;

- (i) $n = 3$ and each $X = \text{Gly}$;
- (j) $n = 2$ and at least one $X = \text{Gly}$ (with the remaining amino acid residue(s) X being independently chosen from any naturally occurring amino acid but preferably being independently chosen from Val, Leu and/or Ile);
- (k) $n = 3$ and at least one $X = \text{Gly}$ (with the remaining amino acid residue(s) X being independently chosen from any naturally occurring amino acid but preferably being independently chosen from Val, Leu and/or Ile);
- (l) $n = 3$ and at least two $X = \text{Gly}$ (with the remaining amino acid residue(s) X being independently chosen from any naturally occurring amino acid but preferably being independently chosen from Val, Leu and/or Ile);
- (m) $n = 2$ and each $X = \text{Ala}$ or Gly ;
- (n) $n = 3$ and each $X = \text{Ala}$ or Gly ;
- (o) $n = 3$ and at least one $X = \text{Ala}$ or Gly (with the remaining amino acid residue(s) X being independently chosen from any naturally occurring amino acid but preferably being independently chosen from Val, Leu and/or Ile); or
- (p) $n = 3$ and at least two $X = \text{Ala}$ or Gly (with the remaining amino acid residue(s) X being independently chosen from any naturally occurring amino acid but preferably being independently chosen from Val, Leu and/or Ile);

with aspects (a), (b), (c), (g), (h), (i), (m) and (n) being particularly preferred, with aspects in which $n = 1$ or 2 being preferred and aspects in which $n = 1$ being particularly preferred.

It should also be noted that, preferably, any C-terminal extension present in a VH domain of the invention does not contain a (free) cysteine residue (unless said cysteine residue is used or intended for further functionalization, for example for pegylation).

Also, the preferences that are indicated on pages 35 to 41 of WO 12/175741 for the C-terminal extensions used according to WO 12/175741 (which are also the preferred C-terminal extensions used in the VH domains according to the present invention) also apply to the C-terminal extensions used in the VH domains of the inventions, and these preferences according to WO 12/175741 are also included herein by reference.

Preferably, when a VH domain of the invention contains a C-terminal extension ($X)_n$, $n = 1, 2$ or 3 , and each X is either Ala or Gly . More preferably, each X is Ala , and $n = 1$ or 2 , and preferably 1 .

When the VH domains of the invention contain a C-terminal extension, they will usually be present at (and often form) the C-terminal end of the protein, polypeptide, compound, construct or other chemical entity in which it is present. Again, such a protein,

polypeptide, compound, construct or other chemical entity may contain one or more other VH domains of the invention (i.e. not at the C-terminal end); in such a case, said other VH domains of the invention will contain a lysine (K) or glutamine (Q) at position 112 (and be as further described herein), but will not contain a C-terminal extension (instead, they may be linked (optionally via one or more suitable linkers) at their C-terminus to one or more other amino acid sequences, moieties, binding domains or binding units present in the protein, polypeptide, compound, construct or other chemical entity, such as the VH domain of the invention with the C-terminal extension that is present at the C-terminal end).

As the VH domains of the invention (and the proteins, polypeptides, compounds, constructs and other chemical entities comprising the same as further described herein) are particularly useful in (and intended for) use pharmaceutical uses (such as the prevention, treatment and/or diagnosis of diseases and disorders in human subjects in need of the same), they preferably have a high degree of sequence homology in their framework regions with the framework sequences of human VH domains. In particular, the VH domains of the invention preferably have an overall degree of sequence identity (determined as further described herein, and taking into account only the framework regions and not the CDR's, and also not taking into account the substitution at position 112 and any C-terminal extension if present) with at least one human germline sequence (such as DP-47, DP-51 or DP-29) of at least 80%, preferably at least 85%, such as 90% or more. More in particular, the VH domains of the invention preferably have an overall degree of sequence identity (determined as further described herein, and taking into account only the framework regions and not the CDR's, and also not taking into account the substitution at position 112 and any C-terminal extension if present) of at least 80%, preferably at least 85%, such as 90% or more with at least one of the following human germline sequences: DP-47, DP-51 and/or DP-29.

As further described herein, according to one aspect of the invention, the VH domain of the invention can be a heavy-chain variable domain that, in the protein, polypeptide, protein or construct in which it is present, interacts/associates (or is intended to interact/associate) with a VL domain in order to form an antigen binding site, in which at least the VH domain has an exposed C-terminal end or region. For example, a VH domain according to this aspect of the invention can be a VH domain that is present and/or used in an ScFv and/or a diabody, where it will associate with a VL domain to form an antigen binding site.

However, according to a preferred aspect of the invention, the VH domain of the invention is an (heavy-chain) immunoglobulin single variable domain or “ISVD”, meaning a

heavy-chain variable domain that can form a functional antigen binding site without interaction with a VL domain. For example, the VH domain of the invention can be a Nanobody (including a VHH, a humanized VHH and/or a camelized VHs such as camelized human VH's), a (single domain) antibody is a VH domain or that is derived from a VH domain, or a dAb that is a VH domain or that is derived from a VH domain. The VH domain of the invention is preferably a nanobody (and more preferably VHH domain, a humanized VHH domain or a camelized VH domain such as a camelized human VH domain).

In the present specification:

- the term "Nanobody" is generally as defined in or WO 08/020079 or WO 09/138519, and thus in a specific aspect generally denotes a VHH, a humanized VHH or a camelized VH (such as a camelized human VH) or generally a sequence optimized VHH (such as e.g. optimized for chemical stability and/or solubility, maximum overlap with known human framework regions and maximum expression). It is noted that the terms Nanobody or Nanobodies are registered trademarks of Ablynx N.V. and thus may also be referred to as Nanobody® and/or Nanobodies®);
- the term "ISVD" (or "ISV") as used herein in its broadest sense also includes "ISVD-based biologicals" and, when the ISVD is a Nanobody, "Nanobody-based biologicals". An "ISVD-based biological" is defined herein as a protein, polypeptide or other biological drug that comprises or essentially consist of at least one (such as one, two or three) ISVD's. Similarly, a "Nanobody-based biological" is defined as a protein, polypeptide or other biological drug that comprises or essentially consist of at least one (such as one, two or three) Nanobodies. As with the term "ISVD", whenever the term "ISVD-based biological" is used, it should be understood that such an ISVD-based biological is preferably a Nanobody-based biological. Within the context of the present invention, both an "ISVD-based biological" and a "Nanobody-based biological" may for example be a monovalent, bivalent (or multivalent), bispecific (or multispecific), and biparatopic (or "multiparatopic) ISVD construct or Nanobody construct, respectively. Also, any ISVD-based or Nanobody-based biological may for example, in addition to the one or more (such as one, two or three) ISVD's or Nanobodies, optionally further comprise one or more (such as one or two) other further therapeutic moieties and/or one or more (such as one or two) other moieties that influence the pharmacokinetic or pharmacodynamic properties of the ISVD-based or Nanobody-based biological (such as its half-life). Suitable examples of such further therapeutic or other moieties will be clear to the skilled

person, and for example generally can include any therapeutically active protein, polypeptide or other binding domain or binding unit, as well as for example modifications such as those described on pages 149 to 152 of WO 09/138159. An ISVD-based biological or Nanobody-based biological is preferably a therapeutic or intended for use as a therapeutic (which includes prophylaxis and diagnosis) and for this purpose preferably contains at least one ISVD against a therapeutically relevant target (such as for example RANK-L, vWF, IgE, RSV, CXCR4, IL-23 or other interleukins, etc.). For some specific but non-limiting examples of such ISVD-based or Nanobody-based biologicals, reference is to Examples 8 to 18 and also for example made to the various applications by Ablynx N.V. (such as for example and without limitation WO 2004/062551, WO 2006/122825, WO 2008/020079 and WO 2009/068627), as well as for example (and without limitation) to applications such as WO 06/038027, WO 06/059108, WO 07/063308, WO 07/063311, WO 07/066016 and WO 07/085814. Also, as further described herein, an ISVD or Nanobody as described herein may be directed against a (human) serum protein such as (human) serum albumin, and such an ISVD or Nanobody may also find therapeutic uses, in particular in and/or for extending the half-life of therapeutic moieties and compounds (such as in or for the ISV-based biologicals described herein). Reference is for example made to WO 2004/041865, WO 2006/122787 and WO 2012/175400, which generally describe the use of serum-albumin binding nanobodies for half-life extension. Also, in the present specification, unless explicitly mentioned otherwise herein, all terms mentioned herein have the meaning given in WO 09/138519 (or in the prior art cited in WO 09/138519) or WO 08/020079 (or in the prior art cited in WO 08/020079). Also, where a method or technique is not specifically described herein, it can be performed as described in WO 09/138519 (or in the prior art cited in WO 09/138519) or WO 08/020079 (or in the prior art cited in WO 08/020079).

Also, when used in the present specification or claims, the following terms have the same meaning as given on, and/or where applicable can be determined in the manner described in, pages 62-75 of WO 09/138519: “*agonist*”, “*antagonist*”, “*inverse agonist*”, “*non-polar, uncharged amino acid residue*”, “*polar uncharged amino acid residue*”, “*polar, charged amino acid residue*”, “*sequence identity*”, “*exactly the same*” and “*amino acid difference*” (when referring to a sequence comparison of two amino acid sequences), “*(in) essentially isolated (form)*”, “*domain*”, “*binding domain*”, “*antigenic determinant*”, “*epitope*”, “*against*” or “*directed against*” (an antigen), “*specificity*” and “*half-life*”. In

addition, the terms “*modulating*” and “*to modulate*”, “*interaction site*”, “*specific for*”, “*cross-block*”, “*cross-blocked*” and “*cross-blocking*” and “*essentially independent of the pH*” are as defined on (and/or can be determined as described on) pages 74-79 of WO 10/130832 of applicant. Also, when referring to a construct, compound, protein or polypeptide of the invention, terms like “*monovalent*”, “*bivalent*” (or “*multivalent*”), “*bispecific*” (or “*multispecific*”), and “*biparatopic*” (or “*multiparatopic*”) may have the meaning given in WO 09/138.519, WO 10/130832 or WO 08/020079.

The term “half-life” as used herein relation to an ISVD, Nanobody, ISVD-based biological, Nanobody-based biological or any other amino acid sequence, compound or 10 polypeptide referred to herein can generally be defined as described in paragraph o) on page 57 of WO 08/020079 and as mentioned therein refers to the time taken for the serum concentration of the amino acid sequence, compound or polypeptide to be reduced by 50%, in vivo, for example due to degradation of the sequence or compound and/or clearance or sequestration of the sequence or compound by natural mechanisms. The in vivo half-life of an amino acid sequence, compound or polypeptide of the invention can be determined in any manner known per se, such as by pharmacokinetic analysis. Suitable techniques will be clear to the person skilled in the art, and may for example generally be as described in paragraph o) on page 57 of WO 08/020079. As also mentioned in paragraph o) on page 57 of WO 08/020079, the half-life can be expressed using parameters such as the t_{1/2}-alpha, t_{1/2}-beta 20 and the area under the curve (AUC). In this respect it should be noted that the term “half-life” as used herein in particular refers to the t_{1/2}-beta or terminal half-life (in which the t_{1/2}-alpha and/or the AUC or both may be kept out of considerations). Reference is for example made to the Experimental Part below, as well as to the standard handbooks, such as Kenneth, A et al: Chemical Stability of Pharmaceuticals: A Handbook for Pharmacists and Peters et al, Pharmacokinete analysis: A Practical Approach (1996). Reference is also made to “Pharmacokinetics”, M Gibaldi & D Perron, published by Marcel Dekker, 2nd Rev. edition (1982). Similarly, the terms “increase in half-life” or “increased half-life” as also as defined in paragraph o) on page 57 of WO 08/020079 and in particular refer to an increase in the t_{1/2}-beta, either with or without an increase in the t_{1/2}-alpha and/or the AUC or both.

30 When a term is not specifically defined herein, it has its usual meaning in the art, which will be clear to the skilled person. Reference is for example made to the standard handbooks, such as Sambrook et al, “Molecular Cloning: A Laboratory Manual” (2nd.Ed.), Vols. 1-3, Cold Spring Harbor Laboratory Press (1989); F. Ausubel et al, eds., “Current protocols in molecular biology”, Green Publishing and Wiley Interscience, New York (1987);

Lewin, "Genes II", John Wiley & Sons, New York, N.Y., (1985); Old et al., "Principles of Gene Manipulation: An Introduction to Genetic Engineering", 2nd edition, University of California Press, Berkeley, CA (1981); Roitt et al., "Immunology" (6th. Ed.), Mosby/Elsevier, Edinburgh (2001); Roitt et al., Roitt's Essential Immunology, 10th Ed. Blackwell Publishing, UK (2001); and Janeway et al., "Immunobiology" (6th Ed.), Garland Science Publishing/Churchill Livingstone, New York (2005), as well as to the general background art cited herein.

Also, as already indicated herein, the amino acid residues of a Nanobody are numbered according to the general numbering for VH domains given by Kabat et al.

10 ("Sequence of proteins of immunological interest", US Public Health Services, NIH Bethesda, MD, Publication No. 91), as applied to VHH domains from Camelids in the article of Riechmann and Muyldermans, *J. Immunol. Methods* 2000 Jun 23; 240 (1-2): 185-195; or referred to herein. According to this numbering, FR1 of a Nanobody comprises the amino acid residues at positions 1-30, CDR1 of a Nanobody comprises the amino acid residues at positions 31-35, FR2 of a Nanobody comprises the amino acids at positions 36-49, CDR2 of a Nanobody comprises the amino acid residues at positions 50-65, FR3 of a Nanobody comprises the amino acid residues at positions 66-94, CDR3 of a Nanobody comprises the amino acid residues at positions 95-102, and FR4 of a Nanobody comprises the amino acid residues at positions 103-113. [In this respect, it should be noted that - as is well known in the art for VH domains and for VHH domains - the total number of amino acid residues in each of the CDR's may vary and may not correspond to the total number of amino acid residues indicated by the Kabat numbering (that is, one or more positions according to the Kabat numbering may not be occupied in the actual sequence, or the actual sequence may contain more amino acid residues than the number allowed for by the Kabat numbering). This means that, generally, the numbering according to Kabat may or may not correspond to the actual numbering of the amino acid residues in the actual sequence. Generally, however, it can be said that, according to the numbering of Kabat and irrespective of the number of amino acid residues in the CDR's, position 1 according to the Kabat numbering corresponds to the start of FR1 and vice versa, position 36 according to the Kabat numbering corresponds to the start of FR2 and vice versa, position 66 according to the Kabat numbering corresponds to the start of FR3 and vice versa, and position 103 according to the Kabat numbering corresponds to the start of FR4 and vice versa.].

Alternative methods for numbering the amino acid residues of VH domains, which methods can also be applied in an analogous manner to VHH domains from Camelids and to

Nanobodies, are the method described by Chothia et al. (Nature 342, 877-883 (1989)), the so-called “AbM definition” and the so-called “contact definition”. However, in the present description, aspects and figures, the numbering according to Kabat as applied to VHH domains by Riechmann and Muyldermans will be followed, unless indicated otherwise.

It should also be noted that the Figures, any Sequence Listing and the Experimental Part/Examples are only given to further illustrate the invention and should not be interpreted or construed as limiting the scope of the invention and/or of the appended claims in any way, unless explicitly indicated otherwise herein.

The VH domains of the invention can be directed against any suitable or desired 10 antigen or target, including any pharmaceutically and/or therapeutically relevant target as described herein.

According to one specific aspect of the invention, the VH domains of the invention are directed against a serum protein, and in particular a human serum protein. According to a preferred aspect, when a VH domain of the invention is directed against a serum protein, it is directed against serum albumin, and in particular human serum albumin. Thus, the invention also relates to a VH domain of the invention (as defined herein, including the preferences defined for the VH domains of the invention) that can specifically bind to a serum protein, in particular a human serum protein, and that can preferably specifically bind to serum albumin, and more preferably to human serum albumin. Again, such a VH domain is preferably an 20 ISVD (as described herein) and more preferably a Nanobody.

For example, a VH domain of the invention against serum albumin can be one of the Nanobodies against (human) serum albumin that are described in WO 2004/041865, and in particular in WO 2006/122787 and WO 2012/175400 (all applications from applicant/assignee), in which the amino acid at position 112 is substituted by either K or Q, and which is optionally provided with a C-terminal extension as described herein (and can also for example also contain one or more of the other specific amino acid residues/ substitutions mentioned herein, such as 11L, L11V, L11K, 14A, P14A, 14P, A14P, 89T, V89T, 89L, V89L, 108L, Q108L, 110Q, T110Q, 110K and/or T110K; although usually the presence of an additional substitution at position 110 will not often not be required when 30 position 112 is K or Q, in which case position 110 is preferably T). Furthermore, it is envisaged that the present invention can also be applied to other serum-albumin binding heavy-chain ISVD's, such as those described in WO 03/035694, WO 04/003019, WO 05/118642, WO 06/059106, WO 08/096158, WO 09/121804 WO 10/108937 or US 2013/0129727, i.e. by suitably introducing the substitutions described herein (i.e. at least one

of S112K, S112Q and/or V89T, and optionally one or more of the other amino acid residues/substitutions described herein, such as L11V) and optionally (and usually preferably as outlined herein) adding a C-terminal extension (as further described herein).

Some preferred but non-limiting examples of such serum albumin binding Nanobodies of the invention are humanized variants of the amino acid sequence of SEQ ID NO: 52 of WO 2006/122787 (called “Alb-1” in WO 2006/122787), in which the amino acid at position 112 is substituted by either K or Q (and which is optionally provided with a C-terminal extension as described herein), such as the humanized variants of Alb-1 that are given in SEQ ID NO’s: 57 to 64 of WO 2006/122787 (in each case, with a S112K or S112Q substitution, and optionally

10 with a C-terminal extension) or the humanized variants of Alb-1 that are given in SEQ ID NO’s 3 to 11 of WO 2012/175400 (again, in each case, with a S112K or S112Q substitution), of which SEQ ID NO’s 3, 4 and 5 can optionally contain a C-terminal extension, and SEQ ID NO’s 6 to 11 already contain a C-terminal extension (and again, such variants can contain one or more of the other specific amino acid residues/ substitutions mentioned herein, such as 11L, L11V, L11K, 14A, P14A, 14P, A14P, 89T, V89T, 89L, V89L, 108L, Q108L, 110Q, T110Q, 110K and/or T110K; although usually the presence of an additional substitution at position 110 will not often not be required when position 112 is K or Q, in which case position 110 is preferably T). Also: (i) position 41 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of 20 WO 08/020079 for position 41 and may in particular be (or be chosen from) proline (P), serine (S), threonine (T), alanine (A) or leucine (L), which are some of the amino acid residues that most frequently occur at this position in either humans or llamas, and may more in particular be either proline (P) or alanine (A); and/or (ii) position 42 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 42 and may in particular be (or be chosen from) glycine (G) or glutamic acid (E); and/or (iii) position 87 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-7 of WO 08/020079 for position 87 and may in particular be (or be chosen from) threonine (T) or alanine (A).

30 Thus, in a further aspect, the invention relates to a Nanobody of the invention (as defined herein) that can bind (and in particular specifically bind) to serum albumin (and in particular human serum albumin) in which:

- CDR1 is the amino acid sequence SFGMS (SEQ ID NO:41);

- CDR2 is the amino acid sequence SISGSGSDTLYADSVKG (SEQ ID NO:42);
- CDR3 is the amino acid sequence GGSLSR (SEQ ID NO:43);
- the amino acid residue at position 112 is either K or Q;

and that optionally contains at its C-terminal end a C-terminal extension (X)_n in which n is 1 to 10, preferably 1 to 5, such as 1, 2, 3, 4 or 5 (and preferably 1 or 2, such as 1); and each X is an (preferably naturally occurring) amino acid residue that is independently chosen, and preferably independently chosen from the group consisting of alanine (A), glycine (G), valine (V), leucine (L) or isoleucine (I) (again, such a C-terminal extension is preferably as further described herein, and again such a Nanobody can also for example also contain one or more

10 of the other specific amino acid residues/ substitutions mentioned herein, such as 11L, L11V, L11K, 14A, P14A, 14P, A14P, 89T, V89T, 89L, V89L, 108L, Q108L, 110Q, T110Q, 110K and/or T110K; although usually the presence of an additional substitution at position 110 will not often not be required when position 112 is K or Q, in which case position 110 is preferably T). Also: (i) position 41 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 41 and may in particular be (or be chosen from) proline (P), serine (S), threonine (T), alanine (A) or leucine (L), which are some of the amino acid residues that most frequently occur at this position in either humans or llamas, and may more in particular be either proline (P) or alanine (A); and/or (ii) position 42 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 42 and may in particular be (or be chosen from) glycine (G) or glutamic acid (E); and/or (iii) position 87 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-7 of WO 08/020079 for position 87 and may in particular be (or be chosen from) threonine (T) or alanine (A).

In a particular aspect, the invention relates to a Nanobody of the invention (as defined herein) that can bind (and in particular specifically bind) to serum albumin (and in particular human serum albumin) that is a humanized variant of SEQ ID NO: 52 of WO 2006/122787 in which:

30

- CDR1 is the amino acid sequence SFGMS (SEQ ID NO:41);
- CDR2 is the amino acid sequence SISGSGSDTLYADSVKG (SEQ ID NO:42);
- CDR3 is the amino acid sequence GGSLSR (SEQ ID NO:43);
- the amino acid residue at position 112 is either K or Q;

and that optionally contains at its C-terminal end a C-terminal extension (X)_n in which n is 1 to 10, preferably 1 to 5, such as 1, 2, 3, 4 or 5 (and preferably 1 or 2, such as 1); and each X is an (preferably naturally occurring) amino acid residue that is independently chosen, and preferably independently chosen from the group consisting of alanine (A), glycine (G), valine (V), leucine (L) or isoleucine (I) (again, such a C-terminal extension is preferably as further described herein, and again such a Nanobody can also for example also contain one or more of the other specific amino acid residues/ substitutions mentioned herein, such as 11L, L11V, L11K, 14A, P14A, 14P, A14P, 89T, V89T, 89L, V89L, 108L, Q108L, 110Q, T110Q, 110K and/or T110K; although usually the presence of an additional substitution at position 110 will 10 not often not be required when position 112 is K or Q, in which case position 110 is preferably T). Also: (i) position 41 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 41 and may in particular be (or be chosen from) proline (P), serine (S), threonine (T), alanine (A) or leucine (L), which are some of the amino acid residues that most frequently occur at this position in either humans or llamas, and may more in particular be either proline (P) or alanine (A); and/or (ii) position 42 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 42 and may in particular be (or be chosen from) glycine (G) or glutamic acid (E); and/or (iii) position 87 may for example be one of the amino acid 20 residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-7 of WO 08/020079 for position 87 and may in particular be (or be chosen from) threonine (T) or alanine (A).

In a particular aspect, the invention relates to a Nanobody of the invention (as defined herein) that can bind (and in particular specifically bind) to serum albumin (and in particular human serum albumin) that has at least 80%, preferably at least 85%, more preferably at least 90% such as at least 95% sequence identity with at least one of Alb-1 (SEQ ID NO: 52 of WO 2006/122787), Alb-8 (SEQ ID NO: 46 herein) and/or Alb-23 (SEQ ID NO: 61 herein) (taking into account both the framework sequences and the CDR's, but not any C-terminal extension), in which the amino acid residue at position 112 is either K or Q, and that 30 optionally contains at its C-terminal end a C-terminal extension (X)_n in which n is 1 to 10, preferably 1 to 5, such as 1, 2, 3, 4 or 5 (and preferably 1 or 2, such as 1); and each X is an (preferably naturally occurring) amino acid residue that is independently chosen, and preferably independently chosen from the group consisting of alanine (A), glycine (G), valine (V), leucine (L) or isoleucine (I) (again, such a C-terminal extension is preferably as further

described herein, and again such a Nanobody can also for example also contain one or more of the other specific amino acid residues/ substitutions mentioned herein, such as 11L, L11V, L11K, 14A, P14A, 14P, A14P, 89T, V89T, 89L, V89L, 108L, Q108L, 110Q, T110Q, 110K and/or T110K; although usually the presence of an additional substitution at position 110 will not often not be required when position 112 is K or Q, in which case position 110 is preferably T). Also: (i) position 41 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 41 and may in particular be (or be chosen from) proline (P), serine (S), threonine (T), alanine (A) or leucine (L), which are some of the amino acid residues that most frequently occur at this position in either humans or llamas, and may more in particular be either proline (P) or alanine (A); and/or (ii) position 42 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 42 and may in particular be (or be chosen from) glycine (G) or glutamic acid (E); and/or (iii) position 87 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-7 of WO 08/020079 for position 87 and may in particular be (or be chosen from) threonine (T) or alanine (A).

Such a Nanobody of the invention is again preferably a humanized variant of Alb-1 (but with a S112K or S112Q substitution), and more preferably has at least one, in particular any two, and more in particular all three of CDR1, CDR2 and/or CDR3 given in SEQ ID NO's 41 to 43, respectively.

According to one specific aspect, any serum albumin-binding Nanobody of the invention can also have the amino acid residues that are characteristic of Alb-23 and its variants as described in WO 12/175400 (i.e. the amino acid motif GP on positions 44 and 45, the amino acid motif SKN on positions 74 to 76, and preferably a G at position 16 and optionally also an R at position 83).

Some preferred, but non-limiting examples of Nanobodies of the invention that are directed against human serum albumin are given in Table 4 and Example 20.

Table 4: Non-limiting examples of VH domains of the invention directed against human serum albumin.

SEQ ID:	Sequence name	Amino acid at position 112	C-terminal extension	Sequence
46	Alb-11 (WO 06/122787)	S (reference)	<i>[none]</i>	EVQLVESGGGLVQPGNRLSCAASGFTFSSFGMSWVRQAPGKGLIEWVSSISGGSDETLYADSVKGRFTISRDNAKTTLYLQMNSLRPDTAVYYCTIGGSLSRSQGTLVTVSS
47	Alb-11 + 112K	K	<i>[none]</i>	EVQLVESGGGLVQPGNRLSCAASGFTFSSFGMSWVRQAPGKGLIEWVSSISGGSDETLYADSVKGRFTISRDNAKTTLYLQMNSLRPDTAVYYCTIGGSLSRSQGTLVTVKS
48	Alb-11 + 112K + A	K	A	EVQLVESGGGLVQPGNRLSCAASGFTFSSFGMSWVRQAPGKGLIEWVSSISGGSDETLYADSVKGRFTISRDNAKTTLYLQMNSLRPDTAVYYCTIGGSLSRSQGTLVTVKSA
49	Alb-11 + 112K + AA	K	AA	EVQLVESGGGLVQPGNRLSCAASGFTFSSFGMSWVRQAPGKGLIEWVSSISGGSDETLYADSVKGRFTISRDNAKTTLYLQMNSLRPDTAVYYCTIGGSLSRSQGTLVTVKSA
50	Alb-11 + 112K + AAA	K	AAA	EVQLVESGGGLVQPGNRLSCAASGFTFSSFGMSWVRQAPGKGLIEWVSSISGGSDETLYADSVKGRFTISRDNAKTTLYLQMNSLRPDTAVYYCTIGGSLSRSQGTLVTVKSA
51	Alb-11 + 112K + G	K	G	EVQLVESGGGLVQPGNRLSCAASGFTFSSFGMSWVRQAPGKGLIEWVSSISGGSDETLYADSVKGRFTISRDNAKTTLYLQMNSLRPDTAVYYCTIGGSLSRSQGTLVTVKSG
52	Alb-11 + 112K + GG	K	GG	EVQLVESGGGLVQPGNRLSCAASGFTFSSFGMSWVRQAPGKGLIEWVSSISGGSDETLYADSVKGRFTISRDNAKTTLYLQMNSLRPDTAVYYCTIGGSLSRSQGTLVTVKSGG

Table 4 (continued):

53	Alb-11 + 112K + GGG	K	GGG	EVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMMSWVRQAPGKGLEWVSSIS GSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRLPDTAVYYCTIGGSLSR SQGTLVTVQSGGG
54	Alb-11 + 112Q	Q	[none]	EVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMMSWVRQAPGKGLEWVSSIS GSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRLPDTAVYYCTIGGSLSR SQGTLVTVQSGGG
55	Alb-11 + 112Q + A	Q	A	EVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMMSWVRQAPGKGLEWVSSIS GSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRLPDTAVYYCTIGGSLSR SQGTLVTVQSA
56	Alb-11 + 112Q + AA	Q	AA	EVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMMSWVRQAPGKGLEWVSSIS GSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRLPDTAVYYCTIGGSLSR SQGTLVTVQSA
57	Alb-11 + 112Q + AAA	Q	AAA	EVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMMSWVRQAPGKGLEWVSSIS GSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRLPDTAVYYCTIGGSLSR SQGTLVTVQAAA
58	Alb-11 + 112Q + G	Q	G	EVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMMSWVRQAPGKGLEWVSSIS GSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRLPDTAVYYCTIGGSLSR SQGTLVTVQSG
59	Alb-11 + 112Q + GG	Q	GG	EVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMMSWVRQAPGKGLEWVSSIS GSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRLPDTAVYYCTIGGSLSR SQGTLVTVQSGG

Table 4 (continued):

60	Alb-11 + 112Q + GGG	Q	GGG	EVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMSWVRQAPGKGLEWVSSIS GGSDDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSRSS SQGTLVTVQSGGG
61	Alb-23 (WO 12/175400)	S (reference)	[none]	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSFGMSWVRQAPGKGPEWVSSISG SGSDDTLYADSVKGRFTISRDNSKNTLYLQMNSLRPEDTAVYYCTIGGSLSRSS QGTLVTVSS
62	Alb-23 + 112K	K	[none]	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSFGMSWVRQAPGKGPEWVSSISG SGSDDTLYADSVKGRFTISRDNSKNTLYLQMNSLRPEDTAVYYCTIGGSLSRSS QGTLVTVKS
63	Alb-23 + 112K +A	K	A	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSFGMSWVRQAPGKGPEWVSSISG SGSDDTLYADSVKGRFTISRDNSKNTLYLQMNSLRPEDTAVYYCTIGGSLSRSS QGTLVTVKSAA
64	Alb-23 + 112K +AA	K	AA	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSFGMSWVRQAPGKGPEWVSSISG SGSDDTLYADSVKGRFTISRDNSKNTLYLQMNSLRPEDTAVYYCTIGGSLSRSS QGTLVTVKSAA
65	Alb-23 + 112K +AAA	K	AAA	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSFGMSWVRQAPGKGPEWVSSISG SGSDDTLYADSVKGRFTISRDNSKNTLYLQMNSLRPEDTAVYYCTIGGSLSRSS QGTLVTVKSAAA
66	Alb-23 + 112K +G	K	G	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSFGMSWVRQAPGKGPEWVSSISG SGSDDTLYADSVKGRFTISRDNSKNTLYLQMNSLRPEDTAVYYCTIGGSLSRSS QGTLVTVKS
67	Alb-23 + 112K +GG	K	GG	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSFGMSWVRQAPGKGPEWVSSISG SGSDDTLYADSVKGRFTISRDNSKNTLYLQMNSLRPEDTAVYYCTIGGSLSRSS QGTLVTVKSGG
68	Alb-23 + 112K +GGG	K	GGG	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSFGMSWVRQAPGKGPEWVSSISG SGSDDTLYADSVKGRFTISRDNSKNTLYLQMNSLRPEDTAVYYCTIGGSLSRSS QGTLVTVKSGGG

Table 4 (continued):

69	Alb-23 + 112Q	Q	[none]	EVQLESGGGLVQPGGSLRLSCAASGFTFRSFGMSWVRQAPGKGPEWVSSISG SGSDTLYADSVKGRFTISRDNSKNTLYLQMNSLRPEDTAVYYCTIGGSLSRSS QGTLVTVQSA
70	Alb-23 + 112Q +A	Q	A	EVQLESGGGLVQPGGSLRLSCAASGFTFRSFGMSWVRQAPGKGPEWVSSISG SGSDTLYADSVKGRFTISRDNSKNTLYLQMNSLRPEDTAVYYCTIGGSLSRSS QGTLVTVQSA
71	Alb-23 + 112Q +AA	Q	AA	EVQLESGGGLVQPGGSLRLSCAASGFTFRSFGMSWVRQAPGKGPEWVSSISG SGSDTLYADSVKGRFTISRDNSKNTLYLQMNSLRPEDTAVYYCTIGGSLSRSS QGTLVTVQSA
72	Alb-23 + 112Q +AAA	Q	AAA	EVQLESGGGLVQPGGSLRLSCAASGFTFRSFGMSWVRQAPGKGPEWVSSISG SGSDTLYADSVKGRFTISRDNSKNTLYLQMNSLRPEDTAVYYCTIGGSLSRSS QGTLVTVQSAAA
73	Alb-23 + 112Q +G	Q	G	EVQLESGGGLVQPGGSLRLSCAASGFTFRSFGMSWVRQAPGKGPEWVSSISG SGSDTLYADSVKGRFTISRDNSKNTLYLQMNSLRPEDTAVYYCTIGGSLSRSS QGTLVTVQSA
74	Alb-23 + 112Q +GG	Q	GG	EVQLESGGGLVQPGGSLRLSCAASGFTFRSFGMSWVRQAPGKGPEWVSSISG SGSDTLYADSVKGRFTISRDNSKNTLYLQMNSLRPEDTAVYYCTIGGSLSRSS QGTLVTVQSGG
75	Alb-23 + 112Q +GGG	Q	GGG	EVQLESGGGLVQPGGSLRLSCAASGFTFRSFGMSWVRQAPGKGPEWVSSISG SGSDTLYADSVKGRFTISRDNSKNTLYLQMNSLRPEDTAVYYCTIGGSLSRSS QGTLVTVQSGGG

In another aspect, the invention relates to a VH domain, and in particular an ISVD, and more in particular an Nanobody, that has:

a) a FW 4 sequence that is one of the following FW4 sequences:

Table 5: FW4 sequences

SSQGTLTVKS (SEQ ID NO:99)
SSQGTLTVQS (SEQ ID NO:100)
SSQGTLVKVSS (SEQ ID NO:101)
SSQGTLVQVSS (SEQ ID NO:102)
SSQGTLTVKS(X) _n (SEQ ID NO:103)
SSQGTLTVQS(X) _n (SEQ ID NO:104)
SSQGTLVKVSS(X) _n (SEQ ID NO:105)
SSQGTLVQVSS(X) _n (SEQ ID NO:106)

in which (i) the amino acid residues of the FW4 sequences that precede the (X)_n C-terminal extension in SEQ ID NO's: 23 to 40 correspond to the amino acid positions of FW4 of a VH domain (i.e. positions 103 to 113 according to the Kabat numbering); (ii) n is 1 to 10, preferably 1 to 5, such as 1, 2, 3, 4 or 5 (and preferably 1 or 2, such as 1); and (iii) each X is an (preferably naturally occurring) amino acid residue that is independently chosen, and preferably independently chosen from the group consisting of alanine (A), glycine (G), valine (V), leucine (L) or isoleucine (I); or

c) an amino acid sequence that has no more than three, preferably no more than two, amino acid differences with at least one of the amino acid sequences SEQ ID NO's: 99 to 106 (in which said amino acid differences are at the positions that correspond to the amino acid positions of FW4 of a VH domain, i.e. at positions 103 to 113 according to the Kabat numbering, with any amino acid differences within the C-terminal extension (X)_n being disregarded), in which: (i) when the amino acid residue at the position corresponding to position 112 of the Kabat numbering is either K or Q, said amino acid differences are at another amino acid position than 112, and the amino acid residue at position 89 of the VH domain is preferably chosen from V, T or L (and is most preferably V); (ii) when the amino acid residue at the position corresponding to position 110 of the Kabat numbering is either K or Q, then said amino acid differences are at another amino acid position than 110, and position 89 is the VH domain is L; (iii) n is 1 to 10, preferably 1 to 5, such as 1,

2, 3, 4 or 5 (and preferably 1 or 2, such as 1); and (iv) each X is an (preferably naturally occurring) amino acid residue that is independently chosen, and preferably independently chosen from the group consisting of alanine (A), glycine (G), valine (V), leucine (L) or isoleucine (I). Again, further to features (i) to (iv) as mentioned in the previous sentence, in such an amino acid sequence: (v) the amino acid residue at the position corresponding to position 103 of the Kabat numbering is preferably S; (vi) the amino acid residue at the position corresponding to position 104 of the Kabat numbering is preferably S; (vii) the amino acid residue at the position corresponding to position 106 of the Kabat numbering is preferably G; (viii) the amino acid residue at the position corresponding to position 107 of the Kabat numbering is preferably T; (ix) the amino acid residue at the position corresponding to position 108 of the Kabat numbering is preferably Q or L (and in humanized nanobodies preferably L); (ix) the amino acid residue at the position corresponding to position 109 of the Kabat numbering is preferably V; and reference is again made to the Table 2 for possible amino acid residues that can be present at each position.

Again, in such VH domains of the invention: (a) the amino acid residue at position 11 is one of L, V or K (and more preferably V); the amino acid residue at position 14 is preferably one of A or P; the amino acid residue at position 41 is preferably one of A or P. Also, such a VH domain of the invention is preferably an ISVD, and more preferably a Nanobody; and may again be directed against human serum albumin (in which case it preferably has CDR1, CDR2 and CDR3 respectively that correspond to SEQ ID NO's 41, 42 and 43, respectively). Also, when said VH domains are ISVD's or nanobodies against human serum albumin, they can further be as described herein for nanobodies of the invention that are directed against human serum albumin.

The VH domains of the invention that are directed against serum albumin (and in particular a serum-albumin binding ISVD of the invention) can be used to increase the half-life of therapeutically active compounds, (poly)peptides, proteins, binding domains, binding units or other therapeutically active entities or moieties, essentially in the manner described in WO 2004/041865, WO 2006/122787 and/or WO 2012/175400 for the use of the serum albumin-binding nanobodies that are disclosed in said references (i.e. by suitably linking the serum albumin-binding ISVD to the protein, polypeptide, compound or other entities, optionally via a suitable linker. For example, WO 12/175400 on pages 12 and 13 gives some examples of the manner in which suitable fusion proteins can be constructed).

In another aspect, the invention relates to an immunoglobulin heavy-chain variable domain (VH domain) in which the amino acid residue at position 89 (Kabat numbering) is threonine (T) and the amino acid residue at position 112 is either a serine (S), lysine (K) residue or glutamine (Q) residue. Such immunoglobulin heavy-chain variable domains (VH domain) with a T at position 89 are also included in the term “VH domains of the invention” as used herein in its broadest sense and can further be as described herein for the VH domains of the invention that comprise a K or Q at position 112. Accordingly, such an immunoglobulin heavy-chain variable domain (VH domain) can have a C-terminal extension as further described herein (including the indicated preferences for such a C-terminal extension); can be an ISVD and in particular a Nanobody as further described herein.

Again, if such an VH domain of the invention has an exposed C-terminal region (for example, because it forms the C-terminal end of the protein, polypeptide or other construct in which it is present), it preferably contains a C-terminal extension (reference is made to the data shown in Table C below).

Also, Nanobodies of the invention in which position 89 is T (i.e. with or without a C-terminal extension) preferably contain an amino acid at position 11 that is chosen from L (the most often occurring amino acid residue in VHH's), E, K, M, S, V,W or Y; more preferably from L, E, K, V or Y, and even more preferably from L, K or V (with V being most preferred). For example, they can contain an L11K or L11V substitution, as well as for example a P14A or A14P substitution, a Q108L substitution, and/or a T110K, T110Q, S112K and/or S112Q substitution (although usually the presence of one or two additional substitutions at position 110 and/or 112 will not often not be required when position 89 is T, in which case position 110 is preferably T and position 112 is preferably S).

In particular, an immunoglobulin heavy-chain variable domain (VH domain) of the invention according to this particular aspect has a T at position 89 (Kabat) and a C-terminal end that is one of VTVSS (SEQ ID NO:76), VTVSS(X)n (SEQ ID NO:77), VTVKS (SEQ ID NO:1), VTVKS(X)n (SEQ ID NO:21), VTVQS (SEQ ID NO:2), VTVQS(X)n (SEQ ID NO:22), VKVSS (SEQ ID NO: 95), VKVSS(X)n (SEQ ID NO:97), VQVSS (SEQ ID NO: 96), VQVSS(X)n (SEQ ID NO: 98), VZVZS (SEQ ID NO: 107, in which each amino acid residue Z is independently K or Q) or VZVZSX(n) (SEQ ID NO: 108, in which each amino acid residue Z is independently K or Q) (and in particular one of VTVKS (SEQ ID NO:1), VTVQS (SEQ ID NO:2), VTVSS (SEQ ID NO:76), VTVKS(X)n (SEQ ID NO:21), VTVQS(X)n (SEQ ID NO:22) or VTVSS(X)n (SEQ ID NO:77), and more in particular be either VTVSS (SEQ ID NO:76) or VTVSS(X)n (SEQ ID NO:77)), in which n and X are as

further described herein for the VH domains of the invention in which position 112 is Q or K (and in which any C-terminal extension is preferably as further described herein for the VH domains of the invention in which position 112 is Q or K). Also, as is the case for the VH domains of the invention in which position 112 is Q or K, when such a VH domain with a T at position 89 is a nanobody, position 11 is preferably a leucine (L), position 14 can in particular be alanine (A) or proline (P) and position 108 can in particular be Q or L (and in humanized nanobodies preferably L); and such a Nanobody with a T at position 89 can contain one or more nanobody hallmark residues and/or can be suitably humanized. Also: (i) position 41 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 41 and may in particular be (or be chosen from) proline (P), serine (S), threonine (T), alanine (A) or leucine (L), which are some of the amino acid residues that most frequently occur at this position in either humans or llamas, and may more in particular be either proline (P) or alanine (A); and/or (ii) position 42 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 42 and may in particular be (or be chosen from) glycine (G) or glutamic acid (E); and/or (iii) position 87 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-7 of WO 08/020079 for position 87 and may in particular be (or be chosen from) threonine (T) or alanine (A).

Such a VH domain of the invention with a T at position 89 can again also be a serum albumin Nanobody as further described herein. For example, such a serum albumin-binding Nanobody can be one of the sequences of SEQ ID NOs: 46 to 75, but with a T at position 89; or another serum albumin binding Nanobody with a T at position 89 that has at least 80%, preferably at least 85%, more preferably at least 90% such as at least 95% sequence identity with at least one of Alb-1 (SEQ ID NO: 52 of WO 2006/122787), Alb-8 (SEQ ID NO: 46 herein) and/or Alb-23 (SEQ ID NO: 61 herein) (taking into account both the framework sequences and the CDR's, but not any C-terminal extension). Some other examples of such Nanobodies with a T at position 89 are given in SEQ ID NO's: 78 to 91 (these are further variants of Alb-1/Alb-8 or Alb-23 with a T at position 89 and an S at position 112).

More generally, a VH domain against serum albumin according to this aspect of the invention can be one of the Nanobodies against (human) serum albumin that are described in WO 2004/041865, and in particular in WO 2006/122787 and WO 2012/175400 (all applications from applicant/assignee), in which the amino acid at position 89 is a threonine

(T), and which is optionally provided with a C-terminal extension as described herein (and can also for example also suitably contain one or more of the other specific amino acid residues/ substitutions mentioned herein, such as 11L, L11V, L11K, 14A, P14A, 14P, A14P, 108L, Q108L, 110K, T110K, 110Q, T110Q, S112K and/or S112Q; although usually the presence of additional substitutions at positions 110 and/or 112 will not often not be required when a T is present at position 89, in which case that position 110 is preferably T and position 112 is preferably S). Also: (i) position 41 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 41 and may in particular be (or be chosen from) proline (P), serine (S), threonine (T), alanine (A) or leucine (L), which are some of the amino acid residues that most frequently occur at this position in either humans or llamas, and may more in particular be either proline (P) or alanine (A); and/or (ii) position 42 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 42 and may in particular be (or be chosen from) glycine (G) or glutamic acid (E); and/or (iii) position 87 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-7 of WO 08/020079 for position 87 and may in particular be (or be chosen from) threonine (T) or alanine (A). Furthermore, it is envisaged that the present invention can also be applied other serum-albumin binding heavy-chain ISVD's, such as those described in WO 03/035694, WO 04/003019, WO 05/118642, WO 06/059106, WO 08/096158, WO 09/121804 WO 10/108937 or US 2013/0129727, i.e. by suitably introducing threonine (T) at position 89, and optionally one or more of the other amino acid residues/substitutions described herein) and optionally (and usually preferably as outlined herein) adding a C-terminal extension (as further described herein).

Some preferred but non-limiting examples of such serum albumin binding Nanobodies of the invention are humanized variants of the amino acid sequence of SEQ ID NO: 52 of WO 2006/122787 (called "Alb-1" in WO 2006/122787), in which the amino acid at position 89 is T (and which is optionally provided with a C-terminal extension as described herein), such as the humanized variants of Alb-1 that are given in SEQ ID NO's: 57 to 64 of WO 2006/122787 (in each case, with a V89T substitution, and optionally with a C-terminal extension) or the humanized variants of Alb-1 that are given in SEQ ID NO's 3 to 11 of WO 2012/175400 (again, in each case, with a V89T substitution), of which SEQ ID NO's 3, 4 and 5 can optionally contain a C-terminal extension, and SEQ ID NO's 6 to 11 already contain a C-terminal extension (and again, such variants can contain one or more of the other specific

amino acid residues/ substitutions mentioned herein, such as 11L, L11V, L11K, 14A, P14A, 14P, A14P, 108L, Q108L, 110K, T110K, 110Q, T110Q, 112Q, 112K, S112Q and/or S112K; although usually the presence of one or two additional substitutions at positions 110 and/or 112 will not often not be required when position 89 is T, in which case position 110 is preferably T and position 112 is preferably S). Also: (i) position 41 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 41 and may in particular be (or be chosen from) proline (P), serine (S), threonine (T), alanine (A) or leucine (L), which are some of the amino acid residues that most frequently occur at this position in either humans or 10 llamas, and may more in particular be either proline (P) or alanine (A); and/or (ii) position 42 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 42 and may in particular be (or be chosen from) glycine (G) or glutamic acid (E); and/or (iii) position 87 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-7 of WO 08/020079 for position 87 and may in particular be (or be chosen from) threonine (T) or alanine (A).

Thus, in a further aspect, the invention relates to a Nanobody of the invention (as defined herein) that can bind (and in particular specifically bind) to serum albumin (and in particular human serum albumin) in which:

20 - CDR1 is the amino acid sequence SFGMS (SEQ ID NO:41);
- CDR2 is the amino acid sequence SISGSGSDTLYADSVKG (SEQ ID NO:42);
- CDR3 is the amino acid sequence GGSLSR (SEQ ID NO:43);
- the amino acid residue at position 89 is T;

and that optionally contains at its C-terminal end a C-terminal extension (X)_n in which n is 1 to 10, preferably 1 to 5, such as 1, 2, 3, 4 or 5 (and preferably 1 or 2, such as 1); and each X is an (preferably naturally occurring) amino acid residue that is independently chosen, and preferably independently chosen from the group consisting of alanine (A), glycine (G), valine (V), leucine (L) or isoleucine (I) (again, such a C-terminal extension is preferably as further described herein, and again such a Nanobody can also for example also contain one or more 30 of the other specific amino acid residues/ substitutions mentioned herein, such as 11L, L11V, L11K, 14A, P14A, 14P, A14P, 108L, Q108L, 110K, T110K, 110Q, T110Q, 112Q, 112K, S112Q and/or S112K; although usually the presence of one or two additional substitutions at positions 110 and/or 112 will not often not be required when position 89 is T, in which case

position 110 is preferably T and position 112 is preferably S). Also: (i) position 41 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 41 and may in particular be (or be chosen from) proline (P), serine (S), threonine (T), alanine (A) or leucine (L), which are some of the amino acid residues that most frequently occur at this position in either humans or llamas, and may more in particular be either proline (P) or alanine (A); and/or (ii) position 42 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 42 and may in particular be (or be chosen from) glycine (G) or glutamic acid (E); and/or (iii) position 10 87 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-7 of WO 08/020079 for position 87 and may in particular be (or be chosen from) threonine (T) or alanine (A).

In a particular aspect, the invention relates to a Nanobody of the invention (as defined herein) that can bind (and in particular specifically bind) to serum albumin (and in particular human serum albumin) that is a humanized variant of SEQ ID NO: 52 of WO 2006/122787 in which:

- CDR1 is the amino acid sequence SFGMS (SEQ ID NO:41);
- CDR2 is the amino acid sequence SISGSGSDTLYADSVKG (SEQ ID NO:42);
- CDR3 is the amino acid sequence GGSLSR (SEQ ID NO:43);
- 20 - the amino acid residue at position 89 is T;

and that optionally contains at its C-terminal end a C-terminal extension (X)_n in which n is 1 to 10, preferably 1 to 5, such as 1, 2, 3, 4 or 5 (and preferably 1 or 2, such as 1); and each X is an (preferably naturally occurring) amino acid residue that is independently chosen, and preferably independently chosen from the group consisting of alanine (A), glycine (G), valine (V), leucine (L) or isoleucine (I) (again, such a C-terminal extension is preferably as further described herein, and again such a Nanobody can also for example also contain one or more of the other specific amino acid residues/ substitutions mentioned herein, such as 11L, L11V, L11K, 14A, P14A, 14P, A14P, 108L, Q108L, 110K, T110K, 110Q, T110Q, 112Q, 112K, S112Q and/or S112K; although usually the presence of one or two additional substitutions at 30 positions 110 and/or 112 will not often not be required when position 89 is T, in which case position 110 is preferably T and position 112 is preferably S). Also: (i) position 41 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 41 and may in particular be

(or be chosen from) proline (P), serine (S), threonine (T), alanine (A) or leucine (L), which are some of the amino acid residues that most frequently occur at this position in either humans or llamas, and may more in particular be either proline (P) or alanine (A); and/or (ii) position 42 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 42 and may in particular be (or be chosen from) glycine (G) or glutamic acid (E); and/or (iii) position 87 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-7 of WO 08/020079 for position 87 and may in particular be (or be chosen from) threonine (T) or alanine (A).

10 In a particular aspect, the invention relates to a Nanobody of the invention (as defined herein) that can bind (and in particular specifically bind) to serum albumin (and in particular human serum albumin) that has at least 80%, preferably at least 85%, more preferably at least 90% such as at least 95% sequence identity with at least one of Alb-1 (SEQ ID NO: 52 of WO 2006/122787), Alb-8 (SEQ ID NO: 46 herein) and/or Alb-23 (SEQ ID NO: 61 herein) (taking into account both the framework sequences and the CDR's, but not any C-terminal extension), in which the amino acid residue at position 89 is T, and that optionally contains at its C-terminal end a C-terminal extension (X)_n in which n is 1 to 10, preferably 1 to 5, such as 1, 2, 3, 4 or 5 (and preferably 1 or 2, such as 1); and each X is an (preferably naturally occurring) amino acid residue that is independently chosen, and preferably independently chosen from the group consisting of alanine (A), glycine (G), valine (V), leucine (L) or isoleucine (I) (again, such a C-terminal extension is preferably as further described herein, and again such a Nanobody can also for example also contain one or more of the other specific amino acid residues/ substitutions mentioned herein, such as 11L, L11V, L11K, 14A, P14A, 14P, A14P, 108L, Q108L, 110K, T110K, 110Q, T110Q, 112Q, 112K, S112Q and/or S112K; although usually the presence of one or two additional substitutions at positions 110 and/or 112 will not often not be required when position 89 is T, in which case position 110 is preferably T and position 112 is preferably S). Also: (i) position 41 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 41 and may in particular be (or be chosen from) proline (P), serine (S), threonine (T), alanine (A) or leucine (L), which are some of the amino acid residues that most frequently occur at this position in either humans or llamas, and may more in particular be either proline (P) or alanine (A); and/or (ii) position 42 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 42 and may in

particular be (or be chosen from) glycine (G) or glutamic acid (E); and/or (iii) position 87 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-7 of WO 08/020079 for position 87 and may in particular be (or be chosen from) threonine (T) or alanine (A).

According to one specific aspect, any such serum albumin-binding Nanobody of the invention with a T at position 89 can also have the amino acid residues that are characteristic of Alb-23 and its variants as described in WO 12/175400 (i.e. the amino acid motif GP on positions 44 and 45, the amino acid motif SKN on positions 74 to 76, and preferably a G at position 16 and optionally also an R at position 83).

10 As with the VH domains of the invention that contain an Q or K at position 112, the VH domains of the invention that contain a T at position 89 (optionally together with a Q or K at position 112 and/or together with a C-terminal extension) show reduced binding by pre-existing antibodies, and in particular by such pre-existing antibodies (as for example are found in samples obtained from SLE patients) that are capable of binding to VH domains and Nanobodies in the presence of a C-terminal extension.

20 In yet another aspect, the invention relates to an immunoglobulin heavy-chain variable domain (VH domain) in which the amino acid residue at position 89 (Kabat numbering) is leucine (L) and the amino acid residue at position 110 is either a lysine (K) residue or glutamine (Q) residue. Such immunoglobulin heavy-chain variable domains (VH domain) with an L at position 89 and a K or Q at position 110 are also included in the term “VH domains of the invention” as used herein in its broadest sense and can further be as described herein for the other VH domains of the invention (i.e. those that comprise a K or Q at position 112 or that comprise a T at position 89). Accordingly, such an immunoglobulin heavy-chain variable domain (VH domain) can have a C-terminal extension as further described herein (including the indicated preferences for such a C-terminal extension); can be an ISVD and in particular a Nanobody as further described herein.

30 Again, if such a VH domain of the invention has an exposed C-terminal region (for example, because it forms the C-terminal end of the protein, polypeptide or other construct in which it is present), it preferably contains a C-terminal extension (reference is made to the data shown in Table C below).

Also, Nanobodies of the invention in which position 89 is L and a K or Q at position 110 (i.e. with or without a C-terminal extension) preferably contain an amino acid at position 11 that is chosen from L (the most often occurring amino acid residue in VHH's), E, K, M, S, V, W or Y; more preferably from L, E, K, V or Y, and even more preferably from L, K or V

(with V being most preferred). For example, they can contain an L11K or L11V substitution, as well as for example a P14A or A14P substitution and/or a Q108L substitution (they can also suitably contain an S112K and/or S112Q mutation, although usually the presence of an additional substitution at positions 112 will not often not be required when position 89 is L and position 110 is K or Q, in which case position 112 is preferably S). Also: (i) position 41 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 41 and may in particular be (or be chosen from) proline (P), serine (S), threonine (T), alanine (A) or leucine (L), which are some of the amino acid residues that most frequently occur at this position in 10 either humans or llamas, and may more in particular be either proline (P) or alanine (A); and/or (ii) position 42 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 42 and may in particular be (or be chosen from) glycine (G) or glutamic acid (E); and/or (iii) position 87 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-7 of WO 08/020079 for position 87 and may in particular be (or be chosen from) threonine (T) or alanine (A).

Also, in one aspect, in such VH domains of the invention in which 89 is L and 110 is K or Q, the amino acid residue at position 112 is serine (S). More in particular, the C-terminal end of such a VH domain may be one of (and preferably is one of) VKVSS (SEQ ID NO: 95), 20 VQVSS (SEQ ID NO: 96), VKVSS(X)_n (SEQ ID NO: 97) or VQVSS(X)_n (SEQ ID NO: 98), in which n and X are as further described herein for the VH domains of the invention in which position 112 is Q or K (and in which any C-terminal extension is preferably as further described herein for the VH domains of the invention in which position 112 is Q or K). Also, as is the case for the VH domains of the invention in which position 112 is Q or K or position 89 is T, when such a VH domain with an L at position 89 and a K or Q at position 110 is a nanobody, position 11 is preferably a leucine (L), position 14 can in particular be alanine (A) or proline (P) and position 108 can in particular be Q or L (and in humanized nanobodies preferably L); and such a Nanobody with an L at position 89 and a K or Q at position 110 can contain one or more nanobody hallmark residues and/or can be suitably humanized. Also: (i) 30 position 41 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 41 and may in particular be (or be chosen from) proline (P), serine (S), threonine (T), alanine (A) or leucine (L), which are some of the amino acid residues that most frequently occur at this position in either humans or llamas, and may more in particular be either proline (P) or

alanine (A); and/or (ii) position 42 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 42 and may in particular be (or be chosen from) glycine (G) or glutamic acid (E); and/or (iii) position 87 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-7 of WO 08/020079 for position 87 and may in particular be (or be chosen from) threonine (T) or alanine (A).

Such a VH domain of the invention with an L at position 89 and a K or Q at position 110 can again also be a serum albumin Nanobody as further described herein. For example, 10 such a serum albumin-binding Nanobody can be one of the sequences of SEQ ID NOS: 46 to 75, but with an L at position 89 and a K or Q at position 110; or another serum albumin binding Nanobody with an L at position 89 and a K or Q at position 110 that has at least 80%, preferably at least 85%, more preferably at least 90% such as at least 95% sequence identity with at least one of Alb-1 (SEQ ID NO: 52 of WO 2006/122787), Alb-8 (SEQ ID NO: 46 herein) and/or Alb-23 (SEQ ID NO: 61 herein) (taking into account both the framework sequences and the CDR's, but not any C-terminal extension).

More generally, a VH domain against serum albumin according to this aspect of the invention can be one of the Nanobodies against (human) serum albumin that are described in WO 2004/041865, and in particular in WO 2006/122787 and WO 2012/175400 (all 20 applications from applicant/assignee), in which the amino acid at position 89 is a leucine (L) and the amino acid residue at position 110 is of K or Q, and which is optionally provided with a C-terminal extension as described herein (and can also for example also contain one or more of the other specific amino acid residues/ substitutions mentioned herein, such as 11L, L11V, L11K, 14A, P14A, 14P, A14P, 108L and/or Q108L; as well as S112K or S112Q, although usually the presence of an additional substitution at position 112 will not often not be required when position 89 is L and position 110 is K or Q, in which case position 112 is preferably S). Furthermore, it is envisaged that the present invention can also be applied other serum-albumin binding heavy-chain ISVD's, such as those described in WO 03/035694, WO 04/003019, WO 05/118642, WO 06/059106, WO 08/096158, WO 09/121804 WO 10/108937 30 or US 2013/0129727, i.e. by suitably introducing leucine (L) at position 89 and either K or Q at position 110, and optionally one or more of the other amino acid residues/substitutions described herein) and optionally (and usually preferably as outlined herein) adding a C-terminal extension (as further described herein). In these VH domains against serum albumin, the amino acid at position 112 is preferably S, and said VH domains preferably have a C-

terminal end that is one of SEQ ID NO's: 95 to 98. Also: (i) position 41 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 41 and may in particular be (or be chosen from) proline (P), serine (S), threonine (T), alanine (A) or leucine (L), which are some of the amino acid residues that most frequently occur at this position in either humans or llamas, and may more in particular be either proline (P) or alanine (A); and/or (ii) position 42 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 42 and may in particular be (or be chosen from) glycine (G) or glutamic acid (E); and/or (iii) position 87 10 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-7 of WO 08/020079 for position 87 and may in particular be (or be chosen from) threonine (T) or alanine (A).

Some preferred but non-limiting examples of such serum albumin binding Nanobodies of the invention are humanized variants of the amino acid sequence of SEQ ID NO: 52 of WO 2006/122787 (called "Alb-1" in WO 2006/122787), in which the amino acid at position 89 is L and the amino acid at position 110 is K or Q (and which is optionally provided with a C-terminal extension as described herein), such as the humanized variants of Alb-1 that are given in SEQ ID NO's: 57 to 64 of WO 2006/122787 (in each case, with a V89L substitution and a T110Q or T110K substitution, and optionally with a C-terminal extension) or the 20 humanized variants of Alb-1 that are given in SEQ ID NO's 3 to 11 of WO 2012/175400 (again, in each case, with a V89L substitution and a T110Q or T110K substitution), of which SEQ ID NO's 3, 4 and 5 can optionally contain a C-terminal extension, and SEQ ID NO's 6 to 11 already contain a C-terminal extension (and again, such variants can contain one or more of the other specific amino acid residues/ substitutions mentioned herein, such as 11L, L11V, L11K, 14A, P14A, 14P, A14P, 108L and/or Q108L; as well as S112K or S112Q, although usually the presence of an additional substitution at position 112 will not often not be required when position 89 is L and position 110 is K or Q, in which case position 112 is preferably S). In these VH domains against serum albumin, the amino acid at position 112 is preferably S, and said VH domains preferably have a C-terminal end that is one of SEQ ID 30 NO's: 95 to 98. Also: (i) position 41 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 41 and may in particular be (or be chosen from) proline (P), serine (S), threonine (T), alanine (A) or leucine (L), which are some of the amino acid residues that most frequently occur at this position in either humans or llamas, and may more in particular be

either proline (P) or alanine (A); and/or (ii) position 42 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 42 and may in particular be (or be chosen from) glycine (G) or glutamic acid (E); and/or (iii) position 87 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-7 of WO 08/020079 for position 87 and may in particular be (or be chosen from) threonine (T) or alanine (A).

Thus, in a further aspect, the invention relates to a Nanobody of the invention (as defined herein) that can bind (and in particular specifically bind) to serum albumin (and in particular human serum albumin) in which:

- CDR1 is the amino acid sequence SFGMS (SEQ ID NO:41);
- CDR2 is the amino acid sequence SISGSGSDTLYADSVKG (SEQ ID NO:42);
- CDR3 is the amino acid sequence GGSLSR (SEQ ID NO:43);
- the amino acid residue at position 89 is L;
- the amino acid residue at position 110 is K or Q;

and that optionally contains at its C-terminal end a C-terminal extension (X)_n in which n is 1 to 10, preferably 1 to 5, such as 1, 2, 3, 4 or 5 (and preferably 1 or 2, such as 1); and each X is an (preferably naturally occurring) amino acid residue that is independently chosen, and preferably independently chosen from the group consisting of alanine (A), glycine (G), valine (V), leucine (L) or isoleucine (I) (again, such a C-terminal extension is preferably as further described herein, and again such a Nanobody can also for example also contain one or more of the other specific amino acid residues/ substitutions mentioned herein, such as 11L, L11V, L11K, 14A, P14A, 14P, A14P, 108L and/or Q108L; as well as S112K or S112Q, although usually the presence of an additional substitution at position 112 will not often not be required when position 89 is L and position 110 is K or Q, in which case position 112 is preferably S).

In these VH domains against serum albumin, the amino acid at position 112 is preferably S, and said VH domains preferably have a C-terminal end that is one of SEQ ID NO's: 95 to 98. Also: (i) position 41 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for

position 41 and may in particular be (or be chosen from) proline (P), serine (S), threonine (T), alanine (A) or leucine (L), which are some of the amino acid residues that most frequently occur at this position in either humans or llamas, and may more in particular be either proline (P) or alanine (A); and/or (ii) position 42 may for example be one of the amino acid residues

(i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 42 and may in particular be (or be chosen from) glycine (G) or glutamic acid (E); and/or (iii) position 87 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-7 of WO 08/020079 for position 87 and may in particular be (or be chosen from) threonine (T) or alanine (A).

In a particular aspect, the invention relates to a Nanobody of the invention (as defined herein) that can bind (and in particular specifically bind) to serum albumin (and in particular human serum albumin) that is a humanized variant of SEQ ID NO: 52 of WO 2006/122787 in which:

- CDR1 is the amino acid sequence SFGMS (SEQ ID NO:41);
- CDR2 is the amino acid sequence SISGSGSDTLYADSVKG (SEQ ID NO:42);
- CDR3 is the amino acid sequence GGSLSR (SEQ ID NO:43);
- the amino acid residue at position 89 is L;
- the amino acid residue at position 110 is K or Q;

and that optionally contains at its C-terminal end a C-terminal extension (X)_n in which n is 1 to 10, preferably 1 to 5, such as 1, 2, 3, 4 or 5 (and preferably 1 or 2, such as 1); and each X is an (preferably naturally occurring) amino acid residue that is independently chosen, and preferably independently chosen from the group consisting of alanine (A), glycine (G), valine (V), leucine (L) or isoleucine (I) (again, such a C-terminal extension is preferably as further described herein, and again such a Nanobody can also for example also contain one or more of the other specific amino acid residues/ substitutions mentioned herein, such as 11L, L11V, L11K, 14A, P14A, 14P, A14P, 108L and/or Q108L; as well as S112K or S112Q, although usually the presence of an additional substitution at position 112 will not often not be required when position 89 is L and position 110 is K or Q, in which case position 112 is preferably S)).

In these VH domains against serum albumin, the amino acid at position 112 is preferably S, and said VH domains preferably have a C-terminal end that is one of SEQ ID NO's: 95 to 98. Also: (i) position 41 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for

position 41 and may in particular be (or be chosen from) proline (P), serine (S), threonine (T), alanine (A) or leucine (L), which are some of the amino acid residues that most frequently occur at this position in either humans or llamas, and may more in particular be either proline (P) or alanine (A); and/or (ii) position 42 may for example be one of the amino acid residues

(i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 42 and may in particular be (or be chosen from) glycine (G) or glutamic acid (E); and/or (iii) position 87 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-7 of WO 08/020079 for position 87 and may in particular be (or be chosen from) threonine (T) or alanine (A).

In a particular aspect, the invention relates to a Nanobody of the invention (as defined herein) that can bind (and in particular specifically bind) to serum albumin (and in particular human serum albumin) that has at least 80%, preferably at least 85%, more preferably at least 10 90% such as at least 95% sequence identity with at least one of Alb-1 (SEQ ID NO: 52 of WO 2006/122787), Alb-8 (SEQ ID NO: 46 herein) and/or Alb-23 (SEQ ID NO: 61 herein) (taking into account both the framework sequences and the CDR's, but not any C-terminal extension), in which the amino acid residue at position 89 is L and the amino acid residue at position 110 is K or Q, and that optionally contains at its C-terminal end a C-terminal extension (X)_n in which n is 1 to 10, preferably 1 to 5, such as 1, 2, 3, 4 or 5 (and preferably 1 or 2, such as 1); and each X is an (preferably naturally occurring) amino acid residue that is independently chosen, and preferably independently chosen from the group consisting of alanine (A), glycine (G), valine (V), leucine (L) or isoleucine (I) (again, such a C-terminal extension is preferably as further described herein, and again such a Nanobody can also for 20 example also contain one or more of the other specific amino acid residues/ substitutions mentioned herein, such as 11L, L11V, L11K, 14A, P14A, 14P, A14P, 108L and/or Q108L; as well as S112K or S112Q, although usually the presence of an additional substitution at position 112 will not often not be required when position 89 is L and position 110 is K or Q, in which case position 112 is preferably S). Such a Nanobody of the invention is again preferably a humanized variant of Alb-1 (but with a V89L and T110K or T110Q substitution), and more preferably has at least one, in particular any two, and more in particular all three of CDR1, CDR2 and/or CDR3 given in SEQ ID NO's 41 to 43, respectively. In these VH domains against serum albumin, the amino acid at position 112 is preferably S, and said VH domains preferably have a C-terminal end that is one of SEQ ID NO's: 95 to 98. Also: (i) 30 position 41 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 41 and may in particular be (or be chosen from) proline (P), serine (S), threonine (T), alanine (A) or leucine (L), which are some of the amino acid residues that most frequently occur at this position in either humans or llamas, and may more in particular be either proline (P) or

alanine (A); and/or (ii) position 42 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 42 and may in particular be (or be chosen from) glycine (G) or glutamic acid (E); and/or (iii) position 87 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-7 of WO 08/020079 for position 87 and may in particular be (or be chosen from) threonine (T) or alanine (A).

According to one specific aspect, any such serum albumin-binding Nanobody of the invention with an L at position 89 and a K or Q at position 110 can also have the amino acid residues that are characteristic of Alb-23 and its variants as described in WO 12/175400 (i.e. the amino acid motif GP on positions 44 and 45, the amino acid motif SKN on positions 74 to 76, and preferably a G at position 16 and optionally also an R at position 83). Also: (i) position 41 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 41 and may in particular be (or be chosen from) proline (P), serine (S), threonine (T), alanine (A) or leucine (L), which are some of the amino acid residues that most frequently occur at this position in either humans or llamas, and may more in particular be either proline (P) or alanine (A); and/or (ii) position 42 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 42 and may in particular be (or be chosen from) glycine (G) or glutamic acid (E); and/or (iii) position 87 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-7 of WO 08/020079 for position 87 and may in particular be (or be chosen from) threonine (T) or alanine (A).

As with the VH domains of the invention that contain an Q or K at position 112 or that have a T at position 89, the VH domains of the invention that contain an L at position 89 and a K or Q at position 110 show reduced binding by pre-existing antibodies, and in particular by such pre-existing antibodies (as for example are found in samples obtained from SLE patients) that are capable of binding to VH domains and Nanobodies in the presence of a C-terminal extension.

Some non-limiting examples of VH domains of the invention that have an L at position 89 and a K at position 110 (and in addition, a V at position 11) are given in Figure 2 as SEQ ID NO's: 123-136. These are VH domains binding to human serum albumin and have

the CDR's indicated herein for the preferred serum albumin binding VH domains of the invention.

In yet another aspect, the invention relates to an immunoglobulin heavy-chain variable domain (VH domain) in which the amino acid residue at position 89 (Kabat numbering) is leucine (L) and the amino acid residue at position 11 is valine (V). Such immunoglobulin heavy-chain variable domains (VH domain) with an L at position 89 and a V at position 11 are also included in the term "VH domains of the invention" as used herein in its broadest sense and can further be as described herein for the other VH domains of the invention described herein (i.e. those that comprise a K or Q at position 112, that comprise a T at position 89, or that comprise an L at position 89 and a K or Q at position 110; albeit that for the VH domains according to the current aspect, the amino acid residue at position 89 will be L, at amino acid residue at position 11 will be V, and the amino acid residues at positions 110 and 112, respectively, can be any amino acid residue suitable for these positions). Accordingly, such an immunoglobulin heavy-chain variable domain (VH domain) can have a C-terminal extension as further described herein (including the indicated preferences for such a C-terminal extension); can be an ISVD and in particular a Nanobody as further described herein.

Again, if such a VH domain of the invention has an exposed C-terminal region (for example, because it forms the C-terminal end of the protein, polypeptide or other construct in which it is present), it preferably contains a C-terminal extension (reference is made to the data shown in Table C below).

Also, Nanobodies of the invention in which position 89 is L and position 11 is V (i.e. with or without a C-terminal extension): (i) preferably contain an amino acid at position 110 that is chosen from T, I, A, K or Q (and preferably from T, K or Q, and that in particular can be T); (ii) preferably contain an amino acid at position 112 that is chosen from S, F, K or Q (and more preferably S, K or Q, and that in particular can be S); and (iii) can for example also contain a P14A or A14P substitution and/or a Q108L substitution. According to one specific embodiment, in the VH domains according to this aspect of the invention, the amino acid residue at position 110 is T and the amino acid residue at position 112 is S, and more preferably the C-terminal end is either VTVSS (SEQ ID NO: 76) or VTVSS(X)n (SEQ ID NO: 77), in which X and n are as defined herein for the C-terminal extension of the other VH domains of the invention. Also, in the VH domains according to this aspect of the invention: (i) position 41 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 41 and

may in particular be (or be chosen from) proline (P), serine (S), threonine (T), alanine (A) or leucine (L), which are some of the amino acid residues that most frequently occur at this position in either humans or llamas, and may more in particular be either proline (P) or alanine (A); and/or (ii) position 42 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 42 and may in particular be (or be chosen from) glycine (G) or glutamic acid (E); and/or (iii) position 87 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-7 of WO 08/020079 for position 87 and may in particular be (or be chosen from) threonine (T) or alanine (A).

Thus, for example, in such VH domains of the invention in which 89 is L and 11 is V, the C-terminal end of such a VH domain may be one of (and preferably is one of) VTVSS (SEQ ID NO:76), VTVSS(X)n (SEQ ID NO:77), VTVKS (SEQ ID NO:1), VTVKS(X)n (SEQ ID NO:21), VTVQS (SEQ ID NO:2), VTVQS(X)n (SEQ ID NO:22), VKVSS (SEQ ID NO: 95), VKVSS(X)n (SEQ ID NO:97), VQVSS (SEQ ID NO: 96), VQVSS(X)n (SEQ ID NO: 98), VZVZS (SEQ ID NO: 107, in which each amino acid residue Z is independently K or Q) or VZVZSX(n) (SEQ ID NO:108, in which each amino acid residue Z is independently K or Q) (and is in particular one of VTVSS , VKVSS (SEQ ID NO: 95), VQVSS (SEQ ID NO: 96), VKVSS(X)n (SEQ ID NO:97) or VQVSS(X)n (SEQ ID NO: 98), and may more in particular be either VTVSS (SEQ ID NO:76) or VTVSS(X)n (SEQ ID NO:77)), in which n and X are as further described herein for the VH domains of the invention in which position 112 is Q or K (and in which any C-terminal extension is preferably as further described herein for the VH domains of the invention in which position 112 is Q or K). Also, as is the case for the VH domains of the invention in which position 112 is Q or K or position 89 is T, when such a VH domain with an L at position 89 and a V at position 11 is a nanobody, position 14 can in particular be alanine (A) or proline (P) and position 108 can be Q or L (and in humanized nanobodies preferably L); and such a Nanobody with an L at position 89 and a V at position 11 can contain one or more nanobody hallmark residues and/or can be suitably humanized. Also: (i) position 41 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 41 and may in particular be (or be chosen from) proline (P), serine (S), threonine (T), alanine (A) or leucine (L), which are some of the amino acid residues that most frequently occur at this position in either humans or llamas, and may more in particular be either proline (P) or alanine (A); and/or (ii) position 42 may for example be one of the amino

acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 42 and may in particular be (or be chosen from) glycine (G) or glutamic acid (E); and/or (iii) position 87 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-7 of WO 08/020079 for position 87 and may in particular be (or be chosen from) threonine (T) or alanine (A).

Such a VH domain of the invention with an L at position 89 and a V at position 11 can again also be a serum albumin Nanobody as further described herein. For example, such a serum albumin-binding Nanobody can be one of the sequences of SEQ ID NOs: 46 to 75, but with an L at position 89 and a V at position 11; or another serum albumin binding Nanobody with an L at position 89 and a V at position 11 that has at least 80%, preferably at least 85%, more preferably at least 90% such as at least 95% sequence identity with at least one of Alb-1 (SEQ ID NO: 52 of WO 2006/122787), Alb-8 (SEQ ID NO: 46 herein) and/or Alb-23 (SEQ ID NO: 61 herein) (taking into account both the framework sequences and the CDR's, but not any C-terminal extension).

More generally, a VH domain against serum albumin according to this aspect of the invention can be one of the Nanobodies against (human) serum albumin that are described in WO 2004/041865, and in particular in WO 2006/122787 and WO 2012/175400 (all applications from applicant/assignee), in which the amino acid at position 89 is a leucine (L) and the amino acid residue at position 11 is V, and which is optionally provided with a C-terminal extension as described herein (and can also for example also suitably contain one or more of the other specific amino acid residues/ substitutions mentioned herein, such as 14A, P14A, 14P, A14P, 108L, Q108L, V110K, V110Q, S112K and/or S112Q). Furthermore, it is envisaged that the present invention can also be applied other serum-albumin binding heavy-chain ISVD's, such as those described in WO 03/035694, WO 04/003019, WO 05/118642, WO 06/059106, WO 08/096158, WO 09/121804 WO 10/108937 or US 2013/0129727, i.e. by suitably introducing leucine (L) at position 89 and valine at position 11, and optionally one or more of the other amino acid residues/substitutions described herein) and optionally (and usually preferably as outlined herein) adding a C-terminal extension (as further described herein). In these VH domains against serum albumin, the amino acid at position 112 is preferably S, and said VH domains preferably have a C-terminal end that is one of SEQ ID NO's: 95 to 98. Also: (i) position 41 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 41 and may in particular be (or be chosen from) proline (P), serine (S),

threonine (T), alanine (A) or leucine (L), which are some of the amino acid residues that most frequently occur at this position in either humans or llamas, and may more in particular be either proline (P) or alanine (A); and/or (ii) position 42 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 42 and may in particular be (or be chosen from) glycine (G) or glutamic acid (E); and/or (iii) position 87 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-7 of WO 08/020079 for position 87 and may in particular be (or be chosen from) threonine (T) or alanine (A).

10 Some preferred but non-limiting examples of such serum albumin binding Nanobodies of the invention are humanized variants of the amino acid sequence of SEQ ID NO: 52 of WO 2006/122787 (called “Alb-1” in WO 2006/122787), in which the amino acid at position 89 is L and the amino acid at position 11 is V (and which is optionally provided with a C-terminal extension as described herein), such as the humanized variants of Alb-1 that are given in SEQ ID NO’s: 57 to 64 of WO 2006/122787 (in each case, with a V89L substitution and a L11V substitution, and optionally with a C-terminal extension) or the humanized variants of Alb-1 that are given in SEQ ID NO’s 3 to 11 of WO 2012/175400 (again, in each case, with a V89L substitution and a L11V), of which SEQ ID NO’s 3, 4 and 5 can optionally contain a C-terminal extension, and SEQ ID NO’s 6 to 11 already contain a C-terminal extension (and again, such variants can suitably contain one or more of the other specific amino acid residues/ substitutions mentioned herein, such as 14A, P14A, 14P, A14P, 108L, Q108L, T110K, T110Q, S112K and/or S112Q). In these VH domains against serum albumin with an L at position 89 and a V at position 11, the amino acid at position 110 is preferably T and the amino acid residue at position 112 is preferably S, and said VH domains preferably have a C-terminal end that is one of SEQ ID NO’s: 95 to 98. Also: (i) position 41 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 41 and may in particular be (or be chosen from) proline (P), serine (S), threonine (T), alanine (A) or leucine (L), which are some of the amino acid residues that most frequently occur at this position in either humans or llamas, and may more in particular be either proline (P) or alanine (A); and/or (ii) position 42 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 42 and may in particular be (or be chosen from) glycine (G) or glutamic acid (E); and/or (iii) position 87 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid

VHH residues) mentioned in Table A-7 of WO 08/020079 for position 87 and may in particular be (or be chosen from) threonine (T) or alanine (A).

Thus, in a further aspect, the invention relates to a Nanobody of the invention (as defined herein) that can bind (and in particular specifically bind) to serum albumin (and in particular human serum albumin) in which:

- CDR1 is the amino acid sequence SFGMS (SEQ ID NO:41);
- CDR2 is the amino acid sequence SISGSGSDTLYADSVKG (SEQ ID NO:42);
- CDR3 is the amino acid sequence GGSLSR (SEQ ID NO:43);
- the amino acid residue at position 89 is L;
- 10 - the amino acid residue at position 11 is V;

in which preferably

- the amino acid residue at position 110 is one of K, Q or T, and more preferably T;
- the amino acid residue at position 112 is one of K, Q or S, and more preferably S;

and that optionally contains at its C-terminal end a C-terminal extension (X)_n in which n is 1 to 10, preferably 1 to 5, such as 1, 2, 3, 4 or 5 (and preferably 1 or 2, such as 1); and each X is an (preferably naturally occurring) amino acid residue that is independently chosen, and preferably independently chosen from the group consisting of alanine (A), glycine (G), valine (V), leucine (L) or isoleucine (I) (again, such a C-terminal extension is preferably as further described herein, and again such a Nanobody can also for example also suitably contain one or more of the other specific amino acid residues/ substitutions mentioned herein, such as

20 14A, P14A, 14P, A14P, 108L, Q108L). Again, in these VH domains against serum albumin with an L at position 89 and a V at position 11, the amino acid at position 110 is preferably T and the amino acid at position 112 is preferably S, and said VH domains preferably have a C-terminal end that is one of SEQ ID NO's: 95 to 98. Also: (i) position 41 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 41 and may in particular be (or be chosen from) proline (P), serine (S), threonine (T), alanine (A) or leucine (L), which are some of the amino acid residues that most frequently occur at this position in either humans or llamas, and may more in particular be either proline (P) or alanine (A); and/or (ii) position 42 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 42 and may in particular be (or be chosen from) glycine (G) or glutamic acid (E); and/or (iii) position 87

may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-7 of WO 08/020079 for position 87 and may in particular be (or be chosen from) threonine (T) or alanine (A).

In a particular aspect, the invention relates to a Nanobody of the invention (as defined herein) that can bind (and in particular specifically bind) to serum albumin (and in particular human serum albumin) that is a humanized variant of SEQ ID NO: 52 of WO 2006/122787 in which:

- CDR1 is the amino acid sequence SFGMS (SEQ ID NO:41);
- CDR2 is the amino acid sequence SISGSGSDTLYADSVKG (SEQ ID NO:42);
- 10 - CDR3 is the amino acid sequence GGSLSR (SEQ ID NO:43);
- the amino acid residue at position 89 is L;
- the amino acid residue at position 11 is V;
- and preferably:
- the amino acid residue at position 110 is one of K, Q or T, and more preferably T;
- the amino acid residue at position 112 is one of K, Q or S, and more preferably S;

and that optionally contains at its C-terminal end a C-terminal extension (X)_n in which n is 1 to 10, preferably 1 to 5, such as 1, 2, 3, 4 or 5 (and preferably 1 or 2, such as 1); and each X is an (preferably naturally occurring) amino acid residue that is independently chosen, and

20 preferably independently chosen from the group consisting of alanine (A), glycine (G), valine (V), leucine (L) or isoleucine (I) (again, such a C-terminal extension is preferably as further described herein, and again such a Nanobody can also for example also contain one or more of the other specific amino acid residues/ substitutions mentioned herein, such as 11L, L11V, L11K, 14A, P14A, 14P, A14P, 108L and/or Q108L). In these VH domains against serum albumin with an L at position 89 and a V at position 11, the amino acid residue at position 110 is preferably T and the amino acid residue at position 112 is preferably S, and said VH domains preferably have a C-terminal end that is one of SEQ ID NO's: 95 to 98. Also: (i) position 41 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 41 and 30 may in particular be (or be chosen from) proline (P), serine (S), threonine (T), alanine (A) or leucine (L), which are some of the amino acid residues that most frequently occur at this position in either humans or llamas, and may more in particular be either proline (P) or alanine (A); and/or (ii) position 42 may for example be one of the amino acid residues (i.e.

human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 42 and may in particular be (or be chosen from) glycine (G) or glutamic acid (E); and/or (iii) position 87 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-7 of WO 08/020079 for position 87 and may in particular be (or be chosen from) threonine (T) or alanine (A).

In a particular aspect, the invention relates to a Nanobody of the invention (as defined herein) that can bind (and in particular specifically bind) to serum albumin (and in particular human serum albumin) that has at least 80%, preferably at least 85%, more preferably at least 90% such as at least 95% sequence identity with at least one of Alb-1 (SEQ ID NO: 52 of WO 2006/122787), Alb-8 (SEQ ID NO: 46 herein) and/or Alb-23 (SEQ ID NO:61 herein) (taking into account both the framework sequences and the CDR's, but not any C-terminal extension), in which the amino acid residue at position 89 is L and the amino acid residue at position 11 is V, and that optionally contains at its C-terminal end a C-terminal extension (X)_n in which n is 1 to 10, preferably 1 to 5, such as 1, 2, 3, 4 or 5 (and preferably 1 or 2, such as 1); and each X is an (preferably naturally occurring) amino acid residue that is independently chosen, and preferably independently chosen from the group consisting of alanine (A), glycine (G), valine (V), leucine (L) or isoleucine (I) (again, such a C-terminal extension is preferably as further described herein, and again such a Nanobody can also for example also suitably contain one or more of the other specific amino acid residues/ substitutions mentioned herein, such as 14A, P14A, 14P, A14P, 108L, Q108L, T110K, T110Q, S112K and/or S112Q). Such a Nanobody of the invention is again preferably a humanized variant of Alb-1 (but with a V89L and L11V substitution), and more preferably has at least one, in particular any two, and more in particular all three of CDR1, CDR2 and/or CDR3 given in SEQ ID NO's 41 to 43, respectively. In these VH domains against serum albumin, the amino acid at position 112 is preferably S, and said VH domains preferably have a C-terminal end that is one of SEQ ID NO's: 95 to 98. Also: (i) position 41 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 41 and may in particular be (or be chosen from) proline (P), serine (S), threonine (T), alanine (A) or leucine (L), which are some of the amino acid residues that most frequently occur at this position in either humans or llamas, and may more in particular be either proline (P) or alanine (A); and/or (ii) position 42 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 42 and may in particular be (or be

chosen from) glycine (G) or glutamic acid (E); and/or (iii) position 87 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-7 of WO 08/020079 for position 87 and may in particular be (or be chosen from) threonine (T) or alanine (A).

According to one specific aspect, any such serum albumin-binding Nanobody of the invention with an L at position 89 and a V at position 11 can also have the amino acid residues that are characteristic of Alb-23 and its variants as described in WO 12/175400 (i.e. the amino acid motif GP on positions 44 and 45, the amino acid motif SKN on positions 74 to 76, and preferably a G at position 16 and optionally also an R at position 83). Also: (i)

10 position 41 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 41 and may in particular be (or be chosen from) proline (P), serine (S), threonine (T), alanine (A) or leucine (L), which are some of the amino acid residues that most frequently occur at this position in either humans or llamas, and may more in particular be either proline (P) or alanine (A); and/or (ii) position 42 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 42 and may in particular be (or be chosen from) glycine (G) or glutamic acid (E); and/or (iii) position 87 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-7 of WO 20 08/020079 for position 87 and may in particular be (or be chosen from) threonine (T) or alanine (A).

As with the VH domains of the invention that contain an Q or K at position 112 or that have a T at position 89, the VH domains of the invention that contain an L at position 89 and a V at position 11 show reduced binding by pre-existing antibodies, and in particular by such pre-existing antibodies (as for example are found in samples obtained from SLE patients) that are capable of binding to VH domains and Nanobodies in the presence of a C-terminal extension. One further thing to note with the VH domains of the invention is which position 89 is L and position 11 is V is that these substitutions are known to occur with some frequency in human VH domains (see Table A-5 of WO 08/020079 for position 11 and Table 30 A-7 of WO 08/020079 of position 89).

Some non-limiting examples of VH domains of the invention that have a V at position 11 and a T at position 89 are given in Figure 2 as SEQ ID NO's: 109-136. Of these VH domains, the sequences given as SEQ ID NO's: 123-136 contain, in addition to the L11V and V89L mutations, also a T110K mutation. These are VH domains binding to human serum

albumin and have the CDR's indicated herein for the preferred serum albumin binding VH domains of the invention.

In a further aspect, the invention relates to a VH domain (and in particular a VH domain that is an ISVD, and more in particular a VH domain that is a nanobody), in which:

- the amino acid residue at position 11 is V; and
- the amino acid residue at position 14 is one of A or P; and
- the amino acid residue at position 41 is one of A or P; and
- the amino acid residue at position 89 is L; and
- the amino acid residue at position 108 is one of Q or L; and
- 10 - the amino acid residue at position 110 is one of T, K or Q; and
- the amino acid residue at position 112 is one of S, K or Q;

and in which said VH domain optionally contains a C-terminal extension (X)_n, in which n is 1 to 10, preferably 1 to 5, such as 1, 2, 3, 4 or 5 (and preferably 1 or 2, such as 1); and each X is an (preferably naturally occurring) amino acid residue that is independently chosen, and preferably independently chosen from the group consisting of alanine (A), glycine (G), valine (V), leucine (L) or isoleucine (I) (which C-terminal extension is preferably as further described herein). Also: (i) position 42 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 42 and may in particular be (or be chosen from) glycine (G) or 20 glutamic acid (E); and/or (ii) position 87 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-7 of WO 08/020079 for position 87 and may in particular be (or be chosen from) threonine (T) or alanine (A). Preferably, in the VH domains according to this paragraph, the amino acid residue at position 110 is T and the amino acid residue at position 112 is S. Again, as with the other VH domains of the invention, such a VH domain may be directed against any suitable target (and in particular a therapeutically relevant target). According to one specific aspect, such a VH domain is directed to serum albumin.

In a further aspect, the invention relates to a VH domain (and in particular a VH domain that is an ISVD, and more in particular a VH domain that is a nanobody), in which:

- 30 - the amino acid residue at position 11 is one of L, V or K; and
- the amino acid residue at position 14 is one of A or P; and
- the amino acid residue at position 41 is one of A or P; and

- the amino acid residue at position 89 is one of T, V or L; and
- the amino acid residue at position 108 is one of Q or L; and
- the amino acid residue at position 110 is one of T, K or Q; and
- the amino acid residue at position 112 is one of S, K or Q;

in which either (i) the amino acid residue at position 112 is one of K or Q; and/or (ii) the amino acid residue at position 89 is T; and/or (iii) the amino acid residue at position 89 is L and the amino acid residue at position 110 is one of K or Q; and (iv) in each of cases (i) to (iii), the amino acid at position 11 is preferably V; and

in which said VH domain optionally contains a C-terminal extension (X)_n, in which n is 1 to

10 10, preferably 1 to 5, such as 1, 2, 3, 4 or 5 (and preferably 1 or 2, such as 1); and each X is an (preferably naturally occurring) amino acid residue that is independently chosen, and preferably independently chosen from the group consisting of alanine (A), glycine (G), valine (V), leucine (L) or isoleucine (I) (which C-terminal extension is preferably as further described herein). Also: (i) position 42 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 42 and may in particular be (or be chosen from) glycine (G) or glutamic acid (E); and/or (ii) position 87 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-7 of WO 08/020079 for position 87 and may in particular be (or be chosen from) threonine (T) or alanine (A). Another aspect of the invention relates to a VH domain (and in particular a VH domain that is an ISVD, and more in particular a VH domain that is a nanobody) which is as described in this paragraph, in which the amino acid residue at position 11 is V and the amino acid residue at position 110 is either K or Q (and in which the amino acid residues at positions 14, 41, 89, 108 and 112 can be as listed in the above bullet points, the amino acid residues at positions 42 and 87 can for example be as described in this paragraph, and the VH domain can optionally contain a C-terminal extension (X)_n as described in this paragraph).

In a further aspect, the invention relates to a VH domain (and in particular a VH domain that is an ISVD, and more in particular a VH domain that is a nanobody), in which:

- the amino acid residue at position 11 is one of L, V or K; and
- the amino acid residue at position 14 is one of A or P; and
- the amino acid residue at position 41 is one of A or P; and
- the amino acid residue at position 89 is one of T, V or L; and
- the amino acid residue at position 108 is one of Q or L; and

- the amino acid residue at position 110 is one of T, K or Q; and
- the amino acid residue at position 112 is one of S, K or Q;

in which either (i) the amino acid residue at position 112 is one of K or Q, the amino acid residue at position 89 is one of T, V or L (and is preferably V), and the amino acid residue at position 110 is one of T, K or Q (and is preferably T); and/or (ii) the amino acid residue at position 89 is T, and the amino acid residue at position 112 is one of S, K or Q (and is preferably S), and the amino acid residue at position 110 is one of T, K or Q (and is preferably T); and/or (iii) the amino acid residue at position 89 is L and the amino acid residue at position 110 is one of K or Q, and the amino acid residue at position 112 is one of S, K or Q (and is preferably S);

10 and (iv) in each of cases (i) to (iii), the amino acid at position 11 is preferably V; and in which said VH domain optionally contains a C-terminal extension (X)_n, in which n is 1 to 10, preferably 1 to 5, such as 1, 2, 3, 4 or 5 (and preferably 1 or 2, such as 1); and each X is an (preferably naturally occurring) amino acid residue that is independently chosen, and preferably independently chosen from the group consisting of alanine (A), glycine (G), valine (V), leucine (L) or isoleucine (I) (which C-terminal extension is preferably as further described herein). Also: (i) position 42 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 42 and may in particular be (or be chosen from) glycine (G) or glutamic acid (E); and/or (ii) position 87 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-7 of WO 20 08/020079 for position 87 and may in particular be (or be chosen from) threonine (T) or alanine (A). Another aspect of the invention relates to a VH domain (and in particular a VH domain that is an ISVD, and more in particular a VH domain that is a nanobody) which is as described in this paragraph, in which the amino acid residue at position 11 is V and the amino acid residue at position 110 is either K or Q (and in which the amino acid residues at positions 14, 41, 89, 108 and 112 can be as listed in the above bullet points, the amino acid residues at positions 42 and 87 can for example be as described in this paragraph, and the VH domain can optionally contain a C-terminal extension (X)_n as described in this paragraph).

30 In a further aspect, the invention relates to a VH domain (and in particular a VH domain that is an ISVD, and more in particular a VH domain that is a nanobody), in which:

- the amino acid residue at position 11 is one of L, V or K; and
- the amino acid residue at position 14 is one of A or P; and
- the amino acid residue at position 41 is one of A or P; and

- the amino acid residue at position 89 is one of T, V or L; and
- the amino acid residue at position 108 is one of Q or L; and
- the amino acid residue at position 110 is one of T, K or Q; and
- the amino acid residue at position 112 is one of S, K or Q;

in which either (i) the amino acid residue at position 112 is one of K or Q; or (ii) the amino acid residue at position 89 is T; or (iii) the amino acid residue at position 89 is L and the amino acid residue at position 110 is one of K or Q; and (iv) in each of cases (i) to (iii), the amino acid at position 11 is preferably V; and

in which said VH domain optionally contains a C-terminal extension (X)_n, in which n is 1 to

10 10, preferably 1 to 5, such as 1, 2, 3, 4 or 5 (and preferably 1 or 2, such as 1); and each X is an (preferably naturally occurring) amino acid residue that is independently chosen, and preferably independently chosen from the group consisting of alanine (A), glycine (G), valine (V), leucine (L) or isoleucine (I) (which C-terminal extension is preferably as further described herein). Also: (i) position 42 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 42 and may in particular be (or be chosen from) glycine (G) or glutamic acid (E); and/or (ii) position 87 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-7 of WO 08/020079 for position 87 and may in particular be (or be chosen from) threonine (T) or alanine (A). Another aspect of the invention relates to a VH domain (and in particular a VH domain that is an ISVD, and more in particular a VH domain that is a nanobody) which is as described in this paragraph, in which the amino acid residue at position 11 is V and the amino acid residue at position 110 is either K or Q (and in which the amino acid residues at positions 14, 41, 89, 108 and 112 can be as listed in the above bullet points, the amino acid residues at positions 42 and 87 can for example be as described in this paragraph, and the VH domain can optionally contain a C-terminal extension (X)_n as described in this paragraph).

In a further aspect, the invention relates to a VH domain (and in particular a VH domain that is an ISVD, and more in particular a VH domain that is a nanobody), in which:

- the amino acid residue at position 11 is one of L, V or K; and
- the amino acid residue at position 14 is one of A or P; and
- the amino acid residue at position 41 is one of A or P; and
- the amino acid residue at position 89 is one of T, V or L; and
- the amino acid residue at position 108 is one of Q or L; and

- the amino acid residue at position 110 is one of T, K or Q; and
- the amino acid residue at position 112 is one of S, K or Q;

in which either (i) the amino acid residue at position 112 is one of K or Q, the amino acid residue at position 89 is one of T, V or L (and is preferably V), and the amino acid residue at position 110 is one of T, K or Q (and is preferably T); or (ii) the amino acid residue at position 89 is T, and the amino acid residue at position 112 is one of S, K or Q (and is preferably S), and the amino acid residue at position 110 is one of T, K or Q (and is preferably T); or (iii) the amino acid residue at position 89 is L, and the amino acid residue at position 110 is one of K or Q, and the amino acid residue at position 112 is one of S, K or Q (and is preferably S); and (iv)

10 in each of cases (i) to (iii), the amino acid at position 11 is preferably V; and in which said VH domain optionally contains a C-terminal extension (X)_n, in which n is 1 to 10, preferably 1 to 5, such as 1, 2, 3, 4 or 5 (and preferably 1 or 2, such as 1); and each X is an (preferably naturally occurring) amino acid residue that is independently chosen, and preferably independently chosen from the group consisting of alanine (A), glycine (G), valine (V), leucine (L) or isoleucine (I) (which C-terminal extension is preferably as further described herein). Also: (i) position 42 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 42 and may in particular be (or be chosen from) glycine (G) or glutamic acid (E); and/or (ii) position 87 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-7 of WO 20 20 08/020079 for position 87 and may in particular be (or be chosen from) threonine (T) or alanine (A). Another aspect of the invention relates to a VH domain (and in particular a VH domain that is an ISVD, and more in particular a VH domain that is a nanobody) which is as described in this paragraph, in which the amino acid residue at position 11 is V and the amino acid residue at position 110 is either K or Q (and in which the amino acid residues at positions 14, 41, 89, 108 and 112 can be as listed in the above bullet points, the amino acid residues at positions 42 and 87 can for example be as described in this paragraph, and the VH domain can optionally contain a C-terminal extension (X)_n as described in this paragraph).

30 In a further aspect, the invention relates to a VH domain (and in particular a VH domain that is an ISVD, and more in particular a VH domain that is a nanobody), in which:

- the amino acid residue at position 11 is one of L, V or K; and
- the amino acid residue at position 14 is one of A or P; and
- the amino acid residue at position 41 is one of A or P; and

- the amino acid residue at position 89 is one of T, V or L; and
- the amino acid residue at position 108 is one of Q or L; and
- the amino acid residue at position 110 is one of T, K or Q; and
- the amino acid residue at position 112 is one of S, K or Q;

in which either (i) the amino acid residue at position 112 is one of K or Q, the amino at position 89 is V, and the amino acid residue at position 110 is T; or (ii) the amino acid residue at position 89 is T, the amino acid residue at position 112 is S, and the amino acid residue at position 110 is T; or (iii) the amino acid residue at position 89 is L and the amino acid residue at position 110 is one of K or Q, and the amino acid residue at position 112 is S (and is

10 preferably S); and (iv) in each of cases (i) to (iii), the amino acid at position 11 is preferably V; and

in which said VH domain optionally contains a C-terminal extension (X)_n, in which n is 1 to 10, preferably 1 to 5, such as 1, 2, 3, 4 or 5 (and preferably 1 or 2, such as 1); and each X is an (preferably naturally occurring) amino acid residue that is independently chosen, and preferably independently chosen from the group consisting of alanine (A), glycine (G), valine (V), leucine (L) or isoleucine (I) (which C-terminal extension is preferably as further described herein). Also: (i) position 42 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 42 and may in particular be (or be chosen from) glycine (G) or

20 glutamic acid (E); and/or (ii) position 87 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-7 of WO 08/020079 for position 87 and may in particular be (or be chosen from) threonine (T) or alanine (A). Another aspect of the invention relates to a VH domain (and in particular a VH domain that is an ISVD, and more in particular a VH domain that is a nanobody) which is as described in this paragraph, in which the amino acid residue at position 11 is V and the amino acid residue at position 110 is either K or Q (and in which the amino acid residues at positions 14, 41, 89, 108 and 112 can be as listed in the above bullet points, the amino acid residues at positions 42 and 87 can for example be as described in this paragraph, and the VH domain can optionally contain a C-terminal extension (X)_n as described in this paragraph).

30 In a further aspect, the invention relates to a VH domain (and in particular a VH domain that is an ISVD, and more in particular a VH domain that is a nanobody), in which:

- the amino acid residue at position 11 is one of L, V or K; and
- the amino acid residue at position 14 is one of A or P; and

- the amino acid residue at position 41 is one of A or P; and
- the amino acid residue at position 89 is one of T, V or L; and
- the amino acid residue at position 108 is one of Q or L; and
- the amino acid residue at position 110 is one of T, K or Q; and
- the amino acid residue at position 112 is one of S, K or Q;

in which either (i) the amino acid residue at position 112 is one of K or Q; and/or (ii) the amino acid residue at position 89 is T; and/or (iii) the amino acid residue at position 89 is L and the amino acid residue at position 110 is one of K or Q; and (iv) in each of cases (i) to (iii), the amino acid at position 11 is preferably V; and

10 in which said VH domain contains a C-terminal extension (X)_n, in which n is 1 to 10, preferably 1 to 5, such as 1, 2, 3, 4 or 5 (and preferably 1 or 2, such as 1); and each X is an (preferably naturally occurring) amino acid residue that is independently chosen, and preferably independently chosen from the group consisting of alanine (A), glycine (G), valine (V), leucine (L) or isoleucine (I) (which C-terminal extension is preferably as further described herein). Also: (i) position 42 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 42 and may in particular be (or be chosen from) glycine (G) or glutamic acid (E); and/or (ii) position 87 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-7 of WO 20 08/020079 for position 87 and may in particular be (or be chosen from) threonine (T) or alanine (A). Another aspect of the invention relates to a VH domain (and in particular a VH domain that is an ISVD, and more in particular a VH domain that is a nanobody) which is as described in this paragraph, in which the amino acid residue at position 11 is V and the amino acid residue at position 110 is either K or Q (and in which the amino acid residues at positions 14, 41, 89, 108 and 112 can be as listed in the above bullet points, the amino acid residues at positions 42 and 87 can for example be as described in this paragraph, and the VH domain can optionally contain a C-terminal extension (X)_n as described in this paragraph).

In a further aspect, the invention relates to a VH domain (and in particular a VH domain that is an ISVD, and more in particular a VH domain that is a nanobody), in which:

30 - the amino acid residue at position 11 is one of L, V or K; and

- the amino acid residue at position 14 is one of A or P; and
- the amino acid residue at position 41 is one of A or P; and
- the amino acid residue at position 89 is one of T, V or L; and

- the amino acid residue at position 108 is one of Q or L; and
- the amino acid residue at position 110 is one of T, K or Q; and
- the amino acid residue at position 112 is one of S, K or Q;

in which either (i) the amino acid residue at position 112 is one of K or Q, the amino at position 89 is one of T, V or L (and is preferably V), and the amino acid residue at position 110 is one of T, K or Q (and is preferably T); and/or (ii) the amino acid residue at position 89 is T, and the amino acid residue at position 112 is one of S, K or Q (and is preferably S), and the amino acid residue at position 110 is one of T, K or Q (and is preferably T); and/or (iii) the amino acid residue at position 89 is L and the amino acid residue at position 110 is one of

10 K or Q, and the amino acid residue at position 112 is one of S, K or Q (and is preferably S); and (iv) in each of cases (i) to (iii), the amino acid at position 11 is preferably V; and in which said VH domain contains a C-terminal extension (X)_n, in which n is 1 to 10, preferably 1 to 5, such as 1, 2, 3, 4 or 5 (and preferably 1 or 2, such as 1); and each X is an (preferably naturally occurring) amino acid residue that is independently chosen, and preferably independently chosen from the group consisting of alanine (A), glycine (G), valine (V), leucine (L) or isoleucine (I) (which C-terminal extension is preferably as further described herein). Also: (i) position 42 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 42 and may in particular be (or be chosen from) glycine (G) or 20 glutamic acid (E); and/or (ii) position 87 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-7 of WO 08/020079 for position 87 and may in particular be (or be chosen from) threonine (T) or alanine (A). Another aspect of the invention relates to a VH domain (and in particular a VH domain that is an ISVD, and more in particular a VH domain that is a nanobody) which is as described in this paragraph, in which the amino acid residue at position 11 is V and the amino acid residue at position 110 is either K or Q (and in which the amino acid residues at positions 14, 41, 89, 108 and 112 can be as listed in the above bullet points, the amino acid residues at positions 42 and 87 can for example be as described in this paragraph, and the VH domain can optionally contain a C-terminal extension (X)_n as described in this paragraph).

30 In a further aspect, the invention relates to a VH domain (and in particular a VH domain that is an ISVD, and more in particular a VH domain that is a nanobody), in which:

- the amino acid residue at position 11 is one of L, V or K; and
- the amino acid residue at position 14 is one of A or P; and

- the amino acid residue at position 41 is one of A or P; and
- the amino acid residue at position 89 is one of T, V or L; and
- the amino acid residue at position 108 is one of Q or L; and
- the amino acid residue at position 110 is one of T, K or Q; and
- the amino acid residue at position 112 is one of S, K or Q;

in which either (i) the amino acid residue at position 112 is one of K or Q; or (ii) the amino acid residue at position 89 is T; or (iii) the amino acid residue at position 89 is L and the amino acid residue at position 110 is one of K or Q; and (iv) in each of cases (i) to (iii), the amino acid at position 11 is preferably V; and

10 in which said VH domain contains a C-terminal extension $(X)_n$, in which n is 1 to 10, preferably 1 to 5, such as 1, 2, 3, 4 or 5 (and preferably 1 or 2, such as 1); and each X is an (preferably naturally occurring) amino acid residue that is independently chosen, and preferably independently chosen from the group consisting of alanine (A), glycine (G), valine (V), leucine (L) or isoleucine (I) (which C-terminal extension is preferably as further described herein). Also: (i) position 42 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 42 and may in particular be (or be chosen from) glycine (G) or glutamic acid (E); and/or (ii) position 87 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-7 of WO 20 08/020079 for position 87 and may in particular be (or be chosen from) threonine (T) or alanine (A). Another aspect of the invention relates to a VH domain (and in particular a VH domain that is an ISVD, and more in particular a VH domain that is a nanobody) which is as described in this paragraph, in which the amino acid residue at position 11 is V and the amino acid residue at position 110 is either K or Q (and in which the amino acid residues at positions 14, 41, 89, 108 and 112 can be as listed in the above bullet points, the amino acid residues at positions 42 and 87 can for example be as described in this paragraph, and the VH domain can optionally contain a C-terminal extension $(X)_n$ as described in this paragraph).

In a further aspect, the invention relates to a VH domain (and in particular a VH domain that is an ISVD, and more in particular a VH domain that is a nanobody), in which:

30 - the amino acid residue at position 11 is one of L, V or K; and

- the amino acid residue at position 14 is one of A or P; and
- the amino acid residue at position 41 is one of A or P; and
- the amino acid residue at position 89 is one of T, V or L; and

- the amino acid residue at position 108 is one of Q or L; and
- the amino acid residue at position 110 is one of T, K or Q; and
- the amino acid residue at position 112 is one of S, K or Q;

in which either (i) the amino acid residue at position 112 is one of K or Q, the amino acid at position 89 is one of T, V or L (and is preferably V), and the amino acid residue at position 110 is one of T, K or Q (and is preferably T); or (ii) the amino acid residue at position 89 is T, and the amino acid residue at position 112 is one of S, K or Q (and is preferably S), and the amino acid residue at position 110 is one of T, K or Q (and is preferably T); or (iii) the amino acid residue at position 89 is L, and the amino acid residue at position 110 is one of K or Q,

10 and the amino acid residue at position 112 is one of S, K or Q (and is preferably S); and (iv) in each of cases (i) to (iii), the amino acid at position 11 is preferably V; and in which said VH domain contains a C-terminal extension (X)_n, in which n is 1 to 10, preferably 1 to 5, such as 1, 2, 3, 4 or 5 (and preferably 1 or 2, such as 1); and each X is an (preferably naturally occurring) amino acid residue that is independently chosen, and preferably independently chosen from the group consisting of alanine (A), glycine (G), valine (V), leucine (L) or isoleucine (I) (which C-terminal extension is preferably as further described herein). Also: (i) position 42 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 42 and may in particular be (or be chosen from) glycine (G) or 20 glutamic acid (E); and/or (ii) position 87 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-7 of WO 08/020079 for position 87 and may in particular be (or be chosen from) threonine (T) or alanine (A). Another aspect of the invention relates to a VH domain (and in particular a VH domain that is an ISVD, and more in particular a VH domain that is a nanobody) which is as described in this paragraph, in which the amino acid residue at position 11 is V and the amino acid residue at position 110 is either K or Q (and in which the amino acid residues at positions 14, 41, 89, 108 and 112 can be as listed in the above bullet points, the amino acid residues at positions 42 and 87 can for example be as described in this paragraph, and the VH domain can optionally contain a C-terminal extension (X)_n as described in this paragraph).

30 In a further aspect, the invention relates to a VH domain (and in particular a VH domain that is an ISVD, and more in particular a VH domain that is a nanobody), in which:

- the amino acid residue at position 11 is one of L, V or K; and
- the amino acid residue at position 14 is one of A or P; and

- the amino acid residue at position 41 is one of A or P; and
- the amino acid residue at position 89 is one of T, V or L; and
- the amino acid residue at position 108 is one of Q or L; and
- the amino acid residue at position 110 is one of T, K or Q; and
- the amino acid residue at position 112 is one of S, K or Q;

in which either (i) the amino acid residue at position 112 is one of K or Q, the amino at position 89 is V, and the amino acid residue at position 110 is T; or (ii) the amino acid residue at position 89 is T, the amino acid residue at position 112 is S, and the amino acid residue at position 110 is T; or (iii) the amino acid residue at position 89 is L and the amino acid residue

10 at position 110 is one of K or Q, and the amino acid residue at position 112 is S (and is preferably S); and (iv) in each of cases (i) to (iii), the amino acid at position 11 is preferably V; and

in which said VH domain contains a C-terminal extension (X)_n, in which n is 1 to 10, preferably 1 to 5, such as 1, 2, 3, 4 or 5 (and preferably 1 or 2, such as 1); and each X is an (preferably naturally occurring) amino acid residue that is independently chosen, and preferably independently chosen from the group consisting of alanine (A), glycine (G), valine (V), leucine (L) or isoleucine (I) (which C-terminal extension is preferably as further described herein). Also: (i) position 42 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO

20 08/020079 for position 42 and may in particular be (or be chosen from) glycine (G) or glutamic acid (E); and/or (ii) position 87 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-7 of WO 08/020079 for position 87 and may in particular be (or be chosen from) threonine (T) or alanine (A). Another aspect of the invention relates to a VH domain (and in particular a VH domain that is an ISVD, and more in particular a VH domain that is a nanobody) which is as described in this paragraph, in which the amino acid residue at position 11 is V and the amino acid residue at position 110 is either K or Q (and in which the amino acid residues at positions 14, 41, 89, 108 and 112 can be as listed in the above bullet points, the amino acid residues at positions 42 and 87 can for example be as described in this paragraph, and the VH domain

30 can optionally contain a C-terminal extension (X)_n as described in this paragraph).

Again, in the VH domains of the invention as defined herein, the amino acid residues at positions that are not explicitly defined herein can be any amino acid residue that is suitable at such a position for VH domains, and in particular for ISVD's and more in particular for

nanobodies (including humanized VHH domains). Reference is again made to the prior art cited herein, such as for example Tables A-3 and A-5 to A-8 of WO 08/020079. Preferably, in each case, the amino acid residue at position 11 is L or V, and more preferably V. Also: (i) position 41 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 41 and may in particular be (or be chosen from) proline (P), serine (S), threonine (T), alanine (A) or leucine (L), which are some of the amino acid residues that most frequently occur at this position in either humans or llamas, and may more in particular be either proline (P) or alanine (A); and/or (ii) position 42 may for example be one of the amino acid residues (i.e.

10 human VH3 residues and/or Camelid VHH residues) mentioned in Table A-6 of WO 08/020079 for position 42 and may in particular be (or be chosen from) glycine (G) or glutamic acid (E); and/or (iii) position 87 may for example be one of the amino acid residues (i.e. human VH3 residues and/or Camelid VHH residues) mentioned in Table A-7 of WO 08/020079 for position 87 and may in particular be (or be chosen from) threonine (T) or alanine (A).

Also, said VH domain of the invention can be directed against any suitable target, and in particular a therapeutic target. In one aspect, they are directed against a human serum protein such as human serum albumin.

20 The invention also relates to proteins, polypeptides, constructs, compounds or other chemical entities that comprise at least one VH domain of the invention (also collectively referred to herein as "*compounds of the invention*").

As further described herein, according to one specific aspect, in a compound of the invention, the VH domain of the invention is present at/forms the C-terminal end of the same. In such a case, the VH domain of the invention that forms/is present at the C-terminal end of the compound of the invention preferably has a C-terminal extension as described herein.

As also further described herein, the compounds of the invention can be a ScFv, diabody or another protein, polypeptide or construct in which the one or more VH domains of the invention are associated with one or more VL domains to form one or more functional antigen-binding sites.

30 However, according to a preferred aspect of the invention, the VH domains of the invention are ISVD's and the compounds of the invention are proteins, polypeptides, constructs, compounds or other chemical entities that comprise or essentially consist of at least one ISVD of the invention and optionally one or more further amino acid sequences, moieties, binding domains or binding units (suitably linked to each other, optionally via one

or more linkers). In particular, such compounds of the invention can comprise or essentially consist of one or more ISVD's, at least one of which is an ISVD of the invention. Such a compound of the invention may in particular have an ISVD of the invention at its C-terminal end, in which case the ISVD of the invention also preferably has a C-terminal extensions as described herein. Also, if such a compound of the invention contains two or more ISVDs, two or more or essentially all of the ISVD's present may be ISVD's of the invention (i.e. each having at least one of the following amino acid residues/substitutions: 112K, 112Q, S112K, S112Q, 89T and/or V89T, or the combination of V89L with T110K or T110Q; and optionally one or more of the further substitutions mentioned herein for ISVD's of the invention, such as 10 L11V). Also, in such a compound of the invention, the ISVD of the invention is preferably a Nanobody of the invention, and all or essentially all of the ISVD's present in the compound of the invention may be (and preferably are) Nanobodies (and in particular Nanobodies of the invention, i.e. each having at least one of the following amino acid residues/substitutions: 112K, 112Q, S112K, S112Q, 89T and/or V89T, or the combination of V89L with T110K or T110Q; and optionally one or more of the further substitutions mentioned herein for Nanobodies of the invention, such as L11V). Examples of such compounds of the invention will be clear to the skilled person based on the further disclosure herein.

Some non-limiting examples of proteins, polypeptides, constructs, compounds or other chemical entities that comprise one or more ISVD's (including at least one ISVD of the 20 invention) are multivalent, multispecific (such as bispecific) or multiparatopic (such as biparatopic) constructs that contain two or more ISVD's linked directly or via one or more suitable linkers. Again, the ISVD's are preferably Nanobodies. For some non-limiting examples of such constructs and a general teaching on how such constructs can be made (in particular based on Nanobodies) reference is for example made to Conrath et al., JBC 276, 10(9), 7346 (2001) as well as to the review article by Muyldeermans. Reviews in Mol. Biotechnol., 74: 27 (2001).

For example, such a compound of the invention containing two or more ISVD's (at least one of which is an ISVD of the invention) may be a bivalent, trivalent, tetravalent or pentavalent construct, and/or may be a monospecific, bispecific, trispecific construct, and/or 30 may be a biparatopic or triparatopic construct. Reference is again made to the prior art on IVSD-based and Nanobody-based biologicals cited herein. Also, such a compound of the invention may have been provided with an increased half-life by functionalization and/or by including in the construct a moiety or binding unit that increases the half-life of the construct. Examples of such functionalization, moieties or binding units will be clear to the skilled

person and may for example be as described herein, and for example may include pegylation, fusion to serum albumin, or fusion to a peptide or binding unit that can bind to a serum protein such as serum albumin. Such a serum-albumin binding peptide or binding domain may be any suitable serum-albumin binding peptide or binding domain capable of increasing the half-life of the construct (compared to the same construct without the serum-albumin binding peptide or binding domain), and may in particular be serum albumin binding peptides as described in WO 2008/068280 by applicant (and in particular WO 2009/127691 and the non-prepublished US application 61/301,819, both by applicant), or a serum-albumin binding ISV (such as a serum-albumin binding Nanobody; for example Alb-1 or a humanized version 10 of Alb-1 such as Alb-8, for which reference is for example made to WO 06/122787), or an ISVD of the invention that is directed against a (human) serum protein such as (human) serum albumin (as further described herein). Generally, any compound of the invention with increased half-life will preferably have a half-life (as defined herein) in human subjects of at least 1 day, preferably at least 3 days, more preferably at least 7 days, such as at least 10 days.

When the compound of the invention comprises at least one (and preferably one) ISVD of the invention (and in particular Nanobody of the invention) that is directed against a (human) serum protein and in particular against (human) serum albumin, the compound of the invention will usually further contain one or more other therapeutically active amino acid sequences, moieties, binding domains or binding units (i.e. directed against a therapeutically relevant target, pathway or mechanism), and the ISVD of the invention will function to extend the half-life of the same (and of the entire compound). Again, said one or more further therapeutically active moieties are preferably ISVD's (and more preferably Nanobodies), and may also be IVSD's of the invention (and more preferably Nanobodies of the invention). In such compounds of the invention, the ISVD of the invention that is directed against human serum albumin may again be present at/forms the C-terminal end of the compound, and in that case may (and preferably does) comprise a C-terminal extension as described herein. When a compound of the invention contains an ISVD of the invention that is directed against (human) serum albumin, said the compound of the invention preferably has a half-life (as defined herein) of at least 1 day, preferably at least 3 days, more preferably at least 7 days, such as at 20 least 10 days in the human subject to which the same is/has been administered. Some non-limiting examples of ISVD's of the invention against human serum albumin that can be used for this purpose are as further described herein.

In one aspect, all of the ISVD's or nanobodies present in said compound of the invention are ISVD's of the invention (meaning that they have the amino acid

residues/substitutions that are characteristic of the VH domains of the invention as defined herein, i.e. at least 112K or Q, or at least 89T, or at least 89L in combination with 110K or 110Q). When all the ISVD's in the compound of the invention are ISVD's of the invention, they can have the same substitutions (for example all have an S112K or S112Q substitution) or different substitutions (for example, one can have an S1112K or S112Q substitution, and another can have a V89L mutation in combination with T110K or T110Q). Also, usually only the ISVD at the C-terminal end of the compound of the invention will have a C-terminal extension (as the others will likely be linked at their C-terminal end to another ISVD present in the compound).

10 Thus, in a further aspect, the invention relates a protein, polypeptide or other compound or molecule that comprises or essentially consists of an ISVD of the invention (as further described herein).

The invention further relates to a protein, polypeptide or other compound or molecule that comprises at least one ISVD of the invention and at least one other therapeutic moiety or entity (either linked directly or via a suitable linker).

The invention further relates to a protein, polypeptide or other compound or molecule that comprises at least one ISVD of the invention that is directed against a (human) serum protein (and preferably against human serum albumin) and at least one other therapeutic moiety or entity (either linked directly or via a suitable linker).

20 The invention further relates to a protein, polypeptide or other compound or molecule that comprises at least two (such as two, three or four) immunoglobulin single variable domains (either linked directly or via a suitable linker), at least one of which is an ISVD of the invention. In this aspect: (i) the ISVD's present may suitably be the same or different; and when they are different they may be directed against the same target (for example, they may have different sequences and/or be directed against different epitopes on the same target) or against two or more different targets (i.e. such that the resulting protein, polypeptide or other compound or molecule is a bi- or multispecific construct); and/or (ii) the ISVD present at the C-terminal end of the protein, polypeptide or other compound or molecule may or may not be an ISVD of the invention (but preferably is); and/or (iii) when an ISVD of the invention is present at the C-terminal end of the protein, polypeptide or other compound or molecule, it preferably has a C-terminal extension as described herein; and/or (iv) essentially all of the ISVD's present in the protein, polypeptide or other compound or molecule may be ISVD's of the invention. Also, when the ISVD's are directed against different targets (as least one of which is a therapeutic target), according to one further aspect at least one of the ISVD's

present may be directed against a (human) serum protein such as human serum albumin (and this ISVD may or may not be an ISVD of the invention; and when it is an ISVD of the invention, it is preferably a nanobody against human serum albumin that is as further described herein).

The invention further relates to such a protein, polypeptide or other compound or molecule that comprises or essentially consists of two immunoglobulin single variable domains (either linked directly or via a suitable linker).

The invention further relates to such a protein, polypeptide or other compound or molecule that comprises or essentially consists of three immunoglobulin single variable domains (either linked directly or via a suitable linker).

10 The invention further relates to such a protein, polypeptide or other compound or molecule comprises or essentially consists of four immunoglobulin single variable domains (either linked directly or via a suitable linker).

The invention further relates to such a protein, polypeptide or other compound or molecule that further comprises at least one moiety, binding domain or binding unit that confers an increased half-life to said protein, polypeptide or other compound or molecule (i.e. compared to the corresponding protein, polypeptide or other compound or molecule without said moiety, binding domain or binding unit). According to a more specific aspect, said at least one moiety, binding domain or binding unit that confers an increased half-life to said 20 protein, polypeptide or other compound or molecule is an immunoglobulin single variable domain, more in particular an immunoglobulin single variable domain that is directed against a serum protein (such as serum albumin), and in particular against a human serum protein (such as human serum albumin); and as described herein may in particular be an ISVD of the invention. Said ISVD against the serum protein may be at the N-terminal end of the protein, polypeptide or other compound or molecule, at the C-terminal end, or (if the protein, polypeptide or other compound or molecule comprises more than two ISVD's) in the middle of the molecule.

The invention further relates to such a protein, polypeptide or other compound or molecule comprises or essentially consists of either:

30 - two immunoglobulin single variable domains (either linked directly or via a suitable linker), i.e. (said) one immunoglobulin single variable domain (such as a nanobody) that confers an increased half-life and one other immunoglobulin single variable domain (such as a nanobody) that may in particular be directed against a therapeutic target;

- three immunoglobulin single variable domains (either linked directly or via a suitable linker), i.e. (said) one immunoglobulin single variable domain (such as a nanobody) that confers an increased half-life and two other immunoglobulin single variable domains (such as two other nanobodies) that may in particular be directed against a therapeutic target (in which said two other immunoglobulin single variable domains may be directed against the same target, against two different targets or against two different epitopes on the same target); or
- four immunoglobulin single variable domains (either linked directly or via a suitable linker), i.e. (said) one immunoglobulin single variable domain (such as a nanobody) that confers an increased half-life and two other immunoglobulin single variable domains (such as two other nanobodies) that may in particular be directed against a therapeutic target (in which said three other immunoglobulin single variable domains may be directed against the same target, against two or three different targets and/or against two or three different epitopes on the same target).

Again, in such a protein, polypeptide or other compound or molecule: (i) the ISVD's present may suitably be the same or different; and when they are different they may be directed against the same target (for example, they may have different sequences and/or be directed against different epitopes on the same target) or against two or more different targets (i.e. such that the resulting protein, polypeptide or other compound or molecule is a bi- or multispecific construct); and/or (ii) the ISVD present at the C-terminal end of the protein, polypeptide or other compound or molecule may or may not be an ISVD of the invention (but preferably is); and/or (iii) when an ISVD of the invention is present at the C-terminal end of the protein, polypeptide or other compound or molecule, it preferably has a C-terminal extension as described herein; and/or (iv) essentially all of the ISVD's present in the protein, polypeptide or other compound or molecule may be ISVD's of the invention.

The invention further relates to methods for expressing/producing/manufacturing the VH domains of the invention and the compounds of the invention (as further described herein). For example, a VH domain of the invention can be expressed/produced by suitably expressing a nucleic acid that encodes the same in a suitable host organism. Reference is for example made to WO 08/020079 (as well as to some of the other patent applications of applicant/assignee cited herein), that generally describes suitable methods and techniques for expressing/producing Nanobodies, which methods can also suitably be used to express/produce Nanobodies of the invention. Methods for expressing VH domains of the

invention other than nanobodies will also be clear to the skilled person based on the disclosure and prior art cited herein. Compounds of the invention can be suitably manufactured-produced by suitably linking (usually via covalent bonds) one or more VH domains of the invention to the one or more further amino acid residues (and/or other groups or moieties) that are to be present in the final compound of the invention, optionally via one or more linkers or spacers. Alternatively, when a compound of the invention is a protein or polypeptide, it can be manufactured-produced by suitably expressing a nucleic acid that encodes the same in a suitable host organism. Reference is again for example made to the general methods described in WO 08/020079 and in some of the other patent applications of applicant/assignee cited herein.

10 The invention also relates to a nucleotide sequence and/or nucleic acid that encodes a VH domain of the invention or a compound of the invention. Such a nucleic acid can be DNA or RNA; and is preferably DNA and can be in the form of a plasmid or vector. Reference is again for example made to WO 08/020079 and to some of the other patent applications of applicant/assignee cited herein.

The invention also relates to a composition that comprises at least one VH domain of the invention, compound of the invention or nucleic acid encoding either of the same.

20 The invention further relates to a pharmaceutical composition that comprises an ISV (and preferably a therapeutic ISV) or a protein or polypeptide comprising at least one ISV (and preferably at least one therapeutic ISV), wherein said ISV, protein or polypeptide is as further described herein (i.e. an ISV, protein or polypeptide according to one or more of the aspects described herein, and in particular according to one or more of the aspects described on the preceding pages; and more in particular an ISV, protein or polypeptide that has a C-terminal end/sequence that is according to one or more of the aspects described herein), and at least one suitable carrier, diluent or excipient (i.e. suitable for pharmaceutical use), and optionally one or more further active substances. Such compositions, carriers, diluents or excipients can for example be as described in WO 08/020079 for pharmaceutical compositions that comprise a Nanobody or a protein or polypeptide that comprises at least one Nanobody (and as already mentioned, according to the present invention, the ISV is also preferably a Nanobody).

30 The invention further relates to an ISV or a protein or polypeptide comprising at least one ISV for use in therapy of a disease in a human being (e.g. a patient in need of such therapy), wherein said ISV, protein or polypeptide is as further described herein (i.e. an ISV, protein or polypeptide according to one or more of the aspects described herein, and in

particular according to one or more of the aspects described on the preceding pages; and more in particular an ISV, protein or polypeptide that has a C-terminal end/sequence that is according to one or more of the aspects described herein).

The invention further relates to the use of an ISV or a protein or polypeptide comprising at least one ISV in the preparation of a pharmaceutical composition, wherein said ISV, protein or polypeptide is as further described herein (i.e. an ISV, protein or polypeptide according to one or more of the aspects described herein, and in particular according to one or more of the aspects described on the preceding pages; and more in particular an ISV, protein or polypeptide that has a C-terminal end/sequence that is according to one or more of the aspects described herein).

10 aspects described herein).

The invention further relates to a method of treatment which comprises administering to a human subject (e.g to a patient in need of such treatment) an ISV or a protein or polypeptide comprising at least one ISV in the preparation of a pharmaceutical composition, wherein said ISV, protein or polypeptide is as further described herein (i.e. an ISV, protein or polypeptide according to one or more of the aspects described herein, and in particular according to one or more of the aspects described on the preceding pages; and more in particular an ISV, protein or polypeptide that has a C-terminal end/sequence that is according to one or more of the aspects described herein); or a pharmaceutical composition (as described above) that comprises at least one such ISV, protein or polypeptide.

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With respect to the above, it will be clear that the therapeutic use of the ISV's, proteins and polypeptides described herein are a very important aspect of the invention, as such therapeutic use (or the clinical development of such ISV's, proteins and polypeptides for such therapeutic use) may involve the use of ADA assays to determine whether said ISV, protein or polypeptide is immunogenic (i.e. can give rise to ADA's when administered to a human subject). In this respect, it will also be clear that concerns about possible immunogenicity will in particular have to be addressed when a therapeutic is either used for longer periods of time (for during weeks, months or years), and/or has a half-life (preferably expressed as t_{1/2}-beta) in a human subject of at least 3 days, such as at least one week, and up to 10 days or more.

30

Thus, according to one specific aspect, the invention relates to an ISV, protein, polypeptide, compound or molecule of the invention as described herein (or pharmaceutical composition the same) that is intended for treatment of a chronic disease in a human being, and/or such ISV, protein, polypeptide as described herein is intended to be present in the circulation of the subject (i.e. at pharmacologically active levels) to which it is administered (i.e. at a therapeutically active dose) for at least a period of one week, preferably at least two

weeks, such as at least a months; and/or such ISV, protein, polypeptide as described herein is such that it has a half-life (preferably expressed as t_{1/2}-beta) in a human subject of at least 3 days, such as at least one week, and up to 10 days or more; and/or such an ISV, protein, polypeptide or pharmaceutical composition as described herein is intended to be administered to a human being as two or more doses that are administered over a period of at least 3 days, such as at least one week, for example at least two weeks or at least one month, or even longer (i.e. at least 3 months, at least 6 months or at least one year), or even chronically administered.

Also, as will be clear to the skilled person based on the disclosure herein, the

10 improvements to VH domains described herein and the resulting improved VH domains will find particular use in proteins, polypeptides or other compounds or molecules that are intended for administration to human subjects (and in particular patients) whose blood/serum contains (or is suspected to contain) pre-existing antibodies of the kind that - according to the present invention - have been found in samples obtained from SLE patients, i.e. pre-existing antibodies that can bind to the C-terminal region of a VH-domain even in the presence of a C-terminal extension as described herein. In particular, the improvements to VH domains described herein and the resulting improved VH domains will find particular use in proteins, polypeptides or other compounds or molecules that are intended to treat or prevent diseases or disorders in such patients. This may be any disease or disorder, but may in particular be a

20 disease or disorder that results in and/or is associated with the presence or emergence of such pre-existing antibodies (one example being SLE, but it is expected that other severe (auto-)immune disorders may also lead to such pre-existing antibodies. This can be easily ascertained by testing samples obtained from the relevant patient population for the presence of such pre-existing antibodies, essentially in a manner analogous to the tests performed on samples from SLE patients in the Experimental Part below).

Thus, according to one specific aspect, the invention relates to an ISV, protein, polypeptide, compound or molecule of the invention as described herein (or a pharmaceutical composition the same) that is intended for administration to a human subject whose blood contains pre-existing antibodies that can bind to the exposed C-terminal region of a VH domain even when said VH-domain contains a C-terminal extension as described herein (or where the C-terminal end of the VH domain is linked to another protein or polypeptide, such as another ISV, optionally via a suitable linker).

In particular, the invention relates to an ISV, protein, polypeptide, compound or molecule of the invention as described herein (or a pharmaceutical composition the same) for

use in the treatment of a disease or disorder in a human subject whose blood contains pre-existing antibodies that can bind to the exposed C-terminal region of a VH domain even when said VH-domain contains a C-terminal extension as described herein (or where the C-terminal end of the VH domain is linked to another protein or polypeptide, such as another ISV, optionally via a suitable linker). Said disease or disorder can be any disease or disorder, but can in particular be a disease or disorder that leads to, results into or otherwise is associated with the presence of such pre-existing antibodies in the blood of such a patient, such as SLE or another (severe) autoimmune disease.

Thus, according to a more specific aspect, the invention relates to an ISV, protein, 10 polypeptide, compound or molecule of the invention as described herein (or a pharmaceutical composition the same) for use in the treatment of a disease or disorder in a human subject/patient, wherein said disease or disorder is a disease or disorder that leads to, results into or otherwise is associated with the presence of pre-existing antibodies in the blood of said human subject/patient that can bind to the exposed C-terminal region of a VH domain even when said VH-domain contains a C-terminal extension as described herein (or where the C-terminal end of the VH domain is linked to another protein or polypeptide, such as another ISV, optionally via a suitable linker). For example, such an ISV, protein, polypeptide, compound or molecule of the invention as described herein (or a pharmaceutical composition the same) for use in the treatment of SLE or another (severe) auto-immune disease in a human 20 subject/patient.

As will be clear to the skilled person, when a protein, polypeptide, compound or molecule is intended for the prevention or treatment of such a disease or disorder, it will contain at least one (such as one, two, three or four) domains, binding units or moieties or entities that are therapeutically active against the relevant disease or disorder (e.g. directed against a target or pathway that is therapeutically relevant for the pertinent disease or disorder). Again, such binding domains or binding units may for example be (other) ISVD's, and according to one aspect may in particular be VH domains or ISVD's of the invention. Another general example of such a protein, polypeptide, compound or molecule is a protein, polypeptide, compound or molecule in which said one or more therapeutic domains, binding 30 units or moieties or entities may not be ISVD's (but for example derived from another scaffold), but that contains a VH domain of the invention to extend the half-life of the same (such as a serum albumin binder as described herein).

In a further aspect, the VH domains, ISVD's or compounds of the invention (as described herein) are directed towards the ion channel Kv1.3. Some preferred, but non-

limiting examples of such VH domains, ISVD's or compounds are given in Example 7, and the VH domains against Kv1.3 described in said example (as well as compounds of the invention comprising the same) as well as the specific compounds of the invention against Kv1.3 described in said example form further aspects of the present invention.

For example and without limitation, a compound of the invention that is directed towards Kv1.3 can comprise or essentially consist of a single VH domain - and preferably Nanobody - of the invention directed against Kv1.3 or can comprise or essentially consist of at least two (such as two or three) VH domains - and preferably Nanobodies - of the invention directed against Kv1.3. When such a polypeptide contains two or more VH domains of the invention against Kv1.3, these VH domains can be the same or different, and when they are different they can be directed against the same epitope on Kv1.3 or subunit on Kv1.3 or against different epitopes or subunits.

Again, as generally described herein for the compounds of the invention, such compounds can suitably contain one or more linkers, can contain a C-terminal extension (i.e. as further described herein) and can also contain one or more further binding units or binding domains (or other amino acid sequences or moieties), such as a further ISVD directed against a different target than Kv1.3. For example and without limitation, the compounds of the invention can (also) contain a binding domain or binding unit that provides for extended half-life, such as an ISVD against a serum protein such as serum albumin (for example, a

20 Nanobody against human serum albumin such as a Nanobody of the invention against human serum albumin).

In further aspects, the invention relates to (synthetic) libraries of immunoglobulin variable domain sequences that are as described herein (i.e. containing the amino acid residues/mutations/substitutions as described herein). Such libraries will usually contain at least 100 different sequences, such as at least 1000 different sequences, in particular more than 10^5 different sequences, more in particular more than 10^6 , such as 10^8 to 10^{10} or more different sequences (meaning in its broadest sense, with at least one amino acid difference between the sequences), usually all with (essentially) the same framework sequences (said framework sequences containing the amino acid residues/mutations indicated herein) and different CDRs (meaning that each sequence in the library has at least "one amino acid difference" in at least one of its CDRs compared to the other sequences in the library).

Synthetic libraries of immunoglobulin single variable domain sequences (for example based on human VH sequences or camelid-derived VHH sequences) and methods of generating/constructing them (including libraries based on pre-determined scaffolds and/or

containing one or more specific amino acid residues/mutations in the framework regions) are well known in the art. Reference is for example made to Tanha et al., *J. Biol. Chem.*, Vol. 276, pp. 24774–24780, 2001; Bond et al., *J. Mol. Biol.* (2003) 332, 643–655; Mandrup et al., *PLOS One*, October 2013, Volume 8, Issue 10, e76834; Goldman et al., *Anal. Chem.*, 2006, 78, 8245-8255; Hussak et al., *Protein Engineering, Design & Selection* vol. 25 no. 6 pp. 313–318, 2012; and Chen et al., *Methods Mol. Biol.*, 2009, 525, 81. The techniques described therein (and similar techniques known per se) can be suitably used or adapted for generating the immunoglobulin single variable domain libraries according to the invention.

The ISVD's present in such libraries can suitably contain any suitable CDR's from 10 any suitable source, such as CDR's obtained/generated starting from the immune repertoire from a “naïve” mammal (such as a species of camelid or human sequences), CDR's obtained/generated starting from the immune repertoire from an animal (such as a species of camelid) that has been suitably immunized with an antigen; a fully synthetic CDR repertoire; or a repertoire that has been obtained through techniques such as mutagenesis (for example random mutagenesis or site-specific mutagenesis). Such a library can for example also be a library that has been generated in the course of affinity maturation procedures known per se.

The framework regions of the ISVD's present in such libraries can be suitably derived from any suitable starting sequence/scaffold, for example based on a scaffold that has been derived starting from a VH sequence (such as a human VH sequence) or starting from a 20 nanobody sequence (such as a VHH sequence or a humanized VH sequences). It is also possible that a library contains ISVD's that are derived from two or more different sources or that are based on two or more different scaffolds (for example, because the library has been obtained by combining two or more libraries obtained from different sources or based on different scaffolds).

Also, (the ISVD's present in) the libraries may be in the form of proteins or in the form of a DNA or RNA encoding the relevant ISVD's. For example, the libraries may be in the form of an expression library suitable for screening and/or selection techniques, and may for this purpose for example be in a form that can be displayed using suitable display techniques such as phage display library, a yeast display library or a ribosome display library.

30 Thus, generally, the invention also relates to libraries (as described herein) containing VH domains of the invention (as further described herein). Preferably, according to one specific aspect of such a library, the VH domains present all have the same (or essentially the same) framework sequences, but different CDR sequences (again, as mentioned, this means

that each of the individual VH domains in the library has at least one amino acid difference in at least one CDR compared to the other VH domains in the library).

In one aspect, such a library of the invention is a library of ISVD's of the invention (as further described herein, including a library of suitable nucleic acids encoding said ISVD's) in which:

- the amino acid residue at position 11 is one of L, V or K; and
- the amino acid residue at position 14 is one of A or P; and
- the amino acid residue at position 41 is one of A or P; and
- the amino acid residue at position 89 is one of T, V or L; and
- 10 - the amino acid residue at position 108 is one of Q or L; and
- the amino acid residue at position 110 is one of T, K or Q; and
- the amino acid residue at position 112 is one of S, K or Q;

in which either (i) the amino acid residue at position 112 is one of K or Q; and/or (ii) the amino acid residue at position 89 is T; and/or (iii) the amino acid residue at position 89 is L and the amino acid residue at position 110 is one of K or Q; and (iv) in each of cases (i) to (iii), the amino acid at position 11 is preferably V. Optionally, the ISVD's present in such a library may also contain a C-terminal extension (as further described herein for the VH domains of the invention) and/or suitably contain a suitable tag (such as a histidine tag).

In another aspect, such a library of the invention is a library of ISVD's of the invention (as further described herein, including a library of suitable nucleic acids encoding said ISVD's) in which:

- the amino acid residue at position 11 is V; and
- the amino acid residue at position 14 is one of A or P; and
- the amino acid residue at position 41 is one of A or P; and
- the amino acid residue at position 89 is one of L; and
- the amino acid residue at position 108 is one of Q or L; and
- the amino acid residue at position 110 is one of T, K or Q; and
- the amino acid residue at position 112 is one of S, K or Q;

30 Optionally, the ISVD's present in such a library may also contain a C-terminal extension (as further described herein for the VH domains of the invention) and/or suitably contain a suitable tag (such as a histidine tag).

The libraries of the invention may be used for any suitable/intended purpose known per se. For example, they may for example be used for screening and/or selection purpose (or as part of a screening and/or selection process), be used for/as part of affinity maturation purposes or other processes intended to yield improved VH domains, or for example for alanine scanning. In practice, usually, the size, design and other features of the library will be adapted to its intended use, as will be within the skill of the artisan.

The invention will now be further described by means of the following non-limiting preferred aspects, examples and figures, in which:

- Figure 1 is a table listing some of the amino acid positions that will be specifically referred to herein and their numbering according to some alternative numbering systems (such as Aho and IMGT);
- Figure 2 lists the sequences referred to herein;
- Figure 3 is a plot showing data points obtained in Example 4 when 96 serum samples were tested for binding a representative Nanobody with an S112K mutation (Reference A + S 112K + C-terminal alanine, indicated as (2) in Figure 3), compared to a reference Nanobody without an S112K mutation (Reference A, SEQ ID NO: 44, indicated as (1) in Figure 3);
- Figure 4 is a plot showing data points obtained in Example 4 when 129 serum samples were tested for binding a representative Nanobody with an V89T mutation (Reference A + L11V + V89T + C-terminal alanine, indicated as (2) in Figure 4), compared to a reference Nanobody without an V89T mutation (Reference A, SEQ ID NO: 44, indicated as (1) in Figure 4);
- Figure 5 is a plot showing data points obtained in Example 5 when 100 serum samples were tested for binding representative Nanobodies with V89L, T110K and/or T110Q mutations (Reference A + L11V + V89L + C-terminal Ala, indicated as (2) in Figure 5; Reference A + L11V + V89L + T110K + C-terminal Ala, indicated as (3) in Figure 5; Reference A + L11V + V89L + T110Q + C-terminal Ala, indicated as (4) in Figure 5) and Reference A + L11V + T87A + V89L + C-terminal Ala, indicated as (5) in Figure 5), compared to a reference Nanobody without any of these mutations (Reference A, SEQ ID NO: 44, indicated as (1) in Figure 5).
- Figure 6 is a plot showing data points obtained in Example 6 when 98 serum samples obtained from healthy volunteers were tested for binding representative trivalent Nanobody constructs. Each dot represents a data point collected by testing of the indicated construct against one of the 98 serum samples. Legenda: (1) = Reference X (Nanobody A-35GS-Nanobody A-35GS-Nanobody B); (2) = Reference X + C-terminal Ala; (3) = Reference X + L11V + V89L + C-terminal Ala; (4) = Reference X + L11V + T87A +

V89L + C-terminal Ala; (5) = Reference X + L11V + V89L + T110K + C-terminal Ala; (6) = Reference X + L11V + V89L + T110Q + C-terminal Ala.

- Figure 7 is a plot showing data points obtained in Example 6 when 30 serum samples obtained from healthy volunteers (samples selected for high titers of pre-existing antibodies or presence of pre-existing antibodies with high degree of binding even in the presence of a C-terminal alanine extension) were tested for binding representative trivalent Nanobody constructs. Each dot represents a data point collected by testing of the indicated construct against one of the 30 serum samples. Legenda: (1) = Reference X + C-terminal Ala; (2) = Reference X + L11V + V89L + C-terminal Ala; (4) = Reference X + L11V + T87A + V89L + C-terminal Ala; (5) = Reference X + L11V + V89L + T110K + C-terminal Ala.
- Figure 8 is a plot showing data points obtained in Example 6 when 98 serum samples obtained from healthy volunteers were tested for binding representative bivalent Nanobody constructs. Each dot represents a data point collected by testing of the indicated construct against one of the 30 serum samples. Legenda: (1) = Reference Y (Nanobody A-35GS- Nanobody B); (2) = Reference Y + C-terminal Ala; (3) = Reference Y + L11V + V89L + C-terminal Ala; (4) = Reference Y + L11V + T87A + V89L + C-terminal Ala; (5) = Reference Y + L11V + V89L + T110K + C-terminal Ala; (6) = Reference Y + L11V + V89L + T110Q + C-terminal Ala;
- Figures 9A and 9B show preferred but non-limiting examples of monovalent Nanobodies of the invention (Figure 9A) and trivalent bispecific half-life extended compounds of the invention (Figure 9B) against the ion channel Kv1.3; and Figure 9C lists some preferred CDRs (classification according to Kabat and Abm, respectively) for ISVDs against Kv1.3.
- Figure 10 is a plot showing data points obtained in Example 7 when 47 serum samples obtained from diabetic human subjects were tested for binding representative trivalent bispecific half-life extended compounds of the invention against Kv1.3. Each dot represents a data point collected by testing of the indicated construct against one of the 47 serum samples. The SEQ ID NO's refer to the relevant sequences listed in Figure 9;
- Figure 11 is a plot showing data points obtained in Example 7 when 90 serum samples obtained from healthy volunteers were tested for binding representative trivalent bispecific half-life extended compounds of the invention against Kv1.3. Each dot represents a data point collected by testing of the indicated construct against one of the 47 serum samples. The SEQ ID NO's refer to the relevant sequences listed in Figure 9.

- Figures 12A and 12B list the CDR's and amino sequences of some preferred, but non-limiting examples of Nanobodies of the invention against IL-23 that are based on the indicated reference sequences. See also Example 8;
- Figure 13 lists the CDR's and amino sequences of some preferred, but non-limiting examples of Nanobodies of the invention against OX40-L that are based on the indicated reference sequence. See also Example 9;
- Figure 14 lists the CDR's and amino sequences of some preferred, but non-limiting examples of Nanobodies of the invention against IgE that are based on the indicated reference sequence. See also Example 10;

10 - Figures 15A and 15B list the CDR's and amino sequences of some preferred, but non-limiting examples of Nanobodies of the invention against CXCR-4 that are based on the indicated reference sequences. See also Example 11;

- Figures 16A and 16B list the CDR's and amino sequences of some preferred, but non-limiting examples of Nanobodies of the invention against HER-3 that are based on the indicated reference sequences. See also Example 12;
- Figures 17A and 17B list the CDR's and amino sequences of some preferred, but non-limiting examples of Nanobodies of the invention against TNF that are based on the indicated reference sequences. See also Examples 13 and 14;
- Figures 18A and 18B list the CDR's and amino sequences of some preferred, but non-limiting examples of Nanobodies of the invention against c-Met that are based on the indicated reference sequences. See also Example 15;

20 - Figure 19 lists the CDR's and amino sequences of some preferred, but non-limiting examples of Nanobodies of the invention against RANK-L that are based on the indicated reference sequence. See also Example 16;

- Figures 20A to 20C list the CDR's and amino sequences of some preferred, but non-limiting examples of Nanobodies of the invention against CXCR-7 that are based on the indicated reference sequences. See also Example 17;
- Figures 21A and 21B list the CDR's and amino sequences of some preferred, but non-limiting examples of Nanobodies of the invention against A-beta that are based on the indicated reference sequences. See also Example 18;

30 - Figure 22 gives the amino acid sequences of some preferred but non-limiting examples of compounds of the invention against IL-23;

- Figure 23 gives the amino acid sequences of some preferred but non-limiting examples of compounds of the invention against OX40-L;

- Figure 24 gives the amino acid sequences of some preferred but non-limiting examples of compounds of the invention against IgE;
- Figure 25 gives the amino acid sequences of some preferred but non-limiting examples of compounds of the invention against CXCR-4;
- Figure 26 gives the amino acid sequences of some preferred but non-limiting examples of compounds of the invention against HER-3;
- Figure 27 gives the amino acid sequences of some preferred but non-limiting examples of compounds of the invention against TNF;
- Figures 28A and 28B give the amino acid sequences of some preferred but non-limiting examples of compounds of the invention against c-Met;
- Figure 29 gives the amino acid sequences of some preferred but non-limiting examples of compounds of the invention against RANK-L;
- Figure 30 gives the amino acid sequences of some preferred but non-limiting examples of compounds of the invention against A-beta;
- Figure 31A is a plot showing data points obtained in Example 19 when 92 serum samples obtained from healthy volunteers were tested for binding representative trivalent bispecific half-life extended compounds of the invention against A-beta. Each dot represents a data point collected by testing of the indicated construct against one of the 92 serum samples. The reference numbers are as listed in Table CC-1. Similarly, Figure 30B is a plot showing data points obtained in Example 19 when 92 serum samples obtained from healthy volunteers were tested for binding the (monovalent) C-terminal Nanobodies that are present in the constructs tested in Figure 31A. Each dot represents a data point collected by testing of the indicated construct against one of the 92 serum samples. The reference numbers are as listed in Table CC-2.
- Figure 32 gives the amino acid sequence of SEQ ID 52 of WO 2006/122787.

Experimental Part

The human samples used in the Experimental Part below were either obtained from commercial sources or from human volunteers (after all required consents and approvals were obtained) and were used in according with the applicable legal and regulatory requirements (including but not limited to those regarding medical secret and patient privacy)

In the Examples below, the binding of pre-existing antibodies that are present in the samples used (i.e. from healthy volunteers, rheumatoid arthritis (RA) patients and SLE patients) to the Nanobodies tested was determined using ProteOn as follows: Binding of pre-existing antibodies on Nanobodies captured on human serum albumin (HSA) was evaluated

using the ProteOn XPR36 (Bio-Rad Laboratories, Inc.). PBS/Tween (phosphate buffered saline, pH7.4, 0.005% Tween20) was used as running buffer and the experiments were performed at 25°C. The ligand lanes of a ProteOn GLC Sensor Chip were activated with EDC/NHS (flow rate 30µl/min) and HSA was injected at 10µg/ml in ProteOn Acetate buffer pH4.5 (flow rate 100µl/min) to render immobilization levels of approximately 3200 RU. After immobilization, surfaces were deactivated with ethanolamine HCl (flow rate 30µl/min).

Nanobodies were injected for 2 minutes at 45µl/min over the HSA surface to render a Nanobody capture level of approximately 200 RU. The samples containing pre-existing antibodies were centrifuged for 2 minutes at 14,000rpm and supernatant was diluted 1:10 in

10 PBS-Tween20 (0.005%) before being injected for 2 minutes at 45µl/min followed by a subsequent 400 seconds dissociation step. After each cycle (i.e. before a new Nanobody capture and blood sample injection step) the HSA surfaces were regenerated with a 2 minute injection of HCl (100mM) at 45µl/min. Sensorgram processing and data analysis was performed with ProteOn Manager 3.1.0 (Bio-Rad Laboratories, Inc.). Sensorgrams showing pre-existing antibody binding were obtained after double referencing by subtracting 1) Nanobody-HSA dissociation and 2) non-specific binding to reference ligand lane. Binding levels of pre-existing antibodies were determined by setting report points at 125 seconds (5 seconds after end of association). Percentage reduction in pre-existing antibody binding was calculated relative to the binding levels at 125 seconds of a reference Nanobody.

20

Example 1: S112K mutation inhibits binding of pre-existing antibodies

The influence of a substitution at position 112 on the binding of pre-existing antibodies in human samples to Nanobodies was determined and compared to the influence of a C-terminal alanine extension as described in WO 12/175741.

Two reference compounds (Reference A without a C-terminal alanine extension and Reference B with a C-terminal alanine extension) and variants of these reference compounds with different mutations at position 112 were tested against sera obtained from six different RA patients and eight sera obtained from different healthy human subjects. Binding of pre-existing antibodies in the samples to the Nanobodies tested was measured on ProteOn according to the general protocol outlined above. The results are shown in Table A below.

30 As can be seen, of the mutations at position 112 that were tested, the S112K mutation gave a reduction of binding of the pre-existing antibodies that were present in the tested sera that was comparable to that of the C-terminal alanine extension (even without the C-terminal

alanine extension being present in the S112K variant). Similar results were obtained with three human plasma samples (data not shown).

Table A: comparison of mutations at position 112 to a C-terminal alanine extension on binding of pre-existing antibodies present in sera from RA patients and human volunteers

	RA sera						healthy human sera							
Average binding on Reference A (RU)	75	96	44	11	117	141	242	81	121	179	93	92	91	92
Inhibition compared to average binding on Reference A (%)														
Reference A	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Reference B	70	90	100	88	84	97	53	78	83	93	93	81	86	86
Reference A (S112E)	51	67	63	65	66	84	31	82	72	59	73	100	74	70
Reference A (S112F)	75	51	85	100	79	39	56	86	69	60	78	93	76	79
Reference A (S112K)	88	88	94	100	94	100	86	93	87	87	95	100	84	91
Reference A (S112L)	69	45	63	54	50	81	37	74	59	42	75	97	68	83

Example 2: Influence of S112K mutation on binding of pre-existing antibodies that are present in human SLE samples

The same Nanobody variants as used in Example 1 were tested for binding by pre-existing antibodies from 7 serum samples obtained from patients who were confirmed positive for systemic lupus erythematosus (SLE). For comparison, plasma samples from two healthy human volunteers were included.

Binding of pre-existing antibodies in the samples to the Nanobodies tested was measured on ProteOn according to the general protocol outlined above. The results are shown in Table B below.

10 As can be seen from a comparison of the binding data for Reference A and Reference B and nanobodies of the invention , the samples obtained from some of the SLE patients appear to contain certain pre-existing antibodies that can still bind to Nanobodies even in the presence of a C-terminal alanine residue (the C-terminal alanine residue did essentially prevent/remove (partially or essentially fully) all binding of the pre-existing antibodies that were present in the plasma samples from healthy volunteers).

It can further be seen that the binding of these pre-existing antibodies from SLE samples could be greatly reduced by mutations at positions 11 and 112 (and in case of position 112, in particular S112K).

Table B: comparison of mutations at positions 11 and 112 to a C-terminal alanine extension on binding of pre-existing antibodies present in sera from SLE patients

	Serum samples obtained from SLE patients				Plasma samples obtained from healthy volunteers				
Average binding on Reference A (RU)	45	61	38	40	43	20	69	128	171
Inhibition compared to binding on Reference A (%)									
Reference B	20	16	13	45	53	86	101	95	90
Reference A (L11E)	63	88	117	61	87	88	92	68	21
Reference A (L11K)	87	97	107	54	106	79	102	100	61
Reference A (L11V)	68	84	49	56	95	91	21	23	6
Reference A (L11Y)	27	71	111	37	84	74	72	13	3
Reference A (S112E)	13	56	91	77	74	91	94	84	22
Reference A (S112F)	-6	18	26	-13	62	69	117	74	43
Reference A (S112K)	71	77	105	80	116	86	120	87	62
Reference A (S112L)	-36	36	48	-24	123	19	84	91	3

Example 3: Influence of combined framework mutations and C-terminal extensions on binding of pre-existing antibodies that are present in human SLE samples

Four different Nanobodies (with specific framework mutations and with or without C-terminal alanine extension) were tested for binding of pre-existing antibodies from 5 serum samples obtained from patients who were confirmed positive for systemic lupus erythemathosus (SLE). For comparison, one plasma sample from a healthy human volunteer was included.

Binding of pre-existing antibodies in the samples to the Nanobodies tested was measured on ProteOn according to the general protocol outlined above. The results are shown 10 in Tables C and D below.

As can be seen from a comparison of the binding data for Reference A and Reference B, the samples obtained from SLE patients appear to contain a certain pre-existing antibodies that can still bind to Nanobodies even in the presence of a C-terminal alanine residue (the C-terminal alanine residue did essentially prevent/remove all binding of the pre-existing antibodies that were present in the plasma samples from the healthy volunteer).

It can further be seen that the binding of these pre-existing antibodies from SLE samples could be greatly reduced by mutations at positions 11 and 112 (and in case of position 112, in particular S112K).

20 Example 4: influence of a V89T mutation on binding of pre-existing antibodies in samples from SLE patients.

As described herein, samples obtained from certain SLE patients appear to contain pre-existing antibodies/factors that can bind to the exposed C-terminal end of a VH domain, even when a C-terminal extension is present. It was investigated whether a V89T mutation could reduce or prevent/remove such binding, with or without the presence of a C-terminal extension. The results are also shown in Tables C and E below.

As can be seen, a V89T mutation could essentially prevent/remove binding of pre-existing antibodies that are present in samples obtained from SLE patients, to a similar degree as an S112K mutation. However, as can be seen from comparing the data given in Tables C 30 and E for nanobodies with a V89T mutation without a C-terminal extension with similar nanobodies with an S112K mutation and without a C-terminal extension, having a mutation at position 112 in a nanobody without a C-terminal extension generally reduces binding of pre-existing antibodies in samples from a healthy volunteer to a larger degree than a V89T mutation (i.e. 100%, 85% and 64% of S112K nanobodies vs. 9%, 11% and 16% for V89T

nanobodies, respectively). For this reason, the use of a mutation at position 112 (and in particular S112K or S112K) will often be preferred over the use of a mutation at position 89 (such as V89T).

However, as can also be seen from the data in Tables C and E, adding a C-terminal alanine to a V89T nanobody completely prevented/removed the binding of pre-existing antibodies in a sample obtained from healthy volunteers, and for this reason a combination of a V89T mutation and a C-terminal extension as described herein will usually be preferred (i.e. over the use of a V89T without C-terminal extension) if the V89T nanobody or VH domain has, or is intended to have, an exposed C-terminal region in the protein or polypeptide in

10 which it will be present (for example, because it forms the C-terminal end of the same).

Table C: influence of different mutations of binding by pre-existing antibodies in samples obtained from SLE patients and human volunteers

Table D: influence of different mutations of binding by pre-existing antibodies in samples obtained from SLE patients and human volunteers

Mutation	Samples obtained from SLE patients		Sample obtained from healthy volunteer
	02-004-030-ABL	02-004-030-ABL	
L11V	ST12Q	SL125	SL13025-14
V89L	I14A	SL137	SL13025-14
L11V	ST12Q	SL137	SL13025-14
		ND	ND
		71	51
		ND	ND
		41	41
		180	180

Table E: influence of different mutations on binding by pre-existing antibodies in samples from SLE patients and human volunteers

	Mutation(s)	Samples obtained from SLE patients				Sample from healthy volunteer	
		SLE25	SLE37	SLE39	SLE41	NB13025-14	02-030-ABL
Average binding to Reference A							
Reference A				28	44	26	33
						30	151
Inhibition compared to average binding to Reference A captured on HSA (%)							
Reference A + V89L, no C-terminal extension	x		77	64	53	63	41
Reference A + V89L + C-terminal alanine	x	x	35	27	63	42	46
Reference A + V89T, no C-terminal extension	x		68	12	84	100	71
Reference A + V89T + C-terminal alanine	x	x	46	35	71	100	97
Reference A + V89T + L11V, no C-terminal extension	x	x	100	97	100	100	97
Reference A + V89T + L11V + C-terminal alanine (*)	x	x	x	100	100	100	100
Reference A + S112K + V89L, no C-terminal extension	x	x	100	100	100	100	100
Reference A + S112K + V89L C-terminal alanine	x	x	x	100	100	100	100
Reference A + S112K + L11V, no C-terminal extension	x	x	100	100	100	100	100
Reference A + S112K + L11V + C-terminal alanine	x	x	x	100	100	100	100

(*) Note: this Nanobody was also used to generate the data shown in Figure 4 and Table G (see below)

To confirm that the results/findings from the table above are broadly applicable, representative Nanobodies with S112K and/or V89T mutations were tested against a test panel of 96 (S112k) and 129 (V89T) human serum samples. Binding was determined on ProteOn using the protocol set out above.

The results are summarized Figure 3 and Table F (representative Nanobody with an S112K mutation) and Figure 4 and Table G (representative Nanobody with a V89T mutation).

In Figure 3, a Nanobody with an S112K mutation (Reference A + S112K + C-terminal alanine – see Table C above) was compared to a reference Nanobody (Reference A; SEQ ID NO:44). The Nanobody with the S112K mutation and Reference A were both tested against 10 each of the serum samples, and the binding level at 125 seconds (RU) was determined. The data was then plotted in Figure 3, with each point presenting the binding measured in one sample for either Reference A (indicated as (1) in Figure 3) or for the S112K mutant (indicated as (2) in Figure 3). The dotted line indicates a measured binding level of 20 RU.

The same data is also represented numerically in Table F, which mentions - for Reference A and the S112K mutant, respectively - the total number of samples tested that gave a level of binding at 125 seconds of more than 20RU, less than 20 RU (i.e. between 0 and 20 RU) and less than 10 RU.

As can be seen from the data plotted in Figure 3 and shown in Table F, for Reference A, more than half of the 96 samples tested gave a binding level of more than 20 RU (in some 20 cases, as high as 150-200 RU), indicating that the pre-existing antibodies present in the sample were binding to Reference A. By comparison, for the S112K mutant, no sample gave a binding level of more than 20 RU (and most less than 10 RU), indicating that the S122K mutation was essentially capable of reducing/preventing binding of the pre-existing antibodies in all of the 96 samples tested.

A similar plot and similar data is shown in Figure 4 and Table G, respectively, for a representative Nanobody with a V89T mutation (Reference A + L11V + V89T + C-terminal alanine; see Table E above), tested against 129 serum samples and again compared to Reference A (indicated by (1) in Figure 4; the V89T mutant is indicated by (2) in Figure 4). Again, from the plot in Figure 4 and the data in Table G, it can be seen that with a few 30 exceptions (i.e. less than 10% of samples tested, which then each gave an absolute binding value after 125 seconds of about 100 RU or less), the V89T mutation was capable of reducing/preventing binding of the pre-existing antibodies in most of the 129 samples tested, whereas the reference without the V89T mutation was bound by pre-existing antibodies in most of the samples tested.

Table F: testing of representative Nanobody with S112K mutation against 96 serum samples.

Nanobody tested	Binding level at 125 seconds < 10 RU	Binding level at 125 seconds < 20 RU	Binding level at 125 seconds > 20 RU
Reference A	34	41	55
Reference A + S112K + C-terminal alanine	92	96	0

Table G: testing of Nanobody mutants with V89L and/or T100K/Q mutations against 129 serum samples.

Nanobody tested	Binding level at 125 seconds < 10 RU	Binding level at 125 seconds < 20 RU	Binding level at 125 seconds > 20 RU
Reference A	27	40	89
Reference A + L11V + V89T + C-terminal alanine	110	119	10

10 Example 5: influence of a V89L mutation combined with a T110K or T110Q mutation on binding of pre-existing antibodies in samples from SLE patients.

As described herein, samples obtained from certain SLE patients appear to contain pre-existing antibodies/factors that can bind to the exposed C-terminal end of a VH domain, even when a C-terminal extension is present. It was investigated whether a V89L and/or a T110Q or T110K mutation (or a combination thereof) could reduce or prevent/remove such binding, with or without the presence of a C-terminal extension. The results are also shown in Tables H and I, which present the data from two separate experiments (Table D above also shows data for an S112Q mutation of the invention combined with a V89L mutation). The Nanobodies used in Table I were also used in generating the data shown in Figure 5 and Table J.

Table H: influence of different mutations on binding by pre-existing antibodies in samples from SLE patients and human volunteers

		Mutation(s)						Samples obtained from SLE patients				Sample from healthy volunteer	
		L11Y	V89L	T110K	T110Q	114A		SLFE37	SLFE39	SLFE41	NB13025-14	004-030-ABL-02	
Average binding to Reference A													
Reference A								28	44	26	33	30	151
Reference A + L11V+ V89L + T110K, no C-terminal extension		x						77	64	53	63	41	35
Reference A + V89L + C-terminal alanine		x					x	35	27	63	42	46	83
Reference A + L11V+ V89L, no C-terminal extension		x	x					100	100	8	95	100	29
Reference A + L11V+ V89L + C-terminal alanine (*)		x	x			x	x	94	70	100	78	100	89
Reference A + V89L + T110K, no C-terminal extension		x	x					100	77	100	100	100	65
Reference A + V89L + T110K, C-terminal alanine		x	x			x	x	96	70	100	100	100	100
Reference A + L11V+ T110K, no C-terminal extension		x	x			x	x	100	0	100	100	100	43
Reference A + L11V+ T110K + C-terminal alanine		x	x			x	x	96	0	100	100	100	99

(*) This Nanobody was also used in generating the data shown in Figure 5 and Table J

Table I: influence of different mutations on binding by pre-existing antibodies in samples from SLE patients and human volunteers.

		Mutation(s)						Samples obtained from SLE patients					
		L11V	T87A	V89L	T110K	T110Q	L11A	SLE25	SLE37	SLE39	SLE41	NB13025-14	
		Average binding to Reference A											
		Reference A											
		50	72	55	56	58							
Inhibition compared to average binding to Reference A captured on HSA (%)													
Reference A + L11V+ V89L + C-terminal alanine	x	x	x				x		x	100	100	98	100
Reference A + L11V+ V89L+ T110K + C-terminal alanine	x	x	x	x			x	100	81	98	99	98	
Reference A + L11V+ V89L+ T110Q + C-terminal alanine	x	x	x	x	x		x	100	100	87	98	81	
Reference A + L11V+ T87A+V89L + C-terminal alanine	x	x	x	x	x	x	x	100	100	100	100	100	

To confirm that the results/findings from the table above are broadly applicable, representative Nanobodies with V89L, T110K and/or T110Q mutations were again tested against a panel of 99 human serum samples. Binding data was again obtained and plotted as indicated in Example 4 for the results and data shown in Figures 3 and 4 and Tables F and G.

The Nanobodies tested were (the numbers correspond to the numbering used in Figure 5): (1) Reference A; (2) Reference A + L11V + V89L + C-terminal Ala; (3) Reference A + L11V + V89L + T110K + C-terminal Ala; (4) Reference A + L11V + V89L + T110Q + C-terminal Ala; (5) Reference A + L11V + T87A + V89L + C-terminal Ala. The results are shown in Figure 5 and Table I.

As can be seen, introducing the mutations tested again greatly reduced the number of samples in which the pre-existing antibodies were capable of binding the Nanobody tested. It can also be seen that, for Nanobody (2) in Figure 5 (Reference A + L11V + V89L + C-terminal Ala), still some of the samples showed binding of pre-existing antibodies after 125 seconds at levels of more than 20 RU (but already much less than 100 RU). However, when the V89L mutation was combined with a T110K mutation (Nanobody (3)) or a T110Q mutation (Nanobody (4)), then essentially all of the 99 samples tested showed a binding level of less than 20RU (and in fact less than 10RU, see Table J).

Table J: testing of representative Nanobodies with V89L, T110K and/or T110Q mutations against 99 serum samples.

Nanobody tested	Binding level at 125 seconds < 10 RU	Binding level at 125 seconds < 20 RU	Binding level at 125 seconds > 20 RU
Reference A	52	64	35
Reference A + L11V + V89L + C-terminal Ala	94	95	4
Reference A + L11V + V89L + T110K + C-terminal Ala	99	99	0
Reference A + L11V + V89L + T110Q + C-terminal Ala	99	99	0
Reference A + L11V + T87A + V89L + C-terminal Ala	99	99	0

Example 6: testing of multivalent constructs for binding of pre-existing antibodies

Multivalent constructs are made based on the following nanobodies:

Nanobody A (directed against a therapeutic target):

EVQLVESGGGLVQPGGSLRLSCAASGRTFNNYAMGWFRQAPGKEREVAAIT
 RSGVRSGVSAIYGDSVKDRFTISRDNAKNTLYLQMNSLRPEDTAVYYCAASAI
 GSGALRRFEYDYSQQGTLTVSS (SEQ ID NO:92)

Nanobody B (directed against serum albumin):

EVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISG
 SGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSRSS
 QGTLTVSS (SEQ ID NO:93)

Nanobody C (directed against a therapeutic target):

EVQLVESGGGLVQPGGSLRLSCAASRSIGRLDRMGWYRHRPGEPELVATITG
GSSINYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTAVYYCNFNKYVTSRDT
WGQGTLTVSS (SEQ ID NO:94)

The constructs made are listed in Table K below (with in each case, the introduced substitution(s) in the relevant nanobody (if any) mentioned between parentheses. “HIS6” denotes an N-terminal his-tag of 6 histidine residues, and “-Ala” denotes a C-terminal extension of 1 alanine residue).

Table K: multivalent constructs tested

HIS6-Nanobody A(E1D,L11V, S112K)-35GS-Nanobody B-Ala
HIS6-Nanobody A(E1D,L11V, S112K)-35GS-Nanobody B(L11V,S112K)-Ala
HIS6-Nanobody A(E1D)-35GS-Nanobody B
HIS6-Nanobody A(E1D)-35GS-Nanobody B-Ala
HIS6-Nanobody A(E1D,L11V, S112K)-35GS-Nanobody B(L11V, S112K)
HIS6-Nanobody A(E1D, S112K)-35GS-Nanobody B(S112K)-Ala
HIS6-Nanobody A(E1D, S112Q)-35GS-Nanobody B(S112Q)-Ala
HIS6-Nanobody A(E1D, V89L, S112K)-35GS-Nanobody B(V89L, S112K)-Ala
HIS6-Nanobody A(E1D,L11V, S112Q)-35GS-Nanobody B(L11V, S112Q)-Ala
HIS6-Nanobody B(E1D)-35GS-Nanobody A
HIS6-Nanobody B(E1D)-35GS-Nanobody A-Ala
HIS6-Nanobody A(E1D)-35GS-Nanobody B(L11V, S112K)-Ala
HIS6-Nanobody B(E1D,L11V, S112K)-35GS-Nanobody A-Ala
HIS6-Nanobody B(E1D,)-35GS-Nanobody A(L11V, S112K)-Ala
HIS6-Nanobody A(E1D,V89L, S112Q)-35GS-Nanobody B(V89L, S112Q)-Ala
HIS6-Nanobody B(E1D,L11V, S112K)-35GS-Nanobody A(L11V, S112K)-Ala
HIS6-Nanobody B(S112K)-Ala
Nanobody B(L11V, S112K)-Ala
Nanobody B(L11V, S112Q)-Ala
Nanobody B(S112Q)-Ala

Table K (continued)

HIS6-Nanobody A(E1D, S112K)-35GS-Nanobody A(S112K)-35GS-Nanobody B(S112K)-Ala
HIS6-Nanobody A(E1D, S112Q)-35GS-Nanobody A(S112Q)-35GS-Nanobody B(S112Q)-Ala
HIS6-Nanobody A(E1D,L11V,S112K)-35GS-Nanobody A(L11V, S112K)-35GS-Nanobody B(L11V, S112K)-Ala
HIS6-Nanobody A(E1D,V89L, S112K)-35GS-Nanobody A(V89L, S112K)-35GS-Nanobody B(V89L, S112K)-Ala
HIS6-Nanobody A(E1D)-35GS-Nanobody A-35GS-Nanobody B
HIS6-Nanobody A(E1D)-35GS-Nanobody A -35GS-Nanobody B-Ala
Nanobody C(E1D)-9GS-AlaLB11-9GS-Nanobody C
HIS6-Nanobody A(E1D,L11V, S112K)-35GS-Nanobody A(L11V, S112K)-35GS-Nanobody B-Ala
HIS6-Nanobody C(E1D,L11V, S112K)-9GS-Nanobody B(L11V, S112K)-9GS-Nanobody C(L11V,S112K)-Ala
Nanobody C(E1D)-9GS-AlaLB11-9GS-Nanobody C-Ala
HIS6-Nanobody A(E1D,L11V, S112Q)-35GS-Nanobody A(L11V, S112Q)-35GS-Nanobody B(L11V, S112Q)-Ala
HIS6-Nanobody A(E1D, V89L, S112Q)-35GS-Nanobody A(V89L, S112Q)-35GS-Nanobody B(V89L, S112Q)-Ala
HIS6-Nanobody C(E1D, S112K)-9GS-Nanobody B(S112K)-9GS-Nanobody C(S112K)-Ala
HIS6-Nanobody C(E1D, S112Q)-9GS-Nanobody B(S112Q)-9GS-Nanobody C(S112Q)-Ala
HIS6-Nanobody C(E1D,L11V, S112Q)-9GS-Nanobody B(L11V, S112Q)-9GS-Nanobody C(L11V,S112Q)-Ala
HIS6-Nanobody C(E1D,V89L, S112K)-9GS-Nanobody B(V89L, S112K)-9GS-Nanobody C(V89L,S112K)-Ala
HIS6-Nanobody C(E1D, V89L, S112Q)-9GS-Nanobody B(V89L, S112Q)-9GS-Nanobody C(V89L, S112Q)-Ala
HIS6-Nanobody A(E1D,L11V,A14P,R39Q,K83R,V89L,T91Y,Q108L)-35GS-Nanobody B(L11V,R30S,E44G,P45L,K83R,V89L,Q108L)-Ala

Table K (continued)

HIS6-Nanobody A(E1D,L11V,A14P,R39Q,K83R,T87A,V89L,T91Y,Q108L)-35GS-Nanobody B(L11V,R30S,E44G,P45L,K83R,T87A,V89L,Q108L)-Ala
HIS6-Nanobody A(E1D,L11V,A14P,R39Q,K83R,V89L,T91Y,Q108L,T110Q)-35GS-Nanobody B(L11V,R30S,E44G,P45L,K83R,V89L,Q108L,T110Q)-Ala
HIS6-Nanobody A(E1D,L11V,A14P,R39Q,K83R,V89L,T91Y,Q108L,T110K)-35GS-Nanobody B(L11V,R30S,E44G,P45L,K83R,V89L,Q108L,T110K)-Ala
HIS6-Nanobody A(E1D,L11V,A14P,R39Q,K83R,V89L,T91Y,Q108L)-35GS-Nanobody A(E1D,L11V,A14P,R39Q,K83R,V89L,T91Y,Q108L)-35GS-Nanobody B(L11V,R30S,E44G,P45L,K83R,V89L,Q108L)-Ala
HIS6-Nanobody A(E1D,L11V,A14P,R39Q,K83R,T87A,V89L,T91Y,Q108L)-35GS-Nanobody A(E1D,L11V,A14P,R39Q,K83R,T87A,V89L,T91Y,Q108L)-35GS-Nanobody B(L11V,R30S,E44G,P45L,K83R,T87A,V89L,Q108L)-Ala
HIS6-Nanobody A(E1D,L11V,A14P,R39Q,K83R,V89L,T91Y,Q108L,T110Q)-35GS-Nanobody A(E1D,L11V,A14P,R39Q,K83R,V89L,T91Y,Q108L,T110Q)-35GS-Nanobody B(L11V,R30S,E44G,P45L,K83R,V89L,Q108L,T110Q)-Ala
HIS6-Nanobody A(E1D,L11V,A14P,R39Q,K83R,V89L,T91Y,Q108L,T110K)-35GS-Nanobody A(E1D,L11V,A14P,R39Q,K83R,V89L,T91Y,Q108L,T110K)-35GS-Nanobody B(L11V,R30S,E44G,P45L,K83R,V89L,Q108L,T110K)-Ala

Representative multivalent constructs were tested for binding by pre-existing antibodies that are present in a blood or serum sample obtained from patients with SLE and healthy volunteers. Both were determined using ProteOn, essentially as described above.

The representative constructs tested are listed in Tables L (trivalent constructs) and M (bivalent constructs), and the results are shown in Figures 6-8 and Tables N-Q. The trivalent constructs tested were derived from the reference construct Nanobody A-35GS-Nanobody A-35GS-Nanobody B (“Reference X”) and the bivalent constructs were derived from the reference construct Nanobody A-35GS- Nanobody B (“Reference X”). All of the constructs (except for the reference constructs) had, were indicated, a C-terminal alanine residue as well as, in each of the “Nanobody A” and “Nanobody B” building blocks, the indicated mutations.

Table L: trivalent constructs tested.

Trivalent constructs	Mutation(s)					
	L11V	T87A	V89L	T110K	T110Q	114A
The constructs (except for the reference constructs) had, were indicated, a C-terminal alanine residue as well as, in each of the building blocks, the indicated mutations.						
Reference X (= Nanobody A-35GS-Nanobody A-35GS-Nanobody B)						
Reference X + C-terminal Ala						x
Reference X + L11V + V89L + C-terminal Ala	x		x			x
Reference X + L11V + V89L + T110K+ C-terminal Ala	x		x	x		x
Reference X + L11V + T87A+ V89L + C-terminal Ala	x	x	x			x
Reference X + L11V + V89L + T110Q+ C-terminal Ala	x		x		x	x

Table M: bivalent constructs tested.

Bivalent constructs	Mutation(s)					
	L11V	T87A	V89L	T110K	T110Q	114A
The constructs (except for the reference constructs) had, were indicated, a C-terminal alanine residue as well as, in each of the building blocks, the indicated mutations.						
Reference Y (= Nanobody A-35GS- Nanobody B)						
Reference Y + C-terminal Ala						x
Reference Y + L11V + V89L + C-terminal Ala	x		x			x
Reference Y + L11V + V89L + T110K+ C-terminal Ala	x		x	x		x
Reference Y + L11V + T87A+ V89L + C-terminal Ala	x	x	x			x
Reference Y + L11V + V89L + T110Q+ C-terminal Ala	x		x		x	x

Table N: results of testing trivalent constructs for binding by pre-existing antibodies present in 98 serum samples obtained from healthy human volunteers. Results are also represented in Figure 6 as a plot in which each dot represents a data point collected by testing of the indicated construct against one of the 98 serum samples.

Nanobody tested on 98 samples (healthy subjects)	Lane number in the plot shown in Figure 6	Binding level at 125 seconds < 10 RU	Binding level at 125 seconds < 20 RU	Binding level at 125 seconds > 20 RU
Reference X	(1)	38	48	50
Reference X + C-terminal Ala	(2)	64	75	23
Reference X + L11V + V89L + C-terminal Ala	(3)	94	95	3
Reference X + L11V + V89L + T110K + C-terminal Ala	(5)	95	96	2
Reference X + L11V + V89L + T110Q + C-terminal Ala	(6)	95	96	2
Reference X + L11V + T87A + V89L + C-terminal Ala	(4)	92	95	3

Table O: results of testing trivalent constructs for binding by pre-existing antibodies present in 30 selected serum samples obtained from healthy human volunteers. The 30 samples used were pre-selected for either having a known high titer of pre-existing antibodies or because it was known that the pre-existing antibodies present in the sample still has a high degree of binding even if a C-terminal alanine residue is present. Results are also represented in Figure 7 as a plot in which each dot represents a data point collected by testing of the indicated construct against one of the selected 30 serum samples.

Nanobody tested on selected set of 30 samples	Lane number in the plot shown in Figure 7	Binding level at 125 seconds < 10 RU	Binding level at 125 seconds < 20 RU	Binding level at 125 seconds > 20 RU
Reference X + C-terminal Ala	(1)	12	13	17
Reference X + L11V + V89L + C-terminal Ala	(2)	18	22	8
Reference X + L11V + T87A + V89L + C-terminal Ala	(3)	27	27	3
Reference X + L11V + V89L + T110K + C-terminal Ala	(4)	26	26	4

Table P: results of testing bivalent constructs for binding by pre-existing antibodies present in 98 serum samples obtained from healthy human volunteers. Results are also represented in Figure 8 as a plot in which each dot represents a data point collected by testing of the indicated construct against one of the 98 serum samples.

Nanobody tested on 98 samples (healthy subjects)	Lane number in the plot shown in Figure 8	Binding level at 125 seconds < 10 RU	Binding level at 125 seconds < 20 RU	Binding level at 125 seconds > 20 RU
Reference Y	(1)	54	67	31
Reference Y + C-terminal Ala	(2)	90	92	6
Reference Y + L11V + V89L + C-terminal Ala	(3)	97	98	0
Reference Y + L11V + T87A + V89L + C-terminal Ala	(4)	98	98	0
Reference Y + L11V + V89L + T110K + C-terminal Ala	(5)	96	98	0
Reference Y + L11V + V89L + T110Q + C-terminal Ala	(6)	98	98	0

Three representative trivalent constructs were also tested against serum samples obtained from SLE patients. The results are shown in Table Q.

Table Q: testing of representative trivalent constructs against serum samples obtained from HLE patients.

The constructs (had, were indicated, a C-terminal alanine residue as well as, in each of the building blocks, the indicated mutations.		Mutation(s)		Samples obtained from SLE patients		Sample from healthy volunteer								
		L11V	T87A	V89L	T110K	T110Q	II4A	SL3E25	SL3E37	SL3E39	SL3E41	NB13025-14	004-030-ABL-	02
Average binding to [Reference X + C-terminal Ala]														
Reference X + C-terminal alanine									142	194	126	108	102	27
Inhibition compared to average binding to [Reference X + C-terminal Ala] captured on HSA (%)														
Reference X + L11V+ V89L + C-terminal alanine	x	x	x			x	x	100	95	100	88	100	0	
Reference X + L11V+ V89L+ T110K + C-terminal alanine	x	x	x	x	x	x	x	100	76	100	100	100	100	
Reference X + L11V+87A + V89L + C-terminal alanine	x	x	x	x	x	x	x	100	100	100	100	97	100	

Example 7: Nanobodies and nanobody-constructs against the ion channel Kv1.3.

In one specific aspect, the VH domains of the invention (and in particular ISVDs of the invention and more in particular Nanobodies of the invention) and compounds of the invention may be directed against the ion channel Kv.1.3.

The co-pending US provisional application USSN 62/014,023 (title: "*Kv1.3 binding immunoglobulins*"; assignee: Ablynx N.V.; filing date: June 18, 2014) as well as the subsequent filed US provisional application of the same title filed on March 16, 2015 (assignee: Ablynx N.V.) *inter alia* describe immunoglobulin single variable domains (and in particular Nanobodies) that are directed against the potassium selective voltage-gated ion channel Kv1.3, as well as proteins, polypeptides and other Nanobody-based constructs that comprise at least one such Nanobody against Kv1.3.

The mutations described in the present application (optionally suitably combined with a C-terminal extension as described in herein and/or in WO 12/175741) may also be suitably applied to the Nanobodies, proteins, polypeptides and other Nanobody-based constructs against Kv1.3 that are described in these two US provisional applications.

Thus, in one aspect, the invention relates to a VH domain that is directed against Kv1.3 and that is as further described herein for the ISVD's of the invention (i.e. comprising the amino acid residues/mutations as described herein).

Again, as with other aspects and embodiments of the invention described herein, when a specific ISVD (such as the ISVD against Kv1.3 described in this Example) or compound comprising the same is said to be "according to the invention" or "as further described herein", the preferred aspects/embodiments and preferences that are generally described herein for the ISVD's or compounds of the invention also specifically apply to said specific ISVD or compound, respectively, unless explicitly indicated otherwise or unless the specific technical context requires otherwise.

Thus, in a particular aspect, the present invention relates to a VH domain that is directed against Kv1.3, in which (i) position 112 is K or Q; or (ii) position 110 is K or Q and position 11 is V; or (iii) position 89 is T; or (iv) position 89 is L and position 110 is K or Q; or (v) position 11 is V and position 89 is L; or any suitable combination of (i) to (v). In particular, in such VH domains against Kv1.3:

- the amino acid residue at position 11 is preferably chosen from L, V or K (and is most preferably V); and
- the amino acid residue at position 14 is preferably suitably chosen from A or P; and

- the amino acid residue at position 41 is preferably suitably chosen from A or P; and
- the amino acid residue at position 89 is preferably suitably chosen from T, V or L; and
- the amino acid residue at position 108 is preferably suitably chosen from Q or L; and
- the amino acid residue at position 110 is preferably suitably chosen from T, K or Q; and
- the amino acid residue at position 112 is preferably suitably chosen from S, K or Q;

such that either (i) position 112 is K or Q; or (ii) position 110 is K or Q and position 11 is V; or (iii) position 89 is T; or (iv) position 89 is L and position 110 is K or Q; or (v) position 11 is V and position 89 is L; or any suitable combination of (i) to (v).

The VH domains against Kv1.3 referred to in this Example may in particular have CDR's that are as described on pages 5-10 of USSN 62/014,023 (including any preferred aspects/embodiments of such CDRs) or sequence-optimized versions thereof, as described in the other US provisional application referred to above.

In particular, the VH domains against Kv 1.3 referred to in this Example may in particular have a combination of CDR1, CDR2 and CDR3 that is chosen from one of the combination of CDR 1, CDR2 and CDR3 that are listed as preferred aspects in the list that bridges pages 9 and 10 of USSN 62/014,023.

In some preferred, but non-limiting aspect of the inventions:

- in a VH domain of the invention: (i) CDR1 (according to Kabat) is the sequence of SED ID NO:166 or an amino acid sequence that has one or two amino acid differences with the sequence of SEQ ID NO:166; (ii) CDR2 (according to Kabat) is the sequence of SED ID NO:167 or an amino acid sequence that has one or two amino acid differences with the sequence of SEQ ID NO:167; and (iii) CDR3 (according to Kabat) is the sequence of SED ID NO:168 or an amino acid sequence that has one or two amino acid differences with the sequence of SEQ ID NO:168; and even more preferably: (i) CDR1 (according to Kabat) is the sequence of SED ID NO:166; (ii) CDR2 (according to Kabat) is the sequence of SED ID NO:167; and (iii) CDR3 (according to Kabat) is the sequence of SED ID NO:168; and/or
- in a VH domain of the invention: (i) CDR1 (according to Abm) is the sequence of SED ID NO:169 or an amino acid sequence that has one or two amino acid differences with the sequence of SEQ ID NO:169; (ii) CDR2 (according to Abm) is the sequence of SED ID NO:170 or an amino acid sequence that has one or two amino acid differences with the sequence of SEQ ID NO:170; and (iii) CDR3 (according to Abm) is the sequence of SED ID NO:171 or an amino acid sequence that has one or two amino acid differences with the

sequence of SEQ ID NO:171; and even more preferably: (i) CDR1 (according to Abm) is the sequence of SED ID NO:169; (ii) CDR2 (according to Abm) is the sequence of SED ID NO:170; and (iii) CDR3 (according to Abm) is the sequence of SED ID NO:178.

The VH domains of the invention against Kv1.3 may further be as described herein and may again in particular be an ISVD (and more in particular a Nanobody) against Kv1.3 or a protein, polypeptide or other compound or construct that comprises at least one such ISVD. Such a protein, polypeptide or other compound or construct may also be as further described herein, and may for example have an increased half-life (i.e. as described herein, e.g. a half-life - expressed as $t_{1/2}$ beta - in human subjects of in human subjects of at least 1 day, preferably at least 3 days, more preferably at least 7 days, such as at least 10 days), and for this purpose may for example comprise a serum-albumin binding Nanobody, which may also be a serum-albumin binding Nanobody of the invention (again, as described herein).

Also, such an ISVD may suitably have a C-terminal extension (as further described herein and in WO 12/175741), in particular when said ISVD forms the C-terminal end of a protein, polypeptide or other compound or construct comprising the same (again, as further described herein).

For example and without limitation, the VH domains of the invention against Kv1.3 may be one of the sequences listed in Table A-1 of USSN 62/014,023 (SEQ ID NO's: 1 to 123 in USSN 62/014,023) or one of the sequences of listed in Table A-1 of US provisional application entitled "*Kv1.3 binding immunoglobulins*" (assignee: Ablynx N.V.; filing date: March 16, 2015) (SEQ ID NO's: 1 to 123, 495, 498 to 513 or 523 to 540 in said US provisional; and in particular the sequence of SEQ ID NO: 495), but suitably with the mutations/specific amino acid residues described herein for the ISVDs of the invention, and optionally suitably with a C-terminal extension.

In one specific aspect, a Nanobody of the invention against Kv1.3 is a variant of the Nanobody of SEQ ID NO:137 (with at least 90% sequence identity with SEQ ID NO:137), in which:

- the amino acid residue at position 11 is preferably chosen from L, V or K (and is most preferably V); and
- the amino acid residue at position 14 is preferably suitably chosen from A or P; and
- the amino acid residue at position 41 is preferably suitably chosen from A or P; and
- the amino acid residue at position 89 is preferably suitably chosen from T, V or L; and
- the amino acid residue at position 108 is preferably suitably chosen from Q or L; and

- the amino acid residue at position 110 is preferably suitably chosen from T, K or Q; and
- the amino acid residue at position 112 is preferably suitably chosen from S, K or Q;

such that either (i) position 112 is K or Q; or (ii) position 110 is K or Q and position 11 is V; or (iii) position 89 is T; or (iv) position 89 is L and position 110 is K or Q; or (v) position 11 is V and position 89 is L; or any suitable combination of (i) to (v).

Some specifically preferred, but non-limiting examples of Nanobodies of the invention against Kv1.3 and of compounds of the invention comprising the same are listed in Figure 9A (monovalent Nanobodies: SEQ ID NO's: 138 to 155) and Figure 9B (trivalent bispecific half-life extended constructs: SEQ ID NO's: 156 to 164). Compounds of the invention that comprise or essentially consist of at least one (such as one, two or three) anti-Kv1.3 Nanobody chosen from the anti-Kv1.3 Nanobodies of SEQ ID NO's: 138 to 155 form a further aspect of the invention. Also, each of the compounds of SEQ ID NO's: 156 to 164 forms a further aspect of the invention. In one specific aspect, such compounds contain two such Nanobodies of the invention against Kv1.3 and one Nanobody against human serum albumin (which is preferably also a Nanobody of the invention). Also, again, such a construct may contain suitable linkers and a C-terminal extension.

The monovalent anti-Kv1.3 Nanobodies of SEQ ID NO's: 138 to 155 were generated by introducing the L11V and V89L mutations of the invention into the starting sequence of SEQ ID NO: 137 (reference). In addition, different combinations of humanizing (or other sequence-optimizing) mutations were introduced, such as E1D, A14P, G19R, M53A or M53Q or M53Y, T62S, A74S, K83R, S94G and/or T97E). The specific mutations introduced in each of the sequences of SEQ ID NO: 138 to 155 is given in Figure 9A.

Some of the monovalent anti-Kv1.3 Nanobodies from Figure 9A were also formatted as trivalent bispecific constructs comprising two Nanobodies of the invention against Kv1.3 and one half-life extending Nanobody of the invention against human serum albumin (SEQ ID NO:109, also referred to as "ALB-82" in Figure 9B). 35GS linkers were used, and all the constructs have a C-terminal extension (a single C-terminal alanine residue). The sequences of the resulting constructs are given in SEQ ID NO's 156 to 164. Of these, three constructs (SEQ ID NOs: 156, 157 and 160) were tested for binding by pre-existing antibodies in samples obtained from 47 diabetic human subjects and 90 healthy human subjects, using the general protocol described herein. The binding by pre-existing antibodies by samples from these two sets were compared to the reference construct of SEQ ID NO:165, which is a corresponding trivalent bispecific construct based on the reference anti-Kv1.3 building block

of SEQ ID NO:137 and the serum albumin binder Alb-8 (SEQ ID NO:46), again combined with a C-terminal alanine extension. The results are shown in Figure 10 (samples from 47 diabetic patients) and Figure 11 (samples from 90 healthy volunteers). In each case, the constructs with the L11V and V89L mutations of the invention showed reduced binding by pre-existing antibodies compared to the reference construct.

Example 8: VH domains (and in particular Nanobodies) against IL-23, and compounds of the invention comprising the same.

In one specific aspect, the VH domains of the invention (and in particular ISVDs of the invention and more in particular Nanobodies of the invention) and compounds of the invention may be directed against IL-23.

Such a VH domain of the invention against IL-23 will generally comprise: (i) suitable framework sequences that suitably comprise the amino acid residues/mutations of the invention as described herein; as well as (ii) CDR sequences that allow the VH domain of the invention to specifically bind to IL-23. In addition, such a VH domain of the invention against IL-23 may also suitably have a C-terminal extension as described herein, in particular when said VH domain is monovalent or forms the C-terminal end of the compound of the invention in which said VH domain is present (again, as further described herein). Such VH domains of the invention against IL-23 may further be as further described herein, and may in particular be ISVD's.

Again, as with other aspects and embodiments of the invention described herein, when a specific ISVD (such as the ISVD against IL-23 described in this Example) or compound comprising the same is said to be "according to the invention" or "as further described herein", the preferred aspects/embodiments and preferences that are generally described herein for the ISVD's or compounds of the invention also specifically apply to said specific ISVD or compound, respectively, unless explicitly indicated otherwise or unless the specific technical context requires otherwise.

Thus, in a particular aspect, the present invention relates to a VH domain (and in particular an ISVD) that is directed against IL-23, in which (i) position 112 is K or Q; or (ii) position 110 is K or Q and position 11 is V; or (iii) position 89 is T; or (iv) position 89 is L and position 110 is K or Q; or (v) position 11 is V and position 89 is L; or any suitable combination of (i) to (v). In particular, in such VH domains against IL-23:

- the amino acid residue at position 11 is preferably chosen from L, V or K (and is most preferably V); and
- the amino acid residue at position 14 is preferably suitably chosen from A or P; and
- the amino acid residue at position 41 is preferably suitably chosen from A or P; and
- the amino acid residue at position 89 is preferably suitably chosen from T, V or L; and
- the amino acid residue at position 108 is preferably suitably chosen from Q or L; and
- the amino acid residue at position 110 is preferably suitably chosen from T, K or Q; and
- the amino acid residue at position 112 is preferably suitably chosen from S, K or Q;

such that either (i) position 112 is K or Q; or (ii) position 110 is K or Q and position 11 is V; or (iii) position 89 is T; or (iv) position 89 is L and position 110 is K or Q; or (v) position 11 is V and position 89 is L; or any suitable combination of (i) to (v).

The VH domains of the invention against IL-23 may further be as described herein and may again in particular be an ISVD (and more in particular a Nanobody) against IL-23 or a protein, polypeptide or other compound or construct that comprises as least one such ISVD. Such a protein, polypeptide or other compound or construct may also be as further described herein, and may for example have an increased half-life (i.e. as described herein, e.g. a half-life - expressed as $t_{1/2}$ beta - in human subjects of in human subjects of at least 1 day, preferably at least 3 days, more preferably at least 7 days, such as at least 10 days), and for this purpose may for example comprise a serum-albumin binding Nanobody, which may also be a serum-albumin binding Nanobody of the invention (again, as described herein).

Also, such an ISVD may suitably have a C-terminal extension (as further described herein and in WO 12/175741), in particular when said ISVD forms the C-terminal end of a protein, polypeptide or other compound or construct comprising the same (again, as further described herein).

In one preferred aspect, the VH domains of the invention against IL-23 comprise (i) a CDR1 sequence that is the sequence of SEQ ID NO: 173 (which is preferred) or that is an amino acid sequence that has only one amino acid difference with the sequence of SEQ ID NO: 173; (ii) a CDR2 sequence that is the sequence of SEQ ID NO: 174 (which is preferred) or that is an amino acid sequence that has only one or two amino acid differences with the sequence of SEQ ID NO: 174; and (iii) a CDR3 sequence that is the sequence of SEQ ID NO: 175 (which is preferred) or that is an amino acid sequence that has only one or two amino acid differences with the sequence of SEQ ID NO: 175.

More preferably, in a VH domain of the invention against IL-23 according to this aspect: (i) CDR1 is SEQ ID NO:173; (ii) CDR2 is SEQ ID NO: 174; and (iii) CDR3 is SEQ ID NO: 175.

In one specific aspect, a Nanobody of the invention against IL-23 is a variant of the Nanobody of SEQ ID NO:172 (with at least 90% sequence identity, such as at least 95% sequence identity, with SEQ ID NO:172), in which:

- the amino acid residue at position 11 is preferably chosen from L, V or K (and is most preferably V); and
- the amino acid residue at position 14 is preferably suitably chosen from A or P; and
- the amino acid residue at position 41 is preferably suitably chosen from A or P; and
- the amino acid residue at position 89 is preferably suitably chosen from T, V or L; and
- the amino acid residue at position 108 is preferably suitably chosen from Q or L; and
- the amino acid residue at position 110 is preferably suitably chosen from T, K or Q; and
- the amino acid residue at position 112 is preferably suitably chosen from S, K or Q;

such that either (i) position 112 is K or Q; or (ii) position 110 is K or Q and position 11 is V; or (iii) position 89 is T; or (iv) position 89 is L and position 110 is K or Q; or (v) position 11 is V and position 89 is L; or any suitable combination of (i) to (v). The CDR's of such an ISV are preferably as defined in the preceding two paragraphs.

In another preferred aspect, the VH domains of the invention against IL-23 comprise (i) a CDR1 sequence that is the sequence of SEQ ID NO: 191 (which is preferred) or that is an amino acid sequence that has only one amino acid difference with the sequence of SEQ ID NO: 191; (ii) a CDR2 sequence that is the sequence of SEQ ID NO: 192 (which is preferred) or that is an amino acid sequence that has only one or two amino acid differences with the sequence of SEQ ID NO: 192; and (iii) a CDR3 sequence that is the sequence of SEQ ID NO: 193 (which is preferred) or that is an amino acid sequence that has only one or two amino acid differences with the sequence of SEQ ID NO: 193.

More preferably, in a VH domain of the invention against IL-23 according to this aspect: (i) CDR1 is SEQ ID NO: 191; (ii) CDR2 is SEQ ID NO: 192; and (iii) CDR3 is SEQ ID NO: 193.

In one specific aspect, a Nanobody of the invention against IL-23 is a variant of the Nanobody of SEQ ID NO:172 (with at least 90% sequence identity, such as at least 95% sequence identity, with SEQ ID NO:190), in which:

- the amino acid residue at position 11 is preferably chosen from L, V or K (and is most preferably V); and
- the amino acid residue at position 14 is preferably suitably chosen from A or P; and
- the amino acid residue at position 41 is preferably suitably chosen from A or P; and
- the amino acid residue at position 89 is preferably suitably chosen from T, V or L; and
- the amino acid residue at position 108 is preferably suitably chosen from Q or L; and
- the amino acid residue at position 110 is preferably suitably chosen from T, K or Q; and
- the amino acid residue at position 112 is preferably suitably chosen from S, K or Q;

such that either (i) position 112 is K or Q; or (ii) position 110 is K or Q and position 11 is V; or (iii) position 89 is T; or (iv) position 89 is L and position 110 is K or Q; or (v) position 11 is V and position 89 is L; or any suitable combination of (i) to (v). Again, the CDR's of such an ISV are preferably as defined in the preceding two paragraphs.

Some specifically preferred, but non-limiting examples of such Nanobodies of the invention against IL-23 are listed in Figure 12A as SEQ ID NO's: 176 to 189 and Figure 12B as SEQ ID NO's: 194 to 207, respectively; and each of these Nanobodies form a further aspect of the invention.

The invention also relates to a compound of the invention against IL-23 that comprises at least one (such as one, two or three) of the Nanobodies of the invention of SEQ ID NO's: 176 to 189 and/or 194 to 207. Such compounds of the invention against IL-23 may again be as further described herein, and thus for example may comprise suitable linkers, may comprise a C-terminal extension as described herein, and may be half-life extended (for example because they comprise a Nanobody against human serum albumin, such as (preferably) a Nanobody of the invention against human serum albumin). Reference is made to Table R below.

As described in for example WO 2009/068627, WO 2010/142534 and WO2011/135026, on particularly preferred class of Nanobody-based compounds against IL-23 are biparatopic compounds. Thus, in one aspect of the invention, a compound of the invention against IL-23 is a biparatopic construct that comprises one ISV that is either SEQ ID NO: 172 or (preferably) an ISV of the invention that has been derived from SEQ ID NO:172 (as described in this Example 8) and one ISV that is either SEQ ID NO: 190 or (preferably) an ISV of the invention that has been derived from SEQ ID NO: 190 (as described in this Example 8), provided that at least one (and preferably both) of these ISV's are ISV's of the invention. Such biparatopic constructs may also be half-life extended (i.e. by

means of a serum albumin-binding ISV). Some specific examples of such biparatopic constructs are given in SEQ ID NO: 514 to 549.

Some specifically preferred examples of compounds of the invention against IL-23 are given in Figure 22 as SEQ ID NO's: 514 to 549; and each of these compounds form a further aspect of the invention. Thus, in another aspect, the invention relates to a polypeptide that is directed against IL-23 and that has an amino acid sequence that is chosen from the group consisting of SEQ ID NO's: 514 to 549. More generally, compounds of the invention against IL-23 may be as described in WO 2009/068627, WO 2010/142534 and WO2011/135026, but comprising ISV's of the invention. They may also be used for the purposes described in WO 2009/068627, WO 2010/142534 and WO2011/135026.

Table R: Examples of compounds of the invention against II-23.

Polypeptide/ construct ¹)	General formula	ISV building blocks and linkers
Monovalent	[IL-23]	[IL-23] = one of SEQ ID NO's: 464 to 477 and/or 482 to 495
Monovalent/ C-terminal extension	[IL-23]-X(n)	[IL-23] = one of SEQ ID NO's: 464 to 477 and/or 482 to 495
Monovalent/ half-life extended	[IL-23]-L _t -[SA] [SA]-L _t -[IL-23]	[IL-23] = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 [SA] = (see legend below) L _t = (see legend below)
Monovalent/ half-life extended/C- terminal extension	[IL-23] - L _t - [SA]-X(n) [SA]- L _t -[IL-23] -X(n)	[IL-23] = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 [SA] = (see legend below) L _t = (see legend below) X(n) = (see legend below)
Bivalent ²)	[IL-23]-L _t -[IL-23]	At least one [IL-23] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 ⁽⁴⁾ L _t = (see legend below)

Table R (continued)

Polypeptide/ construct(¹)	General formula	ISV building blocks and linkers
Bivalent/ C-terminal extension(²)	[IL-23]- L ₁ -[IL-23]-X(n)	At least one [IL-23] = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (⁴) L ₁ = (see legend below) X(n) = (see legend below)
Bivalent/ half-life extended(²)	[IL-23]- L ₁ -[IL-23]- L ₂ -[SA] [IL-23]- L ₁ -[SA]- L ₂ -[IL-23] [SA]- L ₁ -[IL-23]- L ₂ -[IL-23]	At least one [IL-23] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (⁴) [SA] = (see legend below) L ₁ = (see legend below) L ₂ = (see legend below)
Bivalent/ half-life extended/ C-terminal extension(²)	[IL-23]- L ₁ -[IL-23]- L ₂ -[SA] -X(n) [IL-23]- L ₁ -[SA]- L ₂ -[IL-23] -X(n) [SA]- L ₁ -[IL-23]- L ₂ -[IL-23] -X(n)	At least one [IL-23] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (⁴) [SA] = (see legend below) L ₁ = (see legend below) L ₂ = (see legend below) X(n) = (see legend below)

Table R (continued)

Polypeptide/ construct(⁴)	General formula	ISV building blocks and linkers
Bispecific (2)	$[\text{IL-23}] \cdot L_1 \cdot [\text{Nb}]$ $[\text{Nb}] \cdot L_1 \cdot [\text{IL-23}]$ $[\text{IL-23}] \cdot L_1 \cdot [\text{IL-23}] \cdot L_2 \cdot [\text{Nb}]$ $[\text{IL-23}] \cdot L_1 \cdot [\text{Nb}] \cdot L_2 \cdot [\text{IL-23}]$ $[\text{Nb}] \cdot L_1 \cdot [\text{IL-23}] \cdot L_2 \cdot [\text{IL-23}]$	<p>At least one [IL-23] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (⁴)</p> <p>L_1 = (see legend below)</p> <p>L_2 = (see legend below)</p> <p>[\Nb] = (see legend below)</p>
Bispecific/ C-terminal extension (3)	$[\text{IL-23}] \cdot L_1 \cdot [\text{Nb}] \cdot X(n)$ $[\text{Nb}] \cdot L_1 \cdot [\text{IL-23}] \cdot X(n)$ $[\text{IL-23}] \cdot L_1 \cdot [\text{IL-23}] \cdot L_2 \cdot [\text{Nb}] \cdot X(n)$ $[\text{IL-23}] \cdot L_1 \cdot [\text{Nb}] \cdot L_2 \cdot [\text{IL-23}] \cdot X(n)$ $[\text{Nb}] \cdot L_1 \cdot [\text{IL-23}] \cdot L_2 \cdot [\text{IL-23}] \cdot X(n)$	<p>At least one [IL-23] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (⁴)</p> <p>L_1 = (see legend below)</p> <p>L_2 = (see legend below)</p> <p>$X(n)$ = (see legend below)</p> <p>[\Nb] = (see legend below)</p>
Bispecific/ half-life extended (4)	$[\text{IL-23}] \cdot L_1 \cdot [\text{Nb}] \cdot L_2 \cdot [\text{SA}]$ $[\text{IL-23}] \cdot L_1 \cdot [\text{SA}] \cdot L_2 \cdot [\text{Nb}]$ $[\text{Nb}] \cdot L_1 \cdot [\text{SA}] \cdot L_2 \cdot [\text{IL-23}]$ $[\text{Nb}] \cdot L_1 \cdot [\text{IL-23}] \cdot L_2 \cdot [\text{SA}]$ $[\text{SA}] \cdot L_1 \cdot [\text{IL-23}] \cdot L_2 \cdot [\text{Nb}]$ $[\text{SA}] \cdot L_1 \cdot [\text{Nb}] \cdot L_2 \cdot [\text{IL-23}]$	<p>At least one [IL-23] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (⁴)</p> <p>[\SA] = (see legend below)</p> <p>L_1, L_2, L_3 (see legend below)</p> <p>[\Nb] = (see legend below)</p>

Table R (continued)

Polypeptide/ construct(¹)	General formula	ISV building blocks and linkers
Bispecific/ half-life extended (³)	$[\text{IL-23}] \cdot L_1 \cdot [\text{IL-23}] \cdot L_2 \cdot [\text{Nb}] \cdot L_3 \cdot [\text{SA}]$ $[\text{Nb}] \cdot L_1 \cdot [\text{IL-23}] \cdot L_2 \cdot [\text{IL-23}] \cdot L_3 \cdot [\text{SA}]$ $[\text{SA}] \cdot L_1 \cdot [\text{IL-23}] \cdot L_2 \cdot [\text{Nb}] \cdot L_3 \cdot [\text{IL-23}]$ $[\text{SA}] \cdot L_1 \cdot [\text{IL-23}] \cdot L_2 \cdot [\text{Nb}] \cdot L_3 \cdot [\text{IL-23}]$ $[\text{IL-23}] \cdot L_1 \cdot [\text{Nb}] \cdot L_2 \cdot [\text{IL-23}] \cdot L_3 \cdot [\text{SA}]$	At least one [IL-23] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (⁴) [SA] = (see legend below) L ₁ , L ₂ , L ₃ (see legend below) [Nb] = (see legend below)
Bispecific/ half-life extended/ C-terminal extension (³)	$[\text{IL-23}] \cdot L_1 \cdot [\text{Nb}] \cdot L_2 \cdot [\text{SA}] \cdot X(n)$ $[\text{IL-23}] \cdot L_1 \cdot [\text{SA}] \cdot L_2 \cdot [\text{Nb}] \cdot X(n)$ $[\text{Nb}] \cdot L_1 \cdot [\text{SA}] \cdot L_2 \cdot [\text{IL-23}] \cdot X(n)$ $[\text{Nb}] \cdot L_1 \cdot [\text{IL-23}] \cdot L_2 \cdot [\text{SA}] \cdot X(n)$ $[\text{SA}] \cdot L_1 \cdot [\text{IL-23}] \cdot L_2 \cdot [\text{Nb}] \cdot X(n)$ $[\text{SA}] \cdot L_1 \cdot [\text{Nb}] \cdot L_2 \cdot [\text{IL-23}] \cdot X(n)$ $[\text{IL-23}] \cdot L_1 \cdot [\text{IL-23}] \cdot L_2 \cdot [\text{Nb}] \cdot L_3 \cdot [\text{SA}] \cdot X(n)$ $[\text{Nb}] \cdot L_1 \cdot [\text{IL-23}] \cdot L_2 \cdot [\text{IL-23}] \cdot L_3 \cdot [\text{SA}] \cdot X(n)$ $[\text{SA}] \cdot L_1 \cdot [\text{IL-23}] \cdot L_2 \cdot [\text{Nb}] \cdot L_3 \cdot [\text{IL-23}] \cdot X(n)$ $[\text{SA}] \cdot L_1 \cdot [\text{IL-23}] \cdot L_2 \cdot [\text{Nb}] \cdot L_3 \cdot [\text{IL-23}] \cdot X(n)$ $[\text{IL-23}] \cdot L_1 \cdot [\text{Nb}] \cdot L_2 \cdot [\text{IL-23}] \cdot L_3 \cdot [\text{SA}] \cdot X(n)$	At least one [IL-23] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (⁴) [SA] = (see legend below) L ₁ , L ₂ , L ₃ (see legend below) X(n) = (see legend below) [Nb] = (see legend below)

Table R (continued)

Legend:	<ul style="list-style-type: none"> - [SA] is an ISV against (human) serum albumin, preferably an ISV of the invention against (human) serum albumin, more preferably one of SEQ ID NO's: 46 or 61 or even more preferably one of the ISVD's of the invention of SEQ ID NO's: 47, 54, 62, 69, 78, 86, 109, 116, 123, 130 or 496 to 513. - Each of L₁, L₂ and L₃ is (independently) a suitable linker. Each of L₁, L₂ and L₃ may (independently) be present or not. Non-limiting examples of suitable linkers are the gly-ser linkers referred to herein, such as the 9GS, 30GS or 35GS linker. - X(n) = a C-terminal extension as a C-terminal extension as described in herein and/or in WO 12/175741 - [Nb] is an ISV against another therapeutic target. 					
Notes:	<p>(1) In this Table:</p> <ul style="list-style-type: none"> - "Monovalent" generally refers to polypeptides/constructs comprising a single ISV against IL-23. These may further comprise a half-life extending ISV (such as an ISV against serum albumin). - "Bivalent" generally refers to polypeptides/constructs comprising two ISV's against IL-23 (which may be the same or different). These may again further comprise a half-life extending ISV (such as an ISV against serum albumin). - "Bispecific" generally refers to polypeptides/constructs comprising at least one (such as 1 or 2) ISV's against IL-23 and at least one (such as 1 or 2) other ISV against a therapeutic target. These may further comprise a half-life extending ISV (such as an ISV against serum albumin). - In the polypeptides/constructs described in this table, at least one of the ISV's against IL-23 present is an ISV of the invention, and preferably all of the ISV's against IL-23 present in such polypeptide/construct are ISV's of the invention. Also, when a half-life extending ISV and/or an ISV against another therapeutic target is present in such polypeptide/construct, each of these (and preferably all of these) may also be (and preferably are) ISV's of the invention (2): All "bivalent" constructs in this Table may also be biparatopic, meaning that they comprise at least two (such as two) ISV's against IL-23, which are directed against different epitopes on IL-23. <p>(3): As will be clear to the skilled person, other/further bispecific constructs than those listed can be made using the building blocks and linkers mentioned.</p> <p>(4) Preferably, each [IL-23] present is independently chosen from SEQ ID NO's: 464 to 477 and/or 482 to 495. Also, the [IL-23] present may be the same or different; in a biparatopic polypeptide/construct they will be directed against different epitopes on IL-23.</p> <p>(5) Each of the polypeptides/constructs mentioned to in this column by means of reference to a SEQ ID forms an individual specific aspect of the invention.</p>					

Example 9: VH domains (and in particular Nanobodies) against OX40-L, and compounds of the invention comprising the same.

In one specific aspect, the VH domains of the invention (and in particular ISVDs of the invention and more in particular Nanobodies of the invention) and compounds of the invention may be directed against OX40-L.

Such a VH domain of the invention against OX40-L will generally comprise: (i) suitable framework sequences that suitably comprise the amino acid residues/mutations of the invention as described herein; as well as (ii) CDR sequences that allow the VH domain of the invention to specifically bind to OX40-L. In addition, such a VH domain of the invention against OX40-L may also suitably have a C-terminal extension as described herein, in particular when said VH domain is monovalent or forms the C-terminal end of the compound of the invention in which said VH domain is present (again, as further described herein). Such VH domains of the invention against OX40-L may further be as further described herein, and may in particular be ISVD's.

Again, as with other aspects and embodiments of the invention described herein, when a specific ISVD (such as the ISVD against OX40-L described in this Example) or compound comprising the same is said to be "according to the invention" or "as further described herein", the preferred aspects/embodiments and preferences that are generally described herein for the ISVD's or compounds of the invention also specifically apply to said specific ISVD or compound, respectively, unless explicitly indicated otherwise or unless the specific technical context requires otherwise.

Thus, in a particular aspect, the present invention relates to a VH domain (and in particular an ISVD) that is directed against OX40-L, in which (i) position 112 is K or Q; or (ii) position 110 is K or Q and position 11 is V; or (iii) position 89 is T; or (iv) position 89 is L and position 110 is K or Q; or (v) position 11 is V and position 89 is L; or any suitable combination of (i) to (v). In particular, in such VH domains against OX40-L:

- the amino acid residue at position 11 is preferably chosen from L, V or K (and is most preferably V); and
- the amino acid residue at position 14 is preferably suitably chosen from A or P; and
- the amino acid residue at position 41 is preferably suitably chosen from A or P; and
- the amino acid residue at position 89 is preferably suitably chosen from T, V or L; and
- the amino acid residue at position 108 is preferably suitably chosen from Q or L; and
- the amino acid residue at position 110 is preferably suitably chosen from T, K or Q; and

- the amino acid residue at position 112 is preferably suitably chosen from S, K or Q; such that either (i) position 112 is K or Q; or (ii) position 110 is K or Q and position 11 is V; or (iii) position 89 is T; or (iv) position 89 is L and position 110 is K or Q; or (v) position 11 is V and position 89 is L; or any suitable combination of (i) to (v).

The VH domains of the invention against OX40-L may further be as described herein and may again in particular be an ISVD (and more in particular a Nanobody) against OX40-L or a protein, polypeptide or other compound or construct that comprises as least one such ISVD. Such a protein, polypeptide or other compound or construct may also be as further described herein, and may for example have an increased half-life (i.e. as described herein, e.g. a half-life - expressed as $t_{1/2}$ beta - in human subjects of in human subjects of at least 1 day, preferably at least 3 days, more preferably at least 7 days, such as at least 10 days), and for this purpose may for example comprise a serum-albumin binding Nanobody, which may also be a serum-albumin binding Nanobody of the invention (again, as described herein).

Also, such an ISVD may suitably have a C-terminal extension (as further described herein and in WO 12/175741), in particular when said ISVD forms the C-terminal end of a protein, polypeptide or other compound or construct comprising the same (again, as further described herein).

In one preferred aspect, the VH domains of the invention against OX40-L comprise (i) a CDR1 sequence that is the sequence of SEQ ID NO: 209 (which is preferred) or that is an amino acid sequence that has only one amino acid difference with the sequence of SEQ ID NO: 209; (ii) a CDR2 sequence that is the sequence of SEQ ID NO: 210 (which is preferred) or that is an amino acid sequence that has only one or two amino acid differences with the sequence of SEQ ID NO: 210; and (iii) a CDR3 sequence that is the sequence of SEQ ID NO: 211 (which is preferred) or that is an amino acid sequence that has only one or two amino acid differences with the sequence of SEQ ID NO: 211.

More preferably, in a VH domain of the invention against OX40-L according to this aspect: (i) CDR1 is SEQ ID NO:209; (ii) CDR2 is SEQ ID NO: 210; and (iii) CDR3 is SEQ ID NO: 211.

In one specific aspect, a Nanobody of the invention against OX40-L is a variant of the Nanobody of SEQ ID NO:208 (with at least 90% sequence identity, such as at least 95% sequence identity, with SEQ ID NO:208), in which:

- the amino acid residue at position 11 is preferably chosen from L, V or K (and is most preferably V); and

- the amino acid residue at position 14 is preferably suitably chosen from A or P; and
- the amino acid residue at position 41 is preferably suitably chosen from A or P; and
- the amino acid residue at position 89 is preferably suitably chosen from T, V or L; and
- the amino acid residue at position 108 is preferably suitably chosen from Q or L; and
- the amino acid residue at position 110 is preferably suitably chosen from T, K or Q; and
- the amino acid residue at position 112 is preferably suitably chosen from S, K or Q;

such that either (i) position 112 is K or Q; or (ii) position 110 is K or Q and position 11 is V; or (iii) position 89 is T; or (iv) position 89 is L and position 110 is K or Q; or (v) position 11 is V and position 89 is L; or any suitable combination of (i) to (v). The CDR's of such an ISV are preferably as defined in the preceding two paragraphs.

Some specifically preferred, but non-limiting examples of Nanobodies of the invention against OX40-L are listed in Figure 13 as SEQ ID NO's: 212 to 225; and each of these Nanobodies form a further aspect of the invention.

The invention also relates to a compound of the invention against OX40-L that comprises at least one (such as one, two or three) of the Nanobodies of the invention of SEQ ID NO's: 212 to 225. Such compounds of the invention against OX40-L may again be as further described herein, and thus for example may comprise suitable linkers, may comprise a C-terminal extension as described herein, and may be half-life extended (for example because they comprise a Nanobody against human serum albumin, such as (preferably) a Nanobody of the invention against human serum albumin). Reference is made to Table S below.

Some specifically preferred examples of compounds of the invention against OX40-L are given in Figure 23 as SEQ ID NO's: 550 to 585; and each of these compounds form a further aspect of the invention. Thus, in another aspect, the invention relates to a polypeptide that is directed against OX40-L and that has an amino acid sequence that is chosen from the group consisting of SEQ ID NO's: 550 to 585. More generally, compounds of the invention against OX40-L may be as described in WO 2011/073180, but comprising ISV's of the invention. They may also be used for the purposes described in WO 2011/073180.

Table S: Examples of compounds of the invention against OX40-L.

Polypeptide/ construct¹⁾	General formula	ISV building blocks and linkers
Monovalent	[OX40-L]	[OX40-L] = one of SEQ ID NO's: 464 to 477 and/or 482 to 495
Monovalent/ C-terminal extension	[OX40-L]-X(n)	[OX40-L] = one of SEQ ID NO's: 464 to 477 and/or 482 to 495
Monovalent/ half-life extended	[OX40-L]-L ₁ -[SA] [SA]-L ₁ -[OX40-L]	[OX40-L] = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 [SA] = (see legend below) L ₁ = (see legend below)
Monovalent/ half-life extended/C- terminal extension	[OX40-L]-L ₁ -[SA]-X(n) [SA]-L ₁ -[OX40-L]-X(n)	[OX40-L] = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 [SA] = (see legend below) L ₁ = (see legend below) X(n) = (see legend below)
Bivalent(²)	[OX40-L]-L ₁ -[OX40-L]	At least one [OX40-L] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (⁴) L ₁ = (see legend below)

Table S (continued)

Polypeptide/ construct ¹)	General formula	ISV building blocks and linkers
Bivalent/ C-terminal extension ²)	[OX40-L]- L ₁ -[OX40-L] -X(n)	At least one [OX40-L] = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (⁴) L ₁ = (see legend below) X(n) = (see legend below)
Bivalent/ half-life extended ²)	[OX40-L]- L ₁ -[OX40-L]- L ₂ -[SA] [OX40-L]- L ₁ -[SA]- L ₂ -[OX40-L] [SA]- L ₁ -[OX40-L]- L ₂ -[OX40-L]	At least one [OX40-L] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (⁴) [SA] = (see legend below) L ₁ = (see legend below) L ₂ = (see legend below)
Bivalent/ half-life extended/ C-terminal extension ²)	[OX40-L]- L ₁ -[OX40-L]- L ₂ -[SA] -X(n) [OX40-L]- L ₁ -[SA]- L ₂ -[OX40-L] -X(n) [SA]- L ₁ -[OX40-L]- L ₂ -[OX40-L] -X(n)	At least one [OX40-L] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (⁴) [SA] = (see legend below) L ₁ = (see legend below) L ₂ = (see legend below) X(n) = (see legend below)

Table S (continued)

Polypeptide/ construct ⁽³⁾	General formula	ISV building blocks and linkers
Bispecific (3)	[OX40-L]-L ₁ -[Nb] [Nb]-L ₁ -[OX40-L] [OX40-L]-L ₁ -[OX40-L]-L ₂ -[Nb] [OX40-L]-L ₁ -[Nb]-L ₂ -[OX40-L] [Nb]-L ₁ -[OX40-L]-L ₂ -[OX40-L]	At least one [OX40-L] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (4) L ₁ = (see legend below) L ₂ = (see legend below) [Nb] = (see legend below)
Bispecific/ C-terminal extension (3)	[OX40-L]-L ₁ -[Nb]-X(n) [Nb]-L ₁ -[OX40-L]-X(n) [OX40-L]-L ₁ -[OX40-L]-L ₂ -[Nb]-X(n) [OX40-L]-L ₁ -[Nb]-L ₂ -[OX40-L]-X(n) [Nb]-L ₁ -[OX40-L]-L ₂ -[OX40-L]-X(n)	At least one [OX40-L] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (4) L ₁ = (see legend below) L ₂ = (see legend below) X(n) = (see legend below) [Nb] = (see legend below)
Bispecific/ half-life extended (3)	[OX40-L]-L ₁ -[Nb]-L ₂ -[SA] [OX40-L]-L ₁ -[SA]-L ₂ -[Nb] [Nb]-L ₁ -[SA]-L ₂ -[OX40-L] [Nb]-L ₁ -[OX40-L]-L ₂ -[SA] [SA]-L ₁ -[OX40-L]-L ₂ -[Nb] [SA]-L ₁ -[Nb]-L ₂ -[OX40-L]	At least one [OX40-L] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (4) [SA] = (see legend below) L ₁ , L ₂ , L ₃ (see legend below) [Nb] = (see legend below)

Table S (continued)

Polypeptide/ construct ¹⁾	General formula	ISV building blocks and linkers
Bispecific/ half-life extended ⁽³⁾	[OX40-L]-L ₁ -[OX40-L]-L ₂ -[Nb]-L ₃ -[SA] [Nb]-L ₁ -[OX40-L]-L ₂ -[OX40-L]-L ₃ -[SA] [SA]-L ₁ -[OX40-L]-L ₂ -[OX40-L]-L ₃ -[Nb] [SA]-L ₁ -[OX40-L]-L ₂ -[Nb]-L ₃ -[OX40-L] [OX40-L]-L ₁ -[Nb]-L ₂ -[OX40-L]-L ₃ -[SA]	At least one [OX40-L] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (') [SA] = (see legend below) L ₁ , L ₂ , L ₃ (see legend below) [Nb] = (see legend below)
Bispecific/ half-life extended/ C-terminal extension ⁽³⁾	[OX40-L]-L ₁ -[Nb]-L ₂ -[SA]-X(n) [OX40-L]-L ₁ -[SA]-L ₂ -[Nb]-X(n) [Nb]-L ₁ -[SA]-L ₂ -[OX40-L]-X(n) [Nb]-L ₁ -[OX40-L]-L ₂ -[SA]-X(n) [SA]-L ₁ -[OX40-L]-L ₂ -[Nb]-X(n) [SA]-L ₁ -[Nb]-L ₂ -[OX40-L]-X(n) [OX40-L]-L ₁ -[OX40-L]-L ₂ -[Nb]-L ₃ -[SA]-X(n) [Nb]-L ₁ -[OX40-L]-L ₂ -[OX40-L]-L ₃ -[SA]-X(n) [SA]-L ₁ -[OX40-L]-L ₂ -[OX40-L]-L ₃ -[Nb]-X(n) [SA]-L ₁ -[OX40-L]-L ₂ -[Nb]-L ₃ -[OX40-L]-X(n) [OX40-L]-L ₁ -[Nb]-L ₂ -[OX40-L]-L ₃ -[SA]-X(n)	At least one [OX40-L] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (') [SA] = (see legend below) L ₁ , L ₂ , L ₃ (see legend below) X(n) = (see legend below) [Nb] = (see legend below)

Table S (continued)

Legend:	<ul style="list-style-type: none"> - [SA] is an ISV against (human) serum albumin, preferably an ISV of the invention against (human) serum albumin, more preferably one of SEQ ID NO's: 46 or 61 or even more preferably one of the ISVD's of the invention of SEQ ID NO's: 47, 54, 62, 69, 78, 86, 109, 116, 123, 130 or 496 to 513. - Each of L₁, L₂ and L₃ is (independently) a suitable linker. Each of L₁, L₂ and L₃ may (independently) be present or not. Non-limiting examples of suitable linkers are the gly-ser linkers referred to herein, such as the 9GS, 30GS or 35GS linker. - X(n) = a C-terminal extension as a C-terminal extension as described in herein and/or in WO 12/175741 - [Nb] is an ISV against another therapeutic target.
Notes:	
(¹) In this Table:	
	<ul style="list-style-type: none"> - “<i>Monovalent</i>” generally refers to polypeptides/constructs comprising a single ISV against OX40-L. These may further comprise a half-life extending ISV (such as an ISV against serum albumin). - “<i>Bivalent</i>” generally refers to polypeptides/constructs comprising two ISV's against OX40-L (which may be the same or different). These may again further comprise a half-life extending ISV (such as an ISV against serum albumin). - “<i>Bispecific</i>” generally refers to polypeptides/constructs comprising at least one (such as 1 or 2) ISV's against OX40-L and at least one (such as 1 or 2) other ISV against a therapeutic target. These may again further comprise a half-life extending ISV (such as an ISV against serum albumin). - In the polypeptides/constructs described in this table, at least one of the ISV's against OX40-L present is an ISV of the invention, and preferably all of the ISV's against OX40-L present in such polypeptide/construct are ISV's of the invention. Also, when a half-life extending ISV and/or an ISV against another therapeutic target is present in such polypeptide/construct, each of these (and preferably all of these) may also be (and preferably are) ISV's of the invention (²): All “bivalent” constructs in this Table may also be biparatopic, meaning that they comprise at least two (such as two) ISV's against OX40-L, which are directed against different epitopes on OX40-L.
	(³): As will be clear to the skilled person, other/further bispecific constructs than those listed can be made using the building blocks and linkers mentioned.
	(⁴): Preferably, each [OX40-L] present is independently chosen from SEQ ID NO's: 464 to 477 and/or 482 to 495. Also, the [OX40-L] present may be the same or different; in a biparatopic polypeptide/construct they will be directed against different epitopes on OX40-L.
	(⁵): Each of the polypeptides/constructs mentioned to in this column by means of reference to a SEQ ID forms an individual specific aspect of the invention.

Example 10: VH domains (and in particular Nanobodies) against IgE, and compounds of the invention comprising the same.

In one specific aspect, the VH domains of the invention (and in particular ISVDs of the invention and more in particular Nanobodies of the invention) and compounds of the invention may be directed against IgE.

Such a VH domain of the invention against IgE will generally comprise: (i) suitable framework sequences that suitably comprise the amino acid residues/mutations of the invention as described herein; as well as (ii) CDR sequences that allow the VH domain of the invention to specifically bind to IgE. In addition, such a VH domain of the invention against IgE may also suitably have a C-terminal extension as described herein, in particular when said VH domain is monovalent or forms the C-terminal end of the compound of the invention in which said VH domain is present (again, as further described herein). Such VH domains of the invention against IgE may further be as further described herein, and may in particular be ISVD's.

Again, as with other aspects and embodiments of the invention described herein, when a specific ISVD (such as the ISVD against IgE described in this Example) or compound comprising the same is said to be "according to the invention" or "as further described herein", the preferred aspects/embodiments and preferences that are generally described herein for the ISVD's or compounds of the invention also specifically apply to said specific ISVD or compound, respectively, unless explicitly indicated otherwise or unless the specific technical context requires otherwise.

Thus, in a particular aspect, the present invention relates to a VH domain (and in particular an ISVD) that is directed against IgE, in which (i) position 112 is K or Q; or (ii) position 110 is K or Q and position 11 is V; or (iii) position 89 is T; or (iv) position 89 is L and position 110 is K or Q; or (v) position 11 is V and position 89 is L; or any suitable combination of (i) to (v). In particular, in such VH domains against IgE:

- the amino acid residue at position 11 is preferably chosen from L, V or K (and is most preferably V); and
- the amino acid residue at position 14 is preferably suitably chosen from A or P; and
- the amino acid residue at position 41 is preferably suitably chosen from A or P; and
- the amino acid residue at position 89 is preferably suitably chosen from T, V or L; and
- the amino acid residue at position 108 is preferably suitably chosen from Q or L; and
- the amino acid residue at position 110 is preferably suitably chosen from T, K or Q; and

- the amino acid residue at position 112 is preferably suitably chosen from S, K or Q; such that either (i) position 112 is K or Q; or (ii) position 110 is K or Q and position 11 is V; or (iii) position 89 is T; or (iv) position 89 is L and position 110 is K or Q; or (v) position 11 is V and position 89 is L; or any suitable combination of (i) to (v).

The VH domains of the invention against IgE may further be as described herein and may again in particular be an ISVD (and more in particular a Nanobody) against IgE or a protein, polypeptide or other compound or construct that comprises at least one such ISVD. Such a protein, polypeptide or other compound or construct may also be as further described herein, and may for example have an increased half-life (i.e. as described herein, e.g. a half-life - expressed as $t_{1/2}$ beta - in human subjects of in human subjects of at least 1 day, preferably at least 3 days, more preferably at least 7 days, such as at least 10 days), and for this purpose may for example comprise a serum-albumin binding Nanobody, which may also be a serum-albumin binding Nanobody of the invention (again, as described herein).

Also, such an ISVD may suitably have a C-terminal extension (as further described herein and in WO 12/175741), in particular when said ISVD forms the C-terminal end of a protein, polypeptide or other compound or construct comprising the same (again, as further described herein).

In one preferred aspect, the VH domains of the invention against IgE comprise (i) a CDR1 sequence that is the sequence of SEQ ID NO: 227 (which is preferred) or that is an amino acid sequence that has only one amino acid difference with the sequence of SEQ ID NO: 227; (ii) a CDR2 sequence that is the sequence of SEQ ID NO: 228 (which is preferred) or that is an amino acid sequence that has only one or two amino acid differences with the sequence of SEQ ID NO: 228; and (iii) a CDR3 sequence that is the sequence of SEQ ID NO: 229 (which is preferred) or that is an amino acid sequence that has only one or two amino acid differences with the sequence of SEQ ID NO: 229.

More preferably, in a VH domain of the invention against IgE according to this aspect: (i) CDR1 is SEQ ID NO: 227; (ii) CDR2 is SEQ ID NO: 228; and (iii) CDR3 is SEQ ID NO: 229.

In one specific aspect, a Nanobody of the invention against IgE is a variant of the Nanobody of SEQ ID NO: 226 (with at least 90% sequence identity, such as at least 95% sequence identity, with SEQ ID NO: 226), in which:

- the amino acid residue at position 11 is preferably chosen from L, V or K (and is most preferably V); and

- the amino acid residue at position 14 is preferably suitably chosen from A or P; and
- the amino acid residue at position 41 is preferably suitably chosen from A or P; and
- the amino acid residue at position 89 is preferably suitably chosen from T, V or L; and
- the amino acid residue at position 108 is preferably suitably chosen from Q or L; and
- the amino acid residue at position 110 is preferably suitably chosen from T, K or Q; and
- the amino acid residue at position 112 is preferably suitably chosen from S, K or Q;

such that either (i) position 112 is K or Q; or (ii) position 110 is K or Q and position 11 is V; or (iii) position 89 is T; or (iv) position 89 is L and position 110 is K or Q; or (v) position 11 is V and position 89 is L; or any suitable combination of (i) to (v). The CDR's of such an ISV are preferably as defined in the preceding two paragraphs.

Some specifically preferred, but non-limiting examples of Nanobodies of the invention against IgE are listed in Figure 14 as SEQ ID NO's: 230 to 243; and each of these Nanobodies form a further aspect of the invention.

The invention also relates to a compound of the invention against IgE that comprises at least one (such as one, two or three) of the Nanobodies of the invention of SEQ ID NO's: 230 to 243. Such compounds of the invention against IgE may again be as further described herein, and thus for example may comprise suitable linkers, may comprise a C-terminal extension as described herein, and may be half-life extended (for example because they comprise a Nanobody against human serum albumin, such as (preferably) a Nanobody of the invention against human serum albumin). Reference is made to Table T below.

Some specifically preferred examples of compounds of the invention against IgE are given in Figure 24 as SEQ ID NO's: 586 to 594; and each of these compounds form a further aspect of the invention. Thus, in another aspect, the invention relates to a polypeptide that is directed against IgE and that has an amino acid sequence that is chosen from the group consisting of SEQ ID NO's: 586 to 594.

More generally, compounds of the invention against IgE may be as described in WO 2012/175740 and the relevant parts of WO2012/175400, but comprising ISV's of the invention. They may also be used for the purposes described in WO 2012/175740.

Table T: Examples of compounds of the invention against IgE.

Polypeptide/ construct ¹⁾	General formula	ISV building blocks and linkers
Monovalent	[IgE]	[IgE] = one of SEQ ID NO's: 464 to 477 and/or 482 to 495
Monovalent/ C-terminal extension	[IgE]-X(n)	[IgE] = one of SEQ ID NO's: 464 to 477 and/or 482 to 495
Monovalent/ half-life extended	[IgE]- L ₁ -[SA] [SA]- L ₁ -[IgE]	[IgE] = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 [SA] = (see legend below) L ₁ = (see legend below)
Monovalent/ half-life extended/C- terminal extension	[IgE] - L ₁ - [SA]-X(n) [SA]- L ₁ -[IgE] -X(n)	[IgE] = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 [SA] = (see legend below) L ₁ = (see legend below) X(n) = (see legend below)
Bivalent ²⁾	[IgE]- L ₁ -[IgE]	At least one [IgE] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 ⁽⁴⁾ L ₁ = (see legend below)

Table T (continued)

Polypeptide/ construct ⁽¹⁾	General formula	ISV building blocks and linkers
Bivalent/ C-terminal extension ⁽²⁾	[IgE]-L ₁ -[IgE]-X(n)	<p>At least one [IgE] = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (')</p> <p>L₁ = (see legend below)</p> <p>X(n) = (see legend below)</p>
Bivalent/ half-life extended ⁽²⁾	$ \begin{aligned} &[\text{IgE}]-\text{L}_1\text{-}[\text{IgE}]\text{-}\text{L}_2\text{-}[\text{SA}] \\ &[\text{IgE}]\text{-}\text{L}_1\text{-}[\text{SA}]\text{-}\text{L}_2\text{-}[\text{IgE}] \\ &[\text{SA}]\text{-}\text{L}_1\text{-}[\text{IgE}]\text{-}\text{L}_2\text{-}[\text{IgE}] \end{aligned} $	<p>At least one [IgE] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (')</p> <p>[SA] = (see legend below)</p> <p>L₁ = (see legend below)</p> <p>L₂ = (see legend below)</p>
Bivalent/ half-life extended/ C-terminal extension ⁽²⁾	$ \begin{aligned} &[\text{IgE}]\text{-}\text{L}_1\text{-}[\text{IgE}]\text{-}\text{L}_2\text{-}[\text{SA}]\text{-}X(n) \\ &[\text{IgE}]\text{-}\text{L}_1\text{-}[\text{SA}]\text{-}\text{L}_2\text{-}[\text{IgE}]\text{-}X(n) \\ &[\text{SA}]\text{-}\text{L}_1\text{-}[\text{IgE}]\text{-}\text{L}_2\text{-}[\text{IgE}]\text{-}X(n) \end{aligned} $	<p>At least one [IgE] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (')</p> <p>[SA] = (see legend below)</p> <p>L₁ = (see legend below)</p> <p>L₂ = (see legend below)</p> <p>X(n) = (see legend below)</p>

Table T (continued)

Polypeptide/ construct ⁽¹⁾	General formula	ISV building blocks and linkers
Bispecific ⁽²⁾	$[\text{IgE}] \cdot L_1 \cdot [\text{Nb}]$ $[\text{Nb}] \cdot L_1 \cdot [\text{IgE}]$ $[\text{IgE}] \cdot L_1 \cdot [\text{IgE}] \cdot L_2 \cdot [\text{Nb}]$ $[\text{IgE}] \cdot L_1 \cdot [\text{Nb}] \cdot L_2 \cdot [\text{IgE}]$ $[\text{Nb}] \cdot L_1 \cdot [\text{IgE}] \cdot L_2 \cdot [\text{IgE}]$	At least one [IgE] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (4) $L_1 =$ (see legend below) $L_2 =$ (see legend below) $[\text{Nb}] =$ (see legend below)
Bispecific/ C-terminal extension (3)	$[\text{IgE}] \cdot L_1 \cdot [\text{Nb}] \cdot X(n)$ $[\text{Nb}] \cdot L_1 \cdot [\text{IgE}] \cdot X(n)$ $[\text{IgE}] \cdot L_1 \cdot [\text{IgE}] \cdot L_2 \cdot [\text{Nb}] \cdot X(n)$ $[\text{IgE}] \cdot L_1 \cdot [\text{Nb}] \cdot L_2 \cdot [\text{IgE}] \cdot X(n)$ $[\text{Nb}] \cdot L_1 \cdot [\text{IgE}] \cdot L_2 \cdot [\text{IgE}] \cdot X(n)$	At least one [IgE] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (4) $L_1 =$ (see legend below) $L_2 =$ (see legend below) $X(n) =$ (see legend below) $[\text{Nb}] =$ (see legend below)
Bispecific/ half-life extended ⁽³⁾	$[\text{IgE}] \cdot L_1 \cdot [\text{Nb}] \cdot L_2 \cdot [\text{SA}]$ $[\text{IgE}] \cdot L_1 \cdot [\text{SA}] \cdot L_2 \cdot [\text{Nb}]$ $[\text{Nb}] \cdot L_1 \cdot [\text{SA}] \cdot L_2 \cdot [\text{IgE}]$ $[\text{Nb}] \cdot L_1 \cdot [\text{IgE}] \cdot L_2 \cdot [\text{SA}]$ $[\text{SA}] \cdot L_1 \cdot [\text{IgE}] \cdot L_2 \cdot [\text{Nb}]$ $[\text{SA}] \cdot L_1 \cdot [\text{Nb}] \cdot L_2 \cdot [\text{IgE}]$	At least one [IgE] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (4) $[\text{SA}] =$ (see legend below) L_1, L_2, L_3 (see legend below) $[\text{Nb}] =$ (see legend below)

Table T (continued)

Polypeptide/ construct ⁽³⁾)	General formula	ISV building blocks and linkers
Bispecific/ half-life extended ⁽³⁾)	$[\text{IgE}] \cdot L_1 \cdot [\text{IgE}] \cdot L_2 \cdot [\text{Nb}] \cdot L_3 \cdot [\text{SA}]$ $[\text{Nb}] \cdot L_1 \cdot [\text{IgE}] \cdot L_2 \cdot [\text{IgE}] \cdot L_3 \cdot [\text{SA}]$ $[\text{SA}] \cdot L_1 \cdot [\text{IgE}] \cdot L_2 \cdot [\text{IgE}] \cdot L_3 \cdot [\text{Nb}]$ $[\text{SA}] \cdot L_1 \cdot [\text{IgE}] \cdot L_2 \cdot [\text{Nb}] \cdot L_3 \cdot [\text{IgE}]$ $[\text{IgE}] \cdot L_1 \cdot [\text{Nb}] \cdot L_2 \cdot [\text{IgE}] \cdot L_3 \cdot [\text{SA}]$	<p>At least one [IgE] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (4)</p> <p>[SA] = (see legend below)</p> <p>L₁, L₂, L₃(see legend below)</p> <p>[Nb] = (see legend below)</p>
Bispecific/ half-life extended/ C-terminal extension ⁽³⁾)	$[\text{IgE}] \cdot L_1 \cdot [\text{Nb}] \cdot L_2 \cdot [\text{SA}] \cdot X(n)$ $[\text{IgE}] \cdot L_1 \cdot [\text{SA}] \cdot L_2 \cdot [\text{Nb}] \cdot X(n)$ $[\text{Nb}] \cdot L_1 \cdot [\text{SA}] \cdot L_2 \cdot [\text{IgE}] \cdot X(n)$ $[\text{Nb}] \cdot L_1 \cdot [\text{IgE}] \cdot L_2 \cdot [\text{SA}] \cdot X(n)$ $[\text{SA}] \cdot L_1 \cdot [\text{IgE}] \cdot L_2 \cdot [\text{Nb}] \cdot X(n)$ $[\text{SA}] \cdot L_1 \cdot [\text{Nb}] \cdot L_2 \cdot [\text{IgE}] \cdot X(n)$ $[\text{IgE}] \cdot L_1 \cdot [\text{IgE}] \cdot L_2 \cdot [\text{Nb}] \cdot L_3 \cdot [\text{SA}] \cdot X(n)$ $[\text{Nb}] \cdot L_1 \cdot [\text{IgE}] \cdot L_2 \cdot [\text{IgE}] \cdot L_3 \cdot [\text{SA}] \cdot X(n)$ $[\text{SA}] \cdot L_1 \cdot [\text{IgE}] \cdot L_2 \cdot [\text{IgE}] \cdot L_3 \cdot [\text{Nb}] \cdot X(n)$ $[\text{SA}] \cdot L_1 \cdot [\text{IgE}] \cdot L_2 \cdot [\text{Nb}] \cdot L_3 \cdot [\text{IgE}] \cdot X(n)$ $[\text{IgE}] \cdot L_1 \cdot [\text{Nb}] \cdot L_2 \cdot [\text{IgE}] \cdot L_3 \cdot [\text{SA}] \cdot X(n)$	<p>At least one [IgE] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (4)</p> <p>[SA] = (see legend below)</p> <p>L₁, L₂, L₃(see legend below)</p> <p>X(n) = (see legend below)</p> <p>[Nb] = (see legend below)</p>

Table T (continued)

Legend:	<ul style="list-style-type: none"> - [SA] is an ISV against (human) serum albumin, preferably an ISV of the invention against (human) serum albumin, more preferably one of SEQ ID NO's: 46 or 61 or even more preferably one of the ISVD's of the invention of SEQ ID NO's: 47, 54, 62, 69, 78, 86, 109, 116, 123, 130 or 496 to 513. - Each of L₁, L₂ and L₃ is (independently) a suitable linker. Each of L₁, L₂ and L₃ may (independently) be present or not. Non-limiting examples of suitable linkers are the gly-ser linkers referred to herein, such as the 9GS, 30GS or 35GS linker. - X(n) = a C-terminal extension as a C-terminal extension as described in herein and/or in WO 12/175741 - [Nb] is an ISV against another therapeutic target.
Notes:	<p>(¹) In this Table:</p> <ul style="list-style-type: none"> - "<i>Monovalent</i>" generally refers to polypeptides/constructs comprising a single ISV against IgE. These may further comprise a half-life extending ISV (such as an ISV against serum albumin). - "<i>Bivalent</i>" generally refers to polypeptides/constructs comprising two ISV's against IgE (which may be the same or different). These may again further comprise a half-life extending ISV (such as an ISV against serum albumin). - "<i>Bispecific</i>" generally refers to polypeptides/constructs comprising at least one (such as 1 or 2) ISV's against IgE and at least one (such as 1 or 2) other ISV against a therapeutic target. These may further comprise a half-life extending ISV (such as an ISV against serum albumin). - In the polypeptides/constructs described in this table, at least one of the ISV's against IgE present is an ISV of the invention, and preferably all of the ISV's against IgE present in such polypeptide/construct are ISV's of the invention. Also, when a half-life extending ISV and/or an ISV against another therapeutic target is present in such polypeptide/construct, each of these (and preferably all of these) may also be (and preferably are) ISV's of the invention
	<p>(²): All "<i>bivalent</i>" constructs in this Table may also be biparatopic, meaning that they comprise at least two (such as two) ISV's against IgE, which are directed against different epitopes on IgE.</p> <p>(³): As will be clear to the skilled person, other/further bispecific constructs than those listed can be made using the building blocks and linkers mentioned.</p> <p>(⁴) Preferably, each [IgE] present is independently chosen from SEQ ID NO's: 464 to 477 and/or 482 to 495. Also, the [IgE] present may be the same or different; in a biparatopic polypeptide/construct they will be directed against different epitopes on IgE.</p> <p>(⁵) Each of the polypeptides/constructs mentioned to in this column by means of reference to a SEQ ID forms an individual specific aspect of the invention.</p>

Example 11: VH domains (and in particular Nanobodies) against CXCR4, and compounds of the invention comprising the same.

In one specific aspect, the VH domains of the invention (and in particular ISVDs of the invention and more in particular Nanobodies of the invention) and compounds of the invention may be directed against CXCR4.

Such a VH domain of the invention against CXCR4 will generally comprise: (i) suitable framework sequences that suitably comprise the amino acid residues/mutations of the invention as described herein; as well as (ii) CDR sequences that allow the VH domain of the invention to specifically bind to CXCR4. In addition, such a VH domain of the invention against CXCR4 may also suitably have a C-terminal extension as described herein, in particular when said VH domain is monovalent or forms the C-terminal end of the compound of the invention in which said VH domain is present (again, as further described herein). Such VH domains of the invention against CXCR4 may further be as further described herein, and may in particular be ISVD's.

Again, as with other aspects and embodiments of the invention described herein, when a specific ISVD (such as the ISVD against CXCR4 described in this Example) or compound comprising the same is said to be "according to the invention" or "as further described herein", the preferred aspects/embodiments and preferences that are generally described herein for the ISVD's or compounds of the invention also specifically apply to said specific ISVD or compound, respectively, unless explicitly indicated otherwise or unless the specific technical context requires otherwise.

Thus, in a particular aspect, the present invention relates to a VH domain (and in particular an ISVD) that is directed against CXCR4, in which (i) position 112 is K or Q; or (ii) position 110 is K or Q and position 11 is V; or (iii) position 89 is T; or (iv) position 89 is L and position 110 is K or Q; or (v) position 11 is V and position 89 is L; or any suitable combination of (i) to (v). In particular, in such VH domains against CXCR4:

- the amino acid residue at position 11 is preferably chosen from L, V or K (and is most preferably V); and
- the amino acid residue at position 14 is preferably suitably chosen from A or P; and
- the amino acid residue at position 41 is preferably suitably chosen from A or P; and
- the amino acid residue at position 89 is preferably suitably chosen from T, V or L; and
- the amino acid residue at position 108 is preferably suitably chosen from Q or L; and
- the amino acid residue at position 110 is preferably suitably chosen from T, K or Q; and

- the amino acid residue at position 112 is preferably suitably chosen from S, K or Q; such that either (i) position 112 is K or Q; or (ii) position 110 is K or Q and position 11 is V; or (iii) position 89 is T; or (iv) position 89 is L and position 110 is K or Q; or (v) position 11 is V and position 89 is L; or any suitable combination of (i) to (v).

The VH domains of the invention against CXCR4 may further be as described herein and may again in particular be an ISVD (and more in particular a Nanobody) against CXCR4 or a protein, polypeptide or other compound or construct that comprises as least one such ISVD. Such a protein, polypeptide or other compound or construct may also be as further described herein, and may for example have an increased half-life (i.e. as described herein, e.g. a half-life - expressed as $t_{1/2}$ beta - in human subjects of in human subjects of at least 1 day, preferably at least 3 days, more preferably at least 7 days, such as at least 10 days), and for this purpose may for example comprise a serum-albumin binding Nanobody, which may also be a serum-albumin binding Nanobody of the invention (again, as described herein).

Also, such an ISVD may suitably have a C-terminal extension (as further described herein and in WO 12/175741), in particular when said ISVD forms the C-terminal end of a protein, polypeptide or other compound or construct comprising the same (again, as further described herein).

In one preferred aspect, the VH domains of the invention against CXCR4 comprise (i) a CDR1 sequence that is the sequence of SEQ ID NO: 245 (which is preferred) or that is an amino acid sequence that has only one amino acid difference with the sequence of SEQ ID NO: 245; (ii) a CDR2 sequence that is the sequence of SEQ ID NO: 246 (which is preferred) or that is an amino acid sequence that has only one or two amino acid differences with the sequence of SEQ ID NO: 246; and (iii) a CDR3 sequence that is the sequence of SEQ ID NO: 247 (which is preferred) or that is an amino acid sequence that has only one or two amino acid differences with the sequence of SEQ ID NO: 247.

More preferably, in a VH domain of the invention against CXCR4 according to this aspect: (i) CDR1 is SEQ ID NO: 245; (ii) CDR2 is SEQ ID NO: 246; and (iii) CDR3 is SEQ ID NO: 247.

In one specific aspect, a Nanobody of the invention against CXCR4 is a variant of the Nanobody of SEQ ID NO: 244 (with at least 90% sequence identity, such as at least 95% sequence identity, with SEQ ID NO: 244), in which:

- the amino acid residue at position 11 is preferably chosen from L, V or K (and is most preferably V); and

- the amino acid residue at position 14 is preferably suitably chosen from A or P; and
- the amino acid residue at position 41 is preferably suitably chosen from A or P; and
- the amino acid residue at position 89 is preferably suitably chosen from T, V or L; and
- the amino acid residue at position 108 is preferably suitably chosen from Q or L; and
- the amino acid residue at position 110 is preferably suitably chosen from T, K or Q; and
- the amino acid residue at position 112 is preferably suitably chosen from S, K or Q;

such that either (i) position 112 is K or Q; or (ii) position 110 is K or Q and position 11 is V; or (iii) position 89 is T; or (iv) position 89 is L and position 110 is K or Q; or (v) position 11 is V and position 89 is L; or any suitable combination of (i) to (v). The CDR's of such an ISV are preferably as defined in the preceding two paragraphs.

In another preferred aspect, the VH domains of the invention against CXCR4 comprise (i) a CDR1 sequence that is the sequence of SEQ ID NO: 263 (which is preferred) or that is an amino acid sequence that has only one amino acid difference with the sequence of SEQ ID NO: 263; (ii) a CDR2 sequence that is the sequence of SEQ ID NO: 264 (which is preferred) or that is an amino acid sequence that has only one or two amino acid differences with the sequence of SEQ ID NO: 264; and (iii) a CDR3 sequence that is the sequence of SEQ ID NO: 265 (which is preferred) or that is an amino acid sequence that has only one or two amino acid differences with the sequence of SEQ ID NO: 265.

More preferably, in a VH domain of the invention against CXCR-4 according to this aspect: (i) CDR1 is SEQ ID NO: 263; (ii) CDR2 is SEQ ID NO: 264; and (iii) CDR3 is SEQ ID NO: 265.

In one specific aspect, a Nanobody of the invention against IL-23 is a variant of the Nanobody of SEQ ID NO: 262 (with at least 90% sequence identity, such as at least 95% sequence identity, with SEQ ID NO: 262), in which:

- the amino acid residue at position 11 is preferably chosen from L, V or K (and is most preferably V); and
- the amino acid residue at position 14 is preferably suitably chosen from A or P; and
- the amino acid residue at position 41 is preferably suitably chosen from A or P; and
- the amino acid residue at position 89 is preferably suitably chosen from T, V or L; and
- the amino acid residue at position 108 is preferably suitably chosen from Q or L; and
- the amino acid residue at position 110 is preferably suitably chosen from T, K or Q; and
- the amino acid residue at position 112 is preferably suitably chosen from S, K or Q;

such that either (i) position 112 is K or Q; or (ii) position 110 is K or Q and position 11 is V; or (iii) position 89 is T; or (iv) position 89 is L and position 110 is K or Q; or (v) position 11 is V and position 89 is L; or any suitable combination of (i) to (v). Again, the CDR's of such an ISV are preferably as defined in the preceding two paragraphs.

Some specifically preferred, but non-limiting examples of Nanobodies of the invention against CXCR4 are listed in Figure 15A as SEQ ID NO's: 248 to 261 and in Figure 15B as SEQ ID NO's: 266 to 279; and each of these Nanobodies form a further aspect of the invention.

The invention also relates to a compound of the invention against CXCR4 that comprises at least one (such as one, two or three) of the Nanobodies of the invention of SEQ ID NO's: 248 to 261 and/or 266 to 279. Such compounds of the invention against CXCR4 may again be as further described herein, and thus for example may comprise suitable linkers, may comprise a C-terminal extension as described herein, and may be half-life extended (for example because they comprise a Nanobody against human serum albumin, such as (preferably) a Nanobody of the invention against human serum albumin). Reference is made to Table U below.

As described in for example WO 2009/138519, WO 2011/042398 and WO 2011/161266, one particularly preferred class of Nanobody-based compounds against CXCR4 are biparatopic compounds. Thus, in one aspect of the invention, a compound of the invention against CXCR4 is a biparatopic construct that comprises one ISV that is either SEQ ID NO: 244 or (preferably) an ISV of the invention that has been derived from SEQ ID NO: 244 (as described in this Example 11) and one ISV that is either SEQ ID NO: 262 or (preferably) an ISV of the invention that has been derived from SEQ ID NO: 262 (as described in this Example 11), provided that at least one (and preferably both) of these ISV's are ISV's of the invention. Such biparatopic constructs may also be half-life extended (i.e. by means of a serum albumin-binding ISV). Some specific examples of such biparatopic constructs are given in SEQ ID NO: 595 to 603.

Some specifically preferred examples of compounds of the invention against CXCR-4 are given in Figure 25 as SEQ ID NO's: 595 to 603; and each of these compounds form a further aspect of the invention. Thus, in another aspect, the invention relates to a polypeptide that is directed against CXCR-4 and that has an amino acid sequence that is chosen from the group consisting of SEQ ID NO's: 595 to 603. More generally, compounds of the invention against CXCR-4 may be as described in WO 2009/138519, WO 2011/042398 and WO 2011/161266WO 2011/144749, but comprising ISV's of the invention. They may also be

used for the purposes described in WO 2009/138519, WO 2011/042398 and WO 2011/161266.

Table U: Examples of compounds of the invention against CXCR-4.

Polypeptide/ construct ⁽¹⁾	General formula	ISV building blocks and linkers
Monovalent	[CXCR-4]	[CXCR-4] = one of SEQ ID NO's: 464 to 477 and/or 482 to 495
Monovalent/ C-terminal extension	[CXCR-4]-X(n)	[CXCR-4] = one of SEQ ID NO's: 464 to 477 and/or 482 to 495
Monovalent/ half-life extended	[CXCR-4]-L ₁ -[SA] [SA]-L ₁ -[CXCR-4]	[CXCR-4] = one of SEQ ID NO's: 464 to 477 and/or 482 to 495
Monovalent/ half-life extended/C- terminal extension	[CXCR-4]-L ₁ -[SA]-X(n) [SA]-L ₁ -[CXCR-4]-X(n)	[CXCR-4] = one of SEQ ID NO's: 464 to 477 and/or 482 to 495
Bivalent ⁽²⁾	[CXCR-4]-L ₁ -[CXCR-4]	At least one [CXCR-4] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 ⁽⁴⁾
		L ₁ = (see legend below)

Table U (continued)

Polypeptide/ construct ¹)	General formula	ISV building blocks and linkers
Bivalent/ C-terminal extension ²)	[CXCR-4]- L ₁ -[CXCR-4] -X(n)	<p>At least one [CXCR-4] = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (↑)</p> <p>L₁ = (see legend below)</p> <p>X(n) = (see legend below)</p>
Bivalent/ half-life extended ²)	<p>[CXCR-4]- L₁-[CXCR-4]- L₂-[SA]</p> <p>[CXCR-4]- L₁-[SA]- L₂-[CXCR-4]</p> <p>[SA]- L₁-[CXCR-4]- L₂-[CXCR-4]</p>	<p>At least one [CXCR-4] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (↑)</p> <p>[SA] = (see legend below)</p> <p>L₁ = (see legend below)</p> <p>L₂ = (see legend below)</p>
Bivalent/ half-life extended/ C-terminal extension ²)	<p>[CXCR-4]- L₁-[CXCR-4]- L₂-[SA] -X(n)</p> <p>[CXCR-4]- L₁-[SA]- L₂-[CXCR-4] -X(n)</p> <p>[SA]- L₁-[CXCR-4]- L₂-[CXCR-4] -X(n)</p>	<p>At least one [CXCR-4] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (↑)</p> <p>[SA] = (see legend below)</p> <p>L₁ = (see legend below)</p> <p>L₂ = (see legend below)</p> <p>X(n) = (see legend below)</p>

Table U (continued)

Polypeptide/ construct(¹)	General formula	ISV building blocks and linkers
Bispecific (')	$[CXCR-4]-L_1-[Nb]$ $[Nb]-L_1-[CXCR-4]$ $[CXCR-4]-L_1-[CXCR-4]-L_2-[Nb]$ $[CXCR-4]-L_1-[Nb]-L_2-[CXCR-4]$ $[Nb]-L_1-[CXCR-4]-L_2-[CXCR-4]$	At least one [CXCR-4] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (⁴) L ₁ = (see legend below) L ₂ = (see legend below) [Nb] = (see legend below)
Bispecific/ C-terminal extension (3)	$[CXCR-4]-L_1-[Nb]-X(n)$ $[Nb]-L_1-[CXCR-4]-X(n)$ $[CXCR-4]-L_1-[CXCR-4]-L_2-[Nb]-X(n)$ $[CXCR-4]-L_1-[Nb]-L_2-[CXCR-4]-X(n)$ $[Nb]-L_1-[CXCR-4]-L_2-[CXCR-4]-X(n)$	At least one [CXCR-4] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (⁴) L ₁ = (see legend below) L ₂ = (see legend below) X(n) = (see legend below) [Nb] = (see legend below)
Bispecific/ half-life extended (')	$[CXCR-4]-L_1-[Nb]-L_2-[SA]$ $[CXCR-4]-L_1-[SA]-L_2-[Nb]$ $[Nb]-L_1-[SA]-L_2-[CXCR-4]$ $[Nb]-L_1-[CXCR-4]-L_2-[SA]$ $[SA]-L_1-[CXCR-4]-L_2-[Nb]$ $[SA]-L_1-[Nb]-L_2-[CXCR-4]$	At least one [CXCR-4] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (⁴) [SA] = (see legend below) L ₁ , L ₂ , L ₃ (see legend below) [Nb] = (see legend below)

Table U (continued)

Polypeptide/ construct ¹)	General formula	ISV building blocks and linkers
Bispecific/ half-life extended ²)	$[\text{CXCR-4}] \cdot L_1 \cdot [\text{CXCR-4}] \cdot L_2 \cdot [\text{Nb}] \cdot L_3 \cdot [\text{SA}]$ $[\text{Nb}] \cdot L_1 \cdot [\text{CXCR-4}] \cdot L_2 \cdot [\text{CXCR-4}] \cdot L_3 \cdot [\text{SA}]$ $[\text{SA}] \cdot L_1 \cdot [\text{CXCR-4}] \cdot L_2 \cdot [\text{CXCR-4}] \cdot L_3 \cdot [\text{Nb}]$ $[\text{SA}] \cdot L_1 \cdot [\text{CXCR-4}] \cdot L_2 \cdot [\text{Nb}] \cdot L_3 \cdot [\text{CXCR-4}]$ $[\text{CXCR-4}] \cdot L_1 \cdot [\text{Nb}] \cdot L_2 \cdot [\text{CXCR-4}] \cdot L_3 \cdot [\text{SA}]$	At least one [CXCR-4] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 ⁴) [SA] = (see legend below) L ₁ , L ₂ , L ₃ (see legend below) [Nb] = (see legend below)
Bispecific/ half-life extended/ C-terminal extension ³)	$[\text{CXCR-4}] \cdot L_1 \cdot [\text{Nb}] \cdot L_2 \cdot [\text{SA}] \cdot X(n)$ $[\text{CXCR-4}] \cdot L_1 \cdot [\text{SA}] \cdot L_2 \cdot [\text{Nb}] \cdot X(n)$ $[\text{Nb}] \cdot L_1 \cdot [\text{SA}] \cdot L_2 \cdot [\text{CXCR-4}] \cdot X(n)$ $[\text{Nb}] \cdot L_1 \cdot [\text{CXCR-4}] \cdot L_2 \cdot [\text{SA}] \cdot X(n)$ $[\text{SA}] \cdot L_1 \cdot [\text{CXCR-4}] \cdot L_2 \cdot [\text{Nb}] \cdot X(n)$ $[\text{SA}] \cdot L_1 \cdot [\text{Nb}] \cdot L_2 \cdot [\text{CXCR-4}] \cdot X(n)$ $[\text{CXCR-4}] \cdot L_1 \cdot [\text{CXCR-4}] \cdot L_2 \cdot [\text{Nb}] \cdot L_3 \cdot [\text{SA}] \cdot X(n)$ $[\text{Nb}] \cdot L_1 \cdot [\text{CXCR-4}] \cdot L_2 \cdot [\text{CXCR-4}] \cdot L_3 \cdot [\text{SA}] \cdot X(n)$ $[\text{SA}] \cdot L_1 \cdot [\text{CXCR-4}] \cdot L_2 \cdot [\text{CXCR-4}] \cdot L_3 \cdot [\text{Nb}] \cdot X(n)$ $[\text{SA}] \cdot L_1 \cdot [\text{CXCR-4}] \cdot L_2 \cdot [\text{Nb}] \cdot L_3 \cdot [\text{CXCR-4}] \cdot X(n)$ $[\text{CXCR-4}] \cdot L_1 \cdot [\text{Nb}] \cdot L_2 \cdot [\text{CXCR-4}] \cdot L_3 \cdot [\text{SA}] \cdot X(n)$	At least one [CXCR-4] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 ⁴) [SA] = (see legend below) L ₁ , L ₂ , L ₃ (see legend below) X(n) = (see legend below) [Nb] = (see legend below)

Table U (continued)

Legend:	<ul style="list-style-type: none"> [SA] is an ISV against (human) serum albumin, preferably an ISV of the invention against (human) serum albumin, more preferably one of SEQ ID NO's: 46 or 61 or even more preferably one of the ISVD's of the invention of SEQ ID NO's: 47, 54, 62, 69, 78, 86, 109, 116, 123, 130 or 496 to 513. Each of L₁, L₂ and L₃ is (independently) a suitable linker. Each of L₁, L₂ and L₃ may (independently) be present or not. Non-limiting examples of suitable linkers are the gly-ser linkers referred to herein, such as the 9GS, 30GS or 35GS linker. X(n) = a C-terminal extension as a C-terminal extension as described in herein and/or in WO 12/175741 [Nb] is an ISV against another therapeutic target.
Notes:	<p>(¹) In this Table:</p> <ul style="list-style-type: none"> “<i>Monovalent</i>” generally refers to polypeptides/constructs comprising a single ISV against CXCR-4. These may further comprise a half-life extending ISV (such as an ISV against serum albumin). “<i>Bivalent</i>” generally refers to polypeptides/constructs comprising two ISV's against CXCR-4 (which may be the same or different). These may again further comprise a half-life extending ISV (such as an ISV against serum albumin). “<i>Bispecific</i>” generally refers to polypeptides/constructs comprising at least one (such as 1 or 2) ISV's against CXCR-4 and at least one (such as 1 or 2) other ISV against a therapeutic target. These may further comprise a half-life extending ISV (such as an ISV against serum albumin).
	<ul style="list-style-type: none"> In the polypeptides/constructs described in this table, at least one of the ISV's against CXCR-4 present is an ISV of the invention, and preferably all of the ISV's against CXCR-4 present in such polypeptide/construct are ISV's of the invention. Also, when a half-life extending ISV and/or an ISV against another therapeutic target is present in such polypeptide/construct, each of these (and preferably all of these) may also be (and preferably are) ISV's of the invention
	<p>(²): All “bivalent” constructs in this Table may also be biparatopic, meaning that they comprise at least two (such as two) ISV's against CXCR-4, which are directed against different epitopes on CXCR-4.</p> <p>(³): As will be clear to the skilled person, other/further bispecific constructs than those listed can be made using the building blocks and linkers mentioned.</p> <p>(⁴) Preferably, each [CXCR-4] present is independently chosen from SEQ ID NO's: 464 to 477 and/or 482 to 495. Also, the [CXCR-4] present may be the same or different; in a biparatopic polypeptide/construct they will be directed against different epitopes on CXCR-4.</p> <p>(⁵) Each of the polypeptides/constructs mentioned to in this column by means of reference to a SEQ ID forms an individual specific aspect of the invention.</p>

Example 12: VH domains (and in particular Nanobodies) against HER-3, and compounds of the invention comprising the same.

In one specific aspect, the VH domains of the invention (and in particular ISVDs of the invention and more in particular Nanobodies of the invention) and compounds of the invention may be directed against HER-3.

Such a VH domain of the invention against HER-3 will generally comprise: (i) suitable framework sequences that suitably comprise the amino acid residues/mutations of the invention as described herein; as well as (ii) CDR sequences that allow the VH domain of the invention to specifically bind to HER-3. In addition, such a VH domain of the invention against HER-3 may also suitably have a C-terminal extension as described herein, in particular when said VH domain is monovalent or forms the C-terminal end of the compound of the invention in which said VH domain is present (again, as further described herein). Such VH domains of the invention against HER-3 may further be as further described herein, and may in particular be ISVD's.

Again, as with other aspects and embodiments of the invention described herein, when a specific ISVD (such as the ISVD against HER-3 described in this Example) or compound comprising the same is said to be "according to the invention" or "as further described herein", the preferred aspects/embodiments and preferences that are generally described herein for the ISVD's or compounds of the invention also specifically apply to said specific ISVD or compound, respectively, unless explicitly indicated otherwise or unless the specific technical context requires otherwise.

Thus, in a particular aspect, the present invention relates to a VH domain (and in particular an ISVD) that is directed against HER-3, in which (i) position 112 is K or Q; or (ii) position 110 is K or Q and position 11 is V; or (iii) position 89 is T; or (iv) position 89 is L and position 110 is K or Q; or (v) position 11 is V and position 89 is L; or any suitable combination of (i) to (v). In particular, in such VH domains against HER-3:

- the amino acid residue at position 11 is preferably chosen from L, V or K (and is most preferably V); and
- the amino acid residue at position 14 is preferably suitably chosen from A or P; and
- the amino acid residue at position 41 is preferably suitably chosen from A or P; and
- the amino acid residue at position 89 is preferably suitably chosen from T, V or L; and
- the amino acid residue at position 108 is preferably suitably chosen from Q or L; and
- the amino acid residue at position 110 is preferably suitably chosen from T, K or Q; and

- the amino acid residue at position 112 is preferably suitably chosen from S, K or Q; such that either (i) position 112 is K or Q; or (ii) position 110 is K or Q and position 11 is V; or (iii) position 89 is T; or (iv) position 89 is L and position 110 is K or Q; or (v) position 11 is V and position 89 is L; or any suitable combination of (i) to (v).

The VH domains of the invention against HER-3 may further be as described herein and may again in particular be an ISVD (and more in particular a Nanobody) against HER-3 or a protein, polypeptide or other compound or construct that comprises as least one such ISVD. Such a protein, polypeptide or other compound or construct may also be as further described herein, and may for example have an increased half-life (i.e. as described herein, e.g. a half-life - expressed as $t_{1/2}$ beta - in human subjects of in human subjects of at least 1 day, preferably at least 3 days, more preferably at least 7 days, such as at least 10 days), and for this purpose may for example comprise a serum-albumin binding Nanobody, which may also be a serum-albumin binding Nanobody of the invention (again, as described herein).

Also, such an ISVD may suitably have a C-terminal extension (as further described herein and in WO 12/175741), in particular when said ISVD forms the C-terminal end of a protein, polypeptide or other compound or construct comprising the same (again, as further described herein).

In one preferred aspect, the VH domains of the invention against HER-3 comprise (i) a CDR1 sequence that is the sequence of SEQ ID NO: 281 (which is preferred) or that is an amino acid sequence that has only one amino acid difference with the sequence of SEQ ID NO: 281; (ii) a CDR2 sequence that is the sequence of SEQ ID NO: 282 (which is preferred) or that is an amino acid sequence that has only one or two amino acid differences with the sequence of SEQ ID NO: 282; and (iii) a CDR3 sequence that is the sequence of SEQ ID NO: 283 (which is preferred) or that is an amino acid sequence that has only one or two amino acid differences with the sequence of SEQ ID NO: 283.

More preferably, in a VH domain of the invention against HER-3 according to this aspect: (i) CDR1 is SEQ ID NO: 281; (ii) CDR2 is SEQ ID NO: 282; and (iii) CDR3 is SEQ ID NO: 283.

In one specific aspect, a Nanobody of the invention against HER-3 is a variant of the Nanobody of SEQ ID NO: 280 (with at least 90% sequence identity, such as at least 95% sequence identity, with SEQ ID NO: 280), in which:

- the amino acid residue at position 11 is preferably chosen from L, V or K (and is most preferably V); and

- the amino acid residue at position 14 is preferably suitably chosen from A or P; and
- the amino acid residue at position 41 is preferably suitably chosen from A or P; and
- the amino acid residue at position 89 is preferably suitably chosen from T, V or L; and
- the amino acid residue at position 108 is preferably suitably chosen from Q or L; and
- the amino acid residue at position 110 is preferably suitably chosen from T, K or Q; and
- the amino acid residue at position 112 is preferably suitably chosen from S, K or Q;

such that either (i) position 112 is K or Q; or (ii) position 110 is K or Q and position 11 is V; or (iii) position 89 is T; or (iv) position 89 is L and position 110 is K or Q; or (v) position 11 is V and position 89 is L; or any suitable combination of (i) to (v). The CDR's of such an ISV are preferably as defined in the preceding two paragraphs.

In another preferred aspect, the VH domains of the invention against HER-3 comprise (i) a CDR1 sequence that is the sequence of SEQ ID NO: 299 (which is preferred) or that is an amino acid sequence that has only one amino acid difference with the sequence of SEQ ID NO: 299; (ii) a CDR2 sequence that is the sequence of SEQ ID NO: 300 (which is preferred) or that is an amino acid sequence that has only one or two amino acid differences with the sequence of SEQ ID NO: 300; and (iii) a CDR3 sequence that is the sequence of SEQ ID NO: 301 (which is preferred) or that is an amino acid sequence that has only one or two amino acid differences with the sequence of SEQ ID NO: 301.

More preferably, in a VH domain of the invention against HER-3 according to this aspect: (i) CDR1 is SEQ ID NO: 299; (ii) CDR2 is SEQ ID NO: 300; and (iii) CDR3 is SEQ ID NO: 301.

In one specific aspect, a Nanobody of the invention against HER-3 is a variant of the Nanobody of SEQ ID NO: 298 (with at least 90% sequence identity, such as at least 95% sequence identity, with SEQ ID NO: 298), in which:

- the amino acid residue at position 11 is preferably chosen from L, V or K (and is most preferably V); and
- the amino acid residue at position 14 is preferably suitably chosen from A or P; and
- the amino acid residue at position 41 is preferably suitably chosen from A or P; and
- the amino acid residue at position 89 is preferably suitably chosen from T, V or L; and
- the amino acid residue at position 108 is preferably suitably chosen from Q or L; and
- the amino acid residue at position 110 is preferably suitably chosen from T, K or Q; and
- the amino acid residue at position 112 is preferably suitably chosen from S, K or Q;

such that either (i) position 112 is K or Q; or (ii) position 110 is K or Q and position 11 is V; or (iii) position 89 is T; or (iv) position 89 is L and position 110 is K or Q; or (v) position 11 is V and position 89 is L; or any suitable combination of (i) to (v). Again, the CDR's of such an ISV are preferably as defined in the preceding two paragraphs.

Some specifically preferred, but non-limiting examples of Nanobodies of the invention against HER-3 are listed in Figure 16A as SEQ ID NO's: 284 to 297 and Figure 16B as SEQ ID NO's: 302 to 315, respectively; and each of these Nanobodies form a further aspect of the invention.

The invention also relates to a compound of the invention against HER-3 that comprises at least one (such as one, two or three) of the Nanobodies of the invention of SEQ ID NO's: 284 to 297 and/or 302 to 315. Such compounds of the invention against HER-3 may again be as further described herein, and thus for example may comprise suitable linkers, may comprise a C-terminal extension as described herein, and may be half-life extended (for example because they comprise a Nanobody against human serum albumin, such as (preferably) a Nanobody of the invention against human serum albumin). Reference is made to Table V below.

As described in for example WO 2011/144749, one particularly preferred class of Nanobody-based compounds against HER-3 are biparatopic compounds. Thus, in one aspect of the invention, a compound of the invention against HER-3 is a biparatopic construct that comprises one ISV that is either SEQ ID NO: 280 or (preferably) an ISV of the invention that has been derived from SEQ ID NO: 280 (as described in this Example 12) and one ISV that is either SEQ ID NO: 298 or (preferably) an ISV of the invention that has been derived from SEQ ID NO: 298 (as described in this Example 12), provided that at least one (and preferably both) of these ISV's are ISV's of the invention. Such biparatopic constructs may also be half-life extended (i.e. by means of a serum albumin-binding ISV). Some specific examples of such biparatopic constructs are given in SEQ ID NO: 604 to 639.

Some specifically preferred examples of compounds of the invention against HER-3 are given in Figure 26 as SEQ ID NO's: 604 to 639; and each of these compounds form a further aspect of the invention. Thus, in another aspect, the invention relates to a polypeptide that is directed against HER-3 and that has an amino acid sequence that is chosen from the group consisting of SEQ ID NO's: 604 to 639. More generally, compounds of the invention against HER-3 may be as described in WO 2011/144749, but comprising ISV's of the invention. They may also be used for the purposes described in WO 2011/144749.

Table V: Examples of compounds of the invention against HER-3.

Polypeptide/ construct ⁽¹⁾	General formula	ISV building blocks and linkers
Monovalent	[HER-3]	[HER-3] = one of SEQ ID NO's: 464 to 477 and/or 482 to 495
Monovalent/ C-terminal extension	[HER-3]-X(n)	[HER-3] = one of SEQ ID NO's: 464 to 477 and/or 482 to 495
Monovalent/ half-life extended	[HER-3]- L ₁ -[SA] [SA]- L ₁ -[HER-3]	[HER-3] = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 [SA] = (see legend below) L ₁ = (see legend below)
Monovalent/ half-life extended/C- terminal extension	[HER-3] - L ₁ - [SA]-X(n) [SA]- L ₁ -[HER-3] -X(n)	[HER-3] = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 [SA] = (see legend below) L ₁ = (see legend below) X(n) = (see legend below)
Bivalent ⁽²⁾	[HER-3]- L ₁ -[HER-3]	At least one [HER-3] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 ⁽³⁾
		L ₁ = (see legend below)

Table V (continued)

Polypeptide/ construct(¹)	General formula	ISV building blocks and linkers
Bivalent/ C-terminal extension(²)	[HER-3]-L ₁ -[HER-3]-X(n)	At least one [HER-3] = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (⁴) L ₁ = (see legend below) X(n) = (see legend below)
Bivalent/ half-life extended(²)	[HER-3]-L ₁ -[HER-3]-L ₂ -[SA] [HER-3]-L ₁ -[SA]-L ₂ -[HER-3] [SA]-L ₁ -[HER-3]-L ₂ -[HER-3]	At least one [HER-3] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (⁴) [SA] = (see legend below) L ₁ = (see legend below) L ₂ = (see legend below)
Bivalent/ half-life extended/ C-terminal extension(²)	[HER-3]-L ₁ -[HER-3]-L ₂ -[SA]-X(n) [HER-3]-L ₁ -[SA]-L ₂ -[HER-3]-X(n) [SA]-L ₁ -[HER-3]-L ₂ -[HER-3]-X(n)	At least one [HER-3] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (⁴) [SA] = (see legend below) L ₁ = (see legend below) L ₂ = (see legend below) X(n) = (see legend below)

Table V (continued)

Polypeptide/ construct(³)	General formula	ISV building blocks and linkers
Bispecific (')	[HER-3]-L ₁ -[Nb] [Nb]-L ₁ -[HER-3] [HER-3]-L ₁ -[HER-3]-L ₂ -[Nb] [HER-3]-L ₁ -[Nb]-L ₂ -[HER-3] [Nb]-L ₁ -[HER-3]-L ₂ -[HER-3]	At least one [HER-3] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (') L ₁ = (see legend below) L ₂ = (see legend below) [Nb] = (see legend below)
Bispecific/ C-terminal extension (3)	[HER-3]-L ₁ -[Nb]-X(n) [Nb]-L ₁ -[HER-3]-X(n) [HER-3]-L ₁ -[HER-3]-L ₂ -[Nb]-X(n) [HER-3]-L ₁ -[Nb]-L ₂ -[HER-3]-X(n) [Nb]-L ₁ -[HER-3]-L ₂ -[HER-3]-X(n)	At least one [HER-3] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (') L ₁ = (see legend below) L ₂ = (see legend below) X(n) = (see legend below) [Nb] = (see legend below)
Bispecific/ half-life extended (')	[HER-3]-L ₁ -[Nb]-L ₂ -[SA] [HER-3]-L ₁ -[SA]-L ₂ -[Nb] [Nb]-L ₁ -[SA]-L ₂ -[HER-3] [Nb]-L ₁ -[HER-3]-L ₂ -[SA] [SA]-L ₁ -[HER-3]-L ₂ -[Nb] [SA]-L ₁ -[Nb]-L ₂ -[HER-3]	At least one [HER-3] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (') [SA] = (see legend below) L ₁ , L ₂ , L ₃ (see legend below) [Nb] = (see legend below)

Table V (continued)

Polypeptide/ construct(¹)	General formula	ISV building blocks and linkers
Bispecific/ half-life extended (³)	[HER-3]-L ₁ -[HER-3]-L ₂ -[Nb]-L ₃ -[SA] [Nb]-L ₁ -[HER-3]-L ₂ -[HER-3]-L ₃ -[SA] [SA]-L ₁ -[HER-3]-L ₂ -[HER-3]-L ₃ -[Nb] [SA]-L ₁ -[HER-3]-L ₂ -[Nb]-L ₃ -[HER-3] [HER-3]-L ₁ -[Nb]-L ₂ -[HER-3]-L ₃ -[SA]	At least one [HER-3] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (⁴) [SA] = (see legend below) L ₁ , L ₂ , L ₃ (see legend below) [Nb] = (see legend below)
Bispecific/ half-life extended/ C-terminal extension (³)	[HER-3]-L ₁ -[Nb]-L ₂ -[SA]-X(n) [HER-3]-L ₁ -[SA]-L ₂ -[Nb]-X(n) [Nb]-L ₁ -[SA]-L ₂ -[HER-3]-X(n) [Nb]-L ₁ -[HER-3]-L ₂ -[SA]-X(n) [SA]-L ₁ -[HER-3]-L ₂ -[Nb]-X(n) [SA]-L ₁ -[Nb]-L ₂ -[HER-3]-X(n) [HER-3]-L ₁ -[HER-3]-L ₂ -[Nb]-L ₃ -[SA]-X(n) [Nb]-L ₁ -[HER-3]-L ₂ -[HER-3]-L ₃ -[SA]-X(n) [SA]-L ₁ -[HER-3]-L ₂ -[HER-3]-L ₃ -[Nb]-X(n) [SA]-L ₁ -[HER-3]-L ₂ -[Nb]-L ₃ -[HER-3]-X(n) [HER-3]-L ₁ -[Nb]-L ₂ -[HER-3]-L ₃ -[SA]-X(n)	At least one [HER-3] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (⁴) [SA] = (see legend below) L ₁ , L ₂ , L ₃ (see legend below) X(n) = (see legend below) [Nb] = (see legend below)

Table V (continued)

Legend:	<ul style="list-style-type: none"> - [SA] is an ISV against (human) serum albumin, preferably an ISV of the invention against (human) serum albumin, more preferably one of SEQ ID NO's: 46 or 61 or even more preferably one of the ISV's of the invention of SEQ ID NO's: 47, 54, 62, 69, 78, 86, 109, 116, 123, 130 or 496 to 513. - Each of L₁, L₂ and L₃ is (independently) a suitable linker. Each of L₁, L₂ and L₃ may (independently) be present or not. Non-limiting examples of suitable linkers are the gly-ser linkers referred to herein, such as the 9GS, 30GS or 35GS linker. - X(n) = a C-terminal extension as a C-terminal extension as described in herein and/or in WO 12/175741 - [Nb] is an ISV against another therapeutic target.
Notes:	
(¹) In this Table:	
	<ul style="list-style-type: none"> - “<i>Monovalent</i>” generally refers to polypeptides/constructs comprising a single ISV against HER-3. These may further comprise a half-life extending ISV (such as an ISV against serum albumin). - “<i>Bivalent</i>” generally refers to polypeptides/constructs comprising two ISV's against HER-3 (which may be the same or different). These may again further comprise a half-life extending ISV (such as an ISV against serum albumin). - “<i>Bispecific</i>” generally refers to polypeptides/constructs comprising at least one (such as 1 or 2) ISV's against HER-3 and at least one (such as 1 or 2) other ISV against a therapeutic target. These may again further comprise a half-life extending ISV (such as an ISV against serum albumin). - In the polypeptides/constructs described in this table, at least one of the ISV's against HER-3 present is an ISV of the invention, and preferably all of the ISV's against HER-3 present in such polypeptide/construct are ISV's of the invention. Also, when a half-life extending ISV and/or an ISV against another therapeutic target is present in such polypeptide/construct, each of these (and preferably all of these) may also be (and preferably are) ISV's of the invention
	(²): All “bivalent” constructs in this Table may also be biparatopic, meaning that they comprise at least two (such as two) ISV's against HER-3, which are directed against different epitopes on HER-3.
	(³): As will be clear to the skilled person, other/further bispecific constructs than those listed can be made using the building blocks and linkers mentioned.
	(⁴): Preferably, each [HER-3] present is independently chosen from SEQ ID NO's: 464 to 477 and/or 482 to 495. Also, the [HER-3] present may be the same or different; in a biparatopic polypeptide/construct they will be directed against different epitopes on HER-3.
	(⁵): Each of the polypeptides/constructs mentioned to in this column by means of reference to a SEQ ID forms an individual specific aspect of the invention.

Example 13: VH domains (and in particular Nanobodies) against TNF, and compounds of the invention comprising the same.

In one specific aspect, the VH domains of the invention (and in particular ISVDs of the invention and more in particular Nanobodies of the invention) and compounds of the invention may be directed against TNF.

Such a VH domain of the invention against TNF will generally comprise: (i) suitable framework sequences that suitably comprise the amino acid residues/mutations of the invention as described herein; as well as (ii) CDR sequences that allow the VH domain of the invention to specifically bind to TNF. In addition, such a VH domain of the invention against TNF may also suitably have a C-terminal extension as described herein, in particular when said VH domain is monovalent or forms the C-terminal end of the compound of the invention in which said VH domain is present (again, as further described herein). Such VH domains of the invention against TNF may further be as further described herein, and may in particular be ISVD's.

Again, as with other aspects and embodiments of the invention described herein, when a specific ISVD (such as the ISVD against TNF described in this Example) or compound comprising the same is said to be "according to the invention" or "as further described herein", the preferred aspects/embodiments and preferences that are generally described herein for the ISVD's or compounds of the invention also specifically apply to said specific ISVD or compound, respectively, unless explicitly indicated otherwise or unless the specific technical context requires otherwise.

Thus, in a particular aspect, the present invention relates to a VH domain (and in particular an ISVD) that is directed against TNF, in which (i) position 112 is K or Q; or (ii) position 110 is K or Q and position 11 is V; or (iii) position 89 is T; or (iv) position 89 is L and position 110 is K or Q; or (v) position 11 is V and position 89 is L; or any suitable combination of (i) to (v). In particular, in such VH domains against TNF:

- the amino acid residue at position 11 is preferably chosen from L, V or K (and is most preferably V); and
- the amino acid residue at position 14 is preferably suitably chosen from A or P; and
- the amino acid residue at position 41 is preferably suitably chosen from A or P; and
- the amino acid residue at position 89 is preferably suitably chosen from T, V or L; and
- the amino acid residue at position 108 is preferably suitably chosen from Q or L; and
- the amino acid residue at position 110 is preferably suitably chosen from T, K or Q; and

- the amino acid residue at position 112 is preferably suitably chosen from S, K or Q; such that either (i) position 112 is K or Q; or (ii) position 110 is K or Q and position 11 is V; or (iii) position 89 is T; or (iv) position 89 is L and position 110 is K or Q; or (v) position 11 is V and position 89 is L; or any suitable combination of (i) to (v).

The VH domains of the invention against TNF may further be as described herein and may again in particular be an ISVD (and more in particular a Nanobody) against TNF or a protein, polypeptide or other compound or construct that comprises at least one such ISVD. Such a protein, polypeptide or other compound or construct may also be as further described herein, and may for example have an increased half-life (i.e. as described herein, e.g. a half-life - expressed as $t_{1/2}$ beta - in human subjects of in human subjects of at least 1 day, preferably at least 3 days, more preferably at least 7 days, such as at least 10 days), and for this purpose may for example comprise a serum-albumin binding Nanobody, which may also be a serum-albumin binding Nanobody of the invention (again, as described herein).

Also, such an ISVD may suitably have a C-terminal extension (as further described herein and in WO 12/175741), in particular when said ISVD forms the C-terminal end of a protein, polypeptide or other compound or construct comprising the same (again, as further described herein).

In one preferred aspect, the VH domains of the invention against TNF comprise (i) a CDR1 sequence that is the sequence of SEQ ID NO: 317 (which is preferred) or that is an amino acid sequence that has only one amino acid difference with the sequence of SEQ ID NO: 317; (ii) a CDR2 sequence that is the sequence of SEQ ID NO: 318 (which is preferred) or that is an amino acid sequence that has only one or two amino acid differences with the sequence of SEQ ID NO: 318; and (iii) a CDR3 sequence that is the sequence of SEQ ID NO: 319 (which is preferred) or that is an amino acid sequence that has only one or two amino acid differences with the sequence of SEQ ID NO: 319.

More preferably, in a VH domain of the invention against TNF according to this aspect: (i) CDR1 is SEQ ID NO: 317; (ii) CDR2 is SEQ ID NO: 318; and (iii) CDR3 is SEQ ID NO: 319.

In one specific aspect, a Nanobody of the invention against TNF is a variant of the Nanobody of SEQ ID NO: 316 (with at least 90% sequence identity, such as at least 95% sequence identity, with SEQ ID NO: 316), in which:

- the amino acid residue at position 11 is preferably chosen from L, V or K (and is most preferably V); and

- the amino acid residue at position 14 is preferably suitably chosen from A or P; and
- the amino acid residue at position 41 is preferably suitably chosen from A or P; and
- the amino acid residue at position 89 is preferably suitably chosen from T, V or L; and
- the amino acid residue at position 108 is preferably suitably chosen from Q or L; and
- the amino acid residue at position 110 is preferably suitably chosen from T, K or Q; and
- the amino acid residue at position 112 is preferably suitably chosen from S, K or Q;

such that either (i) position 112 is K or Q; or (ii) position 110 is K or Q and position 11 is V; or (iii) position 89 is T; or (iv) position 89 is L and position 110 is K or Q; or (v) position 11 is V and position 89 is L; or any suitable combination of (i) to (v). The CDR's of such an ISV are preferably as defined in the preceding two paragraphs.

Some specifically preferred, but non-limiting examples of Nanobodies of the invention against TNF are listed in Figure 17A as SEQ ID NO's: 320 to 333; and each of these Nanobodies form a further aspect of the invention.

The invention also relates to a compound of the invention against TNF that comprises at least one (such as one, two or three) of the Nanobodies of the invention of SEQ ID NO's: 320 to 333. Such compounds of the invention against TNF may again be as further described herein, and thus for example may comprise suitable linkers, may comprise a C-terminal extension as described herein, and may be half-life extended (for example because they comprise a Nanobody against human serum albumin, such as (preferably) a Nanobody of the invention against human serum albumin). Reference is made to Table W below. Generally, as TNF is a multivalent target, compounds of the invention comprising two or three anti-TNF ISV's (and linkers of suitable length, see WO 06/122786) are preferred)

Some specifically preferred examples of compounds of the invention against TNF are given in Figure 27 as SEQ ID NO's: 640 to 675; and each of these compounds form a further aspect of the invention. Thus, in another aspect, the invention relates to a polypeptide that is directed against TNF and that has an amino acid sequence that is chosen from the group consisting of SEQ ID NO's: 640 to 675. More generally, compounds of the invention against TNF may be as described in WO 2006/122786, but comprising ISV's of the invention. They may also be used for the purposes described in WO 2006/122786.

Table W: Examples of compounds of the invention against TNF.

Polypeptide/ construct(¹)	General formula	ISV building blocks and linkers
Monovalent	[TNF]	[TNF] = one of SEQ ID NO's: 464 to 477 and/or 482 to 495
Monovalent/ C-terminal extension	[TNF]-X(n)	[TNF] = one of SEQ ID NO's: 464 to 477 and/or 482 to 495
Monovalent/ half-life extended	[TNF]- L ₁ -[SA] [SA]- L ₁ -[TNF]	[TNF] = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 [SA] = (see legend below) L ₁ = (see legend below)
Monovalent/ half-life extended/C- terminal extension	[TNF] - L ₁ - [SA]-X(n) [SA]- L ₁ -[TNF] -X(n)	[TNF] = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 [SA] = (see legend below) L ₁ = (see legend below) X(n) = (see legend below)
Bivalent(²)	[TNF]- L ₁ -[TNF]	At least one [TNF] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (⁴) L ₁ = (see legend below)

Table W (continued)

Polypeptide/ construct ⁽¹⁾	General formula	ISV building blocks and linkers
Bivalent/ C-terminal extension ⁽²⁾	[TNF]-L ₁ -[TNF]-X(n)	At least one [TNF] = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 ⁽⁴⁾ L ₁ = (see legend below) X(n) = (see legend below)
Bivalent/ half-life extended ⁽²⁾	$ \begin{aligned} &[TNF]-L_1-[TNF]-L_2-[SA] \\ &[TNF]-L_1-[SA]-L_2-[TNF] \\ &[SA]-L_1-[TNF]-L_2-[TNF] \end{aligned} $	At least one [TNF] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 ⁽⁴⁾ [SA] = (see legend below) L ₁ = (see legend below) L ₂ = (see legend below)
Bivalent/ half-life extended/ C-terminal extension ⁽²⁾	$ \begin{aligned} &[TNF]-L_1-[TNF]-L_2-[SA]-X(n) \\ &[TNF]-L_1-[SA]-L_2-[TNF]-X(n) \\ &[SA]-L_1-[TNF]-L_2-[TNF]-X(n) \end{aligned} $	At least one [TNF] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 ⁽⁴⁾ [SA] = (see legend below) L ₁ = (see legend below) L ₂ = (see legend below) X(n) = (see legend below)

Table W (continued)

Polypeptide/ construct ⁽³⁾	General formula	ISV building blocks and linkers
Bispecific (3)	$[\text{TNF}]\text{-}L_1\text{-}[\text{Nb}]$ $[\text{Nb}]\text{-}L_1\text{-}[\text{TNF}]$ $[\text{TNF}]\text{-}L_1\text{-}[\text{TNF}]\text{-}L_2\text{-}[\text{Nb}]$ $[\text{TNF}]\text{-}L_1\text{-}[\text{Nb}]\text{-}L_2\text{-}[\text{TNF}]$ $[\text{Nb}]\text{-}L_1\text{-}[\text{TNF}]\text{-}L_2\text{-}[\text{TNF}]$	At least one [TNF] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 ⁽⁴⁾ $L_1 = (\text{see legend below})$ $L_2 = (\text{see legend below})$ $[\text{Nb}] = (\text{see legend below})$
Bispecific/ C-terminal extension (3)	$[\text{TNF}]\text{-}L_1\text{-}[\text{Nb}]\text{-}X(n)$ $[\text{Nb}]\text{-}L_1\text{-}[\text{TNF}]\text{-}X(n)$ $[\text{TNF}]\text{-}L_1\text{-}[\text{TNF}]\text{-}L_2\text{-}[\text{Nb}]\text{-}X(n)$ $[\text{TNF}]\text{-}L_1\text{-}[\text{Nb}]\text{-}L_2\text{-}[\text{TNF}]\text{-}X(n)$ $[\text{Nb}]\text{-}L_1\text{-}[\text{TNF}]\text{-}L_2\text{-}[\text{TNF}]\text{-}X(n)$	At least one [TNF] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 ⁽⁴⁾ $L_1 = (\text{see legend below})$ $L_2 = (\text{see legend below})$ $X(n) = (\text{see legend below})$ $[\text{Nb}] = (\text{see legend below})$
Bispecific/ half-life extended (3)	$[\text{TNF}]\text{-}L_1\text{-}[\text{Nb}]\text{-}L_2\text{-}[\text{SA}]$ $[\text{TNF}]\text{-}L_1\text{-}[\text{SA}]\text{-}L_2\text{-}[\text{Nb}]$ $[\text{Nb}]\text{-}L_1\text{-}[\text{SA}]\text{-}L_2\text{-}[\text{TNF}]$ $[\text{Nb}]\text{-}L_1\text{-}[\text{TNF}]\text{-}L_2\text{-}[\text{SA}]$ $[\text{SA}]\text{-}L_1\text{-}[\text{TNF}]\text{-}L_2\text{-}[\text{Nb}]$ $[\text{SA}]\text{-}L_1\text{-}[\text{Nb}]\text{-}L_2\text{-}[\text{TNF}]$	At least one [TNF] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 ⁽⁴⁾ $[\text{SA}] = (\text{see legend below})$ $L_1, L_2, L_3 (\text{see legend below})$ $[\text{Nb}] = (\text{see legend below})$

Table W (continued)

Polypeptide/ construct(‘)	General formula	ISV building blocks and linkers
Bispecific/ half-life extended (‘)	[TNF]-L ₁ -[TNF]-L ₂ -[Nb]-L ₃ -[SA] [Nb]-L ₁ -[TNF]-L ₂ -[TNF]-L ₃ -[SA] [SA]-L ₁ -[TNF]-L ₂ -[TNF]-L ₃ -[Nb] [SA]-L ₁ -[TNF]-L ₂ -[Nb]-L ₃ -[TNF] [TNF]-L ₁ -[Nb]-L ₂ -[TNF]-L ₃ -[SA]	At least one [TNF] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (‘) [SA] = (see legend below) L ₁ , L ₂ , L ₃ (see legend below) [Nb] = (see legend below)
Bispecific/ half-life extended/ C-terminal extension (‘)	[TNF]-L ₁ -[Nb]-L ₂ -[SA]-X(n) [TNF]-L ₁ -[SA]-L ₂ -[Nb]-X(n) [Nb]-L ₁ -[SA]-L ₂ -[TNF]-X(n) [Nb]-L ₁ -[TNF]-L ₂ -[SA]-X(n) [SA]-L ₁ -[TNF]-L ₂ -[Nb]-X(n) [SA]-L ₁ -[Nb]-L ₂ -[TNF]-X(n) [TNF]-L ₁ -[TNF]-L ₂ -[Nb]-L ₃ -[SA]-X(n) [Nb]-L ₁ -[TNF]-L ₂ -[TNF]-L ₃ -[SA]-X(n) [SA]-L ₁ -[TNF]-L ₂ -[TNF]-L ₃ -[Nb]-X(n) [SA]-L ₁ -[TNF]-L ₂ -[Nb]-L ₃ -[TNF]-X(n) [TNF]-L ₁ -[Nb]-L ₂ -[TNF]-L ₃ -[SA]-X(n)	At least one [TNF] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (‘) [SA] = (see legend below) L ₁ , L ₂ , L ₃ (see legend below) X(n) = (see legend below) [Nb] = (see legend below)

Table W (continued)

Legend:	<ul style="list-style-type: none"> - [SA] is an ISV against (human) serum albumin, preferably an ISV of the invention against (human) serum albumin, more preferably one of SEQ ID NO's: 46 or 61 or even more preferably one of the ISVD's of the invention of SEQ ID NO's: 47, 54, 62, 69, 78, 86, 109, 116, 123, 130 or 496 to 513. * Each of L₁, L₂ and L₃ is (independently) a suitable linker. Each of L₁, L₂ and L₃ may (independently) be present or not. Non-limiting examples of suitable linkers are the gly-ser linkers referred to herein, such as the 9GS, 30GS or 35GS linker. - X(n) = a C-terminal extension as a C-terminal extension as described in herein and/or in WO 12/175741 - [Nb] is an ISV against another therapeutic target. 	
Notes:	<p>(¹) In this Table:</p> <ul style="list-style-type: none"> - “<i>Monovalent</i>” generally refers to polypeptides/constructs comprising a single ISV against TNF. These may further comprise a half-life extending ISV (such as an ISV against serum albumin). - “<i>Bivalent</i>” generally refers to polypeptides/constructs comprising two ISV's against TNF (which may be the same or different). These may again further comprise a half-life extending ISV (such as 1 or 2 ISV's against TNF and at least one (such as 1 or 2) other ISV against a therapeutic target. These may further comprise a half-life extending ISV (such as an ISV against serum albumin). - “<i>Bispecific</i>” generally refers to polypeptides/constructs comprising at least one (such as 1 or 2) ISV's against TNF and at least one (such as 1 or 2) other ISV against a therapeutic target. These may further comprise a half-life extending ISV (such as an ISV against serum albumin). - In the polypeptides/constructs described in this table, at least one of the ISV's against TNF present is an ISV of the invention, and preferably all of the ISV's against TNF present in such polypeptide/construct are ISV's of the invention. Also, when a half-life extending ISV and/or an ISV against another therapeutic target is present in such polypeptide/construct, each of these (and preferably all of these) may also be (and preferably are) ISV's of the invention (²): All “bivalent” constructs in this Table may also be biparatopic, meaning that they comprise at least two (such as two) ISV's against TNF, which are directed against different epitopes on TNF. (³): As will be clear to the skilled person, other/further bispecific constructs than those listed can be made using the building blocks and linkers mentioned. (⁴): Preferably, each [TNF] present is independently chosen from SEQ ID NO's: 464 to 477 and/or 482 to 495. Also, the [TNF] present may be the same or different; in a biparatopic polypeptide/construct they will be directed against different epitopes on TNF. (⁵): Each of the polypeptides/constructs mentioned to in this column by means of reference to a SEQ ID forms an individual specific aspect of the invention. 	

Example 14: Further VH domains (and in particular Nanobodies) against TNF, and compounds of the invention comprising the same.

In one specific aspect, the VH domains of the invention (and in particular ISVDs of the invention and more in particular Nanobodies of the invention) and compounds of the invention may be directed against TNF.

Such a VH domain of the invention against TNF will generally comprise: (i) suitable framework sequences that suitably comprise the amino acid residues/mutations of the invention as described herein; as well as (ii) CDR sequences that allow the VH domain of the invention to specifically bind to TNF. In addition, such a VH domain of the invention against TNF may also suitably have a C-terminal extension as described herein, in particular when said VH domain is monovalent or forms the C-terminal end of the compound of the invention in which said VH domain is present (again, as further described herein). Such VH domains of the invention against TNF may further be as further described herein, and may in particular be ISVD's.

Again, as with other aspects and embodiments of the invention described herein, when a specific ISVD (such as the ISVD against TNF described in this Example) or compound comprising the same is said to be "according to the invention" or "as further described herein", the preferred aspects/embodiments and preferences that are generally described herein for the ISVD's or compounds of the invention also specifically apply to said specific ISVD or compound, respectively, unless explicitly indicated otherwise or unless the specific technical context requires otherwise.

Thus, in a particular aspect, the present invention relates to a VH domain (and in particular an ISVD) that is directed against TNF, in which (i) position 112 is K or Q; or (ii) position 110 is K or Q and position 11 is V; or (iii) position 89 is T; or (iv) position 89 is L and position 110 is K or Q; or (v) position 11 is V and position 89 is L; or any suitable combination of (i) to (v). In particular, in such VH domains against TNF:

- the amino acid residue at position 11 is preferably chosen from L, V or K (and is most preferably V); and
- the amino acid residue at position 14 is preferably suitably chosen from A or P; and
- the amino acid residue at position 41 is preferably suitably chosen from A or P; and
- the amino acid residue at position 89 is preferably suitably chosen from T, V or L; and
- the amino acid residue at position 108 is preferably suitably chosen from Q or L; and
- the amino acid residue at position 110 is preferably suitably chosen from T, K or Q; and

- the amino acid residue at position 112 is preferably suitably chosen from S, K or Q; such that either (i) position 112 is K or Q; or (ii) position 110 is K or Q and position 11 is V; or (iii) position 89 is T; or (iv) position 89 is L and position 110 is K or Q; or (v) position 11 is V and position 89 is L; or any suitable combination of (i) to (v).

The VH domains of the invention against TNF may further be as described herein and may again in particular be an ISVD (and more in particular a Nanobody) against TNF or a protein, polypeptide or other compound or construct that comprises at least one such ISVD. Such a protein, polypeptide or other compound or construct may also be as further described herein, and may for example have an increased half-life (i.e. as described herein, e.g. a half-life - expressed as $t_{1/2}$ beta - in human subjects of in human subjects of at least 1 day, preferably at least 3 days, more preferably at least 7 days, such as at least 10 days), and for this purpose may for example comprise a serum-albumin binding Nanobody, which may also be a serum-albumin binding Nanobody of the invention (again, as described herein).

Also, such an ISVD may suitably have a C-terminal extension (as further described herein and in WO 12/175741), in particular when said ISVD forms the C-terminal end of a protein, polypeptide or other compound or construct comprising the same (again, as further described herein).

In one preferred aspect, the VH domains of the invention against TNF comprise (i) a CDR1 sequence that is the sequence of SEQ ID NO: 335 (which is preferred) or that is an amino acid sequence that has only one amino acid difference with the sequence of SEQ ID NO: 335; (ii) a CDR2 sequence that is the sequence of SEQ ID NO: 336 (which is preferred) or that is an amino acid sequence that has only one or two amino acid differences with the sequence of SEQ ID NO: 336; and (iii) a CDR3 sequence that is the sequence of SEQ ID NO: 337 (which is preferred) or that is an amino acid sequence that has only one or two amino acid differences with the sequence of SEQ ID NO: 337.

More preferably, in a VH domain of the invention against TNF according to this aspect: (i) CDR1 is SEQ ID NO: 335; (ii) CDR2 is SEQ ID NO: 336; and (iii) CDR3 is SEQ ID NO: 337.

In one specific aspect, a Nanobody of the invention against TNF is a variant of the Nanobody of SEQ ID NO: 334 (with at least 90% sequence identity, such as at least 95% sequence identity, with SEQ ID NO: 334), in which:

- the amino acid residue at position 11 is preferably chosen from L, V or K (and is most preferably V); and

- the amino acid residue at position 14 is preferably suitably chosen from A or P; and
- the amino acid residue at position 41 is preferably suitably chosen from A or P; and
- the amino acid residue at position 89 is preferably suitably chosen from T, V or L; and
- the amino acid residue at position 108 is preferably suitably chosen from Q or L; and
- the amino acid residue at position 110 is preferably suitably chosen from T, K or Q; and
- the amino acid residue at position 112 is preferably suitably chosen from S, K or Q;

such that either (i) position 112 is K or Q; or (ii) position 110 is K or Q and position 11 is V; or (iii) position 89 is T; or (iv) position 89 is L and position 110 is K or Q; or (v) position 11 is V and position 89 is L; or any suitable combination of (i) to (v). The CDR's of such an ISV are preferably as defined in the preceding two paragraphs.

Some specifically preferred, but non-limiting examples of Nanobodies of the invention against TNF are listed in Figure 17B as SEQ ID NO's: 338 to 351; and each of these Nanobodies form a further aspect of the invention.

The invention also relates to a compound of the invention against TNF that comprises at least one (such as one, two or three) of the Nanobodies of the invention of SEQ ID NO's: 338 to 251. Such compounds of the invention against TNF may again be as further described herein, and thus for example may comprise suitable linkers, may comprise a C-terminal extension as described herein, and may be half-life extended (for example because they comprise a Nanobody against human serum albumin, such as (preferably) a Nanobody of the invention against human serum albumin). Reference is made to Table X below. Generally, as TNF is a multivalent target, compounds of the invention comprising two or three anti-TNF ISV's are preferred.

Table X: Examples of compounds of the invention against TNF.

Polypeptide/ construct(¹)	General formula	ISV building blocks and linkers
Monovalent	[TNF]	[TNF] = one of SEQ ID NO's: 464 to 477 and/or 482 to 495
Monovalent/ C-terminal extension	[TNF]-X(n)	[TNF] = one of SEQ ID NO's: 464 to 477 and/or 482 to 495
Monovalent/ half-life extended	[TNF]- L ₁ -[SA] [SA]- L ₁ -[TNF]	[TNF] = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 [SA] = (see legend below) L ₁ = (see legend below)
Monovalent/ half-life extended/C- terminal extension	[TNF] - L ₁ - [SA]-X(n) [SA]- L ₁ -[TNF] -X(n)	[TNF] = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 [SA] = (see legend below) L ₁ = (see legend below) X(n) = (see legend below)
Bivalent(²)	[TNF]- L ₁ -[TNF]	At least one [TNF] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (⁴) L ₁ = (see legend below)

Table X (continued)

Polypeptide/ construct ¹)	General formula	ISV building blocks and linkers
Bivalent/ C-terminal extension ²)	[TNF]- L ₁ -[TNF] -X(n)	At least one [TNF] = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (⁴) L ₁ = (see legend below) X(n) = (see legend below)
Bivalent/ half-life extended ²)	[TNF]- L ₁ -[TNF]- L ₂ -[SA] [TNF]- L ₁ -[SA]- L ₂ -[TNF] [SA]- L ₁ -[TNF]- L ₂ -[TNF]	At least one [TNF] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (⁴) [SA] = (see legend below) L ₁ = (see legend below) L ₂ = (see legend below)
Bivalent/ half-life extended/ C-terminal extension ²)	[TNF]- L ₁ -[TNF]- L ₂ -[SA] -X(n) [TNF]- L ₁ -[SA]- L ₂ -[TNF] -X(n) [SA]- L ₁ -[TNF]- L ₂ -[TNF] -X(n)	At least one [TNF] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (⁴) [SA] = (see legend below) L ₁ = (see legend below) L ₂ = (see legend below) X(n) = (see legend below)

Table X (continued)

Polypeptide/ construct(¹)	General formula	ISV building blocks and linkers
Bispecific ()	$[\text{TNF}]\text{-L}_1\text{-[Nb]}$ $[\text{Nb}]\text{-L}_1\text{-}[\text{TNF}]$ $[\text{TNF}]\text{-L}_1\text{-}[\text{TNF}]\text{-L}_2\text{-[Nb]}$ $[\text{TNF}]\text{-L}_1\text{-[Nb]}\text{-L}_2\text{-}[\text{TNF}]$ $[\text{Nb}]\text{-L}_1\text{-}[\text{TNF}]\text{-L}_2\text{-}[\text{TNF}]$	At least one [TNF] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (⁴) L_1 = (see legend below) L_2 = (see legend below) [Nb] = (see legend below)
Bispecific/ C-terminal extension (3)	$[\text{TNF}]\text{-L}_1\text{-[Nb]}\text{-}X(n)$ $[\text{Nb}]\text{-L}_1\text{-}[\text{TNF}]\text{-}X(n)$ $[\text{TNF}]\text{-L}_1\text{-}[\text{TNF}]\text{-L}_2\text{-[Nb]}\text{-}X(n)$ $[\text{TNF}]\text{-L}_1\text{-[Nb]}\text{-L}_2\text{-}[\text{TNF}]\text{-}X(n)$ $[\text{Nb}]\text{-L}_1\text{-}[\text{TNF}]\text{-L}_2\text{-}[\text{TNF}]\text{-}X(n)$	At least one [TNF] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (⁴) L_1 = (see legend below) L_2 = (see legend below) X(n) = (see legend below) [Nb] = (see legend below)
Bispecific/ half-life extended (³)	$[\text{TNF}]\text{-L}_1\text{-[Nb]}\text{-}L_2\text{-[SA]}$ $[\text{TNF}]\text{-L}_1\text{-[SA]}\text{-L}_2\text{-[Nb]}$ $[\text{Nb}]\text{-L}_1\text{-[SA]}\text{-L}_2\text{-}[\text{TNF}]$ $[\text{Nb}]\text{-L}_1\text{-}[\text{TNF}]\text{-L}_2\text{-[SA]}$ $[\text{SA}]\text{-L}_1\text{-}[\text{TNF}]\text{-L}_2\text{-[Nb]}$ $[\text{SA}]\text{-L}_1\text{-[Nb]}\text{-L}_2\text{-}[\text{TNF}]$	At least one [TNF] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (⁴) [SA] = (see legend below) L_1 , L_2 , L_3 (see legend below) [Nb] = (see legend below)

Table X (continued)

Polypeptide/ construct(⁴)	General formula	ISV building blocks and linkers
Bispecific/ half-life extended (⁵)	[TNF]-L ₁ -[TNF]-L ₂ -[Nb]-L ₃ -[SA] [Nb]-L ₁ -[TNF]-L ₂ -[TNF]-L ₃ -[SA] [SA]-L ₁ -[TNF]-L ₂ -[TNF]-L ₃ -[Nb] [SA]-L ₁ -[TNF]-L ₂ -[Nb]-L ₃ -[TNF] [TNF]-L ₁ -[Nb]-L ₂ -[TNF]-L ₃ -[SA]	At least one [TNF] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (⁴) [SA] = (see legend below) L ₁ , L ₂ , L ₃ (see legend below) [Nb] = (see legend below)
Bispecific/ half-life extended/ C-terminal extension (⁵)	[TNF]-L ₁ -[Nb]-L ₂ -[SA]-X(n) [TNF]-L ₁ -[SA]-L ₂ -[Nb]-X(n) [Nb]-L ₁ -[SA]-L ₂ -[TNF]-X(n) [Nb]-L ₁ -[TNF]-L ₂ -[SA]-X(n) [SA]-L ₁ -[TNF]-L ₂ -[Nb]-X(n) [SA]-L ₁ -[Nb]-L ₂ -[TNF]-X(n) [TNF]-L ₁ -[TNF]-L ₂ -[Nb]-L ₃ -[SA]-X(n) [Nb]-L ₁ -[TNF]-L ₂ -[TNF]-L ₃ -[SA]-X(n) [SA]-L ₁ -[TNF]-L ₂ -[TNF]-L ₃ -[Nb]-X(n) [SA]-L ₁ -[TNF]-L ₂ -[Nb]-L ₃ -[TNF]-X(n) [TNF]-L ₁ -[Nb]-L ₂ -[TNF]-L ₃ -[SA]-X(n)	At least one [TNF] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (⁴) [SA] = (see legend below) L ₁ , L ₂ , L ₃ (see legend below) X(n) = (see legend below) [Nb] = (see legend below)

Table X (continued)

Legend:	<ul style="list-style-type: none"> - [SA] is an ISV against (human) serum albumin, preferably an ISV of the invention against (human) serum albumin, more preferably one of SEQ ID NO's: 46 or 61 or even more preferably one of the ISVD's of the invention of SEQ ID NO's: 47, 54, 62, 69, 78, 86, 109, 116, 123, 130 or 496 to 513. - Each of L₁, L₂ and L₃ is (independently) a suitable linker. Each of L₁, L₂ and L₃ may (independently) be present or not. Non-limiting examples of suitable linkers are the gly-ser linkers referred to herein, such as the 9GS, 30GS or 35GS linker. - X(n) = a C-terminal extension as a C-terminal extension as described in herein and/or in WO 12/175741 - [Nb] is an ISV against another therapeutic target.
Notes:	
(¹) In this Table:	
	<ul style="list-style-type: none"> - “<i>Monovalent</i>” generally refers to polypeptides/constructs comprising a single ISV against TNF. These may further comprise a half-life extending ISV (such as an ISV against serum albumin). - “<i>Bivalent</i>” generally refers to polypeptides/constructs comprising two ISV's against TNF (which may be the same or different). These may again further comprise a half-life extending ISV (such as an ISV against serum albumin). - “<i>Bispecific</i>” generally refers to polypeptides/constructs comprising at least one (such as 1 or 2) ISV's against TNF and at least one (such as 1 or 2) other ISV against a therapeutic target. These may further comprise a half-life extending ISV (such as an ISV against serum albumin). - In the polypeptides/constructs described in this table, at least one of the ISV's against TNF present is an ISV of the invention, and preferably all of the ISV's against TNF present in such polypeptide/construct are ISV's of the invention. Also, when a half-life extending ISV and/or an ISV against another therapeutic target is present in such polypeptide/construct, each of these (and preferably all of these) may also be (and preferably are) ISV's of the invention
	(²): All “bivalent” constructs in this Table may also be biparatopic, meaning that they comprise at least two (such as two) ISV's against TNF, which are directed against different epitopes on TNF.
	(³): As will be clear to the skilled person, other/further bispecific constructs than those listed can be made using the building blocks and linkers mentioned.
	(⁴): Preferably, each [TNF] present is independently chosen from SEQ ID NO's: 464 to 477 and/or 482 to 495. Also, the [TNF] present may be the same or different, in a biparatopic polypeptide/construct they will be directed against different epitopes on TNF.
	(⁵): Each of the polypeptides/constructs mentioned to in this column by means of reference to a SEQ ID forms an individual specific aspect of the invention.

Example 15: VH domains (and in particular Nanobodies) against c-Met, and compounds of the invention comprising the same.

In one specific aspect, the VH domains of the invention (and in particular ISVDs of the invention and more in particular Nanobodies of the invention) and compounds of the invention may be directed against c-Met.

Such a VH domain of the invention against c-Met will generally comprise: (i) suitable framework sequences that suitably comprise the amino acid residues/mutations of the invention as described herein; as well as (ii) CDR sequences that allow the VH domain of the invention to specifically bind to c-Met. In addition, such a VH domain of the invention against c-Met may also suitably have a C-terminal extension as described herein, in particular when said VH domain is monovalent or forms the C-terminal end of the compound of the invention in which said VH domain is present (again, as further described herein). Such VH domains of the invention against c-Met may further be as further described herein, and may in particular be ISVD's.

Again, as with other aspects and embodiments of the invention described herein, when a specific ISVD (such as the ISVD against c-Met described in this Example) or compound comprising the same is said to be "according to the invention" or "as further described herein", the preferred aspects/embodiments and preferences that are generally described herein for the ISVD's or compounds of the invention also specifically apply to said specific ISVD or compound, respectively, unless explicitly indicated otherwise or unless the specific technical context requires otherwise.

Thus, in a particular aspect, the present invention relates to a VH domain (and in particular an ISVD) that is directed against c-Met, in which (i) position 112 is K or Q; or (ii) position 110 is K or Q and position 11 is V; or (iii) position 89 is T; or (iv) position 89 is L and position 110 is K or Q; or (v) position 11 is V and position 89 is L; or any suitable combination of (i) to (v). In particular, in such VH domains against c-Met:

- the amino acid residue at position 11 is preferably chosen from L, V or K (and is most preferably V); and
- the amino acid residue at position 14 is preferably suitably chosen from A or P; and
- the amino acid residue at position 41 is preferably suitably chosen from A or P; and
- the amino acid residue at position 89 is preferably suitably chosen from T, V or L; and
- the amino acid residue at position 108 is preferably suitably chosen from Q or L; and
- the amino acid residue at position 110 is preferably suitably chosen from T, K or Q; and

- the amino acid residue at position 112 is preferably suitably chosen from S, K or Q; such that either (i) position 112 is K or Q; or (ii) position 110 is K or Q and position 11 is V; or (iii) position 89 is T; or (iv) position 89 is L and position 110 is K or Q; or (v) position 11 is V and position 89 is L; or any suitable combination of (i) to (v).

The VH domains of the invention against c-Met may further be as described herein and may again in particular be an ISVD (and more in particular a Nanobody) against c-Met or a protein, polypeptide or other compound or construct that comprises at least one such ISVD. Such a protein, polypeptide or other compound or construct may also be as further described herein, and may for example have an increased half-life (i.e. as described herein, e.g. a half-life - expressed as $t_{1/2}$ beta - in human subjects of in human subjects of at least 1 day, preferably at least 3 days, more preferably at least 7 days, such as at least 10 days), and for this purpose may for example comprise a serum-albumin binding Nanobody, which may also be a serum-albumin binding Nanobody of the invention (again, as described herein).

Also, such an ISVD may suitably have a C-terminal extension (as further described herein and in WO 12/175741), in particular when said ISVD forms the C-terminal end of a protein, polypeptide or other compound or construct comprising the same (again, as further described herein).

In one preferred aspect, the VH domains of the invention against c-Met comprise (i) a CDR1 sequence that is the sequence of SEQ ID NO: 353 (which is preferred) or that is an amino acid sequence that has only one amino acid difference with the sequence of SEQ ID NO: 353; (ii) a CDR2 sequence that is the sequence of SEQ ID NO: 354 (which is preferred) or that is an amino acid sequence that has only one or two amino acid differences with the sequence of SEQ ID NO: 354; and (iii) a CDR3 sequence that is the sequence of SEQ ID NO: 355 (which is preferred) or that is an amino acid sequence that has only one or two amino acid differences with the sequence of SEQ ID NO: 355.

More preferably, in a VH domain of the invention against c-Met according to this aspect: (i) CDR1 is SEQ ID NO: 353; (ii) CDR2 is SEQ ID NO: 354; and (iii) CDR3 is SEQ ID NO: 355.

In one specific aspect, a Nanobody of the invention against c-Met is a variant of the Nanobody of SEQ ID NO: 352 (with at least 90% sequence identity, such as at least 95% sequence identity, with SEQ ID NO: 352), in which:

- the amino acid residue at position 11 is preferably chosen from L, V or K (and is most preferably V); and

- the amino acid residue at position 14 is preferably suitably chosen from A or P; and
- the amino acid residue at position 41 is preferably suitably chosen from A or P; and
- the amino acid residue at position 89 is preferably suitably chosen from T, V or L; and
- the amino acid residue at position 108 is preferably suitably chosen from Q or L; and
- the amino acid residue at position 110 is preferably suitably chosen from T, K or Q; and
- the amino acid residue at position 112 is preferably suitably chosen from S, K or Q;

such that either (i) position 112 is K or Q; or (ii) position 110 is K or Q and position 11 is V; or (iii) position 89 is T; or (iv) position 89 is L and position 110 is K or Q; or (v) position 11 is V and position 89 is L; or any suitable combination of (i) to (v). The CDR's of such an ISV are preferably as defined in the preceding two paragraphs.

In another preferred aspect, the VH domains of the invention against c-Met comprise (i) a CDR1 sequence that is the sequence of SEQ ID NO: 371 (which is preferred) or that is an amino acid sequence that has only one amino acid difference with the sequence of SEQ ID NO: 371; (ii) a CDR2 sequence that is the sequence of SEQ ID NO: 372 (which is preferred) or that is an amino acid sequence that has only one or two amino acid differences with the sequence of SEQ ID NO: 372; and (iii) a CDR3 sequence that is the sequence of SEQ ID NO: 373 (which is preferred) or that is an amino acid sequence that has only one or two amino acid differences with the sequence of SEQ ID NO: 373.

More preferably, in such a VH domain of the invention against c-Met according to this aspect: (i) CDR1 is SEQ ID NO: 371; (ii) CDR2 is SEQ ID NO: 372; and (iii) CDR3 is SEQ ID NO: 373.

In one specific aspect, a Nanobody of the invention against c-Met is a variant of the Nanobody of SEQ ID NO: 370 (with at least 90% sequence identity, such as at least 95% sequence identity, with SEQ ID NO: 370), in which:

- the amino acid residue at position 11 is preferably chosen from L, V or K (and is most preferably V); and
- the amino acid residue at position 14 is preferably suitably chosen from A or P; and
- the amino acid residue at position 41 is preferably suitably chosen from A or P; and
- the amino acid residue at position 89 is preferably suitably chosen from T, V or L; and
- the amino acid residue at position 108 is preferably suitably chosen from Q or L; and
- the amino acid residue at position 110 is preferably suitably chosen from T, K or Q; and
- the amino acid residue at position 112 is preferably suitably chosen from S, K or Q;

such that either (i) position 112 is K or Q; or (ii) position 110 is K or Q and position 11 is V; or (iii) position 89 is T; or (iv) position 89 is L and position 110 is K or Q; or (v) position 11 is V and position 89 is L; or any suitable combination of (i) to (v). Again, the CDR's of such an ISV are preferably as defined in the preceding two paragraphs.

Some specifically preferred, but non-limiting examples of Nanobodies of the invention against c-Met are listed in Figure 18A as SEQ ID NO's: 356 to 369 and in Figure 18B as SEQ ID NO's: 374 to 387, respectively; and each of these Nanobodies form a further aspect of the invention.

The invention also relates to a compound of the invention against c-Met that comprises at least one (such as one, two or three) of the Nanobodies of the invention of SEQ ID NO's: 356 to 369 and/or 374 to 387. Such compounds of the invention against c-Met may again be as further described herein, and thus for example may comprise suitable linkers, may comprise a C-terminal extension as described herein, and may be half-life extended (for example because they comprise a Nanobody against human serum albumin, such as (preferably) a Nanobody of the invention against human serum albumin). Reference is made to Table Y below.

As described in for example WO 2013/045707, one particularly preferred class of Nanobody-based compounds against c-Met are biparatopic compounds. Thus, in one aspect of the invention, a compound of the invention against c-Met is a biparatopic construct that comprises one ISV that is either SEQ ID NO: 352 or (preferably) an ISV of the invention that has been derived from SEQ ID NO: 352 (as described in this Example 15) and one ISV that is either SEQ ID NO: 370 or (preferably) an ISV of the invention that has been derived from SEQ ID NO: 370 (as described in this Example 15), provided that at least one (and preferably both) of these ISV's are ISV's of the invention. Such biparatopic constructs may also be half-life extended (i.e. by means of a serum albumin-binding ISV). Some specific examples of such biparatopic constructs are given in SEQ ID NO: 676 to 693. Also, bispecific constructs against c-Met may also comprise an ISV against VEGF or EGFR. Reference is again made to WO 2014/341309.

Some specifically preferred examples of compounds of the invention against c-Met are given in Figures 28A and 28B SEQ ID NO's: 676 to 694; and each of these compounds form a further aspect of the invention. Thus, in another aspect, the invention relates to a polypeptide that is directed against c-Met and that has an amino acid sequence that is chosen from the group consisting of SEQ ID NO's: 676 to 694. More generally, compounds of the

invention against c-Met may be as described in WO 2013/045707, but comprising ISV's of the invention. They may also be used for the purposes described in WO 2013/045707.

Table Y: Examples of compounds of the invention against c-Met.

Polypeptide/ construct ⁽¹⁾	General formula	ISV building blocks and linkers
Monovalent	[c-Met]	[c-Met] = one of SEQ ID NO's: 464 to 477 and/or 482 to 495
Monovalent/ C-terminal extension	[c-Met]-X(n)	[c-Met] = one of SEQ ID NO's: 464 to 477 and/or 482 to 495
Monovalent/ half-life extended	[c-Met]- L ₁ -[SA] [SA]- L ₁ -[c-Met]	[c-Met] = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 [SA] = (see legend below) L ₁ = (see legend below)
Monovalent/ half-life extended/C- terminal extension	[c-Met] - L ₁ - [SA]-X(n) [SA]- L ₁ -[c-Met] -X(n)	[c-Met] = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 [SA] = (see legend below) L ₁ = (see legend below) X(n) = (see legend below)
Bivalent ⁽²⁾	[c-Met]- L ₁ -[c-Met]	At least one [c-Met] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 ⁽⁴⁾ L ₁ = (see legend below)

Table Y (continued)

Polypeptide/ construct ¹)	General formula	ISV building blocks and linkers
Bivalent/ C-terminal extension ⁽²⁾)	[c-Met]- L ₁ -[c-Met]- X(n)	At least one [c-Met] = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (⁴) L ₁ = (see legend below) X(n) = (see legend below)
Bivalent/ half-life extended ⁽²⁾)	[c-Met]- L ₁ -[c-Met]- L ₂ -[SA] [c-Met]- L ₁ -[SA]- L ₂ -[c-Met] [SA]- L ₁ -[c-Met]- L ₂ -[c-Met]	At least one [c-Met] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (⁴) [SA] = (see legend below) L ₁ = (see legend below) L ₂ = (see legend below)
Bivalent/ half-life extended/ C-terminal extension ⁽²⁾)	[c-Met]- L ₁ -[c-Met]- L ₂ -[SA]- X(n) [c-Met]- L ₁ -[SA]- L ₂ -[c-Met]- X(n) [SA]- L ₁ -[c-Met]- L ₂ -[c-Met]- X(n)	At least one [c-Met] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (⁴) [SA] = (see legend below) L ₁ = (see legend below) L ₂ = (see legend below) X(n) = (see legend below)

Table Y (continued)

Polypeptide/ construct(¹)	General formula	ISV building blocks and linkers
Bispecific (1)	[c-Met]-L ₁ -[Nb] [Nb]-L ₁ -[c-Met] [c-Met]-L ₁ -[c-Met]-L ₂ -[Nb] [c-Met]-L ₁ -[Nb]-L ₂ -[c-Met] [Nb]-L ₁ -[c-Met]-L ₂ -[c-Met]	At least one [c-Met] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (⁴) L ₁ = (see legend below) L ₂ = (see legend below) [Nb] = (see legend below)
Bispecific/ C-terminal extension (3)	[c-Met]-L ₁ -[Nb]-X(n) [Nb]-L ₁ -[c-Met]-X(n) [c-Met]-L ₁ -[c-Met]-L ₂ -[Nb]-X(n) [c-Met]-L ₁ -[Nb]-L ₂ -[c-Met]-X(n) [Nb]-L ₁ -[c-Met]-L ₂ -[c-Met]-X(n)	At least one [c-Met] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (⁴) L ₁ = (see legend below) L ₂ = (see legend below) X(n) = (see legend below) [Nb] = (see legend below)
Bispecific/ half-life extended (1)	[c-Met]-L ₁ -[Nb]-L ₂ -[SA] [c-Met]-L ₁ -[SA]-L ₂ -[Nb] [Nb]-L ₁ -[SA]-L ₂ -[c-Met] [Nb]-L ₁ -[c-Met]-L ₂ -[SA] [SA]-L ₁ -[c-Met]-L ₂ -[Nb] [SA]-L ₁ -[Nb]-L ₂ -[c-Met]	At least one [c-Met] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (⁴) [SA] = (see legend below) L ₁ , L ₂ , L ₃ (see legend below) [Nb] = (see legend below)

Table Y (continued)

Polypeptide/ construct ¹⁾	General formula	ISV building blocks and linkers
Bispecific/ half-life extended ²⁾	[c-Met]-L ₁ -[c-Met]-L ₂ -[Nb]-L ₃ -[SA] [Nb]-L ₁ -[c-Met]-L ₂ -[c-Met]-L ₃ -[SA] [SA]-L ₁ -[c-Met]-L ₂ -[c-Met]-L ₃ -[Nb] [SA]-L ₁ -[c-Met]-L ₂ -[Nb]-L ₃ -[c-Met] [c-Met]-L ₁ -[Nb]-L ₂ -[c-Met]-L ₃ -[SA]	At least one [c-Met] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 ⁽⁴⁾ [SA] = (see legend below) L ₁ , L ₂ , L ₃ (see legend below) [Nb] = (see legend below)
Bispecific/ half-life extended/ C-terminal extension ²⁾	[c-Met]-L ₁ -[Nb]-L ₂ -[SA]-X(n) [c-Met]-L ₁ -[SA]-L ₂ -[Nb]-X(n) [Nb]-L ₁ -[SA]-L ₂ -[c-Met]-X(n) [Nb]-L ₁ -[c-Met]-L ₂ -[SA]-X(n) [SA]-L ₁ -[c-Met]-L ₂ -[Nb]-X(n) [SA]-L ₁ -[Nb]-L ₂ -[c-Met]-X(n) [c-Met]-L ₁ -[c-Met]-L ₂ -[Nb]-L ₃ -[SA]-X(n) [Nb]-L ₁ -[c-Met]-L ₂ -[c-Met]-L ₃ -[SA]-X(n) [SA]-L ₁ -[c-Met]-L ₂ -[c-Met]-L ₃ -[Nb]-X(n) [SA]-L ₁ -[c-Met]-L ₂ -[Nb]-L ₃ -[c-Met]-X(n) [c-Met]-L ₁ -[Nb]-L ₂ -[c-Met]-L ₃ -[SA]-X(n)	At least one [c-Met] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 ⁽⁴⁾ [SA] = (see legend below) L ₁ , L ₂ , L ₃ (see legend below) X(n) = (see legend below) [Nb] = (see legend below)

Table Y (continued)

Legend:	<ul style="list-style-type: none"> - [SA] is an ISV against (human) serum albumin, preferably an ISV of the invention against (human) serum albumin, more preferably one of SEQ ID NO's: 46 or 61 or even more preferably one of the ISVD's of the invention of SEQ ID NO's: 47, 54, 62, 69, 78, 86, 109, 116, 123, 130 or 496 to 513. - Each of L₁, L₂ and L₃ is (independently) a suitable linker. Each of L₁, L₂ and L₃ may (independently) be present or not. Non-limiting examples of suitable linkers are the gly-ser linkers referred to herein, such as the 9GS, 30GS or 35GS linker. - X(n) = a C-terminal extension as a C-terminal extension as described in herein and/or in WO 12/175741 - [Nb] is an ISV against another therapeutic target.
Notes:	
(¹) In this Table:	
	<ul style="list-style-type: none"> - “<i>Monovalent</i>” generally refers to polypeptides/constructs comprising a single ISV against c-Met. These may further comprise a half-life extending ISV (such as an ISV against serum albumin). - “<i>Bivalent</i>” generally refers to polypeptides/constructs comprising two ISV's against c-Met (which may be the same or different). These may again further comprise a half-life extending ISV (such as an ISV against serum albumin). - “<i>Bispecific</i>” generally refers to polypeptides/constructs comprising at least one (such as 1 or 2) ISV's against c-Met and at least one (such as 1 or 2) other ISV against a therapeutic target. These may further comprise a half-life extending ISV (such as an ISV against serum albumin). - In the polypeptides/constructs described in this table, at least one of the ISV's against c-Met present is an ISV of the invention, and preferably all of the ISV's against c-Met present in such polypeptide/construct are ISV's of the invention. Also, when a half-life extending ISV and/or an ISV against another therapeutic target is present in such polypeptide/construct, each of these (and preferably all of these) may also be (and preferably are) ISV's of the invention
(²):	All “bivalent” constructs in this Table may also be biparatopic, meaning that they comprise at least two (such as two) ISV's against c-Met, which are directed against different epitopes on c-Met.
(³):	As will be clear to the skilled person, other/further bispecific constructs than those listed can be made using the building blocks and linkers mentioned.
(⁴):	Preferably, each [c-Met] present is independently chosen from SEQ ID NO's: 464 to 477 and/or 482 to 495. Also, the [c-Met] present may be the same or different; in a biparatopic polypeptide/construct they will be directed against different epitopes on c-Met.
(⁵):	Each of the polypeptides/constructs mentioned in this column by means of reference to a SEQ ID forms an individual specific aspect of the invention.

Example 16: VH domains (and in particular Nanobodies) against RANK-L, and compounds of the invention comprising the same.

In one specific aspect, the VH domains of the invention (and in particular ISVDs of the invention and more in particular Nanobodies of the invention) and compounds of the invention may be directed against RANK-L.

Such a VH domain of the invention against RANK-L will generally comprise: (i) suitable framework sequences that suitably comprise the amino acid residues/mutations of the invention as described herein; as well as (ii) CDR sequences that allow the VH domain of the invention to specifically bind to RANK-L. In addition, such a VH domain of the invention against RANK-L may also suitably have a C-terminal extension as described herein, in particular when said VH domain is monovalent or forms the C-terminal end of the compound of the invention in which said VH domain is present (again, as further described herein). Such VH domains of the invention against RANK-L may further be as further described herein, and may in particular be ISVD's.

Again, as with other aspects and embodiments of the invention described herein, when a specific ISVD (such as the ISVD against RANK-L described in this Example) or compound comprising the same is said to be "according to the invention" or "as further described herein", the preferred aspects/embodiments and preferences that are generally described herein for the ISVD's or compounds of the invention also specifically apply to said specific ISVD or compound, respectively, unless explicitly indicated otherwise or unless the specific technical context requires otherwise.

Thus, in a particular aspect, the present invention relates to a VH domain (and in particular an ISVD) that is directed against RANK-L, in which (i) position 112 is K or Q; or (ii) position 110 is K or Q and position 11 is V; or (iii) position 89 is T; or (iv) position 89 is L and position 110 is K or Q; or (v) position 11 is V and position 89 is L; or any suitable combination of (i) to (v). In particular, in such VH domains against RANK-L:

- the amino acid residue at position 11 is preferably chosen from L, V or K (and is most preferably V); and
- the amino acid residue at position 14 is preferably suitably chosen from A or P; and
- the amino acid residue at position 41 is preferably suitably chosen from A or P; and
- the amino acid residue at position 89 is preferably suitably chosen from T, V or L; and
- the amino acid residue at position 108 is preferably suitably chosen from Q or L; and
- the amino acid residue at position 110 is preferably suitably chosen from T, K or Q; and

- the amino acid residue at position 112 is preferably suitably chosen from S, K or Q; such that either (i) position 112 is K or Q; or (ii) position 110 is K or Q and position 11 is V; or (iii) position 89 is T; or (iv) position 89 is L and position 110 is K or Q; or (v) position 11 is V and position 89 is L; or any suitable combination of (i) to (v).

The VH domains of the invention against RANK-L may further be as described herein and may again in particular be an ISVD (and more in particular a Nanobody) against RANK-L or a protein, polypeptide or other compound or construct that comprises at least one such ISVD. Such a protein, polypeptide or other compound or construct may also be as further described herein, and may for example have an increased half-life (i.e. as described herein, e.g. a half-life - expressed as $t_{1/2}$ beta - in human subjects of in human subjects of at least 1 day, preferably at least 3 days, more preferably at least 7 days, such as at least 10 days), and for this purpose may for example comprise a serum-albumin binding Nanobody, which may also be a serum-albumin binding Nanobody of the invention (again, as described herein).

Also, such an ISVD may suitably have a C-terminal extension (as further described herein and in WO 12/175741), in particular when said ISVD forms the C-terminal end of a protein, polypeptide or other compound or construct comprising the same (again, as further described herein).

In one preferred aspect, the VH domains of the invention against RANK-L comprise (i) a CDR1 sequence that is the sequence of SEQ ID NO: 389 (which is preferred) or that is an amino acid sequence that has only one amino acid difference with the sequence of SEQ ID NO: 389; (ii) a CDR2 sequence that is the sequence of SEQ ID NO: 390 (which is preferred) or that is an amino acid sequence that has only one or two amino acid differences with the sequence of SEQ ID NO: 390; and (iii) a CDR3 sequence that is the sequence of SEQ ID NO: 391 (which is preferred) or that is an amino acid sequence that has only one or two amino acid differences with the sequence of SEQ ID NO: 391.

More preferably, in a VH domain of the invention against RANK-L according to this aspect: (i) CDR1 is SEQ ID NO: 389; (ii) CDR2 is SEQ ID NO: 390; and (iii) CDR3 is SEQ ID NO: 391.

In one specific aspect, a Nanobody of the invention against RANK-L is a variant of the Nanobody of SEQ ID NO: 388 (with at least 90% sequence identity, such as at least 95% sequence identity, with SEQ ID NO: 388), in which:

- the amino acid residue at position 11 is preferably chosen from L, V or K (and is most preferably V); and

- the amino acid residue at position 14 is preferably suitably chosen from A or P; and
- the amino acid residue at position 41 is preferably suitably chosen from A or P; and
- the amino acid residue at position 89 is preferably suitably chosen from T, V or L; and
- the amino acid residue at position 108 is preferably suitably chosen from Q or L; and
- the amino acid residue at position 110 is preferably suitably chosen from T, K or Q; and
- the amino acid residue at position 112 is preferably suitably chosen from S, K or Q;

such that either (i) position 112 is K or Q; or (ii) position 110 is K or Q and position 11 is V; or (iii) position 89 is T; or (iv) position 89 is L and position 110 is K or Q; or (v) position 11 is V and position 89 is L; or any suitable combination of (i) to (v). The CDR's of such an ISV are preferably as defined in the preceding two paragraphs.

Some specifically preferred, but non-limiting examples of Nanobodies of the invention against RANK-L are listed in Figure 19 as SEQ ID NO's: 392 to 405; and each of these Nanobodies form a further aspect of the invention.

The invention also relates to a compound of the invention against RANK-L that comprises at least one (such as one, two or three) of the Nanobodies of the invention of SEQ ID NO's: 392 to 405. Such compounds of the invention against RANK-L may again be as further described herein, and thus for example may comprise suitable linkers, may comprise a C-terminal extension as described herein, and may be half-life extended (for example because they comprise a Nanobody against human serum albumin, such as (preferably) a Nanobody of the invention against human serum albumin). Reference is made to Table Z below.

Some specifically preferred examples of compounds of the invention against RANK-L are given in Figure 29 as SEQ ID NO's: 694 to 729; and each of these compounds form a further aspect of the invention. Thus, in another aspect, the invention relates to a polypeptide that is directed against RANK-L and that has an amino acid sequence that is chosen from the group consisting of SEQ ID NO's: 694 to 729.

More generally, compounds of the invention against RANK-L may be as described in WO 2008/142164, but comprising ISV's of the invention. They may also be used for the purposes described in WO 2008/142164.

Table Z: Examples of compounds of the invention against RANK-L.

Polypeptide/ construct ⁽¹⁾	General formula	ISV building blocks and linkers
Monovalent	[RANK-L]	[RANK-L] = one of SEQ ID NO's: 464 to 477 and/or 482 to 495
Monovalent/ C-terminal extension	[RANK-L]-X(n)	[RANK-L] = one of SEQ ID NO's: 464 to 477 and/or 482 to 495
Monovalent/ half-life extended	[RANK-L]-L ₁ -[SA] [SA]-L ₁ -[RANK-L]	[RANK-L] = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 [SA] = (see legend below) L ₁ = (see legend below)
Monovalent/ half-life extended/C- terminal extension	[RANK-L]-L ₁ -[SA]-X(n) [SA]-L ₁ -[RANK-L]-X(n)	[RANK-L] = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 [SA] = (see legend below) L ₁ = (see legend below) X(n) = (see legend below)
Bivalent ⁽²⁾	[RANK-L]-L ₁ -[RANK-L]	At least one [RANK-L] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 ⁽⁴⁾ L ₁ = (see legend below)

Table Z (continued)

Polypeptide/ construct ⁽¹⁾	General formula	ISV building blocks and linkers
Bivalent/ C-terminal extension ⁽²⁾	[RANK-L]-L ₁ -[RANK-L]-X(n)	At least one [RANK-L] = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 ⁽⁴⁾ L ₁ = (see legend below) X(n) = (see legend below)
Bivalent/ half-life extended ⁽²⁾	[RANK-L]-L ₁ -[RANK-L]-L ₂ -[SA] [RANK-L]-L ₁ -[SA]-L ₂ -[RANK-L] [SA]-L ₁ -[RANK-L]-L ₂ -[RANK-L]	At least one [RANK-L] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 ⁽⁴⁾ [SA] = (see legend below) L ₁ = (see legend below) L ₂ = (see legend below)
Bivalent/ half-life extended/ C-terminal extension ⁽²⁾	[RANK-L]-L ₁ -[RANK-L]-L ₂ -[SA]-X(n) [RANK-L]-L ₁ -[SA]-L ₂ -[RANK-L]-X(n) [SA]-L ₁ -[RANK-L]-L ₂ -[RANK-L]-X(n)	At least one [RANK-L] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 ⁽⁴⁾ [SA] = (see legend below) L ₁ = (see legend below) L ₂ = (see legend below) X(n) = (see legend below)

Table Z (continued)

Polypeptide/ construct(¹)	General formula	ISV building blocks and linkers
Bispecific (1)	$[RANK-L] \cdot L_1 \cdot [Nb]$ $[Nb] \cdot L_1 \cdot [RANK-L]$ $[RANK-L] \cdot L_1 \cdot [RANK-L] \cdot L_2 \cdot [Nb]$ $[RANK-L] \cdot L_1 \cdot [Nb] \cdot L_2 \cdot [RANK-L]$ $[Nb] \cdot L_1 \cdot [RANK-L] \cdot L_2 \cdot [RANK-L]$	At least one [RANK-L] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (⁴) L ₁ = (see legend below) L ₂ = (see legend below) [Nb] = (see legend below)
Bispecific/ C-terminal extension (3)	$[RANK-L] \cdot L_1 \cdot [Nb] \cdot X(n)$ $[Nb] \cdot L_1 \cdot [RANK-L] \cdot X(n)$ $[RANK-L] \cdot L_1 \cdot [RANK-L] \cdot L_2 \cdot [Nb] \cdot X(n)$ $[RANK-L] \cdot L_1 \cdot [Nb] \cdot L_2 \cdot [RANK-L] \cdot X(n)$ $[Nb] \cdot L_1 \cdot [RANK-L] \cdot L_2 \cdot [RANK-L] \cdot X(n)$	At least one [RANK-L] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (⁴) L ₁ = (see legend below) L ₂ = (see legend below) X(n) = (see legend below) [Nb] = (see legend below)
Bispecific/ half-life extended (3)	$[RANK-L] \cdot L_1 \cdot [Nb] \cdot L_2 \cdot [SA]$ $[RANK-L] \cdot L_1 \cdot [SA] \cdot L_2 \cdot [Nb]$ $[Nb] \cdot L_1 \cdot [SA] \cdot L_2 \cdot [RANK-L]$ $[Nb] \cdot L_1 \cdot [RANK-L] \cdot L_2 \cdot [SA]$ $[SA] \cdot L_1 \cdot [RANK-L] \cdot L_2 \cdot [Nb]$ $[SA] \cdot L_1 \cdot [Nb] \cdot L_2 \cdot [RANK-L]$	At least one [RANK-L] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (⁴) [SA] = (see legend below) L ₁ , L ₂ , L ₃ (see legend below) [Nb] = (see legend below)

Table Z (continued)

Polypeptide/ construct(¹)	General formula	ISV building blocks and linkers
Bispecific/ half-life extended (³)	$[\text{RANK-L}] \cdot L_1 \cdot [\text{RANK-L}] \cdot L_2 \cdot [\text{Nb}] \cdot L_3 \cdot [\text{SA}]$ $[\text{Nb}] \cdot L_1 \cdot [\text{RANK-L}] \cdot L_2 \cdot [\text{RANK-L}] \cdot L_3 \cdot [\text{SA}]$ $[\text{SA}] \cdot L_1 \cdot [\text{RANK-L}] \cdot L_2 \cdot [\text{RANK-L}] \cdot L_3 \cdot [\text{Nb}]$ $[\text{SA}] \cdot L_1 \cdot [\text{RANK-L}] \cdot L_2 \cdot [\text{Nb}] \cdot L_3 \cdot [\text{RANK-L}]$ $[\text{RANK-L}] \cdot L_1 \cdot [\text{Nb}] \cdot L_2 \cdot [\text{RANK-L}] \cdot L_3 \cdot [\text{SA}]$	At least one [RANK-L] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (⁴) [SA] = (see legend below) L ₁ , L ₂ , L ₃ (see legend below) [Nb] = (see legend below)
Bispecific/ half-life extended/ C-terminal extension (³)	$[\text{RANK-L}] \cdot L_1 \cdot [\text{Nb}] \cdot L_2 \cdot [\text{SA}] \cdot X(n)$ $[\text{RANK-L}] \cdot L_1 \cdot [\text{SA}] \cdot L_2 \cdot [\text{Nb}] \cdot X(n)$ $[\text{Nb}] \cdot L_1 \cdot [\text{SA}] \cdot L_2 \cdot [\text{RANK-L}] \cdot X(n)$ $[\text{Nb}] \cdot L_1 \cdot [\text{RANK-L}] \cdot L_2 \cdot [\text{SA}] \cdot X(n)$ $[\text{SA}] \cdot L_1 \cdot [\text{RANK-L}] \cdot L_2 \cdot [\text{Nb}] \cdot X(n)$ $[\text{SA}] \cdot L_1 \cdot [\text{Nb}] \cdot L_2 \cdot [\text{RANK-L}] \cdot X(n)$ $[\text{RANK-L}] \cdot L_1 \cdot [\text{RANK-L}] \cdot L_2 \cdot [\text{Nb}] \cdot L_3 \cdot [\text{SA}] \cdot X(n)$ $[\text{Nb}] \cdot L_1 \cdot [\text{RANK-L}] \cdot L_2 \cdot [\text{RANK-L}] \cdot L_3 \cdot [\text{SA}] \cdot X(n)$ $[\text{SA}] \cdot L_1 \cdot [\text{RANK-L}] \cdot L_2 \cdot [\text{RANK-L}] \cdot L_3 \cdot [\text{Nb}] \cdot X(n)$ $[\text{SA}] \cdot L_1 \cdot [\text{RANK-L}] \cdot L_2 \cdot [\text{Nb}] \cdot L_3 \cdot [\text{RANK-L}] \cdot X(n)$ $[\text{RANK-L}] \cdot L_1 \cdot [\text{Nb}] \cdot L_2 \cdot [\text{RANK-L}] \cdot L_3 \cdot [\text{SA}] \cdot X(n)$	At least one [RANK-L] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (⁴) [SA] = (see legend below) L ₁ , L ₂ , L ₃ (see legend below) X(n) = (see legend below) [Nb] = (see legend below)

Table Z (continued)

Legend:		
- [SA] is an ISV against (human) serum albumin, preferably an ISV of the invention against (human) serum albumin, more preferably one of SEQ ID NO's: 46 or 61 or even more preferably one of the ISVD's of the invention of SEQ ID NO's: 47, 54, 62, 69, 78, 86, 109, 116, 123, 130 or 496 to 513.		
- Each of L ₁ , L ₂ and L ₃ is (independently) a suitable linker. Each of L ₁ , L ₂ and L ₃ may (independently) be present or not. Non-limiting examples of suitable linkers are the gly-ser linkers referred to herein, such as the 9GGS, 30GGS or 35GGS linker.		
- X(n) = a C-terminal extension as a C-terminal extension as described in herein and/or in WO 12/175741		
- [Nb] is an ISV against another therapeutic target.		
Notes:		
(¹) In this Table:		
- “ <i>Monovalent</i> ” generally refers to polypeptides/constructs comprising a single ISV against RANK-L. These may further comprise a half-life extending ISV (such as an ISV against serum albumin).		
- “ <i>Bivalent</i> ” generally refers to polypeptides/constructs comprising two ISV's against RANK-L (which may be the same or different). These may again further comprise a half-life extending ISV (such as an ISV against serum albumin).		
- “ <i>Bispecific</i> ” generally refers to polypeptides/constructs comprising at least one (such as 1 or 2) ISV's against RANK-L and at least one (such as 1 or 2) other ISV against a therapeutic target. These may further comprise a half-life extending ISV (such as an ISV against serum albumin).		
- In the polypeptides/constructs described in this table, at least one of the ISV's against RANK-L present is an ISV of the invention, and preferably all of the ISV's against RANK-L present in such polypeptide/construct are ISV's of the invention. Also, when a half-life extending ISV and/or an ISV against another therapeutic target is present in such polypeptide/construct, each of these (and preferably all of these) may also be (and preferably are) ISV's of the invention		
(²): All “bivalent” constructs in this Table may also be biparatopic, meaning that they comprise at least two (such as two) ISV's against RANK-L, which are directed against different epitopes on RANK-L.		
(³): As will be clear to the skilled person, other/further bispecific constructs than those listed can be made using the building blocks and linkers mentioned.		
(⁴) Preferably, each [RANK-L] present is independently chosen from SEQ ID NO's: 464 to 477 and/or 482 to 495. Also, the [RANK-L] present may be the same or different; in a biparatopic polypeptide/construct they will be directed against different epitopes on RANK-L.		
(⁵) Each of the polypeptides/constructs mentioned to in this column by means of reference to a SEQ ID forms an individual specific aspect of the invention.		

Example 17: VH domains (and in particular Nanobodies) against CXCR-7, and compounds of the invention comprising the same.

In one specific aspect, the VH domains of the invention (and in particular ISVDs of the invention and more in particular Nanobodies of the invention) and compounds of the invention may be directed against CXCR-7.

Such a VH domain of the invention against CXCR-7 will generally comprise: (i) suitable framework sequences that suitably comprise the amino acid residues/mutations of the invention as described herein; as well as (ii) CDR sequences that allow the VH domain of the invention to specifically bind to CXCR-7. In addition, such a VH domain of the invention against CXCR-7 may also suitably have a C-terminal extension as described herein, in particular when said VH domain is monovalent or forms the C-terminal end of the compound of the invention in which said VH domain is present (again, as further described herein). Such VH domains of the invention against CXCR-7 may further be as further described herein, and may in particular be ISVD's.

Again, as with other aspects and embodiments of the invention described herein, when a specific ISVD (such as the ISVD against CXCR-7 described in this Example) or compound comprising the same is said to be "according to the invention" or "as further described herein", the preferred aspects/embodiments and preferences that are generally described herein for the ISVD's or compounds of the invention also specifically apply to said specific ISVD or compound, respectively, unless explicitly indicated otherwise or unless the specific technical context requires otherwise.

Thus, in a particular aspect, the present invention relates to a VH domain (and in particular an ISVD) that is directed against CXCR-7, in which (i) position 112 is K or Q; or (ii) position 110 is K or Q and position 11 is V; or (iii) position 89 is T; or (iv) position 89 is L and position 110 is K or Q; or (v) position 11 is V and position 89 is L; or any suitable combination of (i) to (v). In particular, in such VH domains against CXCR-7:

- the amino acid residue at position 11 is preferably chosen from L, V or K (and is most preferably V); and
- the amino acid residue at position 14 is preferably suitably chosen from A or P; and
- the amino acid residue at position 41 is preferably suitably chosen from A or P; and
- the amino acid residue at position 89 is preferably suitably chosen from T, V or L; and
- the amino acid residue at position 108 is preferably suitably chosen from Q or L; and
- the amino acid residue at position 110 is preferably suitably chosen from T, K or Q; and

- the amino acid residue at position 112 is preferably suitably chosen from S, K or Q; such that either (i) position 112 is K or Q; or (ii) position 110 is K or Q and position 11 is V; or (iii) position 89 is T; or (iv) position 89 is L and position 110 is K or Q; or (v) position 11 is V and position 89 is L; or any suitable combination of (i) to (v).

The VH domains of the invention against CXCR-7 may further be as described herein and may again in particular be an ISVD (and more in particular a Nanobody) against CXCR-7 or a protein, polypeptide or other compound or construct that comprises as least one such ISVD. Such a protein, polypeptide or other compound or construct may also be as further described herein, and may for example have an increased half-life (i.e. as described herein, e.g. a half-life - expressed as t_{1/2} beta - in human subjects of in human subjects of at least 1 day, preferably at least 3 days, more preferably at least 7 days, such as at least 10 days), and for this purpose may for example comprise a serum-albumin binding Nanobody, which may also be a serum-albumin binding Nanobody of the invention (again, as described herein).

Also, such an ISVD may suitably have a C-terminal extension (as further described herein and in WO 12/175741), in particular when said ISVD forms the C-terminal end of a protein, polypeptide or other compound or construct comprising the same (again, as further described herein).

In one preferred aspect, the VH domains of the invention against CXCR-7 comprise (i) a CDR1 sequence that is the sequence of SEQ ID NO: 407 (which is preferred) or that is an amino acid sequence that has only one amino acid difference with the sequence of SEQ ID NO: 407; (ii) a CDR2 sequence that is the sequence of SEQ ID NO: 408 (which is preferred) or that is an amino acid sequence that has only one or two amino acid differences with the sequence of SEQ ID NO: 408; and (iii) a CDR3 sequence that is the sequence of SEQ ID NO: 409 (which is preferred) or that is an amino acid sequence that has only one or two amino acid differences with the sequence of SEQ ID NO: 409.

More preferably, in a VH domain of the invention against CXCR-7 according to this aspect: (i) CDR1 is SEQ ID NO: 407; (ii) CDR2 is SEQ ID NO: 408; and (iii) CDR3 is SEQ ID NO: 409.

In one specific aspect, a Nanobody of the invention against CXCR-7 is a variant of the Nanobody of SEQ ID NO: 406 (with at least 90% sequence identity, such as at least 95% sequence identity, with SEQ ID NO: 406), in which:

- the amino acid residue at position 11 is preferably chosen from L, V or K (and is most preferably V); and

- the amino acid residue at position 14 is preferably suitably chosen from A or P; and
- the amino acid residue at position 41 is preferably suitably chosen from A or P; and
- the amino acid residue at position 89 is preferably suitably chosen from T, V or L; and
- the amino acid residue at position 108 is preferably suitably chosen from Q or L; and
- the amino acid residue at position 110 is preferably suitably chosen from T, K or Q; and
- the amino acid residue at position 112 is preferably suitably chosen from S, K or Q;

such that either (i) position 112 is K or Q; or (ii) position 110 is K or Q and position 11 is V; or (iii) position 89 is T; or (iv) position 89 is L and position 110 is K or Q; or (v) position 11 is V and position 89 is L; or any suitable combination of (i) to (v). The CDR's of such an ISV are preferably as defined in the preceding two paragraphs.

In another preferred aspect, the VH domains of the invention against CXCR-7 comprise (i) a CDR1 sequence that is the sequence of SEQ ID NO: 425 (which is preferred) or that is an amino acid sequence that has only one amino acid difference with the sequence of SEQ ID NO: 425; (ii) a CDR2 sequence that is the sequence of SEQ ID NO: 426 (which is preferred) or that is an amino acid sequence that has only one or two amino acid differences with the sequence of SEQ ID NO: 426; and (iii) a CDR3 sequence that is the sequence of SEQ ID NO: 427 (which is preferred) or that is an amino acid sequence that has only one or two amino acid differences with the sequence of SEQ ID NO: 427.

More preferably, in a VH domain of the invention against CXCR-7 according to this aspect: (i) CDR1 is SEQ ID NO: 425; (ii) CDR2 is SEQ ID NO: 426; and (iii) CDR3 is SEQ ID NO: 427.

In one specific aspect, a Nanobody of the invention against CXCR-7 is a variant of the Nanobody of SEQ ID NO: 424 (with at least 90% sequence identity, such as at least 95% sequence identity, with SEQ ID NO: 424), in which:

- the amino acid residue at position 11 is preferably chosen from L, V or K (and is most preferably V); and
- the amino acid residue at position 14 is preferably suitably chosen from A or P; and
- the amino acid residue at position 41 is preferably suitably chosen from A or P; and
- the amino acid residue at position 89 is preferably suitably chosen from T, V or L; and
- the amino acid residue at position 108 is preferably suitably chosen from Q or L; and
- the amino acid residue at position 110 is preferably suitably chosen from T, K or Q; and
- the amino acid residue at position 112 is preferably suitably chosen from S, K or Q;

such that either (i) position 112 is K or Q; or (ii) position 110 is K or Q and position 11 is V; or (iii) position 89 is T; or (iv) position 89 is L and position 110 is K or Q; or (v) position 11 is V and position 89 is L; or any suitable combination of (i) to (v). Again, the CDR's of such an ISV are preferably as defined in the preceding two paragraphs.

Some specifically preferred, but non-limiting examples of Nanobodies of the invention against CXCR-7 are listed in Figure 20A as SEQ ID NO's: 410 to 423 and in Figure 20B as SEQ ID NO's: 428 to 441; and each of these Nanobodies form a further aspect of the invention.

The invention also relates to a compound of the invention against CXCR-7 that comprises at least one (such as one, two or three) of the Nanobodies of the invention of SEQ ID NO's: 410 to 423 and/or 428 to 441. Such compounds of the invention against CXCR-7 may again be as further described herein, and thus for example may comprise suitable linkers, may comprise a C-terminal extension as described herein, and may be half-life extended (for example because they comprise a Nanobody against human serum albumin, such as (preferably) a Nanobody of the invention against human serum albumin). Reference is made to Table AA below.

As described in for example WO2012/130874, one particularly preferred class of Nanobody-based compounds against CXCR7 are biparatopic compounds. Thus, in one aspect of the invention, a compound of the invention against CXCR-7 is a biparatopic construct that comprises one ISV that is either SEQ ID NO: 406 or (preferably) an ISV of the invention that has been derived from SEQ ID NO: 406 (as described in this Example 17) and one ISV that is either SEQ ID NO: 424 or (preferably) an ISV of the invention that has been derived from SEQ ID NO: 424 (as described in this Example 17), provided that at least one (and preferably both) of these ISV's are ISV's of the invention. Such biparatopic constructs may also be half-life extended (i.e. by means of a serum albumin-binding ISV).

More generally, compounds of the invention against CXCR-7 may be as described in WO2012/130874, but comprising ISV's of the invention. They may also be used for the purposes described in WO2012/130874.

Table AA: Examples of compounds of the invention against CXCR-7.

Polypeptide/ construct ⁽¹⁾	General formula	ISV building blocks and linkers
Monovalent	[CXCR-7]	[CXCR-7] = one of SEQ ID NO's: 464 to 477 and/or 482 to 495
Monovalent/ C-terminal extension	[CXCR-7]-X(n)	[CXCR-7] = one of SEQ ID NO's: 464 to 477 and/or 482 to 495
Monovalent/ half-life extended	[CXCR-7]-L ₁ -[SA] [SA]-L ₁ -[CXCR-7]	[CXCR-7] = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 [SA] = (see legend below) L ₁ = (see legend below)
Monovalent/ half-life extended/C- terminal extension	[CXCR-7] - L ₁ - [SA]-X(n) [SA]-L ₁ -[CXCR-7] - X(n)	[CXCR-7] = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 [SA] = (see legend below) L ₁ = (see legend below) X(n) = (see legend below)
Bivalent ⁽²⁾	[CXCR-7]- L ₁ -[CXCR-7]	At least one [CXCR-7] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 ⁽⁴⁾ L ₁ = (see legend below)

Table AA (continued)

Polypeptide/ construct(¹)	General formula	ISV building blocks and linkers
Bivalent/ C-terminal extension(²)	[CXCR-7]-L ₁ -[CXCR-7]-X(n)	At least one [CXCR-7] = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (⁴) L ₁ = (see legend below) X(n) = (see legend below)
Bivalent/ half-life extended(²)	[CXCR-7]-L ₁ -[CXCR-7]-L ₂ -[SA] [CXCR-7]-L ₁ -[SA]-L ₂ -[CXCR-7] [SA]-L ₁ -[CXCR-7]-L ₂ -[CXCR-7]	At least one [CXCR-7] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (⁴) [SA] = (see legend below) L ₁ = (see legend below) L ₂ = (see legend below)
Bivalent/ half-life extended/ C-terminal extension(²)	[CXCR-7]-L ₁ -[CXCR-7]-L ₂ -[SA] -X(n) [CXCR-7]-L ₁ -[SA]-L ₂ -[CXCR-7] -X(n) [SA]-L ₁ -[CXCR-7]-L ₂ -[CXCR-7] -X(n)	At least one [CXCR-7] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (⁴) [SA] = (see legend below) L ₁ = (see legend below) L ₂ = (see legend below) X(n) = (see legend below)

Table AA (continued)

Polypeptide/ construct(¹)	General formula	ISV building blocks and linkers
Bispecific (1)	$[\text{CXCR-7}] \cdot L_1 \cdot [\text{Nb}]$ $[\text{Nb}] \cdot L_1 \cdot [\text{CXCR-7}]$ $[\text{CXCR-7}] \cdot L_1 \cdot [\text{CXCR-7}] \cdot L_2 \cdot [\text{Nb}]$ $[\text{CXCR-7}] \cdot L_1 \cdot [\text{Nb}] \cdot L_2 \cdot [\text{CXCR-7}]$ $[\text{Nb}] \cdot L_1 \cdot [\text{CXCR-7}] \cdot L_2 \cdot [\text{CXCR-7}]$	At least one [CXCR-7] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (⁴) L ₁ = (see legend below) L ₂ = (see legend below) [Nb] = (see legend below)
Bispecific/ C-terminal extension (3)	$[\text{CXCR-7}] \cdot L_1 \cdot [\text{Nb}] \cdot X(n)$ $[\text{Nb}] \cdot L_1 \cdot [\text{CXCR-7}] \cdot X(n)$ $[\text{CXCR-7}] \cdot L_1 \cdot [\text{CXCR-7}] \cdot L_2 \cdot [\text{Nb}] \cdot X(n)$ $[\text{CXCR-7}] \cdot L_1 \cdot [\text{Nb}] \cdot L_2 \cdot [\text{CXCR-7}] \cdot X(n)$ $[\text{Nb}] \cdot L_1 \cdot [\text{CXCR-7}] \cdot L_2 \cdot [\text{CXCR-7}] \cdot X(n)$	At least one [CXCR-7] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (⁴) L ₁ = (see legend below) L ₂ = (see legend below) X(n) = (see legend below) [Nb] = (see legend below)
Bispecific/ half-life extended (1)	$[\text{CXCR-7}] \cdot L_1 \cdot [\text{Nb}] \cdot L_2 \cdot [\text{SA}]$ $[\text{CXCR-7}] \cdot L_1 \cdot [\text{SA}] \cdot L_2 \cdot [\text{Nb}]$ $[\text{Nb}] \cdot L_1 \cdot [\text{SA}] \cdot L_2 \cdot [\text{CXCR-7}]$ $[\text{Nb}] \cdot L_1 \cdot [\text{CXCR-7}] \cdot L_2 \cdot [\text{SA}]$ $[\text{SA}] \cdot L_1 \cdot [\text{CXCR-7}] \cdot L_2 \cdot [\text{Nb}]$ $[\text{SA}] \cdot L_1 \cdot [\text{Nb}] \cdot L_2 \cdot [\text{CXCR-7}]$	At least one [CXCR-7] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (⁴) [SA] = (see legend below) L ₁ , L ₂ , L ₃ (see legend below) [Nb] = (see legend below)

Table AA (continued)

Polypeptide/ construct(¹)	General formula	ISV building blocks and linkers
Bispecific/ half-life extended (³)	$[\text{CXCR-7}] \cdot L_1 \cdot [\text{CXCR-7}] \cdot L_2 \cdot [\text{Nb}] \cdot L_3 \cdot [\text{SA}]$ $[\text{Nb}] \cdot L_1 \cdot [\text{CXCR-7}] \cdot L_2 \cdot [\text{CXCR-7}] \cdot L_3 \cdot [\text{SA}]$ $[\text{SA}] \cdot L_1 \cdot [\text{CXCR-7}] \cdot L_2 \cdot [\text{CXCR-7}] \cdot L_3 \cdot [\text{Nb}]$ $[\text{SA}] \cdot L_1 \cdot [\text{CXCR-7}] \cdot L_2 \cdot [\text{Nb}] \cdot L_3 \cdot [\text{CXCR-7}]$ $[\text{CXCR-7}] \cdot L_1 \cdot [\text{Nb}] \cdot L_2 \cdot [\text{CXCR-7}] \cdot L_3 \cdot [\text{SA}]$	At least one [CXCR-7] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (⁴) [SA] = (see legend below) L ₁ , L ₂ , L ₃ (see legend below) [Nb] = (see legend below)
Bispecific/ half-life extended/ C-terminal extension (³)	$[\text{CXCR-7}] \cdot L_1 \cdot [\text{Nb}] \cdot L_2 \cdot [\text{SA}] \cdot X(n)$ $[\text{CXCR-7}] \cdot L_1 \cdot [\text{SA}] \cdot L_2 \cdot [\text{Nb}] \cdot X(n)$ $[\text{Nb}] \cdot L_1 \cdot [\text{SA}] \cdot L_2 \cdot [\text{CXCR-7}] \cdot X(n)$ $[\text{Nb}] \cdot L_1 \cdot [\text{CXCR-7}] \cdot L_2 \cdot [\text{SA}] \cdot X(n)$ $[\text{SA}] \cdot L_1 \cdot [\text{CXCR-7}] \cdot L_2 \cdot [\text{Nb}] \cdot X(n)$ $[\text{SA}] \cdot L_1 \cdot [\text{Nb}] \cdot L_2 \cdot [\text{CXCR-7}] \cdot X(n)$ $[\text{CXCR-7}] \cdot L_1 \cdot [\text{CXCR-7}] \cdot L_2 \cdot [\text{Nb}] \cdot L_3 \cdot [\text{SA}] \cdot X(n)$ $[\text{Nb}] \cdot L_1 \cdot [\text{CXCR-7}] \cdot L_2 \cdot [\text{CXCR-7}] \cdot L_3 \cdot [\text{SA}] \cdot X(n)$ $[\text{SA}] \cdot L_1 \cdot [\text{CXCR-7}] \cdot L_2 \cdot [\text{CXCR-7}] \cdot L_3 \cdot [\text{Nb}] \cdot X(n)$ $[\text{SA}] \cdot L_1 \cdot [\text{CXCR-7}] \cdot L_2 \cdot [\text{Nb}] \cdot L_3 \cdot [\text{CXCR-7}] \cdot X(n)$ $[\text{CXCR-7}] \cdot L_1 \cdot [\text{Nb}] \cdot L_2 \cdot [\text{CXCR-7}] \cdot L_3 \cdot [\text{SA}] \cdot X(n)$	At least one [CXCR-7] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (⁴) [SA] = (see legend below) L ₁ , L ₂ , L ₃ (see legend below) X(n) = (see legend below) [Nb] = (see legend below)

Table AA (continued)

Legend:	Notes:	
- [SA] is an ISV against (human) serum albumin, preferably an ISV of the invention against (human) serum albumin, more preferably one of SEQ ID NO's: 46 or 61 or even more preferably one of the ISVD's of the invention of SEQ ID NO's: 47, 54, 62, 69, 78, 86, 109, 116, 123, 130 or 496 to 513.		
- Each of L ₁ , L ₂ and L ₃ is (independently) a suitable linker. Each of L ₁ , L ₂ and L ₃ may (independently) be present or not. Non-limiting examples of suitable linkers are the gly-ser linkers referred to herein, such as the 9GS, 30GS or 35GS linker.		
- X(n) = a C-terminal extension as a C-terminal extension as described in herein and/or in WO 12/175741		
- [Nb] is an ISV against another therapeutic target.		
<p>⁽¹⁾ In this Table:</p> <ul style="list-style-type: none"> - “<i>Monovalent</i>” generally refers to polypeptides/constructs comprising two ISV's against CXCR-7 (which may be the same or different). These may further comprise a half-life extending ISV (such as an ISV against serum albumin). - “<i>Bivalent</i>” generally refers to polypeptides/constructs comprising at least one (such as 1 or 2) ISV's against CXCR-7 and at least one (such as 1 or 2) other comprise a half-life extending ISV (such as an ISV against serum albumin). - “<i>Bispecific</i>” generally refers to polypeptides/constructs comprising at least one (such as 1 or 2) ISV's against CXCR-7 and at least one (such as 1 or 2) other ISV against a therapeutic target. These may further comprise a half-life extending ISV (such as an ISV against serum albumin). - In the polypeptides/constructs described in this table, at least one of the ISV's against CXCR-7 present is an ISV of the invention, and preferably all of the ISV's against CXCR-7 present in such polypeptide/construct are ISV's of the invention. Also, when a half-life extending ISV and/or an ISV against another therapeutic target is present in such polypeptide/construct, each of these (and preferably all of these) may also be (and preferably are) ISV's of the invention <p>(²): All “bivalent” constructs in this Table may also be biparatopic, meaning that they comprise at least two (such as two) ISV's against CXCR-7, which are directed against different epitopes on CXCR-7.</p> <p>(³): As will be clear to the skilled person, other/further bispecific constructs than those listed can be made using the building blocks and linkers mentioned.</p> <p>(⁴): Preferably, each [CXCR-7] present is independently chosen from SEQ ID NO's: 464 to 477 and/or 482 to 495. Also, the [CXCR-7] present may be the same or different; in a biparatopic polypeptide/construct they will be directed against different epitopes on CXCR-7.</p> <p>(⁵): Each of the polypeptides/constructs mentioned to in this column by means of reference to a SEQ ID forms an individual specific aspect of the invention.</p>		

Example 18: VH domains (and in particular Nanobodies) against A-beta, and compounds of the invention comprising the same.

In one specific aspect, the VH domains of the invention (and in particular ISVDs of the invention and more in particular Nanobodies of the invention) and compounds of the invention may be directed against A-beta.

Such a VH domain of the invention against A-beta will generally comprise: (i) suitable framework sequences that suitably comprise the amino acid residues/mutations of the invention as described herein; as well as (ii) CDR sequences that allow the VH domain of the invention to specifically bind to A-beta. In addition, such a VH domain of the invention against A-beta may also suitably have a C-terminal extension as described herein, in particular when said VH domain is monovalent or forms the C-terminal end of the compound of the invention in which said VH domain is present (again, as further described herein). Such VH domains of the invention against A-beta may further be as further described herein, and may in particular be ISVD's.

Again, as with other aspects and embodiments of the invention described herein, when a specific ISVD (such as the ISVD against A-beta described in this Example) or compound comprising the same is said to be "according to the invention" or "as further described herein", the preferred aspects/embodiments and preferences that are generally described herein for the ISVD's or compounds of the invention also specifically apply to said specific ISVD or compound, respectively, unless explicitly indicated otherwise or unless the specific technical context requires otherwise.

Thus, in a particular aspect, the present invention relates to a VH domain (and in particular an ISVD) that is directed against A-beta, in which (i) position 112 is K or Q; or (ii) position 110 is K or Q and position 11 is V; or (iii) position 89 is T; or (iv) position 89 is L and position 110 is K or Q; or (v) position 11 is V and position 89 is L; or any suitable combination of (i) to (v). In particular, in such VH domains against A-beta:

- the amino acid residue at position 11 is preferably chosen from L, V or K (and is most preferably V); and
- the amino acid residue at position 14 is preferably suitably chosen from A or P; and
- the amino acid residue at position 41 is preferably suitably chosen from A or P; and
- the amino acid residue at position 89 is preferably suitably chosen from T, V or L; and
- the amino acid residue at position 108 is preferably suitably chosen from Q or L; and
- the amino acid residue at position 110 is preferably suitably chosen from T, K or Q; and

- the amino acid residue at position 112 is preferably suitably chosen from S, K or Q; such that either (i) position 112 is K or Q; or (ii) position 110 is K or Q and position 11 is V; or (iii) position 89 is T; or (iv) position 89 is L and position 110 is K or Q; or (v) position 11 is V and position 89 is L; or any suitable combination of (i) to (v).

The VH domains of the invention against A-beta may further be as described herein and may again in particular be an ISVD (and more in particular a Nanobody) against A-beta or a protein, polypeptide or other compound or construct that comprises as least one such ISVD. Such a protein, polypeptide or other compound or construct may also be as further described herein, and may for example have an increased half-life (i.e. as described herein, e.g. a half-life - expressed as $t_{1/2}$ beta - in human subjects of in human subjects of at least 1 day, preferably at least 3 days, more preferably at least 7 days, such as at least 10 days), and for this purpose may for example comprise a serum-albumin binding Nanobody, which may also be a serum-albumin binding Nanobody of the invention (again, as described herein).

Also, such an ISVD may suitably have a C-terminal extension (as further described herein and in WO 12/175741), in particular when said ISVD forms the C-terminal end of a protein, polypeptide or other compound or construct comprising the same (again, as further described herein).

In one preferred aspect, the VH domains of the invention against A-beta comprise (i) a CDR1 sequence that is the sequence of SEQ ID NO: 461 (which is preferred) or that is an amino acid sequence that has only one amino acid difference with the sequence of SEQ ID NO: 461; (ii) a CDR2 sequence that is the sequence of SEQ ID NO: 462 (which is preferred) or that is an amino acid sequence that has only one or two amino acid differences with the sequence of SEQ ID NO: 462; and (iii) a CDR3 sequence that is the sequence of SEQ ID NO: 463 (which is preferred) or that is an amino acid sequence that has only one or two amino acid differences with the sequence of SEQ ID NO: 463.

More preferably, in a VH domain of the invention against A-beta according to this aspect: (i) CDR1 is SEQ ID NO: 461; (ii) CDR2 is SEQ ID NO: 462; and (iii) CDR3 is SEQ ID NO: 463.

In one specific aspect, a Nanobody of the invention against A-beta is a variant of the Nanobody of SEQ ID NO: 460 (with at least 90% sequence identity, such as at least 95% sequence identity, with SEQ ID NO: 460), in which:

- the amino acid residue at position 11 is preferably chosen from L, V or K (and is most preferably V); and

- the amino acid residue at position 14 is preferably suitably chosen from A or P; and
- the amino acid residue at position 41 is preferably suitably chosen from A or P; and
- the amino acid residue at position 89 is preferably suitably chosen from T, V or L; and
- the amino acid residue at position 108 is preferably suitably chosen from Q or L; and
- the amino acid residue at position 110 is preferably suitably chosen from T, K or Q; and
- the amino acid residue at position 112 is preferably suitably chosen from S, K or Q;

such that either (i) position 112 is K or Q; or (ii) position 110 is K or Q and position 11 is V; or (iii) position 89 is T; or (iv) position 89 is L and position 110 is K or Q; or (v) position 11 is V and position 89 is L; or any suitable combination of (i) to (v). The CDR's of such an ISV are preferably as defined in the preceding two paragraphs.

In another preferred aspect, the VH domains of the invention against A-beta comprise (i) a CDR1 sequence that is the sequence of SEQ ID NO: 479 (which is preferred) or that is an amino acid sequence that has only one amino acid difference with the sequence of SEQ ID NO: 479; (ii) a CDR2 sequence that is the sequence of SEQ ID NO: 480 (which is preferred) or that is an amino acid sequence that has only one or two amino acid differences with the sequence of SEQ ID NO: 480; and (iii) a CDR3 sequence that is the sequence of SEQ ID NO: 481 (which is preferred) or that is an amino acid sequence that has only one or two amino acid differences with the sequence of SEQ ID NO: 481.

More preferably, in a VH domain of the invention against A-beta according to this aspect: (i) CDR1 is SEQ ID NO: 479; (ii) CDR2 is SEQ ID NO: 480; and (iii) CDR3 is SEQ ID NO: 481.

In one specific aspect, a Nanobody of the invention against A-beta is a variant of the Nanobody of SEQ ID NO: 478 (with at least 90% sequence identity, such as at least 95% sequence identity, with SEQ ID NO: 478), in which:

- the amino acid residue at position 11 is preferably chosen from L, V or K (and is most preferably V); and
- the amino acid residue at position 14 is preferably suitably chosen from A or P; and
- the amino acid residue at position 41 is preferably suitably chosen from A or P; and
- the amino acid residue at position 89 is preferably suitably chosen from T, V or L; and
- the amino acid residue at position 108 is preferably suitably chosen from Q or L; and
- the amino acid residue at position 110 is preferably suitably chosen from T, K or Q; and
- the amino acid residue at position 112 is preferably suitably chosen from S, K or Q;

such that either (i) position 112 is K or Q; or (ii) position 110 is K or Q and position 11 is V; or (iii) position 89 is T; or (iv) position 89 is L and position 110 is K or Q; or (v) position 11 is V and position 89 is L; or any suitable combination of (i) to (v). Again, the CDR's of such an ISV are preferably as defined in the preceding two paragraphs.

Some specifically preferred, but non-limiting examples of Nanobodies of the invention against A-beta are listed in Figure 21A as SEQ ID NO's: 464 to 477 and in Figure 21B as SEQ ID NO's: 482 to 495; and each of these Nanobodies form a further aspect of the invention.

The invention also relates to a compound of the invention against A-beta that comprises at least one (such as one, two or three) of the Nanobodies of the invention of SEQ ID NO's: 464 to 477 and/or 482 to 495. Such compounds of the invention against A-beta may again be as further described herein, and thus for example may comprise suitable linkers, may comprise a C-terminal extension as described herein, and may be half-life extended (for example because they comprise a Nanobody against human serum albumin, such as (preferably) a Nanobody of the invention against human serum albumin). Reference is made to Table BB below.

As described in for example WO 2006/040153 and in particular as described in EP2542579, one particularly preferred class of Nanobody-based compounds against A-beta are biparatopic compounds. Thus, in one aspect of the invention, a compound of the invention against A-beta is a biparatopic construct that comprises one ISV that is either SEQ ID NO: 460 or (preferably) an ISV of the invention that has been derived from SEQ ID NO: 460 (as described in this Example 17) and one ISV that is either SEQ ID NO: 478 or (preferably) an ISV of the invention that has been derived from SEQ ID NO: 478 (as described in this Example 17), provided that at least one (and preferably both) of these ISV's are ISV's of the invention. Such biparatopic constructs may also be half-life extended (i.e. by means of a serum albumin-binding ISV). Some specific examples of such biparatopic constructs are given in SEQ ID NO: 730 to 766.

Some specifically preferred examples of compounds of the invention against A-beta are given in Figure 30 as SEQ ID NO's: 730 to 766; and each of these compounds form a further aspect of the invention. Thus, in another aspect, the invention relates to a polypeptide that is directed against A-beta and that has an amino acid sequence that is chosen from the group consisting of SEQ ID NO's: 730 to 766. More generally, compounds of the invention against A-beta may be as described in WO 2006/040153 and in particular as described in

EP2542579, but comprising ISV's of the invention. They may also be used for the purposes described in WO 2006/040153 and in particular EP2542579.

Table BB: Examples of compounds of the invention against Λ -beta.

Polypeptide/ construct ⁽¹⁾	General formula	ISV building blocks and linkers
Monovalent	[Λ -beta]	[Λ -beta] = one of SEQ ID NO's: 464 to 477 and/or 482 to 495
Monovalent/ C-terminal extension	[Λ -beta]-X(n)	[Λ -beta] = one of SEQ ID NO's: 464 to 477 and/or 482 to 495
Monovalent/ half-life extended	[Λ -beta]-L ₁ -[SA] [SA]-L ₁ -[Λ -beta]	[Λ -beta] = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 [SA] = (see legend below) L ₁ = (see legend below)
Monovalent/ half-life extended/C- terminal extension	[Λ -beta]-L ₁ -[SA]-X(n) [SA]-L ₁ -[Λ -beta]-X(n)	[Λ -beta] = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 [SA] = (see legend below) L ₁ = (see legend below) X(n) = (see legend below)
Bivalent ⁽²⁾	[Λ -beta]-L ₁ -[Λ -beta]	At least one [Λ -beta] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 ⁽⁴⁾ L ₁ = (see legend below)

Table BB (continued)

Polypeptide/ construct ¹)	General formula	ISV building blocks and linkers
Bivalent/ C-terminal extension ⁽²⁾)	[A-beta]- L ₁ -[A-beta] -X(n)	At least one [A-beta] = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (⁴) L ₁ = (see legend below) X(n) = (see legend below)
Bivalent/ half-life extended ⁽²⁾)	[A-beta]- L ₁ -[A-beta]- L ₂ -[SA] [A-beta]- L ₁ -[SA]- L ₂ -[A-beta] [SA]- L ₁ -[A-beta]- L ₂ -[A-beta]	At least one [A-beta] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (⁴) [SA] = (see legend below) L ₁ = (see legend below) L ₂ = (see legend below)
Bivalent/ half-life extended/ C-terminal extension ⁽²⁾)	[A-beta]- L ₁ -[A-beta]- L ₂ -[SA] -X(n) [A-beta]- L ₁ -[SA]- L ₂ -[A-beta] -X(n) [SA]- L ₁ -[A-beta]- L ₂ -[A-beta] -X(n)	At least one [A-beta] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (⁴) [SA] = (see legend below) L ₁ = (see legend below) L ₂ = (see legend below) X(n) = (see legend below)

Table BB (continued)

Polypeptide/ construct ⁽³⁾	General formula	ISV building blocks and linkers
Bispecific (3)	$[\text{A-beta}] \cdot L_1 \cdot [\text{Nb}]$ $[\text{Nb}] \cdot L_1 \cdot [\text{A-beta}]$ $[\text{A-beta}] \cdot L_1 \cdot [\text{A-beta}] \cdot L_2 \cdot [\text{Nb}]$ $[\text{A-beta}] \cdot L_1 \cdot [\text{Nb}] \cdot L_2 \cdot [\text{A-beta}]$ $[\text{Nb}] \cdot L_1 \cdot [\text{A-beta}] \cdot L_2 \cdot [\text{A-beta}]$	<p>At least one [A-beta] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (4)</p> <p>L_1 = (see legend below)</p> <p>L_2 = (see legend below)</p> <p>[\Nb] = (see legend below)</p>
Bispecific/ C-terminal extension (3)	$[\text{A-beta}] \cdot L_1 \cdot [\text{Nb}] \cdot X(n)$ $[\text{Nb}] \cdot L_1 \cdot [\text{A-beta}] \cdot X(n)$ $[\text{A-beta}] \cdot L_1 \cdot [\text{A-beta}] \cdot L_2 \cdot [\text{Nb}] \cdot X(n)$ $[\text{A-beta}] \cdot L_1 \cdot [\text{Nb}] \cdot L_2 \cdot [\text{A-beta}] \cdot X(n)$ $[\text{Nb}] \cdot L_1 \cdot [\text{A-beta}] \cdot L_2 \cdot [\text{A-beta}] \cdot X(n)$	<p>At least one [A-beta] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (4)</p> <p>L_1 = (see legend below)</p> <p>L_2 = (see legend below)</p> <p>$X(n)$ = (see legend below)</p> <p>[\Nb] = (see legend below)</p>
Bispecific/ half-life extended (3)	$[\text{A-beta}] \cdot L_1 \cdot [\text{Nb}] \cdot L_2 \cdot [\text{SA}]$ $[\text{A-beta}] \cdot L_1 \cdot [\text{SA}] \cdot L_2 \cdot [\text{Nb}]$ $[\text{Nb}] \cdot L_1 \cdot [\text{SA}] \cdot L_2 \cdot [\text{A-beta}]$ $[\text{Nb}] \cdot L_1 \cdot [\text{A-beta}] \cdot L_2 \cdot [\text{SA}]$ $[\text{SA}] \cdot L_1 \cdot [\text{A-beta}] \cdot L_2 \cdot [\text{Nb}]$ $[\text{SA}] \cdot L_1 \cdot [\text{Nb}] \cdot L_2 \cdot [\text{A-beta}]$	<p>At least one [A-beta] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 (4)</p> <p>[\SA] = (see legend below)</p> <p>L_1, L_2, L_3 (see legend below)</p> <p>[\Nb] = (see legend below)</p>

Table BB (continued)

Polypeptide/ construct ⁽¹⁾	General formula	ISV building blocks and linkers
Bispecific/ half-life extended ⁽³⁾	$[\text{A-beta}] \cdot L_1 \cdot [\text{A-beta}] \cdot L_2 \cdot [\text{Nb}] \cdot L_3 \cdot [\text{SA}]$ $[\text{Nb}] \cdot L_1 \cdot [\text{A-beta}] \cdot L_2 \cdot [\text{A-beta}] \cdot L_3 \cdot [\text{SA}]$ $[\text{SA}] \cdot L_1 \cdot [\text{A-beta}] \cdot L_2 \cdot [\text{A-beta}] \cdot L_3 \cdot [\text{Nb}]$ $[\text{SA}] \cdot L_1 \cdot [\text{A-beta}] \cdot L_2 \cdot [\text{Nb}] \cdot L_3 \cdot [\text{A-beta}]$ $[\text{A-beta}] \cdot L_1 \cdot [\text{Nb}] \cdot L_2 \cdot [\text{A-beta}] \cdot L_3 \cdot [\text{SA}]$	At least one [A-beta] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 ⁽⁴⁾ [SA] = (see legend below) L ₁ , L ₂ , L ₃ (see legend below) [Nb] = (see legend below)
Bispecific/ half-life extended/ C-terminal extension ⁽³⁾	$[\text{A-beta}] \cdot L_1 \cdot [\text{Nb}] \cdot L_2 \cdot [\text{SA}] \cdot X(n)$ $[\text{A-beta}] \cdot L_1 \cdot [\text{SA}] \cdot L_2 \cdot [\text{Nb}] \cdot X(n)$ $[\text{Nb}] \cdot L_1 \cdot [\text{SA}] \cdot L_2 \cdot [\text{A-beta}] \cdot X(n)$ $[\text{Nb}] \cdot L_1 \cdot [\text{A-beta}] \cdot L_2 \cdot [\text{SA}] \cdot X(n)$ $[\text{SA}] \cdot L_1 \cdot [\text{A-beta}] \cdot L_2 \cdot [\text{Nb}] \cdot X(n)$ $[\text{SA}] \cdot L_1 \cdot [\text{Nb}] \cdot L_2 \cdot [12345] \cdot X(n)$ $[\text{A-beta}] \cdot L_1 \cdot [\text{A-beta}] \cdot L_2 \cdot [\text{Nb}] \cdot L_3 \cdot [\text{SA}] \cdot X(n)$ $[\text{Nb}] \cdot L_1 \cdot [\text{A-beta}] \cdot L_2 \cdot [\text{A-beta}] \cdot L_3 \cdot [\text{SA}] \cdot X(n)$ $[\text{SA}] \cdot L_1 \cdot [\text{A-beta}] \cdot L_2 \cdot [\text{A-beta}] \cdot L_3 \cdot [\text{Nb}] \cdot X(n)$ $[\text{SA}] \cdot L_1 \cdot [\text{A-beta}] \cdot L_2 \cdot [\text{Nb}] \cdot L_3 \cdot [\text{A-beta}] \cdot X(n)$ $[\text{A-beta}] \cdot L_1 \cdot [\text{Nb}] \cdot L_2 \cdot [\text{A-beta}] \cdot L_3 \cdot [\text{SA}] \cdot X(n)$	At least one [A-beta] present is = one of SEQ ID NO's: 464 to 477 and/or 482 to 495 ⁽⁴⁾ [SA] = (see legend below) L ₁ , L ₂ , L ₃ (see legend below) X(n) = (see legend below) [Nb] = (see legend below)

Table BB (continued)**Legend:**

- [SA] is an ISV against (human) serum albumin, preferably an ISV of the invention against (human) serum albumin, more preferably one of SEQ ID NO's: 46 or 61 or even more preferably one of the ISVD's of the invention of SEQ ID NO's: 47, 54, 62, 69, 78, 86, 109, 116, 123, 130 or 496 to 513.
- Each of L₁, L₂ and L₃ is (independently) a suitable linker. Each of L₁, L₂ and L₃ may (independently) be present or not. Non-limiting examples of suitable linkers are the gly-ser linkers referred to herein, such as the 9GS, 30GS or 35GS linker.
- X(n) = a C-terminal extension as a C-terminal extension as described in herein and/or in WO 12/175741
- [Nb] is an ISV against another therapeutic target.

Notes:

(1) In this Table:

- “*Monovalent*” generally refers to polypeptides/constructs comprising a single ISV against A-beta. These may further comprise a half-life extending ISV (such as an ISV against serum albumin).
- “*Bivalent*” generally refers to polypeptides/constructs comprising two ISV's against A-beta (which may be the same or different). These may again further comprise a half-life extending ISV (such as an ISV against serum albumin).
- “*Bispecific*” generally refers to polypeptides/constructs comprising at least one (such as 1 or 2) ISV's against A-beta and at least one (such as 1 or 2) other ISV against a therapeutic target. These may further comprise a half-life extending ISV (such as an ISV against serum albumin).
- In the polypeptides/constructs described in this table, at least one of the ISV's against A-beta present is an ISV of the invention, and preferably all of the ISV's against A-beta present in such polypeptide/construct are ISV's of the invention. Also, when a half-life extending ISV and/or an ISV against another therapeutic target is present in such polypeptide/construct, each of these (and preferably all of these) may also be (and preferably are) ISV's of the invention
- (2) All “bivalent” constructs in this Table may also be biparatopic, meaning that they comprise at least two (such as two) ISV's against A-beta, which are directed against different epitopes on A-beta.
- (3) As will be clear to the skilled person, other/further bispecific constructs than those listed can be made using the building blocks and linkers mentioned.
- (4) Preferably, each [A-beta] present is independently chosen from SEQ ID NO's: 464 to 477 and/or 482 to 495. Also, the [A-beta] present may be the same or different; in a biparatopic polypeptide/construct they will be directed against different epitopes on A-beta.
- (5) Each of the polypeptides/constructs mentioned to in this column by means of reference to a SEQ ID forms an individual specific aspect of the invention.

Example 19: Testing of anti-A-beta constructs for binding by pre-existing antibodies.

Three half-life extended anti-A-beta constructs (with the general formula *[A-beta-1]-9GS-ALB8-9GS-[A-beta-2]-A*) were tested and compared for binding by pre-existing antibodies, using the general protocol described herein. The two constructs according to the invention had the indicated mutations of the invention in all three building blocks (i.e. in the two anti-A-beta Nanobodies and in the serum albumin-binding Nanobody). The reference construct (SEQ ID NO:766) had no mutations of the invention in any of the building blocks. All constructs tested has a C-terminal alanine. The results are given in Table CC-1 and Figure 31A

Table CC-1: testing of anti-A-beta constructs for binding by pre-existing antibodies

Nanobodies tested on 92 samples (healthy subjects)	Ref. no. in Figure 30A	Binding Level at 125 seconds <10 RU	Binding Level at 125 seconds <20 RU	Binding Level at 125 seconds >20 RU
SEQ ID NO: 766 (reference)	(1)	0	1	91
SEQ ID NO: 733 (invention: L11V + V89L)	(2)	11	41	51
SEQ ID NO: 749 (invention: L11V + V89L + T110K)	(3)	16	56	36

The anti-A-beta Nanobodies that were present at the C-terminal end of the constructs were also tested separately as monovalent constructs (with a C-terminal alanine). The results are given in Table CC-2 and Figure 31A.

Table CC-2: testing of monovalent anti-A-beta Nanobodies for binding by pre-existing antibodies

Nanobodies tested on 145 samples (healthy subjects)	Ref. no. in Figure 30A	Binding Level at 125 seconds <10 RU	Binding Level at 125 seconds <20 RU	Binding Level at 125 seconds >20 RU
SEQ ID NO: 478 (reference) (*)	(1)	67	87	58
SEQ ID NO:489 (invention: L11V + V89L) (*)	(2)	74	103	42
SEQ ID NO: 490 (invention: L11V + V89L + T110K) (*)	(3)	116	138	7
(*) all three monovalent Nanobodies tested had a C-terminal alanine added				

Example 20: Overview of serum albumin binders of the invention

Tables DD and EE below give some preferred, but non-limiting examples of serum albumin binding Nanobodies of the invention, based on Alb-8 (Table DD) and Alb-23 (Table EE), respectively.

As mentioned, the invention also relates to a polypeptide, protein, compound or construct (and in particular a compound of the invention) that comprises one of the serum albumin-binding Nanobodies listed in Table DD or EE below. Such a polypeptide, protein, compound or construct (and in particular a compound of the invention) may further comprise at least one (such as one, two or three) binding domain or binding unit (such as an ISVD, and in particular an ISV of the invention) that is directed against at least one therapeutic target. Such a polypeptide, protein, compound or construct may again suitably be monospecific, bispecific or trispecific with respect to the therapeutic target(s), and may be bivalent, trivalent, tetravalent or of higher valency. It will usually also contain suitable linkers, and may comprise a C-terminal extension as described herein.

In particular, such a polypeptide, protein, compound or construct may be a compound of the invention (as described herein) and/or may be as further described herein for the compounds of the invention (including preferred embodiments for compounds of the invention. Thus compounds comprising ISVD's and in particular Nanobodies are particularly

preferred). Accordingly compounds of the invention comprising one of the serum albumin binding Nanobodies listed in Table DD or EE form further aspects of the invention.

Table DD: Alb-8 (reference) and Alb-8 variants according to the invention

SEQ ID NO:	Variant	Sequence
46	Alb-8 (WO 06/122787)	EVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISR DNAKTTLYLQMNSLRPEDTAVYYCTIGGSSLRSSQGTLYTVSS
496	89L + 110K	EVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISR DNAKTTLYLQMNSLRPEDTALYYCTIGGSSLRSSQGTLYKVSS
497	89L + 110Q	EVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISR DNAKTTLYLQMNSLRPEDTALYYCTIGGSSLRSSQGTLYQVSS
498	110K	EVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISR DNAKTTLYLQMNSLRPEDTAVYYCTIGGSSLRSSQGTLYKVSS
499	110Q	EVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISR DNAKTTLYLQMNSLRPEDTAVYYCTIGGSSLRSSQGTLYQVSS
47	112K	EVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISR DNAKTTLYLQMNSLRPEDTAVYYCTIGGSSLRSSQGTLYTVKS
54	112Q	EVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISR DNAKTTLYLQMNSLRPEDTAVYYCTIGGSSLRSSQGTLYTVQS
78	89T	EVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISR DNAKTTLYLQMNSLRPEDTATYYCTIGGSSLRSSQGTLYTVSS

Table DD (continued):

SEQ ID NO:	Variant	Sequence
109	11V + 89L	EVQLVESGGVVQPGNSLRLSCAASGFTSSFGMISWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISR DNAKTTLYLQMNSLRPEDTALYYCTIGGSSLRSSQGTLYVTVSS
123	11V + 89L + 110K	EVQLVESGGVVQPGNSLRLSCAASGFTSSFGMISWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISR DNAKTTLYLQMNSLRPEDTALYYCTIGGSSLRSSQGTLYVTVSS
500	11V + 89L + 110Q	EVQLVESGGVVQPGNSLRLSCAASGFTSSFGMISWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISR DNAKTTLYLQMNSLRPEDTALYYCTIGGSSLRSSQGTLYVQVSS
501	11V + 110K	EVQLVESGGVVQPGNSLRLSCAASGFTSSFGMISWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISR DNAKTTLYLQMNSLRPEDTAVYYCTIGGSSLRSSQGTLYVQVSS
502	11V + 110Q	EVQLVESGGVVQPGNSLRLSCAASGFTSSFGMISWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISR DNAKTTLYLQMNSLRPEDTAVYYCTIGGSSLRSSQGTLYVQVSS
503	11V + 112K	EVQLVESGGVVQPGNSLRLSCAASGFTSSFGMISWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISR DNAKTTLYLQMNSLRPEDTAVYYCTIGGSSLRSSQGTLYVTVKS
504	11V + 112Q	EVQLVESGGVVQPGNSLRLSCAASGFTSSFGMISWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISR DNAKTTLYLQMNSLRPEDTAVYYCTIGGSSLRSSQGTLYVTVQS

Table EE: Alb-23 (reference) and Alb-23 variants according to the invention

SEQ ID NO:	Variant	Sequence
61	Alb-23 (WO 12/17540)	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSFGMSWVRQAPGKGPEWVSSISGGSDTLYADSVKGRFTISR DNSKNTLYLQMNSLRPDTAVYYCTIGGSLSRSSQGTLYTVVSS
505	89L + 110K	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSFGMSWVRQAPGKGPEWVSSISGGSDTLYADSVKGRFTISR DNSKNTLYLQMNSLRPDTALYYCTIGGSLSRSSQGTLYVQVSS
506	89L + 110Q	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSFGMSWVRQAPGKGPEWVSSISGGSDTLYADSVKGRFTISR DNSKNTLYLQMNSLRPDTALYYCTIGGSLSRSSQGTLYVQVSS
507	110K	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSFGMSWVRQAPGKGPEWVSSISGGSDTLYADSVKGRFTISR DNSKNTLYLQMNSLRPDTAVYYCTIGGSLSRSSQGTLYVQVSS
508	110Q	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSFGMSWVRQAPGKGPEWVSSISGGSDTLYADSVKGRFTISR DNSKNTLYLQMNSLRPDTAVYYCTIGGSLSRSSQGTLYVQVSS
62	112K	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSFGMSWVRQAPGKGPEWVSSISGGSDTLYADSVKGRFTISR DNSKNTLYLQMNSLRPDTAVYYCTIGGSLSRSSQGTLYTVVKS
69	112Q	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSFGMSWVRQAPGKGPEWVSSISGGSDTLYADSVKGRFTISR DNSKNTLYLQMNSLRPDTAVYYCTIGGSLSRSSQGTLYTVQS
86	89T	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSFGMSWVRQAPGKGPEWVSSISGGSDTLYADSVKGRFTISR DNSKNTLYLQMNSLRPDTATYYCTIGGSLSRSSQGTLYTVVSS

Table EE (continued):

SEQ ID NO:	Variant	Sequence
116	11V + 89L	EVQLESGGGVVQPGGSLRLSCAASGFTFRSFGMSWVRQAPGKGPEWVSSISGSGSDTLYADSVKGRFTISR DNSKNTLYLQMNSLRPEDTALYYCTIGGSSLRSSQQGTLVTVSS
130	11V + 89L + 110K	EVQLESGGGVVQPGGSLRLSCAASGFTFRSFGMSWVRQAPGKGPEWVSSISGSGSDTLYADSVKGRFTISR DNSKNTLYLQMNSLRPEDTALYYCTIGGSSLRSSQQGTLVTVSS
509	11V + 89L + 110Q	EVQLESGGGVVQPGGSLRLSCAASGFTFRSFGMSWVRQAPGKGPEWVSSISGSGSDTLYADSVKGRFTISR DNSKNTLYLQMNSLRPEDTALYYCTIGGSSLRSSQQGTLVTVSS
510	11V + 110K	EVQLESGGGVVQPGGSLRLSCAASGFTFRSFGMSWVRQAPGKGPEWVSSISGSGSDTLYADSVKGRFTISR DNSKNTLYLQMNSLRPEDTALYYCTIGGSSLRSSQQGTLVTVSS
511	11V + 110Q	EVQLESGGGVVQPGGSLRLSCAASGFTFRSFGMSWVRQAPGKGPEWVSSISGSGSDTLYADSVKGRFTISR DNSKNTLYLQMNSLRPEDTAVYYCTIGGSSLRSSQQGTLVTVSS
512	11V + 112K	EVQLESGGGVVQPGGSLRLSCAASGFTFRSFGMSWVRQAPGKGPEWVSSISGSGSDTLYADSVKGRFTISR DNSKNTLYLQMNSLRPEDTAVYYCTIGGSSLRSSQQGTLVTVKS
513	11V + 112Q	EVQLESGGGVVQPGGSLRLSCAASGFTFRSFGMSWVRQAPGKGPEWVSSISGSGSDTLYADSVKGRFTISR DNSKNTLYLQMNSLRPEDTAVYYCTIGGSSLRSSQQGTLVTVQS

C L A I M S

1. A heavy-chain immunoglobulin single variable domain (ISVD), in which the amino acid residue at position 89 is L and the amino acid residue at position 11 is V, wherein the amino acid residues/positions are indicated with the numbering according to Kabat.
2. The heavy-chain ISVD according to claim 1 that contains an amino acid at position 110 that is chosen from T, I, A, K or Q; (ii) contains an amino acid at position 112 that is chosen from S, F, K or Q; and (iii) optionally contains a P14A or A14P substitution and/or a Q108L substitution.
3. The heavy-chain ISVD according to claim 2 that contains an amino acid at position 110 that is chosen from T, K or Q; (ii) contains an amino acid at position 112 that is chosen from S, K or Q; and (iii) optionally contains a P14A or A14P substitution and/or a Q108L substitution.
4. The heavy-chain ISVD according to claim 3 that contains an amino acid at position 110 that is T; (ii) contains an amino acid at position 112 that is chosen from S; and (iii) optionally contains a P14A or A14P substitution and/or a Q108L substitution.
5. The heavy-chain ISVD according to any one of claims 1 to 4, in which said VH domain contains a C-terminal extension (X)_n, in which n is 1 to 10, preferably 1 to 5, such as 1, 2, 3, 4 or 5 (and preferably 1 or 2, such as 1); and each X is an (preferably naturally occurring) amino acid residue that is independently chosen, and preferably independently chosen from the group consisting of alanine (A), glycine (G), valine (V), leucine (L) or isoleucine (I).
6. The heavy-chain ISVD according to claim 4 or claim 5, respectively, in which the C-terminal end is the C-terminal end is either VTVSS (SEQ ID NO: 76) or VTVSS(X)_n (SEQ ID NO: 77), respectively, in which X and n are as defined in claim 5.
7. The heavy-chain ISVD according to claim 6, which is a nanobody.
8. The heavy-chain ISVD according to claim 1, in which the C-terminal end of the VH domain is one of: VTVSS (SEQ ID NO:76), VTVSS(X)n (SEQ ID NO:77), VTVKS (SEQ ID NO:1), VTVKS(X)n (SEQ ID NO:21), VTVQS (SEQ ID NO:2), VTVQS(X)n (SEQ ID

NO:22), VKVSS (SEQ ID NO: 95), VKVSS(X)n (SEQ ID NO:97), VQVSS (SEQ ID NO: 96), VQVSS(X)n (SEQ ID NO: 98), VZVZS (SEQ ID NO: 107, in which each amino acid residue Z is independently K or Q) or VZVZSX(n) (SEQ ID NO:108, in which each amino acid residue Z is independently K or Q), in which n is 1 to 10, preferably 1 to 5, such as 1, 2, 3, 4 or 5 (and preferably 1 or 2, such as 1); and each X is an (preferably naturally occurring) amino acid residue that is independently chosen, and preferably independently chosen from the group consisting of alanine (A), glycine (G), valine (V), leucine (L) or isoleucine (I).

9. Heavy-chain ISVD according to claim 8, in which the C-terminal end of the VH domain is one of VTVSS (SEQ ID NO:76), VKVSS (SEQ ID NO: 95), VQVSS (SEQ ID NO: 96), VKVSS(X)n (SEQ ID NO:97) or VQVSS(X)n (SEQ ID NO: 98), in which X and n are as defined in claim 8.

10. Heavy-chain ISVD according to claim 8 or claim 9, in which the C-terminal end of the VH domain is one of VTVSS (SEQ ID NO:76) or VTVSS(X)n (SEQ ID NO:77), in which X and n are as defined in claim 8.

11. Heavy-chain ISVD according to any one of claims 8 to 10, which is an immunoglobulin single variable domain.

12. Heavy-chain ISVD according to claim 11, which is a nanobody.

13. Heavy-chain ISVD, in which:

- the amino acid residue at position 11 is V; and
- the amino acid residue at position 14 is one of A or P; and
- the amino acid residue at position 41 is one of A or P; and
- the amino acid residue at position 89 is L; and
- the amino acid residue at position 108 is one of Q or L; and
- the amino acid residue at position 110 is one of T, K or Q; and
- the amino acid residue at position 112 is one of S, K or Q;

and in which said VH domain optionally contains a C-terminal extension (X)n , in which n is 1 to 10, preferably 1 to 5, such as 1, 2, 3, 4 or 5 (and preferably 1 or 2, such as 1); and each X is an (preferably naturally occurring) amino acid residue that is independently chosen, and preferably independently chosen from the group consisting of alanine (A), glycine (G), valine (V), leucine (L) or isoleucine (I),

wherein the amino acid residues/positions are indicated with the numbering according to Kabat.

14. Heavy-chain ISVD according to claim 13, which is a nanobody.

15. Heavy-chain ISVD according to any one of the preceding claims, which is directed to serum albumin.

16. Heavy-chain ISVD according to claim 15, in which:

- CDR1 is the amino acid sequence SFGMS (SEQ ID NO:41);
- CDR2 is the amino acid sequence SISGSGSDTLYADSVKG (SEQ ID NO:42);
- CDR3 is the amino acid sequence GGSLSR (SEQ ID NO:43).

17. Heavy-chain ISVD according to claim 16, which has at least 95% sequence identity with at least one of Alb-1 (SEQ ID NO: 52 of WO 2006/122787 as defined in Figure 32), Alb-8 (SEQ ID NO: 46) and/or Alb-23 (SEQ ID NO:61).

18. Library of heavy-chain ISVDs according to any one of claims 1 to 17.

19. Library of nucleic acid residues encoding heavy-chain ISVDs according to any of claims 1 to 17.

20. Library according to claim 19, which is an expression library.

21. Library according to any one of claims 18 to 20, which is a synthetic library.

22. Library according to any one of claims 18 to 21, which contains at least 100 different sequences, such as at least 1000 different sequences, in particular more than 10^5 different sequences, more in particular more than 10^6 different sequences, such as 10^8 to 10^{10} or more different sequences.

23. Polypeptide, construct or compound that comprises at least one heavy-chain immunoglobulin single variable domain according to any one of claims 1 to 17.

24. Nucleic acid that encodes the heavy-chain immunoglobulin single variable domain according to any one of claims 1 to 17 or the polypeptide, construct or compound according to claim 23.

25. A method for producing the heavy-chain immunoglobulin single variable domain according to any one of claims 1 to 17 or the polypeptide, construct or compound according to claim 23, optionally comprising expressing the nucleic acid according to claim 24 in a suitable host organism.

26. A composition comprising the heavy-chain immunoglobulin single variable domain according to any one of claims 1 to 17, the polypeptide, construct or compound according to claim 23 or the nucleic acid according to claim 24, wherein the composition is optionally a pharmaceutical composition.

27. The heavy-chain immunoglobulin single variable domain according to any one of claims 1 to 17 or the polypeptide, construct or compound according to claim 23 for use in medicine.

Figure 1

Numbering according to Kabat (VH)	Numbering according to Chotia (VH)	Aho numbering	IMGT
11	11	12	12
14	14	15	15
41	41	48	46
42	42	49	47
87	87	101	99
89	89	103	101
108	108	144	---
110	110	146	---
112	112	148	---

Source: <http://www.bioc.uzh.ch/phueckthum/antibody/Numbering/NumFrame.html>

Figure 2

SEQ ID NO:1	C-terminal end	VTVKS
SEQ ID NO:2	C-terminal end	VTVQS
SEQ ID NO:3	FR4 sequence	WGQGTQVTVKS
SEQ ID NO:4	FR4 sequence	WGKGTLVTVKS
SEQ ID NO:5	FR4 sequence	RGQGTRVTVKS
SEQ ID NO:6	FR4 sequence	WGLGTQVTIIS
SEQ ID NO:7	FR4 sequence	GSQGTQVTVKS
SEQ ID NO:8	FR4 sequence	LRGGTQVTVKS
SEQ ID NO:9	FR4 sequence	RGQGTLVTVKS
SEQ ID NO:10	FR4 sequence	RSRGIQVTVKS
SEQ ID NO:11	FR4 sequence	WGKGQTQVTVKS
SEQ ID NO:12	FR4 sequence	WGQGTQVTVQS
SEQ ID NO:13	FR4 sequence	WGKGTLVTVQS
SEQ ID NO:14	FR4 sequence	RGQGTRVTVQS
SEQ ID NO:15	FR4 sequence	WGLGTQVTIIS
SEQ ID NO:16	FR4 sequence	GSQGTQVTVQS
SEQ ID NO:17	FR4 sequence	LRGGTQVTVQS
SEQ ID NO:18	FR4 sequence	RGQGTLVTVQS
SEQ ID NO:19	FR4 sequence	RSRGIQVTVQS
SEQ ID NO:20	FR4 sequence	WGKGQTQVTVQS
SEQ ID NO:21	C-terminal end with C-terminal extension	VTVKS(X) _n

Figure 2 (continued)

SEQ ID NO:22	C-terminal end with C- terminal extension	VTVQS(X) _n
SEQ ID NO:23	FR4 sequence with C- terminal extension	WGQGTQVTVKS(X) _n
SEQ ID NO:24	FR4 sequence with C- terminal extension	WGKGTLVTVKS(X) _n
SEQ ID NO:25	FR4 sequence with C- terminal extension	RGQGTRVTVKS(X) _n
SEQ ID NO:26	FR4 sequence with C- terminal extension	WGLGTQVTIIS(X) _n
SEQ ID NO:27	FR4 sequence with C- terminal extension	GSQGTQVTVKS(X) _n
SEQ ID NO:28	FR4 sequence with C- terminal extension	LRGGTQVTVKS(X) _n
SEQ ID NO:29	FR4 sequence with C- terminal extension	RGQGTLVTVKS(X) _n
SEQ ID NO:30	FR4 sequence with C- terminal extension	RSRGQVTVKS(X) _n

Figure 2 (continued)

SEQ ID NO:31	FR4 sequence with C- terminal extension	WGKGTQVTVKS(X) _n
SEQ ID NO:32	FR4 sequence with C- terminal extension	WGQGTQVTVQS(X) _n
SEQ ID NO:33	FR4 sequence with C- terminal extension	WGKGTLVTVQS(X) _n
SEQ ID NO:34	FR4 sequence with C- terminal extension	RGQGTRVTVQS(X) _n
SEQ ID NO:35	FR4 sequence with C- terminal extension	WGLGTQVTIIS(X) _n
SEQ ID NO:36	FR4 sequence with C- terminal extension	GSQGTQVTVQS(X) _n
SEQ ID NO:37	FR4 sequence with C- terminal extension	LRGGTQVTVQS(X) _n
SEQ ID NO:38	FR4 sequence with C- terminal extension	RGQGTLVTVQS(X) _n
SEQ ID NO:39	FR4 sequence with C- terminal extension	RSRGIQVTVQS(X) _n

Figure 2 (continued)

SEQ ID NO:40	FR4 sequence with C-terminal extension	WGKGTQVTVQS(X) _n
SEQ ID NO:41	CDR1 sequence	SFGMS
SEQ ID NO:42	CDR2 sequence	SISGSGSDTLYADSVKG
SEQ ID NO:43	CDR3 sequence	GGSLSR
SEQ ID NO:44	Reference A.	HHHHHHEVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSRSSQGT LTVSS
SEQ ID NO:45	Reference B. SEQ ID NO:37 from WO 12/175741	HHHHHHEVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSRSSQGT LTVSSA
SEQ ID NO:46	Alb-8 (WO 06/122787)	EVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSRSSQGT LTVSS
SEQ ID NO:47	Alb-8 + 112K	EVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSRSSQGT LTVKS
SEQ ID NO:48	Alb-8 + 112K + A	EVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSRSSQGT LTVKSA
SEQ ID NO:49	Alb-8 + 112K + AA	EVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSRSSQGT LTVKSA A
SEQ ID NO:50	Alb-8 + 112K + AAA	EVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSRSSQGT LTVKSA AA
SEQ ID NO:51	Alb-8 + 112K + G	EVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSRSSQGT LTVKSG
SEQ ID NO:52	Alb-8 + 112K + GG	EVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSRSSQGT LTVKSG G

Figure 2 (continued)

SEQ ID NO:53	Alb-8 + 112K + GGG	EVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMSWVR QAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKT TLYLQMNSLRPEDTAVYYCTIGGSLSRSSQGTLTVKSG GG
SEQ ID NO:54	Alb-8 + 112Q	EVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMSWVR QAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKT TLYLQMNSLRPEDTAVYYCTIGGSLSRSSQGTLTVQSA
SEQ ID NO:55	Alb-8 + 112Q + A	EVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMSWVR QAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKT TLYLQMNSLRPEDTAVYYCTIGGSLSRSSQGTLTVQSA
SEQ ID NO:56	Alb-8 + 112Q + AA	EVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMSWVR QAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKT TLYLQMNSLRPEDTAVYYCTIGGSLSRSSQGTLTVQSA A
SEQ ID NO:57	Alb-8 + 112Q + AAA	EVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMSWVR QAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKT TLYLQMNSLRPEDTAVYYCTIGGSLSRSSQGTLTVQSA AA
SEQ ID NO:58	Alb-8 + 112Q + G	EVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMSWVR QAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKT TLYLQMNSLRPEDTAVYYCTIGGSLSRSSQGTLTVQSG
SEQ ID NO:59	Alb-8 + 112Q + GG	EVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMSWVR QAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKT TLYLQMNSLRPEDTAVYYCTIGGSLSRSSQGTLTVQSG G
SEQ ID NO:60	Alb-8 + 112Q + GGG	EVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMSWVR QAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKT TLYLQMNSLRPEDTAVYYCTIGGSLSRSSQGTLTVQSG GG
SEQ ID NO:61	Alb-23 (WO 12/175400)	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSGMSWVR QAPGKPEWVSSISGSGSDTLYADSVKGRFTISRDNSKN TLYLQMNSLRPEDTAVYYCTIGGSLSRSSQGTLTVSS
SEQ ID NO:62	Alb-23 + 112K	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSGMSWVR QAPGKPEWVSSISGSGSDTLYADSVKGRFTISRDNSKN TLYLQMNSLRPEDTAVYYCTIGGSLSRSSQGTLTVKS
SEQ ID NO:63	Alb-23 + 112K +A	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSGMSWVR QAPGKPEWVSSISGSGSDTLYADSVKGRFTISRDNSKN TLYLQMNSLRPEDTAVYYCTIGGSLSRSSQGTLTVKSA
SEQ ID NO:64	Alb-23 + 112K +AA	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSGMSWVR QAPGKPEWVSSISGSGSDTLYADSVKGRFTISRDNSKN TLYLQMNSLRPEDTAVYYCTIGGSLSRSSQGTLTVKSA A
SEQ ID NO:65	Alb-23 + 112K +AAA	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSGMSWVR QAPGKPEWVSSISGSGSDTLYADSVKGRFTISRDNSKN TLYLQMNSLRPEDTAVYYCTIGGSLSRSSQGTLTVKSA AA

Figure 2 (continued)

SEQ ID NO:66	Alb-23 + 112K +G	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSGMSWVR QAPGKGPEWVSSISGSGSDTLYADSVKGRFTISRDNSKN TLYLQMNSLRPEDTAVYYCTIGGSLSRSSQGTLVTVKSG
SEQ ID NO:67	Alb-23 + 112K +GG	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSGMSWVR QAPGKGPEWVSSISGSGSDTLYADSVKGRFTISRDNSKN TLYLQMNSLRPEDTAVYYCTIGGSLSRSSQGTLVTVKSG G
SEQ ID NO:68	Alb-23 + 112K +GGG	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSGMSWVR QAPGKGPEWVSSISGSGSDTLYADSVKGRFTISRDNSKN TLYLQMNSLRPEDTAVYYCTIGGSLSRSSQGTLVTVKSG GG
SEQ ID NO:69	Alb-23 + 112Q	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSGMSWVR QAPGKGPEWVSSISGSGSDTLYADSVKGRFTISRDNSKN TLYLQMNSLRPEDTAVYYCTIGGSLSRSSQGTLVTVQS
SEQ ID NO:70	Alb-23 + 112Q +A	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSGMSWVR QAPGKGPEWVSSISGSGSDTLYADSVKGRFTISRDNSKN TLYLQMNSLRPEDTAVYYCTIGGSLSRSSQGTLVTVQSA
SEQ ID NO:71	Alb-23 + 112Q +AA	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSGMSWVR QAPGKGPEWVSSISGSGSDTLYADSVKGRFTISRDNSKN TLYLQMNSLRPEDTAVYYCTIGGSLSRSSQGTLVTVQSA A
SEQ ID NO:72	Alb-23 + 112Q +AAA	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSGMSWVR QAPGKGPEWVSSISGSGSDTLYADSVKGRFTISRDNSKN TLYLQMNSLRPEDTAVYYCTIGGSLSRSSQGTLVTVQSA AA
SEQ ID NO:73	Alb-23 + 112Q +G	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSGMSWVR QAPGKGPEWVSSISGSGSDTLYADSVKGRFTISRDNSKN TLYLQMNSLRPEDTAVYYCTIGGSLSRSSQGTLVTVQSG
SEQ ID NO:74	Alb-23 + 112Q +GG	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSGMSWVR QAPGKGPEWVSSISGSGSDTLYADSVKGRFTISRDNSKN TLYLQMNSLRPEDTAVYYCTIGGSLSRSSQGTLVTVQSG G
SEQ ID NO:75	Alb-23 + 112Q +GGG	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSGMSWVR QAPGKGPEWVSSISGSGSDTLYADSVKGRFTISRDNSKN TLYLQMNSLRPEDTAVYYCTIGGSLSRSSQGTLVTVQSG GG
SEQ ID NO:76	C-terminal end	VTVSS
SEQ ID NO:77	C-terminal end with C-terminal extension	VTVSS(X) _n
SEQ ID NO:78	Serum albumin-binding nanobody with V89T substitution	EVQLVESGGGLVQPGNRLSCAASGFTFSSFGMSWVR QAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKT TLYLQMNSLRPEDTATYYCTIGGSLSRSSQGTLVTVSS

Figure 2 (continued)

SEQ ID NO:79	Serum albumin-binding nanobody with V89T substitution	EVQLVESGGGLVQPGNSLRLSCAASGFTSSFGMSWVR QAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKT TLYLQMNSLRPEDTATYYCTIGGSLSRSSQGTLVTVSSA
SEQ ID NO:80	Serum albumin-binding nanobody with V89T substitution	EVQLVESGGGLVQPGNSLRLSCAASGFTSSFGMSWVR QAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKT TLYLQMNSLRPEDTATYYCTIGGSLSRSSQGTLVTVSSA A
SEQ ID NO:81	Serum albumin-binding nanobody with V89T substitution	EVQLVESGGGLVQPGNSLRLSCAASGFTSSFGMSWVR QAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKT TLYLQMNSLRPEDTATYYCTIGGSLSRSSQGTLVTVSSA AA
SEQ ID NO:82	Serum albumin-binding nanobody with V89T substitution	EVQLVESGGGLVQPGNSLRLSCAASGFTSSFGMSWVR QAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKT TLYLQMNSLRPEDTATYYCTIGGSLSRSSQGTLVTVSSG
SEQ ID NO:83	Serum albumin-binding nanobody with V89T substitution	EVQLVESGGGLVQPGNSLRLSCAASGFTSSFGMSWVR QAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKT TLYLQMNSLRPEDTATYYCTIGGSLSRSSQGTLVTVSSG G
SEQ ID NO:84	Serum albumin-binding nanobody with V89T substitution	EVQLVESGGGLVQPGNSLRLSCAASGFTSSFGMSWVR QAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKT TLYLQMNSLRPEDTATYYCTIGGSLSRSSQGTLVTVSSG GG
SEQ ID NO:85	Serum albumin-binding nanobody with V89T substitution	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSGMSWVR QAPGKGPEWVSSISGSGSDTLYADSVKGRFTISRDNSKN TLYLQMNSLRPEDTATYYCTIGGSLSRSSQGTLVTVSS
SEQ ID NO:86	Serum albumin-binding nanobody with V89T substitution	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSGMSWVR QAPGKGPEWVSSISGSGSDTLYADSVKGRFTISRDNSKN TLYLQMNSLRPEDTATYYCTIGGSLSRSSQGTLVTVSSA

Figure 2 (continued)

SEQ ID NO:87	Serum albumin-binding nanobody with V89T substitution	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSGMSWVR QAPGKGPEWVSSISGSGSDTLYADSVKGRFTISRDNSKN TLYLQMNSLRPEDTATYYCTIGGSLSRSSQGTLTVSSA A
SEQ ID NO:88	Serum albumin-binding nanobody with V89T substitution	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSGMSWVR QAPGKGPEWVSSISGSGSDTLYADSVKGRFTISRDNSKN TLYLQMNSLRPEDTATYYCTIGGSLSRSSQGTLTVSSA AA
SEQ ID NO:89	Serum albumin-binding nanobody with V89T substitution	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSGMSWVR QAPGKGPEWVSSISGSGSDTLYADSVKGRFTISRDNSKN TLYLQMNSLRPEDTATYYCTIGGSLSRSSQGTLTVSSG
SEQ ID NO:90	Serum albumin-binding nanobody with V89T substitution	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSGMSWVR QAPGKGPEWVSSISGSGSDTLYADSVKGRFTISRDNSKN TLYLQMNSLRPEDTATYYCTIGGSLSRSSQGTLTVSSG G
SEQ ID NO:91	Serum albumin-binding nanobody with V89T substitution	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSGMSWVR QAPGKGPEWVSSISGSGSDTLYADSVKGRFTISRDNSKN TLYLQMNSLRPEDTATYYCTIGGSLSRSSQGTLTVSSG GG
SEQ ID NO:92	Nanobody A used in Example 6	EVQLVESGGGLVQPGGSLRLSCAASGRTFNNYAMGWF RQAPGKEREVAAITRSGVRSVSAIYGDSVKDRFTISR DNAKNTLYLQMNSLRPEDTAVYYCAASAIGSGALRRFE YDYSQQGTLTVSS
SEQ ID NO:93	Nanobody B used in Example 6	EVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMSWVR QAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKT TLYLQMNSLRPEDTAVYYCTIGGSLSRSSQGTLTVSS
SEQ ID NO:94	Nanobody C used in Example 6	EVQLVESGGGLVQPGGSLRLSCAASRSIGRLDRMGWYR HRPGEPRELVATITGGSSINYGDSVKGRFTISIDNSKNTV YLQMNSLRPEDTAVYYCNFNKYVTSRDTWGQQGTLTV SS

Figure 2 (continued)

SEQ ID NO:95	C-terminal end	VKVSS
SEQ ID NO:96	C-terminal end	VQVSS
SEQ ID NO:97	C-terminal end	VKVSS(X)n
SEQ ID NO:98	C-terminal end	VQVSS(X)n
SEQ ID NO:99	FR4 sequence	SSQGTLTVKVS
SEQ ID NO:100	FR4 sequence	SSQGTLTVQVS
SEQ ID NO:101	FR4 sequence	SSQGTLVKVSS
SEQ ID NO:102	FR4 sequence	SSQGTLVQVSS
SEQ ID NO:103	FR4 sequence with C-terminal extension	SSQGTLTVKVS(X)n
SEQ ID NO:104	FR4 sequence with C-terminal extension	SSQGTLTVQVS(X)n
SEQ ID NO:105	FR4 sequence with C-terminal extension	SSQGTLVKVSS(X)n
SEQ ID NO:106	FR4 sequence with C-terminal extension	SSQGTLVQVSS(X)n
SEQ ID NO:107	C-terminal sequence	VZVZS
SEQ ID NO:108	C-terminal sequence	VZVZS(X)n
SEQ ID NO:109	Serum albumin-binding nanobody with L11V + V89L substitution	EVQLVESGGVVQPGNSLRLSCAASGFTFSSFGMSWVR QAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKT TLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLTVSS

Figure 2 (continued)

SEQ ID NO:110	Serum albumin-binding nanobody with L11V + V89L substitution	EVQLVESGGVVQPGNSLRLSCAASGFTSSFGMSWVR QAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKT TLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLVTVSSA
SEQ ID NO:111	Serum albumin-binding nanobody with L11V + V89L substitution	EVQLVESGGVVQPGNSLRLSCAASGFTSSFGMSWVR QAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKT TLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLVTVSSA A
SEQ ID NO:112	Serum albumin-binding nanobody with L11V + V89L substitution	EVQLVESGGVVQPGNSLRLSCAASGFTSSFGMSWVR QAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKT TLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLVTVSSA AA
SEQ ID NO:113	Serum albumin-binding nanobody with L11V + V89L substitution	EVQLVESGGVVQPGNSLRLSCAASGFTSSFGMSWVR QAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKT TLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLVTVSSG
SEQ ID NO:114	Serum albumin-binding nanobody with L11V + V89L substitution	EVQLVESGGVVQPGNSLRLSCAASGFTSSFGMSWVR QAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKT TLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLVTVSSG G
SEQ ID NO:115	Serum albumin-binding nanobody with L11V + V89L substitution	EVQLVESGGVVQPGNSLRLSCAASGFTSSFGMSWVR QAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKT TLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLVTVSSG GG

Figure 2 (continued)

SEQ ID NO:116	Serum albumin-binding nanobody with L11V + V89L substitution	EVQLLESGGGVVQPGGSLRLSCAASGFTFRSGMSWVR QAPGKGPEWVSSISGSGSDTLYADSVKGRFTISRDNSKN TLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLVTVSS
SEQ ID NO:117	Serum albumin-binding nanobody with L11V + V89L substitution	EVQLLESGGGVVQPGGSLRLSCAASGFTFRSGMSWVR QAPGKGPEWVSSISGSGSDTLYADSVKGRFTISRDNSKN TLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLVTVSSA
SEQ ID NO:118	Serum albumin-binding nanobody with L11V + V89L substitution	EVQLLESGGGVVQPGGSLRLSCAASGFTFRSGMSWVR QAPGKGPEWVSSISGSGSDTLYADSVKGRFTISRDNSKN TLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLVTVSSAA
SEQ ID NO:119	Serum albumin-binding nanobody with L11V + V89L substitution	EVQLLESGGGVVQPGGSLRLSCAASGFTFRSGMSWVR QAPGKGPEWVSSISGSGSDTLYADSVKGRFTISRDNSKN TLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLVTVSSAA
SEQ ID NO:120	Serum albumin-binding nanobody with L11V + V89L substitution	EVQLLESGGGVVQPGGSLRLSCAASGFTFRSGMSWVR QAPGKGPEWVSSISGSGSDTLYADSVKGRFTISRDNSKN TLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLVTVSSG
SEQ ID NO:121	Serum albumin-binding nanobody with L11V + V89L substitution	EVQLLESGGGVVQPGGSLRLSCAASGFTFRSGMSWVR QAPGKGPEWVSSISGSGSDTLYADSVKGRFTISRDNSKN TLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLVTVSSGG

Figure 2 (continued)

SEQ ID NO:122	Serum albumin-binding nanobody with L11V + V89L substitution	EVQLLESGGGVVQPGNSRLSCAASGFTFRSGMSWVR QAPGKGPEWVSSISGSGSDTLYADSVKGRFTISRDNSKN TLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLTVSSG GG
SEQ ID NO:123	Serum albumin-binding nanobody with L11V + V89L + T110K substitution	EVQLVESGGGVVQPGNSRLSCAASGFTSSFGMSWVR QAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKT TLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLVKVSS
SEQ ID NO:124	Serum albumin-binding nanobody with L11V + V89L + T110K substitution	EVQLVESGGGVVQPGNSRLSCAASGFTSSFGMSWVR QAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKT TLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLVKVSSA
SEQ ID NO:125	Serum albumin-binding nanobody with L11V + V89L + T110K substitution	EVQLVESGGGVVQPGNSRLSCAASGFTSSFGMSWVR QAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKT TLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLVKVSSA A
SEQ ID NO:126	Serum albumin-binding nanobody with L11V + V89L + T110K substitution	EVQLVESGGGVVQPGNSRLSCAASGFTSSFGMSWVR QAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKT TLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLVKVSSA AA
SEQ ID NO:127	Serum albumin-binding nanobody with L11V + V89L + T110K substitution	EVQLVESGGGVVQPGNSRLSCAASGFTSSFGMSWVR QAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKT TLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLVKVSSG

Figure 2 (continued)

SEQ ID NO:128	Serum albumin-binding nanobody with L11V + V89L + T110K substitution	EVQLVESGGVVQPGNSRLSCAASGFTSSFGMSWVR QAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKT TLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLVKVSSG G
SEQ ID NO:129	Serum albumin-binding nanobody with L11V + V89L + T110K substitution	EVQLVESGGVVQPGNSRLSCAASGFTSSFGMSWVR QAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKT TLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLVKVSSG GG
SEQ ID NO:130	Serum albumin-binding nanobody with L11V + V89L + T110K substitution	EVQLLESGGVVQPGGSLRLSCAASGFTFRSGMSWVR QAPGKGPEWVSSISGSGSDTLYADSVKGRFTISRDNSKN TLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLVKVSS
SEQ ID NO:131	Serum albumin-binding nanobody with L11V + V89L + T110K substitution	EVQLLESGGVVQPGGSLRLSCAASGFTFRSGMSWVR QAPGKGPEWVSSISGSGSDTLYADSVKGRFTISRDNSKN TLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLVKVSSA
SEQ ID NO:132	Serum albumin-binding nanobody with L11V + V89L + T110K substitution	EVQLLESGGVVQPGGSLRLSCAASGFTFRSGMSWVR QAPGKGPEWVSSISGSGSDTLYADSVKGRFTISRDNSKN TLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLVKVSSA A
SEQ ID NO:133	Serum albumin-binding nanobody with L11V + V89L + T110K substitution	EVQLLESGGVVQPGGSLRLSCAASGFTFRSGMSWVR QAPGKGPEWVSSISGSGSDTLYADSVKGRFTISRDNSKN TLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLVKVSSA AA

Figure 2 (continued)

SEQ ID NO:134	Serum albumin-binding nanobody with L11V + V89L + T110K substitution	EVQLLESGGGVVQPGGSLRLSCAASGFTFRSGMSWVR QAPGKGPEWVSSISGSGSDTLYADSVKGRFTISRDNSKN TLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLVKVSSG
SEQ ID NO:135	Serum albumin-binding nanobody with L11V + V89L + T110K substitution	EVQLLESGGGVVQPGGSLRLSCAASGFTFRSGMSWVR QAPGKGPEWVSSISGSGSDTLYADSVKGRFTISRDNSKN TLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLVKVSSG
SEQ ID NO:136	Serum albumin-binding nanobody with L11V + V89L + T110K substitution	EVQLLESGGGVVQPGGSLRLSCAASGFTFRSGMSWVR QAPGKGPEWVSSISGSGSDTLYADSVKGRFTISRDNSKN TLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLVKVSSG
Note: In the sequences above, whenever (X) _n is present, it represents a C-terminal extension, with n = 1, 2, 3, 4 or 5 (preferably 1, 2 or 3, more preferably 1 or 2, most preferably 1) and each X being independently chosen from suitable amino acids (preferably from naturally occurring amino acid residues, more preferably from the group consisting of A, G, V, L or I, with A and/or G being particularly preferred).		
Note: In the sequences of SEQ ID NO: 107 (VZVZS) and 108 (VZVZS(X)n), each Z is independently K or Q.		

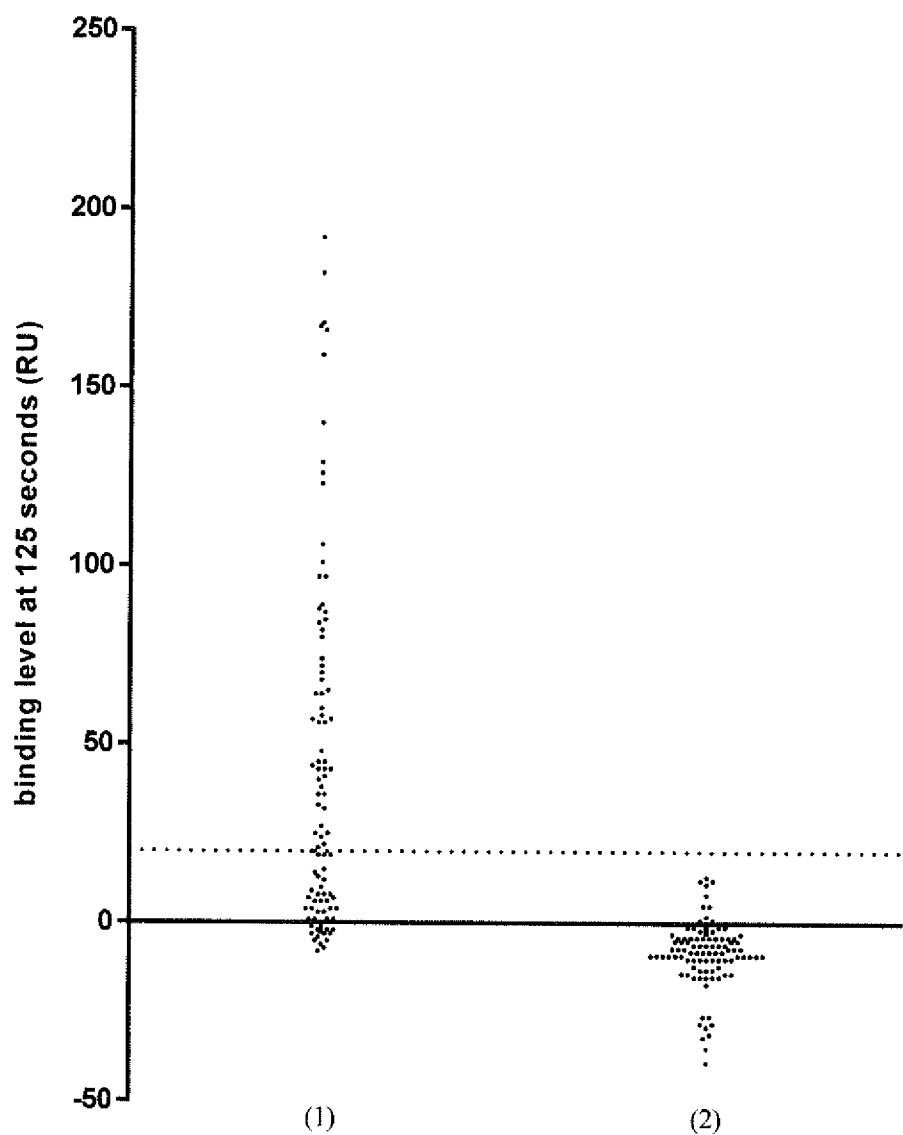
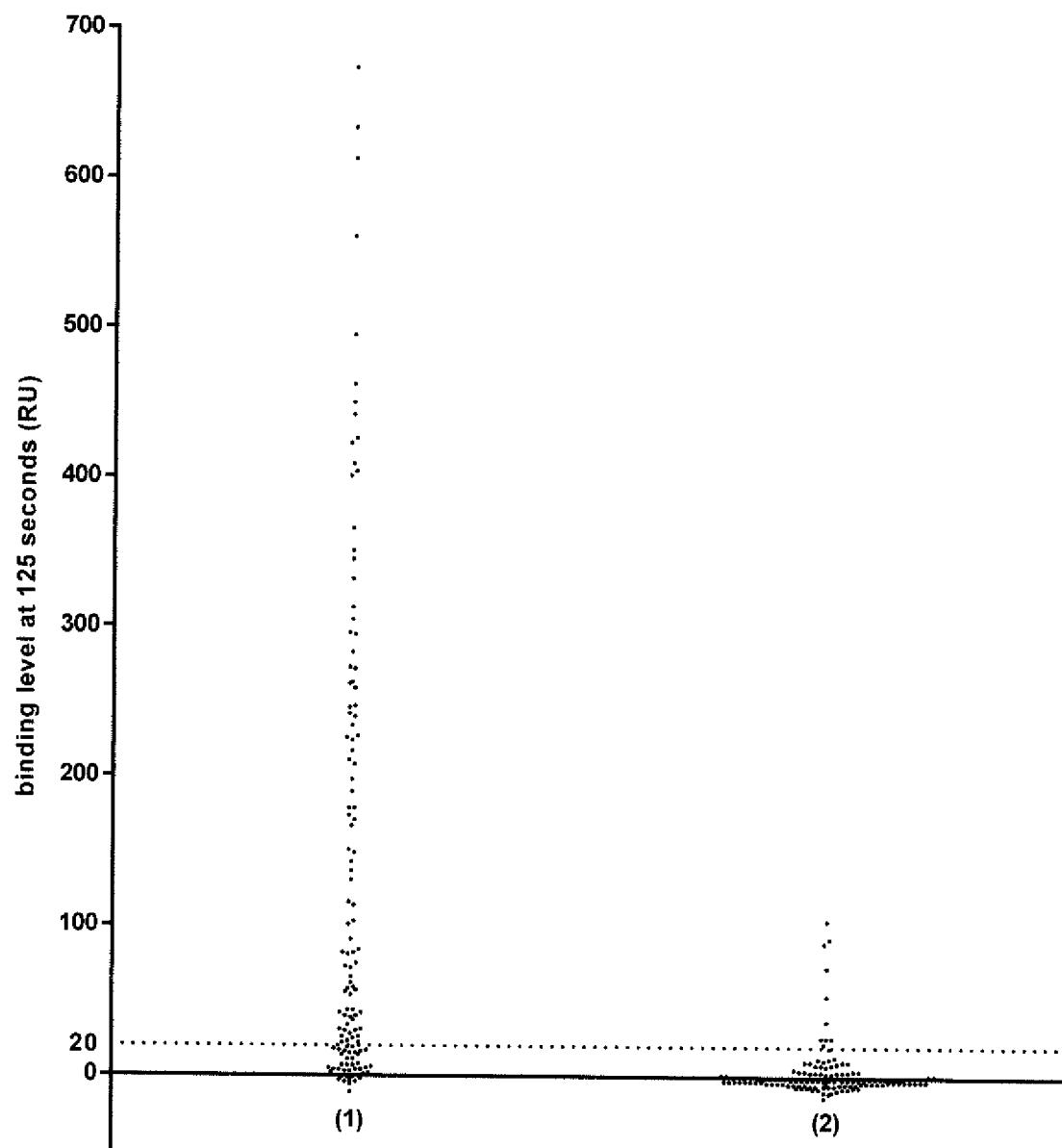
Figure 3

Figure 4

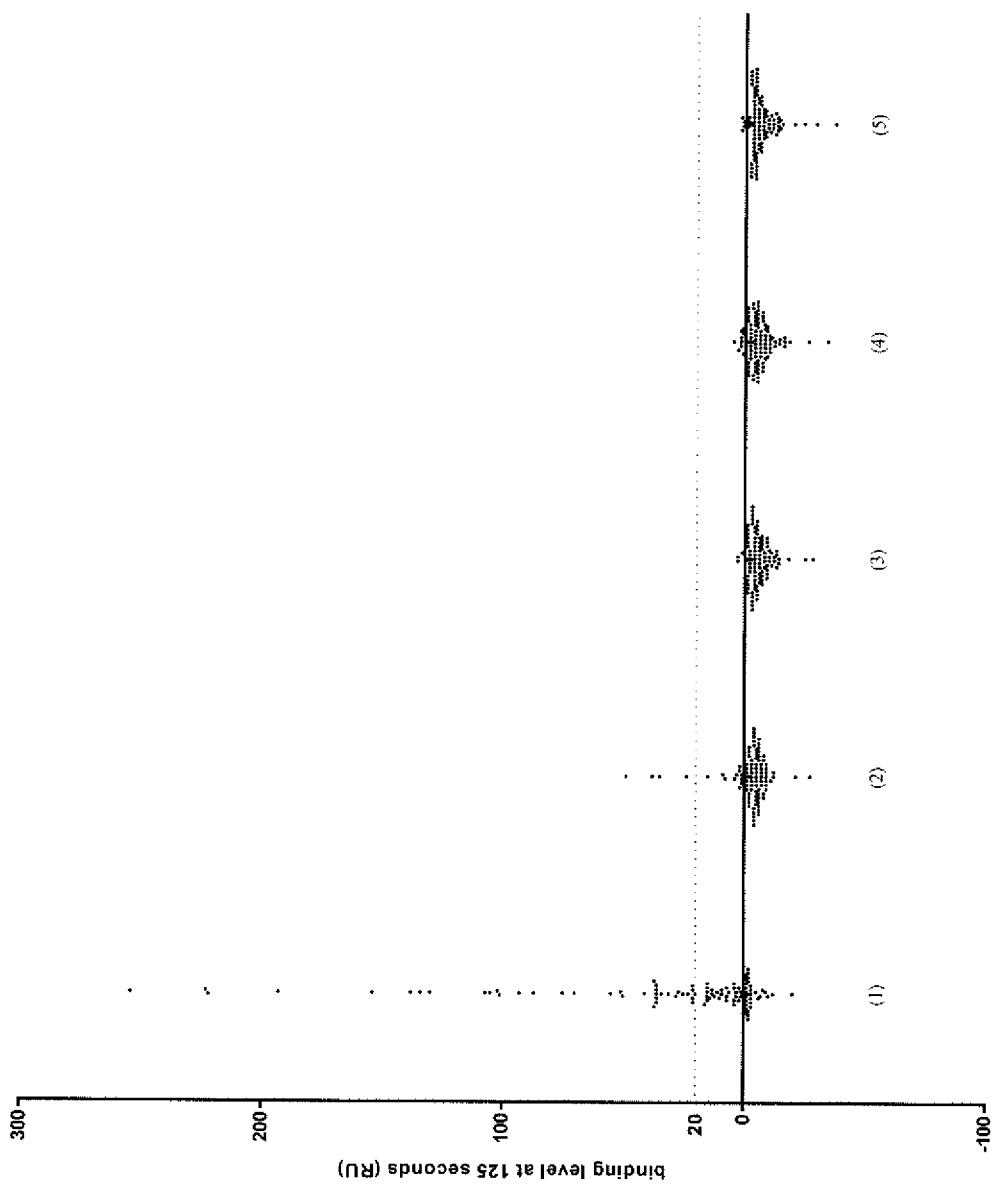


Figure 5

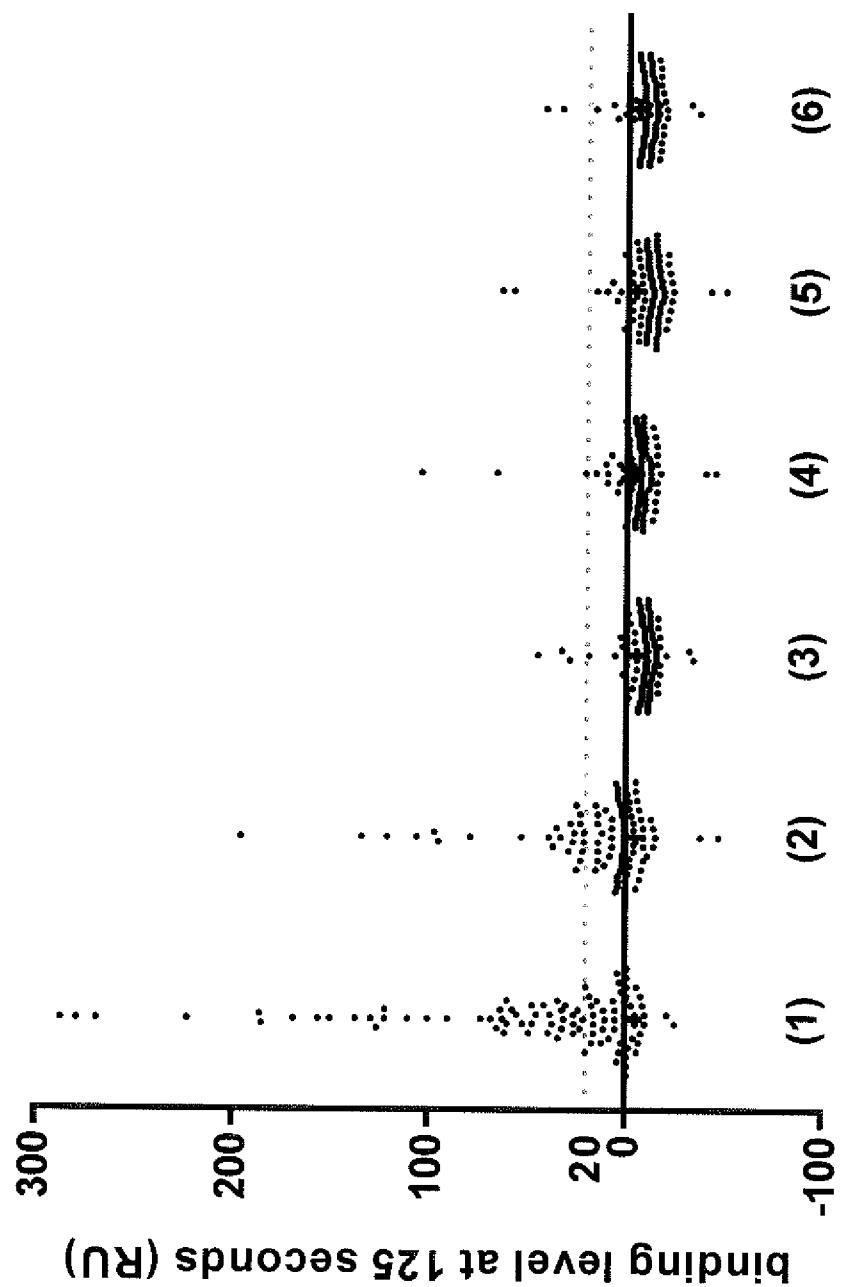


Figure 6

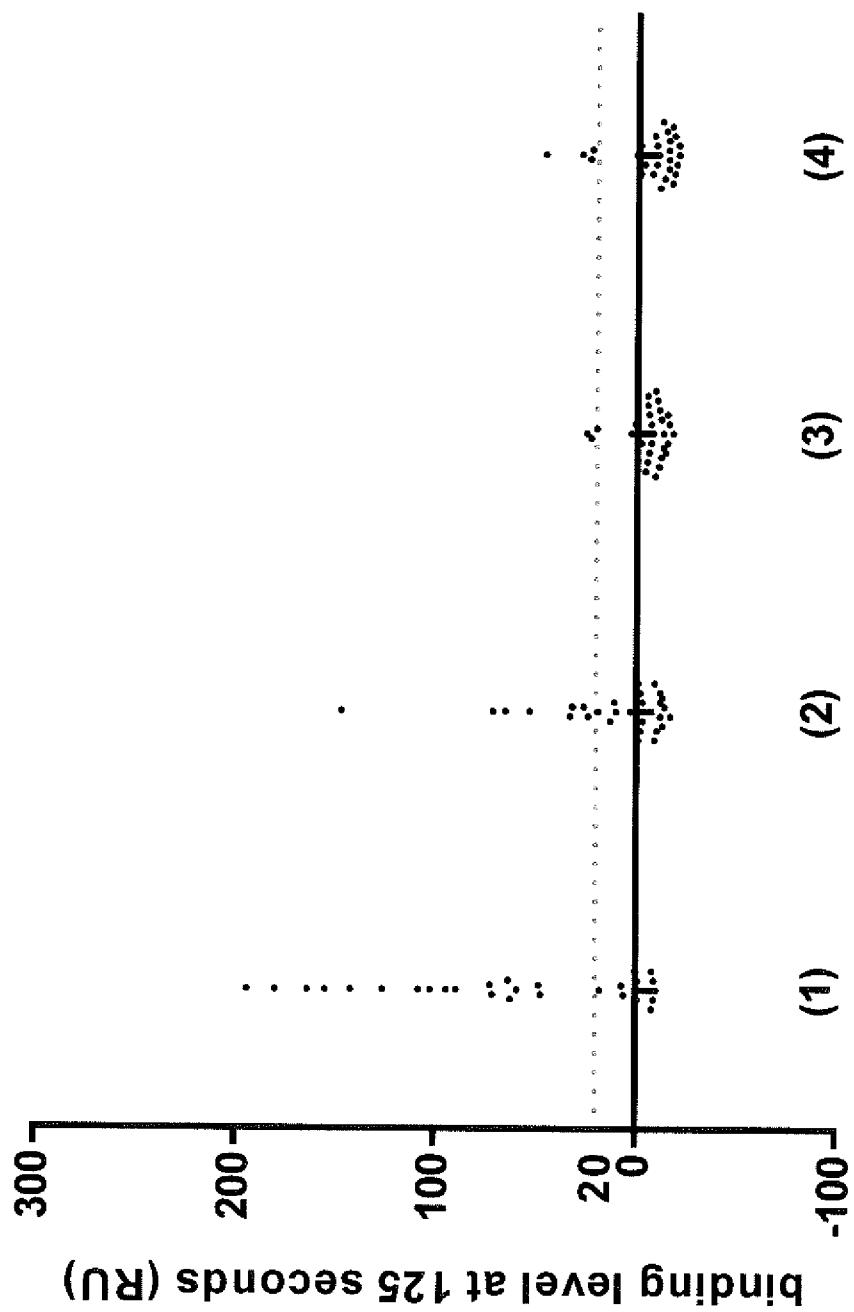


Figure 7

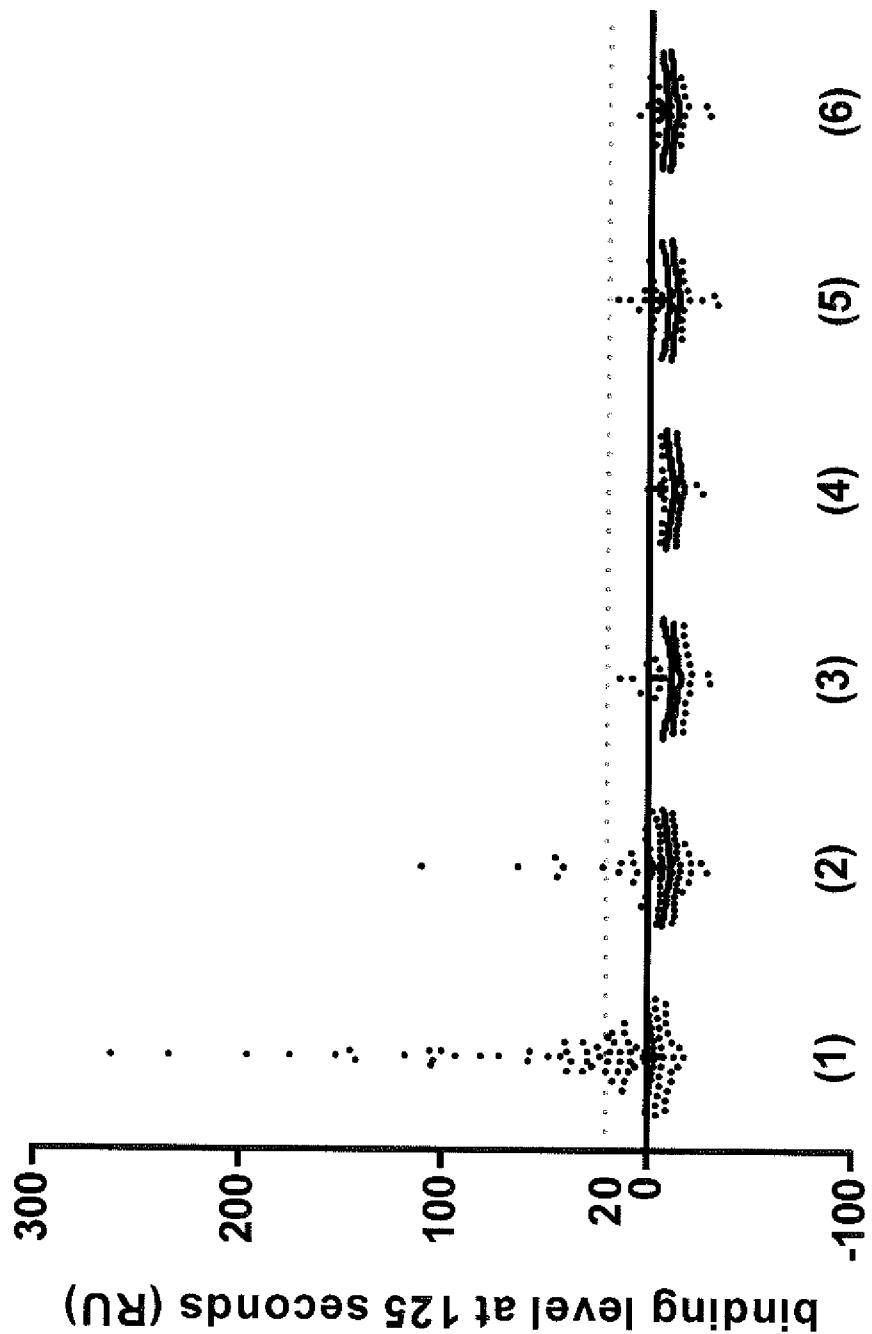


Figure 8

Figure 9A

Clone	SEQ ID NO:	Sequence
A0194009G09 (reference)	137 (495)*	EVQLVESGGGLVQAGGSLGLSCSAGLLFSRNSAGWYRQAPGKQREFVARIRMGGSINYADTVKG RFTISRDNAKNTVYLQMNSLKPEDTAVYYCSSWRTGFYEWGQQGTLVTVSS
A0194009G09 (E1D,L11V,A14P,G19R,M53 A,T62S,A74S,K83R,V89L,S9 4G)	138 (523)	DVQLVESGGGVVQPGGSLRLSCSAGLLFSRNSAGWYRQAPGKQREFVARIRAGGSINYADSVKG RFTISRDNSKNTVYLQMNSLRPEDTALYYCSCGWRTGFYEWGQQGTLVTVSS
A0194009G09 (E1D,L11V,A14P,G19R,M53 A,T62S,A74S,K83R,V89L,T9 7E)	139 (524)	DVQLVESGGGVVQPGGSLRLSCSAGLLFSRNSAGWYRQAPGKQREFVARIRAGGSINYADSVKG RFTISRDNSKNTVYLQMNSLRPEDTALYYCSSWREGFYEYWGQQGTLVTVSS
A0194009G09 (E1D,L11V,A14P,G19R,M53 A,T62S,A74S,K83R,V89L,S9 4G,T97E)	140 (525)	DVQLVESGGGVVQPGGSLRLSCSAGLLFSRNSAGWYRQAPGKQREFVARIRAGGSINYADSVKG RFTISRDNSKNTVYLQMNSLRPEDTALYYCSCGWREGFYEYWGQQGTLVTVSS
A0194009G09 (E1D,L11V,A14P,G19R,M53 Q,T62S,A74S,K83R,V89L,S9 4G)	141 (526)	DVQLVESGGGVVQPGGSLRLSCSAGLLFSRNSAGWYRQAPGKQREFVARIRQGGSINYADSVKG RFTISRDNSKNTVYLQMNSLRPEDTALYYCSCGWRTGFYEWGQQGTLVTVSS

(*) In Figures 9A and 9B, the number between parenthesis refers to the SEQ ID NO by which this sequence is listed in the co-pending US provisional application entitled “Kv1.3 binding immunoglobulins” (filing date: March 16, 2015; assignee: Ablynx N.V.).

Figure 9A (continued)

Clone	SEQ ID NO:	Sequence
A0194009G09 (E1D,L11V,A14P,G19R,M53 Q,T62S,A74S,K83R,V89L,T9 7E)	142 (527)	DVQLVESGGVVQPGGSLRLSCSASGLLFSRNSAGWYRQAPGKQREFVARIQGGGSINYADSVKG RFTISRDNSKNTVYIQMNSLRLPEDTALYYCSSWREGFYEYWGQQGTLVTVSS
A0194009G09 (E1D,L11V,A14P,G19R,M53 Q,T62S,A74S,K83R,V89L,S9 4G,T97E)	143 (528)	DVQLVESGGVVQPGGSLRLSCSASGLLFSRNSAGWYRQAPGKQREFVARIQGGGSINYADSVKG RFTISRDNSKNTVYIQMNSLRLPEDTALYYCSGWREGFYEYWGQQGTLVTVSS
A0194009G09 (E1D,L11V,A14P,G19R,M53 Y,T62S,A74S,K83R,V89L,S9 4G)	144 (529)	DVQLVESGGVVQPGGSLRLSCSASGLLFSRNSAGWYRQAPGKQREFVARIYGGGSINYADSVKG RFTISRDNSKNTVYIQMNSLRLPEDTALYYCSGWRTGFYEYWGQQGTLVTVSS
A0194009G09 (E1D,L11V,A14P,G19R,M53 Y,T62S,A74S,K83R,V89L,T9 7E)	145 (530)	DVQLVESGGVVQPGGSLRLSCSASGLLFSRNSAGWYRQAPGKQREFVARIYGGGSINYADSVKG RFTISRDNSKNTVYIQMNSLRLPEDTALYYCSSWREGFYEYWGQQGTLVTVSS
A0194009G09 (E1D,L11V,A14P,G19R,M53 Y,T62S,A74S,K83R,V89L,S9 4G,T97E)	146 (531)	DVQLVESGGVVQPGGSLRLSCSASGLLFSRNSAGWYRQAPGKQREFVARIYGGGSINYADSVKG RFTISRDNSKNTVYIQMNSLRLPEDTALYYCSGWREGFYEYWGQQGTLVTVSS

Figure 9A (continued)

Clone	SEQ ID NO:	Sequence
A0194009G09 (L11V,A14P,G19R,M53A,T62 S,A74S,K83R,V89L, S94G)	147 (532)	EVQLVESGGGVVQPGGSSLRLSCSASGLLFSRNSAGWYRQAPGKQREFVARIAGGSINYADSVKG RFTISRDN SKNTVYLQMNSL RPEDTALYYC SGWRTGFYEYWGQGTLVTVSS
A0194009G09 (L11V,A14P,G19R,M53A,T62 S,A74S,K83R,V89L, T97E)	148 (533)	EVQLVESGGGVVQPGGSSLRLSCSASGLLFSRNSAGWYRQAPGKQREFVARIAGGSINYADSVKG RFTISRDN SKNTVYLQMNSL RPEDTALYYC SSWREGFYEYWGQGTLVTVSS
A0194009G09 (L11V,A14P,G19R,M53A,T62 S,A74S,K83R,V89L, T97E)	149 (534)	EVQLVESGGGVVQPGGSSLRLSCSASGLLFSRNSAGWYRQAPGKQREFVARIAGGSINYADSVKG RFTISRDN SKNTVYLQMNSL RPEDTALYYC SGWREGFYEYWGQGTLVTVSS
A0194009G09 (L11V,A14P,G19R,M53Q,T62 S,A74S,K83R,V89L, S94G,T97E)	150 (535)	EVQLVESGGGVVQPGGSSLRLSCSASGLLFSRNSAGWYRQAPGKQREFVARIQGGGSINYADSVKG RFTISRDN SKNTVYLQMNSL RPEDTALYYC SGWREGFYEYWGQGTLVTVSS
A0194009G09 (L11V,A14P,G19R,M53Q,T62 S,A74S,K83R,V89L, S94G)	151 (536)	EVQLVESGGGVVQPGGSSLRLSCSASGLLFSRNSAGWYRQAPGKQREFVARIQGGGSINYADSVKG RFTISRDN SKNTVYLQMNSL RPEDTALYYC SSWREGFYEYWGQGTLVTVSS
A0194009G09 (L11V,A14P,G19R,M53Q,T62 S,A74S,K83R,V89L, T97E)	152 (537)	EVQLVESGGGVVQPGGSSLRLSCSASGLLFSRNSAGWYRQAPGKQREFVARIQGGGSINYADSVKG RFTISRDN SKNTVYLQMNSL RPEDTALYYC SGWREGFYEYWGQGTLVTVSS

Figure 9A (continued)

Clone	SEQ ID NO:	Sequence
A0194009G09 (L11V,A14P,G19R,M53Y,T62 S,A74S,K83R,V89L, S94G)	153 (538)	EVQLVESGGVVQPGGSLRLSCSASGLLFSRNSAGWYRQAPGKQREFVARRYGGSINYADSVKG RFTISRDNSKNTVYLQMNSLIRPEDTALYYCSCGWRTGFYFYEWGQGTLVTVSS
A0194009G09 (L11V,A14P,G19R,M53Y,T62 S,A74S,K83R,V89L, T97E)	154 (539)	EVQLVESGGVVQPGGSLRLSCSASGLLFSRNSAGWYRQAPGKQREFVARRYGGSINYADSVKG RFTISRDNSKNTVYLQMNSLIRPEDTALYYCSSWREGFYEWGQGTLVTVSS
A0194009G09 (L11V,A14P,G19R,M53Y,T62 S,A74S,K83R,V89L, S94G,T97E)	155 (540)	EVQLVESGGVVQPGGSLRLSCSASGLLFSRNSAGWYRQAPGKQREFVARRYGGSINYADSVKG RFTISRDNSKNTVYLQMNSLIRPEDTALYYCSCGWREGFYEWGQGTLVTVSS

Figure 9B

Clone	SEQ ID No:	Sequence
A0194009G09 (E1D,L11V,A14P,G19R,M53 Q,T62S,A74S,K83R,V89L,S9 4G)-35GS-A0194009G09 (L11V,A14P,G19R,M53Q,T62 S,A74S,K83R,V89L,S94G)- 35GS-ALB82-A ^(*)	156 (514) ^(*)	DVQLVESGGGVVQPGGLSLRLSCSASGLLFSRNSAGWYRQAPGKQREFVARIRQGGSINYADSVVKG RFTISRDNSKNTVYLQMNSLRPEDITALYYCSGWRTGFYFYWQGQTLVTVSSGGGGSGGGGGGGGGGGGGGG GSGGG KQREFVARIROGGSINYADSVKGRFTISRDNSKNTVYLQMNSLRPEDITALYYCSGWRTGFYFYWVG QGTLVTVSSGG SCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSL RPEDTALYYCTIGGSSLRSSSQGTLVTVSSA
A0194009G09 (E1D,L11V,A14P,G19R,M53 Q,T62S,A74S,K83R,V89L,T9 7E)-35GS-A0194009G09 (L11V,A14P,G19R,M53Q,T62 S,A74S,K83R,V89L,T97E)- 35GS-ALB82-A	157 (515)	DVQLVESGGGVVQPGGLSLRLSCSASGLLFSRNSAGWYRQAPGKQREFVARIRQGGSINYADSVVKG RFTISRDNSKNTVYLQMNSLRPEDITALYYCSSWREGFYFYWQGQTLVTVSSGGGGGGGGGGGGGGGGGGGGGG GSGGG KQREFVARIROGGSINYADSVKGRFTISRDNSKNTVYLQMNSLRPEDITALYYCSSWREGFYFYWVG QGTLVTVSSGG SCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSL RPEDTALYYCTIGGSSLRSSSQGTLVTVSSA
<p>(*) In Figures 9A and 9B, the number between parenthesis refers to the SEQ ID NO by which this sequence is listed in the co-pending US provisional application entitled “Kv1.3 binding immunoglobulins” (filing date: March 16, 2015; assignee: Ablynx N.V.).</p> <p>(*)“ALB82” refers to the sequence of SEQ ID NO:109</p>		

Figure 9B (continued)

Clone	SEQ ID NO:	Sequence
A0194009G09 (E1D,L11V,A14P,G19R,M53 A,T62S,A74S,K83R,V89L,S9 4G)-35GS-A0194009G09 (L11V,A14P,G19R,M53A,T62 S,A74S,K83R,V89L,S94G)- 35GS-ALB82-A	158 (516)	DVQLVESGGGVVQPGGSLRI.SCSASGLLFSRNSAGWYRQAPGKQREFVARIRAGGSINYADSVKG RFTISRDNSKNTVYLQMNSLRPEDTALYYCSGWRTGFYEWGQQGTLVTVSSGGCGSGGGGGGG GSGGGGGGGGGGGGGGGGGSEVQLVESGGGVVQPGGSLRLSCSASGLLFSRNSAGWYRQAPG KQREFVARIRAGGSINYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALYYCSGWRTGFYEWG QGTLVTVSSGGGGGGGGGGGGGGGGSEVQLVESGGGVVQPGGNSLRL SCAASGFTSSFGMSWVVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSL RPEDTALYYCTIGGSLSRSSQGTLVTVSSA
A0194009G09 (E1D,L11V,A14P,G19R,M53 A,T62S,A74S,K83R,V89L,T9 7E)-35GS-A0194009G09 (L11V,A14P,G19R,M53A,T62 S,A74S,K83R,V89L,T97E)- 35GS-ALB82-A	159 (517)	DVQLVESGGGVVQPGGSLRI.SCSASGLLFSRNSAGWYRQAPGKQREFVARIRAGGSINYADSVKG RFTISRDNSKNTVYLQMNSLRPEDTALYYCSSWREGFYEWGQQGTLVTVSSGGGGGGGGGG GSGGGGGGGGGGGGGSEVQLVESGGGVVQPGGSLRLSCSASGLLFSRNSAGWYRQAPG KQREFVARIRAGGSINYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALYYCSSWREGFYEWG QGTLVTVSSGGGGGGGGGGGGGGGGSEVQLVESGGGVVQPGGNSLRL SCAASGFTSSFGMSWVVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSL RPEDTALYYCTIGGSLSRSSQGTLVTVSSA
A0194009G09 (E1D,L11V,A14P,G19R,M53 A,T62S,A74S,K83R,V89L,S9 4G,T97E-35GS-0194009G09 (L11V,A14P,G19R,M53A,T62 S,A74S,K83R,V89L,S94G,T9 7E)-35GS-ALB82-A	160 (518)	DVQLVESGGGVVQPGGSLRI.SCSASGLLFSRNSAGWYRQAPGKQREFVARIRAGGSINYADSVKG RFTISRDNSKNTVYLQMNSLRPEDTALYYCSGWREGFYEWGQQGTLVTVSSGGGGGGGG GSGGGGGGGGGGGGGGGGGSEVQLVESGGGVVQPGGSLRLSCSASGLLFSRNSAGWYRQAPG KQREFVARIRAGGSINYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALYYCSGWREGFYEWG QGTLVTVSSGGGGGGGGGGGGGGGGSEVQLVESGGGVVQPGGNSLRL SCAASGFTSSFGMSWVVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSL RPEDTALYYCTIGGSLSRSSQGTLVTVSSA

Figure 9B (continued)

Clone	SEQ ID NO:	Sequence
A0194009G09 (E1D,L11V,A14P,G19R,M53 Y,T62S,A74S,K83R,V89L,S9 4G)-35GS-A0194009G09 (L11V,A14P,G19R,M53Y,T62 S,A74S,K83R,V89L,S94G)- 35GS-ALB82-A	161 (519)	DVQLVESGGGVVQPGGSLRILSCSASGLLFSRNSAGWYRQAPGKQREFVARRIYGGSINYADSVKG RFTISRDNSKNTVYLQMNSLRPEDTALYYCSCGWRTGFYEWGQGTLVTVSSGGGGGGGGGGGGGGGG GSGGGGGGGGGGGGGGGGGSEVQLVESGGGVVQPGGSLRILSCSASGLLFSRNSAGWYRQAPG KQREFVARRIYGGSINYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALYYCSCGWRTGFYEWG QGTLVTVSSGGGGGGGGGGGGGGSEVQLVESGGGVVQPGGSLRILSCSASGLLFSRNSAGWYRQAPG SCAASGFTSSFGMSWVVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSL RPEDTALYYCTIGGSLSRSSQGTIVTSSA
A0194009G09 (E1D,L11V,A14P,G19R,M53 Y,T62S,A74S,K83R,V89L,T9 7E)-35GS-A0194009G09 L11V,A14P,G19R,M53Y,T62 S,A74S,K83R,V89L,T97E)- 35GS-ALB82-A	162 (520)	DVQLVESGGGVVQPGGSLRILSCSASGLLFSRNSAGWYRQAPGKQREFVARRIYGGSINYADSVKG RFTISRDNSKNTVYLQMNSLRPEDTALYYCSCSWREGFYEWGQGTLVTVSSGGGGGGGGGGGGGG GSGGGGGGGGGGGGGGGGGSEVQLVESGGGVVQPGGSLRILSCSASGLLFSRNSAGWYRQAPG KQREFVARRIYGGSINYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALYYCSCSWREGFYEWG QGTLVTVSSGGGGGGGGGGGGGGSEVQLVESGGGVVQPGGSLRILSCSASGLLFSRNSAGWYRQAPG SCAASGFTSSFGMSWVVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSL RPEDTALYYCTIGGSLSRSSQGTIVTSSA
A0194009G09 (E1D,L11V,A14P,G19R,M53 Y,T62S,A74S,K83R,V89L,S9 4G,T97E)-35GS-0194009G09 (L11V,A14P,G19R,M53Y,T62 S,A74S,K83R,V89L,S94G,T9 7E)-35GS-ALB82-A	163 (521)	DVQLVESGGGVVQPGGSLRILSCSASGLLFSRNSAGWYRQAPGKQREFVARRIYGGSINYADSVKG RFTISRDNSKNTVYLQMNSLRPEDTALYYCSCGWREGFYEWGQGTLVTVSSGGGGGGGGGGGGGG GSGGGGGGGGGGGGGGGGGSEVQLVESGGGVVQPGGSLRILSCSASGLLFSRNSAGWYRQAPG KQREFVARRIYGGSINYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALYYCSCGWREGFYEWG QGTLVTVSSGGGGGGGGGGGGGGSEVQLVESGGGVVQPGGSLRILSCSASGLLFSRNSAGWYRQAPG SCAASGFTSSFGMSWVVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSL RPEDTALYYCTIGGSLSRSSQGTIVTSSA

Figure 9B (continued)

Clone	SEQ ID NO:	Sequence
A0194009G09 (E1D,L11V,A14P,G19R,M53 Q,T62S,A74S,K83R,V89L,S9 A4G,T97E)-35GS-0194009G09 (L11V,A14P,G19R,M53Q,T62 S,A74S,K83R,V89L,S94G,T9 E)-35GS-ALB82-A A0194009G09(E1D)-35GS- A0194009G09-35GS-ALB8-A (Reference)	164 (522) 165 (497)	DVQLVESGGGVVQPGGSLRLSCSASGLLFSRNSAGWYRQAPGKQREFVARRQGGSINYADSVKG RFTISRDNSKNTVYLQMNSLRPEDTALYYCSGWREGFYEWGQGTLVTVSSGGCGSGGGGGGGGG GSGGGGGGGGGGGGGGGSEVQLVESGGGVQPGGSLRLSCSASGLLFSRNSAGWYRQAPG KQREFVARRQGGSINYADSVKGRTFISRDNSKNTVYLQMNSLRPEDTALYYCSGWREGFYEWG QGTLVTVSSGGGGGGGGGGGGGGGGGGGGGGGGSEVQLVESGGGVQPGNSLRL SCAASGFTFSSFGMSWVRQAPGKGLIEWVSSISGSGSDILYADSVKGRTFISRDNAKTTLYLQMNSL RPEDTALYYCTIGGSLSRSSQGTLVTVSSA DVQLVESGGGLVQAGGSLGLSCSASGLLFSRNSAGWYRQAPGKQREFVARIQMGGSINYADTVKG RFTISRDNAKNTVYLQMNSLKPEDTAVYYCSSLWRTGFYEWGQGTLVTVSSGGCGGGGGGGGG GSGGGGGGGGGGGGGGGSEVQLVESGGGLVQAGGSLGLSCSASGLLFSRNSAGWYRQAPG KQREFVARIQMGGSINYADTVKGRTFISRDNAKNTVYLQMNSLKPEDTAVYYCSSWRTGFYEW GQGTLVTVSSGGGGGGGGGGGGGGGGGGGGSEVQLVESGGGLVQPGNSLRL LSCAASGFTFSSFGMSWVRQAPGKGLIEWVSSISGSGSDTLYADSVKGRTFISRDNAKTTLYLQMNSL RPEDTAVYYCTIGGSLSRSSQGTLVTVSSA

Figure 9C

Clone	SEQ ID NO:	Sequence
CDR1 (Kabat)	166	RNSAG
CDR2 (Kabat)	167	RIRMGGSINYADTVVKG
CDR3 (Kabat)	168	WRTGFYEY
CDR1 (Abm)	169	GLLFSRNSAG
CDR2 (Abm)	170	RIRMGGSIN
CDR3 (Abm)	171	WRTGFYEY

47 diabetic human subjects

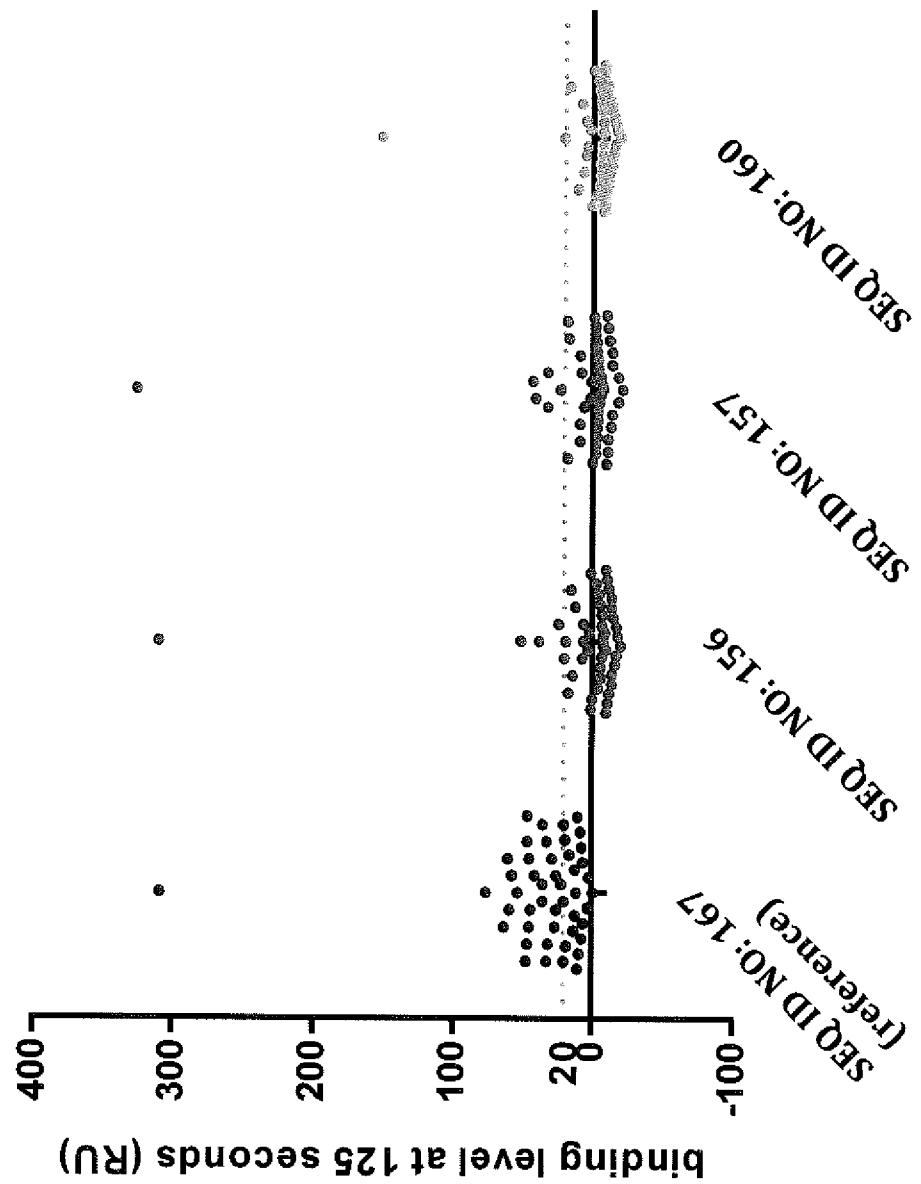


Figure 10

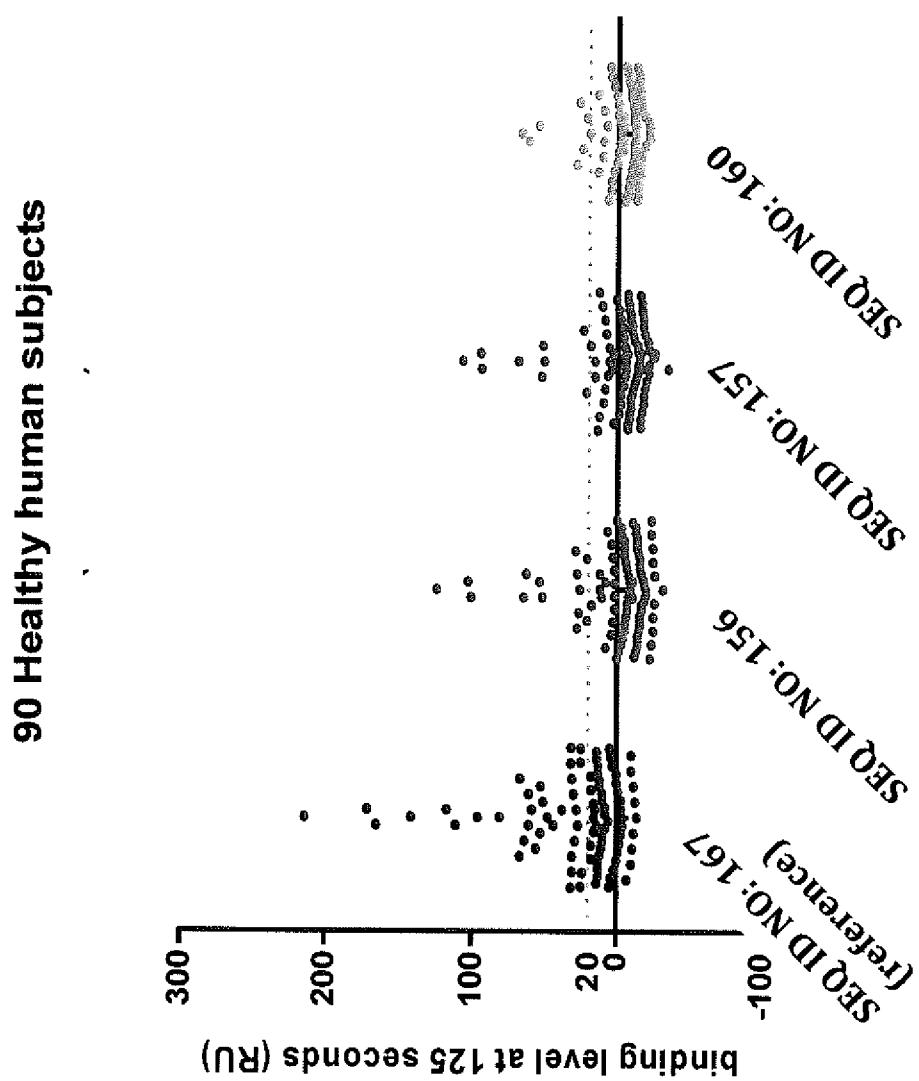


Figure 11

Figure 12A

SEQ ID	Mutation(s)	Sequence
172	None (reference)	EVQLLESGGGLVQPGGSLRLSCAASGRIFSLPASGNIFNLLTIAW YRQAPGKGRELVATINSGSRTYYADSVKGRFTISRDNSKKTVYL QMNSLRPEDTAVYYCQTSGSGSPNFWGQGTLTVSS
173	CDR1	LPASGNIFNLLTIA
174	CDR2	APGKGRELVATINSGSRTYYADSVKG
175	CDR3	SGSGSPNF
176	89L + 110K	EVQLLESGGGLVQPGGSLRLSCAASGRIFSLPASGNIFNLLTIAW YRQAPGKGRELVATINSGSRTYYADSVKGRFTISRDNSKKTVYL QMNSLRPEDTALYYCQTSGSGSPNFWGQGTLVKVSS
177	89L + 110Q	EVQLLESGGGLVQPGGSLRLSCAASGRIFSLPASGNIFNLLTIAW YRQAPGKGRELVATINSGSRTYYADSVKGRFTISRDNSKKTVYL QMNSLRPEDTALYYCQTSGSGSPNFWGQGTLVQVSS
178	110K	EVQLLESGGGLVQPGGSLRLSCAASGRIFSLPASGNIFNLLTIAW YRQAPGKGRELVATINSGSRTYYADSVKGRFTISRDNSKKTVYL QMNSLRPEDTAVYYCQTSGSGSPNFWGQGTLVKVSS
179	110Q	EVQLLESGGGLVQPGGSLRLSCAASGRIFSLPASGNIFNLLTIAW YRQAPGKGRELVATINSGSRTYYADSVKGRFTISRDNSKKTVYL QMNSLRPEDTAVYYCQTSGSGSPNFWGQGTLVQVSS
180	112K	EVQLLESGGGLVQPGGSLRLSCAASGRIFSLPASGNIFNLLTIAW YRQAPGKGRELVATINSGSRTYYADSVKGRFTISRDNSKKTVYL QMNSLRPEDTAVYYCQTSGSGSPNFWGQGTLVTVKS
181	112Q	EVQLLESGGGLVQPGGSLRLSCAASGRIFSLPASGNIFNLLTIAW YRQAPGKGRELVATINSGSRTYYADSVKGRFTISRDNSKKTVYL QMNSLRPEDTAVYYCQTSGSGSPNFWGQGTLVTVQS
182	89T	EVQLLESGGGLVQPGGSLRLSCAASGRIFSLPASGNIFNLLTIAW YRQAPGKGRELVATINSGSRTYYADSVKGRFTISRDNSKKTVYL QMNSLRPEDTATYYCQTSGSGSPNFWGQGTLTVSS
183	11V + 89L	EVQLLESGGGVVQPGGSLRLSCAASGRIFSLPASGNIFNLLTIAW YRQAPGKGRELVATINSGSRTYYADSVKGRFTISRDNSKKTVYL QMNSLRPEDTALYYCQTSGSGSPNFWGQGTLTVSS
184	11V + 89L + 110K	EVQLLESGGGVVQPGGSLRLSCAASGRIFSLPASGNIFNLLTIAW YRQAPGKGRELVATINSGSRTYYADSVKGRFTISRDNSKKTVYL QMNSLRPEDTALYYCQTSGSGSPNFWGQGTLVKVSS
185	11V + 89L + 110Q	EVQLLESGGGVVQPGGSLRLSCAASGRIFSLPASGNIFNLLTIAW YRQAPGKGRELVATINSGSRTYYADSVKGRFTISRDNSKKTVYL QMNSLRPEDTALYYCQTSGSGSPNFWGQGTLVQVSS
186	11V + 110K	EVQLLESGGGVVQPGGSLRLSCAASGRIFSLPASGNIFNLLTIAW YRQAPGKGRELVATINSGSRTYYADSVKGRFTISRDNSKKTVYL QMNSLRPEDTAVYYCQTSGSGSPNFWGQGTLVKVSS
187	11V + 110Q	EVQLLESGGGVVQPGGSLRLSCAASGRIFSLPASGNIFNLLTIAW YRQAPGKGRELVATINSGSRTYYADSVKGRFTISRDNSKKTVYL QMNSLRPEDTAVYYCQTSGSGSPNFWGQGTLVQVSS
188	11V + 112K	EVQLLESGGGVVQPGGSLRLSCAASGRIFSLPASGNIFNLLTIAW YRQAPGKGRELVATINSGSRTYYADSVKGRFTISRDNSKKTVYL QMNSLRPEDTAVYYCQTSGSGSPNFWGQGTLVTVKS
189	11V + 112Q	EVQLLESGGGVVQPGGSLRLSCAASGRIFSLPASGNIFNLLTIAW YRQAPGKGRELVATINSGSRTYYADSVKGRFTISRDNSKKTVYL QMNSLRPEDTAVYYCQTSGSGSPNFWGQGTLVTVQS

Figure 12B

SEQ ID	Mutation(s)	Sequence
190	None (reference)	EVQLLESGGGLVQPGGSLRLSCAASGRTLSSYAMGWFRQAPGK GREFVARISQGGTAIYYADSVKGRFTISRDNSKNTLYLQMNSLR PEDTAVYYCAKDPSYYRGSAYLLSGSYDSWGQGTLTVSS
191	CDR1	SYAMG
192	CDR2	RISQGGTAIYYADSVKG
193	CDR3	DPSYYRGSAYLLSGSYDS
194	89L + 110K	EVQLLESGGGLVQPGGSLRLSCAASGRTLSSYAMGWFRQAPGK GREFVARISQGGTAIYYADSVKGRFTISRDNSKNTLYLQMNSLR PEDTALYYCAKDPSYYRGSAYLLSGSYDSWGQGTLVKVSS
195	89L + 110Q	EVQLLESGGGLVQPGGSLRLSCAASGRTLSSYAMGWFRQAPGK GREFVARISQGGTAIYYADSVKGRFTISRDNSKNTLYLQMNSLR PEDTALYYCAKDPSYYRGSAYLLSGSYDSWGQGTLVQVSS
196	110K	EVQLLESGGGLVQPGGSLRLSCAASGRTLSSYAMGWFRQAPGK GREFVARISQGGTAIYYADSVKGRFTISRDNSKNTLYLQMNSLR PEDTAVYYCAKDPSYYRGSAYLLSGSYDSWGQGTLVKVSS
197	110Q	EVQLLESGGGLVQPGGSLRLSCAASGRTLSSYAMGWFRQAPGK GREFVARISQGGTAIYYADSVKGRFTISRDNSKNTLYLQMNSLR PEDTAVYYCAKDPSYYRGSAYLLSGSYDSWGQGTLVQVSS
198	112K	EVQLLESGGGLVQPGGSLRLSCAASGRTLSSYAMGWFRQAPGK GREFVARISQGGTAIYYADSVKGRFTISRDNSKNTLYLQMNSLR PEDTAVYYCAKDPSYYRGSAYLLSGSYDSWGQGTLVTVKS
199	112Q	EVQLLESGGGLVQPGGSLRLSCAASGRTLSSYAMGWFRQAPGK GREFVARISQGGTAIYYADSVKGRFTISRDNSKNTLYLQMNSLR PEDTAVYYCAKDPSYYRGSAYLLSGSYDSWGQGTLVTVQS
200	89T	EVQLLESGGGLVQPGGSLRLSCAASGRTLSSYAMGWFRQAPGK GREFVARISQGGTAIYYADSVKGRFTISRDNSKNTLYLQMNSLR PEDTATYYCAKDPSYYRGSAYLLSGSYDSWGQGTLTVSS
201	11V + 89L	EVQLLESGGVVQPGGSLRLSCAASGRTLSSYAMGWFRQAPGK GREFVARISQGGTAIYYADSVKGRFTISRDNSKNTLYLQMNSLR PEDTALYYCAKDPSYYRGSAYLLSGSYDSWGQGTLTVSS
202	11V + 89L + 110K	EVQLLESGGVVQPGGSLRLSCAASGRTLSSYAMGWFRQAPGK GREFVARISQGGTAIYYADSVKGRFTISRDNSKNTLYLQMNSLR PEDTALYYCAKDPSYYRGSAYLLSGSYDSWGQGTLVKVSS
203	11V + 89L + 110Q	EVQLLESGGVVQPGGSLRLSCAASGRTLSSYAMGWFRQAPGK GREFVARISQGGTAIYYADSVKGRFTISRDNSKNTLYLQMNSLR PEDTALYYCAKDPSYYRGSAYLLSGSYDSWGQGTLVQVSS
204	11V + 110K	EVQLLESGGVVQPGGSLRLSCAASGRTLSSYAMGWFRQAPGK GREFVARISQGGTAIYYADSVKGRFTISRDNSKNTLYLQMNSLR PEDTAVYYCAKDPSYYRGSAYLLSGSYDSWGQGTLVKVSS

Figure 12B (Continued)

SEQ ID	Mutation(s)	Sequence
205	11V + 110Q	EVQLLESGGVVQPGGSLRLSCAASGRTLSSYAMGWFRQAPGK GREFVARISQGGTAIYYADSVKGRFTISRDNSKNTLYLQMNSLR PEDTAVYYCAKDPSPYYRGSAAYLLSGSYDSWGQGTLVQVSS
206	11V + 112K	EVQLLESGGVVQPGGSLRLSCAASGRTLSSYAMGWFRQAPGK GREFVARISQGGTAIYYADSVKGRFTISRDNSKNTLYLQMNSLR PEDTAVYYCAKDPSPYYRGSAAYLLSGSYDSWGQGTLVTVKs
207	11V + 112Q	EVQLLESGGVVQPGGSLRLSCAASGRTLSSYAMGWFRQAPGK GREFVARISQGGTAIYYADSVKGRFTISRDNSKNTLYLQMNSLR PEDTAVYYCAKDPSPYYRGSAAYLLSGSYDSWGQGTLVTVQS

Figure 13

SEQ ID	Mutation(s)	Sequence
208	None (reference)	EVQLVESGGGLVQPGGSLRLSCAASRSIGRLDRMGWYRHRPGE PRELVATITGGSSINYGDSVKGRFTISIDNSKNTVYLQMNSLRPE DTAVYYCNFNKYVTSRDTWGQGTLTVSS
209	CDR1	LDRMG
210	CDR2	TITGGSSINYGDSVKG
211	CDR3	NKYVTSRDT
212	89L + 110K	EVQLVESGGGLVQPGGSLRLSCAASRSIGRLDRMGWYRHRPGE PRELVATITGGSSINYGDSVKGRFTISIDNSKNTVYLQMNSLRPE DTALYYCNFNKYVTSRDTWGQGTLVKVSS
213	89L + 110Q	EVQLVESGGGLVQPGGSLRLSCAASRSIGRLDRMGWYRHRPGE PRELVATITGGSSINYGDSVKGRFTISIDNSKNTVYLQMNSLRPE DTALYYCNFNKYVTSRDTWGQGTLVQVSS
214	110K	EVQLVESGGGLVQPGGSLRLSCAASRSIGRLDRMGWYRHRPGE PRELVATITGGSSINYGDSVKGRFTISIDNSKNTVYLQMNSLRPE DTAVYYCNFNKYVTSRDTWGQGTLVKVSS
215	110Q	EVQLVESGGGLVQPGGSLRLSCAASRSIGRLDRMGWYRHRPGE PRELVATITGGSSINYGDSVKGRFTISIDNSKNTVYLQMNSLRPE DTAVYYCNFNKYVTSRDTWGQGTLVQVSS
216	112K	EVQLVESGGGLVQPGGSLRLSCAASRSIGRLDRMGWYRHRPGE PRELVATITGGSSINYGDSVKGRFTISIDNSKNTVYLQMNSLRPE DTAVYYCNFNKYVTSRDTWGQGTLVTVKS
217	112Q	EVQLVESGGGLVQPGGSLRLSCAASRSIGRLDRMGWYRHRPGE PRELVATITGGSSINYGDSVKGRFTISIDNSKNTVYLQMNSLRPE DTAVYYCNFNKYVTSRDTWGQGTLVTVQS
218	89T	EVQLVESGGGLVQPGGSLRLSCAASRSIGRLDRMGWYRHRPGE PRELVATITGGSSINYGDSVKGRFTISIDNSKNTVYLQMNSLRPE DTATYYCNFNKYVTSRDTWGQGTLTVSS
219	11V + 89L	EVQLVESGGGVQPGGSLRLSCAASRSIGRLDRMGWYRHRPGE PRELVATITGGSSINYGDSVKGRFTISIDNSKNTVYLQMNSLRPE DTALYYCNFNKYVTSRDTWGQGTLTVSS
220	11V + 89L + 110K	EVQLVESGGGVQPGGSLRLSCAASRSIGRLDRMGWYRHRPGE PRELVATITGGSSINYGDSVKGRFTISIDNSKNTVYLQMNSLRPE DTALYYCNFNKYVTSRDTWGQGTLVKVSS
221	11V + 89L + 110Q	EVQLVESGGGVQPGGSLRLSCAASRSIGRLDRMGWYRHRPGE PRELVATITGGSSINYGDSVKGRFTISIDNSKNTVYLQMNSLRPE DTALYYCNFNKYVTSRDTWGQGTLVQVSS
222	11V + 110K	EVQLVESGGGVQPGGSLRLSCAASRSIGRLDRMGWYRHRPGE PRELVATITGGSSINYGDSVKGRFTISIDNSKNTVYLQMNSLRPE DTAVYYCNFNKYVTSRDTWGQGTLVKVSS

Figure 13 (Continued)

SEQ ID	Mutation(s)	Sequence
223	11V + 110Q	EVQLVESGGVVQPGGSLRLSCAASRSIGRLDRMGWYRHPGE PRELVATITGGSSINYGDSVKGRFTISIDNSKNTVYLQMNSLRPE DTAVYYCNFNKYVTSRDTWGQGTLVQVSS
224	11V + 112K	EVQLVESGGVVQPGGSLRLSCAASRSIGRLDRMGWYRHPGE PRELVATITGGSSINYGDSVKGRFTISIDNSKNTVYLQMNSLRPE DTAVYYCNFNKYVTSRDTWGQGTLVTVKS
225	11V + 112Q	EVQLVESGGVVQPGGSLRLSCAASRSIGRLDRMGWYRHPGE PRELVATITGGSSINYGDSVKGRFTISIDNSKNTVYLQMNSLRPE DTAVYYCNFNKYVTSRDTWGQGTLVTVQS

Figure 14

SEQ ID	Mutation(s)	Sequence
226	None (reference)	DVQLLESGGGLVQPGGSLRLSCAASGFTFGNYDMAWVRQAPG KRPEWVSSIDTGGDITHYADSVKGRFTISRDNAKNTLYLQMNSL RPEDTAVYWCATDEEYALGPNEFDYYGQGTLVTVSS
227	CDR1	NYDMA
228	CDR2	SIDTGGDITHYADSVKG
229	CDR3	DEEYALGPNEFDY
230	89L + 110K	DVQLLESGGGLVQPGGSLRLSCAASGFTFGNYDMAWVRQAPG KRPEWVSSIDTGGDITHYADSVKGRFTISRDNAKNTLYLQMNSL RPEDTALYWCATDEEYALGPNEFDYYGQGTLVKVSS
231	89L + 110Q	DVQLLESGGGLVQPGGSLRLSCAASGFTFGNYDMAWVRQAPG KRPEWVSSIDTGGDITHYADSVKGRFTISRDNAKNTLYLQMNSL RPEDTALYWCATDEEYALGPNEFDYYGQGTLVQVSS
232	110K	DVQLLESGGGLVQPGGSLRLSCAASGFTFGNYDMAWVRQAPG KRPEWVSSIDTGGDITHYADSVKGRFTISRDNAKNTLYLQMNSL RPEDTAVYWCATDEEYALGPNEFDYYGQGTLVKVSS
233	110Q	DVQLLESGGGLVQPGGSLRLSCAASGFTFGNYDMAWVRQAPG KRPEWVSSIDTGGDITHYADSVKGRFTISRDNAKNTLYLQMNSL RPEDTAVYWCATDEEYALGPNEFDYYGQGTLVQVSS
234	112K	DVQLLESGGGLVQPGGSLRLSCAASGFTFGNYDMAWVRQAPG KRPEWVSSIDTGGDITHYADSVKGRFTISRDNAKNTLYLQMNSL RPEDTAVYWCATDEEYALGPNEFDYYGQGTLVTVKS
235	112Q	DVQLLESGGGLVQPGGSLRLSCAASGFTFGNYDMAWVRQAPG KRPEWVSSIDTGGDITHYADSVKGRFTISRDNAKNTLYLQMNSL RPEDTAVYWCATDEEYALGPNEFDYYGQGTLVTVQS
236	89T	DVQLLESGGGLVQPGGSLRLSCAASGFTFGNYDMAWVRQAPG KRPEWVSSIDTGGDITHYADSVKGRFTISRDNAKNTLYLQMNSL RPEDTATYWCATDEEYALGPNEFDYYGQGTLVTVSS
237	11V + 89L	DVQLLESGGVVQPGGSLRLSCAASGFTFGNYDMAWVRQAPG KRPEWVSSIDTGGDITHYADSVKGRFTISRDNAKNTLYLQMNSL RPEDTALYWCATDEEYALGPNEFDYYGQGTLVTVSS
238	11V + 89L + 110K	DVQLLESGGVVQPGGSLRLSCAASGFTFGNYDMAWVRQAPG KRPEWVSSIDTGGDITHYADSVKGRFTISRDNAKNTLYLQMNSL RPEDTALYWCATDEEYALGPNEFDYYGQGTLVKVSS
239	11V + 89L + 110Q	DVQLLESGGVVQPGGSLRLSCAASGFTFGNYDMAWVRQAPG KRPEWVSSIDTGGDITHYADSVKGRFTISRDNAKNTLYLQMNSL RPEDTALYWCATDEEYALGPNEFDYYGQGTLVQVSS

Figure 14 (continued)

SEQ ID	Mutation(s)	Sequence
240	11V + 110K	DVQLLESGGGVVQPGGSLRLSCAASGFTFGNYDMAWVRQAPG KRPEWVSSIDTGGDITHYADSVKGRFTISRDNAKNTLYLQMNSL RPEDTAVYWCATDEEYALGPNEFDYYGQGTLVKVSS
241	11V + 110Q	DVQLLESGGGVVQPGGSLRLSCAASGFTFGNYDMAWVRQAPG KRPEWVSSIDTGGDITHYADSVKGRFTISRDNAKNTLYLQMNSL RPEDTAVYWCATDEEYALGPNEFDYYGQGTLVQVSS
242	11V + 112K	DVQLLESGGGVVQPGGSLRLSCAASGFTFGNYDMAWVRQAPG KRPEWVSSIDTGGDITHYADSVKGRFTISRDNAKNTLYLQMNSL RPEDTAVYWCATDEEYALGPNEFDYYGQGTLVTVKs
243	11V + 112Q	DVQLLESGGGVVQPGGSLRLSCAASGFTFGNYDMAWVRQAPG KRPEWVSSIDTGGDITHYADSVKGRFTISRDNAKNTLYLQMNSL RPEDTAVYWCATDEEYALGPNEFDYYGQGTLVTVQS

Figure 15A

SEQ ID	Mutation(s)	Sequence
244	None (reference)	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGK GLEWVSGIKSSGDSTRYAGSVKGRFTISRDNAKNTLYLQMNSLR PEDTAVYYCAKSRSRTGLYTYDNRGQGTLTVSS
245	CDR1	SYAMS
246	CDR2	GIKSSGDSTRYAGSVKG
247	CDR3	SRVSRTGLYTYDN
248	89L + 110K	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGK GLEWVSGIKSSGDSTRYAGSVKGRFTISRDNAKNTLYLQMNSLR PEDTALYYCAKSRSRTGLYTYDNRGQGTLVKVSS
249	89L + 110Q	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGK GLEWVSGIKSSGDSTRYAGSVKGRFTISRDNAKNTLYLQMNSLR PEDTALYYCAKSRSRTGLYTYDNRGQGTLVQVSS
250	110K	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGK GLEWVSGIKSSGDSTRYAGSVKGRFTISRDNAKNTLYLQMNSLR PEDTAVYYCAKSRSRTGLYTYDNRGQGTLVKVSS
251	110Q	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGK GLEWVSGIKSSGDSTRYAGSVKGRFTISRDNAKNTLYLQMNSLR PEDTAVYYCAKSRSRTGLYTYDNRGQGTLVQVSS
252	112K	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGK GLEWVSGIKSSGDSTRYAGSVKGRFTISRDNAKNTLYLQMNSLR PEDTAVYYCAKSRSRTGLYTYDNRGQGTLTVKS
253	112Q	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGK GLEWVSGIKSSGDSTRYAGSVKGRFTISRDNAKNTLYLQMNSLR PEDTAVYYCAKSRSRTGLYTYDNRGQGTLTVQS
254	89T	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGK GLEWVSGIKSSGDSTRYAGSVKGRFTISRDNAKNTLYLQMNSLR PEDTATYYCAKSRSRTGLYTYDNRGQGTLTVSS
255	11V + 89L	EVQLVESGGGVVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGK GLEWVSGIKSSGDSTRYAGSVKGRFTISRDNAKNTLYLQMNSLR PEDTALYYCAKSRSRTGLYTYDNRGQGTLTVSS
256	11V + 89L + 110K	EVQLVESGGGVVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGK GLEWVSGIKSSGDSTRYAGSVKGRFTISRDNAKNTLYLQMNSLR PEDTALYYCAKSRSRTGLYTYDNRGQGTLVKVSS
257	11V + 89L + 110Q	EVQLVESGGGVVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGK GLEWVSGIKSSGDSTRYAGSVKGRFTISRDNAKNTLYLQMNSLR PEDTALYYCAKSRSRTGLYTYDNRGQGTLVQVSS

Figure 15A (Continued)

SEQ ID	Mutation(s)	Sequence
258	11V + 110K	EVQLVESGGVVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGK GLEWVSGIKSSGDSTRYAGSVKGRFTISRDNAKNTLYLQMNSLR PEDTAVYYCAKSRSRTGLYTYDNRGQGTLVKVSS
259	11V + 110Q	EVQLVESGGVVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGK GLEWVSGIKSSGDSTRYAGSVKGRFTISRDNAKNTLYLQMNSLR PEDTAVYYCAKSRSRTGLYTYDNRGQGTLVQVSS
260	11V + 112K	EVQLVESGGVVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGK GLEWVSGIKSSGDSTRYAGSVKGRFTISRDNAKNTLYLQMNSLR PEDTAVYYCAKSRSRTGLYTYDNRGQGTLTVKS
261	11V + 112Q	EVQLVESGGVVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGK GLEWVSGIKSSGDSTRYAGSVKGRFTISRDNAKNTLYLQMNSLR PEDTAVYYCAKSRSRTGLYTYDNRGQGTLTVQS

Figure 15B

SEQ ID	Mutation(s)	Sequence
262	None (reference)	EVQLVESGGGLVQPGGSLRLSCAASGRTFNNYAMGWFRQAPG KEREFAAITRSGVRSGVSAIYGDSVKDRFTISRDNAKNTLYLQ MNSLRPEDTAVYYCAASAIGSGALRRFEYDYSQGQTLVTVSS
263	CDR1	NYAMG
264	CDR2	AITRSGVRSGVSAIYGDSVKD
265	CDR3	SAIGSGALRRFEYDY
266	89L + 110K	EVQLVESGGGLVQPGGSLRLSCAASGRTFNNYAMGWFRQAPG KEREFAAITRSGVRSGVSAIYGDSVKDRFTISRDNAKNTLYLQ MNSLRPEDTALYYCAASAIGSGALRRFEYDYSQGQTLVKVSS
267	89L + 110Q	EVQLVESGGGLVQPGGSLRLSCAASGRTFNNYAMGWFRQAPG KEREFAAITRSGVRSGVSAIYGDSVKDRFTISRDNAKNTLYLQ MNSLRPEDTALYYCAASAIGSGALRRFEYDYSQGQTLVQVSS
268	110K	EVQLVESGGGLVQPGGSLRLSCAASGRTFNNYAMGWFRQAPG KEREFAAITRSGVRSGVSAIYGDSVKDRFTISRDNAKNTLYLQ MNSLRPEDTAVYYCAASAIGSGALRRFEYDYSQGQTLVKVSS
269	110Q	EVQLVESGGGLVQPGGSLRLSCAASGRTFNNYAMGWFRQAPG KEREFAAITRSGVRSGVSAIYGDSVKDRFTISRDNAKNTLYLQ MNSLRPEDTAVYYCAASAIGSGALRRFEYDYSQGQTLVQVSS
270	112K	EVQLVESGGGLVQPGGSLRLSCAASGRTFNNYAMGWFRQAPG KEREFAAITRSGVRSGVSAIYGDSVKDRFTISRDNAKNTLYLQ MNSLRPEDTAVYYCAASAIGSGALRRFEYDYSQGQTLVTVKS
271	112Q	EVQLVESGGGLVQPGGSLRLSCAASGRTFNNYAMGWFRQAPG KEREFAAITRSGVRSGVSAIYGDSVKDRFTISRDNAKNTLYLQ MNSLRPEDTAVYYCAASAIGSGALRRFEYDYSQGQTLVTVQS
272	89T	EVQLVESGGGLVQPGGSLRLSCAASGRTFNNYAMGWFRQAPG KEREFAAITRSGVRSGVSAIYGDSVKDRFTISRDNAKNTLYLQ MNSLRPEDTATYYCAASAIGSGALRRFEYDYSQGQTLVTVSS
273	11V + 89L	EVQLVESGGGVQPGGSLRLSCAASGRTFNNYAMGWFRQAPG KEREFAAITRSGVRSGVSAIYGDSVKDRFTISRDNAKNTLYLQ MNSLRPEDTALYYCAASAIGSGALRRFEYDYSQGQTLVTVSS
274	11V + 89L + 110K	EVQLVESGGGVQPGGSLRLSCAASGRTFNNYAMGWFRQAPG KEREFAAITRSGVRSGVSAIYGDSVKDRFTISRDNAKNTLYLQ MNSLRPEDTALYYCAASAIGSGALRRFEYDYSQGQTLVKVSS
275	11V + 89L + 110Q	EVQLVESGGGVQPGGSLRLSCAASGRTFNNYAMGWFRQAPG KEREFAAITRSGVRSGVSAIYGDSVKDRFTISRDNAKNTLYLQ MNSLRPEDTALYYCAASAIGSGALRRFEYDYSQGQTLVQVSS

Figure 15B (Continued)

SEQ ID	Mutation(s)	Sequence
276	11V + 110K	EVQLVESGGVVQPGGSLRLSCAASGRTFNNYAMGWFRQAPG KEREFAAITRSGVRSGVSAIYGDSVKDRFTISRDNAKNTLYLQ MNSLRPEDTAVYYCAASAIGSGALRRFEYDYSQGQGTLVKVSS
277	11V + 110Q	EVQLVESGGVVQPGGSLRLSCAASGRTFNNYAMGWFRQAPG KEREFAAITRSGVRSGVSAIYGDSVKDRFTISRDNAKNTLYLQ MNSLRPEDTAVYYCAASAIGSGALRRFEYDYSQGQGTLVQVSS
278	11V + 112K	EVQLVESGGVVQPGGSLRLSCAASGRTFNNYAMGWFRQAPG KEREFAAITRSGVRSGVSAIYGDSVKDRFTISRDNAKNTLYLQ MNSLRPEDTAVYYCAASAIGSGALRRFEYDYSQGQGTLVTVKS
279	11V + 112Q	EVQLVESGGVVQPGGSLRLSCAASGRTFNNYAMGWFRQAPG KEREFAAITRSGVRSGVSAIYGDSVKDRFTISRDNAKNTLYLQ MNSLRPEDTAVYYCAASAIGSGALRRFEYDYSQGQGTLVTVQS

Figure 16A

SEQ ID	Mutation(s)	Sequence
280	None (reference)	DVQLVESGGGLVQPGGSLRLSCAASGSIGGLNAMAWYRQAPG KERELVAGIFGVGSTRYADSVKGRFTISRDNSKNTVYLQMNSLR PEDTAVYYCRMSSVTRGSSDYWGQGTLTVSS
281	CDR1	LNAMA
282	CDR2	GIFGVGSTRYADSVKG
283	CDR3	SSVTRGSSDY
284	89L + 110K	DVQLVESGGGLVQPGGSLRLSCAASGSIGGLNAMAWYRQAPG KERELVAGIFGVGSTRYADSVKGRFTISRDNSKNTVYLQMNSLR PEDTALYYCRMSSVTRGSSDYWGQGTLVKVSS
285	89L + 110Q	DVQLVESGGGLVQPGGSLRLSCAASGSIGGLNAMAWYRQAPG KERELVAGIFGVGSTRYADSVKGRFTISRDNSKNTVYLQMNSLR PEDTALYYCRMSSVTRGSSDYWGQGTLVQVSS
286	110K	DVQLVESGGGLVQPGGSLRLSCAASGSIGGLNAMAWYRQAPG KERELVAGIFGVGSTRYADSVKGRFTISRDNSKNTVYLQMNSLR PEDTAVYYCRMSSVTRGSSDYWGQGTLVKVSS
287	110Q	DVQLVESGGGLVQPGGSLRLSCAASGSIGGLNAMAWYRQAPG KERELVAGIFGVGSTRYADSVKGRFTISRDNSKNTVYLQMNSLR PEDTAVYYCRMSSVTRGSSDYWGQGTLVQVSS
288	112K	DVQLVESGGGLVQPGGSLRLSCAASGSIGGLNAMAWYRQAPG KERELVAGIFGVGSTRYADSVKGRFTISRDNSKNTVYLQMNSLR PEDTAVYYCRMSSVTRGSSDYWGQGTLTVKS
289	112Q	DVQLVESGGGLVQPGGSLRLSCAASGSIGGLNAMAWYRQAPG KERELVAGIFGVGSTRYADSVKGRFTISRDNSKNTVYLQMNSLR PEDTAVYYCRMSSVTRGSSDYWGQGTLTVQS
290	89T	DVQLVESGGGLVQPGGSLRLSCAASGSIGGLNAMAWYRQAPG KERELVAGIFGVGSTRYADSVKGRFTISRDNSKNTVYLQMNSLR PEDTATYYCRMSSVTRGSSDYWGQGTLTVSS
291	11V + 89L	DVQLVESGGGVQPGGSLRLSCAASGSIGGLNAMAWYRQAPG KERELVAGIFGVGSTRYADSVKGRFTISRDNSKNTVYLQMNSLR PEDTALYYCRMSSVTRGSSDYWGQGTLTVSS
292	11V + 89L + 110K	DVQLVESGGGVQPGGSLRLSCAASGSIGGLNAMAWYRQAPG KERELVAGIFGVGSTRYADSVKGRFTISRDNSKNTVYLQMNSLR PEDTALYYCRMSSVTRGSSDYWGQGTLVKVSS
293	11V + 89L + 110Q	DVQLVESGGGVQPGGSLRLSCAASGSIGGLNAMAWYRQAPG KERELVAGIFGVGSTRYADSVKGRFTISRDNSKNTVYLQMNSLR PEDTALYYCRMSSVTRGSSDYWGQGTLVQVSS

Figure 16A (continued)

SEQ ID	Mutation(s)	Sequence
294	11V + 110K	DVQLVESGGVVQPGGSLRLSCAASGSIGGLNAMAWYRQAPG KERELVAGIFGVGSTRYADSVKGRFTISRDNSKNTVYLQMNSLR PEDTAVYYCRMSSVTRGSSDYWGQGTLVKVSS
295	11V + 110Q	DVQLVESGGVVQPGGSLRLSCAASGSIGGLNAMAWYRQAPG KERELVAGIFGVGSTRYADSVKGRFTISRDNSKNTVYLQMNSLR PEDTAVYYCRMSSVTRGSSDYWGQGTLVQVSS
296	11V + 112K	DVQLVESGGVVQPGGSLRLSCAASGSIGGLNAMAWYRQAPG KERELVAGIFGVGSTRYADSVKGRFTISRDNSKNTVYLQMNSLR PEDTAVYYCRMSSVTRGSSDYWGQGTLTVKS
297	11V + 112Q	DVQLVESGGVVQPGGSLRLSCAASGSIGGLNAMAWYRQAPG KERELVAGIFGVGSTRYADSVKGRFTISRDNSKNTVYLQMNSLR PEDTAVYYCRMSSVTRGSSDYWGQGTLTVQS

Figure 16B

SEQ ID	Mutation(s)	Sequence
298	None (reference)	EVQLVESGGGLVQPGGSLRLSCAASGRYYLNAMGWFRQAPG KEREFVAIDWSEGNKDYADSVKGRFTISRDNKNTVYLQMNS LRPEDTAVYYCAADTPPWGPLIYIESYDSWGQQGTLTVSS
299	CDR1	LNAMG
300	CDR2	AIDWSEGNKDYADSVKG
301	CDR3	DTPPWGPIYIESYDS
302	89L + 110K	EVQLVESGGGLVQPGGSLRLSCAASGRYYLNAMGWFRQAPG KEREFVAIDWSEGNKDYADSVKGRFTISRDNKNTVYLQMNS LRPEDTALYYCAADTPPWGPLIYIESYDSWGQQGTLVKVSS
303	89L + 110Q	EVQLVESGGGLVQPGGSLRLSCAASGRYYLNAMGWFRQAPG KEREFVAIDWSEGNKDYADSVKGRFTISRDNKNTVYLQMNS LRPEDTALYYCAADTPPWGPLIYIESYDSWGQQGTLVQVSS
304	110K	EVQLVESGGGLVQPGGSLRLSCAASGRYYLNAMGWFRQAPG KEREFVAIDWSEGNKDYADSVKGRFTISRDNKNTVYLQMNS LRPEDTAVYYCAADTPPWGPLIYIESYDSWGQQGTLVKVSS
305	110Q	EVQLVESGGGLVQPGGSLRLSCAASGRYYLNAMGWFRQAPG KEREFVAIDWSEGNKDYADSVKGRFTISRDNKNTVYLQMNS LRPEDTAVYYCAADTPPWGPLIYIESYDSWGQQGTLVQVSS
306	112K	EVQLVESGGGLVQPGGSLRLSCAASGRYYLNAMGWFRQAPG KEREFVAIDWSEGNKDYADSVKGRFTISRDNKNTVYLQMNS LRPEDTAVYYCAADTPPWGPLIYIESYDSWGQQGTLVTVK
307	112Q	EVQLVESGGGLVQPGGSLRLSCAASGRYYLNAMGWFRQAPG KEREFVAIDWSEGNKDYADSVKGRFTISRDNKNTVYLQMNS LRPEDTAVYYCAADTPPWGPLIYIESYDSWGQQGTLVTVQS
308	89T	EVQLVESGGGLVQPGGSLRLSCAASGRYYLNAMGWFRQAPG KEREFVAIDWSEGNKDYADSVKGRFTISRDNKNTVYLQMNS LRPEDTATYYCAADTPPWGPLIYIESYDSWGQQGTLVTVSS
309	11V + 89L	EVQLVESGGGVQPGGSLRLSCAASGRYYLNAMGWFRQAPG KEREFVAIDWSEGNKDYADSVKGRFTISRDNKNTVYLQMNS LRPEDTALYYCAADTPPWGPLIYIESYDSWGQQGTLVTVSS
310	11V + 89L + 110K	EVQLVESGGGVQPGGSLRLSCAASGRYYLNAMGWFRQAPG KEREFVAIDWSEGNKDYADSVKGRFTISRDNKNTVYLQMNS LRPEDTALYYCAADTPPWGPLIYIESYDSWGQQGTLVKVSS
311	11V + 89L + 110Q	EVQLVESGGGVQPGGSLRLSCAASGRYYLNAMGWFRQAPG KEREFVAIDWSEGNKDYADSVKGRFTISRDNKNTVYLQMNS LRPEDTALYYCAADTPPWGPLIYIESYDSWGQQGTLVQVSS

Figure 16B (continued)

SEQ ID	Mutation(s)	Sequence
312	11V + 110K	EVQLVESGGVVQPGGSLRLSCAASGRYYLNAMGWFRQAPG KEREFAAIDWSEGNKDYADSVKGRFTISRDN SKNTVYLQMNS LRPEDTAVYYCAADTPPWGPLIYIESYDSWGQGTLVKVSS
313	11V + 110Q	EVQLVESGGVVQPGGSLRLSCAASGRYYLNAMGWFRQAPG KEREFAAIDWSEGNKDYADSVKGRFTISRDN SKNTVYLQMNS LRPEDTAVYYCAADTPPWGPLIYIESYDSWGQGTLVQVSS
314	11V + 112K	EVQLVESGGVVQPGGSLRLSCAASGRYYLNAMGWFRQAPG KEREFAAIDWSEGNKDYADSVKGRFTISRDN SKNTVYLQMNS LRPEDTAVYYCAADTPPWGPLIYIESYDSWGQGTLTVKS
315	11V + 112Q	EVQLVESGGVVQPGGSLRLSCAASGRYYLNAMGWFRQAPG KEREFAAIDWSEGNKDYADSVKGRFTISRDN SKNTVYLQMNS LRPEDTAVYYCAADTPPWGPLIYIESYDSWGQGTLTVQS

Figure 17A

SEQ ID	Mutation(s)	Sequence
316	None (reference)	EVQLVESGGGLVQPGGSLRLSCAASGFTFS DYW MYW VRQAPG KG LEW VSE INTN GLITKYPDSVKGRFTISRDNAKNTLYLQMNSL RP EDT A VYY CARSPSGFNRGQGTLVTVSS
317	CDR1	DYW MY
318	CDR2	EINTN GLITKYPDSVKKG
319	CDR3	SPSGFN
320	89L + 110K	EVQLVESGGGLVQPGGSLRLSCAASGFTFS DYW MYW VRQAPG KG LEW VSE INTN GLITKYPDSVKGRFTISRDNAKNTLYLQMNSL RP EDT A VYY CARSPSGFNRGQGTLV KVSS
321	89L + 110Q	EVQLVESGGGLVQPGGSLRLSCAASGFTFS DYW MYW VRQAPG KG LEW VSE INTN GLITKYPDSVKGRFTISRDNAKNTLYLQMNSL RP EDT A VYY CARSPSGFNRGQGTLVQVSS
322	110K	EVQLVESGGGLVQPGGSLRLSCAASGFTFS DYW MYW VRQAPG KG LEW VSE INTN GLITKYPDSVKGRFTISRDNAKNTLYLQMNSL RP EDT A VYY CARSPSGFNRGQGTLV KVSS
323	110Q	EVQLVESGGGLVQPGGSLRLSCAASGFTFS DYW MYW VRQAPG KG LEW VSE INTN GLITKYPDSVKGRFTISRDNAKNTLYLQMNSL RP EDT A VYY CARSPSGFNRGQGTLVQVSS
324	112K	EVQLVESGGGLVQPGGSLRLSCAASGFTFS DYW MYW VRQAPG KG LEW VSE INTN GLITKYPDSVKGRFTISRDNAKNTLYLQMNSL RP EDT A VYY CARSPSGFNRGQGTLVTVKS
325	112Q	EVQLVESGGGLVQPGGSLRLSCAASGFTFS DYW MYW VRQAPG KG LEW VSE INTN GLITKYPDSVKGRFTISRDNAKNTLYLQMNSL RP EDT A VYY CARSPSGFNRGQGTLVTVQS
326	89T	EVQLVESGGGLVQPGGSLRLSCAASGFTFS DYW MYW VRQAPG KG LEW VSE INTN GLITKYPDSVKGRFTISRDNAKNTLYLQMNSL RP EDT A VYY CARSPSGFNRGQGTLVTVSS
327	11V + 89L	EVQLVESGGGVQPGGSLRLSCAASGFTFS DYW MYW VRQAPG KG LEW VSE INTN GLITKYPDSVKGRFTISRDNAKNTLYLQMNSL RP EDT A VYY CARSPSGFNRGQGTLVTVSS
328	11V + 89L + 110K	EVQLVESGGGVQPGGSLRLSCAASGFTFS DYW MYW VRQAPG KG LEW VSE INTN GLITKYPDSVKGRFTISRDNAKNTLYLQMNSL RP EDT A VYY CARSPSGFNRGQGTLV KVSS
329	11V + 89L + 110Q	EVQLVESGGGVQPGGSLRLSCAASGFTFS DYW MYW VRQAPG KG LEW VSE INTN GLITKYPDSVKGRFTISRDNAKNTLYLQMNSL RP EDT A VYY CARSPSGFNRGQGTLVQVSS

Figure 17A (continued)

SEQ ID	Mutation(s)	Sequence
330	11V + 110K	EVQLVESGGVVQPGGSLRLSCAASGFTFSDYWMYWVRQAPG KGLEWVSEINTNGLITKYPDSVKGRFTISRDNAKNTLYLQMNSL RPEDTAVYYCARSPSGFNRGQGTLVKVSS
331	11V + 110Q	EVQLVESGGVVQPGGSLRLSCAASGFTFSDYWMYWVRQAPG KGLEWVSEINTNGLITKYPDSVKGRFTISRDNAKNTLYLQMNSL RPEDTAVYYCARSPSGFNRGQGTLVQVSS
332	11V + 112K	EVQLVESGGVVQPGGSLRLSCAASGFTFSDYWMYWVRQAPG KGLEWVSEINTNGLITKYPDSVKGRFTISRDNAKNTLYLQMNSL RPEDTAVYYCARSPSGFNRGQGTLVTVKs
333	11V + 112Q	EVQLVESGGVVQPGGSLRLSCAASGFTFSDYWMYWVRQAPG KGLEWVSEINTNGLITKYPDSVKGRFTISRDNAKNTLYLQMNSL RPEDTAVYYCARSPSGFNRGQGTLVTVQS

Figure 17B

SEQ ID	Mutation(s)	Sequence
334	None (reference)	EVQLVESGGGLVQPGGSLRLSCTASGFTSTADMGWFRQAPGK GREFVSRISGIDGTTYYDEPVKGRFTISRDNAKNTLYLQMNSLRP EDTAVYYCRSPRYADQWSAYDYWGQGTLVTVSS
335	CDR1	TADMG
336	CDR2	RISGIDGTTYYDEPVKG
337	CDR3	PRYADQWSAYDY
338	89L + 110K	EVQLVESGGGLVQPGGSLRLSCTASGFTSTADMGWFRQAPGK GREFVSRISGIDGTTYYDEPVKGRFTISRDNAKNTLYLQMNSLRP EDTALYYCRSPRYADQWSAYDYWGQGTLVKVSS
339	89L + 110Q	EVQLVESGGGLVQPGGSLRLSCTASGFTSTADMGWFRQAPGK GREFVSRISGIDGTTYYDEPVKGRFTISRDNAKNTLYLQMNSLRP EDTALYYCRSPRYADQWSAYDYWGQGTLVQVSS
340	110K	EVQLVESGGGLVQPGGSLRLSCTASGFTSTADMGWFRQAPGK GREFVSRISGIDGTTYYDEPVKGRFTISRDNAKNTLYLQMNSLRP EDTAVYYCRSPRYADQWSAYDYWGQGTLVKVSS
341	110Q	EVQLVESGGGLVQPGGSLRLSCTASGFTSTADMGWFRQAPGK GREFVSRISGIDGTTYYDEPVKGRFTISRDNAKNTLYLQMNSLRP EDTAVYYCRSPRYADQWSAYDYWGQGTLVQVSS
342	112K	EVQLVESGGGLVQPGGSLRLSCTASGFTSTADMGWFRQAPGK GREFVSRISGIDGTTYYDEPVKGRFTISRDNAKNTLYLQMNSLRP EDTAVYYCRSPRYADQWSAYDYWGQGTLVTVK
343	112Q	EVQLVESGGGLVQPGGSLRLSCTASGFTSTADMGWFRQAPGK GREFVSRISGIDGTTYYDEPVKGRFTISRDNAKNTLYLQMNSLRP EDTAVYYCRSPRYADQWSAYDYWGQGTLVTVQS
344	89T	EVQLVESGGGLVQPGGSLRLSCTASGFTSTADMGWFRQAPGK GREFVSRISGIDGTTYYDEPVKGRFTISRDNAKNTLYLQMNSLRP EDTATYYCRSPRYADQWSAYDYWGQGTLVTVSS
345	11V + 89L	EVQLVESGGGVQPGGSLRLSCTASGFTSTADMGWFRQAPGK GREFVSRISGIDGTTYYDEPVKGRFTISRDNAKNTLYLQMNSLRP EDTALYYCRSPRYADQWSAYDYWGQGTLVTVSS
346	11V + 89L + 110K	EVQLVESGGGVQPGGSLRLSCTASGFTSTADMGWFRQAPGK GREFVSRISGIDGTTYYDEPVKGRFTISRDNAKNTLYLQMNSLRP EDTALYYCRSPRYADQWSAYDYWGQGTLVKVSS
347	11V + 89L + 110Q	EVQLVESGGGVQPGGSLRLSCTASGFTSTADMGWFRQAPGK GREFVSRISGIDGTTYYDEPVKGRFTISRDNAKNTLYLQMNSLRP EDTALYYCRSPRYADQWSAYDYWGQGTLVQVSS

Figure 17B (continued)

SEQ ID	Mutation(s)	Sequence
348	11V + 110K	EVQLVESGGVVQPGGSLRLSCTASGFTFSTADMGWFRQAPGK GREFVSRISGIDGTTYYDEPVKGRFTISRDNAKNTLYLQMNSLRP EDTAVYYCRSPRYADQWSAYDYWGQGTLVKVSS
349	11V + 110Q	EVQLVESGGVVQPGGSLRLSCTASGFTFSTADMGWFRQAPGK GREFVSRISGIDGTTYYDEPVKGRFTISRDNAKNTLYLQMNSLRP EDTAVYYCRSPRYADQWSAYDYWGQGTLVQVSS
350	11V + 112K	EVQLVESGGVVQPGGSLRLSCTASGFTFSTADMGWFRQAPGK GREFVSRISGIDGTTYYDEPVKGRFTISRDNAKNTLYLQMNSLRP EDTAVYYCRSPRYADQWSAYDYWGQGTLVTVKS
351	11V + 112Q	EVQLVESGGVVQPGGSLRLSCTASGFTFSTADMGWFRQAPGK GREFVSRISGIDGTTYYDEPVKGRFTISRDNAKNTLYLQMNSLRP EDTAVYYCRSPRYADQWSAYDYWGQGTLVTVQS

Figure 18A

SEQ ID	Mutation(s)	Sequence
352	None (reference)	DVQLVESGGGLVQPGGSLRLSCAASGFILDYYAIGWFRQAPGKE REGVLCIDASDDITYYADSVKGRFTISRDN SKNTVYLQMNSLRP EDTAVYYCATPIGLSSSCLLEYDYDYWGQGTLTVSS
353	CDR1	YYAIG
354	CDR2	CIDASDDITYYADSVKG
355	CDR3	PIGLSSSCLLEYDYDY
356	89L + 110K	DVQLVESGGGLVQPGGSLRLSCAASGFILDYYAIGWFRQAPGKE REGVLCIDASDDITYYADSVKGRFTISRDN SKNTVYLQMNSLRP EDTALYYCATPIGLSSSCLLEYDYDYWGQGTLVKVSS
357	89L + 110Q	DVQLVESGGGLVQPGGSLRLSCAASGFILDYYAIGWFRQAPGKE REGVLCIDASDDITYYADSVKGRFTISRDN SKNTVYLQMNSLRP EDTALYYCATPIGLSSSCLLEYDYDYWGQGTLVQVSS
358	110K	DVQLVESGGGLVQPGGSLRLSCAASGFILDYYAIGWFRQAPGKE REGVLCIDASDDITYYADSVKGRFTISRDN SKNTVYLQMNSLRP EDTAVYYCATPIGLSSSCLLEYDYDYWGQGTLVKVSS
359	110Q	DVQLVESGGGLVQPGGSLRLSCAASGFILDYYAIGWFRQAPGKE REGVLCIDASDDITYYADSVKGRFTISRDN SKNTVYLQMNSLRP EDTAVYYCATPIGLSSSCLLEYDYDYWGQGTLVQVSS
360	112K	DVQLVESGGGLVQPGGSLRLSCAASGFILDYYAIGWFRQAPGKE REGVLCIDASDDITYYADSVKGRFTISRDN SKNTVYLQMNSLRP EDTAVYYCATPIGLSSSCLLEYDYDYWGQGTLVTVKS
361	112Q	DVQLVESGGGLVQPGGSLRLSCAASGFILDYYAIGWFRQAPGKE REGVLCIDASDDITYYADSVKGRFTISRDN SKNTVYLQMNSLRP EDTAVYYCATPIGLSSSCLLEYDYDYWGQGTLVTVQS
362	89T	DVQLVESGGGLVQPGGSLRLSCAASGFILDYYAIGWFRQAPGKE REGVLCIDASDDITYYADSVKGRFTISRDN SKNTVYLQMNSLRP EDTATYYCATPIGLSSSCLLEYDYDYWGQGTLTVSS
363	11V + 89L	DVQLVESGGGVVQPGGSLRLSCAASGFILDYYAIGWFRQAPGKE EREGVLCIDASDDITYYADSVKGRFTISRDN SKNTVYLQMNSLRP PEDTALYYCATPIGLSSSCLLEYDYDYWGQGTLTVSS
364	11V + 89L + 110K	DVQLVESGGGVVQPGGSLRLSCAASGFILDYYAIGWFRQAPGKE EREGVLCIDASDDITYYADSVKGRFTISRDN SKNTVYLQMNSLRP PEDTALYYCATPIGLSSSCLLEYDYDYWGQGTLVKS
365	11V + 89L + 110Q	DVQLVESGGGVVQPGGSLRLSCAASGFILDYYAIGWFRQAPGKE EREGVLCIDASDDITYYADSVKGRFTISRDN SKNTVYLQMNSLRP PEDTALYYCATPIGLSSSCLLEYDYDYWGQGTLVQVSS

Figure 18A (continued)

SEQ ID	Mutation(s)	Sequence
366	11V + 110K	DVQLVESGGVVQPGGSLRLSCAASGFILDYYAIGWFRQAPGK EREGVL CIDASDDITYYADSVKGRFTISRDNSKNTVYLQMNSLR PEDTAVYYCATPIGLSSSCLLEYDYDYWGQQGTLVKVSS
367	11V + 110Q	DVQLVESGGVVQPGGSLRLSCAASGFILDYYAIGWFRQAPGK EREGVL CIDASDDITYYADSVKGRFTISRDNSKNTVYLQMNSLR PEDTAVYYCATPIGLSSSCLLEYDYDYWGQQGTLVQVSS
368	11V + 112K	DVQLVESGGVVQPGGSLRLSCAASGFILDYYAIGWFRQAPGK EREGVL CIDASDDITYYADSVKGRFTISRDNSKNTVYLQMNSLR PEDTAVYYCATPIGLSSSCLLEYDYDYWGQQGTLVTVKS
369	11V + 112Q	DVQLVESGGVVQPGGSLRLSCAASGFILDYYAIGWFRQAPGK EREGVL CIDASDDITYYADSVKGRFTISRDNSKNTVYLQMNSLR PEDTAVYYCATPIGLSSSCLLEYDYDYWGQQGTLVTVQS

Figure 18B

SEQ ID	Mutation(s)	Sequence
370	None (reference)	DVQLVESGGGLVQPGGSLRLSCAASGFAFDDYAI GWFRQAPGE EREGVSSISSTYGLYYADSVKGRFTISSLNSKNTVYLQMNSLRP EDTAVYYCAATPIGLIGLDAYEYDYWGQGTLTVSS
371	CDR1	DDYAI G
372	CDR2	SISSTYGLYYADSVKG
373	CDR3	TPIGLIGLDAYEYDY
374	89L + 110K	DVQLVESGGGLVQPGGSLRLSCAASGFAFDDYAI GWFRQAPGE EREGVSSISSTYGLYYADSVKGRFTISSLNSKNTVYLQMNSLRP EDTALYYCAATPIGLIGLDAYEYDYWGQGTLVKVSS
375	89L + 110Q	DVQLVESGGGLVQPGGSLRLSCAASGFAFDDYAI GWFRQAPGE EREGVSSISSTYGLYYADSVKGRFTISSLNSKNTVYLQMNSLRP EDTALYYCAATPIGLIGLDAYEYDYWGQGTLVQVSS
376	110K	DVQLVESGGGLVQPGGSLRLSCAASGFAFDDYAI GWFRQAPGE EREGVSSISSTYGLYYADSVKGRFTISSLNSKNTVYLQMNSLRP EDTAVYYCAATPIGLIGLDAYEYDYWGQGTLVKVSS
377	110Q	DVQLVESGGGLVQPGGSLRLSCAASGFAFDDYAI GWFRQAPGE EREGVSSISSTYGLYYADSVKGRFTISSLNSKNTVYLQMNSLRP EDTAVYYCAATPIGLIGLDAYEYDYWGQGTLVQVSS
378	112K	DVQLVESGGGLVQPGGSLRLSCAASGFAFDDYAI GWFRQAPGE EREGVSSISSTYGLYYADSVKGRFTISSLNSKNTVYLQMNSLRP EDTAVYYCAATPIGLIGLDAYEYDYWGQGTLVTVKS
379	112Q	DVQLVESGGGLVQPGGSLRLSCAASGFAFDDYAI GWFRQAPGE EREGVSSISSTYGLYYADSVKGRFTISSLNSKNTVYLQMNSLRP EDTAVYYCAATPIGLIGLDAYEYDYWGQGTLVTVQS
380	89T	DVQLVESGGGLVQPGGSLRLSCAASGFAFDDYAI GWFRQAPGE EREGVSSISSTYGLYYADSVKGRFTISSLNSKNTVYLQMNSLRP EDTATYYCAATPIGLIGLDAYEYDYWGQGTLTVSS
381	11V + 89L	DVQLVESGGGVVQPGGSLRLSCAASGFAFDDYAI GWFRQAPGE EREGVSSISSTYGLYYADSVKGRFTISSLNSKNTVYLQMNSLRP EDTALYYCAATPIGLIGLDAYEYDYWGQGTLVTVSS
382	11V + 89L + 110K	DVQLVESGGGVVQPGGSLRLSCAASGFAFDDYAI GWFRQAPGE EREGVSSISSTYGLYYADSVKGRFTISSLNSKNTVYLQMNSLRP EDTALYYCAATPIGLIGLDAYEYDYWGQGTLVKVSS
383	11V + 89L + 110Q	DVQLVESGGGVVQPGGSLRLSCAASGFAFDDYAI GWFRQAPGE EREGVSSISSTYGLYYADSVKGRFTISSLNSKNTVYLQMNSLRP EDTALYYCAATPIGLIGLDAYEYDYWGQGTLVQVSS

Figure 18B (continued)

SEQ ID	Mutation(s)	Sequence
384	11V + 110K	DVQLVESGGVVQPGGSLRLSCAASGFAFDDYAIGWFRQAPGE EREGVSSISSTYGLTYYADSVKGRFTISSLNSKNTVYLQMNSLRP EDTAVYYCAATPIGLIGLDAYEYDYWGQGTLVKVSS
385	11V + 110Q	DVQLVESGGVVQPGGSLRLSCAASGFAFDDYAIGWFRQAPGE EREGVSSISSTYGLTYYADSVKGRFTISSLNSKNTVYLQMNSLRP EDTAVYYCAATPIGLIGLDAYEYDYWGQGTLVQVSS
386	11V + 112K	DVQLVESGGVVQPGGSLRLSCAASGFAFDDYAIGWFRQAPGE EREGVSSISSTYGLTYYADSVKGRFTISSLNSKNTVYLQMNSLRP EDTAVYYCAATPIGLIGLDAYEYDYWGQGTLTVKS
387	11V + 112Q	DVQLVESGGVVQPGGSLRLSCAASGFAFDDYAIGWFRQAPGE EREGVSSISSTYGLTYYADSVKGRFTISSLNSKNTVYLQMNSLRP EDTAVYYCAATPIGLIGLDAYEYDYWGQGTLTVQS

Figure 19

SEQ ID	Mutation(s)	Sequence
388	None (reference)	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYPMGWFHQAPGK GREFVSSITGSGGSTYYADSVKGRFTISRDNAKNTLYLQMNSLR PEDTAVYYCAAYIRPDTYLSRDYRKYDYWGQGTLVTVSS
389	CDR1	SYPMG
390	CDR2	SITGSGGSTYYADSVKG
391	CDR3	YIRPDTYLSRDYRKYDY
392	89L + 110K	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYPMGWFHQAPGK GREFVSSITGSGGSTYYADSVKGRFTISRDNAKNTLYLQMNSLR PEDTALYYCAAYIRPDTYLSRDYRKYDYWGQGTLVKVSS
393	89L + 110Q	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYPMGWFHQAPGK GREFVSSITGSGGSTYYADSVKGRFTISRDNAKNTLYLQMNSLR PEDTALYYCAAYIRPDTYLSRDYRKYDYWGQGTLVQVSS
394	110K	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYPMGWFHQAPGK GREFVSSITGSGGSTYYADSVKGRFTISRDNAKNTLYLQMNSLR PEDTAVYYCAAYIRPDTYLSRDYRKYDYWGQGTLVKVSS
395	110Q	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYPMGWFHQAPGK GREFVSSITGSGGSTYYADSVKGRFTISRDNAKNTLYLQMNSLR PEDTAVYYCAAYIRPDTYLSRDYRKYDYWGQGTLVQVSS
396	112K	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYPMGWFHQAPGK GREFVSSITGSGGSTYYADSVKGRFTISRDNAKNTLYLQMNSLR PEDTAVYYCAAYIRPDTYLSRDYRKYDYWGQGTLVTVKS
397	112Q	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYPMGWFHQAPGK GREFVSSITGSGGSTYYADSVKGRFTISRDNAKNTLYLQMNSLR PEDTAVYYCAAYIRPDTYLSRDYRKYDYWGQGTLVTVQS
398	89T	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYPMGWFHQAPGK GREFVSSITGSGGSTYYADSVKGRFTISRDNAKNTLYLQMNSLR PEDTATYYCAAYIRPDTYLSRDYRKYDYWGQGTLVTVSS
399	11V + 89L	EVQLVESGGGVVQPGGSLRLSCAASGFTFSSYPMGWFHQAPGK GREFVSSITGSGGSTYYADSVKGRFTISRDNAKNTLYLQMNSLR PEDTALYYCAAYIRPDTYLSRDYRKYDYWGQGTLVTVSS
400	11V + 89L + 110K	EVQLVESGGGVVQPGGSLRLSCAASGFTFSSYPMGWFHQAPGK GREFVSSITGSGGSTYYADSVKGRFTISRDNAKNTLYLQMNSLR PEDTALYYCAAYIRPDTYLSRDYRKYDYWGQGTLVKVSS
401	11V + 89L + 110Q	EVQLVESGGGVVQPGGSLRLSCAASGFTFSSYPMGWFHQAPGK GREFVSSITGSGGSTYYADSVKGRFTISRDNAKNTLYLQMNSLR PEDTALYYCAAYIRPDTYLSRDYRKYDYWGQGTLVQVSS

Figure 19 (continued)

SEQ ID	Mutation(s)	Sequence
402	11V + 110K	EVQLVESGGVVQPGGSLRLSCAASGFTFSSYPMGWFRQAPGK GREFVSSITGSGGSTYYADSVKGRFTISRDNAKNTLYLQMNSLR PEDTAVYYCAAYIRPDTYLSRDYRKYDYWGQGTLVKVSS
403	11V + 110Q	EVQLVESGGVVQPGGSLRLSCAASGFTFSSYPMGWFRQAPGK GREFVSSITGSGGSTYYADSVKGRFTISRDNAKNTLYLQMNSLR PEDTAVYYCAAYIRPDTYLSRDYRKYDYWGQGTLVQVSS
404	11V + 112K	EVQLVESGGVVQPGGSLRLSCAASGFTFSSYPMGWFRQAPGK GREFVSSITGSGGSTYYADSVKGRFTISRDNAKNTLYLQMNSLR PEDTAVYYCAAYIRPDTYLSRDYRKYDYWGQGTLVTVKS
405	11V + 112Q	EVQLVESGGVVQPGGSLRLSCAASGFTFSSYPMGWFRQAPGK GREFVSSITGSGGSTYYADSVKGRFTISRDNAKNTLYLQMNSLR PEDTAVYYCAAYIRPDTYLSRDYRKYDYWGQGTLVTVQS

Figure 20A

SEQ ID	Mutation(s)	Sequence
406	None (reference)	EVQLVESGGGLVQPGGSLRISCAASGSIYLINYM GWYRQAPGKQ RELVATL TSGGSTNYAGSVKGRFAISRDNAKNTVYLQMNSLKP EDTAVYYCNIGGTL YDRRRFESWGQQGTLTVSS
407	CDR1	INYMG
408	CDR2	TLTSGGSTNYAGSVKG
409	CDR3	GGTLYD DRRRFES
410	89L + 110K	EVQLVESGGGLVQPGGSLRISCAASGSIYLINYM GWYRQAPGKQ RELVATL TSGGSTNYAGSVKGRFAISRDNAKNTVYLQMNSLKP EDTALYYCNIGGTL YDRRRFESWGQQGTLVKVSS
411	89L + 110Q	EVQLVESGGGLVQPGGSLRISCAASGSIYLINYM GWYRQAPGKQ RELVATL TSGGSTNYAGSVKGRFAISRDNAKNTVYLQMNSLKP EDTALYYCNIGGTL YDRRRFESWGQQGTLVQVSS
412	110K	EVQLVESGGGLVQPGGSLRISCAASGSIYLINYM GWYRQAPGKQ RELVATL TSGGSTNYAGSVKGRFAISRDNAKNTVYLQMNSLKP EDTAVYYCNIGGTL YDRRRFESWGQQGTLVKVSS
413	110Q	EVQLVESGGGLVQPGGSLRISCAASGSIYLINYM GWYRQAPGKQ RELVATL TSGGSTNYAGSVKGRFAISRDNAKNTVYLQMNSLKP EDTAVYYCNIGGTL YDRRRFESWGQQGTLVQVSS
414	112K	EVQLVESGGGLVQPGGSLRISCAASGSIYLINYM GWYRQAPGKQ RELVATL TSGGSTNYAGSVKGRFAISRDNAKNTVYLQMNSLKP EDTAVYYCNIGGTL YDRRRFESWGQQGTLVTVKS
415	112Q	EVQLVESGGGLVQPGGSLRISCAASGSIYLINYM GWYRQAPGKQ RELVATL TSGGSTNYAGSVKGRFAISRDNAKNTVYLQMNSLKP EDTAVYYCNIGGTL YDRRRFESWGQQGTLTVQS
416	89T	EVQLVESGGGLVQPGGSLRISCAASGSIYLINYM GWYRQAPGKQ RELVATL TSGGSTNYAGSVKGRFAISRDNAKNTVYLQMNSLKP EDTATYYCNIGGTL YDRRRFESWGQQGTLTVSS
417	11V + 89L	EVQLVESGGVVQPGGSLRISCAASGSIYLINYM GWYRQAPGK QRELVATL TSGGSTNYAGSVKGRFAISRDNAKNTVYLQMNSLK PEDTALYYCNIGGTL YDRRRFESWGQQGTLTVSS
418	11V + 89L + 110K	EVQLVESGGVVQPGGSLRISCAASGSIYLINYM GWYRQAPGK QRELVATL TSGGSTNYAGSVKGRFAISRDNAKNTVYLQMNSLK PEDTALYYCNIGGTL YDRRRFESWGQQGTLVKVSS
419	11V + 89L + 110Q	EVQLVESGGVVQPGGSLRISCAASGSIYLINYM GWYRQAPGK QRELVATL TSGGSTNYAGSVKGRFAISRDNAKNTVYLQMNSLK PEDTALYYCNIGGTL YDRRRFESWGQQGTLVQVSS

Figure 20A (continued)

SEQ ID	Mutation(s)	Sequence
420	11V + 110K	EVQLVESGGVVQPGGSLRISCAASGSIYLINYM G WYRQAPGK QRELVATL T SGGSTNYAGSVKGRFAISRDNAKNTVYLQMNSLK PEDTAVYYCNIGGTL Y DRRRFESWGQGTLVKVSS
421	11V + 110Q	EVQLVESGGVVQPGGSLRISCAASGSIYLINYM G WYRQAPGK QRELVATL T SGGSTNYAGSVKGRFAISRDNAKNTVYLQMNSLK PEDTAVYYCNIGGTL Y DRRRFESWGQGTLVQVSS
422	11V + 112K	EVQLVESGGVVQPGGSLRISCAASGSIYLINYM G WYRQAPGK QRELVATL T SGGSTNYAGSVKGRFAISRDNAKNTVYLQMNSLK PEDTAVYYCNIGGTL Y DRRRFESWGQGTLVTVKS
423	11V + 112Q	EVQLVESGGVVQPGGSLRISCAASGSIYLINYM G WYRQAPGK QRELVATL T SGGSTNYAGSVKGRFAISRDNAKNTVYLQMNSLK PEDTAVYYCNIGGTL Y DRRRFESWGQGTLVQVSS

Figure 20B

SEQ ID	Mutation(s)	Sequence
424	None (reference)	EVQLVESGGGLVQTGASLRLSCAASGRTFSNYAMGWFRQAPGK ERERVAAITPRAFTYYADSVKGRFTISRDNAKNTAYLQMVS LK PEDTAVYYCAAQLVGSNSLGRQESYAYWGQGTLVTVSS
425	CDR1	NYAMG
426	CDR2	AITPRAFTYYADSVKG
427	CDR3	QLVGSNSLGRQESYAY
428	89L + 110K	EVQLVESGGGLVQTGASLRLSCAASGRTFSNYAMGWFRQAPGK ERERVAAITPRAFTYYADSVKGRFTISRDNAKNTAYLQMVS LK PEDTALYYCAAQLVGSNSLGRQESYAYWGQGTLVKVSS
429	89L + 110Q	EVQLVESGGGLVQTGASLRLSCAASGRTFSNYAMGWFRQAPGK ERERVAAITPRAFTYYADSVKGRFTISRDNAKNTAYLQMVS LK PEDTALYYCAAQLVGSNSLGRQESYAYWGQGTLVQVSS
430	110K	EVQLVESGGGLVQTGASLRLSCAASGRTFSNYAMGWFRQAPGK ERERVAAITPRAFTYYADSVKGRFTISRDNAKNTAYLQMVS LK PEDTAVYYCAAQLVGSNSLGRQESYAYWGQGTLVKVSS
431	110Q	EVQLVESGGGLVQTGASLRLSCAASGRTFSNYAMGWFRQAPGK ERERVAAITPRAFTYYADSVKGRFTISRDNAKNTAYLQMVS LK PEDTAVYYCAAQLVGSNSLGRQESYAYWGQGTLVQVSS
432	112K	EVQLVESGGGLVQTGASLRLSCAASGRTFSNYAMGWFRQAPGK ERERVAAITPRAFTYYADSVKGRFTISRDNAKNTAYLQMVS LK PEDTAVYYCAAQLVGSNSLGRQESYAYWGQGTLVTVKS
433	112Q	EVQLVESGGGLVQTGASLRLSCAASGRTFSNYAMGWFRQAPGK ERERVAAITPRAFTYYADSVKGRFTISRDNAKNTAYLQMVS LK PEDTAVYYCAAQLVGSNSLGRQESYAYWGQGTLVTVQS
434	89T	EVQLVESGGGLVQTGASLRLSCAASGRTFSNYAMGWFRQAPGK ERERVAAITPRAFTYYADSVKGRFTISRDNAKNTAYLQMVS LK PEDTATYYCAAQLVGSNSLGRQESYAYWGQGTLVTVSS
435	11V + 89L	EVQLVESGGVVQTGASLRLSCAASGRTFSNYAMGWFRQAPG KERERVAAITPRAFTYYADSVKGRFTISRDNAKNTAYLQMVS LK PEDTALYYCAAQLVGSNSLGRQESYAYWGQGTLVTVSS
436	11V + 89L + 110K	EVQLVESGGVVQTGASLRLSCAASGRTFSNYAMGWFRQAPG KERERVAAITPRAFTYYADSVKGRFTISRDNAKNTAYLQMVS LK PEDTALYYCAAQLVGSNSLGRQESYAYWGQGTLVKVSS
437	11V + 89L + 110Q	EVQLVESGGVVQTGASLRLSCAASGRTFSNYAMGWFRQAPG KERERVAAITPRAFTYYADSVKGRFTISRDNAKNTAYLQMVS LK PEDTALYYCAAQLVGSNSLGRQESYAYWGQGTLVQVSS

Figure 20B (continued)

SEQ ID	Mutation(s)	Sequence
438	11V + 110K	EVQLVESGGVVQTGASLRLSCAASGRTFSNYAMGWFRQAPG KERERVAAITPRAFTYYADSVKGRFTISRDNAKNTAYLQMVS KPEDTAVYYCAAQLVGSNSLGRQESYAYWGQGTLVKVSS
439	11V + 110Q	EVQLVESGGVVQTGASLRLSCAASGRTFSNYAMGWFRQAPG KERERVAAITPRAFTYYADSVKGRFTISRDNAKNTAYLQMVS KPEDTAVYYCAAQLVGSNSLGRQESYAYWGQGTLVQVSS
440	11V + 112K	EVQLVESGGVVQTGASLRLSCAASGRTFSNYAMGWFRQAPG KERERVAAITPRAFTYYADSVKGRFTISRDNAKNTAYLQMVS KPEDTAVYYCAAQLVGSNSLGRQESYAYWGQGTLTVKS
441	11V + 112Q	EVQLVESGGVVQTGASLRLSCAASGRTFSNYAMGWFRQAPG KERERVAAITPRAFTYYADSVKGRFTISRDNAKNTAYLQMVS KPEDTAVYYCAAQLVGSNSLGRQESYAYWGQGTLTVQS

Figure 20C

SEQ ID	Mutation(s)	Sequence
442	None (reference)	EVQLVESGGGLVQAGESLTSCAASGRTLSAYIMGWFRQAPGK EREFVAGIWSGGYTHLADSAKGRFSISRDNAKNTVYLQMNGLK PEDTAVYYCAAGLGRQYSNWGQGTLTVSS
443	CDR1	AYIMG
444	CDR2	GIWSGGYTHLADSAKG
445	CDR3	GIWSGGYTHLADSAKG
446	89L + 110K	EVQLVESGGGLVQAGESLTSCAASGRTLSAYIMGWFRQAPGK EREFVAGIWSGGYTHLADSAKGRFSISRDNAKNTVYLQMNGLK PEDTALYYCAAGLGRQYSNWGQGTLVKVSS
447	89L + 110Q	EVQLVESGGGLVQAGESLTSCAASGRTLSAYIMGWFRQAPGK EREFVAGIWSGGYTHLADSAKGRFSISRDNAKNTVYLQMNGLK PEDTALYYCAAGLGRQYSNWGQGTLVQVSS
448	110K	EVQLVESGGGLVQAGESLTSCAASGRTLSAYIMGWFRQAPGK EREFVAGIWSGGYTHLADSAKGRFSISRDNAKNTVYLQMNGLK PEDTAVYYCAAGLGRQYSNWGQGTLVKVSS
449	110Q	EVQLVESGGGLVQAGESLTSCAASGRTLSAYIMGWFRQAPGK EREFVAGIWSGGYTHLADSAKGRFSISRDNAKNTVYLQMNGLK PEDTAVYYCAAGLGRQYSNWGQGTLVQVSS
450	112K	EVQLVESGGGLVQAGESLTSCAASGRTLSAYIMGWFRQAPGK EREFVAGIWSGGYTHLADSAKGRFSISRDNAKNTVYLQMNGLK PEDTAVYYCAAGLGRQYSNWGQGTLTVKS
451	112Q	EVQLVESGGGLVQAGESLTSCAASGRTLSAYIMGWFRQAPGK EREFVAGIWSGGYTHLADSAKGRFSISRDNAKNTVYLQMNGLK PEDTAVYYCAAGLGRQYSNWGQGTLTVKS
452	89T	EVQLVESGGGLVQAGESLTSCAASGRTLSAYIMGWFRQAPGK EREFVAGIWSGGYTHLADSAKGRFSISRDNAKNTVYLQMNGLK PEDTATYYCAAGLGRQYSNWGQGTLTVSS
453	11V + 89L	EVQLVESGGGVVQAGESLTSCAASGRTLSAYIMGWFRQAPGK EREFVAGIWSGGYTHLADSAKGRFSISRDNAKNTVYLQMNGLK PEDTALYYCAAGLGRQYSNWGQGTLTVSS
454	11V + 89L + 110K	EVQLVESGGGVVQAGESLTSCAASGRTLSAYIMGWFRQAPGK EREFVAGIWSGGYTHLADSAKGRFSISRDNAKNTVYLQMNGLK PEDTALYYCAAGLGRQYSNWGQGTLVKVSS
455	11V + 89L + 110Q	EVQLVESGGGVVQAGESLTSCAASGRTLSAYIMGWFRQAPGK EREFVAGIWSGGYTHLADSAKGRFSISRDNAKNTVYLQMNGLK PEDTALYYCAAGLGRQYSNWGQGTLVQVSS

Figure 20C (continued)

SEQ ID	Mutation(s)	Sequence
456	11V + 110K	EVQLVESGGVVQAGESLTSCAASGRTLSAYIMGWFRQAPGK EREFVAGIWSGGYTHLADSAKGRFSISRDNAKNTVYLQMNGLK PEDTAVYYCAAGLGRQYSNWGQQGTLVKVSS
457	11V + 110Q	EVQLVESGGVVQAGESLTSCAASGRTLSAYIMGWFRQAPGK EREFVAGIWSGGYTHLADSAKGRFSISRDNAKNTVYLQMNGLK PEDTAVYYCAAGLGRQYSNWGQQGTLVQVSS
458	11V + 112K	EVQLVESGGVVQAGESLTSCAASGRTLSAYIMGWFRQAPGK EREFVAGIWSGGYTHLADSAKGRFSISRDNAKNTVYLQMNGLK PEDTAVYYCAAGLGRQYSNWGQQGTLTVKS
459	11V + 112Q	EVQLVESGGVVQAGESLTSCAASGRTLSAYIMGWFRQAPGK EREFVAGIWSGGYTHLADSAKGRFSISRDNAKNTVYLQMNGLK PEDTAVYYCAAGLGRQYSNWGQQGTLTVQS

Figure 21A

SEQ ID	Mutation(s)	Sequence
460	lead	EVQLLESGGGLVQPGGSLRLSCVHSGPTFRDTMGWFRQAPGK GREFVAAVTWNSGRINYADSVKGRFTISRDNSKNTAYLQMNSL RPEDTAVYYCAAHRFVVGGRVEDWRYWGQGTLTVSS
461	CDR1	TDTMG
462	CDR2	AVTWNSGRINYADSVKG
463	CDR3	HRFVVGGRVEDWRY
464	89L + 110K	EVQLLESGGGLVQPGGSLRLSCVHSGPTFRDTMGWFRQAPGK GREFVAAVTWNSGRINYADSVKGRFTISRDNSKNTALLQMNSL RPEDTAVYYCAAHRFVVGGRVEDWRYWGQGTLVKVSS
465	89L + 110Q	EVQLLESGGGLVQPGGSLRLSCVHSGPTFRDTMGWFRQAPGK GREFVAAVTWNSGRINYADSVKGRFTISRDNSKNTALLQMNSL RPEDTAVYYCAAHRFVVGGRVEDWRYWGQGTLVQVSS
466	110K	EVQLLESGGGLVQPGGSLRLSCVHSGPTFRDTMGWFRQAPGK GREFVAAVTWNSGRINYADSVKGRFTISRDNSKNTAYLQMNSL RPEDTAVYYCAAHRFVVGGRVEDWRYWGQGTLVKVSS
467	110Q	EVQLLESGGGLVQPGGSLRLSCVHSGPTFRDTMGWFRQAPGK GREFVAAVTWNSGRINYADSVKGRFTISRDNSKNTAYLQMNSL RPEDTAVYYCAAHRFVVGGRVEDWRYWGQGTLVQVSS
468	112K	EVQLLESGGGLVQPGGSLRLSCVHSGPTFRDTMGWFRQAPGK GREFVAAVTWNSGRINYADSVKGRFTISRDNSKNTAYLQMNSL RPEDTAVYYCAAHRFVVGGRVEDWRYWGQGTLVTVKS
469	112Q	EVQLLESGGGLVQPGGSLRLSCVHSGPTFRDTMGWFRQAPGK GREFVAAVTWNSGRINYADSVKGRFTISRDNSKNTAYLQMNSL RPEDTAVYYCAAHRFVVGGRVEDWRYWGQGTLVTVQS
470	89T	EVQLLESGGGLVQPGGSLRLSCVHSGPTFRDTMGWFRQAPGK GREFVAAVTWNSGRINYADSVKGRFTISRDNSKNTATLQMNSL RPEDTAVYYCAAHRFVVGGRVEDWRYWGQGTLTVSS
471	11V + 89L	EVQLLESGGGVVQPGGSLRLSCVHSGPTFRDTMGWFRQAPGK GREFVAAVTWNSGRINYADSVKGRFTISRDNSKNTALLQMNSL RPEDTAVYYCAAHRFVVGGRVEDWRYWGQGTLTVSS
472	11V + 89L + 110K	EVQLLESGGGVVQPGGSLRLSCVHSGPTFRDTMGWFRQAPGK GREFVAAVTWNSGRINYADSVKGRFTISRDNSKNTALLQMNSL RPEDTAVYYCAAHRFVVGGRVEDWRYWGQGTLVKVSS
473	11V + 89L + 110Q	EVQLLESGGGVVQPGGSLRLSCVHSGPTFRDTMGWFRQAPGK GREFVAAVTWNSGRINYADSVKGRFTISRDNSKNTALLQMNSL RPEDTAVYYCAAHRFVVGGRVEDWRYWGQGTLVQVSS

Figure 21A (continued)

SEQ ID	Mutation(s)	Sequence
474	11V + 110K	EVQLLESGGGVVQPGGSLRLSCVHSGPTFRTDTMGWFRQAPGK GREFVAAVTWNSGRINYADSVKGRFTISRDNSKNTAYLQMNSL RPEDTAVYYCAAHRFVVGGNRVEDWRYWGQGTLVKVSS
475	11V + 110Q	EVQLLESGGGVVQPGGSLRLSCVHSGPTFRTDTMGWFRQAPGK GREFVAAVTWNSGRINYADSVKGRFTISRDNSKNTAYLQMNSL RPEDTAVYYCAAHRFVVGGNRVEDWRYWGQGTLVQVSS
476	11V + 112K	EVQLLESGGGVVQPGGSLRLSCVHSGPTFRTDTMGWFRQAPGK GREFVAAVTWNSGRINYADSVKGRFTISRDNSKNTAYLQMNSL RPEDTAVYYCAAHRFVVGGNRVEDWRYWGQGTLVTVK
477	11V + 112Q	EVQLLESGGGVVQPGGSLRLSCVHSGPTFRTDTMGWFRQAPGK GREFVAAVTWNSGRINYADSVKGRFTISRDNSKNTAYLQMNSL RPEDTAVYYCAAHRFVVGGNRVEDWRYWGQGTLVTVQS

Figure 21B

SEQ ID	Mutation(s)	Sequence
478	lead	EVQLLESGGGLVQPGGSLRLSCAASGRTFNNYNMGWFRQAPGK GREFVAAVSRSGVSTYYADSVKGRFTISRDNSKNTVYLQMNSL RPEDTAVYYCAAAYRGTAINVRRSYSSWGQGTLTVSS
479	CDR1	NYNMG
480	CDR2	AVSRSGVSTYYADSVKG
481	CDR3	AYRGTAINVRRSYSS
482	89L + 110K	EVQLLESGGGLVQPGGSLRLSCAASGRTFNNYNMGWFRQAPGK GREFVAAVSRSGVSTYYADSVKGRFTISRDNSKNTVYLQMNSL RPEDTALYYCAAAYRGTAINVRRSYSSWGQGTLVKVSS
483	89L + 110Q	EVQLLESGGGLVQPGGSLRLSCAASGRTFNNYNMGWFRQAPGK GREFVAAVSRSGVSTYYADSVKGRFTISRDNSKNTVYLQMNSL RPEDTALYYCAAAYRGTAINVRRSYSSWGQGTLVQVSS
484	110K	EVQLLESGGGLVQPGGSLRLSCAASGRTFNNYNMGWFRQAPGK GREFVAAVSRSGVSTYYADSVKGRFTISRDNSKNTVYLQMNSL RPEDTAVYYCAAAYRGTAINVRRSYSSWGQGTLVKVSS
485	110Q	EVQLLESGGGLVQPGGSLRLSCAASGRTFNNYNMGWFRQAPGK GREFVAAVSRSGVSTYYADSVKGRFTISRDNSKNTVYLQMNSL RPEDTAVYYCAAAYRGTAINVRRSYSSWGQGTLVQVSS
486	112K	EVQLLESGGGLVQPGGSLRLSCAASGRTFNNYNMGWFRQAPGK GREFVAAVSRSGVSTYYADSVKGRFTISRDNSKNTVYLQMNSL RPEDTAVYYCAAAYRGTAINVRRSYSSWGQGTLVTVKS
487	112Q	EVQLLESGGGLVQPGGSLRLSCAASGRTFNNYNMGWFRQAPGK GREFVAAVSRSGVSTYYADSVKGRFTISRDNSKNTVYLQMNSL RPEDTAVYYCAAAYRGTAINVRRSYSSWGQGTLVTVQS
488	89T	EVQLLESGGGLVQPGGSLRLSCAASGRTFNNYNMGWFRQAPGK GREFVAAVSRSGVSTYYADSVKGRFTISRDNSKNTVYLQMNSL RPEDTATYYCAAAYRGTAINVRRSYSSWGQGTLTVSS
489	11V + 89L	EVQLLESGGGVVQPGGSLRLSCAASGRTFNNYNMGWFRQAPG KGREFVAAVSRSGVSTYYADSVKGRFTISRDNSKNTVYLQMNS LRPEDTALYYCAAAYRGTAINVRRSYSSWGQGTLVTVSS
490	11V + 89L + 110K	EVQLLESGGGVVQPGGSLRLSCAASGRTFNNYNMGWFRQAPG KGREFVAAVSRSGVSTYYADSVKGRFTISRDNSKNTVYLQMNS LRPEDTALYYCAAAYRGTAINVRRSYSSWGQGTLVKVSS
491	11V + 89L + 110Q	EVQLLESGGGVVQPGGSLRLSCAASGRTFNNYNMGWFRQAPG KGREFVAAVSRSGVSTYYADSVKGRFTISRDNSKNTVYLQMNS LRPEDTALYYCAAAYRGTAINVRRSYSSWGQGTLVTVSS

Figure 21B (continued)

SEQ ID	Mutation(s)	Sequence
492	11V + 110K	EVQLLESGGGVVQPGGSLRLSCAASGRTFNNYNMGWFRQAPG KGREFVAAVSRSGVSTYYADSVKGRFTISRDNSKNTVYLQMNS LRPEDTAVYYCAAAYRGTAINVRRSYSSWGQGTLVKVSS
493	11V + 110Q	EVQLLESGGGVVQPGGSLRLSCAASGRTFNNYNMGWFRQAPG KGREFVAAVSRSGVSTYYADSVKGRFTISRDNSKNTVYLQMNS LRPEDTAVYYCAAAYRGTAINVRRSYSSWGQGTLVQVSS
494	11V + 112K	EVQLLESGGGVVQPGGSLRLSCAASGRTFNNYNMGWFRQAPG KGREFVAAVSRSGVSTYYADSVKGRFTISRDNSKNTVYLQMNS LRPEDTAVYYCAAAYRGTAINVRRSYSSWGQGTLVTVKs
495	11V + 112Q	EVQLLESGGGVVQPGGSLRLSCAASGRTFNNYNMGWFRQAPG KGREFVAAVSRSGVSTYYADSVKGRFTISRDNSKNTVYLQMNS LRPEDTAVYYCAAAYRGTAINVRRSYSSWGQGTLTVQS

Figure 22

SEQ ID	Sequence
514	EVQLLESGGGVVQPGGLRLSCAASGRIFSLPASGNIFNLLTIAWYRQAPGKGREL VATINSGSRTYYADSVKGRFTISRDNSKKTVYLQMNSLRPEDTALYYCQTSGSGSP NFWGQGTLTVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSSFG MSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRP EDTAVYYCTIGGSLRSSQGTLTVSSGGGGSGGGSEVQLLESGGGVVQPGGSLRL SCAASGRTLSSYAMGWFRQAPGKGREFVARISQGGTAIYYADSVKGRFTISRDNSK NTLYLQMNSLRPEDTALYYCAKDPSYYRGSAYLLGSYDSWGQGTLTVSSA
515	EVQLLESGGGVVQPGGLRLSCAASGRIFSLPASGNIFNLLTIAWYRQAPGKGREL VATINSGSRTYYADSVKGRFTISRDNSKKTVYLQMNSLRPEDTALYYCQTSGSGSP NFWGQGTLTVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSSFG MSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRP EDTAVYYCTIGGSLRSSQGTLTVSSGGGGSGGGSEVQLLESGGGVVQPGGSLRL SCAASGRTLSSYAMGWFRQAPGKGREFVARISQGGTAIYYADSVKGRFTISRDNSK NTLYLQMNSLRPEDTALYYCAKDPSYYRGSAYLLGSYDSWGQGTLVKVSSA
516	EVQLLESGGGVVQPGGLRLSCAASGRIFSLPASGNIFNLLTIAWYRQAPGKGREL VATINSGSRTYYADSVKGRFTISRDNSKKTVYLQMNSLRPEDTALYYCQTSGSGSP NFWGQGTLTVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSSFG MSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRP EDTAVYYCTIGGSLRSSQGTLTVSSGGGGSGGGSEVQLLESGGGVVQPGGSLRL SCAASGRTLSSYAMGWFRQAPGKGREFVARISQGGTAIYYADSVKGRFTISRDNSK NTLYLQMNSLRPEDTALYYCAKDPSYYRGSAYLLGSYDSWGQGTLVQVSSA
517	EVQLLESGGGVVQPGGLRLSCAASGRIFSLPASGNIFNLLTIAWYRQAPGKGREL VATINSGSRTYYADSVKGRFTISRDNSKKTVYLQMNSLRPEDTALYYCQTSGSGSP NFWGQGTLTVSSGGGGSGGGSEVQLVESGGGVVQPGNSLRLSCAASGFTFSSFG MSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRP EDTALYYCTIGGSLRSSQGTLTVSSGGGGSGGGSEVQLLESGGGVVQPGGSLRL SCAASGRTLSSYAMGWFRQAPGKGREFVARISQGGTAIYYADSVKGRFTISRDNSK NTLYLQMNSLRPEDTALYYCAKDPSYYRGSAYLLGSYDSWGQGTLTVSSA
518	EVQLLESGGGVVQPGGLRLSCAASGRIFSLPASGNIFNLLTIAWYRQAPGKGREL VATINSGSRTYYADSVKGRFTISRDNSKKTVYLQMNSLRPEDTALYYCQTSGSGSP NFWGQGTLTVSSGGGGSGGGSEVQLVESGGGVVQPGNSLRLSCAASGFTFSSFG MSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRP EDTALYYCTIGGSLRSSQGTLTVSSGGGGSGGGSEVQLLESGGGVVQPGGSLRL SCAASGRTLSSYAMGWFRQAPGKGREFVARISQGGTAIYYADSVKGRFTISRDNSK NTLYLQMNSLRPEDTALYYCAKDPSYYRGSAYLLGSYDSWGQGTLVKVSSA
519	EVQLLESGGGVVQPGGLRLSCAASGRIFSLPASGNIFNLLTIAWYRQAPGKGREL VATINSGSRTYYADSVKGRFTISRDNSKKTVYLQMNSLRPEDTALYYCQTSGSGSP NFWGQGTLTVSSGGGGSGGGSEVQLVESGGGVVQPGNSLRLSCAASGFTFSSFG MSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRP EDTALYYCTIGGSLRSSQGTLTVSSGGGGSGGGSEVQLLESGGGVVQPGGSLRL SCAASGRTLSSYAMGWFRQAPGKGREFVARISQGGTAIYYADSVKGRFTISRDNSK NTLYLQMNSLRPEDTALYYCAKDPSYYRGSAYLLGSYDSWGQGTLVQVSSA

Figure 22 (continued)

SEQ ID	Sequence
520	EVQLLESGGVVQPGGLRLSCAASGRIFSLPASGNIFNLLTIAWYRQAPGKGREL VATINSGSRTYYADSVKGRFTISRDNSKKTVYLQMNSLRPEDTALYYCQTSGSGSP NFWGQGTLTVSSGGGGSGGGSEVQLVESGGGVQPGNSLRLSCAASGFTFSSFG MSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRP EDTALYYCTIGGSLRSSQGTLVKVSSGGGGSGGGSEVQLLESGGGVVQPGGSLRL SCAASGRTLSSYAMGWFRQAPGKGREFVARISQGGTAIYYADSVKGRFTISRDNSK NTLYLQMNSLRPEDTALYYCAKDPSYYRGSAYLLSGSYDSWGQGTLTVSSA
521	EVQLLESGGVVQPGGLRLSCAASGRIFSLPASGNIFNLLTIAWYRQAPGKGREL VATINSGSRTYYADSVKGRFTISRDNSKKTVYLQMNSLRPEDTALYYCQTSGSGSP NFWGQGTLTVSSGGGGSGGGSEVQLVESGGGVQPGNSLRLSCAASGFTFSSFG MSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRP EDTALYYCTIGGSLRSSQGTLVKVSSGGGGSGGGSEVQLLESGGGVVQPGGSLRL SCAASGRTLSSYAMGWFRQAPGKGREFVARISQGGTAIYYADSVKGRFTISRDNSK NTLYLQMNSLRPEDTALYYCAKDPSYYRGSAYLLSGSYDSWGQGTLVKVSSA
522	EVQLLESGGVVQPGGLRLSCAASGRIFSLPASGNIFNLLTIAWYRQAPGKGREL VATINSGSRTYYADSVKGRFTISRDNSKKTVYLQMNSLRPEDTALYYCQTSGSGSP NFWGQGTLTVSSGGGGSGGGSEVQLVESGGGVQPGNSLRLSCAASGFTFSSFG MSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRP EDTALYYCTIGGSLRSSQGTLVKVSSGGGGSGGGSEVQLLESGGGVVQPGGSLRL SCAASGRTLSSYAMGWFRQAPGKGREFVARISQGGTAIYYADSVKGRFTISRDNSK NTLYLQMNSLRPEDTALYYCAKDPSYYRGSAYLLSGSYDSWGQGTLVQVSSA
523	EVQLLESGGVVQPGGLRLSCAASGRIFSLPASGNIFNLLTIAWYRQAPGKGREL VATINSGSRTYYADSVKGRFTISRDNSKKTVYLQMNSLRPEDTALYYCQTSGSGSP NFWGQGTLTVSSGGGGSGGGSEVQLVESGGGVQPGNSLRLSCAASGFTFSSFG MSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRP EDTALYYCTIGGSLRSSQGTLVKVSSGGGGSGGGSEVQLLESGGGVVQPGGSLRL SCAASGRTLSSYAMGWFRQAPGKGREFVARISQGGTAIYYADSVKGRFTISRDNSK NTLYLQMNSLRPEDTALYYCAKDPSYYRGSAYLLSGSYDSWGQGTLVQVSSA
524	EVQLLESGGVVQPGGLRLSCAASGRIFSLPASGNIFNLLTIAWYRQAPGKGREL VATINSGSRTYYADSVKGRFTISRDNSKKTVYLQMNSLRPEDTALYYCQTSGSGSP NFWGQGTLTVSSGGGGSGGGSEVQLVESGGGVQPGNSLRLSCAASGFTFSSFG MSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRP EDTALYYCTIGGSLRSSQGTLVKVSSGGGGSGGGSEVQLLESGGGVVQPGGSLRL SCAASGRTLSSYAMGWFRQAPGKGREFVARISQGGTAIYYADSVKGRFTISRDNSK NTLYLQMNSLRPEDTALYYCAKDPSYYRGSAYLLSGSYDSWGQGTLVKVSSA
525	EVQLLESGGVVQPGGLRLSCAASGRIFSLPASGNIFNLLTIAWYRQAPGKGREL VATINSGSRTYYADSVKGRFTISRDNSKKTVYLQMNSLRPEDTALYYCQTSGSGSP NFWGQGTLTVSSGGGGSGGGSEVQLVESGGGVQPGNSLRLSCAASGFTFSSFG MSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRP EDTALYYCTIGGSLRSSQGTLVKVSSGGGGSGGGSEVQLLESGGGVVQPGGSLRL SCAASGRTLSSYAMGWFRQAPGKGREFVARISQGGTAIYYADSVKGRFTISRDNSK NTLYLQMNSLRPEDTALYYCAKDPSYYRGSAYLLSGSYDSWGQGTLVQVSSA

Figure 22 (continued)

SEQ ID	Sequence
526	EVQLLESGGGVVQPGGLRLSCAASGRIFSLPASGNIFNLLTIAWYRQAPGKGREL VATINSGSRTYYADSVKGRFTISRDNSKKTVYLQMNSLRPEDTALYYCQTSGSGSP NFWGQGTLVVKVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSSFG MSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRP EDTAVYYCTIGGSLSRSSQGTLSVSSGGGGSGGGSEVQLLESGGGVVQPGGLRL SCAASGRTLSSYAMGWFRQAPGKGREFVARISQGGTAIYYADSVKGRFTISRDNSK NTLYLQMNSLRPEDTALYYCAKDPSYYRGSAYLLSGSYDSWGQGTLTVSSA
527	EVQLLESGGGVVQPGGLRLSCAASGRIFSLPASGNIFNLLTIAWYRQAPGKGREL VATINSGSRTYYADSVKGRFTISRDNSKKTVYLQMNSLRPEDTALYYCQTSGSGSP NFWGQGTLVVKVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSSFG MSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRP EDTAVYYCTIGGSLSRSSQGTLSVSSGGGGSGGGSEVQLLESGGGVVQPGGLRL SCAASGRTLSSYAMGWFRQAPGKGREFVARISQGGTAIYYADSVKGRFTISRDNSK NTLYLQMNSLRPEDTALYYCAKDPSYYRGSAYLLSGSYDSWGQGTLVKVSSA
528	EVQLLESGGGVVQPGGLRLSCAASGRIFSLPASGNIFNLLTIAWYRQAPGKGREL VATINSGSRTYYADSVKGRFTISRDNSKKTVYLQMNSLRPEDTALYYCQTSGSGSP NFWGQGTLVVKVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSSFG MSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRP EDTAVYYCTIGGSLSRSSQGTLSVSSGGGGSGGGSEVQLLESGGGVVQPGGLRL SCAASGRTLSSYAMGWFRQAPGKGREFVARISQGGTAIYYADSVKGRFTISRDNSK NTLYLQMNSLRPEDTALYYCAKDPSYYRGSAYLLSGSYDSWGQGTLVQVSSA
529	EVQLLESGGGVVQPGGLRLSCAASGRIFSLPASGNIFNLLTIAWYRQAPGKGREL VATINSGSRTYYADSVKGRFTISRDNSKKTVYLQMNSLRPEDTALYYCQTSGSGSP NFWGQGTLVVKVSSGGGGSGGGSEVQLVESGGGVVQPGNSLRLSCAASGFTFSSFG MSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRP EDTAVYYCTIGGSLSRSSQGTLSVSSGGGGSGGGSEVQLLESGGGVVQPGGLRL SCAASGRTLSSYAMGWFRQAPGKGREFVARISQGGTAIYYADSVKGRFTISRDNSK NTLYLQMNSLRPEDTALYYCAKDPSYYRGSAYLLSGSYDSWGQGTLTVSSA
530	EVQLLESGGGVVQPGGLRLSCAASGRIFSLPASGNIFNLLTIAWYRQAPGKGREL VATINSGSRTYYADSVKGRFTISRDNSKKTVYLQMNSLRPEDTALYYCQTSGSGSP NFWGQGTLVVKVSSGGGGSGGGSEVQLVESGGGVVQPGNSLRLSCAASGFTFSSFG MSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRP EDTAVYYCTIGGSLSRSSQGTLSVSSGGGGSGGGSEVQLLESGGGVVQPGGLRL SCAASGRTLSSYAMGWFRQAPGKGREFVARISQGGTAIYYADSVKGRFTISRDNSK NTLYLQMNSLRPEDTALYYCAKDPSYYRGSAYLLSGSYDSWGQGTLVKVSSA
531	EVQLLESGGGVVQPGGLRLSCAASGRIFSLPASGNIFNLLTIAWYRQAPGKGREL VATINSGSRTYYADSVKGRFTISRDNSKKTVYLQMNSLRPEDTALYYCQTSGSGSP NFWGQGTLVVKVSSGGGGSGGGSEVQLVESGGGVVQPGNSLRLSCAASGFTFSSFG MSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRP EDTAVYYCTIGGSLSRSSQGTLSVSSGGGGSGGGSEVQLLESGGGVVQPGGLRL SCAASGRTLSSYAMGWFRQAPGKGREFVARISQGGTAIYYADSVKGRFTISRDNSK NTLYLQMNSLRPEDTALYYCAKDPSYYRGSAYLLSGSYDSWGQGTLVQVSSA

Figure 22 (continued)

SEQ ID	Sequence
532	EVQLLESGGGVVQPGGLRLSCAASGRIFSLPASGNIFNLLTIAWYRQAPGKGREL VATINSGSRTRYADSVKGRFTISRDNSKKTVYLQMNSLRPEDTALYYCQTSGSGSP NFWGQGTLVKVSSGGGSGGGSEVQLVESGGGVQPGNSRLSCAASGFTSSFG MSWVRQAPGKGLEWVSSISGSQDTLYADSVKGRFTISRDNAKTTLYLQMNSLRP EDTALYYCTIGGSLRSSQGTLVKVSSGGGSGGGSEVQLLESGGGVQPGGLRL SCAASGRTLSSYAMGWFRQAPGKGREFVARISQGGTAIYYADSVKGRFTISRDNSK NTLYLQMNSLRPEDTALYYCAKDPSYYRGSAYLLSGSYDSWGQGTLVTVSSA
533	EVQLLESGGGVVQPGGLRLSCAASGRIFSLPASGNIFNLLTIAWYRQAPGKGREL VATINSGSRTRYADSVKGRFTISRDNSKKTVYLQMNSLRPEDTALYYCQTSGSGSP NFWGQGTLVKVSSGGGSGGGSEVQLVESGGGVQPGNSRLSCAASGFTSSFG MSWVRQAPGKGLEWVSSISGSQDTLYADSVKGRFTISRDNAKTTLYLQMNSLRP EDTALYYCTIGGSLRSSQGTLVKVSSGGGSGGGSEVQLLESGGGVQPGGLRL SCAASGRTLSSYAMGWFRQAPGKGREFVARISQGGTAIYYADSVKGRFTISRDNSK NTLYLQMNSLRPEDTALYYCAKDPSYYRGSAYLLSGSYDSWGQGTLVTVSSA
534	EVQLLESGGGVVQPGGLRLSCAASGRIFSLPASGNIFNLLTIAWYRQAPGKGREL VATINSGSRTRYADSVKGRFTISRDNSKKTVYLQMNSLRPEDTALYYCQTSGSGSP NFWGQGTLVKVSSGGGSGGGSEVQLVESGGGVQPGNSRLSCAASGFTSSFG MSWVRQAPGKGLEWVSSISGSQDTLYADSVKGRFTISRDNAKTTLYLQMNSLRP EDTALYYCTIGGSLRSSQGTLVKVSSGGGSGGGSEVQLLESGGGVQPGGLRL SCAASGRTLSSYAMGWFRQAPGKGREFVARISQGGTAIYYADSVKGRFTISRDNSK NTLYLQMNSLRPEDTALYYCAKDPSYYRGSAYLLSGSYDSWGQGTLVQVSSA
535	EVQLLESGGGVVQPGGLRLSCAASGRIFSLPASGNIFNLLTIAWYRQAPGKGREL VATINSGSRTRYADSVKGRFTISRDNSKKTVYLQMNSLRPEDTALYYCQTSGSGSP NFWGQGTLVKVSSGGGSGGGSEVQLVESGGGVQPGNSRLSCAASGFTSSFG MSWVRQAPGKGLEWVSSISGSQDTLYADSVKGRFTISRDNAKTTLYLQMNSLRP EDTALYYCTIGGSLRSSQGTLVKVSSGGGSGGGSEVQLLESGGGVQPGGLRL SCAASGRTLSSYAMGWFRQAPGKGREFVARISQGGTAIYYADSVKGRFTISRDNSK NTLYLQMNSLRPEDTALYYCAKDPSYYRGSAYLLSGSYDSWGQGTLVTVSSA
536	EVQLLESGGGVVQPGGLRLSCAASGRIFSLPASGNIFNLLTIAWYRQAPGKGREL VATINSGSRTRYADSVKGRFTISRDNSKKTVYLQMNSLRPEDTALYYCQTSGSGSP NFWGQGTLVKVSSGGGSGGGSEVQLVESGGGVQPGNSRLSCAASGFTSSFG MSWVRQAPGKGLEWVSSISGSQDTLYADSVKGRFTISRDNAKTTLYLQMNSLRP EDTALYYCTIGGSLRSSQGTLVKVSSGGGSGGGSEVQLLESGGGVQPGGLRL SCAASGRTLSSYAMGWFRQAPGKGREFVARISQGGTAIYYADSVKGRFTISRDNSK NTLYLQMNSLRPEDTALYYCAKDPSYYRGSAYLLSGSYDSWGQGTLVTVSSA
537	EVQLLESGGGVVQPGGLRLSCAASGRIFSLPASGNIFNLLTIAWYRQAPGKGREL VATINSGSRTRYADSVKGRFTISRDNSKKTVYLQMNSLRPEDTALYYCQTSGSGSP NFWGQGTLVKVSSGGGSGGGSEVQLVESGGGVQPGNSRLSCAASGFTSSFG MSWVRQAPGKGLEWVSSISGSQDTLYADSVKGRFTISRDNAKTTLYLQMNSLRP EDTALYYCTIGGSLRSSQGTLVKVSSGGGSGGGSEVQLLESGGGVQPGGLRL SCAASGRTLSSYAMGWFRQAPGKGREFVARISQGGTAIYYADSVKGRFTISRDNSK NTLYLQMNSLRPEDTALYYCAKDPSYYRGSAYLLSGSYDSWGQGTLVQVSSA

Figure 22 (continued)

SEQ ID	Sequence
538	EVQLLESGGGVVQPGGLRLSCAASGRIFSLPASGNIFNLLTIAWYRQAPGKGREL VATINSGSRTYYADSVKGRFTISRDNSKKTVYLQMNSLRPEDTALYYCQTSGSGSP NFWGQGTLVQVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSSFG MSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRP EDTAVYYCTIGGSLSRSSQGTLSVSSGGGGSGGGSEVQLLESGGGVVQPGGLRL SCAASGRTLSSYAMGWFRQAPGKGREFVARISQGGTAIYYADSVKGRFTISRDNSK NTLYLQMNSLRPEDTALYYCAKDPSYYRGSAVLLSGSYDSWGQGTLVTVSSA
539	EVQLLESGGGVVQPGGLRLSCAASGRIFSLPASGNIFNLLTIAWYRQAPGKGREL VATINSGSRTYYADSVKGRFTISRDNSKKTVYLQMNSLRPEDTALYYCQTSGSGSP NFWGQGTLVQVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSSFG MSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRP EDTAVYYCTIGGSLSRSSQGTLSVSSGGGGSGGGSEVQLLESGGGVVQPGGLRL SCAASGRTLSSYAMGWFRQAPGKGREFVARISQGGTAIYYADSVKGRFTISRDNSK NTLYLQMNSLRPEDTALYYCAKDPSYYRGSAVLLSGSYDSWGQGTLVTVSSA
540	EVQLLESGGGVVQPGGLRLSCAASGRIFSLPASGNIFNLLTIAWYRQAPGKGREL VATINSGSRTYYADSVKGRFTISRDNSKKTVYLQMNSLRPEDTALYYCQTSGSGSP NFWGQGTLVQVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSSFG MSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRP EDTAVYYCTIGGSLSRSSQGTLSVSSGGGGSGGGSEVQLLESGGGVVQPGGLRL SCAASGRTLSSYAMGWFRQAPGKGREFVARISQGGTAIYYADSVKGRFTISRDNSK NTLYLQMNSLRPEDTALYYCAKDPSYYRGSAVLLSGSYDSWGQGTLVTVSSA
541	EVQLLESGGGVVQPGGLRLSCAASGRIFSLPASGNIFNLLTIAWYRQAPGKGREL VATINSGSRTYYADSVKGRFTISRDNSKKTVYLQMNSLRPEDTALYYCQTSGSGSP NFWGQGTLVQVSSGGGGSGGGSEVQLVESGGGVVQPGNSLRLSCAASGFTFSSFG MSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRP EDTAVYYCTIGGSLSRSSQGTLSVSSGGGGSGGGSEVQLLESGGGVVQPGGLRL SCAASGRTLSSYAMGWFRQAPGKGREFVARISQGGTAIYYADSVKGRFTISRDNSK NTLYLQMNSLRPEDTALYYCAKDPSYYRGSAVLLSGSYDSWGQGTLVTVSSA
542	EVQLLESGGGVVQPGGLRLSCAASGRIFSLPASGNIFNLLTIAWYRQAPGKGREL VATINSGSRTYYADSVKGRFTISRDNSKKTVYLQMNSLRPEDTALYYCQTSGSGSP NFWGQGTLVQVSSGGGGSGGGSEVQLVESGGGVVQPGNSLRLSCAASGFTFSSFG MSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRP EDTAVYYCTIGGSLSRSSQGTLSVSSGGGGSGGGSEVQLLESGGGVVQPGGLRL SCAASGRTLSSYAMGWFRQAPGKGREFVARISQGGTAIYYADSVKGRFTISRDNSK NTLYLQMNSLRPEDTALYYCAKDPSYYRGSAVLLSGSYDSWGQGTLVTVSSA
543	EVQLLESGGGVVQPGGLRLSCAASGRIFSLPASGNIFNLLTIAWYRQAPGKGREL VATINSGSRTYYADSVKGRFTISRDNSKKTVYLQMNSLRPEDTALYYCQTSGSGSP NFWGQGTLVQVSSGGGGSGGGSEVQLVESGGGVVQPGNSLRLSCAASGFTFSSFG MSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRP EDTAVYYCTIGGSLSRSSQGTLSVSSGGGGSGGGSEVQLLESGGGVVQPGGLRL SCAASGRTLSSYAMGWFRQAPGKGREFVARISQGGTAIYYADSVKGRFTISRDNSK NTLYLQMNSLRPEDTALYYCAKDPSYYRGSAVLLSGSYDSWGQGTLVTVSSA

Figure 22 (continued)

SEQ ID	Sequence
544	EVQLLESGGGVVQPGGLRLSCAASGRIFSLPASGNIFNLLTIAWYRQAPGKGREL VATINSGSRTYYADSVKGRFTISRDNSKKTVYLQMNSLRPEDTALYYCQTSGSGSP NFWGQGTLVQVSSGGGSGGGSEVQLVESGGGVQPGNSLRLSCAASGFTFSSFG MSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRP EDTALYYCTIGGSLRSSQGTLVKVSSGGGSGGGSEVQLLESGGGVQPGGSLRL SCAASGRTLSSYAMGWFRQAPGKGREFVARISQGGTAIYYADSVKGRFTISRDNSK NTLYLQMNSLRPEDTALYYCAKDPSYYRGSAYLLSGSYDSWGQGTLVTVSSA
545	EVQLLESGGGVVQPGGLRLSCAASGRIFSLPASGNIFNLLTIAWYRQAPGKGREL VATINSGSRTYYADSVKGRFTISRDNSKKTVYLQMNSLRPEDTALYYCQTSGSGSP NFWGQGTLVQVSSGGGSGGGSEVQLVESGGGVQPGNSLRLSCAASGFTFSSFG MSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRP EDTALYYCTIGGSLRSSQGTLVKVSSGGGSGGGSEVQLLESGGGVQPGGSLRL SCAASGRTLSSYAMGWFRQAPGKGREFVARISQGGTAIYYADSVKGRFTISRDNSK NTLYLQMNSLRPEDTALYYCAKDPSYYRGSAYLLSGSYDSWGQGTLVKVSSA
546	EVQLLESGGGVVQPGGLRLSCAASGRIFSLPASGNIFNLLTIAWYRQAPGKGREL VATINSGSRTYYADSVKGRFTISRDNSKKTVYLQMNSLRPEDTALYYCQTSGSGSP NFWGQGTLVQVSSGGGSGGGSEVQLVESGGGVQPGNSLRLSCAASGFTFSSFG MSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRP EDTALYYCTIGGSLRSSQGTLVKVSSGGGSGGGSEVQLLESGGGVQPGGSLRL SCAASGRTLSSYAMGWFRQAPGKGREFVARISQGGTAIYYADSVKGRFTISRDNSK NTLYLQMNSLRPEDTALYYCAKDPSYYRGSAYLLSGSYDSWGQGTLVQVSSA
547	EVQLLESGGGVVQPGGLRLSCAASGRIFSLPASGNIFNLLTIAWYRQAPGKGREL VATINSGSRTYYADSVKGRFTISRDNSKKTVYLQMNSLRPEDTALYYCQTSGSGSP NFWGQGTLVQVSSGGGSGGGSEVQLVESGGGVQPGNSLRLSCAASGFTFSSFG MSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRP EDTALYYCTIGGSLRSSQGTLVKVSSGGGSGGGSEVQLLESGGGVQPGGSLRL SCAASGRTLSSYAMGWFRQAPGKGREFVARISQGGTAIYYADSVKGRFTISRDNSK NTLYLQMNSLRPEDTALYYCAKDPSYYRGSAYLLSGSYDSWGQGTLVTVSSA
548	EVQLLESGGGVVQPGGLRLSCAASGRIFSLPASGNIFNLLTIAWYRQAPGKGREL VATINSGSRTYYADSVKGRFTISRDNSKKTVYLQMNSLRPEDTALYYCQTSGSGSP NFWGQGTLVQVSSGGGSGGGSEVQLVESGGGVQPGNSLRLSCAASGFTFSSFG MSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRP EDTALYYCTIGGSLRSSQGTLVKVSSGGGSGGGSEVQLLESGGGVQPGGSLRL SCAASGRTLSSYAMGWFRQAPGKGREFVARISQGGTAIYYADSVKGRFTISRDNSK NTLYLQMNSLRPEDTALYYCAKDPSYYRGSAYLLSGSYDSWGQGTLVKVSSA
549	EVQLLESGGGVVQPGGLRLSCAASGRIFSLPASGNIFNLLTIAWYRQAPGKGREL VATINSGSRTYYADSVKGRFTISRDNSKKTVYLQMNSLRPEDTALYYCQTSGSGSP NFWGQGTLVQVSSGGGSGGGSEVQLVESGGGVQPGNSLRLSCAASGFTFSSFG MSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRP EDTALYYCTIGGSLRSSQGTLVKVSSGGGSGGGSEVQLLESGGGVQPGGSLRL SCAASGRTLSSYAMGWFRQAPGKGREFVARISQGGTAIYYADSVKGRFTISRDNSK NTLYLQMNSLRPEDTALYYCAKDPSYYRGSAYLLSGSYDSWGQGTLVQVSSA

Figure 23

SEQ ID	Sequence
550	EVQLVESGGGVVQPGGSLRLSCAASRSIGRLDRMGWYRHRPGEPRELVATITGGSSI NYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTALYYCNFNKYVTSRDTWGQGTLV TVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMSWVRQAPGK GLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGS LSRSSQGTLTVTSSGGGGSGGGSEVQLVESGGGVVQPGGSLRLSCAASRSIGRLDRM GWYRHRPGEPRELVATITGGSSINYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTAL YYCNFNKYVTSRDTWGQGTLTVSSA
551	EVQLVESGGGVVQPGGSLRLSCAASRSIGRLDRMGWYRHRPGEPRELVATITGGSSI NYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTALYYCNFNKYVTSRDTWGQGTLV TVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMSWVRQAPGK GLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGS LSRSSQGTLTVTSSGGGGSGGGSEVQLVESGGGVVQPGGSLRLSCAASRSIGRLDRM GWYRHRPGEPRELVATITGGSSINYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTAL YYCNFNKYVTSRDTWGQGTLVKVSSA
552	EVQLVESGGGVVQPGGSLRLSCAASRSIGRLDRMGWYRHRPGEPRELVATITGGSSI NYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTALYYCNFNKYVTSRDTWGQGTLV TVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMSWVRQAPGK GLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGS LSRSSQGTLTVTSSGGGGSGGGSEVQLVESGGGVVQPGGSLRLSCAASRSIGRLDRM GWYRHRPGEPRELVATITGGSSINYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTAL YYCNFNKYVTSRDTWGQGTLVQVSSA
553	EVQLVESGGGVVQPGGSLRLSCAASRSIGRLDRMGWYRHRPGEPRELVATITGGSSI NYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTALYYCNFNKYVTSRDTWGQGTLV TVSSGGGGSGGGSEVQLVESGGGVVQPGNSLRLSCAASGFTFSSFGMSWVRQAPGK GLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGS LSRSSQGTLTVTSSGGGGSGGGSEVQLVESGGGVVQPGGSLRLSCAASRSIGRLDRM GWYRHRPGEPRELVATITGGSSINYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTAL YYCNFNKYVTSRDTWGQGTLTVSSA
554	EVQLVESGGGVVQPGGSLRLSCAASRSIGRLDRMGWYRHRPGEPRELVATITGGSSI NYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTALYYCNFNKYVTSRDTWGQGTLV TVSSGGGGSGGGSEVQLVESGGGVVQPGNSLRLSCAASGFTFSSFGMSWVRQAPGK GLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGS LSRSSQGTLTVTSSGGGGSGGGSEVQLVESGGGVVQPGGSLRLSCAASRSIGRLDRM GWYRHRPGEPRELVATITGGSSINYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTAL YYCNFNKYVTSRDTWGQGTLVKVSSA

Figure 23 (continued)

SEQ ID	Sequence
555	EVQLVESGGGVVQPGGSLRLSCAASRSIGRLDRMGWYRHRPGEPRELVATITGGSSI NYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTALYYCNFKYVTSRDTWGQGTLV TVSSGGGGSGGGSEVQLVESGGGVVQPGNSLRLSCAASGFTSSFGMSWVRQAPGK GLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGS LSRSQGTLTVTSSGGGGSGGGSEVQLVESGGGVVQPGGSLRLSCAASRSIGRLDRM GWYRHRPGEPRELVATITGGSSINYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTAL YYCNFKYVTSRDTWGQGTLVQVSSA
556	EVQLVESGGGVVQPGGSLRLSCAASRSIGRLDRMGWYRHRPGEPRELVATITGGSSI NYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTALYYCNFKYVTSRDTWGQGTLV TVSSGGGGSGGGSEVQLVESGGGVVQPGNSLRLSCAASGFTSSFGMSWVRQAPGK GLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGS LSRSQGTLVVKVSSGGGGSGGGSEVQLVESGGGVVQPGGSLRLSCAASRSIGRLDRM GWYRHRPGEPRELVATITGGSSINYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTAL YYCNFKYVTSRDTWGQGTLVTVSSA
557	EVQLVESGGGVVQPGGSLRLSCAASRSIGRLDRMGWYRHRPGEPRELVATITGGSSI NYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTALYYCNFKYVTSRDTWGQGTLV TVSSGGGGSGGGSEVQLVESGGGVVQPGNSLRLSCAASGFTSSFGMSWVRQAPGK GLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGS LSRSQGTLVVKVSSGGGGSGGGSEVQLVESGGGVVQPGGSLRLSCAASRSIGRLDRM GWYRHRPGEPRELVATITGGSSINYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTAL YYCNFKYVTSRDTWGQGTLVKVSSA
558	EVQLVESGGGVVQPGGSLRLSCAASRSIGRLDRMGWYRHRPGEPRELVATITGGSSI NYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTALYYCNFKYVTSRDTWGQGTLV TVSSGGGGSGGGSEVQLVESGGGVVQPGNSLRLSCAASGFTSSFGMSWVRQAPGK GLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGS LSRSQGTLVVKVSSGGGGSGGGSEVQLVESGGGVVQPGGSLRLSCAASRSIGRLDRM GWYRHRPGEPRELVATITGGSSINYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTAL YYCNFKYVTSRDTWGQGTLVQVSSA
559	EVQLVESGGGVVQPGGSLRLSCAASRSIGRLDRMGWYRHRPGEPRELVATITGGSSI NYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTALYYCNFKYVTSRDTWGQGTLV TVSSGGGGSGGGSEVQLVESGGGVVQPGNSLRLSCAASGFTSSFGMSWVRQAPGK GLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGS LSRSQGTLVQVSSGGGGSGGGSEVQLVESGGGVVQPGGSLRLSCAASRSIGRLDRM GWYRHRPGEPRELVATITGGSSINYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTAL YYCNFKYVTSRDTWGQGTLVTVSSA

Figure 23 (continued)

SEQ ID	Sequence
560	EVQLVESGGGVVQPGGLRLSCAASRSIGRLDRMGWYRHRPGEPRELVATITGGSSI NYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTALYYCNFNKYVTSRDTWGQGTLV TVSSGGGGSGGGSEVQLVESGGGVQPGNSLRLSCAASGFTSSFGMSWVRQAPGK GLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGS LSRQQGTLVQVSSGGGGSGGGSEVQLVESGGGVQPGGLRLSCAASRSIGRLDRM GWYRHRPGEPRELVATITGGSSINYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTAL YYCNFNKYVTSRDTWGQGTLVKVSSA
561	EVQLVESGGGVVQPGGLRLSCAASRSIGRLDRMGWYRHRPGEPRELVATITGGSSI NYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTALYYCNFNKYVTSRDTWGQGTLV TVSSGGGGSGGGSEVQLVESGGGVQPGNSLRLSCAASGFTSSFGMSWVRQAPGK GLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGS LSRQQGTLVQVSSGGGGSGGGSEVQLVESGGGVQPGGLRLSCAASRSIGRLDRM GWYRHRPGEPRELVATITGGSSINYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTAL YYCNFNKYVTSRDTWGQGTLVQVSSA
562	EVQLVESGGGVVQPGGLRLSCAASRSIGRLDRMGWYRHRPGEPRELVATITGGSSI NYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTALYYCNFNKYVTSRDTWGQGTLV KVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTSSFGMSWVRQAPGK GLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGS LSRQQGTLVTVSSGGGGSGGGSEVQLVESGGGVQPGGLRLSCAASRSIGRLDRM GWYRHRPGEPRELVATITGGSSINYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTAL YYCNFNKYVTSRDTWGQGTLVTVSSA
563	EVQLVESGGGVVQPGGLRLSCAASRSIGRLDRMGWYRHRPGEPRELVATITGGSSI NYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTALYYCNFNKYVTSRDTWGQGTLV KVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTSSFGMSWVRQAPGK GLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGS LSRQQGTLVTVSSGGGGSGGGSEVQLVESGGGVQPGGLRLSCAASRSIGRLDRM GWYRHRPGEPRELVATITGGSSINYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTAL YYCNFNKYVTSRDTWGQGTLVKVSSA
564	EVQLVESGGGVVQPGGLRLSCAASRSIGRLDRMGWYRHRPGEPRELVATITGGSSI NYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTALYYCNFNKYVTSRDTWGQGTLV KVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTSSFGMSWVRQAPGK GLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGS LSRQQGTLVTVSSGGGGSGGGSEVQLVESGGGVQPGGLRLSCAASRSIGRLDRM GWYRHRPGEPRELVATITGGSSINYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTAL YYCNFNKYVTSRDTWGQGTLVQVSSA

Figure 23 (continued)

SEQ ID	Sequence
565	EVQLVESGGGVVQPGGLRLSCAASRSIGRLDRMGWYRHRPGEPRELVATITGGSSI NYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTALYYCNFNKYVTSRDTWGQGTLV KVSSGGGGSGGGSEVQLVESGGGVVQPGNSLRLSCAASGFTSSFGMSWVRQAPGK GLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGS LSRSSQGTLTVTSSGGGGSGGGSEVQLVESGGGVVQPGGLRLSCAASRSIGRLDRM GWYRHRPGEPRELVATITGGSSINYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTAL YYCNFNKYVTSRDTWGQGTLTVSSA
566	EVQLVESGGGVVQPGGLRLSCAASRSIGRLDRMGWYRHRPGEPRELVATITGGSSI NYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTALYYCNFNKYVTSRDTWGQGTLV KVSSGGGGSGGGSEVQLVESGGGVVQPGNSLRLSCAASGFTSSFGMSWVRQAPGK GLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGS LSRSSQGTLTVTSSGGGGSGGGSEVQLVESGGGVVQPGGLRLSCAASRSIGRLDRM GWYRHRPGEPRELVATITGGSSINYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTAL YYCNFNKYVTSRDTWGQGTLVKVSSA
567	EVQLVESGGGVVQPGGLRLSCAASRSIGRLDRMGWYRHRPGEPRELVATITGGSSI NYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTALYYCNFNKYVTSRDTWGQGTLV KVSSGGGGSGGGSEVQLVESGGGVVQPGNSLRLSCAASGFTSSFGMSWVRQAPGK GLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGS LSRSSQGTLTVTSSGGGGSGGGSEVQLVESGGGVVQPGGLRLSCAASRSIGRLDRM GWYRHRPGEPRELVATITGGSSINYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTAL YYCNFNKYVTSRDTWGQGTLVQVSSA
568	EVQLVESGGGVVQPGGLRLSCAASRSIGRLDRMGWYRHRPGEPRELVATITGGSSI NYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTALYYCNFNKYVTSRDTWGQGTLV KVSSGGGGSGGGSEVQLVESGGGVVQPGNSLRLSCAASGFTSSFGMSWVRQAPGK GLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGS LSRSSQGTLVKVSSGGGGSGGGSEVQLVESGGGVVQPGGLRLSCAASRSIGRLDRM GWYRHRPGEPRELVATITGGSSINYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTAL YYCNFNKYVTSRDTWGQGTLTVSSA
569	EVQLVESGGGVVQPGGLRLSCAASRSIGRLDRMGWYRHRPGEPRELVATITGGSSI NYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTALYYCNFNKYVTSRDTWGQGTLV KVSSGGGGSGGGSEVQLVESGGGVVQPGNSLRLSCAASGFTSSFGMSWVRQAPGK GLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGS LSRSSQGTLVKVSSGGGGSGGGSEVQLVESGGGVVQPGGLRLSCAASRSIGRLDRM GWYRHRPGEPRELVATITGGSSINYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTAL YYCNFNKYVTSRDTWGQGTLVKVSSA

Figure 23 (continued)

SEQ ID	Sequence
570	EVQLVESGGGVVQPGGLRLSCAASRSIGRLDRMGWYRHPGEPRELVATITGGSSI NYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTALYYCNFKYVTSRDTWGQGTLV KVSSGGGGSGGGSEVQLVESGGGVQPGNSLRLSCAASGFTSSFGMSWVRQAPGK GLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGS LSRQQGTLVQVSSGGGGSGGGSEVQLVESGGGVQPGGLRLSCAASRSIGRLDRM GWYRHPGEPRELVATITGGSSINYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTAL YYCNFKYVTSRDTWGQGTLVQVSSA
571	EVQLVESGGGVVQPGGLRLSCAASRSIGRLDRMGWYRHPGEPRELVATITGGSSI NYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTALYYCNFKYVTSRDTWGQGTLV KVSSGGGGSGGGSEVQLVESGGGVQPGNSLRLSCAASGFTSSFGMSWVRQAPGK GLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGS LSRQQGTLVQVSSGGGGSGGGSEVQLVESGGGVQPGGLRLSCAASRSIGRLDRM GWYRHPGEPRELVATITGGSSINYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTAL YYCNFKYVTSRDTWGQGTLVTVSSA
572	EVQLVESGGGVVQPGGLRLSCAASRSIGRLDRMGWYRHPGEPRELVATITGGSSI NYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTALYYCNFKYVTSRDTWGQGTLV KVSSGGGGSGGGSEVQLVESGGGVQPGNSLRLSCAASGFTSSFGMSWVRQAPGK GLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGS LSRQQGTLVQVSSGGGGSGGGSEVQLVESGGGVQPGGLRLSCAASRSIGRLDRM GWYRHPGEPRELVATITGGSSINYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTAL YYCNFKYVTSRDTWGQGTLVQVSSA
573	EVQLVESGGGVVQPGGLRLSCAASRSIGRLDRMGWYRHPGEPRELVATITGGSSI NYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTALYYCNFKYVTSRDTWGQGTLV KVSSGGGGSGGGSEVQLVESGGGVQPGNSLRLSCAASGFTSSFGMSWVRQAPGK GLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGS LSRQQGTLVQVSSGGGGSGGGSEVQLVESGGGVQPGGLRLSCAASRSIGRLDRM GWYRHPGEPRELVATITGGSSINYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTAL YYCNFKYVTSRDTWGQGTLVQVSSA
574	EVQLVESGGGVVQPGGLRLSCAASRSIGRLDRMGWYRHPGEPRELVATITGGSSI NYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTALYYCNFKYVTSRDTWGQGTLV QVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTSSFGMSWVRQAPGK GLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGS LSRQQGTLVTVSSGGGGSGGGSEVQLVESGGGVQPGGLRLSCAASRSIGRLDRM GWYRHPGEPRELVATITGGSSINYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTAL YYCNFKYVTSRDTWGQGTLVTVSSA

Figure 23 (continued)

SEQ ID	Sequence
575	EVQLVESGGGVVQPGGSLRLSCAASRSIGRLDRMGWYRHRPGEPRELVATITGGSSI NYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTALYYCNFNKYVTSRDTWGQGTLV QVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTSSFGMSWVRQAPGK GLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGS LSRQQGTLTVTSSGGGGSGGGSEVQLVESGGGVVQPGGSLRLSCAASRSIGRLDRM GWYRHRPGEPRELVATITGGSSINYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTAL YYCNFNKYVTSRDTWGQGTLVKVSSA
576	EVQLVESGGGVVQPGGSLRLSCAASRSIGRLDRMGWYRHRPGEPRELVATITGGSSI NYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTALYYCNFNKYVTSRDTWGQGTLV QVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTSSFGMSWVRQAPGK GLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGS LSRQQGTLTVTSSGGGGSGGGSEVQLVESGGGVVQPGGSLRLSCAASRSIGRLDRM GWYRHRPGEPRELVATITGGSSINYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTAL YYCNFNKYVTSRDTWGQGTLVQVSSA
577	EVQLVESGGGVVQPGGSLRLSCAASRSIGRLDRMGWYRHRPGEPRELVATITGGSSI NYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTALYYCNFNKYVTSRDTWGQGTLV QVSSGGGGSGGGSEVQLVESGGGVVQPGNSLRLSCAASGFTSSFGMSWVRQAPGK GLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGS LSRQQGTLTVTSSGGGGSGGGSEVQLVESGGGVVQPGGSLRLSCAASRSIGRLDRM GWYRHRPGEPRELVATITGGSSINYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTAL YYCNFNKYVTSRDTWGQGTLVTVSSA
578	EVQLVESGGGVVQPGGSLRLSCAASRSIGRLDRMGWYRHRPGEPRELVATITGGSSI NYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTALYYCNFNKYVTSRDTWGQGTLV QVSSGGGGSGGGSEVQLVESGGGVVQPGNSLRLSCAASGFTSSFGMSWVRQAPGK GLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGS LSRQQGTLTVTSSGGGGSGGGSEVQLVESGGGVVQPGGSLRLSCAASRSIGRLDRM GWYRHRPGEPRELVATITGGSSINYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTAL YYCNFNKYVTSRDTWGQGTLVKVSSA
579	EVQLVESGGGVVQPGGSLRLSCAASRSIGRLDRMGWYRHRPGEPRELVATITGGSSI NYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTALYYCNFNKYVTSRDTWGQGTLV QVSSGGGGSGGGSEVQLVESGGGVVQPGNSLRLSCAASGFTSSFGMSWVRQAPGK GLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGS LSRQQGTLTVTSSGGGGSGGGSEVQLVESGGGVVQPGGSLRLSCAASRSIGRLDRM GWYRHRPGEPRELVATITGGSSINYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTAL YYCNFNKYVTSRDTWGQGTLVQVSSA

Figure 23 (continued)

SEQ ID	Sequence
580	EVQLVESGGGVVQPGGSLRLSCAASRSIGRLDRMGWYRHRPGEPRELVATITGGSSI NYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTALYYCNFNKYVTSRDTWGQGTLV QVSSGGGGSGGGSEVQLVESGGGVVQPGNSLRLSCAASGFTFSSFGMSWVRQAPGK GLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGS LSRSSQGTLV ру VVSSGGGGSGGGSEVQLVESGGGVVQPGGSLRLSCAASRSIGRLDRM GWYRHRPGEPRELVATITGGSSI NYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTAL YYCNFNKYVTSRDTWGQGTLV ру VSSA
581	EVQLVESGGGVVQPGGSLRLSCAASRSIGRLDRMGWYRHRPGEPRELVATITGGSSI NYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTALYYCNFNKYVTSRDTWGQGTLV QVSSGGGGSGGGSEVQLVESGGGVVQPGNSLRLSCAASGFTFSSFGMSWVRQAPGK GLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGS LSRSSQGTLV ру VVSSGGGGSGGGSEVQLVESGGGVVQPGGSLRLSCAASRSIGRLDRM GWYRHRPGEPRELVATITGGSSI NYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTAL YYCNFNKYVTSRDTWGQGTLV ру VSSA
582	EVQLVESGGGVVQPGGSLRLSCAASRSIGRLDRMGWYRHRPGEPRELVATITGGSSI NYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTALYYCNFNKYVTSRDTWGQGTLV QVSSGGGGSGGGSEVQLVESGGGVVQPGNSLRLSCAASGFTFSSFGMSWVRQAPGK GLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGS LSRSSQGTLV ру VVSSGGGGSGGGSEVQLVESGGGVVQPGGSLRLSCAASRSIGRLDRM GWYRHRPGEPRELVATITGGSSI NYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTAL YYCNFNKYVTSRDTWGQGTLV ру VSSA
583	EVQLVESGGGVVQPGGSLRLSCAASRSIGRLDRMGWYRHRPGEPRELVATITGGSSI NYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTALYYCNFNKYVTSRDTWGQGTLV QVSSGGGGSGGGSEVQLVESGGGVVQPGNSLRLSCAASGFTFSSFGMSWVRQAPGK GLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGS LSRSSQGTLV ру VVSSGGGGSGGGSEVQLVESGGGVVQPGGSLRLSCAASRSIGRLDRM GWYRHRPGEPRELVATITGGSSI NYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTAL YYCNFNKYVTSRDTWGQGTLV ру VSSA
584	EVQLVESGGGVVQPGGSLRLSCAASRSIGRLDRMGWYRHRPGEPRELVATITGGSSI NYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTALYYCNFNKYVTSRDTWGQGTLV QVSSGGGGSGGGSEVQLVESGGGVVQPGNSLRLSCAASGFTFSSFGMSWVRQAPGK GLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGS LSRSSQGTLV ру VVSSGGGGSGGGSEVQLVESGGGVVQPGGSLRLSCAASRSIGRLDRM GWYRHRPGEPRELVATITGGSSI NYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTAL YYCNFNKYVTSRDTWGQGTLV ру VSSA
585	EVQLVESGGGVVQPGGSLRLSCAASRSIGRLDRMGWYRHRPGEPRELVATITGGSSI NYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTALYYCNFNKYVTSRDTWGQGTLV QVSSGGGGSGGGSEVQLVESGGGVVQPGNSLRLSCAASGFTFSSFGMSWVRQAPGK GLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGS LSRSSQGTLV ру VVSSGGGGSGGGSEVQLVESGGGVVQPGGSLRLSCAASRSIGRLDRM GWYRHRPGEPRELVATITGGSSI NYGDSVKGRFTISIDNSKNTVYLQMNSLRPEDTAL YYCNFNKYVTSRDTWGQGTLV ру VSSA

Figure 24

SEQ ID	Sequence
586	DVQLLESGGGVVQPGGSLRLSCAASGFTFGNYDMAWVRQAPGKRPEWVSSIDT GGDITHYADSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYWCATDEEYALGPN EFDYYGQGTLTVSSGGGGSGGGSEVQLLESGGGVVQPGGSLRLSCAASGFTFR SFGMSWVRQAPGKGPEWVSSISGSGSDTLYADSVKGRFTISRDNSKNTLYLQMN SLRPEDTALYYCTIGGSLSRSSQGTLTVSSA
587	DVQLLESGGGVVQPGGSLRLSCAASGFTFGNYDMAWVRQAPGKRPEWVSSIDT GGDITHYADSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYWCATDEEYALGPN EFDYYGQGTLTVSSGGGGSGGGSEVQLLESGGGVVQPGGSLRLSCAASGFTFR SFGMSWVRQAPGKGPEWVSSISGSGSDTLYADSVKGRFTISRDNSKNTLYLQMN SLRPEDTALYYCTIGGSLSRSSQGTLVKVSSA
588	DVQLLESGGGVVQPGGSLRLSCAASGFTFGNYDMAWVRQAPGKRPEWVSSIDT GGDITHYADSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYWCATDEEYALGPN EFDYYGQGTLTVSSGGGGSGGGSEVQLLESGGGVVQPGGSLRLSCAASGFTFR SFGMSWVRQAPGKGPEWVSSISGSGSDTLYADSVKGRFTISRDNSKNTLYLQMN SLRPEDTALYYCTIGGSLSRSSQGTLVQVSSA
589	DVQLLESGGGVVQPGGSLRLSCAASGFTFGNYDMAWVRQAPGKRPEWVSSIDT GGDITHYADSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYWCATDEEYALGPN EFDYYGQGTLVKVSSGGGGSGGGSEVQLLESGGGVVQPGGSLRLSCAASGFTFR SFGMSWVRQAPGKGPEWVSSISGSGSDTLYADSVKGRFTISRDNSKNTLYLQMN SLRPEDTALYYCTIGGSLSRSSQGTLTVSSA
590	DVQLLESGGGVVQPGGSLRLSCAASGFTFGNYDMAWVRQAPGKRPEWVSSIDT GGDITHYADSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYWCATDEEYALGPN EFDYYGQGTLVKVSSGGGGSGGGSEVQLLESGGGVVQPGGSLRLSCAASGFTFR SFGMSWVRQAPGKGPEWVSSISGSGSDTLYADSVKGRFTISRDNSKNTLYLQMN SLRPEDTALYYCTIGGSLSRSSQGTLVKVSSA
591	DVQLLESGGGVVQPGGSLRLSCAASGFTFGNYDMAWVRQAPGKRPEWVSSIDT GGDITHYADSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYWCATDEEYALGPN EFDYYGQGTLVKVSSGGGGSGGGSEVQLLESGGGVVQPGGSLRLSCAASGFTFR SFGMSWVRQAPGKGPEWVSSISGSGSDTLYADSVKGRFTISRDNSKNTLYLQMN SLRPEDTALYYCTIGGSLSRSSQGTLVQVSSA
592	DVQLLESGGGVVQPGGSLRLSCAASGFTFGNYDMAWVRQAPGKRPEWVSSIDT GGDITHYADSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYWCATDEEYALGPN EFDYYGQGTLVQVSSGGGGSGGGSEVQLLESGGGVVQPGGSLRLSCAASGFTFR SFGMSWVRQAPGKGPEWVSSISGSGSDTLYADSVKGRFTISRDNSKNTLYLQMN SLRPEDTALYYCTIGGSLSRSSQGTLTVSSA
593	DVQLLESGGGVVQPGGSLRLSCAASGFTFGNYDMAWVRQAPGKRPEWVSSIDT GGDITHYADSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYWCATDEEYALGPN EFDYYGQGTLVQVSSGGGGSGGGSEVQLLESGGGVVQPGGSLRLSCAASGFTFR SFGMSWVRQAPGKGPEWVSSISGSGSDTLYADSVKGRFTISRDNSKNTLYLQMN SLRPEDTALYYCTIGGSLSRSSQGTLVKVSSA
594	DVQLLESGGGVVQPGGSLRLSCAASGFTFGNYDMAWVRQAPGKRPEWVSSIDT GGDITHYADSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYWCATDEEYALGPN EFDYYGQGTLVQVSSGGGGSGGGSEVQLLESGGGVVQPGGSLRLSCAASGFTFR SFGMSWVRQAPGKGPEWVSSISGSGSDTLYADSVKGRFTISRDNSKNTLYLQMN SLRPEDTALYYCTIGGSLSRSSQGTLVQVSSA

Figure 25

SEQ ID	Sequence
595	EVQLVESGGVVQPGGLRLSCAASGFTSSYAMSWVRQAPGKGLEWVSGIKSSG DSTRYAGSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCAKSRSRTGLYTYD NRGQGTLVTVSSGGGGSGGGGGSEVQLVESGGVVQPGGLRLSC AASGRTFNNYAMGWFRQAPGKEREVAAITSGVRSGVSAIYGDSVKDRFTISRD NAKNTLYLQMNSLRPEDTALYYCAASAIGSGALRRFEYDYSQGTLTVSSA
596	EVQLVESGGVVQPGGLRLSCAASGFTSSYAMSWVRQAPGKGLEWVSGIKSSG DSTRYAGSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCAKSRSRTGLYTYD NRGQGTLVTVSSGGGGSGGGGGSEVQLVESGGVVQPGGLRLSC AASGRTFNNYAMGWFRQAPGKEREVAAITSGVRSGVSAIYGDSVKDRFTISRD NAKNTLYLQMNSLRPEDTALYYCAASAIGSGALRRFEYDYSQGTLVQVSSA
597	EVQLVESGGVVQPGGLRLSCAASGFTSSYAMSWVRQAPGKGLEWVSGIKSSG DSTRYAGSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCAKSRSRTGLYTYD NRGQGTLVTVSSGGGGSGGGGGSEVQLVESGGVVQPGGLRLSC AASGRTFNNYAMGWFRQAPGKEREVAAITSGVRSGVSAIYGDSVKDRFTISRD NAKNTLYLQMNSLRPEDTALYYCAASAIGSGALRRFEYDYSQGTLVQVSSA
598	EVQLVESGGVVQPGGLRLSCAASGFTSSYAMSWVRQAPGKGLEWVSGIKSSG DSTRYAGSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCAKSRSRTGLYTYD NRGQGTLVKVSSGGGGSGGGGGSEVQLVESGGVVQPGGLRLSC AASGRTFNNYAMGWFRQAPGKEREVAAITSGVRSGVSAIYGDSVKDRFTISRD NAKNTLYLQMNSLRPEDTALYYCAASAIGSGALRRFEYDYSQGTLTVSSA
599	EVQLVESGGVVQPGGLRLSCAASGFTSSYAMSWVRQAPGKGLEWVSGIKSSG DSTRYAGSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCAKSRSRTGLYTYD NRGQGTLVKVSSGGGGSGGGGGSEVQLVESGGVVQPGGLRLSC AASGRTFNNYAMGWFRQAPGKEREVAAITSGVRSGVSAIYGDSVKDRFTISRD NAKNTLYLQMNSLRPEDTALYYCAASAIGSGALRRFEYDYSQGTLVQVSSA
600	EVQLVESGGVVQPGGLRLSCAASGFTSSYAMSWVRQAPGKGLEWVSGIKSSG DSTRYAGSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCAKSRSRTGLYTYD NRGQGTLVKVSSGGGGSGGGGGSEVQLVESGGVVQPGGLRLSC AASGRTFNNYAMGWFRQAPGKEREVAAITSGVRSGVSAIYGDSVKDRFTISRD NAKNTLYLQMNSLRPEDTALYYCAASAIGSGALRRFEYDYSQGTLVQVSSA
601	EVQLVESGGVVQPGGLRLSCAASGFTSSYAMSWVRQAPGKGLEWVSGIKSSG DSTRYAGSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCAKSRSRTGLYTYD NRGQGTLVKVSSGGGGSGGGGGSEVQLVESGGVVQPGGLRLSC AASGRTFNNYAMGWFRQAPGKEREVAAITSGVRSGVSAIYGDSVKDRFTISRD NAKNTLYLQMNSLRPEDTALYYCAASAIGSGALRRFEYDYSQGTLTVSSA
602	EVQLVESGGVVQPGGLRLSCAASGFTSSYAMSWVRQAPGKGLEWVSGIKSSG DSTRYAGSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCAKSRSRTGLYTYD NRGQGTLVKVSSGGGGSGGGGGSEVQLVESGGVVQPGGLRLSC AASGRTFNNYAMGWFRQAPGKEREVAAITSGVRSGVSAIYGDSVKDRFTISRD NAKNTLYLQMNSLRPEDTALYYCAASAIGSGALRRFEYDYSQGTLVQVSSA
603	EVQLVESGGVVQPGGLRLSCAASGFTSSYAMSWVRQAPGKGLEWVSGIKSSG DSTRYAGSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCAKSRSRTGLYTYD NRGQGTLVKVSSGGGGSGGGGGSEVQLVESGGVVQPGGLRLSC AASGRTFNNYAMGWFRQAPGKEREVAAITSGVRSGVSAIYGDSVKDRFTISRD NAKNTLYLQMNSLRPEDTALYYCAASAIGSGALRRFEYDYSQGTLVQVSSA

Figure 26

SEQ ID	Sequence
604	DVQLVESGGGVVQPGGSLRLSCAASGSIGGLNAMA WYRQAPGKERELVAGIFGV GSTRYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALYYCRMSSVTRGSSDYWG QGTLVTVSSGGGGGGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMSWV RQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAV YYCTIGGSLSRSSQGTLVTVSSGGGGGGGGSEVQLVESGGGVVQPGGSLRLSCAAS GRTYYLNAMGWFRQAPGKEREVAAIDWSEGNKDYADSVKGRFTISRDNSKNTV YLQMNSLRPEDTALYYCAADTPPWGPLIYIESYDSWGQGTLTVVSSA
605	DVQLVESGGGVVQPGGSLRLSCAASGSIGGLNAMA WYRQAPGKERELVAGIFGV GSTRYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALYYCRMSSVTRGSSDYWG QGTLVTVSSGGGGGGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMSWV RQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAV YYCTIGGSLSRSSQGTLVTVSSGGGGGGGGSEVQLVESGGGVVQPGGSLRLSCAAS GRTYYLNAMGWFRQAPGKEREVAAIDWSEGNKDYADSVKGRFTISRDNSKNTV YLQMNSLRPEDTALYYCAADTPPWGPLIYIESYDSWGQGTLVKVSSA
606	DVQLVESGGGVVQPGGSLRLSCAASGSIGGLNAMA WYRQAPGKERELVAGIFGV GSTRYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALYYCRMSSVTRGSSDYWG QGTLVTVSSGGGGGGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMSWV RQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAV YYCTIGGSLSRSSQGTLVTVSSGGGGGGGGSEVQLVESGGGVVQPGGSLRLSCAAS GRTYYLNAMGWFRQAPGKEREVAAIDWSEGNKDYADSVKGRFTISRDNSKNTV YLQMNSLRPEDTALYYCAADTPPWGPLIYIESYDSWGQGTLVQVSSA
607	DVQLVESGGGVVQPGGSLRLSCAASGSIGGLNAMA WYRQAPGKERELVAGIFGV GSTRYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALYYCRMSSVTRGSSDYWG QGTLVTVSSGGGGGGGGSEVQLVESGGGVVQPGNSLRLSCAASGFTFSSFGMSWV RQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAL YYCTIGGSLSRSSQGTLVTVSSGGGGGGGGSEVQLVESGGGVVQPGGSLRLSCAAS GRTYYLNAMGWFRQAPGKEREVAAIDWSEGNKDYADSVKGRFTISRDNSKNTV YLQMNSLRPEDTALYYCAADTPPWGPLIYIESYDSWGQGTLTVVSSA
608	DVQLVESGGGVVQPGGSLRLSCAASGSIGGLNAMA WYRQAPGKERELVAGIFGV GSTRYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALYYCRMSSVTRGSSDYWG QGTLVTVSSGGGGGGGGSEVQLVESGGGVVQPGNSLRLSCAASGFTFSSFGMSWV RQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAL YYCTIGGSLSRSSQGTLVTVSSGGGGGGGGSEVQLVESGGGVVQPGGSLRLSCAAS GRTYYLNAMGWFRQAPGKEREVAAIDWSEGNKDYADSVKGRFTISRDNSKNTV YLQMNSLRPEDTALYYCAADTPPWGPLIYIESYDSWGQGTLVKVSSA
609	DVQLVESGGGVVQPGGSLRLSCAASGSIGGLNAMA WYRQAPGKERELVAGIFGV GSTRYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALYYCRMSSVTRGSSDYWG QGTLVTVSSGGGGGGGGSEVQLVESGGGVVQPGNSLRLSCAASGFTFSSFGMSWV RQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAL YYCTIGGSLSRSSQGTLVTVSSGGGGGGGGSEVQLVESGGGVVQPGGSLRLSCAAS GRTYYLNAMGWFRQAPGKEREVAAIDWSEGNKDYADSVKGRFTISRDNSKNTV YLQMNSLRPEDTALYYCAADTPPWGPLIYIESYDSWGQGTLVQVSSA

Figure 26 (continued)

SEQ ID	Sequence
610	DVQLVESGGVVQPGGLRLSCAASGSIGGLNAMAWYRQAPGKERELVAGIFGV GSTRYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALYYCRMSSVTRGSSDYWG QGTLTVSSGGGGGGSEVQLVESGGGVQPGNSLRLSCAASGFTFSSFGMSWV RQAPGKGLEWVSSISGSQDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAL YYCTIGGSLRSSQGTLVVKVSSGGGGGGSEVQLVESGGGVQPGGLRLSCAAS GRTYYLNAMGWFRQAPGKEREVAAIDWSEGNKDYADSVKGRFTISRDNSKNTV YLQMNSLRPEDTALYYCAADTPPWGPLIYIESYDSWGQGTLTVSSA
611	DVQLVESGGVVQPGGLRLSCAASGSIGGLNAMAWYRQAPGKERELVAGIFGV GSTRYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALYYCRMSSVTRGSSDYWG QGTLTVSSGGGGGGSEVQLVESGGGVQPGNSLRLSCAASGFTFSSFGMSWV RQAPGKGLEWVSSISGSQDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAL YYCTIGGSLRSSQGTLVVKVSSGGGGGGSEVQLVESGGGVQPGGLRLSCAAS GRTYYLNAMGWFRQAPGKEREVAAIDWSEGNKDYADSVKGRFTISRDNSKNTV YLQMNSLRPEDTALYYCAADTPPWGPLIYIESYDSWGQGTLVSSA
612	DVQLVESGGVVQPGGLRLSCAASGSIGGLNAMAWYRQAPGKERELVAGIFGV GSTRYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALYYCRMSSVTRGSSDYWG QGTLTVSSGGGGGGSEVQLVESGGGVQPGNSLRLSCAASGFTFSSFGMSWV RQAPGKGLEWVSSISGSQDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAL YYCTIGGSLRSSQGTLVVKVSSGGGGGGSEVQLVESGGGVQPGGLRLSCAAS GRTYYLNAMGWFRQAPGKEREVAAIDWSEGNKDYADSVKGRFTISRDNSKNTV YLQMNSLRPEDTALYYCAADTPPWGPLIYIESYDSWGQGTLVSSA
613	DVQLVESGGVVQPGGLRLSCAASGSIGGLNAMAWYRQAPGKERELVAGIFGV GSTRYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALYYCRMSSVTRGSSDYWG QGTLTVSSGGGGGGSEVQLVESGGGVQPGNSLRLSCAASGFTFSSFGMSWV RQAPGKGLEWVSSISGSQDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAL YYCTIGGSLRSSQGTLVVKVSSGGGGGGSEVQLVESGGGVQPGGLRLSCAAS GRTYYLNAMGWFRQAPGKEREVAAIDWSEGNKDYADSVKGRFTISRDNSKNTV YLQMNSLRPEDTALYYCAADTPPWGPLIYIESYDSWGQGTLVSSA
614	DVQLVESGGVVQPGGLRLSCAASGSIGGLNAMAWYRQAPGKERELVAGIFGV GSTRYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALYYCRMSSVTRGSSDYWG QGTLTVSSGGGGGGSEVQLVESGGGVQPGNSLRLSCAASGFTFSSFGMSWV RQAPGKGLEWVSSISGSQDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAL YYCTIGGSLRSSQGTLVVKVSSGGGGGGSEVQLVESGGGVQPGGLRLSCAAS GRTYYLNAMGWFRQAPGKEREVAAIDWSEGNKDYADSVKGRFTISRDNSKNTV YLQMNSLRPEDTALYYCAADTPPWGPLIYIESYDSWGQGTLVSSA
615	DVQLVESGGVVQPGGLRLSCAASGSIGGLNAMAWYRQAPGKERELVAGIFGV GSTRYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALYYCRMSSVTRGSSDYWG QGTLTVSSGGGGGGSEVQLVESGGGVQPGNSLRLSCAASGFTFSSFGMSWV RQAPGKGLEWVSSISGSQDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAL YYCTIGGSLRSSQGTLVVKVSSGGGGGGSEVQLVESGGGVQPGGLRLSCAAS GRTYYLNAMGWFRQAPGKEREVAAIDWSEGNKDYADSVKGRFTISRDNSKNTV YLQMNSLRPEDTALYYCAADTPPWGPLIYIESYDSWGQGTLVSSA

Figure 26 (continued)

SEQ ID	Sequence
616	DVQLVESGGVVQPGGLRLSCAASGSIGGLNAMA WYRQAPGKERELVAGIFGV GSTRYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALYYCRMSSVTRGSSDYWG QGTLVKVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMSWV RQAPGKGLEWVSSISGSQDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAV YYCTIGGSLSRSSQGTLTVSSGGGGSGGGSEVQLVESGGGVVQPGGLRLSCAAS GRTYYLNAMGWFRQAPGKEREVAAIDWSEGNKDYADSVKGRFTISRDNSKNTV YLQMNSLRPEDTALYYCAADTPPWGPLIYIESYDSWGQGTLTVSSA
617	DVQLVESGGVVQPGGLRLSCAASGSIGGLNAMA WYRQAPGKERELVAGIFGV GSTRYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALYYCRMSSVTRGSSDYWG QGTLVKVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMSWV RQAPGKGLEWVSSISGSQDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAV YYCTIGGSLSRSSQGTLTVSSGGGGSGGGSEVQLVESGGGVVQPGGLRLSCAAS GRTYYLNAMGWFRQAPGKEREVAAIDWSEGNKDYADSVKGRFTISRDNSKNTV YLQMNSLRPEDTALYYCAADTPPWGPLIYIESYDSWGQGTLVQVSSA
618	DVQLVESGGVVQPGGLRLSCAASGSIGGLNAMA WYRQAPGKERELVAGIFGV GSTRYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALYYCRMSSVTRGSSDYWG QGTLVKVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMSWV RQAPGKGLEWVSSISGSQDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAV YYCTIGGSLSRSSQGTLTVSSGGGGSGGGSEVQLVESGGGVVQPGGLRLSCAAS GRTYYLNAMGWFRQAPGKEREVAAIDWSEGNKDYADSVKGRFTISRDNSKNTV YLQMNSLRPEDTALYYCAADTPPWGPLIYIESYDSWGQGTLVQVSSA
619	DVQLVESGGVVQPGGLRLSCAASGSIGGLNAMA WYRQAPGKERELVAGIFGV GSTRYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALYYCRMSSVTRGSSDYWG QGTLVKVSSGGGGSGGGSEVQLVESGGGVVQPGNSLRLSCAASGFTFSSFGMSWV RQAPGKGLEWVSSISGSQDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAL YYCTIGGSLSRSSQGTLTVSSGGGGSGGGSEVQLVESGGGVVQPGGLRLSCAAS GRTYYLNAMGWFRQAPGKEREVAAIDWSEGNKDYADSVKGRFTISRDNSKNTV YLQMNSLRPEDTALYYCAADTPPWGPLIYIESYDSWGQGTLVQVSSA
620	DVQLVESGGVVQPGGLRLSCAASGSIGGLNAMA WYRQAPGKERELVAGIFGV GSTRYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALYYCRMSSVTRGSSDYWG QGTLVKVSSGGGGSGGGSEVQLVESGGGVVQPGNSLRLSCAASGFTFSSFGMSWV RQAPGKGLEWVSSISGSQDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAL YYCTIGGSLSRSSQGTLTVSSGGGGSGGGSEVQLVESGGGVVQPGGLRLSCAAS GRTYYLNAMGWFRQAPGKEREVAAIDWSEGNKDYADSVKGRFTISRDNSKNTV YLQMNSLRPEDTALYYCAADTPPWGPLIYIESYDSWGQGTLVQVSSA
621	DVQLVESGGVVQPGGLRLSCAASGSIGGLNAMA WYRQAPGKERELVAGIFGV GSTRYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALYYCRMSSVTRGSSDYWG QGTLVKVSSGGGGSGGGSEVQLVESGGGVVQPGNSLRLSCAASGFTFSSFGMSWV RQAPGKGLEWVSSISGSQDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAL YYCTIGGSLSRSSQGTLTVSSGGGGSGGGSEVQLVESGGGVVQPGGLRLSCAAS GRTYYLNAMGWFRQAPGKEREVAAIDWSEGNKDYADSVKGRFTISRDNSKNTV YLQMNSLRPEDTALYYCAADTPPWGPLIYIESYDSWGQGTLVQVSSA

Figure 26 (continued)

SEQ ID	Sequence
622	DVQLVESGGVVQPGGLRLSCAASGSIGGLNAMA WYRQAPGKERELVAGIFGV GSTRYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALYYCRMSSVTRGSSDYWG QGTLVKVSSGGGGSGGGSEVQLVESGGGVQPGNSLRLSCAASGFTFSSFGMSWV RQAPGKGLEWVSSISGSQDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAL YYCTIGGSLRSSQGTLVKVSSGGGGSGGGSEVQLVESGGGVQPGNSLRLSCAAS GRTYYLNAMGWFRQAPGKEREVAAIDWSEGNKDYADSVKGRFTISRDNSKNTV YLQMNSLRPEDTALYYCAADTPPWGPLIYIESYDSWGQGTLVTVSSA
623	DVQLVESGGVVQPGGLRLSCAASGSIGGLNAMA WYRQAPGKERELVAGIFGV GSTRYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALYYCRMSSVTRGSSDYWG QGTLVKVSSGGGGSGGGSEVQLVESGGGVQPGNSLRLSCAASGFTFSSFGMSWV RQAPGKGLEWVSSISGSQDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAL YYCTIGGSLRSSQGTLVKVSSGGGGSGGGSEVQLVESGGGVQPGNSLRLSCAAS GRTYYLNAMGWFRQAPGKEREVAAIDWSEGNKDYADSVKGRFTISRDNSKNTV YLQMNSLRPEDTALYYCAADTPPWGPLIYIESYDSWGQGTLVTVSSA
624	DVQLVESGGVVQPGGLRLSCAASGSIGGLNAMA WYRQAPGKERELVAGIFGV GSTRYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALYYCRMSSVTRGSSDYWG QGTLVKVSSGGGGSGGGSEVQLVESGGGVQPGNSLRLSCAASGFTFSSFGMSWV RQAPGKGLEWVSSISGSQDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAL YYCTIGGSLRSSQGTLVKVSSGGGGSGGGSEVQLVESGGGVQPGNSLRLSCAAS GRTYYLNAMGWFRQAPGKEREVAAIDWSEGNKDYADSVKGRFTISRDNSKNTV YLQMNSLRPEDTALYYCAADTPPWGPLIYIESYDSWGQGTLVTVSSA
625	DVQLVESGGVVQPGGLRLSCAASGSIGGLNAMA WYRQAPGKERELVAGIFGV GSTRYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALYYCRMSSVTRGSSDYWG QGTLVKVSSGGGGSGGGSEVQLVESGGGVQPGNSLRLSCAASGFTFSSFGMSWV RQAPGKGLEWVSSISGSQDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAL YYCTIGGSLRSSQGTLVKVSSGGGGSGGGSEVQLVESGGGVQPGNSLRLSCAAS GRTYYLNAMGWFRQAPGKEREVAAIDWSEGNKDYADSVKGRFTISRDNSKNTV YLQMNSLRPEDTALYYCAADTPPWGPLIYIESYDSWGQGTLVTVSSA
626	DVQLVESGGVVQPGGLRLSCAASGSIGGLNAMA WYRQAPGKERELVAGIFGV GSTRYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALYYCRMSSVTRGSSDYWG QGTLVKVSSGGGGSGGGSEVQLVESGGGVQPGNSLRLSCAASGFTFSSFGMSWV RQAPGKGLEWVSSISGSQDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAL YYCTIGGSLRSSQGTLVKVSSGGGGSGGGSEVQLVESGGGVQPGNSLRLSCAAS GRTYYLNAMGWFRQAPGKEREVAAIDWSEGNKDYADSVKGRFTISRDNSKNTV YLQMNSLRPEDTALYYCAADTPPWGPLIYIESYDSWGQGTLVTVSSA
627	DVQLVESGGVVQPGGLRLSCAASGSIGGLNAMA WYRQAPGKERELVAGIFGV GSTRYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALYYCRMSSVTRGSSDYWG QGTLVKVSSGGGGSGGGSEVQLVESGGGVQPGNSLRLSCAASGFTFSSFGMSWV RQAPGKGLEWVSSISGSQDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAL YYCTIGGSLRSSQGTLVKVSSGGGGSGGGSEVQLVESGGGVQPGNSLRLSCAAS GRTYYLNAMGWFRQAPGKEREVAAIDWSEGNKDYADSVKGRFTISRDNSKNTV YLQMNSLRPEDTALYYCAADTPPWGPLIYIESYDSWGQGTLVTVSSA

Figure 26 (continued)

SEQ ID	Sequence
628	DVQLVESGGVVQPGGLRLSCAASGSIGGLNAMAWYRQAPGKERELVAGIFGV GSTRYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALYYCRMSSVTRGSSDYWG QGTLVQVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMSWV RQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAV YYCTIGGSLSRSSQGTLTVSSGGGGSGGGSEVQLVESGGGVVQPGGLRLSCAAS GRTYYLNAMGWFRQAPGKEREVAAIDWSEGNKDYADSVKGRFTISRDNSKNTV YLQMNSLRPEDTALYYCAADTPPWGPLIYIESYDSWGQGTLTVSSA
629	DVQLVESGGVVQPGGLRLSCAASGSIGGLNAMAWYRQAPGKERELVAGIFGV GSTRYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALYYCRMSSVTRGSSDYWG QGTLVQVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMSWV RQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAV YYCTIGGSLSRSSQGTLTVSSGGGGSGGGSEVQLVESGGGVVQPGGLRLSCAAS GRTYYLNAMGWFRQAPGKEREVAAIDWSEGNKDYADSVKGRFTISRDNSKNTV YLQMNSLRPEDTALYYCAADTPPWGPLIYIESYDSWGQGTLVKVSSA
630	DVQLVESGGVVQPGGLRLSCAASGSIGGLNAMAWYRQAPGKERELVAGIFGV GSTRYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALYYCRMSSVTRGSSDYWG QGTLVQVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMSWV RQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAV YYCTIGGSLSRSSQGTLTVSSGGGGSGGGSEVQLVESGGGVVQPGGLRLSCAAS GRTYYLNAMGWFRQAPGKEREVAAIDWSEGNKDYADSVKGRFTISRDNSKNTV YLQMNSLRPEDTALYYCAADTPPWGPLIYIESYDSWGQGTLVQVSSA
631	DVQLVESGGVVQPGGLRLSCAASGSIGGLNAMAWYRQAPGKERELVAGIFGV GSTRYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALYYCRMSSVTRGSSDYWG QGTLVQVSSGGGGSGGGSEVQLVESGGGVVQPGNSLRLSCAASGFTFSSFGMSWV RQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAL YYCTIGGSLSRSSQGTLTVSSGGGGSGGGSEVQLVESGGGVVQPGGLRLSCAAS GRTYYLNAMGWFRQAPGKEREVAAIDWSEGNKDYADSVKGRFTISRDNSKNTV YLQMNSLRPEDTALYYCAADTPPWGPLIYIESYDSWGQGTLVQVSSA
632	DVQLVESGGVVQPGGLRLSCAASGSIGGLNAMAWYRQAPGKERELVAGIFGV GSTRYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALYYCRMSSVTRGSSDYWG QGTLVQVSSGGGGSGGGSEVQLVESGGGVVQPGNSLRLSCAASGFTFSSFGMSWV RQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAL YYCTIGGSLSRSSQGTLTVSSGGGGSGGGSEVQLVESGGGVVQPGGLRLSCAAS GRTYYLNAMGWFRQAPGKEREVAAIDWSEGNKDYADSVKGRFTISRDNSKNTV YLQMNSLRPEDTALYYCAADTPPWGPLIYIESYDSWGQGTLVKVSSA
633	DVQLVESGGVVQPGGLRLSCAASGSIGGLNAMAWYRQAPGKERELVAGIFGV GSTRYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALYYCRMSSVTRGSSDYWG QGTLVQVSSGGGGSGGGSEVQLVESGGGVVQPGNSLRLSCAASGFTFSSFGMSWV RQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAL YYCTIGGSLSRSSQGTLTVSSGGGGSGGGSEVQLVESGGGVVQPGGLRLSCAAS GRTYYLNAMGWFRQAPGKEREVAAIDWSEGNKDYADSVKGRFTISRDNSKNTV YLQMNSLRPEDTALYYCAADTPPWGPLIYIESYDSWGQGTLVQVSSA

Figure 26 (continued)

SEQ ID	Sequence
634	DVQLVESGGVVQPGGLRLSCAASGSIGGLNAMAWYRQAPGKERELVAGIFGV GSTRYADSVKGRFTISRDNKNTVYLQMNSLRPEDTALYYCRMSSVTRGSSDYWG QGTLVQVSSGGGGGGSEVQLVESGGVVQPGNSLRLSCAASGFTFSSFGMSWV RQAPGKGLEWVSSISGSQDTLYADSVKGRFTISRDNNAKTTLYLQMNSLRPEDTAL YYCTIGGSLSRSSQGTLVKVSSGGGGGGSEVQLVESGGVVQPGGSLRLSCAAS GRTYYLNAMGWFRQAPGKEREVAAIDWSEGNKDYADSVKGRFTISRDNKNTV YLQMNSLRPEDTALYYCAADTPPWGPLIYIESYDSWGQGTLVTVSSA
635	DVQLVESGGVVQPGGLRLSCAASGSIGGLNAMAWYRQAPGKERELVAGIFGV GSTRYADSVKGRFTISRDNKNTVYLQMNSLRPEDTALYYCRMSSVTRGSSDYWG QGTLVQVSSGGGGGGSEVQLVESGGVVQPGNSLRLSCAASGFTFSSFGMSWV RQAPGKGLEWVSSISGSQDTLYADSVKGRFTISRDNNAKTTLYLQMNSLRPEDTAL YYCTIGGSLSRSSQGTLVKVSSGGGGGGSEVQLVESGGVVQPGGSLRLSCAAS GRTYYLNAMGWFRQAPGKEREVAAIDWSEGNKDYADSVKGRFTISRDNKNTV YLQMNSLRPEDTALYYCAADTPPWGPLIYIESYDSWGQGTLVKVSSA
636	DVQLVESGGVVQPGGLRLSCAASGSIGGLNAMAWYRQAPGKERELVAGIFGV GSTRYADSVKGRFTISRDNKNTVYLQMNSLRPEDTALYYCRMSSVTRGSSDYWG QGTLVQVSSGGGGGGSEVQLVESGGVVQPGNSLRLSCAASGFTFSSFGMSWV RQAPGKGLEWVSSISGSQDTLYADSVKGRFTISRDNNAKTTLYLQMNSLRPEDTAL YYCTIGGSLSRSSQGTLVKVSSGGGGGGSEVQLVESGGVVQPGGSLRLSCAAS GRTYYLNAMGWFRQAPGKEREVAAIDWSEGNKDYADSVKGRFTISRDNKNTV YLQMNSLRPEDTALYYCAADTPPWGPLIYIESYDSWGQGTLVQVSSA
637	DVQLVESGGVVQPGGLRLSCAASGSIGGLNAMAWYRQAPGKERELVAGIFGV GSTRYADSVKGRFTISRDNKNTVYLQMNSLRPEDTALYYCRMSSVTRGSSDYWG QGTLVQVSSGGGGGGSEVQLVESGGVVQPGNSLRLSCAASGFTFSSFGMSWV RQAPGKGLEWVSSISGSQDTLYADSVKGRFTISRDNNAKTTLYLQMNSLRPEDTAL YYCTIGGSLSRSSQGTLVKVSSGGGGGGSEVQLVESGGVVQPGGSLRLSCAAS GRTYYLNAMGWFRQAPGKEREVAAIDWSEGNKDYADSVKGRFTISRDNKNTV YLQMNSLRPEDTALYYCAADTPPWGPLIYIESYDSWGQGTLVQVSSA
638	DVQLVESGGVVQPGGLRLSCAASGSIGGLNAMAWYRQAPGKERELVAGIFGV GSTRYADSVKGRFTISRDNKNTVYLQMNSLRPEDTALYYCRMSSVTRGSSDYWG QGTLVQVSSGGGGGGSEVQLVESGGVVQPGNSLRLSCAASGFTFSSFGMSWV RQAPGKGLEWVSSISGSQDTLYADSVKGRFTISRDNNAKTTLYLQMNSLRPEDTAL YYCTIGGSLSRSSQGTLVKVSSGGGGGGSEVQLVESGGVVQPGGSLRLSCAAS GRTYYLNAMGWFRQAPGKEREVAAIDWSEGNKDYADSVKGRFTISRDNKNTV YLQMNSLRPEDTALYYCAADTPPWGPLIYIESYDSWGQGTLVKVSSA
639	DVQLVESGGVVQPGGLRLSCAASGSIGGLNAMAWYRQAPGKERELVAGIFGV GSTRYADSVKGRFTISRDNKNTVYLQMNSLRPEDTALYYCRMSSVTRGSSDYWG QGTLVQVSSGGGGGGSEVQLVESGGVVQPGNSLRLSCAASGFTFSSFGMSWV RQAPGKGLEWVSSISGSQDTLYADSVKGRFTISRDNNAKTTLYLQMNSLRPEDTAL YYCTIGGSLSRSSQGTLVKVSSGGGGGGSEVQLVESGGVVQPGGSLRLSCAAS GRTYYLNAMGWFRQAPGKEREVAAIDWSEGNKDYADSVKGRFTISRDNKNTV YLQMNSLRPEDTALYYCAADTPPWGPLIYIESYDSWGQGTLVQVSSA

Figure 27

SEQ ID	Sequence
640	EVQLVESGGGVVQPGGSLRLSCAASGFTFSDYWMYWVRQAPGKGLEWVSEINTN GLITKYPDSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCARSPSGFNRGQGTL VTVSSGGGSGGGSEVQLVESGGGLVQPGNSRLSCAASGFTFSSFGMSWVRQAP GKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCT IGGSLSRSSQGTLTVTSSGGGSGGGSEVQLVESGGGVVQPGGSLRLSCAASGFTF SDYWMYWVRQAPGKGLEWVSEINTNGLITKYPDSVKGRFTISRDNAKNTLYLQM NSLRPEDTALYYCARSPSGFNRGQGTLTVSSA
641	EVQLVESGGGVVQPGGSLRLSCAASGFTFSDYWMYWVRQAPGKGLEWVSEINTN GLITKYPDSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCARSPSGFNRGQGTL VTVSSGGGSGGGSEVQLVESGGGLVQPGNSRLSCAASGFTFSSFGMSWVRQAP GKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCT IGGSLSRSSQGTLTVTSSGGGSGGGSEVQLVESGGGVVQPGGSLRLSCAASGFTF SDYWMYWVRQAPGKGLEWVSEINTNGLITKYPDSVKGRFTISRDNAKNTLYLQM NSLRPEDTALYYCARSPSGFNRGQGTLVKVSSA
642	EVQLVESGGGVVQPGGSLRLSCAASGFTFSDYWMYWVRQAPGKGLEWVSEINTN GLITKYPDSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCARSPSGFNRGQGTL VTVSSGGGSGGGSEVQLVESGGGLVQPGNSRLSCAASGFTFSSFGMSWVRQAP GKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCT IGGSLSRSSQGTLTVTSSGGGSGGGSEVQLVESGGGVVQPGGSLRLSCAASGFTF SDYWMYWVRQAPGKGLEWVSEINTNGLITKYPDSVKGRFTISRDNAKNTLYLQM NSLRPEDTALYYCARSPSGFNRGQGTLVQVSSA
643	EVQLVESGGGVVQPGGSLRLSCAASGFTFSDYWMYWVRQAPGKGLEWVSEINTN GLITKYPDSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCARSPSGFNRGQGTL VTVSSGGGSGGGSEVQLVESGGGVVQPGNSRLSCAASGFTFSSFGMSWVRQAP GKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCT IGGSLSRSSQGTLTVTSSGGGSGGGSEVQLVESGGGVVQPGGSLRLSCAASGFTF SDYWMYWVRQAPGKGLEWVSEINTNGLITKYPDSVKGRFTISRDNAKNTLYLQM NSLRPEDTALYYCARSPSGFNRGQGTLTVSSA
644	EVQLVESGGGVVQPGGSLRLSCAASGFTFSDYWMYWVRQAPGKGLEWVSEINTN GLITKYPDSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCARSPSGFNRGQGTL VTVSSGGGSGGGSEVQLVESGGGVVQPGNSRLSCAASGFTFSSFGMSWVRQAP GKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCT IGGSLSRSSQGTLTVTSSGGGSGGGSEVQLVESGGGVVQPGGSLRLSCAASGFTF SDYWMYWVRQAPGKGLEWVSEINTNGLITKYPDSVKGRFTISRDNAKNTLYLQM NSLRPEDTALYYCARSPSGFNRGQGTLVKVSSA
645	EVQLVESGGGVVQPGGSLRLSCAASGFTFSDYWMYWVRQAPGKGLEWVSEINTN GLITKYPDSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCARSPSGFNRGQGTL VTVSSGGGSGGGSEVQLVESGGGVVQPGNSRLSCAASGFTFSSFGMSWVRQAP GKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCT IGGSLSRSSQGTLTVTSSGGGSGGGSEVQLVESGGGVVQPGGSLRLSCAASGFTF SDYWMYWVRQAPGKGLEWVSEINTNGLITKYPDSVKGRFTISRDNAKNTLYLQM NSLRPEDTALYYCARSPSGFNRGQGTLVQVSSA

Figure 27 (continued)

SEQ ID	Sequence
646	EVQLVESGGGVVQPGGSLRLSCAASGFTFSDYWMYWVRQAPGKGLEWVSEINTN GLITKYPDSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCARSPSGFNRGQGTL VTVSSGGGSGGGSEVQLVESGGGVQPGNSRLSCAASGFTFSSFGMSWVRQAP GKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCT IGGSLSRSSQGTLVKVSSGGGSGGGSEVQLVESGGGVQPGGSLRLSCAASGFTF SDYWMYWVRQAPGKGLEWVSEINTNGLITKYPDSVKGRFTISRDNAKNTLYLQM NSLRPEDTALYYCARSPSGFNRGQGTLTVSSA
647	EVQLVESGGGVVQPGGSLRLSCAASGFTFSDYWMYWVRQAPGKGLEWVSEINTN GLITKYPDSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCARSPSGFNRGQGTL VTVSSGGGSGGGSEVQLVESGGGVQPGNSRLSCAASGFTFSSFGMSWVRQAP GKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCT IGGSLSRSSQGTLVKVSSGGGSGGGSEVQLVESGGGVQPGGSLRLSCAASGFTF SDYWMYWVRQAPGKGLEWVSEINTNGLITKYPDSVKGRFTISRDNAKNTLYLQM NSLRPEDTALYYCARSPSGFNRGQGTLVKVSSA
648	EVQLVESGGGVVQPGGSLRLSCAASGFTFSDYWMYWVRQAPGKGLEWVSEINTN GLITKYPDSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCARSPSGFNRGQGTL VTVSSGGGSGGGSEVQLVESGGGVQPGNSRLSCAASGFTFSSFGMSWVRQAP GKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCT IGGSLSRSSQGTLVKVSSGGGSGGGSEVQLVESGGGVQPGGSLRLSCAASGFTF SDYWMYWVRQAPGKGLEWVSEINTNGLITKYPDSVKGRFTISRDNAKNTLYLQM NSLRPEDTALYYCARSPSGFNRGQGTLVQVSSA
649	EVQLVESGGGVVQPGGSLRLSCAASGFTFSDYWMYWVRQAPGKGLEWVSEINTN GLITKYPDSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCARSPSGFNRGQGTL VTVSSGGGSGGGSEVQLVESGGGVQPGNSRLSCAASGFTFSSFGMSWVRQAP GKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCT IGGSLSRSSQGTLVKVSSGGGSGGGSEVQLVESGGGVQPGGSLRLSCAASGFTF SDYWMYWVRQAPGKGLEWVSEINTNGLITKYPDSVKGRFTISRDNAKNTLYLQM NSLRPEDTALYYCARSPSGFNRGQGTLTVSSA
650	EVQLVESGGGVVQPGGSLRLSCAASGFTFSDYWMYWVRQAPGKGLEWVSEINTN GLITKYPDSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCARSPSGFNRGQGTL VTVSSGGGSGGGSEVQLVESGGGVQPGNSRLSCAASGFTFSSFGMSWVRQAP GKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCT IGGSLSRSSQGTLVKVSSGGGSGGGSEVQLVESGGGVQPGGSLRLSCAASGFTF SDYWMYWVRQAPGKGLEWVSEINTNGLITKYPDSVKGRFTISRDNAKNTLYLQM NSLRPEDTALYYCARSPSGFNRGQGTLVKVSSA
651	EVQLVESGGGVVQPGGSLRLSCAASGFTFSDYWMYWVRQAPGKGLEWVSEINTN GLITKYPDSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCARSPSGFNRGQGTL VTVSSGGGSGGGSEVQLVESGGGVQPGNSRLSCAASGFTFSSFGMSWVRQAP GKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCT IGGSLSRSSQGTLVKVSSGGGSGGGSEVQLVESGGGVQPGGSLRLSCAASGFTF SDYWMYWVRQAPGKGLEWVSEINTNGLITKYPDSVKGRFTISRDNAKNTLYLQM NSLRPEDTALYYCARSPSGFNRGQGTLVQVSSA

Figure 27 (continued)

SEQ ID	Sequence
652	EVQLVESGGVVQPGGLRLSCAASGFTFSDYWMYWVRQAPGKGLEWVSEINTN GLITKYPDSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCARSPSGFNRGQGTL VKVSSGGGSGGSEVQLVESGGGLVQPGNRLSCAASGFTFSSFGMSWVRQAP GKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCT IGGSLRSSQGTLTVVSSGGGSGGSEVQLVESGGVVQPGGLRLSCAASGFTF SDYWMYWVRQAPGKGLEWVSEINTNGLITKYPDSVKGRFTISRDNAKNTLYLQM NSLRPEDTALYYCARSPSGFNRGQGTLTVSSA
653	EVQLVESGGVVQPGGLRLSCAASGFTFSDYWMYWVRQAPGKGLEWVSEINTN GLITKYPDSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCARSPSGFNRGQGTL VKVSSGGGSGGSEVQLVESGGGLVQPGNRLSCAASGFTFSSFGMSWVRQAP GKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCT IGGSLRSSQGTLTVVSSGGGSGGSEVQLVESGGVVQPGGLRLSCAASGFTF SDYWMYWVRQAPGKGLEWVSEINTNGLITKYPDSVKGRFTISRDNAKNTLYLQM NSLRPEDTALYYCARSPSGFNRGQGTLVKVSSA
654	EVQLVESGGVVQPGGLRLSCAASGFTFSDYWMYWVRQAPGKGLEWVSEINTN GLITKYPDSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCARSPSGFNRGQGTL VKVSSGGGSGGSEVQLVESGGGLVQPGNRLSCAASGFTFSSFGMSWVRQAP GKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCT IGGSLRSSQGTLTVVSSGGGSGGSEVQLVESGGVVQPGGLRLSCAASGFTF SDYWMYWVRQAPGKGLEWVSEINTNGLITKYPDSVKGRFTISRDNAKNTLYLQM NSLRPEDTALYYCARSPSGFNRGQGTLVQVSSA
655	EVQLVESGGVVQPGGLRLSCAASGFTFSDYWMYWVRQAPGKGLEWVSEINTN GLITKYPDSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCARSPSGFNRGQGTL VKVSSGGGSGGSEVQLVESGGVVQPGNRLSCAASGFTFSSFGMSWVRQAP GKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCT IGGSLRSSQGTLTVVSSGGGSGGSEVQLVESGGVVQPGGLRLSCAASGFTF SDYWMYWVRQAPGKGLEWVSEINTNGLITKYPDSVKGRFTISRDNAKNTLYLQM NSLRPEDTALYYCARSPSGFNRGQGTLTVVSSA
656	EVQLVESGGVVQPGGLRLSCAASGFTFSDYWMYWVRQAPGKGLEWVSEINTN GLITKYPDSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCARSPSGFNRGQGTL VKVSSGGGSGGSEVQLVESGGGVQPGNRLSCAASGFTFSSFGMSWVRQAP GKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCT IGGSLRSSQGTLTVVSSGGGSGGSEVQLVESGGVVQPGGLRLSCAASGFTF SDYWMYWVRQAPGKGLEWVSEINTNGLITKYPDSVKGRFTISRDNAKNTLYLQM NSLRPEDTALYYCARSPSGFNRGQGTLVKVSSA
657	EVQLVESGGVVQPGGLRLSCAASGFTFSDYWMYWVRQAPGKGLEWVSEINTN GLITKYPDSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCARSPSGFNRGQGTL VKVSSGGGSGGSEVQLVESGGGVQPGNRLSCAASGFTFSSFGMSWVRQAP GKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCT IGGSLRSSQGTLTVVSSGGGSGGSEVQLVESGGVVQPGGLRLSCAASGFTF SDYWMYWVRQAPGKGLEWVSEINTNGLITKYPDSVKGRFTISRDNAKNTLYLQM NSLRPEDTALYYCARSPSGFNRGQGTLVQVSSA

Figure 27 (continued)

SEQ ID	Sequence
658	EVQLVESGGGVVQPGGSLRLSCAASGFTFSDYWMYWVRQAPGKGLEWVSEINTN GLITKYPDSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCARSPSGFNRGQGTL VKVSSGGGSGGGSEVQLVESGGGVQPGNSRLSCAASGFTFSSFGMSWVRQAP GKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCT IGGSLSRSSQGTLVKVSSGGGSGGSEVQLVESGGGVQPGGSLRLSCAASGFTF SDYWMYWVRQAPGKGLEWVSEINTNGLITKYPDSVKGRFTISRDNAKNTLYLQM NSLRPEDTALYYCARSPSGFNRGQGTLTVSSA
659	EVQLVESGGGVVQPGGSLRLSCAASGFTFSDYWMYWVRQAPGKGLEWVSEINTN GLITKYPDSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCARSPSGFNRGQGTL VKVSSGGGSGGGSEVQLVESGGGVQPGNSRLSCAASGFTFSSFGMSWVRQAP GKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCT IGGSLSRSSQGTLVKVSSGGGSGGSEVQLVESGGGVQPGGSLRLSCAASGFTF SDYWMYWVRQAPGKGLEWVSEINTNGLITKYPDSVKGRFTISRDNAKNTLYLQM NSLRPEDTALYYCARSPSGFNRGQGTLVKVSSA
660	EVQLVESGGGVVQPGGSLRLSCAASGFTFSDYWMYWVRQAPGKGLEWVSEINTN GLITKYPDSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCARSPSGFNRGQGTL VKVSSGGGSGGGSEVQLVESGGGVQPGNSRLSCAASGFTFSSFGMSWVRQAP GKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCT IGGSLSRSSQGTLVKVSSGGGSGGSEVQLVESGGGVQPGGSLRLSCAASGFTF SDYWMYWVRQAPGKGLEWVSEINTNGLITKYPDSVKGRFTISRDNAKNTLYLQM NSLRPEDTALYYCARSPSGFNRGQGTLVQVSSA
661	EVQLVESGGGVVQPGGSLRLSCAASGFTFSDYWMYWVRQAPGKGLEWVSEINTN GLITKYPDSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCARSPSGFNRGQGTL VKVSSGGGSGGGSEVQLVESGGGVQPGNSRLSCAASGFTFSSFGMSWVRQAP GKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCT IGGSLSRSSQGTLVKVSSGGGSGGSEVQLVESGGGVQPGGSLRLSCAASGFTF SDYWMYWVRQAPGKGLEWVSEINTNGLITKYPDSVKGRFTISRDNAKNTLYLQM NSLRPEDTALYYCARSPSGFNRGQGTLTVSSA
662	EVQLVESGGGVVQPGGSLRLSCAASGFTFSDYWMYWVRQAPGKGLEWVSEINTN GLITKYPDSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCARSPSGFNRGQGTL VKVSSGGGSGGGSEVQLVESGGGVQPGNSRLSCAASGFTFSSFGMSWVRQAP GKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCT IGGSLSRSSQGTLVKVSSGGGSGGSEVQLVESGGGVQPGGSLRLSCAASGFTF SDYWMYWVRQAPGKGLEWVSEINTNGLITKYPDSVKGRFTISRDNAKNTLYLQM NSLRPEDTALYYCARSPSGFNRGQGTLVKVSSA
663	EVQLVESGGGVVQPGGSLRLSCAASGFTFSDYWMYWVRQAPGKGLEWVSEINTN GLITKYPDSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCARSPSGFNRGQGTL VKVSSGGGSGGGSEVQLVESGGGVQPGNSRLSCAASGFTFSSFGMSWVRQAP GKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCT IGGSLSRSSQGTLVKVSSGGGSGGSEVQLVESGGGVQPGGSLRLSCAASGFTF SDYWMYWVRQAPGKGLEWVSEINTNGLITKYPDSVKGRFTISRDNAKNTLYLQM NSLRPEDTALYYCARSPSGFNRGQGTLVQVSSA

Figure 27 (continued)

SEQ ID	Sequence
664	EVQLVESGGGVVQPGGSLRLSCAASGFTFSDYWMYWVRQAPGKGLEWVSEINTN GLITKYPDSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCARSPSGFNRGQGTL VQVSSGGGSGGGSEVQLVESGGGLVQPGNSRLSCAASGFTFSSFGMSWVRQAP GKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCT IGGSLSRSSQGTLTVTSSGGGSGGGSEVQLVESGGGVVQPGGSLRLSCAASGFTF SDYWMYWVRQAPGKGLEWVSEINTNGLITKYPDSVKGRFTISRDNAKNTLYLQM NSLRPEDTALYYCARSPSGFNRGQGTLTVSSA
665	EVQLVESGGGVVQPGGSLRLSCAASGFTFSDYWMYWVRQAPGKGLEWVSEINTN GLITKYPDSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCARSPSGFNRGQGTL VQVSSGGGSGGGSEVQLVESGGGLVQPGNSRLSCAASGFTFSSFGMSWVRQAP GKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCT IGGSLSRSSQGTLTVTSSGGGSGGGSEVQLVESGGGVVQPGGSLRLSCAASGFTF SDYWMYWVRQAPGKGLEWVSEINTNGLITKYPDSVKGRFTISRDNAKNTLYLQM NSLRPEDTALYYCARSPSGFNRGQGTLVKSAA
666	EVQLVESGGGVVQPGGSLRLSCAASGFTFSDYWMYWVRQAPGKGLEWVSEINTN GLITKYPDSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCARSPSGFNRGQGTL VQVSSGGGSGGGSEVQLVESGGGLVQPGNSRLSCAASGFTFSSFGMSWVRQAP GKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCT IGGSLSRSSQGTLTVTSSGGGSGGGSEVQLVESGGGVVQPGGSLRLSCAASGFTF SDYWMYWVRQAPGKGLEWVSEINTNGLITKYPDSVKGRFTISRDNAKNTLYLQM NSLRPEDTALYYCARSPSGFNRGQGTLVQVSSA
667	EVQLVESGGGVVQPGGSLRLSCAASGFTFSDYWMYWVRQAPGKGLEWVSEINTN GLITKYPDSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCARSPSGFNRGQGTL VQVSSGGGSGGGSEVQLVESGGGVVQPGNSRLSCAASGFTFSSFGMSWVRQAP GKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCT IGGSLSRSSQGTLTVTSSGGGSGGGSEVQLVESGGGVVQPGGSLRLSCAASGFTF SDYWMYWVRQAPGKGLEWVSEINTNGLITKYPDSVKGRFTISRDNAKNTLYLQM NSLRPEDTALYYCARSPSGFNRGQGTLTVSSA
668	EVQLVESGGGVVQPGGSLRLSCAASGFTFSDYWMYWVRQAPGKGLEWVSEINTN GLITKYPDSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCARSPSGFNRGQGTL VQVSSGGGSGGGSEVQLVESGGGVVQPGNSRLSCAASGFTFSSFGMSWVRQAP GKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCT IGGSLSRSSQGTLTVTSSGGGSGGGSEVQLVESGGGVVQPGGSLRLSCAASGFTF SDYWMYWVRQAPGKGLEWVSEINTNGLITKYPDSVKGRFTISRDNAKNTLYLQM NSLRPEDTALYYCARSPSGFNRGQGTLVKSAA
669	EVQLVESGGGVVQPGGSLRLSCAASGFTFSDYWMYWVRQAPGKGLEWVSEINTN GLITKYPDSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCARSPSGFNRGQGTL VQVSSGGGSGGGSEVQLVESGGGVVQPGNSRLSCAASGFTFSSFGMSWVRQAP GKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCT IGGSLSRSSQGTLTVTSSGGGSGGGSEVQLVESGGGVVQPGGSLRLSCAASGFTF SDYWMYWVRQAPGKGLEWVSEINTNGLITKYPDSVKGRFTISRDNAKNTLYLQM NSLRPEDTALYYCARSPSGFNRGQGTLVQVSSA

Figure 27 (continued)

SEQ ID	Sequence
670	EVQLVESGGGVVQPGGSLRLSCAASGFTFSDYWMYWVRQAPGKGLEWVSEINTN GLITKYPDSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCARSPSGFNRGQGTL VQVSSGGGSGGSEVQLVESGGGVQPGNSRLSCAASGFTFSSFGMSWVRQAP GKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCT IGGSLSRSSQGTLVKVSSGGGSGGSEVQLVESGGGVQPGGSLRLSCAASGFTF SDYWMYWVRQAPGKGLEWVSEINTNGLITKYPDSVKGRFTISRDNAKNTLYLQM NSLRPEDTALYYCARSPSGFNRGQGTLTVSSA
671	EVQLVESGGGVVQPGGSLRLSCAASGFTFSDYWMYWVRQAPGKGLEWVSEINTN GLITKYPDSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCARSPSGFNRGQGTL VQVSSGGGSGGSEVQLVESGGGVQPGNSRLSCAASGFTFSSFGMSWVRQAP GKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCT IGGSLSRSSQGTLVKVSSGGGSGGSEVQLVESGGGVQPGGSLRLSCAASGFTF SDYWMYWVRQAPGKGLEWVSEINTNGLITKYPDSVKGRFTISRDNAKNTLYLQM NSLRPEDTALYYCARSPSGFNRGQGTLVKVSSA
672	EVQLVESGGGVVQPGGSLRLSCAASGFTFSDYWMYWVRQAPGKGLEWVSEINTN GLITKYPDSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCARSPSGFNRGQGTL VQVSSGGGSGGSEVQLVESGGGVQPGNSRLSCAASGFTFSSFGMSWVRQAP GKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCT IGGSLSRSSQGTLVKVSSGGGSGGSEVQLVESGGGVQPGGSLRLSCAASGFTF SDYWMYWVRQAPGKGLEWVSEINTNGLITKYPDSVKGRFTISRDNAKNTLYLQM NSLRPEDTALYYCARSPSGFNRGQGTLVQVSSA
673	EVQLVESGGGVVQPGGSLRLSCAASGFTFSDYWMYWVRQAPGKGLEWVSEINTN GLITKYPDSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCARSPSGFNRGQGTL VQVSSGGGSGGSEVQLVESGGGVQPGNSRLSCAASGFTFSSFGMSWVRQAP GKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCT IGGSLSRSSQGTLVKVSSGGGSGGSEVQLVESGGGVQPGGSLRLSCAASGFTF SDYWMYWVRQAPGKGLEWVSEINTNGLITKYPDSVKGRFTISRDNAKNTLYLQM NSLRPEDTALYYCARSPSGFNRGQGTLTVSSA
674	EVQLVESGGGVVQPGGSLRLSCAASGFTFSDYWMYWVRQAPGKGLEWVSEINTN GLITKYPDSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCARSPSGFNRGQGTL VQVSSGGGSGGSEVQLVESGGGVQPGNSRLSCAASGFTFSSFGMSWVRQAP GKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCT IGGSLSRSSQGTLVKVSSGGGSGGSEVQLVESGGGVQPGGSLRLSCAASGFTF SDYWMYWVRQAPGKGLEWVSEINTNGLITKYPDSVKGRFTISRDNAKNTLYLQM NSLRPEDTALYYCARSPSGFNRGQGTLVKVSSA
675	EVQLVESGGGVVQPGGSLRLSCAASGFTFSDYWMYWVRQAPGKGLEWVSEINTN GLITKYPDSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCARSPSGFNRGQGTL VQVSSGGGSGGSEVQLVESGGGVQPGNSRLSCAASGFTFSSFGMSWVRQAP GKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCT IGGSLSRSSQGTLVKVSSGGGSGGSEVQLVESGGGVQPGGSLRLSCAASGFTF SDYWMYWVRQAPGKGLEWVSEINTNGLITKYPDSVKGRFTISRDNAKNTLYLQM NSLRPEDTALYYCARSPSGFNRGQGTLVQVSSA

Figure 28A

SEQ ID	Sequence
676	DVQLVESGGGVVQPGGSLRLSCAASGFILDYYAIGWFRQAPGKEREGVLCIDAS DDITYYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALYYCATPIGLSSCLLE YDYDYWGQGTLTVSSGGGGSGGGSEVQLLESGGGVQPGGSLRLSCAASGF TFRSGMSWVRQAPGKGPEWSSISGSQDTLYADSVKGRFTISRDNSKNTLYL QMNSLRPEDTALYYCTIGGSLSRSSQGTLTVSSA
677	DVQLVESGGGVVQPGGSLRLSCAASGFILDYYAIGWFRQAPGKEREGVLCIDAS DDITYYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALYYCATPIGLSSCLLE YDYDYWGQGTLTVSSGGGGSGGGSEVQLLESGGGVQPGGSLRLSCAASGF TFRSGMSWVRQAPGKGPEWSSISGSQDTLYADSVKGRFTISRDNSKNTLYL QMNSLRPEDTALYYCTIGGSLSRSSQGTLVKVSSA
678	DVQLVESGGGVVQPGGSLRLSCAASGFILDYYAIGWFRQAPGKEREGVLCIDAS DDITYYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALYYCATPIGLSSCLLE YDYDYWGQGTLTVSSGGGGSGGGSEVQLLESGGGVQPGGSLRLSCAASGF TFRSGMSWVRQAPGKGPEWSSISGSQDTLYADSVKGRFTISRDNSKNTLYL QMNSLRPEDTALYYCTIGGSLSRSSQGTLVQVSSA
679	DVQLVESGGGVVQPGGSLRLSCAASGFILDYYAIGWFRQAPGKEREGVLCIDAS DDITYYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALYYCATPIGLSSCLLE YDYDYWGQGTLVKVSSGGGGSGGGSEVQLLESGGGVQPGGSLRLSCAASGF TFRSGMSWVRQAPGKGPEWSSISGSQDTLYADSVKGRFTISRDNSKNTLYL QMNSLRPEDTALYYCTIGGSLSRSSQGTLVQVSSA
680	DVQLVESGGGVVQPGGSLRLSCAASGFILDYYAIGWFRQAPGKEREGVLCIDAS DDITYYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALYYCATPIGLSSCLLE YDYDYWGQGTLVKVSSGGGGSGGGSEVQLLESGGGVQPGGSLRLSCAASGF TFRSGMSWVRQAPGKGPEWSSISGSQDTLYADSVKGRFTISRDNSKNTLYL QMNSLRPEDTALYYCTIGGSLSRSSQGTLVKVSSA
681	DVQLVESGGGVVQPGGSLRLSCAASGFILDYYAIGWFRQAPGKEREGVLCIDAS DDITYYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALYYCATPIGLSSCLLE YDYDYWGQGTLVKVSSGGGGSGGGSEVQLLESGGGVQPGGSLRLSCAASGF TFRSGMSWVRQAPGKGPEWSSISGSQDTLYADSVKGRFTISRDNSKNTLYL QMNSLRPEDTALYYCTIGGSLSRSSQGTLVQVSSA
682	DVQLVESGGGVVQPGGSLRLSCAASGFILDYYAIGWFRQAPGKEREGVLCIDAS DDITYYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALYYCATPIGLSSCLLE YDYDYWGQGTLVQVSSGGGGSGGGSEVQLLESGGGVQPGGSLRLSCAASGF TFRSGMSWVRQAPGKGPEWSSISGSQDTLYADSVKGRFTISRDNSKNTLYL QMNSLRPEDTALYYCTIGGSLSRSSQGTLVQVSSA
683	DVQLVESGGGVVQPGGSLRLSCAASGFILDYYAIGWFRQAPGKEREGVLCIDAS DDITYYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALYYCATPIGLSSCLLE YDYDYWGQGTLVQVSSGGGGSGGGSEVQLLESGGGVQPGGSLRLSCAASGF TFRSGMSWVRQAPGKGPEWSSISGSQDTLYADSVKGRFTISRDNSKNTLYL QMNSLRPEDTALYYCTIGGSLSRSSQGTLVKVSSA
684	DVQLVESGGGVVQPGGSLRLSCAASGFILDYYAIGWFRQAPGKEREGVLCIDAS DDITYYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALYYCATPIGLSSCLLE YDYDYWGQGTLVQVSSGGGGSGGGSEVQLLESGGGVQPGGSLRLSCAASGF TFRSGMSWVRQAPGKGPEWSSISGSQDTLYADSVKGRFTISRDNSKNTLYL QMNSLRPEDTALYYCTIGGSLSRSSQGTLVQVSSA

Figure 28B

SEQ ID	Sequence
685	DVQLVESGGVVQPGGLRLSCAASGFAFDDYAIWFRQAPGEEREGVSSISSTYGL TYYADSVKGRFTIISDNSKNTVYLQMNSLRPEDTALYYCAATPIGLIGL DAYEYDYWGQGTLVTSSGGGGGGSEVQLVESGGVVQPGNSLRLSCAASGFT FSSFGMSWVRQAPGKGLEWVSSISGSQDTLYADSVKGRFTISRDNA KTTLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLTVSSA
686	DVQLVESGGVVQPGGLRLSCAASGFAFDDYAIWFRQAPGEEREGVSSISSTYGL TYYADSVKGRFTIISDNSKNTVYLQMNSLRPEDTALYYCAATPIGLIGL DAYEYDYWGQGTLVTSSGGGGGGSEVQLVESGGVVQPGNSLRLSCAASGFT FSSFGMSWVRQAPGKGLEWVSSISGSQDTLYADSVKGRFTISRDNA KTTLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLVQVSSA
687	DVQLVESGGVVQPGGLRLSCAASGFAFDDYAIWFRQAPGEEREGVSSISSTYGL TYYADSVKGRFTIISDNSKNTVYLQMNSLRPEDTALYYCAATPIGLIGL DAYEYDYWGQGTLVTSSGGGGGGSEVQLVESGGVVQPGNSLRLSCAASGFT FSSFGMSWVRQAPGKGLEWVSSISGSQDTLYADSVKGRFTISRDNA KTTLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLVQVSSA
688	DVQLVESGGVVQPGGLRLSCAASGFAFDDYAIWFRQAPGEEREGVSSISSTYGL TYYADSVKGRFTIISDNSKNTVYLQMNSLRPEDTALYYCAATPIGLIGL DAYEYDYWGQGTLVKSSEGGGGGGSEVQLVESGGVVQPGNSLRLSCAASGFT FSSFGMSWVRQAPGKGLEWVSSISGSQDTLYADSVKGRFTISRDNA KTTLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLVQVSSA
689	DVQLVESGGVVQPGGLRLSCAASGFAFDDYAIWFRQAPGEEREGVSSISSTYGL TYYADSVKGRFTIISDNSKNTVYLQMNSLRPEDTALYYCAATPIGLIGL DAYEYDYWGQGTLVKSSEGGGGGGSEVQLVESGGVVQPGNSLRLSCAASGFT FSSFGMSWVRQAPGKGLEWVSSISGSQDTLYADSVKGRFTISRDNA KTTLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLVQVSSA
690	DVQLVESGGVVQPGGLRLSCAASGFAFDDYAIWFRQAPGEEREGVSSISSTYGL TYYADSVKGRFTIISDNSKNTVYLQMNSLRPEDTALYYCAATPIGLIGL DAYEYDYWGQGTLVKSSEGGGGGGSEVQLVESGGVVQPGNSLRLSCAASGFT FSSFGMSWVRQAPGKGLEWVSSISGSQDTLYADSVKGRFTISRDNA KTTLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLVQVSSA
691	DVQLVESGGVVQPGGLRLSCAASGFAFDDYAIWFRQAPGEEREGVSSISSTYGL TYYADSVKGRFTIISDNSKNTVYLQMNSLRPEDTALYYCAATPIGLIGL DAYEYDYWGQGTLVKSSEGGGGGGSEVQLVESGGVVQPGNSLRLSCAASGFT FSSFGMSWVRQAPGKGLEWVSSISGSQDTLYADSVKGRFTISRDNA KTTLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLVQVSSA
692	DVQLVESGGVVQPGGLRLSCAASGFAFDDYAIWFRQAPGEEREGVSSISSTYGL TYYADSVKGRFTIISDNSKNTVYLQMNSLRPEDTALYYCAATPIGLIGL DAYEYDYWGQGTLVKSSEGGGGGGSEVQLVESGGVVQPGNSLRLSCAASGFT FSSFGMSWVRQAPGKGLEWVSSISGSQDTLYADSVKGRFTISRDNA KTTLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLVQVSSA
693	DVQLVESGGVVQPGGLRLSCAASGFAFDDYAIWFRQAPGEEREGVSSISSTYGL TYYADSVKGRFTIISDNSKNTVYLQMNSLRPEDTALYYCAATPIGLIGL DAYEYDYWGQGTLVKSSEGGGGGGSEVQLVESGGVVQPGNSLRLSCAASGFT FSSFGMSWVRQAPGKGLEWVSSISGSQDTLYADSVKGRFTISRDNA KTTLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLVQVSSA

Figure 29

SEQ ID	Sequence
694	EVQLVESGGGVVQPGGSLRLSCAASGFTFSSYPMGWFHQAPGKGREFVSSITGS GG STYYADSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCAAYIRPDTYLSRDYR KYDYWGQGTLTVVSSGGGSGGGSEVQLVESGGLVQPGNSRLSCAASGFTFSS FGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSL RPEDTAVYYCTIGGSLSRSSQGTLTVVSSGGGSGGGSEVQLVESGGGVQPGGSL RLSCAASGFTFSSYPMGWFHQAPGKGREFVSSITGSGGSTYYADSVKGRFTISRDN AKNTLYLQMNSLRPEDTALYYCAAYIRPDTYLSRDYRKYDYWGQGTLTVSSA
695	EVQLVESGGGVVQPGGSLRLSCAASGFTFSSYPMGWFHQAPGKGREFVSSITGS GG STYYADSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCAAYIRPDTYLSRDYR KYDYWGQGTLTVVSSGGGSGGGSEVQLVESGGLVQPGNSRLSCAASGFTFSS FGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSL RPEDTAVYYCTIGGSLSRSSQGTLTVVSSGGGSGGGSEVQLVESGGGVQPGGSL RLSCAASGFTFSSYPMGWFHQAPGKGREFVSSITGSGGSTYYADSVKGRFTISRDN AKNTLYLQMNSLRPEDTALYYCAAYIRPDTYLSRDYRKYDYWGQGTLVKVSSA
696	EVQLVESGGGVVQPGGSLRLSCAASGFTFSSYPMGWFHQAPGKGREFVSSITGS GG STYYADSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCAAYIRPDTYLSRDYR KYDYWGQGTLTVVSSGGGSGGGSEVQLVESGGLVQPGNSRLSCAASGFTFSS FGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSL RPEDTAVYYCTIGGSLSRSSQGTLTVVSSGGGSGGGSEVQLVESGGGVQPGGSL RLSCAASGFTFSSYPMGWFHQAPGKGREFVSSITGSGGSTYYADSVKGRFTISRDN AKNTLYLQMNSLRPEDTALYYCAAYIRPDTYLSRDYRKYDYWGQGTLVQVSSA
697	EVQLVESGGGVVQPGGSLRLSCAASGFTFSSYPMGWFHQAPGKGREFVSSITGS GG STYYADSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCAAYIRPDTYLSRDYR KYDYWGQGTLTVVSSGGGSGGGSEVQLVESGGVQPGNSRLSCAASGFTFSS FGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSL RPEDTALYYCTIGGSLSRSSQGTLTVVSSGGGSGGGSEVQLVESGGGVQPGGSL RLSCAASGFTFSSYPMGWFHQAPGKGREFVSSITGSGGSTYYADSVKGRFTISRDN AKNTLYLQMNSLRPEDTALYYCAAYIRPDTYLSRDYRKYDYWGQGTLVTVSSA
698	EVQLVESGGGVVQPGGSLRLSCAASGFTFSSYPMGWFHQAPGKGREFVSSITGS GG STYYADSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCAAYIRPDTYLSRDYR KYDYWGQGTLTVVSSGGGSGGGSEVQLVESGGVQPGNSRLSCAASGFTFSS FGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSL RPEDTALYYCTIGGSLSRSSQGTLTVVSSGGGSGGGSEVQLVESGGGVQPGGSL RLSCAASGFTFSSYPMGWFHQAPGKGREFVSSITGSGGSTYYADSVKGRFTISRDN AKNTLYLQMNSLRPEDTALYYCAAYIRPDTYLSRDYRKYDYWGQGTLVKVSSA
699	EVQLVESGGGVVQPGGSLRLSCAASGFTFSSYPMGWFHQAPGKGREFVSSITGS GG STYYADSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCAAYIRPDTYLSRDYR KYDYWGQGTLTVVSSGGGSGGGSEVQLVESGGVQPGNSRLSCAASGFTFSS FGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSL RPEDTALYYCTIGGSLSRSSQGTLTVVSSGGGSGGGSEVQLVESGGGVQPGGSL RLSCAASGFTFSSYPMGWFHQAPGKGREFVSSITGSGGSTYYADSVKGRFTISRDN AKNTLYLQMNSLRPEDTALYYCAAYIRPDTYLSRDYRKYDYWGQGTLVQVSSA

Figure 29 (continued)

SEQ ID	Sequence
700	EVQLVESGGGVVQPGGLRLSCAASGFTFSSYPMGWFHQAPGKGREFVSSITGS GG STYYADSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCAAYIRPDTYLSRDYR KYDYWGQGTLTVSSGGGGSGGGSEVQLVESGGGVVQPGNSRLSCAASGFTFSS FGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSL RPEDTALYYCTIGGSLSRSSQGTLVKVSSGGGGSGGGSEVQLVESGGGVVQPGGSL RLSCAASGFTFSSYPMGWFHQAPGKGREFVSSITGSGGSTYYADSVKGRFTISRDN AKNTLYLQMNSLRPEDTALYYCAAYIRPDTYLSRDYRKYDYWGQGTLTVSSA
701	EVQLVESGGGVVQPGGLRLSCAASGFTFSSYPMGWFHQAPGKGREFVSSITGS GG STYYADSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCAAYIRPDTYLSRDYR KYDYWGQGTLTVSSGGGGSGGGSEVQLVESGGGVVQPGNSRLSCAASGFTFSS FGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSL RPEDTALYYCTIGGSLSRSSQGTLVKVSSGGGGSGGGSEVQLVESGGGVVQPGGSL RLSCAASGFTFSSYPMGWFHQAPGKGREFVSSITGSGGSTYYADSVKGRFTISRDN AKNTLYLQMNSLRPEDTALYYCAAYIRPDTYLSRDYRKYDYWGQGTLVKVSSA
702	EVQLVESGGGVVQPGGLRLSCAASGFTFSSYPMGWFHQAPGKGREFVSSITGS GG STYYADSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCAAYIRPDTYLSRDYR KYDYWGQGTLTVSSGGGGSGGGSEVQLVESGGGVVQPGNSRLSCAASGFTFSS FGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSL RPEDTALYYCTIGGSLSRSSQGTLVKVSSGGGGSGGGSEVQLVESGGGVVQPGGSL RLSCAASGFTFSSYPMGWFHQAPGKGREFVSSITGSGGSTYYADSVKGRFTISRDN AKNTLYLQMNSLRPEDTALYYCAAYIRPDTYLSRDYRKYDYWGQGTLVQVSSA
703	EVQLVESGGGVVQPGGLRLSCAASGFTFSSYPMGWFHQAPGKGREFVSSITGS GG STYYADSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCAAYIRPDTYLSRDYR KYDYWGQGTLTVSSGGGGSGGGSEVQLVESGGGVVQPGNSRLSCAASGFTFSS FGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSL RPEDTALYYCTIGGSLSRSSQGTLVKVSSGGGGSGGGSEVQLVESGGGVVQPGGSL RLSCAASGFTFSSYPMGWFHQAPGKGREFVSSITGSGGSTYYADSVKGRFTISRDN AKNTLYLQMNSLRPEDTALYYCAAYIRPDTYLSRDYRKYDYWGQGTLVQVSSA
704	EVQLVESGGGVVQPGGLRLSCAASGFTFSSYPMGWFHQAPGKGREFVSSITGS GG STYYADSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCAAYIRPDTYLSRDYR KYDYWGQGTLTVSSGGGGSGGGSEVQLVESGGGVVQPGNSRLSCAASGFTFSS FGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSL RPEDTALYYCTIGGSLSRSSQGTLVKVSSGGGGSGGGSEVQLVESGGGVVQPGGSL RLSCAASGFTFSSYPMGWFHQAPGKGREFVSSITGSGGSTYYADSVKGRFTISRDN AKNTLYLQMNSLRPEDTALYYCAAYIRPDTYLSRDYRKYDYWGQGTLVKVSSA
705	EVQLVESGGGVVQPGGLRLSCAASGFTFSSYPMGWFHQAPGKGREFVSSITGS GG STYYADSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCAAYIRPDTYLSRDYR KYDYWGQGTLTVSSGGGGSGGGSEVQLVESGGGVVQPGNSRLSCAASGFTFSS FGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSL RPEDTALYYCTIGGSLSRSSQGTLVKVSSGGGGSGGGSEVQLVESGGGVVQPGGSL RLSCAASGFTFSSYPMGWFHQAPGKGREFVSSITGSGGSTYYADSVKGRFTISRDN AKNTLYLQMNSLRPEDTALYYCAAYIRPDTYLSRDYRKYDYWGQGTLVQVSSA

Figure 29 (continued)

SEQ ID	Sequence
706	EVQLVESGGGVVQPGNSLRLSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSG SDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLV KVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMSWVRQAPG KGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTI GGSLSRSSQGTLTVSSGGGGSGGGSEVQLVESGGGVVQPGGSLRLSCAASGFTFS SYPMGWFRQAPGKGREFVSSITGSGGSTYYADSVKGRFTISRDNAKNTLYLQMNS LRPEDTALYYCAAYIRPDTYLSRDYRKYDYWGQGTLTVSSA
707	EVQLVESGGGVVQPGNSLRLSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSG SDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLV KVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMSWVRQAPG KGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTI GGSLSRSSQGTLTVSSGGGGSGGGSEVQLVESGGGVVQPGGSLRLSCAASGFTFS SYPMGWFRQAPGKGREFVSSITGSGGSTYYADSVKGRFTISRDNAKNTLYLQMNS LRPEDTALYYCAAYIRPDTYLSRDYRKYDYWGQGTLVKVSSA
708	EVQLVESGGGVVQPGNSLRLSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSG SDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLV KVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMSWVRQAPG KGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTI GGSLSRSSQGTLTVSSGGGGSGGGSEVQLVESGGGVVQPGGSLRLSCAASGFTFS SYPMGWFRQAPGKGREFVSSITGSGGSTYYADSVKGRFTISRDNAKNTLYLQMNS LRPEDTALYYCAAYIRPDTYLSRDYRKYDYWGQGTLVQVSSA
709	EVQLVESGGGVVQPGNSLRLSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSG SDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLV KVSSGGGGSGGGSEVQLVESGGGVVQPGNSLRLSCAASGFTFSSFGMSWVRQAPG KGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTI GGSLSRSSQGTLTVSSGGGGSGGGSEVQLVESGGGVVQPGGSLRLSCAASGFTFS SYPMGWFRQAPGKGREFVSSITGSGGSTYYADSVKGRFTISRDNAKNTLYLQMNS LRPEDTALYYCAAYIRPDTYLSRDYRKYDYWGQGTLVQVSSA
710	EVQLVESGGGVVQPGNSLRLSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSG SDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLV KVSSGGGGSGGGSEVQLVESGGGVVQPGNSLRLSCAASGFTFSSFGMSWVRQAPG KGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTI GGSLSRSSQGTLTVSSGGGGSGGGSEVQLVESGGGVVQPGGSLRLSCAASGFTFS SYPMGWFRQAPGKGREFVSSITGSGGSTYYADSVKGRFTISRDNAKNTLYLQMNS LRPEDTALYYCAAYIRPDTYLSRDYRKYDYWGQGTLVKVSSA
711	EVQLVESGGGVVQPGNSLRLSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSG SDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLV KVSSGGGGSGGGSEVQLVESGGGVVQPGNSLRLSCAASGFTFSSFGMSWVRQAPG KGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTI GGSLSRSSQGTLTVSSGGGGSGGGSEVQLVESGGGVVQPGGSLRLSCAASGFTFS SYPMGWFRQAPGKGREFVSSITGSGGSTYYADSVKGRFTISRDNAKNTLYLQMNS LRPEDTALYYCAAYIRPDTYLSRDYRKYDYWGQGTLVQVSSA

Figure 29 (continued)

SEQ ID	Sequence
712	EVQLVESGGGVVQPGNSLRLSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSG SDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLV KVSSGGGGSGGGSEVQLVESGGGVQPGNSLRLSCAASGFTFSSFGMSWVRQAPG KGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTI GGSLSRSSQGTLVKVSSGGGGSGGGSEVQLVESGGGVQPGGSLRLSCAASGFTFS SYPMGWFRQAPGKGREFVSSITGSGGSTYYADSVKGRFTISRDNAKNTLYLQMNS LRPEDTALYYCAAYIRPDTYLSRDYRKYDYWGQGTLVTVSSA
713	EVQLVESGGGVVQPGNSLRLSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSG SDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLV KVSSGGGGSGGGSEVQLVESGGGVQPGNSLRLSCAASGFTFSSFGMSWVRQAPG KGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTI GGSLSRSSQGTLVKVSSGGGGSGGGSEVQLVESGGGVQPGGSLRLSCAASGFTFS SYPMGWFRQAPGKGREFVSSITGSGGSTYYADSVKGRFTISRDNAKNTLYLQMNS LRPEDTALYYCAAYIRPDTYLSRDYRKYDYWGQGTLVKVSSA
714	EVQLVESGGGVVQPGNSLRLSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSG SDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLV KVSSGGGGSGGGSEVQLVESGGGVQPGNSLRLSCAASGFTFSSFGMSWVRQAPG KGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTI GGSLSRSSQGTLVKVSSGGGGSGGGSEVQLVESGGGVQPGGSLRLSCAASGFTFS SYPMGWFRQAPGKGREFVSSITGSGGSTYYADSVKGRFTISRDNAKNTLYLQMNS LRPEDTALYYCAAYIRPDTYLSRDYRKYDYWGQGTLVQVSSA
715	EVQLVESGGGVVQPGNSLRLSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSG SDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLV KVSSGGGGSGGGSEVQLVESGGGVQPGNSLRLSCAASGFTFSSFGMSWVRQAPG KGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTI GGSLSRSSQGTLVKVSSGGGGSGGGSEVQLVESGGGVQPGGSLRLSCAASGFTFS SYPMGWFRQAPGKGREFVSSITGSGGSTYYADSVKGRFTISRDNAKNTLYLQMNS LRPEDTALYYCAAYIRPDTYLSRDYRKYDYWGQGTLVQVSSA
716	EVQLVESGGGVVQPGNSLRLSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSG SDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLV KVSSGGGGSGGGSEVQLVESGGGVQPGNSLRLSCAASGFTFSSFGMSWVRQAPG KGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTI GGSLSRSSQGTLVKVSSGGGGSGGGSEVQLVESGGGVQPGGSLRLSCAASGFTFS SYPMGWFRQAPGKGREFVSSITGSGGSTYYADSVKGRFTISRDNAKNTLYLQMNS LRPEDTALYYCAAYIRPDTYLSRDYRKYDYWGQGTLVKVSSA
717	EVQLVESGGGVVQPGNSLRLSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSG SDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLV KVSSGGGGSGGGSEVQLVESGGGVQPGNSLRLSCAASGFTFSSFGMSWVRQAPG KGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTI GGSLSRSSQGTLVKVSSGGGGSGGGSEVQLVESGGGVQPGGSLRLSCAASGFTFS SYPMGWFRQAPGKGREFVSSITGSGGSTYYADSVKGRFTISRDNAKNTLYLQMNS LRPEDTALYYCAAYIRPDTYLSRDYRKYDYWGQGTLVQVSSA

Figure 29 (continued)

SEQ ID	Sequence
718	EVQLVESGGGVVQPGNSLRLSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSG SDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLV QVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMSWVRQAPG KGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTI GGSLSRSSQGTLTVSSGGGGSGGGSEVQLVESGGGVVQPGGSLRLSCAASGFTFS SYPMGWFRQAPGKGREFVSSITGSGGSTYYADSVKGRFTISRDNAKNTLYLQMNS LRPEDTALYYCAAYIRPDTYLSRDYRKYDYWGQGTLTVSSA
719	EVQLVESGGGVVQPGNSLRLSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSG SDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLV QVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMSWVRQAPG KGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTI GGSLSRSSQGTLTVSSGGGGSGGGSEVQLVESGGGVVQPGGSLRLSCAASGFTFS SYPMGWFRQAPGKGREFVSSITGSGGSTYYADSVKGRFTISRDNAKNTLYLQMNS LRPEDTALYYCAAYIRPDTYLSRDYRKYDYWGQGTLVKVSSA
720	EVQLVESGGGVVQPGNSLRLSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSG SDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLV QVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMSWVRQAPG KGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTI GGSLSRSSQGTLTVSSGGGGSGGGSEVQLVESGGGVVQPGGSLRLSCAASGFTFS SYPMGWFRQAPGKGREFVSSITGSGGSTYYADSVKGRFTISRDNAKNTLYLQMNS LRPEDTALYYCAAYIRPDTYLSRDYRKYDYWGQGTLVQVSSA
721	EVQLVESGGGVVQPGNSLRLSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSG SDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLV QVSSGGGGSGGGSEVQLVESGGGVVQPGNSLRLSCAASGFTFSSFGMSWVRQAPG KGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTI GGSLSRSSQGTLTVSSGGGGSGGGSEVQLVESGGGVVQPGGSLRLSCAASGFTFS SYPMGWFRQAPGKGREFVSSITGSGGSTYYADSVKGRFTISRDNAKNTLYLQMNS LRPEDTALYYCAAYIRPDTYLSRDYRKYDYWGQGTLVQVSSA
722	EVQLVESGGGVVQPGNSLRLSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSG SDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLV QVSSGGGGSGGGSEVQLVESGGGVVQPGNSLRLSCAASGFTFSSFGMSWVRQAPG KGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTI GGSLSRSSQGTLTVSSGGGGSGGGSEVQLVESGGGVVQPGGSLRLSCAASGFTFS SYPMGWFRQAPGKGREFVSSITGSGGSTYYADSVKGRFTISRDNAKNTLYLQMNS LRPEDTALYYCAAYIRPDTYLSRDYRKYDYWGQGTLVKVSSA
723	EVQLVESGGGVVQPGNSLRLSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSG SDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLV QVSSGGGGSGGGSEVQLVESGGGVVQPGNSLRLSCAASGFTFSSFGMSWVRQAPG KGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTI GGSLSRSSQGTLTVSSGGGGSGGGSEVQLVESGGGVVQPGGSLRLSCAASGFTFS SYPMGWFRQAPGKGREFVSSITGSGGSTYYADSVKGRFTISRDNAKNTLYLQMNS LRPEDTALYYCAAYIRPDTYLSRDYRKYDYWGQGTLVQVSSA

Figure 29 (continued)

SEQ ID	Sequence
724	EVQLVESGGGVVQPGNSRLSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLVQVSSGGGGSGGGSEVQLVESGGGVQPGNSRLSCAASGFTFSSFGMSWVRQAPKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLVQVSSGGGGSGGGSEVQLVESGGGVQPGNSRLSCAASGFTFSSFGMSWVRQAPKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLVQVSSGGGGSGGGSEVQLVESGGGVQPGNSRLSCAASGFTFSYPMGWFRQAPGKGREFVSSITGSGGSTYYADSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCAAYIRPDTYLSRDYRKYDYWGQGTLTVSSA
725	EVQLVESGGGVVQPGNSRLSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLVQVSSGGGGSGGGSEVQLVESGGGVQPGNSRLSCAASGFTFSSFGMSWVRQAPKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLVQVSSGGGGSGGGSEVQLVESGGGVQPGNSRLSCAASGFTFSYPMGWFRQAPGKGREFVSSITGSGGSTYYADSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCAAYIRPDTYLSRDYRKYDYWGQGTLVSSA
726	EVQLVESGGGVVQPGNSRLSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLVQVSSGGGGSGGGSEVQLVESGGGVQPGNSRLSCAASGFTFSSFGMSWVRQAPKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLVQVSSGGGGSGGGSEVQLVESGGGVQPGNSRLSCAASGFTFSYPMGWFRQAPGKGREFVSSITGSGGSTYYADSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCAAYIRPDTYLSRDYRKYDYWGQGTLVQVSSA
727	EVQLVESGGGVVQPGNSRLSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLVQVSSGGGGSGGGSEVQLVESGGGVQPGNSRLSCAASGFTFSSFGMSWVRQAPKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLVQVSSGGGGSGGGSEVQLVESGGGVQPGNSRLSCAASGFTFSYPMGWFRQAPGKGREFVSSITGSGGSTYYADSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCAAYIRPDTYLSRDYRKYDYWGQGTLVQVSSA
728	EVQLVESGGGVVQPGNSRLSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLVQVSSGGGGSGGGSEVQLVESGGGVQPGNSRLSCAASGFTFSSFGMSWVRQAPKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLVQVSSGGGGSGGGSEVQLVESGGGVQPGNSRLSCAASGFTFSYPMGWFRQAPGKGREFVSSITGSGGSTYYADSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCAAYIRPDTYLSRDYRKYDYWGQGTLVQVSSA
729	EVQLVESGGGVVQPGNSRLSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLVQVSSGGGGSGGGSEVQLVESGGGVQPGNSRLSCAASGFTFSSFGMSWVRQAPKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLVQVSSGGGGSGGGSEVQLVESGGGVQPGNSRLSCAASGFTFSYPMGWFRQAPGKGREFVSSITGSGGSTYYADSVKGRFTISRDNAKNTLYLQMNSLRPEDTALYYCAAYIRPDTYLSRDYRKYDYWGQGTLVQVSSA

Figure 30

SEQ ID	Sequence
730	EVQLLESGGGVVQPGGSLRLSCVHSGPTFRDTMGWFRQAPGKGREFVAAVT WNSGRINYADSVKGRFTISRDNSKNTALLQMNSLRPEDTAVYYCAAHRFVVG GNRVEDWRYWGQGTLTVSSGGGGSGGSEVQLVESGGGLVQPGNSLR LSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGR FTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSRSSQGTLTVSSG GGGSGGGSEVQLLESGGGVVQPGGSLRLSCAASGRTFNNYNMGWFRQAPG KGREFVAAVSRSRVSTYYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALY YCAAAYRGTAINVRRSYSSWGQGTLTVSSA
731	EVQLLESGGGVVQPGGSLRLSCVHSGPTFRDTMGWFRQAPGKGREFVAAVT WNSGRINYADSVKGRFTISRDNSKNTALLQMNSLRPEDTAVYYCAAHRFVVG GNRVEDWRYWGQGTLTVSSGGGGSGGSEVQLVESGGGLVQPGNSLR LSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGR FTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSRSSQGTLTVSSG GGGSGGGSEVQLLESGGGVVQPGGSLRLSCAASGRTFNNYNMGWFRQAPG KGREFVAAVSRSRVSTYYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALY YCAAAYRGTAINVRRSYSSWGQGTLVKVSSA
732	EVQLLESGGGVVQPGGSLRLSCVHSGPTFRDTMGWFRQAPGKGREFVAAVT WNSGRINYADSVKGRFTISRDNSKNTALLQMNSLRPEDTAVYYCAAHRFVVG GNRVEDWRYWGQGTLTVSSGGGGSGGSEVQLVESGGGLVQPGNSLR LSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGR FTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSRSSQGTLTVSSG GGGSGGGSEVQLLESGGGVVQPGGSLRLSCAASGRTFNNYNMGWFRQAPG KGREFVAAVSRSRVSTYYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALY YCAAAYRGTAINVRRSYSSWGQGTLTVSSA
733	EVQLLESGGGVVQPGGSLRLSCVHSGPTFRDTMGWFRQAPGKGREFVAAVT WNSGRINYADSVKGRFTISRDNSKNTALLQMNSLRPEDTAVYYCAAHRFVVG GNRVEDWRYWGQGTLTVSSGGGGSGGSEVQLVESGGGVVQPGNSLR LSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGR FTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLTVSSG GGGSGGGSEVQLLESGGGVVQPGGSLRLSCAASGRTFNNYNMGWFRQAPG KGREFVAAVSRSRVSTYYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALY YCAAAYRGTAINVRRSYSSWGQGTLTVSSA
734	EVQLLESGGGVVQPGGSLRLSCVHSGPTFRDTMGWFRQAPGKGREFVAAVT WNSGRINYADSVKGRFTISRDNSKNTALLQMNSLRPEDTAVYYCAAHRFVVG GNRVEDWRYWGQGTLTVSSGGGGSGGSEVQLVESGGGVVQPGNSLR LSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGR FTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLTVSSG GGGSGGGSEVQLLESGGGVVQPGGSLRLSCAASGRTFNNYNMGWFRQAPG KGREFVAAVSRSRVSTYYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALY YCAAAYRGTAINVRRSYSSWGQGTLVKVSSA

Figure 30 (continued)

SEQ ID	Sequence
735	EVQLLESGGVVQPGGSLRLSCVHSGPTFRDTMGWFRQAPGKGREFVAAVT WNSGRINYADSVKGRFTISRDNSKNTALLQMNSLRPEDTAVYYCAAHRFVVG GNRVEDWRYWGQGTLTVSSGGGGGGSEVQLVESGGGVVQPGNSLR LSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGR FTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGSLRSQQGTLTVSSG GGGSGGGSEVQLLESGGGVVQPGGSLRLSCAASGRTFNNYNMGWFRQAPG KGREFVAAVSRSVGSTYYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALY YCAAAYRGTAINVRRSYSSWGQGTLTVSSA
736	EVQLLESGGVVQPGGSLRLSCVHSGPTFRDTMGWFRQAPGKGREFVAAVT WNSGRINYADSVKGRFTISRDNSKNTALLQMNSLRPEDTAVYYCAAHRFVVG GNRVEDWRYWGQGTLTVSSGGGGGGSEVQLVESGGGVVQPGNSLR LSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGR FTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGSLRSQQGTLVKVSSG GGGSGGGSEVQLLESGGGVVQPGGSLRLSCAASGRTFNNYNMGWFRQAPG KGREFVAAVSRSVGSTYYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALY YCAAAYRGTAINVRRSYSSWGQGTLTVSSA
737	EVQLLESGGVVQPGGSLRLSCVHSGPTFRDTMGWFRQAPGKGREFVAAVT WNSGRINYADSVKGRFTISRDNSKNTALLQMNSLRPEDTAVYYCAAHRFVVG GNRVEDWRYWGQGTLTVSSGGGGGGSEVQLVESGGGVVQPGNSLR LSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGR FTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGSLRSQQGTLVKVSSG GGGSGGGSEVQLLESGGGVVQPGGSLRLSCAASGRTFNNYNMGWFRQAPG KGREFVAAVSRSVGSTYYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALY YCAAAYRGTAINVRRSYSSWGQGTLVKVSSA
738	EVQLLESGGVVQPGGSLRLSCVHSGPTFRDTMGWFRQAPGKGREFVAAVT WNSGRINYADSVKGRFTISRDNSKNTALLQMNSLRPEDTAVYYCAAHRFVVG GNRVEDWRYWGQGTLTVSSGGGGGGSEVQLVESGGGVVQPGNSLR LSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGR FTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGSLRSQQGTLVKVSSG GGGSGGGSEVQLLESGGGVVQPGGSLRLSCAASGRTFNNYNMGWFRQAPG KGREFVAAVSRSVGSTYYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALY YCAAAYRGTAINVRRSYSSWGQGTLVKVSSA
739	EVQLLESGGVVQPGGSLRLSCVHSGPTFRDTMGWFRQAPGKGREFVAAVT WNSGRINYADSVKGRFTISRDNSKNTALLQMNSLRPEDTAVYYCAAHRFVVG GNRVEDWRYWGQGTLTVSSGGGGGGSEVQLVESGGGVVQPGNSLR LSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGR FTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGSLRSQQGTLVQVSSG GGGSGGGSEVQLLESGGGVVQPGGSLRLSCAASGRTFNNYNMGWFRQAPG KGREFVAAVSRSVGSTYYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALY YCAAAYRGTAINVRRSYSSWGQGTLTVSSA

Figure 30 (continued)

SEQ ID	Sequence
740	EVQLLESGGGVVQPGGSLRLSCVHSGPTFRDTMGWFRQAPGKGREFVAAVT WNSGRINYADSVKGRFTISRDNSKNTALLQMNSLRPEDTAVYYCAAHRFVVG GNRVEDWRYWGQGTLTVSSGGGGSGGSEVQLVESGGGVQPGNSLR LSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGR FTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGSLRSSQGTLVQVSSG GGGSGGGSEVQLLESGGGVVQPGGSLRLSCAASGRTFNNYNMGWFRQAPG KGREFVAAVSRSVGSTYYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALY YCAAAYRGTAINVRRSYSSWGQGTLVKVSSA
741	EVQLLESGGGVVQPGGSLRLSCVHSGPTFRDTMGWFRQAPGKGREFVAAVT WNSGRINYADSVKGRFTISRDNSKNTALLQMNSLRPEDTAVYYCAAHRFVVG GNRVEDWRYWGQGTLTVSSGGGGSGGSEVQLVESGGGVQPGNSLR LSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGR FTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGSLRSSQGTLVQVSSG GGGSGGGSEVQLLESGGGVVQPGGSLRLSCAASGRTFNNYNMGWFRQAPG KGREFVAAVSRSVGSTYYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALY YCAAAYRGTAINVRRSYSSWGQGTLVTVSSA
742	EVQLLESGGGVVQPGGSLRLSCVHSGPTFRDTMGWFRQAPGKGREFVAAVT WNSGRINYADSVKGRFTISRDNSKNTALLQMNSLRPEDTAVYYCAAHRFVVG GNRVEDWRYWGQGTLVKVSSGGGGSGGSEVQLVESGGGLVQPGNSLR LSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGR FTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLRSSQGTLVTVSSG GGGSGGGSEVQLLESGGGVVQPGGSLRLSCAASGRTFNNYNMGWFRQAPG KGREFVAAVSRSVGSTYYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALY YCAAAYRGTAINVRRSYSSWGQGTLVTVSSA
743	EVQLLESGGGVVQPGGSLRLSCVHSGPTFRDTMGWFRQAPGKGREFVAAVT WNSGRINYADSVKGRFTISRDNSKNTALLQMNSLRPEDTAVYYCAAHRFVVG GNRVEDWRYWGQGTLVKVSSGGGGSGGSEVQLVESGGGLVQPGNSLR LSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGR FTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLRSSQGTLVTVSSG GGGSGGGSEVQLLESGGGVVQPGGSLRLSCAASGRTFNNYNMGWFRQAPG KGREFVAAVSRSVGSTYYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALY YCAAAYRGTAINVRRSYSSWGQGTLVKVSSA
744	EVQLLESGGGVVQPGGSLRLSCVHSGPTFRDTMGWFRQAPGKGREFVAAVT WNSGRINYADSVKGRFTISRDNSKNTALLQMNSLRPEDTAVYYCAAHRFVVG GNRVEDWRYWGQGTLVKVSSGGGGSGGSEVQLVESGGGLVQPGNSLR LSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGR FTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLRSSQGTLVTVSSG GGGSGGGSEVQLLESGGGVVQPGGSLRLSCAASGRTFNNYNMGWFRQAPG KGREFVAAVSRSVGSTYYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALY YCAAAYRGTAINVRRSYSSWGQGTLVTVSSA

Figure 30 (continued)

SEQ ID	Sequence
745	EVQLLESGGGVVQPGGSLRLSCVHSGPTFRDTMGWFRQAPKGREFVAAVT WNSGRINYADSVKGRFTISRDNSKNTALLQMNSLRPEDTAVYYCAAHRFVVG GNRVEDWRYWGQGTLVKVSSGGGGSGGGSEVQLVESGGGVVQPGNSLR LSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGR FTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLTVSSG GGGSGGGSEVQLLESGGGVVQPGGSLRLSCAASGRTFNNYNMGWFRQAPG KGREFVAAVSRSVSTYYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALY YCAAAYRGTAINVRRSYSSWGQGTLTVSSA
746	EVQLLESGGGVVQPGGSLRLSCVHSGPTFRDTMGWFRQAPKGREFVAAVT WNSGRINYADSVKGRFTISRDNSKNTALLQMNSLRPEDTAVYYCAAHRFVVG GNRVEDWRYWGQGTLVKVSSGGGGSGGGSEVQLVESGGGVVQPGNSLR LSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGR FTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLTVSSG GGGSGGGSEVQLLESGGGVVQPGGSLRLSCAASGRTFNNYNMGWFRQAPG KGREFVAAVSRSVSTYYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALY YCAAAYRGTAINVRRSYSSWGQGTLVKVSSA
747	EVQLLESGGGVVQPGGSLRLSCVHSGPTFRDTMGWFRQAPKGREFVAAVT WNSGRINYADSVKGRFTISRDNSKNTALLQMNSLRPEDTAVYYCAAHRFVVG GNRVEDWRYWGQGTLVKVSSGGGGSGGGSEVQLVESGGGVVQPGNSLR LSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGR FTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLTVSSG GGGSGGGSEVQLLESGGGVVQPGGSLRLSCAASGRTFNNYNMGWFRQAPG KGREFVAAVSRSVSTYYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALY YCAAAYRGTAINVRRSYSSWGQGTLTVSSA
748	EVQLLESGGGVVQPGGSLRLSCVHSGPTFRDTMGWFRQAPKGREFVAAVT WNSGRINYADSVKGRFTISRDNSKNTALLQMNSLRPEDTAVYYCAAHRFVVG GNRVEDWRYWGQGTLVKVSSGGGGSGGGSEVQLVESGGGVVQPGNSLR LSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGR FTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLVKVSSG GGGSGGGSEVQLLESGGGVVQPGGSLRLSCAASGRTFNNYNMGWFRQAPG KGREFVAAVSRSVSTYYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALY YCAAAYRGTAINVRRSYSSWGQGTLTVSSA
749	EVQLLESGGGVVQPGGSLRLSCVHSGPTFRDTMGWFRQAPKGREFVAAVT WNSGRINYADSVKGRFTISRDNSKNTALLQMNSLRPEDTAVYYCAAHRFVVG GNRVEDWRYWGQGTLVKVSSGGGGSGGGSEVQLVESGGGVVQPGNSLR LSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGR FTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLVKVSSG GGGSGGGSEVQLLESGGGVVQPGGSLRLSCAASGRTFNNYNMGWFRQAPG KGREFVAAVSRSVSTYYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALY YCAAAYRGTAINVRRSYSSWGQGTLVKVSSA

Figure 30 (continued)

SEQ ID	Sequence
750	EVQLLESGGVVQPGGSLRLSCVHSGPTFRDTMGWFRQAPKGREFVAAVT WNSGRINYADSVKGRFTISRDNSKNTALLQMNSLRPEDTAVYYCAAHRFVVG GNRVEDWRYWGQGTLVKVSSGGGGSGGGSEVQLVESGGGVVQPGNSLR LSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGR FTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGSLRSSQGTLVKVSSG GGGSGGGSEVQLLESGGGVVQPGGSLRLSCAASGRTFNNYNMGWFRQAPG KGREFVAAVSRSRVSTYYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALY YCAAAYRGTAINVRRSYSSWGQGTLTVSSA
751	EVQLLESGGVVQPGGSLRLSCVHSGPTFRDTMGWFRQAPKGREFVAAVT WNSGRINYADSVKGRFTISRDNSKNTALLQMNSLRPEDTAVYYCAAHRFVVG GNRVEDWRYWGQGTLVKVSSGGGGSGGGSEVQLVESGGGVVQPGNSLR LSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGR FTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGSLRSSQGTLVQVSSG GGGSGGGSEVQLLESGGGVVQPGGSLRLSCAASGRTFNNYNMGWFRQAPG KGREFVAAVSRSRVSTYYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALY YCAAAYRGTAINVRRSYSSWGQGTLTVSSA
752	EVQLLESGGVVQPGGSLRLSCVHSGPTFRDTMGWFRQAPKGREFVAAVT WNSGRINYADSVKGRFTISRDNSKNTALLQMNSLRPEDTAVYYCAAHRFVVG GNRVEDWRYWGQGTLVKVSSGGGGSGGGSEVQLVESGGGVVQPGNSLR LSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGR FTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGSLRSSQGTLVQVSSG GGGSGGGSEVQLLESGGGVVQPGGSLRLSCAASGRTFNNYNMGWFRQAPG KGREFVAAVSRSRVSTYYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALY YCAAAYRGTAINVRRSYSSWGQGTLVKVSSA
753	EVQLLESGGVVQPGGSLRLSCVHSGPTFRDTMGWFRQAPKGREFVAAVT WNSGRINYADSVKGRFTISRDNSKNTALLQMNSLRPEDTAVYYCAAHRFVVG GNRVEDWRYWGQGTLVKVSSGGGGSGGGSEVQLVESGGGVVQPGNSLR LSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGR FTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGSLRSSQGTLVQVSSG GGGSGGGSEVQLLESGGGVVQPGGSLRLSCAASGRTFNNYNMGWFRQAPG KGREFVAAVSRSRVSTYYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALY YCAAAYRGTAINVRRSYSSWGQGTLTVSSA
754	EVQLLESGGVVQPGGSLRLSCVHSGPTFRDTMGWFRQAPKGREFVAAVT WNSGRINYADSVKGRFTISRDNSKNTALLQMNSLRPEDTAVYYCAAHRFVVG GNRVEDWRYWGQGTLVKVSSGGGGSGGGSEVQLVESGGGLVQPGNSLR LSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGR FTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLRSSQGTLVTVSSG GGGSGGGSEVQLLESGGGVVQPGGSLRLSCAASGRTFNNYNMGWFRQAPG KGREFVAAVSRSRVSTYYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALY YCAAAYRGTAINVRRSYSSWGQGTLTVSSA

Figure 30 (continued)

SEQ ID	Sequence
755	EVQLLESGGGVVQPGGSLRLSCVHSGPTFRDTMGWFRQAPGKGREFVAAVT WNSGRINYADSVKGRFTISRDN SKNT ALLQMNSLRPEDTAVYYCAAHRFVVG GNRVEDWRYWGQGTLVQVSSGGGGSGGGSEVQLVESGGGLVQPGNSLR LSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGR FTISRDN AKTTLYLQMNSLRPEDTAVYYCTIGGSLSRSSQGTLTVSSG GGGSGGGSEVQLLESGGGVVQPGGSLRLSCAASGRTFNNYNMGWFRQAPG KGREFVAAVSRSVSTYYADSVKGRFTISRDN SKNT VYLQMNSLRPEDTALY YCAAAYRGTAINVRRSYSSWQGQGTLVKVSSA
756	EVQLLESGGGVVQPGGSLRLSCVHSGPTFRDTMGWFRQAPGKGREFVAAVT WNSGRINYADSVKGRFTISRDN SKNT ALLQMNSLRPEDTAVYYCAAHRFVVG GNRVEDWRYWGQGTLVQVSSGGGGSGGGSEVQLVESGGGLVQPGNSLR LSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGR FTISRDN AKTTLYLQMNSLRPEDTAVYYCTIGGSLSRSSQGTLTVSSG GGGSGGGSEVQLLESGGGVVQPGGSLRLSCAASGRTFNNYNMGWFRQAPG KGREFVAAVSRSVSTYYADSVKGRFTISRDN SKNT VYLQMNSLRPEDTALY YCAAAYRGTAINVRRSYSSWQGQGTLVKVSSA
757	EVQLLESGGGVVQPGGSLRLSCVHSGPTFRDTMGWFRQAPGKGREFVAAVT WNSGRINYADSVKGRFTISRDN SKNT ALLQMNSLRPEDTAVYYCAAHRFVVG GNRVEDWRYWGQGTLVQVSSGGGGSGGGSEVQLVESGGGVVQPGNSLR LSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGR FTISRDN AKTTLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLTVSSG GGGSGGGSEVQLLESGGGVVQPGGSLRLSCAASGRTFNNYNMGWFRQAPG KGREFVAAVSRSVSTYYADSVKGRFTISRDN SKNT VYLQMNSLRPEDTALY YCAAAYRGTAINVRRSYSSWQGQGTLVKVSSA
758	EVQLLESGGGVVQPGGSLRLSCVHSGPTFRDTMGWFRQAPGKGREFVAAVT WNSGRINYADSVKGRFTISRDN SKNT ALLQMNSLRPEDTAVYYCAAHRFVVG GNRVEDWRYWGQGTLVQVSSGGGGSGGGSEVQLVESGGGVVQPGNSLR LSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGR FTISRDN AKTTLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLTVSSG GGGSGGGSEVQLLESGGGVVQPGGSLRLSCAASGRTFNNYNMGWFRQAPG KGREFVAAVSRSVSTYYADSVKGRFTISRDN SKNT VYLQMNSLRPEDTALY YCAAAYRGTAINVRRSYSSWQGQGTLVKVSSA
759	EVQLLESGGGVVQPGGSLRLSCVHSGPTFRDTMGWFRQAPGKGREFVAAVT WNSGRINYADSVKGRFTISRDN SKNT ALLQMNSLRPEDTAVYYCAAHRFVVG GNRVEDWRYWGQGTLVQVSSGGGGSGGGSEVQLVESGGGVVQPGNSLR LSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGR FTISRDN AKTTLYLQMNSLRPEDTALYYCTIGGSLSRSSQGTLTVSSG GGGSGGGSEVQLLESGGGVVQPGGSLRLSCAASGRTFNNYNMGWFRQAPG KGREFVAAVSRSVSTYYADSVKGRFTISRDN SKNT VYLQMNSLRPEDTALY YCAAAYRGTAINVRRSYSSWQGQGTLVKVSSA

Figure 30 (continued)

SEQ ID	Sequence
760	EVQLLESGGGVVQPGGSLRLSCVHSGPTFRDTMGWFRQAPGKGREFVAAVT WNSGRINYADSVKGRFTISRDNSKNTALLQMNSLRPEDTAVYYCAAHRFVVG GNRVEDWRYWGQGTLVQVSSGGGGSGGGSEVQLVESGGGVVQPGNSLR LSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGR FTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGSLRSSQGTLVKVSSG GGGSGGGSEVQLLESGGGVVQPGGSLRLSCAASGRTFNNYNMGWFRQAPG KGREFVAAVSRSVGSTYYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALY YCAAAYRGTAINVRRSYSSWGQGTLTVSSA
761	EVQLLESGGGVVQPGGSLRLSCVHSGPTFRDTMGWFRQAPGKGREFVAAVT WNSGRINYADSVKGRFTISRDNSKNTALLQMNSLRPEDTAVYYCAAHRFVVG GNRVEDWRYWGQGTLVQVSSGGGGSGGGSEVQLVESGGGVVQPGNSLR LSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGR FTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGSLRSSQGTLVKVSSG GGGSGGGSEVQLLESGGGVVQPGGSLRLSCAASGRTFNNYNMGWFRQAPG KGREFVAAVSRSVGSTYYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALY YCAAAYRGTAINVRRSYSSWGQGTLVKVSSA
762	EVQLLESGGGVVQPGGSLRLSCVHSGPTFRDTMGWFRQAPGKGREFVAAVT WNSGRINYADSVKGRFTISRDNSKNTALLQMNSLRPEDTAVYYCAAHRFVVG GNRVEDWRYWGQGTLVQVSSGGGGSGGGSEVQLVESGGGVVQPGNSLR LSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGR FTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGSLRSSQGTLVKVSSG GGGSGGGSEVQLLESGGGVVQPGGSLRLSCAASGRTFNNYNMGWFRQAPG KGREFVAAVSRSVGSTYYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALY YCAAAYRGTAINVRRSYSSWGQGTLVKVSSA
763	EVQLLESGGGVVQPGGSLRLSCVHSGPTFRDTMGWFRQAPGKGREFVAAVT WNSGRINYADSVKGRFTISRDNSKNTALLQMNSLRPEDTAVYYCAAHRFVVG GNRVEDWRYWGQGTLVQVSSGGGGSGGGSEVQLVESGGGVVQPGNSLR LSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGR FTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGSLRSSQGTLVQVSSG GGGSGGGSEVQLLESGGGVVQPGGSLRLSCAASGRTFNNYNMGWFRQAPG KGREFVAAVSRSVGSTYYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALY YCAAAYRGTAINVRRSYSSWGQGTLVKVSSA
764	EVQLLESGGGVVQPGGSLRLSCVHSGPTFRDTMGWFRQAPGKGREFVAAVT WNSGRINYADSVKGRFTISRDNSKNTALLQMNSLRPEDTAVYYCAAHRFVVG GNRVEDWRYWGQGTLVQVSSGGGGSGGGSEVQLVESGGGVVQPGNSLR LSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYADSVKGR FTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGSLRSSQGTLVQVSSG GGGSGGGSEVQLLESGGGVVQPGGSLRLSCAASGRTFNNYNMGWFRQAPG KGREFVAAVSRSVGSTYYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALY YCAAAYRGTAINVRRSYSSWGQGTLVKVSSA

Figure 30 (continued)

SEQ ID	Sequence
765	EVQLLESGGVVQPGGSLRLSCVHSGPTFRDTMGWFRQAPGKGREFVAAVT WNSGRINYADSVKGRFTISRDNSKNTALLQMNSLRPEDTAVYYCAAHRFVVG GNRVEDWRYWGQGTLVQVSSGGGGSGGGSEVQLVESGGVVQPGNSLR LSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSQDTLYADSVKGR FTISRDNAKTTLYLQMNSLRPEDTALYYCTIGGSLRSSQGTLVQVSSG GGGSGGGSEVQLLESGGGVQPGGSLRLSCAASGRTFNNYNMGWFRQAPG KGREFVAAVSRSGVSTYYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTALY YCAAAYRGTAINVRRSYSSWGQGTLTVSSA
766	EVQLLESGGGLVQPGGSLRLSCVHSGPTFRDTMGWFRQAPGKGREFVAAVT WNSGRINYADSVKGRFTISRDNSKNTAYLQMNSLRPEDTAVYYCAAHRFVVG GNRVEDWRYWGQGTLTVSSGGGGSGGGSEVQLVESGGGLVQPGNSLR LSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSQDTLYADSVKG RFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLRSSQGTLTVSS GGGGSGGGSEVQLLESGGGLVQPGGSLRLSCAASGRTFNNYNMGWFRQAPG KGREFVAAVSRSGVSTYYADSVKGRFTISRDNSKNTVYLQMNSLRPEDTAV YYCAAAYRGTAINVRRSYSSWGQGTLTVSSA

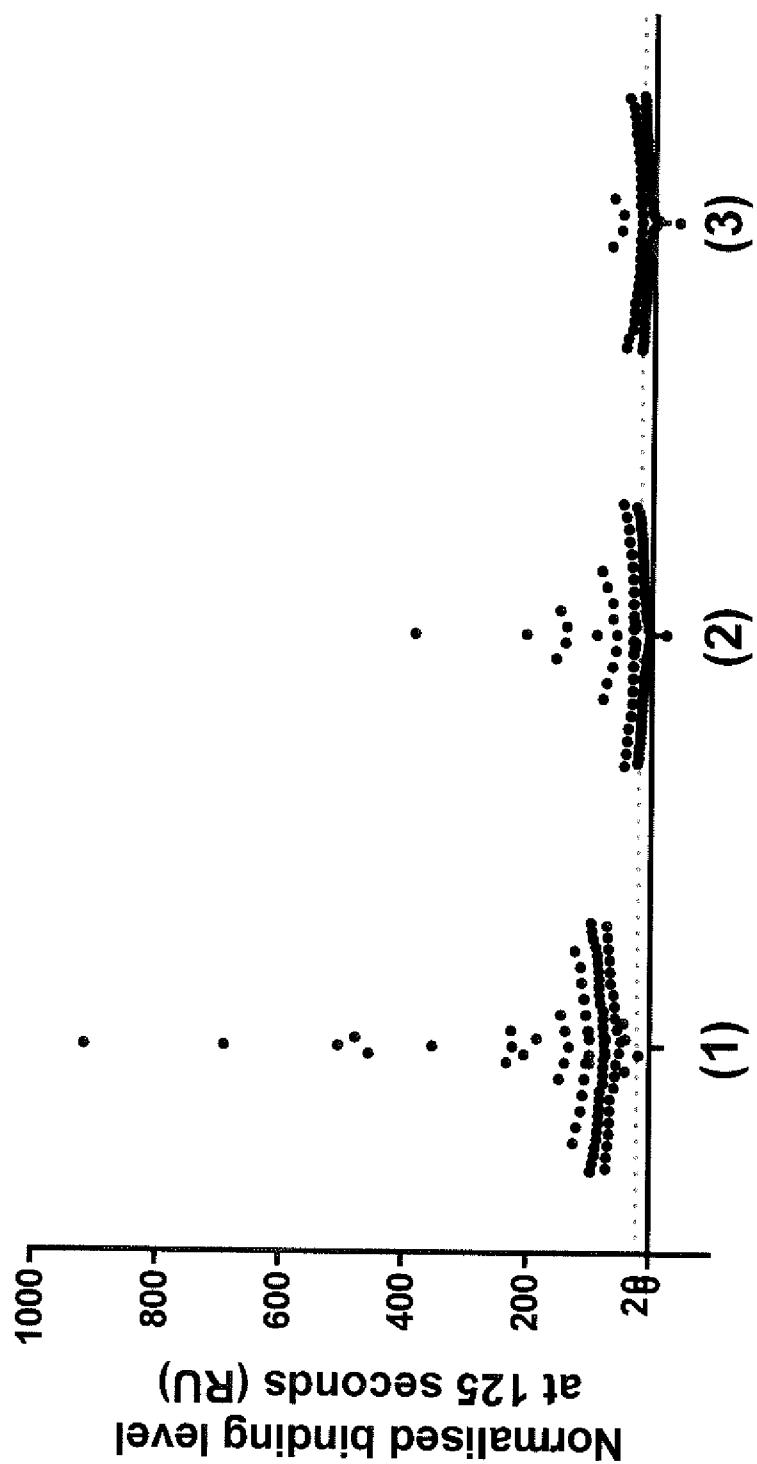


Figure 31A

2015261536 07 Apr 2020

112/112

Figure 31B

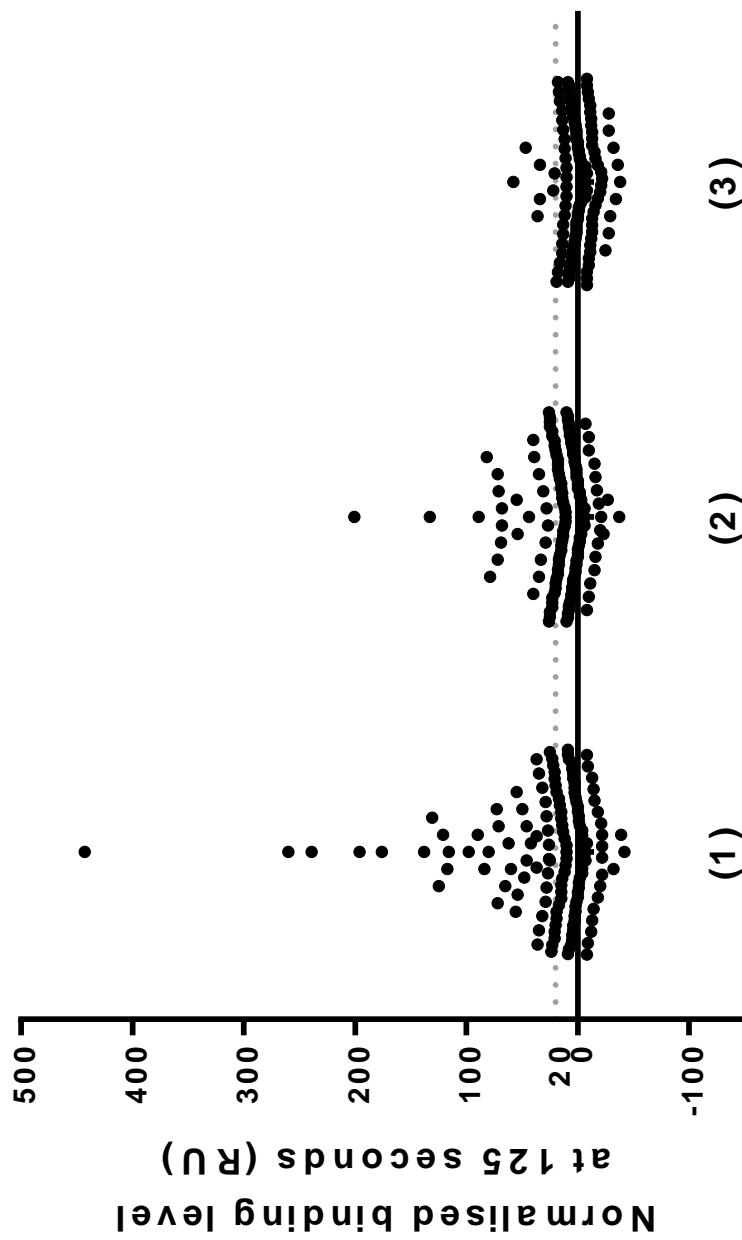


Figure 32

SEQ ID 52 of WO 2006/122787:

AVQLVESGGGLVQPGNLRLSCAAAGFTFRS**FGMSWVRQAPGKEPEWVSSISGSGSDTLYADSVKGRTIS**
RDNNAKTTLYLQMNSLKPEDTAVYYCT**GGSLSRSSQGTQVTVSS**