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(54) Title: ANTIGEN-BINDING CONSTRUCTS

(57) Abstract: The invention relates to a combination of RANKL antagonists with OSM antagonists, and provides antigen-binding constructs which bind to RANKL comprising a protein scaffold which are linked to one or more epitope-binding domains wherein the antigen-binding construct has at least two antigen binding sites at least one of which is from an epitope binding domain and at least one of which is from a paired VH/VL domain, methods of making such constructs and uses thereof.

Antigen-binding constructs

Background

Antibodies are well known for use in therapeutic applications.

Antibodies are heteromultimeric glycoproteins comprising at least two heavy and two light chains. Aside from IgM, intact antibodies are usually heterotetrameric glycoproteins of approximately 150Kda, composed of two identical light (L) chains and two identical heavy (H) chains. Typically, each light chain is linked to a heavy chain by one covalent disulfide bond while the number of disulfide linkages between the heavy chains of different immunoglobulin isotypes varies. Each heavy and light chain also has intrachain disulfide bridges. Each heavy chain has at one end a variable domain (VH) followed by a number of constant regions. Each light chain has a variable domain (VL) and a constant region at its other end; the constant region of the light chain is aligned with the first constant region of the heavy chain and the light chain variable domain is aligned with the variable domain of the heavy chain. The light chains of antibodies from most vertebrate species can be assigned to one of two types called Kappa and Lambda based on the amino acid sequence of the constant region. Depending on the amino acid sequence of the constant region of their heavy chains, human antibodies can be assigned to five different classes, IgA, IgD, IgE, IgG and IgM. IgG and IgA can be further subdivided into subclasses, IgG1, IgG2, IgG3 and IgG4; and IgA1 and IgA2. Species variants exist with mouse and rat having at least IgG2a, IgG2b. The variable domain of the antibody confers binding specificity upon the antibody with certain regions displaying particular variability called complementarity determining regions (CDRs). The more conserved portions of the variable region are called Framework regions (FR). The variable domains of intact heavy and light chains each comprise four FR connected by three CDRs. The CDRs in each chain are held together in close proximity by the FR regions and with the CDRs from the other chain contribute to the formation of the antigen-binding site of antibodies. The constant regions are not directly involved in the binding of the antibody to the antigen but exhibit various effector functions such as participation in antibody dependent cell-mediated cytotoxicity (ADCC), phagocytosis via binding to Fcγ receptor, half-life/clearance rate via neonatal Fc receptor (FcRn) and complement dependent cytotoxicity via the C1q component of the complement cascade.

The nature of the structure of an IgG antibody is such that there are two antigen-binding sites, both of which are specific for the same epitope. They are therefore, monospecific.

A bispecific antibody is an antibody having binding specificities for at least two different epitopes. Methods of making such antibodies are known in the art.

Traditionally, the recombinant production of bispecific antibodies is based on the coexpression of two immunoglobulin H chain-L chain pairs, where the two H chains have different binding specificities see Millstein *et al*, Nature 305 537-539 (1983), WO93/08829 and Traunecker *et al* EMBO, 10, 1991, 3655-3659. Because of the random assortment of H and L chains, a potential mixture of ten different antibody structures are produced of which only one has the desired binding specificity. An alternative approach involves fusing the variable domains with the desired binding specificities to heavy chain constant region comprising at least part of the hinge region, CH2 and CH3 regions. It is preferred to have the CH1 region containing the site necessary for light chain binding present in at least one of the fusions. DNA encoding these fusions, and if desired the L chain are inserted into separate expression vectors and are then cotransfected into a suitable host organism. It is possible though to insert the coding sequences for two or all three chains into one expression vector. In one approach, a bispecific antibody is composed of a H chain with a first binding specificity in one arm and a H-L chain pair, providing a second binding specificity in the other arm, see WO94/04690. Also see Suresh *et al* Methods in Enzymology 121, 210, 1986. Other approaches include antibody molecules which comprise single domain binding sites which is set out in WO2007/095338.

RANKL (Receptor activator of nuclear factor kappa B ligand) is a member of the tumor necrosis family and is involved in osteoclastogenesis and bone resorption. RANK and it's ligand RANK-L act in consort to regulate bone resorption and are part of the normal physiology of bone remodeling. In normal physiology, RANK is expressed on osteoclasts precursors whereas RANKL is expressed on osteoblastic stroma and T-cells. Osteoblasts and T-cells can drive osteoclasts development resulting in osteoclastogenesis and bone resorption. RANKL is believed to play a key role in bone destruction across a range of conditions including osteoporosis, treatment-induced bone loss, rheumatoid- and osteo -arthritis, and fuels a vicious cycle of bone destruction and tumor growth in metastatic disease and multiple myeloma. Joint bone erosion along with cartilage degradation are two structural changes which occur in Rheumatoid- and Osteo-arthritis. RANKL is an integral factor in osteoclast formation, function, and survival. In the joint, RANK-L is expressed on T cells and fibroblast-like synoviocytes in the synovial membrane of RA patients. Research has demonstrated that RANK-L in the synovium stimulates the development of mature osteoclasts found at the synovial pannus-cartilage/subchondral bone interface and that these cells are responsible for the focal bone erosion in rheumatoid arthritis patients.

OSM (Oncostatin M) is a cytokine that belongs to the Interleukin 6 group of cytokines consisting of ciliary neurotrophic factor (CNTF), leukemia inhibitory factor (LIF), interleukin-6 (IL-6), interleukin-11 (IL-11), cardiotrophin-1 (CT-1), and cardiotrophin-like cytokine (CLC). OSM is secreted as a glycoprotein monomer of 28 kDa with a

secondary structure containing four a-helical chains. OSM is produced by monocytes and macrophages, neutrophils and activated T-cells which seem to be the major sources of this cytokine. In humans, OSM binds to two functional OSM receptor complexes: the type I OSM receptor complex consisting of gp130 and LIF receptor (LIFR) subunits, and the type II OSM receptor complex consisting of gp130 and OSM receptor beta. OSM is reported to promote cartilidge and bone changes in combination with IL-1 or TNF. OSM, TNF and IL-1 are reported to be overexpressed in RA and OA synovial fluid. In addition, it is now recognised that OSM can be secreted by neutrophils in the context of solid tumors and that OSM is belived to participate in the angiogenic response see Cancer Research **65** 8896-8904 (2005)

Summary of invention

The present invention relates to the combination of a RANKL antagonist and an OSM antagonist for use in therapy.

The present invention in particular relates to an antigen-binding construct comprising a protein scaffold which is linked to one or more epitope-binding domains wherein the antigen-binding construct has at least two antigen-binding sites at least one of which is from an epitope binding domain and at least one of which is from a paired VH/VL domain, and wherein at least one of the antigen-binding sites binds to RANK Ligand.

The invention also provides a polynucleotide sequence encoding a heavy chain of any of the antigen-binding constructs described herein, and a polynucleotide encoding a light chain of any of the antigen-binding constructs described herein. Such polynucleotides represent the coding sequence which corresponds to the equivalent polypeptide sequences, however it will be understood that such polynucleotide sequences could be cloned into an expression vector along with a start codon, an appropriate signal sequence and a stop codon.
The invention also provides a recombinant transformed or transfected host cell comprising one or more polynucleotides encoding a heavy chain and a light chain of any of the antigen-binding constructs described herein.

The invention further provides a method for the production of any of the antigen-binding constructs described herein which method comprises the step of culturing a host cell comprising a first and second vector, said first vector comprising a polynucleotide encoding a heavy chain of any of the antigen-binding constructs described herein and said second vector comprising a polynucleotide encoding a light chain of any of the antigen-binding constructs described herein, in a suitable culture media, for example serum- free culture media.

The invention further provides a pharmaceutical composition comprising an antigen-binding construct as described herein a pharmaceutically acceptable carrier.

Definitions

The term 'Protein Scaffold' as used herein includes but is not limited to an immunoglobulin (Ig) scaffold, for example an IgG scaffold, which may be a four chain or two chain antibody, or which may comprise only the Fc region of an antibody, or which may comprise one or more constant regions from an antibody, which constant regions may be of human or primate origin, or which may be an artificial chimera of human and primate constant regions. Such protein scaffolds may comprise antigen-binding sites in addition to the one or more constant regions, for example where the protein scaffold comprises a full IgG. Such protein scaffolds will be capable of being linked to other protein domains, for example protein domains which have antigen-binding sites, for example epitope-binding domains or ScFv domains.

A "domain" is a folded protein structure which has tertiary structure independent of the rest of the protein. Generally, domains are responsible for discrete functional properties of proteins and in many cases may be added, removed or transferred to other proteins without loss of function of the remainder of the protein and/or of the domain. An "antibody single variable domain" is a folded polypeptide domain comprising sequences characteristic of antibody variable domains. It therefore includes complete antibody variable domains and modified variable domains, for example, in which one or more loops have been replaced by sequences which are not characteristic of antibody variable domains, or antibody variable domains which have been truncated or comprise N- or C-terminal extensions, as well as folded fragments of variable domains which retain at least the binding activity and specificity of the full-length domain.

The phrase "immunoglobulin single variable domain" refers to an antibody variable domain (V_H, V_{HH}, V_L) that specifically binds an antigen or epitope independently of a different V region or domain. An immunoglobulin single variable domain can be present in a format (*e.g.,* homo- or hetero-multimer) with other, different variable regions or variable domains where the other regions or domains are not required for antigen binding by the single immunoglobulin variable domain (*i.e.*, where the immunoglobulin single variable domain binds antigen independently of the additional variable domains). A "domain antibody" or "dAb" is the same as an "immunoglobulin single variable domain" which is capable of binding to an antigen as the term is used herein. An immunoglobulin single variable domain may be a human antibody variable domain, but also includes single antibody variable domains from other species such as rodent (for example, as disclosed in WO 00/29004), nurse shark and *Camelid* V_{HH} dAbs. Camelid V_{HH} are immunoglobulin single variable domain polypeptides that are derived from species including camel, llama, alpaca, dromedary, and guanaco, which produce heavy chain antibodies naturally devoid of light chains. Such V_{HH} domains may be humanised according to standard techniques available in the art, and such domains are still considered to be "domain antibodies"

according to the invention. As used herein "V_H includes camelid V_{HH} domains. NARV are another type of immunoglobulin single variable domain which were identified in cartilaginous fish including the nurse shark. These domains are also known as Novel Antigen Receptor variable region (commonly abbreviated to V(NAR) or NARV). For
5 further details see Mol. Immunol. **44**, 656-665 (2006) and US20050043519A.

The term "Epitope-binding domain" refers to a domain that specifically binds an antigen or epitope independently of a different V region or domain, this may be a domain antibody (dAb), for example a human, camelid or shark immunoglobulin
10 single variable domain or it may be a domain which is a derivative of a scaffold selected from the group consisting of CTLA-4 (Evibody); lipocalin; Protein A derived molecules such as Z-domain of Protein A (Affibody, SpA), A-domain (Avimer/Maxibody); Heat shock proteins such as GroEl and GroES; transferrin (trans-body); ankyrin repeat protein (DARPin); peptide aptamer; C-type lectin domain
15 (Tetranectin); human γ-crystallin and human ubiquitin (affilins); PDZ domains; scorpion toxinkunitz type domains of human protease inhibitors; and fibronectin (adnectin); which has been subjected to protein engineering in order to obtain binding to a ligand other than the natural ligand.

20 CTLA-4 (Cytotoxic T Lymphocyte-associated Antigen 4) is a CD28-family receptor expressed on mainly CD4+ T-cells. Its extracellular domain has a variable domain-like Ig fold. Loops corresponding to CDRs of antibodies can be substituted with heterologous sequence to confer different binding properties. CTLA-4 molecules engineered to have different binding specificities are also known as Evibodies. For
25 further details see Journal of Immunological Methods **248 (1-2)**, 31-45 (2001)

Lipocalins are a family of extracellular proteins which transport small hydrophobic molecules such as steroids, bilins, retinoids and lipids. They have a rigid β-sheet secondary structure with a numer of loops at the open end of the conical structure
30 which can be engineered to bind to different target antigens. Anticalins are between 160-180 amino acids in size, and are derived from lipocalins. For further details see Biochim Biophys Acta **1482**: 337-350 (2000), US7250297B1 and US20070224633

An affibody is a scaffold derived from Protein A of *Staphylococcus aureus* which can
35 be engineered to bind to antigen. The domain consists of a three-helical bundle of approximately 58 amino acids. Libraries have been generated by randomisation of surface residues. For further details see Protein Eng. Des. Sel. **17**, 455-462 (2004) and EP1641818A1

40 Avimers are multidomain proteins derived from the A-domain scaffold family. The native domains of approximately 35 amino acids adopt a defined disulphide bonded structure. Diversity is generated by shuffling of the natural variation exhibited by the

family of A-domains. For further details see Nature Biotechnology **23(12)**, 1556 - 1561 (2005) and Expert Opinion on Investigational Drugs **16(6)**, 909-917 (June 2007)

A transferrin is a monomeric serum transport glycoprotein. Transferrins can be engineered to bind different target antigens by insertion of peptide sequences in a permissive surface loop. Examples of engineered transferrin scaffolds include the Trans-body. For further details see J. Biol. Chem **274**, 24066-24073 (1999).

Designed Ankyrin Repeat Proteins (DARPins) are derived from Ankyrin which is a family of proteins that mediate attachment of integral membrane proteins to the cytoskeleton. A single ankyrin repeat is a 33 residue motif consisting of two α-helices and a β-turn. They can be engineered to bind different target antigens by randomising residues in the first α-helix and a β-turn of each repeat. Their binding interface can be increased by increasing the number of modules (a method of affinity maturation). For further details see J. Mol. Biol. **332**, 489-503 (2003), PNAS **100(4)**, 1700-1705 (2003) and J. Mol. Biol. 369, 1015-1028 (2007) and US20040132028A1.

Fibronectin is a scaffold which can be engineered to bind to antigen. Adnectins consists of a backbone of the natural amino acid sequence of the 10th domain of the 15 repeating units of human fibronectin type III (FN3). Three loops at one end of the β-sandwich can be engineered to enable an Adnectin to specifically recognize a therapeutic target of interest. For further details see Protein Eng. Des. Sel. **18**, 435-444 (2005), US20080139791, WO2005056764 and US6818418B1.

Peptide aptamers are combinatorial recognition molecules that consist of a constant scaffold protein, typically thioredoxin (TrxA) which contains a constrained variable peptide loop inserted at the active site. For further details see Expert Opin. Biol. Ther. 5, 783-797 (2005).

Microbodies are derived from naturally occurring microproteins of 25-50 amino acids in length which contain 3-4 cysteine bridges – examples of microproteins include KalataB1 and conotoxin and knottins. The microproteins have a loop which can be engineered to include upto 25 amino acids without affecting the overall fold of the microprotein. For further details of engineered knottin domains, see WO2008098796.

Other epitope binding domains include proteins which have been used as a scaffold to engineer different target antigen binding properties include human γ-crystallin and human ubiquitin (affilins), kunitz type domains of human protease inhibitors, PDZ-domains of the Ras-binding protein AF-6, scorpion toxins (charybdotoxin), C-type lectin domain (tetranectins) are reviewed in Chapter 7 – Non-Antibody Scaffolds from Handbook of Therapeutic Antibodies (2007, edited by Stefan Dubel) and Protein Science **15**:14-27 (2006). Epitope binding domains of the present invention could be derived from any of these alternative protein domains.

As used herein, the terms “paired VH domain”, “paired VL domain”, and “paired VH/VL domains” refer to antibody variable domains which specifically bind antigen only when paired with their partner variable domain. There is always one VH and one VL in any pairing, and the term “paired VH domain” refers to the VH partner, the term “paired VL domain” refers to the VL partner, and the term “paired VH/VL domains” refers to the two domains together.

In one embodiment of the invention the antigen-binding site binds to antigen with a Kd of at least 1mM, for example a Kd of 10nM, 1nM, 500pM, 200pM, 100pM, to each antigen as measured by Biacore™ .

As used herein, the term “antigen-binding site” refers to a site on a construct which is capable of specifically binding to antigen, this may be a single domain, for example an epitope-binding domain, or it may be paired VH/VL domains as can be found on a standard antibody. In some aspects of the invention single-chain Fv (ScFv) domains can provide antigen-binding sites.

The terms “mAb/dAb” and dAb/mAb” are used herein to refer to antigen-binding constructs of the present invention. The two terms can be used interchangeably, and are intended to have the same meaning as used herein.

The term “constant heavy chain 1” is used herein to refer to the CH1 domain of an immunoglobulin heavy chain.

The term “constant light chain” is used herein to refer to the constant domain of an immunoglobulin light chain.

Detailed description of Invention

The present invention provides compositions comprising a RANKL antagonist and a OSM antagonist. The present invention also provides the combination of a RANKL antagonist a OSM antagonist, for use in therapy. The present invention also provides a method of treating disease by administering a RANKL antagonist in combination with a OSM antagonist. The RANKL antagonist and the OSM antagonist may be administered separately, sequentially or simultaneously.

Such antagonists may be antibodies or epitope binding domains for example dAbs. The antagonists may be administered as a mixture of separate molecules which are administered at the same time i.e. co-administered, or are administered within 24 hours of each other, for example within 20 hours, or within 15 hours or within 12 hours, or within 10 hours, or within 8 hours, or within 6 hours, or within 4 hours, or within 2 hours, or within 1 hour, or within 30 minutes of each other.

In a further embodiment the antagonists are present as one molecule capable of binding to two or more antigens, for example the invention provides a dual targeting molecule which is capable of binding to RANKL and OSM.

The present invention provides an antigen-binding construct comprising a protein scaffold which is linked to one or more epitope-binding domains wherein the antigen-binding construct has at least two antigen-binding sites at least one of which is from an epitope binding domain and at least one of which is from a paired VH/VL domain and wherein at least one of the antigen-binding sites binds to RANK Ligand.

Such antigen-binding constructs comprise a protein scaffold, for example an Ig scaffold such as IgG, for example a monoclonal antibody, which is linked to one or more epitope-binding domains, for example a domain antibody, wherein the binding construct has at least two antigen-binding sites, at least one of which is from an epitope binding domain, and wherein at least one of the antigen-binding sites binds to RANK Ligand, and to methods of producing and uses thereof, particularly uses in therapy.

Some examples of antigen-binding constructs according to the invention are set out in Figures 1-5.

The antigen-binding constructs of the present invention are also referred to as mAbdAbs or bispecific antibodies.

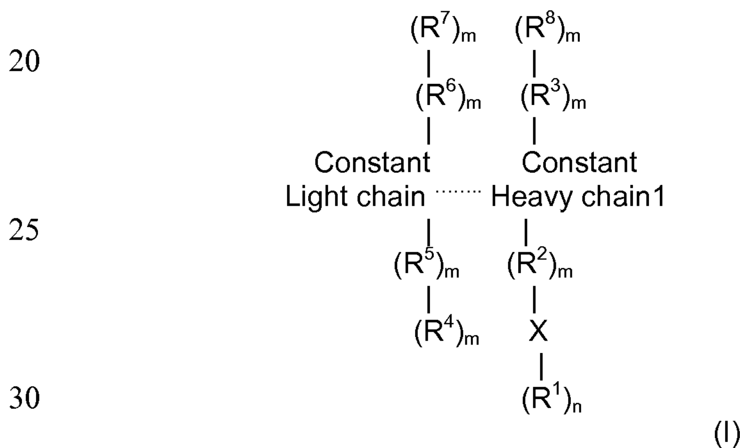
In one embodiment the protein scaffold of the antigen-binding construct of the present invention is an Ig scaffold, for example an IgG scaffold or IgA scaffold. The

IgG scaffold may comprise all the domains of an antibody (i.e. CH1, CH2, CH3, VH, VL). The antigen-binding construct of the present invention may comprise an IgG scaffold selected from IgG1, IgG2, IgG3, IgG4 or IgG4PE.

5 The antigen-binding construct of the present invention has at least two antigen-binding sites, for examples it has two binding sites, for example where the first binding site has specificity for a first epitope on an antigen and the second binding site has specificity for a second epitope on the same antigen. In a further embodiment there are 4 antigen-binding sites, or 6 antigen-binding sites, or 8
10 antigen-binding sites, or 10 or more antigen-binding sites. In one embodiment the antigen-binding construct has specificity for more than one antigen, for example two antigens, or for three antigens, or for four antigens.

In another aspect the invention relates to an antigen-binding construct which is
15 capable of binding to RANKL comprising at least one homodimer comprising two or more structures of formula I:

20



25

30

(I)

wherein

X represents a constant antibody region comprising constant heavy domain 2 and
35 constant heavy domain 3;

R^1, R^4 , R^7 and R^8 represent a domain independently selected from an epitope-binding domain;

40 R^2 represents a domain selected from the group consisting of constant heavy chain 1, and an epitope-binding domain;

R^3 represents a domain selected from the group consisting of a paired VH and an epitope-binding domain;

R^5 represents a domain selected from the group consisting of constant light chain, and an epitope-binding domain;

5 R^6 represents a domain selected from the group consisting of a paired VL and an epitope-binding domain;

n represents an integer independently selected from: 0, 1, 2, 3 and 4;
m represents an integer independently selected from: 0 and 1,

10

wherein the Constant Heavy chain 1 and the Constant Light chain domains are associated;

wherein at least one epitope binding domain is present;

15

and when R^3 represents a paired VH domain, R^6 represents a paired VL domain, so that the two domains are together capable of binding antigen.

In one embodiment R^6 represents a paired VL and R^3 represents a paired VH.

20

In a further embodiment either one or both of R^7 and R^8 represent an epitope binding domain.

In yet a further embodiment either one or both of R^1 and R^4 represent an epitope
25 binding domain.

In one embodiment R^4 is present.

In one embodiment R^1 R^7 and R^8 represent an epitope binding domain.

30

In one embodiment R^1 R^7 and R^8, and R^4 represent an epitope binding domain.

In one embodiment $(R^1)_n$, $(R^2)_m$, $(R^4)_m$ and $(R^5)_m$ = 0, i.e. are not present, R^3 is a paired VH domain, R^6 is a paired VL domain, R^8 is a VH dAb, and R^7 is a VL dAb.

35

In another embodiment $(R^1)_n$, $(R^2)_m$, $(R^4)_m$ and $(R^5)_m$ are 0, i.e. are not present, R^3 is a paired VH domain, R^6 is a paired VL domain, R^8 is a VH dAb, and $(R^7)_m$ = 0 i.e. not present.

40 In another embodiment $(R^2)_m$, and $(R^5)_m$ are 0, i.e. are not present, R^1 is a dAb, R^4 is a dAb, R^3 is a paired VH domain, R^6 is a paired VL domain, $(R^8)_m$ and $(R^7)_m$ = 0 i.e. not present.

In one embodiment of the present invention the epitope binding domain is a dAb.

It will be understood that any of the antigen-binding constructs described herein will be capable of neutralising one or more antigens, for example they will be capable of neutralising RANKL and they will also be capable of neutralising OSM.

The term “neutralises” and grammatical variations thereof as used throughout the present specification in relation to antigen-binding constructs of the invention means that a biological activity of the target is reduced, either totally or partially, in the presence of the antigen-binding constructs of the present invention in comparison to the activity of the target in the absence of such antigen-binding constructs. Neutralisation may be due to but not limited to one or more of blocking ligand binding, preventing the ligand activating the receptor, down regulating the receptor or affecting effector functionality.

Levels of neutralisation can be measured in several ways, for example by use of any of the assays as set out in the examples below, for example in an assay which measures inhibition of ligand binding to receptor which may be carried out for example as described in Example 4. The neutralisation of OSM, in this assay is measured by assessing the decreased binding between the ligand and its receptor (gp130) in the presence of neutralising antigen-binding construct.

Other methods of assessing neutralisation, for example, by assessing the decreased binding between the ligand and its receptor in the presence of neutralising antigen-binding construct are known in the art, and include, for example, Biacore™ assays.

In an alternative aspect of the present invention there is provided antigen-binding constructs which have at least substantially equivalent neutralising activity to the antibodies exemplified herein.

The antigen-binding constructs of the invention have specificity for RANKL, for example they comprise an epitope-binding domain which is capable of binding to RANKL, and/or they comprise a paired VH/VL which binds to RANKL. The antigen-binding construct may comprise an antibody which is capable of binding to RANKL. The antigen-binding construct may comprise a dAb which is capable of binding to RANKL.

In one embodiment the antigen-binding construct of the present invention has specificity for more than one antigen, for example where it is capable of binding RANKL and OSM. In one embodiment the antigen-binding construct of the present invention is capable of binding RANKL and OSM simultaneously.

It will be understood that any of the antigen-binding constructs described herein may be capable of binding two or more antigens simultaneously, for example, as determined by stochiometry analysis by using a suitable assay such as that described in Example 5.

Examples of such antigen-binding constructs include OSM antibodies which have an epitope binding domain which is a RANKL antagonist, for example an anti-RANKL dAb, attached to the c-terminus or the n-terminus of the heavy chain or the c-terminus or n-terminus of the light chain. Other examples of such antigen-binding constructs include OSM antibodies which have an anti- RANKL nanobody, attached to the c-terminus or the n-terminus of the heavy chain or the c-terminus or n-terminus of the light chain. Examples include a antigen binding construct comprising the heavy chain sequence set out in SEQ ID NO:1 and/or the light chain sequence set out in SEQ ID NO:2 wherein one or both of the Heavy and Light chain further comprise one or more epitope-binding domains which bind to RANKL, for example the nanobody set out in SEQ ID NO: 38 or SEQ ID NO: 39.

Examples of such antigen-binding constructs include an antigen binding construct having the heavy chain sequence set out in SEQ ID NO: 40 and the light chain sequence set out in SEQ ID NO: 2 or 41, or an antigen binding construct having the light chain sequence set out in SEQ ID NO: 41 and the heavy chain sequence set out in SEQ ID NO: 1 or 40.

Other examples of such antigen-binding constructs include RANKL antibodies which have an epitope binding domain which is an OSM antagonist, for example an anti-OSM dAb, attached to the c-terminus or the n-terminus of the heavy chain or the c-terminus or n-terminus of the light chain. Other examples of such antigen-binding constructs include RANKL antibodies which have an anti- OSM adnectin attached to the c-terminus or the n-terminus of the heavy chain or the c-terminus or n-terminus of the light chain.

Examples include a antigen binding construct comprising the heavy chain sequence set out in SEQ ID NO: 24, 25, 30, 31, 32 or 36 and/or the light chain sequence set out in SEQ ID NO: 26, 27, 28, 29, 33, 34, 35 or 37 wherein one or both of the Heavy and Light chain further comprise one or more epitope-binding domains which bind to OSM.

Examples of such antigen-binding constructs include an anti-RANKL antibody linked to an epitope binding domain which is a OSM antagonist, wherein the anti-RANKL antibody has the same CDRs as the antibody which has the heavy chain sequence of SEQ ID NO: 24, 25, 30, 31, 32 or 36 and the light chain sequence of SEQ ID NO: 26, 27, 28, 29, 33, 34, 35 or 37.

Such antigen-binding constructs may also have one or more further epitope binding domains with the same or different antigen-specificity attached to the c-terminus and/or the n-terminus of the heavy chain and/ or the c-terminus and/or n-terminus of the light chain.

In one embodiment of the present invention there is provided an antigen-binding construct according to the invention described herein and comprising a constant region such that the antibody has reduced ADCC and/or complement activation or effector functionality. In one such embodiment the heavy chain constant region may comprise a naturally disabled constant region of IgG2 or IgG4 isotype or a mutated IgG1 constant region. Examples of suitable modifications are described in EP0307434. One example comprises the substitutions of alanine residues at positions 235 and 237 (EU index numbering – i.e. kabat numbering).

In one embodiment the antigen-binding constructs of the present invention will retain Fc functionality for example will be capable of one or both of ADCC and CDC activity. Such antigen-binding constructs may comprise an epitope-binding domain located on the light chain, for example on the c-terminus of the light chain.

The invention also provides a method of maintaining ADCC and CDC function of antigen-binding constructs by positioning of the epitope binding domain on the light chain of the antibody in particular, by positioning the epitope binding domain on the c-terminus of the light chain.

The invention also provides a method of reducing CDC function of antigen-binding constructs by positioning of the epitope binding domain on the heavy chain of the antibody, in particular, by positioning the epitope binding domain on the c-terminus of the heavy chain.

In one embodiment, the antigen-binding constructs comprise an epitope-binding domain which is a domain antibody (dAb), for example the epitope binding domain may be a human VH or human VL, or a camelid V_{HH} or a shark dAb (NARV).
In one embodiment the antigen-binding constructs comprise an epitope-binding domain which is a derivative of a scaffold selected from the group consisting of CTLA-4 (Evibody); lipocalin; Protein A derived molecules such as Z-domain of Protein A (Affibody, SpA), A-domain (Avimer/Maxibody); Heat shock proteins such as GroEl and GroES; transferrin (trans-body); ankyrin repeat protein (DARPin); peptide aptamer; C-type lectin domain (Tetranectin); human γ-crystallin and human ubiquitin (affilins); PDZ domains; scorpion toxinkunitz type domains of human protease inhibitors; and fibronectin (adnectin); which has been subjected to protein engineering in order to obtain binding to a ligand other than the natural ligand.

The antigen-binding constructs of the present invention may comprise a protein scaffold attached to an epitope binding domain which is an adnectin, for example an IgG scaffold with an adnectin attached to the c-terminus of the heavy chain, or it may comprise a protein scaffold attached to an adnectin, for example an IgG scaffold with an adnectin attached to the n-terminus of the heavy chain, or it may comprise a protein scaffold attached to an adnectin, for example an IgG scaffold with an adnectin attached to the c-terminus of the light chain, or it may comprise a protein scaffold attached to an adnectin, for example an IgG scaffold with an adnectin attached to the n-terminus of the light chain.

In other embodiments it may comprise a protein scaffold, for example an IgG scaffold, attached to an epitope binding domain which is a CTLA-4, for example an IgG scaffold with a CTLA-4 attached to the n-terminus of the heavy chain, or it may comprise for example an IgG scaffold with a CTLA-4 attached to the c-terminus of the heavy chain, or it may comprise for example an IgG scaffold with CTLA-4 attached to the n-terminus of the light chain, or it may comprise an IgG scaffold with CTLA-4 attached to the c-terminus of the light chain.

In other embodiments it may comprise a protein scaffold, for example an IgG scaffold, attached to an epitope binding domain which is a lipocalin, for example an IgG scaffold with a lipocalin attached to the n-terminus of the heavy chain, or it may comprise for example an IgG scaffold with a lipocalin attached to the c-terminus of the heavy chain, or it may comprise for example an IgG scaffold with a lipocalin attached to the n-terminus of the light chain, or it may comprise an IgG scaffold with a lipocalin attached to the c-terminus of the light chain.

In other embodiments it may comprise a protein scaffold, for example an IgG scaffold, attached to an epitope binding domain which is an SpA, for example an IgG scaffold with an SpA attached to the n-terminus of the heavy chain, or it may comprise for example an IgG scaffold with an SpA attached to the c-terminus of the heavy chain, or it may comprise for example an IgG scaffold with an SpA attached to the n-terminus of the light chain, or it may comprise an IgG scaffold with an SpA attached to the c-terminus of the light chain.

In other embodiments it may comprise a protein scaffold, for example an IgG scaffold, attached to an epitope binding domain which is an affibody, for example an IgG scaffold with an affibody attached to the n-terminus of the heavy chain, or it may comprise for example an IgG scaffold with an affibody attached to the c-terminus of the heavy chain, or it may comprise for example an IgG scaffold with an affibody attached to the n-terminus of the light chain, or it may comprise an IgG scaffold with an affibody attached to the c-terminus of the light chain.

In other embodiments it may comprise a protein scaffold, for example an IgG scaffold, attached to an epitope binding domain which is an affimer, for example an IgG scaffold with an affimer attached to the n-terminus of the heavy chain, or it may comprise for example an IgG scaffold with an affimer attached to the c-terminus of the heavy chain, or it may comprise for example an IgG scaffold with an affimer

attached to the n-terminus of the light chain, or it may comprise an IgG scaffold with an affimer attached to the c-terminus of the light chain.
In other embodiments it may comprise a protein scaffold, for example an IgG scaffold, attached to an epitope binding domain which is a GroEI, for example an IgG scaffold with a GroEI attached to the n-terminus of the heavy chain, or it may comprise for example an IgG scaffold with a GroEI attached to the c-terminus of the heavy chain, or it may comprise for example an IgG scaffold with a GroEI attached to the n-terminus of the light chain, or it may comprise an IgG scaffold with a GroEI attached to the c-terminus of the light chain.
In other embodiments it may comprise a protein scaffold, for example an IgG scaffold, attached to an epitope binding domain which is a transferrin, for example an IgG scaffold with a transferrin attached to the n-terminus of the heavy chain, or it may comprise for example an IgG scaffold with a transferrin attached to the c-terminus of the heavy chain, or it may comprise for example an IgG scaffold with a transferrin attached to the n-terminus of the light chain, or it may comprise an IgG scaffold with a transferrin attached to the c-terminus of the light chain.
In other embodiments it may comprise a protein scaffold, for example an IgG scaffold, attached to an epitope binding domain which is a GroES, for example an IgG scaffold with a GroES attached to the n-terminus of the heavy chain, or it may comprise for example an IgG scaffold with a GroES attached to the c-terminus of the heavy chain, or it may comprise for example an IgG scaffold with a GroES attached to the n-terminus of the light chain, or it may comprise an IgG scaffold with a GroES attached to the c-terminus of the light chain.
In other embodiments it may comprise a protein scaffold, for example an IgG scaffold, attached to an epitope binding domain which is a DARPin, for example an IgG scaffold with a DARPin attached to the n-terminus of the heavy chain, or it may comprise for example an IgG scaffold with a DARPin attached to the c-terminus of the heavy chain, or it may comprise for example an IgG scaffold with a DARPin attached to the n-terminus of the light chain, or it may comprise an IgG scaffold with a DARPin attached to the c-terminus of the light chain.
In other embodiments it may comprise a protein scaffold, for example an IgG scaffold, attached to an epitope binding domain which is a peptide aptamer, for example an IgG scaffold with a peptide aptamer attached to the n-terminus of the heavy chain, or it may comprise for example an IgG scaffold with a peptide aptamer attached to the c-terminus of the heavy chain, or it may comprise for example an IgG scaffold with a peptide aptamer attached to the n-terminus of the light chain, or it may comprise an IgG scaffold with a peptide aptamer attached to the c-terminus of the light chain.

In one embodiment of the present invention there are four epitope binding domains, for example four domain antibodies, two of the epitope binding domains may have specificity for the same antigen, or all of the epitope binding domains present in the antigen-binding construct may have specificity for the same antigen.

Protein scaffolds of the present invention may be linked to epitope-binding domains by the use of linkers. Examples of suitable linkers include amino acid sequences which may be from 1 amino acid to 150 amino acids in length, or from 1 amino acid to 140 amino acids, for example, from 1 amino acid to 130 amino acids, or from 1 to 120 amino acids, or from 1 to 80 amino acids, or from 1 to 50 amino acids, or from 1 to 20 amino acids, or from 1 to 10 amino acids, or from 5 to 18 amino acids. Such sequences may have their own tertiary structure, for example, a linker of the present invention may comprise a single variable domain. The size of a linker in one embodiment is equivalent to a single variable domain. Suitable linkers may be of a size from 1 to 20 angstroms, for example less than 15 angstroms, or less than 10 angstroms, or less than 5 angstroms.

In one embodiment of the present invention at least one of the epitope binding domains is directly attached to the Ig scaffold with a linker comprising from 1 to 150 amino acids, for example 1 to 20 amino acids, for example 1 to 10 amino acids. Such linkers may be selected from any one of those set out in SEQ ID NO: 3 to 8, for example the linker may be 'TVAAPS', or the linker may be 'GGGGS' or multiples of such linkers . Linkers of use in the antigen-binding constructs of the present invention may comprise alone or in addition to other linkers, one or more sets of GS residues, for example 'GSTVAAPS' or 'TVAAPSGS' or 'GSTVAAPSGS' or multiples of such linkers.

In one embodiment the epitope binding domain is linked to the Ig scaffold by the linker '$(PAS)_n(GS)_m$'. In another embodiment the epitope binding domain is linked to the Ig scaffold by the linker '$(GGGGS)_p(GS)_m$'. In another embodiment the epitope binding domain is linked to the Ig scaffold by the linker '$(TVAAPS)_p(GS)_m$'. In another embodiment the epitope binding domain is linked to the Ig scaffold by the linker '$(GS)_m(TVAAPSGS)_p$'. In another embodiment the epitope binding domain is linked to the Ig scaffold by the linker '$(GS)_m(TVAAPS)_p(GS)_m$'. In another embodiment the epitope binding domain is linked to the Ig scaffold by the linker '$(PAVPPP)_n(GS)_m$'. In another embodiment the epitope binding domain is linked to the Ig scaffold by the linker '$(TVSDVP)_n(GS)_m$'. In another embodiment the epitope binding domain is linked to the Ig scaffold by the linker '$(TGLDSP)_n(GS)_m$'. In all such embodiments, n = 1-10, and m = 0-4, and p=2-10.

Examples of such linkers include $(PAS)_n(GS)_m$ wherein n=1 and m=1 (SEQ ID NO: 50), $(PAS)_n(GS)_m$ wherein n=2 and m=1 (SEQ ID NO: 51), $(PAS)_n(GS)_m$ wherein n=3 and m=1 (SEQ ID NO:52), $(PAS)_n(GS)_m$ wherein n=4 and m=1, $(PAS)_n(GS)_m$ wherein n=2 and m=0, $(PAS)_n(GS)_m$ wherein n=3 and m=0, $(PAS)_n(GS)_m$ wherein n=4 and m=0.

Examples of such linkers include $(GGGGS)_p(GS)_m$ wherein p=2 and m=0 (SEQ ID NO: 53), $(GGGGS)_p(GS)_m$ wherein p=3 and m=0 (SEQ ID NO:54), $(GGGGS)_p(GS)_m$ wherein p=4 and m=0.

5 Examples of such linkers include $(GS)_m(TVAAPS)_p$ wherein p=1 and m=1, $(GS)_m(TVAAPS)_p$ wherein p=2 and m=1, $(GS)_m(TVAAPS)_p$ wherein p=3 and m=1, $(GS)_m(TVAAPS)_p$ wherein p=4 and m=1), $(GS)_m(TVAAPS)_p$ wherein p=5 and m=1, or $(GS)_m(TVAAPS)_p$ wherein p=6 and m=1.

10 Examples of such linkers include$(TVAAPS)_p(GS)_m$ wherein p=2 and m=1 (SEQ ID NO:68), $(TVAAPS)_p(GS)_m$ wherein p=3 and m=1 (SEQ ID NO:69), $(TVAAPS)_p(GS)_m$ wherein p=4 and m=1, $(TVAAPS)_p(GS)_m$ wherein p=2 and m=0, $(TVAAPS)_p(GS)_m$ wherein p=3 and m=0, $(TVAAPS)_p(GS)_m$ wherein p=4 and m=0.

15 Examples of such linkers include $(GS)_m(TVAAPSGS)_p$ wherein p=1 and m=0 (SEQ ID NO:8), $(GS)_m(TVAAPSGS)_p$ wherein p=2 and m=1 (SEQ ID NO:45), $(GS)_m(TVAAPSGS)_p$ wherein p=3 and m=1 (SEQ ID NO:46), or $(GS)_m(TVAAPSGS)_p$ wherein p=4 and m=1 (SEQ ID NO:47), $(GS)_m(TVAAPSGS)_p$ wherein p=5 and m=1 (SEQ ID NO:48), $(GS)_m(TVAAPSGS)_p$ wherein p=6 and m=1 (SEQ ID NO:49).

20

Examples of such linkers include$(TVAAPSGS)_p(GS)_m$ wherein p=2 and m=1, $(TVAAPSGS)_p(GS)_m$ wherein p=3 and m=1 , $(TVAAPSGS)_p(GS)_m$ wherein p=4 and m=1, $(TVAAPSGS)_p(GS)_m$ wherein p=2 and m=0, $(TVAAPSGS)_p(GS)_m$ wherein p=3 and m=0, $(TVAAPSGS)_p(GS)_m$ wherein p=4 and m=0.

25

Examples of such linkers include $(PAVPPP)_n(GS)_m$ wherein n=1 and m=1 (SEQ ID NO: 55), $(PAVPPP)_n(GS)_m$ wherein n=2 and m=1 (SEQ ID NO:56), $(PAVPPP)_n(GS)_m$ wherein n=3 and m=1 (SEQ ID NO:57), $(PAVPPP)_n(GS)_m$ wherein n=4 and m=1, $(PAVPPP)_n(GS)_m$ wherein n=2 and m=0, $(PAVPPP)_n(GS)_m$ wherein n=3 and m=0,
30 $(PAVPPP)_n(GS)_m$ wherein n=4 and m=0.

Examples of such linkers include $(TVSDVP)_n(GS)_m$ wherein n=1 and m=1 (SEQ ID NO: 58), $(TVSDVP)_n(GS)_m$ wherein n=2 and m=1 (SEQ ID NO: 59), $(TVSDVP)_n(GS)_m$ wherein n=3 and m=1 (SEQ ID NO:60), $(TVSDVP)_n(GS)_m$ wherein n=4 and m=1,
35 $(TVSDVP)_n(GS)_m$ wherein n=2 and m=0, $(TVSDVP)_n(GS)_m$ wherein n=3 and m=0, $(TVSDVP)_n(GS)_m$ wherein n=4 and m=0.

Examples of such linkers include $(TGLDSP)_n(GS)_m$ wherein n=1 and m=1 (SEQ ID NO: 61), $(TGLDSP)_n(GS)_m$ wherein n=2 and m=1 (SEQ ID NO: 62), $(TGLDSP)_n(GS)_m$
40 wherein n=3 and m=1 (SEQ ID NO:63), $(TGLDSP)_n(GS)_m$ wherein n=4 and m=1, $(TGLDSP)_n(GS)_m$ wherein n=2 and m=0, $(TGLDSP)_n(GS)_m$ wherein n=3 and m=0, $(TGLDSP)_n(GS)_m$ wherein n=4 and m=0.

In another embodiment there is no linker between the epitope binding domain, for example the dAb, and the Ig scaffold. In another embodiment the epitope binding domain, for example a dAb, is linked to the Ig scaffold by the linker 'TVAAPS'. In another embodiment the epitope binding domain, for example a dAb, is linked to the Ig scaffold by the linker 'TVAAPSGS'. In another embodiment the epitope binding domain, for example a dAb, is linked to the Ig scaffold by the linker 'GS'.

In one embodiment, the antigen-binding construct of the present invention comprises at least one antigen-binding site, for example at least one epitope binding domain, which is capable of binding human serum albumin.

In one embodiment, there are at least 3 antigen-binding sites, for example there are 4, or 5 or 6 or 8 or 10 antigen-binding sites and the antigen-binding construct is capable of binding at least 3 or 4 or 5 or 6 or 8 or 10 antigens, for example it is capable of binding 3 or 4 or 5 or 6 or 8 or 10 antigens simultaneously.

The invention also provides the antigen-binding constructs for use in medicine, for example for use in the manufacture of a medicament for treating osteoporosis, or arthritic diseases such as rheumatoid arthritis, erosive arthritis, psoriatic arthritis, polymyalgia rhumatica, ankylosing spondylitis, juvenile rheumatoid arthritis, Paget's disease, osteogenesis imperfecta, osteoporosis, sports or other injuries of the knee, ankle, hand, hip, shoulder or spine, back pain, lupus particularly of the joints and osteoarthritis or cancer, for example Acute Myologenous Leukaemia, breast cancer, lung cancer, prostate cancer, colon cancer, stomach cancer, bladder cancer, uterine cancer, kidney cancer, multiple myeloma or arthritic diseases.

The invention provides a method of treating a patient suffering from osteoporosis, or arthritic diseases such as rheumatoid arthritis, erosive arthritis, psoriatic arthritis, polymyalgia rhumatica, ankylosing spondylitis, juvenile rheumatoid arthritis, Paget's disease, osteogenesis imperfecta, osteoporosis, sports or other injuries of the knee, ankle, hand, hip, shoulder or spine, back pain, lupus particularly of the joints, osteoarthritis or cancer, for example Acute Myologenous Leukaemia, breast cancer, lung cancer, prostate cancer, colon cancer, stomach cancer, bladder cancer, uterine cancer, kidney cancer, multiple myeloma or arthritic diseasescomprising administering a therapeutic amount of an antigen-binding construct of the invention.

The antigen-binding constructs of the invention may be used for the treatment of osteoporosis, or arthritic diseases such as rheumatoid arthritis, erosive arthritis, psoriatic arthritis, polymyalgia rhumatica, ankylosing spondylitis, juvenile rheumatoid arthritis, Paget's disease, osteogenesis imperfecta, osteoporosis, sports or other injuries of the knee, ankle, hand, hip, shoulder or spine, back pain, lupus particularly of the joints, osteoarthritis or cancer, for example Acute Myologenous Leukaemia,

breast cancer, lung cancer, prostate cancer, colon cancer, stomach cancer, bladder cancer, uterine cancer, kidney cancer, multiple myeloma or arthritic diseasesor a disease associated with the over production of RANKL or OSM.

5 The antigen-binding constructs of the invention may have some effector function. For example if the protein scaffold contains an Fc region derived from an antibody with effector function, for example if the protein scaffold comprises CH2 and CH3 from IgG1. Levels of effector function can be varied according to known techniques, for example by mutations in the CH2 domain, for example wherein the IgG1 CH2
10 domain has one or more mutations at positions selected from 239 and 332 and 330, for example the mutations are selected from S239D and I332E and A330L such that the antibody has enhanced effector function, and/or for example altering the glycosylation profile of the antigen-binding construct of the invention such that there is a reduction in fucosylation of the Fc region.
15
Protein scaffolds of use in the present invention include full monoclonal antibody scaffolds comprising all the domains of an antibody, or protein scaffolds of the present invention may comprise a non-conventional antibody structure, such as a monovalent antibody. Such monovalent antibodies may comprise a paired heavy and
20 light chain wherein the hinge region of the heavy chain is modified so that the heavy chain does not homodimerise, such as the monovalent antibody described in WO2007059782. Other monovalent antibodies may comprise a paired heavy and light chain which dimerises with a second heavy chain which is lacking a functional variable region and CH1 region, wherein the first and second heavy chains are
25 modified so that they will form heterodimers rather than homodimers, resulting in a monovalent antibody with two heavy chains and one light chain such as the monovalent antibody described in WO2006015371. Such monovalent antibodies can provide the protein scaffold of the present invention to which epitope binding domains can be linked.
30
Epitope-binding domains of use in the present invention are domains that specifically bind an antigen or epitope independently of a different V region or domain, this may be a domain antibody or may be a domain which is a derivative of a scaffold selected from the group consisting of CTLA-4 (Evibody); lipocalin; Protein A derived molecules
35 such as Z-domain of Protein A (Affibody, SpA), A-domain (Avimer/Maxibody); Heat shock proteins such as GroEl and GroES; transferrin (trans-body); ankyrin repeat protein (DARPin); peptide aptamer; C-type lectin domain (Tetranectin); human γ-crystallin and human ubiquitin (affilins); PDZ domains; scorpion toxinkunitz type domains of human protease inhibitors; and fibronectin (adnectin); which has been
40 subjected to protein engineering in order to obtain binding to a ligand other than the natural ligand. In one embodiment this may be an domain antibody or other suitable domains such as a domain selected from the group consisting of CTLA-4, lipocallin, SpA, an Affibody, an avimer, GroEl, transferrin, GroES and fibronectin. In one

embodiment this may be selected from a dAb, an Affibody, an ankyrin repeat protein (DARPin) and an adnectin. In another embodiment this may be selected from an Affibody, an ankyrin repeat protein (DARPin) and an adnectin. In another embodiment this may be a domain antibody, for example a domain antibody selected
5 from a human, camelid or shark (NARV) domain antibody.

Epitope-binding domains can be linked to the protein scaffold at one or more positions. These positions include the C-terminus and the N-terminus of the protein scaffold, for example at the C-terminus of the heavy chain and/or the C-terminus of
10 the light chain of an IgG, or for example the N-terminus of the heavy chain and/or the N-terminus of the light chain of an IgG.

In one embodiment, a first epitope binding domain is linked to the protein scaffold and a second epitope binding domain is linked to the first epitope binding domain, for
15 example where the protein scaffold is an IgG scaffold, a first epitope binding domain may be linked to the c-terminus of the heavy chain of the IgG scaffold, and that epitope binding domain can be linked at its c-terminus to a second epitope binding domain, or for example a first epitope binding domain may be linked to the c-terminus of the light chain of the IgG scaffold, and that first epitope binding domain may be
20 further linked at its c-terminus to a second epitope binding domain, or for example a first epitope binding domain may be linked to the n-terminus of the light chain of the IgG scaffold, and that first epitope binding domain may be further linked at its n-terminus to a second epitope binding domain, or for example a first epitope binding domain may be linked to the n-terminus of the heavy chain of the IgG scaffold, and
25 that first epitope binding domain may be further linked at its n-terminus to a second epitope binding domain.

When the epitope-binding domain is a domain antibody, some domain antibodies may be suited to particular positions within the scaffold.

30

Domain antibodies of use in the present invention can be linked at the C-terminal end of the heavy chain and/or the light chain of conventional IgGs. In addition some dAbs can be linked to the C-terminal ends of both the heavy chain and the light chain of conventional antibodies.

35

In constructs where the N-terminus of dAbs are fused to an antibody constant domain (either C_H3 or CL), a peptide linker may help the dAb to bind to antigen. Indeed, the N-terminal end of a dAb is located closely to the complementarity-determining regions (CDRS) involved in antigen-binding activity. Thus a short peptide
40 linker acts as a spacer between the epitope-binding, and the constant domain fo the protein scaffold, which may allow the dAb CDRs to more easily reach the antigen, which may therefore bind with high affinity.

The surroundings in which dAbs are linked to the IgG will differ depending on which antibody chain they are fused to:
When fused at the C-terminal end of the antibody light chain of an IgG scaffold, each dAb is expected to be located in the vicinity of the antibody hinge and the Fc portion.
5 It is likely that such dAbs will be located far apart from each other. In conventional antibodies, the angle between Fab fragments and the angle between each Fab fragment and the Fc portion can vary quite significantly. It is likely that – with mAbdAbs – the angle between the Fab fragments will not be widely different, whilst some angular restrictions may be observed with the angle between each Fab
10 fragment and the Fc portion.
When fused at the C-terminal end of the antibody heavy chain of an IgG scaffold, each dAb is expected to be located in the vicinity of the C_H3 domains of the Fc portion. This is not expected to impact on the Fc binding properties to Fc receptors (e.g. FcγRI, II, III an FcRn) as these receptors engage with the C_H2 domains (for the
15 FcγRI, II and III class of receptors) or with the hinge between the C_H2 and C_H3 domains (e.g. FcRn receptor). Another feature of such antigen-binding constructs is that both dAbs are expected to be spatially close to each other and provided that flexibility is provided by provision of appropriate linkers, these dAbs may even form homodimeric species, hence propagating the 'zipped' quaternary structure of the Fc
20 portion, which may enhance stability of the construct.

Such structural considerations can aid in the choice of the most suitable position to link an epitope-binding domain, for example a dAb, on to a protein scaffold, for example an antibody.
25

The size of the antigen, its localization (in blood or on cell surface), its quaternary structure (monomeric or multimeric) can vary. Conventional antibodies are naturally designed to function as adaptor constructs due to the presence of the hinge region, wherein the orientation of the two antigen-binding sites at the tip of the Fab
30 fragments can vary widely and hence adapt to the molecular feature of the antigen and its surroundings. In contrast dAbs linked to an antibody or other protein scaffold, for example a protein scaffold which comprises an antibody with no hinge region, may have less structural flexibility either directly or indirectly.

35 Understanding the solution state and mode of binding at the dAb is also helpful. Evidence has accumulated that *in vitro* dAbs can predominantly exist in monomeric, homo-dimeric or multimeric forms in solution (Reiter et al. (1999) J Mol Biol 290 p685-698; Ewert et al (2003) J Mol Biol 325, p531-553, Jespers et al (2004) J Mol Biol 337 p893-903; Jespers et al (2004) Nat Biotechnol 22 p1161-1165; Martin et al
40 (1997) Protein Eng. 10 p607-614; Sepulvada et al (2003) J Mol Biol 333 p355-365). This is fairly reminiscent to multimerisation events observed *in vivo* with Ig domains such as Bence-Jones proteins (which are dimers of immunoglobulin light chains (Epp et al (1975) Biochemistry 14 p4943-4952; Huan et al (1994) Biochemistry 33 p14848-

14857; Huang et al (1997) Mol immunol 34 p1291-1301) and amyloid fibers (James *et al*. (2007) *J Mol Biol*. **367**:603-8).

For example, it may be desirable to link domain antibodies that tend to dimerise in solution to the C-terminal end of the Fc portion in preference to the C-terminal end of the light chain as linking to the C-terminal end of the Fc will allow those dAbs to dimerise in the context of the antigen-binding construct of the invention.

The antigen-binding constructs of the present invention may comprise antigen-binding sites specific for a single antigen, or may have antigen-binding sites specific for two or more antigens, or for two or more epitopes on a single antigen, or there may be antigen-binding sites each of which is specific for a different epitope on the same or different antigens.

In particular, the antigen-binding constructs of the present invention may be useful in treating diseases associated with RANKL or OSM for example osteoporosis, or arthritic diseases such as rheumatoid arthritis, erosive arthritis, psoriatic arthritis, polymyalgia rhumatica, ankylosing spondylitis, juvenile rheumatoid arthritis, Paget's disease, osteogenesis imperfecta, osteoporosis, sports or other injuries of the knee, ankle, hand, hip, shoulder or spine, back pain, lupus particularly of the joints, osteoarthritis, or cancer, for example Acute Myologenous Leukaemia, breast cancer, lung cancer, prostate cancer, colon cancer, stomach cancer, bladder cancer, uterine cancer, kidney cancer, multiple myeloma or arthritic diseases.

The antigen-binding constructs of the present invention may be produced by transfection of a host cell with an expression vector comprising the coding sequence for the antigen-binding construct of the invention. An expression vector or recombinant plasmid is produced by placing these coding sequences for the antigen-binding construct in operative association with conventional regulatory control sequences capable of controlling the replication and expression in, and/or secretion from, a host cell. Regulatory sequences include promoter sequences, e.g., CMV promoter, and signal sequences which can be derived from other known antibodies. Similarly, a second expression vector can be produced having a DNA sequence which encodes a complementary antigen-binding construct light or heavy chain. In certain embodiments this second expression vector is identical to the first except insofar as the coding sequences and selectable markers are concerned, so to ensure as far as possible that each polypeptide chain is functionally expressed. Alternatively, the heavy and light chain coding sequences for the antigen-binding construct may reside on a single vector, for example in two expression cassettes in the same vector.
A selected host cell is co-transfected by conventional techniques with both the first and second vectors (or simply transfected by a single vector) to create the transfected host cell of the invention comprising both the recombinant or synthetic

light and heavy chains. The transfected cell is then cultured by conventional techniques to produce the engineered antigen-binding construct of the invention. The antigen-binding construct which includes the association of both the recombinant heavy chain and/or light chain is screened from culture by appropriate assay, such as ELISA or RIA. Similar conventional techniques may be employed to construct other antigen-binding constructs.

Suitable vectors for the cloning and subcloning steps employed in the methods and construction of the compositions of this invention may be selected by one of skill in the art. For example, the conventional pUC series of cloning vectors may be used. One vector, pUC19, is commercially available from supply houses, such as Amersham (Buckinghamshire, United Kingdom) or Pharmacia (Uppsala, Sweden). Additionally, any vector which is capable of replicating readily, has an abundance of cloning sites and selectable genes (e.g., antibiotic resistance), and is easily manipulated may be used for cloning. Thus, the selection of the cloning vector is not a limiting factor in this invention.

The expression vectors may also be characterized by genes suitable for amplifying expression of the heterologous DNA sequences, e.g., the mammalian dihydrofolate reductase gene (DHFR). Other preferable vector sequences include a poly A signal sequence, such as from bovine growth hormone (BGH) and the betaglobin promoter sequence (betaglopro). The expression vectors useful herein may be synthesized by techniques well known to those skilled in this art.

The components of such vectors, e.g. replicons, selection genes, enhancers, promoters, signal sequences and the like, may be obtained from commercial or natural sources or synthesized by known procedures for use in directing the expression and/or secretion of the product of the recombinant DNA in a selected host. Other appropriate expression vectors of which numerous types are known in the art for mammalian, bacterial, insect, yeast, and fungal expression may also be selected for this purpose.

The present invention also encompasses a cell line transfected with a recombinant plasmid containing the coding sequences of the antigen-binding constructs of the present invention. Host cells useful for the cloning and other manipulations of these cloning vectors are also conventional. However, cells from various strains of E. coli may be used for replication of the cloning vectors and other steps in the construction of antigen-binding constructs of this invention.

Suitable host cells or cell lines for the expression of the antigen-binding constructs of the invention include mammalian cells such as NS0, Sp2/0, CHO (e.g. DG44), COS, HEK, a fibroblast cell (e.g., 3T3), and myeloma cells, for example it may be expressed in a CHO or a myeloma cell. Human cells may be used, thus enabling the molecule to be modified with human glycosylation patterns. Alternatively, other eukaryotic cell lines may be employed. The selection of suitable mammalian host cells and methods for transformation, culture, amplification, screening and product production and purification are known in the art. See, e.g., Sambrook et al., cited above.

Bacterial cells may prove useful as host cells suitable for the expression of the recombinant Fabs or other embodiments of the present invention (see, e.g., Plückthun, A., Immunol. Rev., 130:151-188 (1992)). However, due to the tendency of proteins expressed in bacterial cells to be in an unfolded or improperly folded form or in a non-glycosylated form, any recombinant Fab produced in a bacterial cell would have to be screened for retention of antigen binding ability. If the molecule expressed by the bacterial cell was produced in a properly folded form, that bacterial cell would be a desirable host, or in alternative embodiments the molecule may express in the bacterial host and then be subsequently re-folded. For example, various strains of E. coli used for expression are well-known as host cells in the field of biotechnology. Various strains of B. subtilis, Streptomyces, other bacilli and the like may also be employed in this method.

Where desired, strains of yeast cells known to those skilled in the art are also available as host cells, as well as insect cells, e.g. Drosophila and Lepidoptera and viral expression systems. See, e.g. Miller et al., Genetic Engineering, 8:277-298, Plenum Press (1986) and references cited therein.

The general methods by which the vectors may be constructed, the transfection methods required to produce the host cells of the invention, and culture methods necessary to produce the antigen-binding construct of the invention from such host cell may all be conventional techniques. Typically, the culture method of the present invention is a serum-free culture method, usually by culturing cells serum-free in suspension. Likewise, once produced, the antigen-binding constructs of the invention may be purified from the cell culture contents according to standard procedures of the art, including ammonium sulfate precipitation, affinity columns, column chromatography, gel electrophoresis and the like. Such techniques are within the skill of the art and do not limit this invention. For example, preparation of altered antibodies are described in WO 99/58679 and WO 96/16990.

Yet another method of expression of the antigen-binding constructs may utilize expression in a transgenic animal, such as described in U. S. Patent No. 4,873,316. This relates to an expression system using the animal's casein promoter which when transgenically incorporated into a mammal permits the female to produce the desired recombinant protein in its milk.

In a further aspect of the invention there is provided a method of producing an antibody of the invention which method comprises the step of culturing a host cell transformed or transfected with a vector encoding the light and/or heavy chain of the antibody of the invention and recovering the antibody thereby produced.

In accordance with the present invention there is provided a method of producing an antigen-binding construct of the present invention which method comprises the steps of;

(a) providing a first vector encoding a heavy chain of the antigen-binding construct;
(b) providing a second vector encoding a light chain of the antigen-binding construct;

(c) transforming a mammalian host cell (e.g. CHO) with said first and second vectors;
(d) culturing the host cell of step (c) under conditions conducive to the secretion of the antigen-binding construct from said host cell into said culture media;
(e) recovering the secreted antigen-binding construct of step (d).

Once expressed by the desired method, the antigen-binding construct is then examined for in vitro activity by use of an appropriate assay. Presently conventional ELISA assay formats are employed to assess qualitative and quantitative binding of the antigen-binding construct to its target. Additionally, other in vitro assays may also be used to verify neutralizing efficacy prior to subsequent human clinical studies performed to evaluate the persistence of the antigen-binding construct in the body despite the usual clearance mechanisms.

The dose and duration of treatment relates to the relative duration of the molecules of the present invention in the human circulation, and can be adjusted by one of skill in the art depending upon the condition being treated and the general health of the patient. It is envisaged that repeated dosing (e.g. once a week or once every two weeks) over an extended time period (e.g. four to six months) maybe required to achieve maximal therapeutic efficacy.

The mode of administration of the therapeutic agent of the invention may be any suitable route which delivers the agent to the host. The antigen-binding constructs, and pharmaceutical compositions of the invention are particularly useful for parenteral administration, i.e., subcutaneously (s.c.), intrathecally, intraperitoneally, intramuscularly (i.m.), intravenously (i.v.), or intranasally.

Therapeutic agents of the invention may be prepared as pharmaceutical compositions containing an effective amount of the antigen-binding construct of the invention as an active ingredient in a pharmaceutically acceptable carrier. In the prophylactic agent of the invention, an aqueous suspension or solution containing the antigen-binding construct, preferably buffered at physiological pH, in a form ready for injection is preferred. The compositions for parenteral administration will commonly comprise a solution of the antigen-binding construct of the invention or a cocktail thereof dissolved in a pharmaceutically acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers may be employed, e.g., 0.9% saline, 0.3% glycine, and the like. These solutions may be made sterile and generally free of particulate matter. These solutions may be sterilized by conventional, well known sterilization techniques (e.g., filtration). The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, etc. The concentration of the antigen-binding construct of the invention in such pharmaceutical formulation can vary widely, i.e., from less than about 0.5%, usually at or at least about 1% to as much as 15 or 20% by weight and will be selected

primarily based on fluid volumes, viscosities, etc., according to the particular mode of administration selected.

Thus, a pharmaceutical composition of the invention for intramuscular injection could be prepared to contain 1 mL sterile buffered water, and between about 1 ng to about 200 mg, e.g. about 50 ng to about 30 mg or more preferably, about 5 mg to about 25 mg, of an antigen-binding construct of the invention. Similarly, a pharmaceutical composition of the invention for intravenous infusion could be made up to contain about 250 ml of sterile Ringer's solution, and about 1 to about 30 and preferably 5 mg to about 25 mg of an antigen-binding construct of the invention per ml of Ringer's solution. Actual methods for preparing parenterally administrable compositions are well known or will be apparent to those skilled in the art and are described in more detail in, for example, Remington's Pharmaceutical Science, 15th ed., Mack Publishing Company, Easton, Pennsylvania. For the preparation of intravenously administrable antigen-binding construct formulations of the invention see Lasmar U and Parkins D "The formulation of Biopharmaceutical products", Pharma. Sci.Tech.today, page 129-137, Vol.3 (3rd April 2000), Wang, W "Instability, stabilisation and formulation of liquid protein pharmaceuticals", Int. J. Pharm 185 (1999) 129-188, Stability of Protein Pharmaceuticals Part A and B ed Ahern T.J., Manning M.C., New York, NY: Plenum Press (1992), Akers,M.J. "Excipient-Drug interactions in Parenteral Formulations", J.Pharm Sci 91 (2002) 2283-2300, Imamura, K et al "Effects of types of sugar on stabilization of Protein in the dried state", J Pharm Sci 92 (2003) 266-274,Izutsu, Kkojima, S. "Excipient crystalinity and its protein-structure-stabilizing effect during freeze-drying", J Pharm. Pharmacol, 54 (2002) 1033-1039, Johnson, R, "Mannitol-sucrose mixtures-versatile formulations for protein lyophilization", J. Pharm. Sci, 91 (2002) 914-922.
Ha,E Wang W, Wang Y.j. "Peroxide formation in polysorbate 80 and protein stability", J. Pharm Sci, 91, 2252-2264,(2002) the entire contents of which are incorporated herein by reference and to which the reader is specifically referred.
It is preferred that the therapeutic agent of the invention, when in a pharmaceutical preparation, be present in unit dose forms. The appropriate therapeutically effective dose will be determined readily by those of skill in the art. Suitable doses may be calculated for patients according to their weight, for example suitable doses may be in the range of 0.01 to 20mg/kg, for example 0.1 to 20mg/kg, for example 1 to 20mg/kg, for example 10 to 20mg/kg or for example 1 to 15mg/kg, for example 10 to 15mg/kg. To effectively treat conditions of use in the present invention in a human, suitable doses may be within the range of 0.01 to 1000 mg, for example 0.1 to 1000mg, for example 0.1 to 500mg, for example 500mg, for example 0.1 to 100mg, or 0.1 to 80mg, or 0.1 to 60mg, or 0.1 to 40mg, or for example 1 to 100mg, or 1 to 50mg, of an antigen-binding construct of this invention, which may be administered parenterally, for example subcutaneously, intravenously or intramuscularly. Such dose may, if necessary, be repeated at appropriate time intervals selected as appropriate by a physician.

The antigen-binding constructs described herein can be lyophilized for storage and reconstituted in a suitable carrier prior to use. This technique has been shown to be effective with conventional immunoglobulins and art-known lyophilization and reconstitution techniques can be employed.

There are several methods known in the art which can be used to find epitope-binding domains of use in the present invention.

The term “library” refers to a mixture of heterogeneous polypeptides or nucleic acids. The library is composed of members, each of which has a single polypeptide or nucleic acid sequence. To this extent, “library” is synonymous with “repertoire.” Sequence differences between library members are responsible for the diversity present in the library. The library may take the form of a simple mixture of polypeptides or nucleic acids, or may be in the form of organisms or cells, for example bacteria, viruses, animal or plant cells and the like, transformed with a library of nucleic acids. In one example, each individual organism or cell contains only one or a limited number of library members. Advantageously, the nucleic acids are incorporated into expression vectors, in order to allow expression of the polypeptides encoded by the nucleic acids. In a one aspect, therefore, a library may take the form of a population of host organisms, each organism containing one or more copies of an expression vector containing a single member of the library in nucleic acid form which can be expressed to produce its corresponding polypeptide member. Thus, the population of host organisms has the potential to encode a large repertoire of diverse polypeptides.

A “universal framework” is a single antibody framework sequence corresponding to the regions of an antibody conserved in sequence as defined by Kabat (“Sequences of Proteins of Immunological Interest”, US Department of Health and Human Services) or corresponding to the human germline immunoglobulin repertoire or structure as defined by Chothia and Lesk, (1987) J. Mol. Biol. 196:910-917. There may be a single framework, or a set of such frameworks, which has been found to permit the derivation of virtually any binding specificity though variation in the hypervariable regions alone.

Amino acid and nucleotide sequence alignments and homology, similarity or identity, as defined herein are in one embodiment prepared and determined using the algorithm BLAST 2 Sequences, using default parameters (Tatusova, T. A. *et al.*, *FEMS Microbiol Lett*, *174*:187-188 (1999)).

When a display system (*e.g.*, a display system that links coding function of a nucleic acid and functional characteristics of the peptide or polypeptide encoded by the nucleic acid) is used in the methods described herein, eg in the selection of a dAb or other epitope binding domain, it is frequently advantageous to amplify or increase the copy number of the nucleic acids that encode the selected peptides or polypeptides. This provides an efficient way of obtaining sufficient quantities of nucleic acids and/or

peptides or polypeptides for additional rounds of selection, using the methods described herein or other suitable methods, or for preparing additional repertoires (*e.g.*, affinity maturation repertoires). Thus, in some embodiments, the methods of selecting epitope binding domains comprises using a display system (*e.g.*, that links coding function of a nucleic acid and functional characteristics of the peptide or polypeptide encoded by the nucleic acid, such as phage display) and further comprises amplifying or increasing the copy number of a nucleic acid that encodes a selected peptide or polypeptide. Nucleic acids can be amplified using any suitable methods, such as by phage amplification, cell growth or polymerase chain reaction.

In one example, the methods employ a display system that links the coding function of a nucleic acid and physical, chemical and/or functional characteristics of the polypeptide encoded by the nucleic acid. Such a display system can comprise a plurality of replicable genetic packages, such as bacteriophage or cells (bacteria). The display system may comprise a library, such as a bacteriophage display library. Bacteriophage display is an example of a display system.
A number of suitable bacteriophage display systems (*e.g.*, monovalent display and multivalent display systems) have been described. (See, *e.g.*, Griffiths *et al.*, U.S. Patent No. 6,555,313 B1 (incorporated herein by reference); Johnson *et al.*, U.S. Patent No. 5,733,743 (incorporated herein by reference); McCafferty *et al.*, U.S. Patent No. 5,969,108 (incorporated herein by reference); Mulligan-Kehoe, U.S. Patent No. 5,702,892 (Incorporated herein by reference); Winter, G. *et al.*, *Annu. Rev. Immunol. 12*:433-455 (1994); Soumillion, P. *et al., Appl. Biochem. Biotechnol.* 47(2-3):175-189 (1994); Castagnoli, L. *et al., Comb. Chem. High Throughput Screen,* 4(2):121-133 (2001).) The peptides or polypeptides displayed in a bacteriophage display system can be displayed on any suitable bacteriophage, such as a filamentous phage (*e.g.*, fd, M13, F1), a lytic phage (*e.g.*, T4, T7, lambda), or an RNA phage (*e.g.*, MS2), for example.
Generally, a library of phage that displays a repertoire of peptides or phagepolypeptides, as fusion proteins with a suitable phage coat protein (*e.g.*, fd pIII protein), is produced or provided. The fusion protein can display the peptides or polypeptides at the tip of the phage coat protein, or if desired at an internal position. For example, the displayed peptide or polypeptide can be present at a position that is amino-terminal to domain 1 of pIII. (Domain 1 of pIII is also referred to as N1.) The displayed polypeptide can be directly fused to pIII (*e.g.*, the N-terminus of domain 1 of pIII) or fused to pIII using a linker. If desired, the fusion can further comprise a tag (*e.g.*, myc epitope, His tag). Libraries that comprise a repertoire of peptides or polypeptides that are displayed as fusion proteins with a phage coat protein,can be produced using any suitable methods, such as by introducing a library of phage vectors or phagemid vectors encoding the displayed peptides or polypeptides into suitable host bacteria, and culturing the resulting bacteria to produce phage (*e.g.*, using a suitable helper phage or complementing plasmid if desired). The library of

phage can be recovered from the culture using any suitable method, such as precipitation and centrifugation.

The display system can comprise a repertoire of peptides or polypeptides that contains any desired amount of diversity. For example, the repertoire can contain peptides or polypeptides that have amino acid sequences that correspond to naturally occurring polypeptides expressed by an organism, group of organisms, desired tissue or desired cell type, or can contain peptides or polypeptides that have random or randomized amino acid sequences. If desired, the polypeptides can share a common core or scaffold. For example, all polypeptides in the repertoire or library can be based on a scaffold selected from protein A, protein L, protein G, a fibronectin domain, an anticalin, CTLA4, a desired enzyme (*e.g.*, a polymerase, a cellulase), or a polypeptide from the immunoglobulin superfamily, such as an antibody or antibody fragment (*e.g.*, an antibody variable domain). The polypeptides in such a repertoire or library can comprise defined regions of random or randomized amino acid sequence and regions of common amino acid sequence. In certain embodiments, all or substantially all polypeptides in a repertoire are of a desired type, such as a desired enzyme (*e.g.*, a polymerase) or a desired antigen-binding fragment of an antibody (*e.g.*, human V_H or human V_L). In some embodiments, the polypeptide display system comprises a repertoire of polypeptides wherein each polypeptide comprises an antibody variable domain. For example, each polypeptide in the repertoire can contain a V_H, a V_L or an Fv (*e.g.*, a single chain Fv).

Amino acid sequence diversity can be introduced into any desired region of a peptide or polypeptide or scaffold using any suitable method. For example, amino acid sequence diversity can be introduced into a target region, such as a complementarity determining region of an antibody variable domain or a hydrophobic domain, by preparing a library of nucleic acids that encode the diversified polypeptides using any suitable mutagenesis methods (*e.g.*, low fidelity PCR, oligonucleotide-mediated or site directed mutagenesis, diversification using NNK codons) or any other suitable method. If desired, a region of a polypeptide to be diversified can be randomized.

The size of the polypeptides that make up the repertoire is largely a matter of choice and uniform polypeptide size is not required. The polypeptides in the repertoire may have at least tertiary structure (form at least one domain).

Selection/Isolation/Recovery

An epitope binding domain or population of domains can be selected, isolated and/or recovered from a repertoire or library (*e.g.*, in a display system) using any suitable method. For example, a domain is selected or isolated based on a selectable characteristic (*e.g.*, physical characteristic, chemical characteristic, functional characteristic). Suitable selectable functional characteristics include biological activities of the peptides or polypeptides in the repertoire, for example, binding to a generic ligand (*e.g.*, a superantigen), binding to a target ligand (*e.g.*, an antigen, an epitope, a substrate), binding to an antibody (*e.g.*, through an epitope expressed on a

peptide or polypeptide), and catalytic activity. (See, *e.g.*, Tomlinson *et al.*, WO 99/20749; WO 01/57065; WO 99/58655.)

In some embodiments, the protease resistant peptide or polypeptide is selected and/or isolated from a library or repertoire of peptides or polypeptides in which
5 substantially all domains share a common selectable feature. For example, the domain can be selected from a library or repertoire in which substantially all domains bind a common generic ligand, bind a common target ligand, bind (or are bound by) a common antibody, or possess a common catalytic activity. This type of selection is particularly useful for preparing a repertoire of domains that are based on a parental
10 peptide or polypeptide that has a desired biological activity, for example, when performing affinity maturation of an immunoglobulin single variable domain.

Selection based on binding to a common generic ligand can yield a collection or population of domains that contain all or substantially all of the domains that were components of the original library or repertoire. For example, domains that bind a
15 target ligand or a generic ligand, such as protein A, protein L or an antibody, can be selected, isolated and/or recovered by panning or using a suitable affinity matrix. Panning can be accomplished by adding a solution of ligand (*e.g.*, generic ligand, target ligand) to a suitable vessel (*e.g.*, tube, petri dish) and allowing the ligand to become deposited or coated onto the walls of the vessel. Excess ligand can be
20 washed away and domains can be added to the vessel and the vessel maintained under conditions suitable for peptides or polypeptides to bind the immobilized ligand. Unbound domains can be washed away and bound domains can be recovered using any suitable method, such as scraping or lowering the pH, for example.

Suitable ligand affinity matrices generally contain a solid support or bead (*e.g.*,
25 agarose) to which a ligand is covalently or noncovalently attached. The affinity matrix can be combined with peptides or polypeptides (*e.g.*, a repertoire that has been incubated with protease) using a batch process, a column process or any other suitable process under conditions suitable for binding of domains to the ligand on the matrix. domains that do not bind the affinity matrix can be washed away and bound
30 domains can be eluted and recovered using any suitable method, such as elution with a lower pH buffer, with a mild denaturing agent (*e.g.*, urea), or with a peptide or domain that competes for binding to the ligand. In one example, a biotinylated target ligand is combined with a repertoire under conditions suitable for domains in the repertoire to bind the target ligand. Bound domains are recovered using immobilized
35 avidin or streptavidin (*e.g.*, on a bead).

In some embodiments, the generic or target ligand is an antibody or antigen binding fragment thereof. Antibodies or antigen binding fragments that bind structural features of peptides or polypeptides that are substantially conserved in the peptides or polypeptides of a library or repertoire are particularly useful as generic ligands.
40 Antibodies and antigen binding fragments suitable for use as ligands for isolating, selecting and/or recovering protease resistant peptides or polypeptides can be monoclonal or polyclonal and can be prepared using any suitable method.

LIBRARIES/REPERTOIRES

Libraries that encode and/or contain protease epitope binding domains can be prepared or obtained using any suitable method. A library can be designed to encode domains based on a domain or scaffold of interest (*e.g.*, a domain selected from a library) or can be selected from another library using the methods described herein. For example, a library enriched in domains can be prepared using a suitable polypeptide display system.

Libraries that encode a repertoire of a desired type of domain can readily be produced using any suitable method. For example, a nucleic acid sequence that encodes a desired type of polypeptide (*e.g.*, an immunoglobulin variable domain) can be obtained and a collection of nucleic acids that each contain one or more mutations can be prepared, for example by amplifying the nucleic acid using an error-prone polymerase chain reaction (PCR) system, by chemical mutagenesis (Deng *et al., J. Biol. Chem.*, 269:9533 (1994)) or using bacterial mutator strains (Low *et al., J. Mol. Biol.*, 260:359 (1996)).

In other embodiments, particular regions of the nucleic acid can be targeted for diversification. Methods for mutating selected positions are also well known in the art and include, for example, the use of mismatched oligonucleotides or degenerate oligonucleotides, with or without the use of PCR. For example, synthetic antibody libraries have been created by targeting mutations to the antigen binding loops. Random or semi-random antibody H3 and L3 regions have been appended to germline immunoblulin V gene segments to produce large libraries with unmutated framework regions (Hoogenboom and Winter (1992) supra; Nissim *et al.* (1994) supra; Griffiths *et al.* (1994) supra; DeKruif *et al.* (1995) supra). Such diversification has been extended to include some or all of the other antigen binding loops (Crameri *et al.* (1996) *Nature Med.*, 2:100; Riechmann *et al.* (1995) *Bio/Technology*, 13:475; Morphosys, WO 97/08320, supra). In other embodiments, particular regions of the nucleic acid can be targeted for diversification by, for example, a two-step PCR strategy employing the product of the first PCR as a "mega-primer." (See, *e.g.*, Landt, O. *et al., Gene 96*:125-128 (1990).) Targeted diversification can also be accomplished, for example, by SOE PCR. (See, *e.g.*, Horton, R.M. *et al., Gene 77*:61-68 (1989).)

Sequence diversity at selected positions can be achieved by altering the coding sequence which specifies the sequence of the polypeptide such that a number of possible amino acids (*e.g.*, all 20 or a subset thereof) can be incorporated at that position. Using the IUPAC nomenclature, the most versatile codon is NNK, which encodes all amino acids as well as the TAG stop codon. The NNK codon may be used in order to introduce the required diversity. Other codons which achieve the same ends are also of use, including the NNN codon, which leads to the production of the additional stop codons TGA and TAA. Such a targeted approach can allow the full sequence space in a target area to be explored.

Some libraries comprise domains that are members of the immunoglobulin superfamily (*e.g.,* antibodies or portions thereof). For example the libraries can

comprise domains that have a known main-chain conformation. (See, *e.g.*, Tomlinson et al., WO 99/20749.) Libraries can be prepared in a suitable plasmid or vector. As used herein, vector refers to a discrete element that is used to introduce heterologous DNA into cells for the expression and/or replication thereof. Any suitable vector can be used, including plasmids (*e.g.*, bacterial plasmids), viral or bacteriophage vectors, artificial chromosomes and episomal vectors. Such vectors may be used for simple cloning and mutagenesis, or an expression vector can be used to drive expression of the library. Vectors and plasmids usually contain one or more cloning sites (*e.g.*, a polylinker), an origin of replication and at least one selectable marker gene. Expression vectors can further contain elements to drive transcription and translation of a polypeptide, such as an enhancer element, promoter, transcription termination signal, signal sequences, and the like. These elements can be arranged in such a way as to be operably linked to a cloned insert encoding a polypeptide, such that the polypeptide is expressed and produced when such an expression vector is maintained under conditions suitable for expression (*e.g.*, in a suitable host cell).

Cloning and expression vectors generally contain nucleic acid sequences that enable the vector to replicate in one or more selected host cells. Typically in cloning vectors, this sequence is one that enables the vector to replicate independently of the host chromosomal DNA and includes origins of replication or autonomously replicating sequences. Such sequences are well known for a variety of bacteria, yeast and viruses. The origin of replication from the plasmid pBR322 is suitable for most Gram-negative bacteria, the 2 micron plasmid origin is suitable for yeast, and various viral origins (*e.g.* SV40, adenovirus) are useful for cloning vectors in mammalian cells. Generally, the origin of replication is not needed for mammalian expression vectors, unless these are used in mammalian cells able to replicate high levels of DNA, such as COS cells.

Cloning or expression vectors can contain a selection gene also referred to as selectable marker. Such marker genes encode a protein necessary for the survival or growth of transformed host cells grown in a selective culture medium. Host cells not transformed with the vector containing the selection gene will therefore not survive in the culture medium. Typical selection genes encode proteins that confer resistance to antibiotics and other toxins, *e.g.* ampicillin, neomycin, methotrexate or tetracycline, complement auxotrophic deficiencies, or supply critical nutrients not available in the growth media.

Suitable expression vectors can contain a number of components, for example, an origin of replication, a selectable marker gene, one or more expression control elements, such as a transcription control element (*e.g.*, promoter, enhancer, terminator) and/or one or more translation signals, a signal sequence or leader sequence, and the like. Expression control elements and a signal or leader sequence, if present, can be provided by the vector or other source. For example, the transcriptional and/or translational control sequences of a cloned nucleic acid encoding an antibody chain can be used to direct expression.

A promoter can be provided for expression in a desired host cell. Promoters can be constitutive or inducible. For example, a promoter can be operably linked to a nucleic acid encoding an antibody, antibody chain or portion thereof, such that it directs transcription of the nucleic acid. A variety of suitable promoters for procaryotic (*e.g.*, the β-lactamase and lactose promoter systems, alkaline phosphatase, the tryptophan (trp) promoter system, lac, tac, T3, T7 promoters for *E. coli*) and eucaryotic (*e.g.*, simian virus 40 early or late promoter, Rous sarcoma virus long terminal repeat promoter, cytomegalovirus promoter, adenovirus late promoter, EG-1a promoter) hosts are available.

In addition, expression vectors typically comprise a selectable marker for selection of host cells carrying the vector, and, in the case of a replicable expression vector, an origin of replication. Genes encoding products which confer antibiotic or drug resistance are common selectable markers and may be used in procaryotic (*e.g.*, β-lactamase gene (ampicillin resistance), *Tet* gene for tetracycline resistance) and eucaryotic cells (*e.g.*, neomycin (G418 or geneticin), gpt (mycophenolic acid), ampicillin, or hygromycin resistance genes). Dihydrofolate reductase marker genes permit selection with methotrexate in a variety of hosts. Genes encoding the gene product of auxotrophic markers of the host (*e.g.*, *LEU2, URA3, HIS3*) are often used as selectable markers in yeast. Use of viral (*e.g.*, baculovirus) or phage vectors, and vectors which are capable of integrating into the genome of the host cell, such as retroviral vectors, are also contemplated.

Suitable expression vectors for expression in prokaryotic (*e.g.*, bacterial cells such as *E. coli*) or mammalian cells include, for example, a pET vector (*e.g.*, pET-12a, pET-36, pET-37, pET-39, pET-40, Novagen and others), a phage vector (*e.g.*, pCANTAB 5 E, Pharmacia), pRIT2T (Protein A fusion vector, Pharmacia), pCDM8, pCDNA1.1/amp, pcDNA3.1, pRc/RSV, pEF-1 (Invitrogen, Carlsbad, CA), pCMV-SCRIPT, pFB, pSG5, pXT1 (Stratagene, La Jolla, CA), pCDEF3 (Goldman, L.A., *et al.*, *Biotechniques*, *21*:1013-1015 (1996)), pSVSPORT (GibcoBRL, Rockville, MD), pEF-Bos (Mizushima, S., *et al.*, *Nucleic Acids Res.*, *18*:5322 (1990)) and the like.

Expression vectors which are suitable for use in various expression hosts, such as prokaryotic cells (*E. coli*), insect cells (*Drosophila* Schnieder S2 cells, Sf9), yeast (*P. methanolica*, *P. pastoris*, *S. cerevisiae*) and mammalian cells (eg, COS cells) are available.

Some examples of vectors are expression vectors that enable the expression of a nucleotide sequence corresponding to a polypeptide library member. Thus, selection with generic and/or target ligands can be performed by separate propagation and expression of a single clone expressing the polypeptide library member. As described above, a particular selection display system is bacteriophage display. Thus, phage or phagemid vectors may be used, for example vectors may be phagemid vectors which have an *E. coli.* origin of replication (for double stranded replication) and also a phage origin of replication (for production of single-stranded DNA). The manipulation and expression of such vectors is well known in the art (Hoogenboom and Winter (1992) supra; Nissim *et al.* (1994) supra). Briefly, the

vector can contain a β-lactamase gene to confer selectivity on the phagemid and a lac promoter upstream of an expression cassette that can contain a suitable leader sequence, a multiple cloning site, one or more peptide tags, one or more TAG stop codons and the phage protein pIII. Thus, using various suppressor and non-suppressor strains of *E. coli* and with the addition of glucose, iso-propyl thio-β-D-galactoside (IPTG) or a helper phage, such as VCS M13, the vector is able to replicate as a plasmid with no expression, produce large quantities of the polypeptide library member only or product phage, some of which contain at least one copy of the polypeptide-pIII fusion on their surface.

Antibody variable domains may comprise a target ligand binding site and/or a generic ligand binding site. In certain embodiments, the generic ligand binding site is a binding site for a superantigen, such as protein A, protein L or protein G. The variable domains can be based on any desired variable domain, for example a human VH (*e.g.*, V_H 1a, V_H 1b, V_H 2, V_H 3, V_H 4, V_H 5, V_H 6), a human Vλ (*e.g.*, VλI, VλII, VλIII, VλIV, VλV, VλVI or Vκ1) or a human Vκ (*e.g.*, Vκ2, Vκ3, Vκ4, Vκ5, Vκ6, Vκ7, Vκ8, Vκ9 or Vκ10).

A still further category of techniques involves the selection of repertoires in artificial compartments, which allow the linkage of a gene with its gene product. For example, a selection system in which nucleic acids encoding desirable gene products may be selected in microcapsules formed by water-in-oil emulsions is described in WO99/02671, WO00/40712 and Tawfik & Griffiths (1998) *Nature Biotechnol* **16**(7), 652-6. Genetic elements encoding a gene product having a desired activity are compartmentalised into microcapsules and then transcribed and/or translated to produce their respective gene products (RNA or protein) within the microcapsules. Genetic elements which produce gene product having desired activity are subsequently sorted. This approach selects gene products of interest by detecting the desired activity by a variety of means.

Characterisation of the epitope binding domains.

The binding of a domain to its specific antigen or epitope can be tested by methods which will be familiar to those skilled in the art and include ELISA. In one example, binding is tested using monoclonal phage ELISA.

Phage ELISA may be performed according to any suitable procedure: an exemplary protocol is set forth below.

Populations of phage produced at each round of selection can be screened for binding by ELISA to the selected antigen or epitope, to identify "polyclonal" phage antibodies. Phage from single infected bacterial colonies from these populations can then be screened by ELISA to identify "monoclonal" phage antibodies. It is also desirable to screen soluble antibody fragments for binding to antigen or epitope, and

this can also be undertaken by ELISA using reagents, for example, against a C- or N-terminal tag (see for example Winter *et al.* (1994) Ann. Rev. Immunology 12, 433-55 and references cited therein.

5 The diversity of the selected phage monoclonal antibodies may also be assessed by gel electrophoresis of PCR products (Marks *et al.* 1991, *supra*; Nissim *et al.* 1994 *supra*), probing (Tomlinson *et al.*, 1992) J. Mol. Biol. 227, 776) or by sequencing of the vector DNA.

10 Structure of dAbs

In the case that the dAbs are selected from V-gene repertoires selected for instance using phage display technology as herein described, then these variable domains comprise a universal framework region, such that is they may be recognised by a
15 specific generic ligand as herein defined. The use of universal frameworks, generic ligands and the like is described in WO99/20749.

Where V-gene repertoires are used variation in polypeptide sequence may be located within the structural loops of the variable domains. The polypeptide
20 sequences of either variable domain may be altered by DNA shuffling or by mutation in order to enhance the interaction of each variable domain with its complementary pair. DNA shuffling is known in the art and taught, for example, by Stemmer, 1994, Nature 370: 389-391 and U.S. Patent No. 6,297,053, both of which are incorporated herein by reference. Other methods of mutagenesis are well known to those of skill
25 in the art.

Scaffolds for use in Constructing dAbs

i. Selection of the main-chain conformation
30 The members of the immunoglobulin superfamily all share a similar fold for their polypeptide chain. For example, although antibodies are highly diverse in terms of their primary sequence, comparison of sequences and crystallographic structures has revealed that, contrary to expectation, five of the six antigen binding loops of antibodies (H1, H2, L1, L2, L3) adopt a limited number of main-chain conformations,
35 or canonical structures (Chothia and Lesk (1987) *J. Mol. Biol.*, **196**: 901; Chothia *et al.* (1989) *Nature*, **342**: 877). Analysis of loop lengths and key residues has therefore enabled prediction of the main-chain conformations of H1, H2, L1, L2 and L3 found in the majority of human antibodies (Chothia *et al.* (1992) *J. Mol. Biol.*, **227**: 799; Tomlinson *et al.* (1995) *EMBO J.*, **14**: 4628; Williams *et al.* (1996) *J. Mol. Biol.*, **264**:
40 220). Although the H3 region is much more diverse in terms of sequence, length and structure (due to the use of D segments), it also forms a limited number of main-chain conformations for short loop lengths which depend on the length and the presence of particular residues, or types of residue, at key positions in the loop and

the antibody framework (Martin *et al.* (1996) *J. Mol. Biol.*, **263**: 800; Shirai *et al.* (1996) *FEBS Letters*, **399**: 1).

The dAbs are advantageously assembled from libraries of domains, such as libraries of V_H domains and/or libraries of V_L domains. In one aspect, libraries of domains are designed in which certain loop lengths and key residues have been chosen to ensure that the main-chain conformation of the members is known. Advantageously, these are real conformations of immunoglobulin superfamily molecules found in nature, to minimise the chances that they are non-functional, as discussed above. Germline V gene segments serve as one suitable basic framework for constructing antibody or T-cell receptor libraries; other sequences are also of use. Variations may occur at a low frequency, such that a small number of functional members may possess an altered main-chain conformation, which does not affect its function.

Canonical structure theory is also of use to assess the number of different main-chain conformations encoded by ligands, to predict the main-chain conformation based on ligand sequences and to chose residues for diversification which do not affect the canonical structure. It is known that, in the human V_κ domain, the L1 loop can adopt one of four canonical structures, the L2 loop has a single canonical structure and that 90% of human V_κ domains adopt one of four or five canonical structures for the L3 loop (Tomlinson *et al.* (1995) supra); thus, in the V_κ domain alone, different canonical structures can combine to create a range of different main-chain conformations. Given that the $V\lambda$ domain encodes a different range of canonical structures for the L1, L2 and L3 loops and that V_κ and $V\lambda$ domains can pair with any V_H domain which can encode several canonical structures for the H1 and H2 loops, the number of canonical structure combinations observed for these five loops is very large. This implies that the generation of diversity in the main-chain conformation may be essential for the production of a wide range of binding specificities. However, by constructing an antibody library based on a single known main-chain conformation it has been found, contrary to expectation, that diversity in the main-chain conformation is not required to generate sufficient diversity to target substantially all antigens. Even more surprisingly, the single main-chain conformation need not be a consensus structure - a single naturally occurring conformation can be used as the basis for an entire library. Thus, in a one particular aspect, the dAbs possess a single known main-chain conformation.

The single main-chain conformation that is chosen may be commonplace among molecules of the immunoglobulin superfamily type in question. A conformation is commonplace when a significant number of naturally occurring molecules are observed to adopt it. Accordingly, in one aspect, the natural occurrence of the different main-chain conformations for each binding loop of an immunoglobulin domain are considered separately and then a naturally occurring variable domain is chosen which possesses the desired combination of main-chain conformations for

the different loops. If none is available, the nearest equivalent may be chosen. The desired combination of main-chain conformations for the different loops may be created by selecting germline gene segments which encode the desired main-chain conformations. In one example, the selected germline gene segments are frequently expressed in nature, and in particular they may be the most frequently expressed of all natural germline gene segments.

In designing libraries the incidence of the different main-chain conformations for each of the six antigen binding loops may be considered separately. For H1, H2, L1, L2 and L3, a given conformation that is adopted by between 20% and 100% of the antigen binding loops of naturally occurring molecules is chosen. Typically, its observed incidence is above 35% (i.e. between 35% and 100%) and, ideally, above 50% or even above 65%. Since the vast majority of H3 loops do not have canonical structures, it is preferable to select a main-chain conformation which is commonplace among those loops which do display canonical structures. For each of the loops, the conformation which is observed most often in the natural repertoire is therefore selected. In human antibodies, the most popular canonical structures (CS) for each loop are as follows: H1 - CS 1 (79% of the expressed repertoire), H2 - CS 3 (46%), L1 - CS 2 of V_κ(39%), L2 - CS 1 (100%), L3 - CS 1 of V_κ(36%) (calculation assumes a κ:λ ratio of 70:30, Hood *et al.* (1967) *Cold Spring Harbor Symp. Quant. Biol.*, **48**: 133). For H3 loops that have canonical structures, a CDR3 length (Kabat *et al.* (1991) *Sequences of proteins of immunological interest*, U.S. Department of Health and Human Services) of seven residues with a salt-bridge from residue 94 to residue 101 appears to be the most common. There are at least 16 human antibody sequences in the EMBL data library with the required H3 length and key residues to form this conformation and at least two crystallographic structures in the protein data bank which can be used as a basis for antibody modelling (2cgr and 1tet). The most frequently expressed germline gene segments that this combination of canonical structures are the V_H segment 3-23 (DP-47), the J_H segment JH4b, the V_κ segment O2/O12 (DPK9) and the J_κ segment J_κ1. V_H segments DP45 and DP38 are also suitable. These segments can therefore be used in combination as a basis to construct a library with the desired single main-chain conformation.

Alternatively, instead of choosing the single main-chain conformation based on the natural occurrence of the different main-chain conformations for each of the binding loops in isolation, the natural occurrence of combinations of main-chain conformations is used as the basis for choosing the single main-chain conformation. In the case of antibodies, for example, the natural occurrence of canonical structure combinations for any two, three, four, five, or for all six of the antigen binding loops can be determined. Here, the chosen conformation may be commonplace in naturally occurring antibodies and may be observed most frequently in the natural repertoire. Thus, in human antibodies, for example, when natural combinations of the five antigen binding loops, H1, H2, L1, L2 and L3, are considered, the most frequent

combination of canonical structures is determined and then combined with the most popular conformation for the H3 loop, as a basis for choosing the single main-chain conformation.

Diversification of the canonical sequence

Having selected several known main-chain conformations or a single known main-chain conformation, dAbs can be constructed by varying the binding site of the molecule in order to generate a repertoire with structural and/or functional diversity. This means that variants are generated such that they possess sufficient diversity in their structure and/or in their function so that they are capable of providing a range of activities.

The desired diversity is typically generated by varying the selected molecule at one or more positions. The positions to be changed can be chosen at random or they may be selected. The variation can then be achieved either by randomisation, during which the resident amino acid is replaced by any amino acid or analogue thereof, natural or synthetic, producing a very large number of variants or by replacing the resident amino acid with one or more of a defined subset of amino acids, producing a more limited number of variants.

Various methods have been reported for introducing such diversity. Error-prone PCR (Hawkins *et al*. (1992) *J. Mol. Biol*., 226: 889), chemical mutagenesis (Deng *et al*. (1994) *J. Biol. Chem*., **269**: 9533) or bacterial mutator strains (Low *et al*. (1996) *J. Mol. Biol.,* **260**: 359) can be used to introduce random mutations into the genes that encode the molecule. Methods for mutating selected positions are also well known in the art and include the use of mismatched oligonucleotides or degenerate oligonucleotides, with or without the use of PCR. For example, several synthetic antibody libraries have been created by targeting mutations to the antigen binding loops. The H3 region of a human tetanus toxoid-binding Fab has been randomised to create a range of new binding specificities (Barbas *et al*. (1992) *Proc. Natl. Acad. Sci. USA*, **89**: 4457). Random or semi-random H3 and L3 regions have been appended to germline V gene segments to produce large libraries with unmutated framework regions (Hoogenboom & Winter (1992) *J. Mol. Biol*., **227**: 381; Barbas *et al*. (1992) *Proc. Natl. Acad. Sci. USA*, **89**: 4457; Nissim *et al*. (1994) *EMBO J*., **13**: 692; Griffiths *et al*. (1994) *EMBO J*., **13**: 3245; De Kruif *et al*. (1995) *J. Mol. Biol*., **248**: 97). Such diversification has been extended to include some or all of the other antigen binding loops (Crameri *et al*. (1996) *Nature Med.,* **2**: 100; Riechmann *et al*. (1995) *Bio/Technology*, **13**: 475; Morphosys, WO97/08320, supra).

Since loop randomisation has the potential to create approximately more than 10^{15} structures for H3 alone and a similarly large number of variants for the other five loops, it is not feasible using current transformation technology or even by using cell free systems to produce a library representing all possible combinations. For

example, in one of the largest libraries constructed to date, 6 x 10^{10} different antibodies, which is only a fraction of the potential diversity for a library of this design, were generated (Griffiths *et al*. (1994) supra).

5 In a one embodiment, only those residues which are directly involved in creating or modifying the desired function of the molecule are diversified. For many molecules, the function will be to bind a target and therefore diversity should be concentrated in the target binding site, while avoiding changing residues which are crucial to the overall packing of the molecule or to maintaining the chosen main-chain
10 conformation.

In one aspect, libraries of dAbs are used in which only those residues in the antigen binding site are varied. These residues are extremely diverse in the human antibody repertoire and are known to make contacts in high-resolution antibody/antigen
15 complexes. For example, in L2 it is known that positions 50 and 53 are diverse in naturally occurring antibodies and are observed to make contact with the antigen. In contrast, the conventional approach would have been to diversify all the residues in the corresponding Complementarity Determining Region (CDR1) as defined by Kabat *et al*. (1991, supra), some seven residues compared to the two diversified in the
20 library.. This represents a significant improvement in terms of the functional diversity required to create a range of antigen binding specificities.

In nature, antibody diversity is the result of two processes: somatic recombination of germline V, D and J gene segments to create a naive primary repertoire (so called
25 germline and junctional diversity) and somatic hypermutation of the resulting rearranged V genes. Analysis of human antibody sequences has shown that diversity in the primary repertoire is focused at the centre of the antigen binding site whereas somatic hypermutation spreads diversity to regions at the periphery of the antigen binding site that are highly conserved in the primary repertoire (see Tomlinson *et al*.
30 (1996) *J. Mol. Biol.*, **256**: 813). This complementarity has probably evolved as an efficient strategy for searching sequence space and, although apparently unique to antibodies, it can easily be applied to other polypeptide repertoires. The residues which are varied are a subset of those that form the binding site for the target. Different (including overlapping) subsets of residues in the target binding site are
35 diversified at different stages during selection, if desired.

In the case of an antibody repertoire, an initial ‘naive’ repertoire is created where some, but not all, of the residues in the antigen binding site are diversified. As used herein in this context, the term “naive” or “dummy” refers to antibody molecules that
40 have no pre-determined target. These molecules resemble those which are encoded by the immunoglobulin genes of an individual who has not undergone immune diversification, as is the case with fetal and newborn individuals, whose immune systems have not yet been challenged by a wide variety of antigenic stimuli. This

repertoire is then selected against a range of antigens or epitopes. If required, further diversity can then be introduced outside the region diversified in the initial repertoire. This matured repertoire can be selected for modified function, specificity or affinity.

5 It will be understood that the sequences described herein include sequences which are substantially identical, for example sequences which are at least 90% identical, for example which are at least 91%, or at least 92%, or at least 93%, or at least 94% or at least 95%, or at least 96%, or at least 97% or at least 98%, or at least 99% identical to the sequences described herein.

10 For nucleic acids, the term “substantial identity” indicates that two nucleic acids, or designated sequences thereof, when optimally aligned and compared, are identical, with appropriate nucleotide insertions or deletions, in at least about 80% of the nucleotides, usually at least about 90% to 95%, and more preferably at least about 98% to 99.5% of the nucleotides. Alternatively, substantial identity exists when the 15 segments will hybridize under selective hybridization conditions, to the complement of the strand.

For nucleotide and amino acid sequences, the term “identical" indicates the degree of identity between two nucleic acid or amino acid sequences when optimally aligned 20 and compared with appropriate insertions or deletions. Alternatively, substantial identity exists when the DNA segments will hybridize under selective hybridization conditions, to the complement of the strand.

The percent identity between two sequences is a function of the number of identical 25 positions shared by the sequences (i.e., % identity = # of identical positions/total # of positions times 100), taking into account the number of gaps, and the length of each gap, which need to be introduced for optimal alignment of the two sequences. The comparison of sequences and determination of percent identity between two sequences can be accomplished using a mathematical algorithm, as described in the 30 non-limiting examples below.

The percent identity between two nucleotide sequences can be determined using the GAP program in the GCG software package, using a NWSgapdna.CMP matrix and a gap weight of 40, 50, 60, 70, or 80 and a length weight of 1, 2, 3, 4, 5, or 6. The 35 percent identity between two nucleotide or amino acid sequences can also be determined using the algorithm of E. Meyers and W. Miller (Comput. Appl. Biosci., 4:11-17 (1988)) which has been incorporated into the ALIGN program (version 2.0), using a PAM120 weight residue table, a gap length penalty of 12 and a gap penalty of 4. In addition, the percent identity between two amino acid sequences can be 40 determined using the Needleman and Wunsch (J. Mol. Biol. 48:444-453 (1970)) algorithm which has been incorporated into the GAP program in the GCG software package, using either a Blossum 62 matrix or a PAM250 matrix, and a gap weight of 16, 14, 12, 10, 8, 6, or 4 and a length weight of 1, 2, 3, 4, 5, or 6.

By way of example, a polypeptide sequence of the present invention may be identical to the reference sequence encoded by SEQ ID NO: 24, that is be 100% identical, or it may include up to a certain integer number of amino acid alterations as compared to the reference sequence such that the % identity is less than 100%. Such alterations are selected from the group consisting of at least one amino acid deletion, substitution, including conservative and non-conservative substitution, or insertion, and wherein said alterations may occur at the amino- or carboxy-terminal positions of the reference polypeptide sequence or anywhere between those terminal positions, interspersed either individually among the amino acids in the reference sequence or in one or more contiguous groups within the reference sequence. The number of amino acid alterations for a given % identity is determined by multiplying the total number of amino acids in the polypeptide sequence encoded by SEQ ID NO: 24 by the numerical percent of the respective percent identity (divided by 100) and then subtracting that product from said total number of amino acids in the polypeptide sequence encoded by SEQ ID NO: 24, or:

$$na \leq xa - (xa \bullet y),$$

wherein na is the number of amino acid alterations, xa is the total number of amino acids in the polypeptide sequence encoded by SEQ ID NO: 24, and y is, for instance 0.70 for 70%, 0.80 for 80%, 0.85 for 85% etc., and wherein any non-integer product of xa and y is rounded down to the nearest integer prior to subtracting it from xa.

Examples

Example 1: Construction of anti-RANKL/anti-OSM antigen binding constructs

5

This example is prophetic

Design of anti-RANKL/anti-OSM antigen binding constructs

10 Anti-RANKL/anti-OSM antigen binding constructs described herein are generated by linking a heavy chain or light chain of an anti-RANKL antibody via an optional linker to an anti-OSM epitope binding domain, or by linking a heavy chain or light chain of an anti-OSM antibody via an optional linker to an anti-RANKL epitope binding domain.

15

A schematic diagram showing examples of antigen binding constructs is given in Figure 6.

Examples of amino acid sequences of various anti-RANKL antibody variable heavy
20 and variable light domains which are of use in the present invention are given in SEQ ID NO: 10-23. These can be linked to any suitable constant region to form a full antibody heavy or light chain.
Examples of amino acid sequences of full length heavy chain and light chains of various anti-RANKL antibodies which are of use in the present invention are given in
25 SEQ ID NO: 24-37.
Further details of an antibody which is of use in the present invention and which comprises the variable heavy and variable light domain sequences of SEQ ID NO: 22 and 23, and the full length heavy chain and light chains of SEQ ID NO: 36 and 37, are given in WO2003002713.
30 Further examples of anti-RANKL variable domain sequences are given in table 1

Table 1

	Code	*code in alignment*	*backmutations*	*SEQ ID NO.*
2A4 VH	86	HZHC2A4-2	none, straight graft	10
	87	HZHC2A4-1	S49A	11
2A4 VL	88	HZLC2A4-1	Q3V, S60D	14
	89	HZLC2A4-3 (= 88 w/o Q3V)	S60D	15
	90	HZLC2A4-4(= 88 w/o S60D	Q3V	13
	91	HZLC2A4-2	None, straight graft	12
19H22 VH	93	HZH19H22-2	Y27F, T30K, R66K, A71T, 93T, 94T	16
	94	HZH19H22-4	Y27F, T28N, F29I, T30K,	17

			A71T, 93T, 94T	
	95	HZH19H22-5	V2I, Y27F, T28N, F29I, T30K, R66K, V67A, A71T, T75P, S76N, 93T, 94T	18
19H22 VL	96	HZLC19H22-2	I58V, F71Y	20
	97	HZLC19H22-3	F71Y	21
	98	HZLC19H22-4	None, straight graft	19

Examples of suitable linker sequences are given in SEQ ID NO: 3-8, or alternatively any naturally occurring or synthetic linker sequence which provides an efficient linkage between the CH3 domain and the epitope binding domain could be used.

5

Examples of anti-RANKL epitope binding domains (in this case anti-RANKL nanobodies) which are of use in the present invention are given in SEQ ID NO: 38 and 39.

10 Amino acid sequences of full length heavy chain and light chains of an anti-OSM antibody which is of use in the present invention are given in SEQ ID NO: 1 and 2.

An example of an antigen binding construct according to the present invention comprising an anti-OSM antibody heavy chain fused to a RANKL epitope binding
15 domain is given in SEQ ID NO: 40. An example of an anti-OSM antibody light chain fused to a RANKL epitope binding domain is given in SEQ ID NO: 41. In both cases, the linker sequence (TVAAPSGS) is underlined.

<u>**Molecular biology and Expression**</u>

20

DNA expression vectors encoding heavy chain or light chain of anti-RANKL/anti-OSM antigen binding constructs can be generated by standard molecular biology techniques including de novo construction from overlapping oligonucleotides by PCR or by overlapping PCR techniques or by site directed mutagenesis or by restriction
25 enzyme cloning or by other recombinant techniques (such as Gateway cloning etc).

In order to express these proteins, it is necessary to add a signal peptide sequence at the N-terminus to direct the fusion proteins for secretion. An example of a suitable signal peptide sequences is given in SEQ ID NO: 9. The full length fusion protein
30 including the signal peptide sequence can be back-translated to obtain a DNA sequence. In some cases it may be useful to codon optimise the DNA sequence for improved expression. In order to facilitate expression, a kozak sequence and stop codons are added. In order to facilitate cloning, restriction enzymes can be included at the 5' and 3' ends. Similarly, restriction enzyme sites can also be engineered into
35 the coding sequence to facilitate the shuffling of domains although in some cases it may be necessary to modify the amino acid sequence to accommodate a restriction site.

Sequence validated clones encoding the heavy and light chains of an anti-RANKL/anti-OSM antigen binding constructs can be co-transfected and expressed in various expression systems such as *E. coli* or eukaryotic cell lines such as CHO-K1, CHO-e1A, HEK293, HEK293-6E or other common expression cell lines.

Examples of anti-RANKL/anti-OSM antigen binding constructs can be expressed by co-transfecting vectors encoding the heavy chain sequence set out in SEQ ID NO: 1 with the light chain sequence set out in SEQ ID NO: 41 or SEQ ID NO: 2, or by co-transfecting vectors endoding the heavy chain sequence set out in and SEQ ID NO: 40 with the light chain sequence set out in SEQ ID NO: 41 or SEQ ID NO: 2.

For mammalian expression systems, antigen binding constructs can be recovered from the supernatant, and can be purified using standard purification technologies such as Protein A sepharose.

The antigen binding constructs can then be tested in a variety of assays to assess binding to RANKL and OSM and for biological activity in a number of assays including ELISA e.g. competition ELISA, receptor neutralisation ELISAs, BIAcore or cell-based assays which will be well known to the skilled man.

Example 2 - Design and Construction of RANKL Bispecific antibodies

A polynucleotide sequence encoding an anti-OSM mAb variable heavy (VH) polynucleotide sequence was cloned into a mammalian expression vector encoding the human IgG1 constant region fused to the humanized anti-RANKL VHH. This allowed the anti-RANKL VHH to be fused onto the C-terminus of the anti-OSM mAb heavy chain via a TVAAPSGS linker (SEQ ID NO: 42 and 40, DNA and Protein sequences of the heavy chain of BPC1845).

A polynucleotide sequence encoding an anti-OSM mAb variable light (VL) polypeptide sequence was cloned into a mammalian expression vector encoding the human kappa constant region (SEQ ID NO:43 and SEQ ID NO: 2, DNA and Protein sequences of the light chain of BPC1845).

The expression plasmids encoding BPC1845 (SEQ ID NO: 42 (heavy chain) and SEQ ID NO:43 (light chain)) were transiently transfected into HEK 293-6E cells using 293fectin (Invitrogen, 12347019). Table 2 sets out the details of these sequences.

A tryptone feed was added to the cell culture after 24 hours. The supernatant was harvested and concentrated after 4 to 5 days and the supernatant was used in the Biacore assays of Example 3.

Table 2:

ANTIBODY ID	DESCRIPTION	SEQ ID No: Polynucleotide sequence	SEQ ID No: Amino acid sequence
BPC1845	Anti-OSM -TVAAPSGS-RANKLVHH Heavy Chain	42	40
	Anti-OSM Light Chain	43	2

Example 3 - OSM and RANKL Binding Biacore method

Protein A was immobilised on a CM5 chip by primary amine coupling. This surface was used to capture BPC1845. The assay was set up so that OSM was passed over the surface first, followed by RANKL. The Protein A surface was regenerated using 50mM NaOH and reused to capture fresh BPC1845. The assay was repeated except this time RANKL was passed over the surface first, followed by OSM. Both RANKL and OSM were used at 256nM.

Figure 1 shows the results of the Biacore assays and confirms that BPC1845 is capable of binding OSM and RANK-L at the same time, irrespective of the order in which they bind.

Example 4: KB assay for OSM activity

This example is prophetic.

KB cells (a human epithelial cell line) express mRNA for gp130 together with LIF and OSM receptors (Mosley, J. Biol Chem., 271 (50) 32635-32643). Both OSM and LIF induce IL-6 release from KB cells. This cell line can be used to identify antigen binding constructs which modulate the interaction between OSM and gp130.

KB cells are obtained from ECACC (Accession no 94050408) and maintained in DMEM + 10% heat inactivated FCS, supplemented with glutamine ("KB medium"). Cells grow as a monolayer and can be split twice weekly. Sigma non-enzymatic cell dissociation medium or Versene can be used to detach the cells. Cells are incubated overnight (37°C, 5% CO_2). OSM standards are made up in culture media. 1ng/ml OSM + antigen binding construct are made up and incubated for 1h at RT. Media is carefully removed from KB cell plate and OSM standards and OSM-antigen binding construct mixtures are added. This is incubated for ~16-18h at 37°C. Culture medium is then removed and assayed for IL-6.

Example 5
Stoichiometry assessment of antigen binding constructs (using Biacore™)

This example is prophetic.

5

Anti-human IgG is immobilised onto a CM5 biosensor chip by primary amine coupling. Antigen binding constructs are captured onto this surface after which a single concentration of RANKL or OSM is passed over, this concentration is enough to saturate the binding surface and the binding signal observed reached full R-max.
10 Stoichiometries are then calculated using the given formula:

Stoich=Rmax * Mw (ligand) / Mw (analyte)* R (ligand immobilised or captured)

Where the stoichiometries are calculated for more than one analyte binding at the
15 same time, the different antigens are passed over sequentially at the saturating antigen concentration and the stoichometries calculated as above. The work can be carried out on the Biacore 3000, at 25°C using HBS-EP running buffer.

Sequences

Description (amino acid sequence)	SEQ ID NO: Amino acid sequence	SEQ ID NO: Polynucleotide sequence
Anti-OSM antibody Heavy chain	1	
Anti-OSM antibody Light chain	2	43
GSSSS (G4S) Linker	3	
TVAAPS Linker	4	
ASTKGPT Linker	5	
ASTKGPS Linker	6	
GS Linker	7	
TVAAPSGS Linker	8	
Signal peptide sequence	9	
Humanised heavy chain variable region sequence HZVH2A4-2 straight graft (86)	10	
Humanised heavy chain variable region sequence HZVH2A4-1 S49A (87)	11	
Humanised light chain variable region sequence HZLC2A4-2 straight graft (91)	12	
Humanised light chain variable region sequence HZLC2A4-3 Q3V (90)	13	
Humanised light chain variable region sequence HZLC2A4-1 Q3V, S60D (88)	14	
Humanised light chain variable region sequence HZLC2A4-4 S60D (89)	15	
Humanised heavy chain variable region sequence HZ19H22-2 (93) Y27F, T30K, R66K, A71T, 93T, 94T	16	
Humanised heavy chain variable region sequence HZ19H22-4 (94) Y27F, T28N, F29I, T30K, A71T, 93T, 94T	17	
Humanised heavy chain variable region sequence HZ19H22-5 (95) V2I, Y27F, T28N, F29I, T30K, R66K, V67A, A71T, T75P, S76N, 93T, 94T	18	
Humanised light chain variable region sequence	19	

HZK19H22-4 (98) straight graft		
Humanised light chain variable region sequence HZK19H22-2 (96) I58V, F71Y	20	
Humanised light chain variable region sequence HZK19H22-3 (97) F71Y	21	
αOPGL-1 heavy chain variable region amino acid sequence SEQ ID13 WO2003002713A2[1] (AMG-162 VH)	22	
αOPGL-1 light chain variable region amino acid sequence SEQ ID14 WO2003002713A2[1] (AMG-162 VL)	23	
Humanised heavy chain sequence HZVH2A4-2 (86)	24	
Humanised heavy chain sequence HZVH2A4-1 (87)	25	
Humanised light chain sequence HZLC2A4-2 (91)	26	
Humanised light chain sequence HZLC2A4-3 (90)	27	
Humanised light chain sequence HZLC2A4-1 (88)	28	
Humanised light chain sequence HZLC2A4-4 (89)	29	
Humanised heavy chain sequence HZ19H22-2 (93)	30	
Humanised heavy chain sequence HZ19H22-4 (94)	31	
Humanised heavy chain sequence HZ19H22-5 (95)	32	
Humanised light chain sequence HZK19H22-4 (98)	33	
Humanised light chain sequence HZK19H22-2 (96)	34	
Humanised light chain sequence HZK19H22-3 (97)	35	
αOPGL-1 heavy chain sequence (AMG-162 VH)	36	
αOPGL-1 light chain sequence (AMG-162 VL)	37	
Anti-RANKL nanobody RANKL13	38	
Humanised anti-RANKL nanobody RANKL13hum5	39	
Anti-OSM antibody Heavy chain + humanised anti-RANKL nanobody RANKL13hum5	40	42
Anti-OSM antibody light chain + humanised anti-RANKL nanobody RANKL13hum5	41	
$GS(TVAAPSGS)_1$	44	
$GS(TVAAPSGS)_2$	45	
$GS(TVAAPSGS)_3$	46	
$GS(TVAAPSGS)_4$	47	

GS(TVAAPSGS)$_5$	48	
GS(TVAAPSGS)$_6$	49	
(PAS)$_1$GS	50	
(PAS)$_2$GS	51	
(PAS)$_3$GS	52	
(G$_4$S)$_2$	53	
(G$_4$S)$_3$	54	
(PAVPPP)$_1$GS	55	
(PAVPPP)$_2$GS	56	
(PAVPPP)$_3$GS	57	
(TVSDVP)$_1$GS	58	
(TVSDVP)$_2$GS	59	
(TVSDVP)$_3$GS	60	
(TGLDSP)$_1$GS	61	
(TGLDSP)$_2$GS	62	
(TGLDSP)$_3$GS	63	
PAS linker	64	
PAVPPP linker	65	
TVSDVP linker	66	
TGLDSP linker	67	
(TVAAPS)$_2$(GS)$_1$	68	
(TVAAPS)$_3$(GS)$_1$	69	

SEQ ID NO: 1 (Anti-OSM antibody Heavy Chain)

QVQLVESGGGVVQPGRSLRLSCAASGFSLTNYGVHWVRQAPGKGLEWVAVIWRGGSTDYNAA
FMSRFTISKDNSKNTLYLQMNSLRAEDTAVYYCAKSPNSNFYWYFDVWGRGTLVTVSSASTK
GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLS
SVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT
VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA
LHNHYTQKSLSLSPGK

SEQ ID NO: 2 (Anti-OSM antibody Light Chain)

EIVLTQSPATLSLSPGERATLSCSGSSSVSYMYWYQQKPGQAPRLLIEDTSNLASGIPARFS
GSGSGTDYTLTISNLEPEDFAVYYCQQWSSYPPTFGQGTKLEIKRTVAAPSVFIFPPSDEQL
KSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE
KHKVYACEVTHQGLSSPVTKSFNRGEC

5

SEQ ID NO: 3 (G4S linker)

GGGGS

SEQ ID NO: 4 (linker)

10 TVAAPS

SEQ ID NO: 5 (linker)

ASTKGPT

15 **SEQ ID NO: 6 (linker)**

ASTKGPS

SEQ ID NO: 7 (linker)

GS

20

SEQ ID NO: 8 (linker)

TVAAPSGS

SEQ ID NO: 9 (Example signal peptide sequence)

25 MGWSCIILFLVATATGVHS

SEQ ID NO: 10 (Humanised heavy chain variable region sequence HZVH2A4-2 (86) straight graft)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSRYGMSWVRQAPGKGLEWVSTISSGGSYIYYPD
30 SVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARLDGYNYRWYFDVWGQGTMVTVSS

SEQ ID NO:11 (Humanised heavy chain variable region sequence HZVH2A4-1 S49A (87))

EVQLVESGGGLVQPGGSLRLSCAASGFTFSRYGMSWVRQAPGKGLEWVATISSGGSYIYYPD
35 SVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARLDGYNYRWYFDVWGQGTMVTVSS

SEQ ID NO: 12 (Humanised light chain variable region sequence HZLC2A4-2 straight graft)

DIQMTQSPSSLSASVGDRVTITCKASQDVSTAVAWYQQKPGKAPKLLIYSASYRYTGVPSRF
SGSGSGTDFTLTISSLQPEDFATYYCQQHYSSPRTFGGGTKVEIKRT

5

SEQ ID NO: 13 (Humanised light chain variable region sequence HZLC2A4-3 Q3V (90))

DIVMTQSPSSLSASVGDRVTITCKASQDVSTAVAWYQQKPGKAPKLLIYSASYRYTGVPSRF
SGSGSGTDFTLTISSLQPEDFATYYCQQHYSSPRTFGGGTKVEIKRT

10

SEQ ID NO: 14 (Humanised light chain variable region sequence HZLC2A4-1 Q3V, S60D (88))

DIVMTQSPSSLSASVGDRVTITCKASQDVSTAVAWYQQKPGKAPKLLIYSASYRYTGVPDRF
SGSGSGTDFTLTISSLQPEDFATYYCQQHYSSPRTFGGGTKVEIKRT

15

SEQ ID NO: 15 (Humanised light chain variable region sequence HZLC2A4-4 S60D (89))

DIQMTQSPSSLSASVGDRVTITCKASQDVSTAVAWYQQKPGKAPKLLIYSASYRYTGVPDRF
SGSGSGTDFTLTISSLQPEDFATYYCQQHYSSPRTFGGGTKVEIKRT

20

SEQ ID NO: 16 - Humanised heavy chain variable sequence HZ19H22-2 (93) Y27F, T30K, R66K, A71T, 93T, 94T

QVQLVQSGAEVKKPGASVKVSCKASGFTFKGTYMHWVRQAPGQGLEWMGRIDPANGNTKYDP
KFQGKVTITTDTSTSTAYMELSSLRSEDTAVYYCTTQFHYYGYGGVYWGQGTMVTVSS

25

SEQ ID NO : 17 - Humanised heavy chain variable sequence HZ19H22-4 (94) Y27F, T28N, F29I, T30K, A71T, 93T, 94T

QVQLVQSGAEVKKPGASVKVSCKASGFNIKGTYMHWVRQAPGQGLEWMGRIDPANGNTKYDP
KFQGRVTITTDTSTSTAYMELSSLRSEDTAVYYCTTQFHYYGYGGVYWGQGTMVTVSS

30

SEQ ID NO: 18 - Humanised heavy chain variable sequence HZ19H22-5 (95) V2I, Y27F, T28N, F29I, T30K, R66K, V67A, A71T, T75P, S76N, 93T, 94T

QIQLVQSGAEVKKPGASVKVSCKASGFNIKGTYMHWVRQAPGQGLEWMGRIDPANGNTKYDP
KFQGKATITTDTSPNTAYMELSSLRSEDTAVYYCTTQFHYYGYGGVYWGQGTMVTVSS

35

SEQ ID NO: 19 - Humanised light chain variable region sequence HZK19H22-4 (98) straight graft

EIVLTQSPGTLSLSPGERATLSCSASSSVSYMYWYQQKPGQAPRLLIYDTSNLASGIPDRFS
GSGSGTDFTLTISRLEPEDFAVYYCQQWSNFPLTFGQGTKVEIKRT

SEQ ID NO: 20 - Humanised light chain variable region sequence HZK19H22-2 (96) I58V, F71Y

EIVLTQSPGTLSLSPGERATLSCSASSSVSYMYWYQQKPGQAPRLLIYDTSNLASGVPDRFS
GSGSGTDYTLTISRLEPEDFAVYYCQQWSNFPLTFGQGTKVEIKRT

SEQ ID NO: 21 - Humanised light chain variable region sequence HZK19H22-3 (97) F71Y

EIVLTQSPGTLSLSPGERATLSCSASSSVSYMYWYQQKPGQAPRLLIYDTSNLASGIPDRFS
GSGSGTDYTLTISRLEPEDFAVYYCQQWSNFPLTFGQGTKVEIKRT

SEQ ID NO: 22 - αOPGL-1 heavy chain variable region (AMG-162 VH)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSGITGSGGSTYYAD
SVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDPGTTVIMSWFDPWGQGTLVTVSS

SEQ ID NO: 23 - αOPGL-1 light chain variable region (AMG-162 VL)

EIVLTQSPGTLSLSPGERATLSCRASQSVRGRYLAWYQQKPGQAPRLLIYGASSRATGIPDR
FSGSGSGTDFTLTISRLEPEDFAVFYCQQYGSSPRTFGQGTKVEIKRT

SEQ ID NO: 24 – Humanised heavy chain sequence HZVH2A4-2 (86)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSRYGMSWVRQAPGKGLEWVSTISSGGSYIYYPD
SVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARLDGYNYRWYFDVWGQGTMVTVSSAST
KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL
SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFP
PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL
TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL
VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE
ALHNHYTQKSLSLSPGK

SEQ ID NO: 25 – Humanised heavy chain sequence HZVH2A4-1 (87)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSRYGMSWVRQAPGKGLEWVATISSGGSYIYYPD
SVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARLDGYNYRWYFDVWGQGTMVTVSSAST
KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL
SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFP

PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL
TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL
VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE
ALHNHYTQKSLSLSPGK

5

SEQ ID NO: 26 (Humanised light chain sequence HZLC2A4-2 (91))

DIQMTQSPSSLSASVGDRVTITCKASQDVSTAVAWYQQKPGKAPKLLIYSASYRYTGVPSRF
SGSGSGTDFTLTISSLQPEDFATYYCQQHYSSPRTFGGGTKVEIKRTVAAPSVFIFPPSDEQ
LKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADY
10 EKHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO: 27 (Humanised light chain sequence HZLC2A4-3 (90))

DIVMTQSPSSLSASVGDRVTITCKASQDVSTAVAWYQQKPGKAPKLLIYSASYRYTGVPSRF
SGSGSGTDFTLTISSLQPEDFATYYCQQHYSSPRTFGGGTKVEIKRTVAAPSVFIFPPSDEQ
15 LKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADY
EKHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO: 28 (Humanised sequence HZLC2A4-1 (88))

20 DIVMTQSPSSLSASVGDRVTITCKASQDVSTAVAWYQQKPGKAPKLLIYSASYRYTGVPDRF
SGSGSGTDFTLTISSLQPEDFATYYCQQHYSSPRTFGGGTKVEIKRTVAAPSVFIFPPSDEQ
LKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADY
EKHKVYACEVTHQGLSSPVTKSFNRGEC

25

SEQ ID NO: 29 (Humanised light chain sequence HZLC2A4-4 (89))

DIQMTQSPSSLSASVGDRVTITCKASQDVSTAVAWYQQKPGKAPKLLIYSASYRYTGVPDRF
SGSGSGTDFTLTISSLQPEDFATYYCQQHYSSPRTFGGGTKVEIKRTVAAPSVFIFPPSDEQ
LKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADY
30 EKHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO: 30 (Humanised heavy chain sequence HZ19H22-2 (93))

QVQLVQSGAEVKKPGASVKVSCKASGFTFKGTYMHWVRQAPGQGLEWMGRIDPANGNTKYDP
KFQGKVTITTDTSTSTAYMELSSLRSEDTAVYYCTTQFHYYGYGGVYWGQGTMVTVSSASTK
35 GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLS
SVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT

VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA
LHNHYTQKSLSLSPGK

5 **SEQ ID NO: 31 (Humanised heavy chain sequence HZ19H22-4 (94))**
QVQLVQSGAEVKKPGASVKVSCKASGFNIKGTYMHWVRQAPGQGLEWMGRIDPANGNTKYDP
KFQGRVTITTDTSTSTAYMELSSLRSEDTAVYYCTTQFHYYGYGGVYWGQGTMVTVS**S**ASTK
GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLS
SVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPP
10 KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT
VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA
LHNHYTQKSLSLSPGK

15 **SEQ ID NO: 32 (Humanised heavy chain sequence HZ19H22-5 (95))**
QIQLVQSGAEVKKPGASVKVSCKASGFNIKGTYMHWVRQAPGQGLEWMGRIDPANGNTKYDP
KFQGKATITTDTSPNTAYMELSSLRSEDTAVYYCTTQFHYYGYGGVYWGQGTMVTVS**S**ASTK
GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLS
SVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPP
20 KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT
VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA
LHNHYTQKSLSLSPGK

25 **SEQ ID NO: 33 (Humanised light chain sequence HZK19H22-4 (98))**
EIVLTQSPGTLSLSPGERATLSCSASSSVSYMYWYQQKPGQAPRLLIYDTSNLASGIPDRFS
GSGSGTDFTLTISRLEPEDFAVYYCQQWSNFPLTFGQGTKVEIKRTVAAPSVFIFPPSDEQL
KSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE
KHKVYACEVTHQGLSSPVTKSFNRGEC

30

SEQ ID NO: 34 (Humanised light chain sequence HZK19H22-2 (96))
EIVLTQSPGTLSLSPGERATLSCSASSSVSYMYWYQQKPGQAPRLLIYDTSNLASGvPDRFS
GSGSGTDyTLTISRLEPEDFAVYYCQQWSNFPLTFGQGTKVEIKRTVAAPSVFIFPPSDEQL
KSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE
35 KHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO: 35 (Humanised light chain sequence HZK19H22-3 (97))

EIVLTQSPGTLSLSPGERATLSCSASSSVSYMYWYQQKPGQAPRLLIYDTSNLASGIPDRFS
GSGSGTDyTLTISRLEPEDFAVYYCQQWSNFPLTFGQGTKVEIKRTVAAPSVFIFPPSDEQL
KSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE
KHKVYACEVTHQGLSSPVTKSFNRGEC

5

SEQ ID NO: 36 (αOPGL-1 heavy chain sequence (AMG-162 VH))

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSGITGSGGSTYYAD
SVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDPGTTVIMSWFDPWGQGTLVTVSSAS
TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS
10 LSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLF
PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTC
LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH
EALHNHYTQKSLSLSPGK

15

SEQ ID NO: 37 (αOPGL-1 light chain sequence (AMG-162 VL))

EIVLTQSPGTLSLSPGERATLSCRASQSVRGRYLAWYQQKPGQAPRLLIYGASSRATGIPDR
FSGSGSGTDFTLTISRLEPEDFAVFYCQQYGSSPRTFGQGTKVEIKRTVAAPSVFIFPPSDE
QLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKAD
20 YEKHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO: 38 (Anti-RANKL nanobody RANKL13)

EVQLVESGGGLVQAGGSLRLSCAASGRTFRSYPMGWFRQAPGKEREFVASITGSGGSTYYAD
25 SVKGRFTISRDNAKNTVYLQMNSLRPEDTAVYSCAAYIRPDTYLSRDYRKYDYWGQGTQVTV
SS

SEQ ID NO: 39 (Humanised anti-RANKL nanobody RANKL13hum5)

30 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYPMGWFRQAPGKGREFVSSITGSGGSTYYAD
SVKGRFTISRDNAKNTLYLQMNSLRPEDTAVYYCAAYIRPDTYLSRDYRKYDYWGQGTLVTV
SS

**SEQ ID NO: 40 (Anti-OSM antibody Heavy Chain + humanised anti-RANKL
35 nanobody RANKL13hum5)**

QVQLVESGGGVVQPGRSLRLSCAASGFSLTNYGVHWVRQAPGKGLEWVAVIWRGGSTDYNAA
FMSRFTISKDNSKNTLYLQMNSLRAEDTAVYYCAKSPNSNFYWYFDVWGRGTLVTVSSASTK
GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLS
40 SVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPP

KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT
VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA
LHNHYTQKSLSLSPGK**TVAAPSGS**EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYPMGWFR
5 QAPGKGREFVSSITGSGGSTYYADSVKGRFTISRDNAKNTLYLQMNSLRPEDTAVYYCAAYI
RPDTYLSRDYRKYDYWGQGTLVTVSS

SEQ ID NO: 41 (Anti-OSM antibody Light Chain + humanised anti-RANKL
10 **nanobody RANKL13hum5)**

EIVLTQSPATLSLSPGERATLSCSGSSSVSYMYWYQQKPGQAPRLLIEDTSNLASGIPARFS
GSGSGTDYTLTISNLEPEDFAVYYCQQWSSYPPTFGQGTKLEIKRTVAAPSVFIFPPSDEQL
KSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE
15 KHKVYACEVTHQGLSSPVTKSFNRGEC**TVAAPSGS**EVQLVESGGGLVQPGGSLRLSCAASGF
TFSSYPMGWFRQAPGKGREFVSSITGSGGSTYYADSVKGRFTISRDNAKNTLYLQMNSLRPE
DTAVYYCAAYIRPDTYLSRDYRKYDYWGQGTLVTVSS

SEQ ID NO: 42 (polynucleotide sequence of BPC1845 heavy chain)

20 CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGA
CTCTCCTGTGCAGCGTCTGGATTCTCATTAACTAATTATGGTGTACACTGGGTCCGC
CAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTGATATGGAGAGGTGGAAGCACA
GACTACAATGCAGCTTTCATGTCCCGATTCACCATCTCCAAGGACAATTCCAAGAAC
ACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGT
25 GCGAAAAGTCCGAATAGTAACTTTTACTGGTATTTCGATGTCTGGGGCCGTGGCACA
CTAGTGACCGTGTCCAGCGCCAGCACCAAGGGCCCCAGCGTGTTCCCCCTGGCCCCC
AGCAGCAAGAGCACCAGCGGCGGCACAGCCGCCCTGGGCTGCCTGGTGAAGGACTAC
TTCCCCGAACCGGTGACCGTGTCCTGGAACAGCGGAGCCCTGACCAGCGGCGTGCAC
ACCTTCCCCGCCGTGCTGCAGAGCAGCGGCCTGTACAGCCTGAGCAGCGTGGTGACC
30 GTGCCCAGCAGCAGCCTGGGCACCCAGACCTACATCTGTAACGTGAACCACAAGCCC
AGCAACACCAAGGTGGACAAGAAGGTGGAGCCCAAGAGCTGTGACAAGACCCACACC
TGCCCCCCCTGCCCTGCCCCCGAGCTGCTGGGAGGCCCCAGCGTGTTCCTGTTCCCC
CCCAAGCCTAAGGACACCCTGATGATCAGCAGAACCCCCGAGGTGACCTGTGTGGTG
GTGGATGTGAGCCACGAGGACCCTGAGGTGAAGTTCAACTGGTACGTGGACGGCGTG
35 GAGGTGCACAATGCCAAGACCAAGCCCAGGGAGGAGCAGTACAACAGCACCTACCGG
GTGGTGTCCGTGCTGACCGTGCTGCACCAGGATTGGCTGAACGGCAAGGAGTACAAG
TGTAAGGTGTCCAACAAGGCCCTGCCTGCCCCTATCGAGAAAACCATCAGCAAGGCC
AAGGGCCAGCCCAGAGAGCCCCAGGTGTACACCCTGCCCCCTAGCAGAGATGAGCTG
ACCAAGAACCAGGTGTCCCTGACCTGCCTGGTGAAGGGCTTCTACCCCAGCGACATC
40 GCCGTGGAGTGGGAGAGCAACGGCCAGCCCGAGAACAACTACAAGACCACCCCCCCT
GTGCTGGACAGCGATGGCAGCTTCTTCCTGTACAGCAAGCTGACCGTGGACAAGAGC
AGATGGCAGCAGGGCAACGTGTTCAGCTGCTCCGTGATGCACGAGGCCCTGCACAAT
CACTACACCCAGAAGAGCCTGAGCCTGTCCCCTGGCAAGACCGTGGCCGCCCCCTCG
GGATCCGAGGTCCAGCTGGTGGAGAGCGGCGGAGGCCTGGTGCAGCCCGGCGGCAGC
45 CTCAGGCTGAGCTGCGCCGCCAGCGGCTTCACCTTCAGCAGCTACCCCATGGGCTGG
TTTAGGCAGGCTCCCGGCAAGGGCAGGGAGTTCGTGTCCAGCATCACCGGGAGCGGC

GGCTCTACCTACTACGCCGACAGCGTGAAGGGCAGGTTCACCATCAGCCGCGACAAC
GCCAAGAACACCCTGTACCTGCAGATGAACAGCCTGAGGCCCGAGGATACCGCCGTG
TACTATTGCGCCGCCTACATCAGGCCCGACACCTACCTGAGCCGGGACTACAGGAAG
TACGACTACTGGGGCCAGGGCACTCTGGTGACCGTGAGCAGC

SEQ ID NO: 43 (polynucleotide sequence of BPC1845 light chain)

GAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGGGAAAGAGCC
ACCCTCTCCTGCAGTGGCAGCTCAAGTGTAAGTTACATGTATTGGTACCAACAGAAA
CCTGGCCAGGCTCCCAGGCTCCTCATCGAAGACACATCCAACCTGGCTTCTGGCATC
CCAGCCAGGTTCAGTGGCAGTGGGTCTGGGACAGACTACACTCTCACCATCAGCAAC
CTAGAGCCTGAAGATTTTGCAGTTTATTACTGTCAACAGTGGAGTAGTTATCCACCC
ACGTTTGGCCAGGGGACCAAGCTGGAGATCAAACGTACGGTGGCCGCCCCCAGCGTG
TTCATCTTCCCCCCCAGCGATGAGCAGCTGAAGAGCGGCACCGCCAGCGTGGTGTGT
CTGCTGAACAACTTCTACCCCCGGGAGGCCAAGGTGCAGTGGAAGGTGGACAATGCC
CTGCAGAGCGGCAACAGCCAGGAGAGCGTGACCGAGCAGGACAGCAAGGACTCCACC
TACAGCCTGAGCAGCACCCTGACCCTGAGCAAGGCCGACTACGAGAAGCACAAGGTG
TACGCCTGTGAGGTGACCCACCAGGGCCTGTCCAGCCCCGTGACCAAGAGCTTCAAC
CGGGGCGAGTGC

SEQ ID NO:44
GSTVAAPSGS

SEQ ID NO:45
GSTVAAPSGSTVAAPSGS

SEQ ID NO:46
GSTVAAPSGSTVAAPSGSTVAAPSGS

SEQ ID NO:47
GSTVAAPSGSTVAAPSGSTVAAPSGSTVAAPSGS

SEQ ID NO:48
GSTVAAPSGSTVAAPSGSTVAAPSGSTVAAPSGSTVAAPSGS

SEQ ID NO:49
GSTVAAPSGSTVAAPSGSTVAAPSGSTVAAPSGSTVAAPSGSTVAAPSGS

SEQ ID NO:50
PASGS

SEQ ID NO:51
PASPASGS

SEQ ID NO:52
PASPASPASGS

SEQ ID NO:53
GGGGSGGGGS

SEQ ID NO:54
GGGGSGGGGSGGGGS

SEQ ID NO:55
PAVPPPGS

SEQ ID NO:56
PAVPPPPAVPPPGS

SEQ ID NO:57
PAVPPPPAVPPPPAVPPPGS

SEQ ID NO:58
TVSDVPGS

SEQ ID NO:59
TVSDVPTVSDVPGS

SEQ ID NO:60
TVSDVPTVSDVPTVSDVPGS

SEQ ID NO:61
TGLDSPGS

SEQ ID NO:62
TGLDSPTGLDSPGS

SEQ ID NO:63
TGLDSPTGLDSPTGLDSPGS

SEQ ID NO:64
PAS

SEQ ID NO:65
PAVPPP

SEQ ID NO:66
TVSDVP

SEQ ID NO: 67
TGLDSP

SEQ ID NO:68
TVAAPSTVAAPSGS

SEQ ID NO:69
TVAAPSTVAAPSTVAAPSGS

Brief Description of Figures

Figures 1 to 5: Examples of antigen-binding constructs
Figure 6: Schematic diagram of antigen binding constructs.

Figure 7a) and b):Results of the Biacore assays. Confirms that BPC1845 can bind to both OSM and RANK-L irrespective of the order in which they bind.

Claims

1. An antigen-binding construct comprising a protein scaffold which is linked to one or more epitope-binding domains wherein the antigen-binding construct has at least two antigen binding sites at least one of which is from an epitope binding domain and at least one of which is from a paired VH/VL domain and wherein at least one of the antigen binding sites is capable of binding RANKL.

2. An antigen-binding construct according to claim 1 wherein at least one epitope binding domain is a dAb.

3. An antigen-binding construct according to claim 2 wherein the dAb is a human dAb.

4. An antigen-binding construct according to claim 2 wherein the dAb is a camelid dAb.

5. An antigen-binding construct according to claim 2 wherein the dAb is a shark dAb (NARV).

6. An antigen-binding construct according to any one of claims 1 to 5 wherein at least one epitope binding domain is derived from a scaffold selected from CTLA-4 (Evibody); lipocalin; Protein A derived molecules such as Z-domain of Protein A (Affibody, SpA), A-domain (Avimer/Maxibody); Heat shock proteins such as GroEl and GroES; transferrin (trans-body); ankyrin repeat protein (DARPin); peptide aptamer; C-type lectin domain (Tetranectin); human γ-crystallin and human ubiquitin (affilins); PDZ domains; scorpion toxinkunitz type domains of human protease inhibitors; and fibronectin (adnectin).

7. An antigen-binding construct according to claim 6 wherein the epitope binding domain is derived from a scaffold selected from an Affibody, an ankyrin repeat protein (DARPin) and an adnectin.

8. An antigen-binding construct of any preceding claim wherein the binding construct has specificity for more than one antigen.

9. An antigen-binding construct according to any preceding claim wherein at least one paired VH/VL domain is capable of binding RANKL.

10. An antigen-binding construct according to any preceding claim wherein at least one epitope binding domain is capable of binding RANKL.

11. An antigen-binding construct according to any one of claims 1 to 10 wherein the antigen-binding construct is capable of binding two or more antigens selected from RANKL and OSM.

12. An antigen-binding construct according to any preceding claim wherein the protein scaffold is an Ig scaffold.

13. An antigen-binding construct according to claim 12 wherein the Ig scaffold is an IgG scaffold.

14. An antigen-binding construct according to claim 13 wherein the IgG scaffold is selected from IgG1, IgG2, IgG3 and IgG4.

15. An antigen-binding construct according to claim 14 wherein the protein scaffold comprises a monovalent antibody.

16. An antigen-binding construct according to any one of claims 12 to 14 wherein the IgG scaffold comprises all the domains of an antibody.

17. An antigen-binding construct according to any previous claim which comprises four epitope binding domains.

18. An antigen-binding construct according to claim 17wherein two of the epitope binding domains have specificity for the same antigen.

19. An antigen-binding construct according to claim 18 wherein all of the epitope binding domains have specificity for the same antigen.

20. An antigen-binding construct according to any preceding claim wherein at least one of the epitope binding domains is directly attached to the Ig scaffold with a linker comprising from 1 to 150 amino acids.

21. An antigen-binding construct according to claim 20 wherein at least one of the epitope binding domains is directly attached to the Ig scaffold with a linker comprising from 1 to 20 amino acids.

22. An antigen-binding construct according to claim 21 wherein at least one of the epitope binding domains is directly attached to the Ig scaffold with a linker selected from any one of those set out in SEQ ID NO: 3 to 8, or any combination thereof.

23. An antigen-binding construct according to any preceding claim wherein at least one of the epitope binding domains binds human serum albumin.

24. An antigen-binding construct according to any one of claims 12 to 23 comprising an epitope binding domain attached to the Ig scaffold at the N-terminus of the light chain.

25. An antigen-binding construct according to any one of claims 12 to 23 comprising an epitope binding domain attached to the Ig scaffold at the N-terminus of the heavy chain.

26. An antigen-binding construct according to any one of claims 12 to 23 comprising an epitope binding domain attached to the Ig scaffold at the C-terminus of the light chain.

27. An antigen-binding construct according to any one of claims 12 to 23 comprising an epitope binding domain attached to the Ig scaffold at the C-terminus of the heavy chain.

28. An antigen-binding construct according to any previous claim which has 4 antigen binding sites and which is capable of binding 4 antigens simultaneously.

29. An antigen-binding construct according to any preceding claim for use in medicine.

30. An antigen-binding construct according to any preceding claim for use in the manufacture of a medicament for treating osteoporosis, or arthritic diseases such as rheumatoid arthritis, erosive arthritis, psoriatic arthritis, polymyalgia rhumatica, ankylosing spondylitis, juvenile rheumatoid arthritis, Paget's disease, osteogenesis imperfecta, osteoporosis, sports or other injuries of the knee, ankle, hand, hip, shoulder or spine, back pain, lupus particularly of the joints, osteoarthritis or cancer, for example Acute Myologenous Leukaemia, breast cancer, lung cancer, prostate cancer, colon cancer, stomach cancer, bladder cancer, uterine cancer, kidney cancer, multiple myeloma or arthritic diseases.

31. A method of treating a patient suffering from osteoporosis, or arthritic diseases such as rheumatoid arthritis, erosive arthritis, psoriatic arthritis, polymyalgia rhumatica, ankylosing spondylitis, juvenile rheumatoid arthritis, Paget's disease, osteogenesis imperfecta, osteoporosis, sports or other injuries of the knee, ankle, hand, hip, shoulder or spine, back pain, lupus particularly of the joints, osteoarthritis, or cancer, for example Acute Myologenous Leukaemia, breast cancer, lung cancer, prostate cancer, colon cancer, stomach cancer, bladder cancer, uterine cancer, kidney cancer, multiple myeloma or arthritic diseasescomprising administering a therapeutic amount of an antigen-binding construct according to any one of claims 1 to 28

32. An antigen-binding construct according to any one of claims 1 to 28 for the treatment of osteoporosis, or arthritic diseases such as rheumatoid arthritis, erosive arthritis, psoriatic arthritis, polymyalgia rhumatica, ankylosing spondylitis, juvenile rheumatoid arthritis, Paget's disease, osteogenesis imperfecta, osteoporosis, sports or other injuries of the knee, ankle, hand, hip, shoulder or spine, back pain, lupus particularly of the joints, osteoarthritis or cancer, for example Acute Myologenous Leukaemia, breast cancer, lung cancer, prostate cancer, colon cancer, stomach cancer, bladder cancer, uterine cancer, kidney cancer, multiple myeloma or arthritic diseasesr.

33. A polynucleotide sequence encoding a heavy chain of an antigen-binding construct according to any one of claims 1 to 28

34. A polynucleotide encoding a light chain of an antigen-binding construct according to any one of claims 1 to 28

35. A recombinant transformed or transfected host cell comprising one or more polynucleotide sequences encoding a heavy chain and a light chain of an antigen-binding construct of any preceding claim.

36. A method for the production of an antigen-binding construct according to claims 1 to 28 which method comprises the step of culturing a host cell of claim 35 and isolating the antigen-binding construct.

37. A pharmaceutical composition comprising an antigen-binding construct of any one of claims 1 to 28 and a pharmaceutically acceptable carrier.

5 **Figure 1**

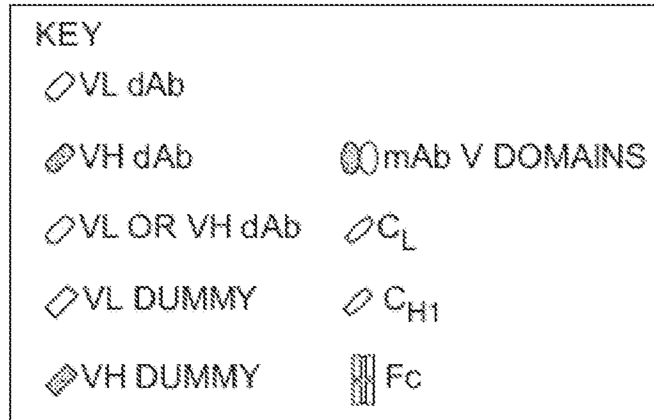


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Figure 2

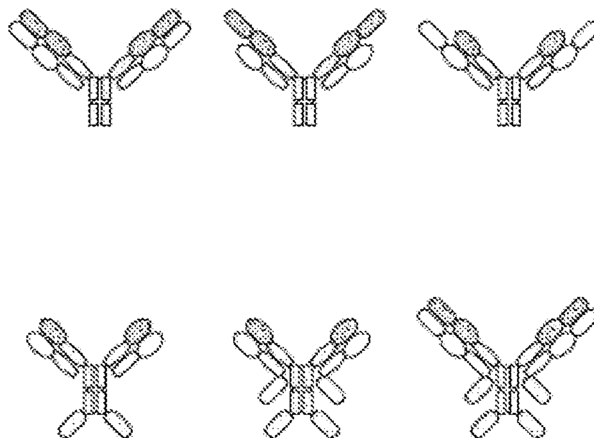

Figure 3

CATEGORY 2:
DUMMY IgG + VARIABLE DOMAINS (Fv AND/OR dAbs)

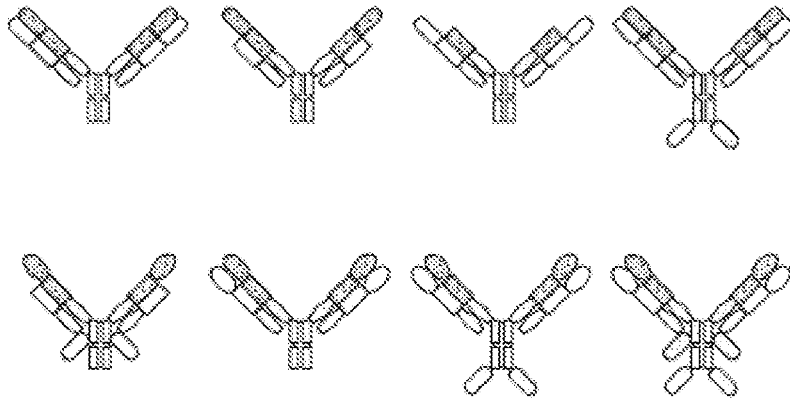

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Figure 4

CATEGORY 3:
PORTION OF DUMMY IgG + VARIABLE DOMAINS (Fv AND/OR dAbs)

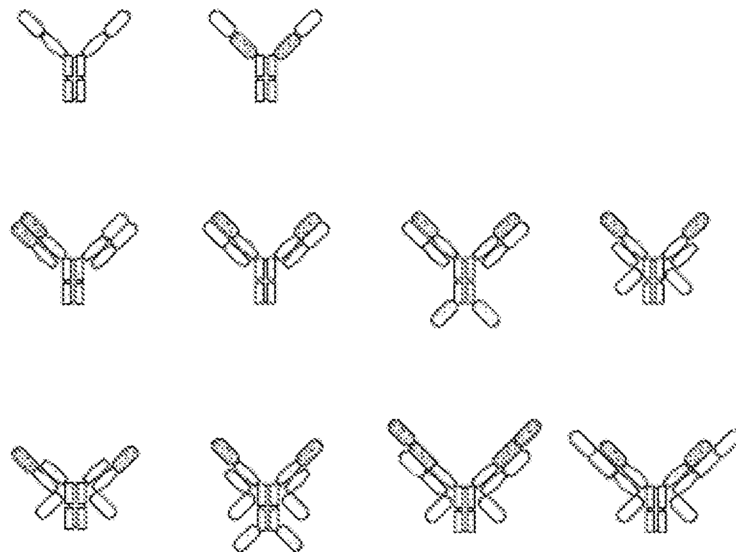

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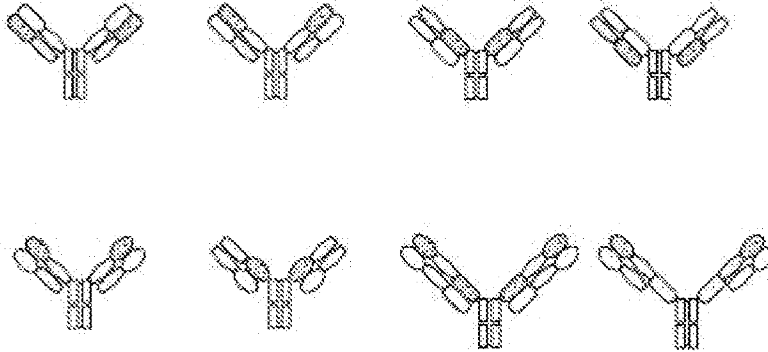
Figure 5a



5 **Figure 5b**

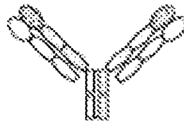


Figure 5c

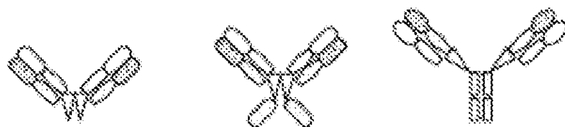


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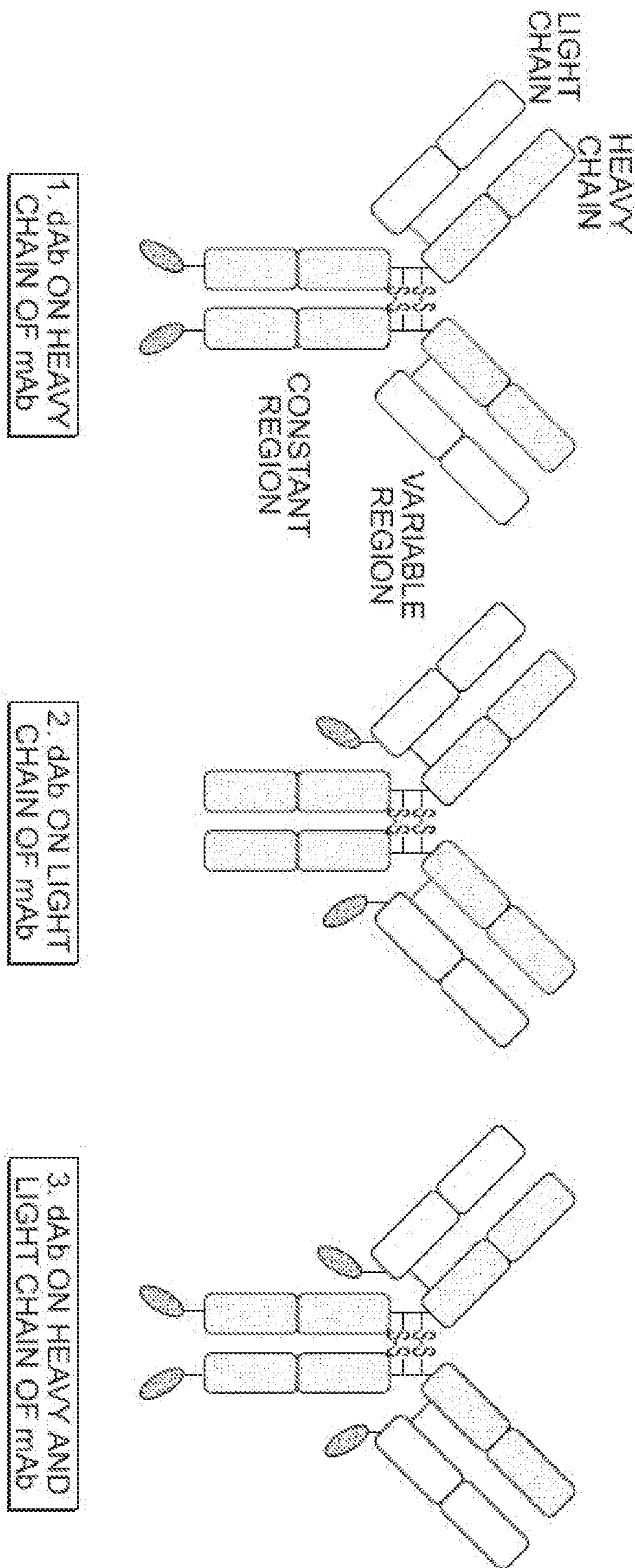
Figure 6



5 **Figure 7a**

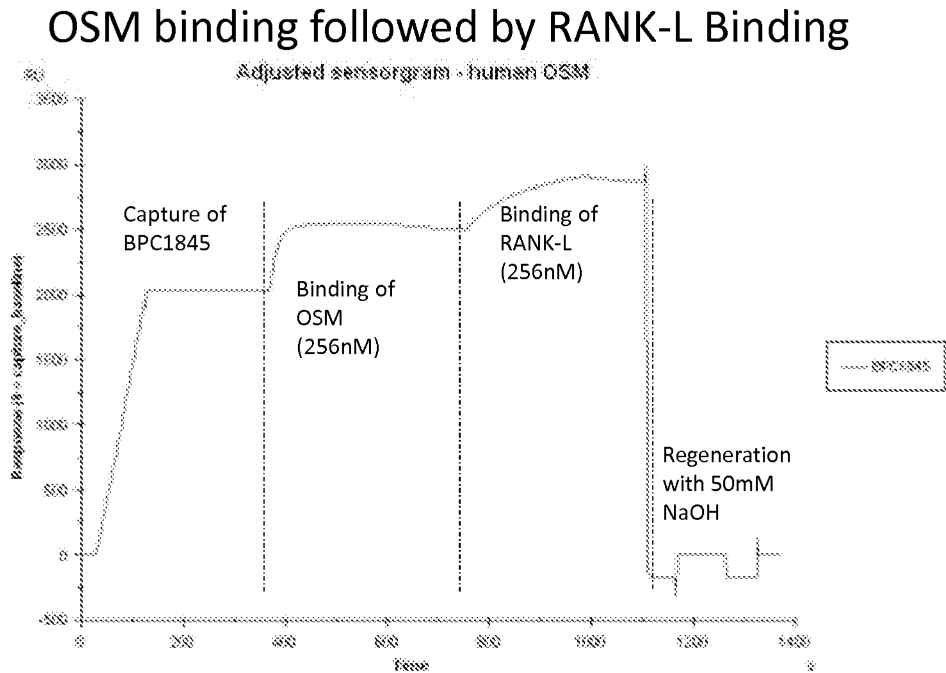
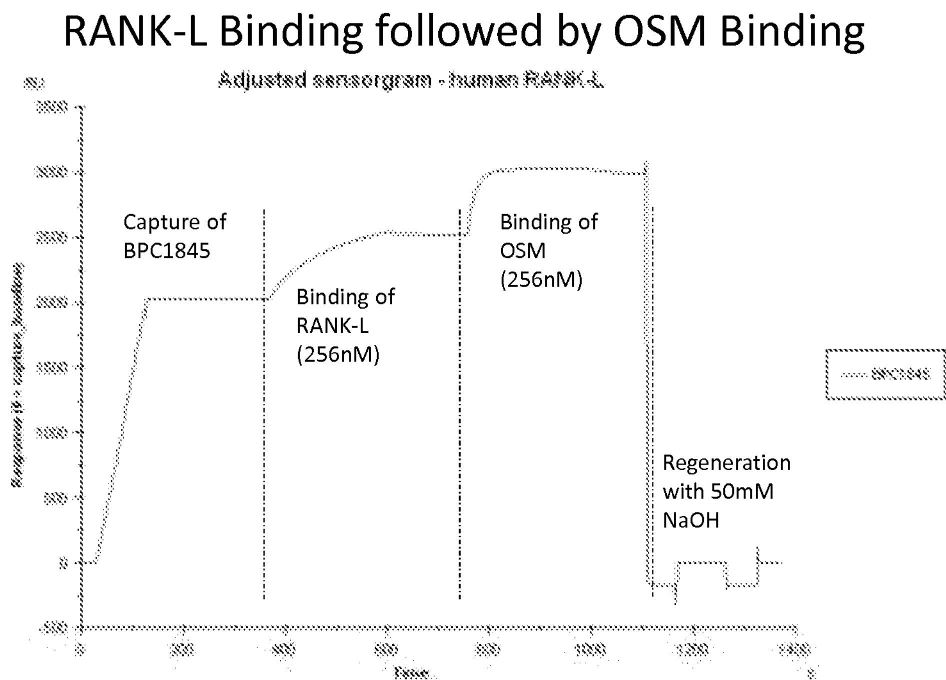


Figure 7b



INTERNATIONAL SEARCH REPORT

International application No
PCT/EP2010/052284

A. CLASSIFICATION OF SUBJECT MATTER
INV. C07K16/24 C07K16/28 C07K16/46
ADD.

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

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
C07K

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

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, EMBASE, BIOSIS

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	WO 2008/142164 A2 (ABLYNX NV [BE]; BEIRNAERT ELS [BE]; CORNELIS SIGRID [BE]; HOOGENBOOM H) 27 November 2008 (2008-11-27) example 11 page 159, line 31 - line 33	1-37

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[X] Further documents are listed in the continuation of Box C.

[X] See patent family annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance
"E" earlier document but published on or after the international filing date
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"P" document published prior to the international filing date but later than the priority date claimed

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"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
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"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
4 May 2010	19/05/2010

Name and mailing address of the ISA/	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Fax: (+31-70) 340-3016	Bumb, Peter

INTERNATIONAL SEARCH REPORT

International application No
PCT/EP2010/052284

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	KAMIJO S ET AL: "Amelioration of bone loss in collagen-induced arthritis by neutralizing anti-RANKL monoclonal antibody" BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, ACADEMIC PRESS INC. ORLANDO, FL, US LNKD- DOI:10.1016/J.BBRC.2006.06.098, vol. 347, no. 1, 18 August 2006 (2006-08-18), pages 124-132, XP024925477 ISSN: 0006-291X [retrieved on 2006-08-18] the whole document	1,2,4,9, 10, 12-16, 20-22, 29-37
Y	WO 2007/095338 A2 (IMCLONE SYSTEMS INC [US]; ZHU ZHENPING [US]) 23 August 2007 (2007-08-23) figures 1,7	1-37
Y	LUCY J HOLT ET AL: "Anti-serum albumin domain antibodies for extending the half-lives of short lived drugs" PROTEIN ENGINEERING, DESIGN AND SELECTION, OXFORD JOURNAL, LONDON, GB LNKD- DOI:10.1093/PROTEIN/GZM067, vol. 21, 1 January 2008 (2008-01-01), pages 283-288, XP007911765 ISSN: 1741-0126 [retrieved on 2008-04-02] the whole document	23
A	HUI WANG ET AL: "A model of inflammatory arthritis highlights a role for oncostatin M in pro-inflammatory cytokine-induced bone destruction via RANK/RANKL" ARTHRITIS RESEARCH, CURRENT SCIENCE, LONDON, GB LNKD- DOI:10.1186/AR1460, vol. 7, no. 1, 10 November 2004 (2004-11-10), pages R57-R64, XP021011547 ISSN: 1465-9905 the whole document	11

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No
PCT/EP2010/052284

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