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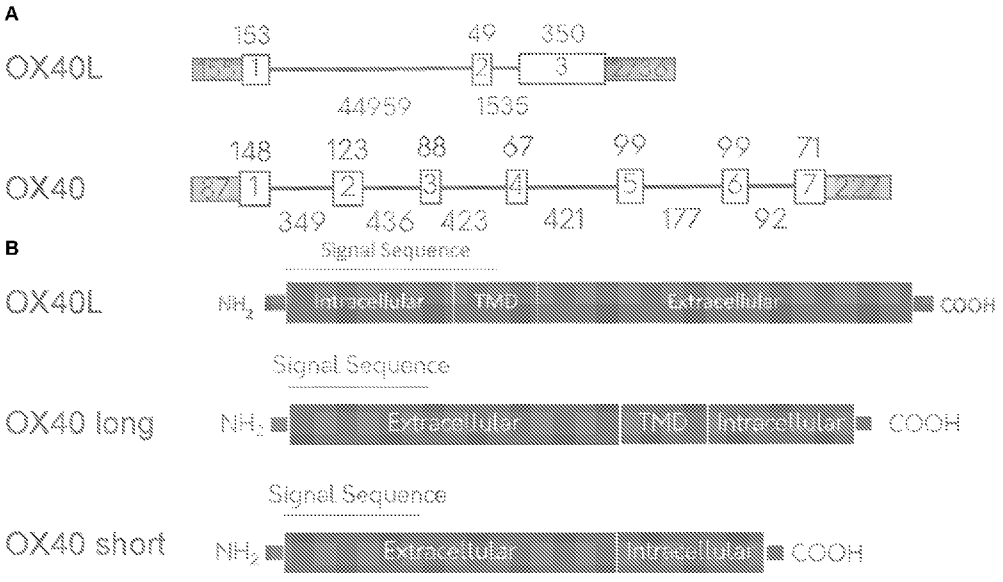
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(54) Title: THERAPEUTIC ANTIBODIES

Figure 1



(57) Abstract: The invention relates to antibodies which modulate the OX40 signalling pathway to treat inflammatory diseases in companion animals, for example atopic dermatitis (AD) and/or eczema. Related methods and uses are also described.

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Therapeutic antibodies

Introduction

The present invention relates to antibodies which modulate the OX40 signalling pathway to treat inflammatory diseases in companion animals.

Atopic dermatitis (AD) and/or eczema, characterised by chronic, dry, itchy, red skin, is a significant problem in dogs, effecting 10-15 % of pet dogs.

Cytopoint is an existing treatment for Atopic Dermatitis in dogs that has a recommended minimum dose of 1 mg kg^{-1}, by injection, once a month. Cytopoint is an anti-IL31 Ab (described for example in WO2013/011407A1 and WO2019/177697), specifically intended to treat the itch (pruritus) associated with atopic dermatitis. However, there are at least one third of canine AD patients that do not satisfactorily respond to Cytopoint, and in some instances, efficacy can decrease following the first injection (see, for example "CVMP assessment report for CYTOPOINT EMA/118401/2017 (EMEA/V/C/003939/0000)", and World Association for Veterinary Dermatology, Cytopoint roundtable May 2017, https://wavd.org/wp-content/uploads/cytopoint-roundtable-2017-05.pdf). The most common side effects of Cytopoint (which may affect up to 1 in 1,000 animals) are allergic reactions such as anaphylaxis, facial oedema and urticaria. Cytopoint must not be given to dogs weighing less than 3 kg. (https://www.ema.europa.eu/en/documents/product-information/cytopoint-epar-product-information_en.pdf).

There is a need for improved treatments as well as for drugs that treat the underlying cause of the disease rather than the symptoms. In particular, there is a need for a treatment that is safe, has a long duration of action, and has efficacy to cover a wider spectrum of patients, particularly non-responders.

Advantageously, targeting OX40/OX40L which are upstream in the inflammatory cascade, offers the possibility to modulate multiple cytokines simultaneously.

Canine OX40L is described in US 10,196,435. The protein sequence of canine OX40 has not been reported in the scientific or patent literature to date.

A monoclonal antibody (7D6) that binds feline CD134 (OX40) and its effect on the feline immunodeficiency virus is described in Willett et al, Journal of Virology, 81 (18), 2007, pages 9665-9679.

The use of an antibody to OX40L or OX40 in the treatment of immune-regulated diseases, such as atopic dermatitis, in companion animals (e.g. dogs) has not been shown before.

Statements of invention

In a first aspect, the invention relates to an antibody or fragment thereof that specifically binds to companion animal OX40L or to companion animal OX40, wherein the antibody is selected from one of the following antibodies:

an antibody comprising a HC CDR1 comprising SEQ ID No: 575 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 576 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 577 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 578 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 579 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 580 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto;
an antibody comprising a HC CDR1 comprising SEQ ID No: 741 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 742 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 743 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 744 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 745 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 746 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto;
an antibody comprising a HC CDR1 comprising SEQ ID No: 275 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 276 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 277 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 278 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 279 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 280 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto;
an antibody comprising a HC CDR1 comprising SEQ ID No: 395 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 396 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 397 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 398 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 399 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 400 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto
an antibody comprising a HC CDR1 comprising SEQ ID No: 15 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 16 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR3 comprising SEQ ID No:

17 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 18 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 19 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 20 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto

an antibody comprising a HC CDR1 comprising SEQ ID No: 45 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 46 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 47 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 48 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 49 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 50 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto

an antibody comprising a HC CDR1 comprising SEQ ID No: 65 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 66 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 67 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 68 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 69 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 70 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 115 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 116 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 117 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 118 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 119 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 120 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 155 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 156 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 157 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 158 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 159 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 160 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 235 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 236 or a sequence

with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 237 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 238 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 239 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 240 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 285 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 286 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 287 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 288 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 289 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 290 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 365 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 366 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 367 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 368 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 369 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 370 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 665 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 666 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 667 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 668 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 669 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 670 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 751 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 752 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 753 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 754 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 755 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 756 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto or

an antibody comprising a HC CDR1 comprising SEQ ID No: 761 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 762or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 763 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 764 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 765 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 766 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto.

The companion animal may be a dog or a cat.
In one embodiment, the antibody or fragment binds to canine OX40L.

In one embodiment, the antibody or fragment is capable of

a) Reducing, inhibiting or neutralising OX40 activity or activation in the companion animal or in a cell of the companion animal;
b) Modifying secretion of a cytokine in the companion animal or in a cell of the companion animal and/or
c) Decreasing proliferation of leukocytes in the companion animal or in a cell of the companion animal.

In one embodiment, the antibody or fragment is capable of

a) Reducing, inhibiting or neutralising OX40 activity or activation in the companion animal or in a cell of the companion animal;
b) Decreasing secretion of inflammatory cytokine in the companion animal or in a cell of the companion animal and/or
c) Decreasing secretion of an inflammatory chemokine or chemokine receptor in the companion animal or in a cell of the companion animal and/or
d) Increasing the secretion of suppressive cytokine(s) in the companion animal or in a cell of the companion animal and/or
e) Increasing the secretion of suppressive chemokines(s) or chemokine receptors in the companion animal or in a cell of the companion animal and/or
f) Decreasing proliferation of leukocytes in the companion animal.

Suitable assays assessing these properties, such as a Mixed Lymphocyte Reaction (MLR) assay or HEK-blue assay for measuring an inhibition of NFkB activity, are described herein, such as the assays shown in the examples, e.g. the PBMC activation assay. Other assays are known to the skilled person and may also be used.

The cytokine or cytokine receptor may be selected from TNF alpha, IL-1Ra, IL-2, IL-3, IL-4, IL-5, IL-6, IL-8, IL-9, IL-10, IL-13, IL-17, RANTES, GM-CSF, TGF-β and interferon gamma.

In one embodiment, the antibody or fragment binds to canine OX40. The antibody or fragment may be capable of reducing, inhibiting or neutralising OX40 activity or activation in the companion animal or in a cell of the companion animal.

In one embodiment of the forgoing and the various aspects of the invention relating to antibodies that bind OX40 or OX40L, the antibody or fragment is a fully canine, chimeric or caninized antibody. The terms fully canine and canine are used interchangeably herein. According to a preferred embodiment, the antibody is canine (i.e. fully canine).

For example, said fragment is selected from a F(ab')2, Fab, Fv, scFv, heavy chain, light chain, variable heavy (VH), variable light (VL) chain, CDR region, single VH or VL domain, maxibodies, minibodies, intrabodies, diabodies, triabodies, tetrabodies, and bis-scFv, and polypeptides that contain at least a portion of an immunoglobulin that is sufficient to confer specific antigen binding to the polypeptide.
In one embodiment, the antibody or fragment is conjugated to another moiety. The antibody or fragment may comprise a therapeutic moiety, half life extending moiety or label.

In another aspect, the invention relates to a binding molecule comprising an antibody or fragment as described above.

In another aspect, the invention relates to an antibody or fragment or the binding molecule as described above for use in the treatment of a disease.

In another aspect, the invention relates to a pharmaceutical composition comprising an antibody or fragment thereof or binding molecule as described above.

In another aspect, the invention relates to an antibody or fragment thereof, binding molecule pharmaceutical as described above for use in the treatment of an OX40 or OX40L-mediated disease.

In another aspect, the invention relates to methods of treating or preventing an OX40 or OX40L-mediated disease comprising administering to a subject in need thereof an antibody or fragment, binding molecule or the pharmaceutical composition as described above.

For example, the disease is selected from an inflammatory or autoimmune disease.

The disease may be an inflammatory skin diseases, including atopic dermatitis, allergic dermatitis, pruritus, psoriasis, scleroderma, or eczema; responses associated with inflammatory bowel disease

(such as Crohn's disease and ulcerative colitis); ischemic reperfusion; adult respiratory distress syndrome; asthma; meningitis; encephalitis; uveitis; autoimmune diseases such as rheumatoid arthritis, Sjorgen's syndrome, vasculitis; diseases involving leukocyte diapedesis; central nervous system (CNS) inflammatory disorder, multiple organ injury syndrome secondary to septicaemia or trauma, bacterial pneumonia, antigen-antibody complex mediated diseases; inflammations of the lung, including pleurisy, alveolitis, vasculitis, pneumonia, chronic bronchitis, bronchiectasis, and cystic fibrosis.

In one embodiment, the antibody or fragment, binding molecule, pharmaceutical composition is administered together with one or more therapeutic agent.

For example, said one or more therapeutic agent is selected from rapamycin (sirolimus), tacrolimus, cyclosporine (e.g. Atopica®), corticosteroids (e.g. methylprednisolone), methotrexate, mycophenolate mofetil, anti-CD28 antibodies, anti-IL12/IL-23 antibodies, anti-CD20 antibodies, anti-CD30 antibodies, CTLA4-Fc molecules, CCR5 receptor antagonists, anti-CD40L antibodies, anti-VI_A4 antibodies, anti-LFA1 antibodies, fludarabine, anti-CD52 antibodies, anti-CD45 antibodies, cyclophosphamide, anti-thymocyte globulins, anti-complement C5 antibodies, anti-a4b7 integrin antibodies, anti-IL6 antibodies, anti-IL6-R antibodies, anti-IL2R antibodies, anti-CD25 antibodies, anti-TNFa (TNFα) / TNFa-Fc molecules, HDAC inhibitors, JAK inhibitors, such as JAK-1 and JAK-3 inhibitors, anti-IL-31 antibodies, SYK inhibitors, anti-IL-4Ra antibodies, anti-IL-13 antibodies, anti-TSLP antibodies, PDE4 inhibitors, lokietmab (Cytopoint®), and oclacitinib (Apoquel®).

In another aspect, the invention relates to a method of decreasing the secretion of cytokines comprising administering to a subject in need thereof an antibody or fragment, binding molecule or a pharmaceutical composition as described above.

In another aspect, the invention relates to a multispecific binding agent comprising an antibody or fragment or a binding molecule as described above.
In another aspect, the invention relates to a combination therapy comprising antibody or fragment, binding molecule or pharmaceutical composition as described above.

In another aspect, the invention relates to an immunoconjugate comprising an antibody or fragment or binding molecule as described above.

In another aspect, the invention relates to a kit comprising an antibody or fragment thereof, binding or pharmaceutical composition as described above.

In another aspect, the invention relates to vector comprising a nucleic acid as above.

In another aspect, the invention relates to host cell comprising a nucleic acid or a vector as described above where the host cell is optionally selected from a mammalian, yeast, plant or bacterial cell.

In another aspect, the invention relates to a method for detecting OX40L or OX40 in a companion animal comprising contacting a test sample with an antibody or fragment or a binding molecule as described above.

In another aspect, the invention relates to a trimeric soluble companion animal OX40L extra cellular domain probe and its use in in a method of screening for companion animal OX40L antibodies.

The invention is described in the following non-limiting figures and tables.

Figures

Figure 1. Canine OX40 and OX40L gene and protein structures. **A.** The predicted number and arrangement of exons within the dog genome. Exons are represented by boxes. Numbers above the line represent the predicted size of each exon in nucleotides. Numbers below the line represent the predicted size of introns in nucleotides, 5' UTR and 3' UTR (shaded boxes). Predicted gene structures were made based on NCBI Assembly ID: 317138 (CanFam3.1). The size and sequence of the predicted transcripts was confirmed by RT-PCR using RNA extracted from activated PBMCs. **B.** Cartoon representations of OX40 and OX40L proteins.

Figure 2. Alignment of the canine OX40 long and short amino acids sequences (SEQ ID Nos. 4 and 6). Based on protein sequence homology with OX40 from other species, exon 6 is predicted to contain the transmembrane domain. Cartoon representations of these sequences are shown in Figure 1B.

Figure 3. Relative abundance of the two canine OX40 splice variants in PHA-activated canine PBMC's, as determined by the number of E.Coli colonies transformed with total OX40 cDNA. The long and short splice variants were identified from individual colonies by diagnostic PCR. Measurements were taken on independent PBMC samples, 1 and 4 days after activation. Insert: PCR discrimination of short (S) and long (L) splice variants. +ve = positive control. 1kb Plus DNA Ladder (NEB), with brighter bands at 0.5, 1.0 and 3.0 bp.

Figure 4. Serum antibody titres from immunised and non-immunised mice, measured using flow cytometry. **A.** In non-immunised mice there was no appreciable antibody binding to untransfected cells (△) or those stably expressing OX40L (○). **B.** Serum from immunised mice was collected 10-days after the first boost and yielded a clear distinction between untransfected/wild-type cells (▽) and those stably expressing OX40L (□). In this example, hydrodynamic tail vein injection of OX40L expression plasmid was used for the prime immunisation and OX40L expressing mouse embryonic fibroblasts was used for subsequent boosts.

Figure 5. Schematic representation of soluble proteins containing canine OX40L extra-cellular domain (ECD) (Seq ID Nos 807-811). **A.** Monomeric canine OX40L probe containing monomeric human IgG1 (mvhfc), 6xhistidine (HIS) tag and tobacco etch virus (TEV) protease cleaving peptide. **B.** Trimeric canine OX40L probes containing chicken tenascin C trimerization domain and either human IgG1 Fc or HIS tags. The term trimeric refers to the conformation of OX40L extra cellular domain.

Figure 6. Single-dose cell based binding assay of canine OX40L antibodies. Histograms show the overlayed intensity of signal obtained by flow cytometry of OX40L expressing HEK293 cells or the parental line stained with candidate OX40L antibodies and subsequently with a fluorescently labelled secondary antibody. All antibodies shown in the figure bind OX40L-expressing HEK cells with higher affinity compared to the parental line, with exception with the one labelled as non-binder. Geo mean intensity data are presented in Table 4.

Figure 7. Functional assay to measure OX40-OX40L interactions. **A.** Representative curves showing the enzymatic activity of secreted alkaline phosphatase, that was liberated 6 hrs, 24 hrs and 48hrs after mixing HEK-Blue-OX40 with HEK-OX40L cells. All curves are baseline subtracted with the signal obtained with culture media alone.

Figure 8. Single-dose cell based blocking assay based on HEK blue system to determine the blocking effect of candidate antibodies on OX40-OX40L interaction. Data are normalised with a maximum signal (100%) defined by the response obtained in the absence of antibodies and a minimum signal (0%) measured in the presence of HEK-blue-OX40 cells alone.

Figure 9. HPLC-SEC chromatogram for antibodies PMX050, 51, 53 and 63. Quantification of the percentage of monomeric for is presented in Table 9.

Figure 10. Candidate antibody biophysical stability measurement using Uncle (Unchained Labs) for antibodies PMX051 and 063. **A.** Data shows the intensity and mass distribution (left and centre graphs, respectively) used to calculate the initial diameter of the molecules, and **B.** SLS/DLS data used to calculate Tm_1 and $Tagg_{266}$. Data are presented in Table 9.

Figure 11. Quantification of the first melting temperature (Tm1) and aggregation temperatures as measured by fluorescence 266nm and 473nm of PMX051, PMX063 PMX 097, PMX098 and PMX154 molecules after incubation at 37°C over a period of 28 days. Data show that the tendency of all 5 molecules to melt or aggregate are relatively stable when incubated at 37°C for 28 days. Data were acquired using an UNCLE machine (UNChained Labs).

Figure 12. Quantification of the average molecule size of PMX051, PMX063 PMX 097, PMX098 and PMX154 molecules after incubation at 37°C over a period of 28 days. Data show the different propensity of the 5 molecules to aggregate over time at 37°C. PMX097 and PMX154 demonstrated the best stability when incubated at 37°C for 28 days. Data were acquired using an UNCLE machine (UNChained Labs).

Figure 13. Pharmacokinetic profile of PMX097 (triangles) and PMX154 (squares) in dog serum after intravenous injection of 3.0 mg of antibody per kg of body weight. Data were analysed by fitting a two-phase decay curve using Prism. Degradation phase: PMX097=8.5 days; PMX154=8.9 days.

Figure 14. Canine interferon gamma (IFNY) ELISpot performed on PBMC isolated from dogs treated with PMX097 or PMX154 at the indicated dose before KLH immunisation accordingly to the protocol exemplified in table 11. The data show the number of spots obtained after culturing PBMC with either no stimulation (**A.**) or in presence of 50µg/ml KLH (**B-C**.). Both PMX097 and PMX154 reduced T cell activation for up to 35 post single dosing when administered at 0.5 mg/kg and for up to 77 days post single dosing when administered at 3.0 mg/kg.

Figure 15. Anti-KLH IgM (A, B) and IgG (C, D) serum titre performed on serum from dogs treated with PMX097 or PMX154 at the indicated dose before KLH immunisation accordingly to the protocol exemplified in table 11. Data show the results obtained from serum isolated from dogs at different time points and a detailed view on days 21 and 98 post dosing. Both PMX097 and PMX154 reduced anti-KLH IgM and IgG serum titre at both 3.0mg/kg and 0.5mg/kg for up to 77 days post single dosing.

Figure 16. Haematoxylin and eosin (HE) staining on sections from skin biopsies collected from dogs treated with PMX097 or PMX154 2 days after intradermal KLH injection. The images show the subcutaneous fat area. **(A, B)** Biopsies from vehicle control injected dogs collected at the KLH injection site (B) or a non-injected skin area (A). **(C, D)** Biopsies collected at the KLH injection site from dogs treated with PMX154 at 3.0 mg/kg (C) or 0.5 mg/kg (D). **(E, F)** Biopsies collected at the KLH injection site from dogs treated with PMX097 at 3.0 mg/kg (E) or 0.5 mg/kg (F). Both PMX097 and PMX154 reduce the presence of immune infiltrates compared to vehicle control dogs. PMX154 nearly completely abrogated the presence of immune infiltrates.

Table 1. Amino Acid Residues and Examples of Conservative Amino Acid Substitutions.

Table 2. Nucleic acid and amino acid sequences.

Table 3. VH and VL gene usage

Table 4. Geomeans obtained from cell binding assay.

Table 5. Normalised cell-based inhibition assay based on HEK blue system, demonstrating the percentage of OX40 signal inhibition of candidate antibodies. Data are normalised with a maximum inhibition (100%) defined as the SEAP activity detected in samples with HEK blue OX40 cells alone and a minimum signal (0%) measured in samples with HEK blue OX40 and HEK OX40L cells, the absence of anti-canine OX40L antibodies.

Table 6: Inhibition of IFN-γ release by candidate OX40L antibodies from activated PBMCs in the presence of OX40L expressing HEK cells. Anti-OX40L antibodies were tested in ten independent

experiments. Level of IFN-γ in control samples in each experiment is also indicated. Activated PBMC only = PBMC activated in presence of CD3-CD28 antibodies only and no anti-OX40L antibody. Activated PBMC plus HEK WT = PBMC activated in presence of CD3-CD28 antibodies and WT HEK cells and no anti-OX40L antibody. Activated PBMC plus HEK OX40L = PBMC activated in presence of CD3-CD28 antibodies and HEK cells expressing OX40L and no anti-OX40L antibody.

Table 7: Normalised IFN-γ levels in supernatant from PBMC activated with CD3 and CD28 antibodies in presence of OX40L expressing HEK cells and the indicated anti-OX40L antibody. Data from Table 6 were normalised using GraphPad as such IFN-γ levels in wells with PBMC activated in presence of CD3-CD28 antibodies only and no anti-OX40L antibody was set as 0% and IFN-γ levels in wells with PBMC activated in presence of CD3-CD28 antibodies and HEK cells expressing OX40L and no anti-OX40L antibody was set as 100%.

Table 8: Functional affinity of anti OX40L antibodies for trimeric canine OX40L determined by surface plasmon resonance (SPR). Data were analysed using Biacore Insight Evaluation Software. Curves were fitted using a bivalent analyte binding model.

Table 9: Protein stability determination of OX40L antibodies. Tm_1 = melting (unfolding) temperature 1; $Tagg_{266}$ = onset aggregation temperature determined by static light scattering at 266nm; initial diameter = average molecule diameter before temperature increase; % monomer (SEC) = % of monomers determined by HLPLC-SEC.

Table 10: Long term stability of PMX097 and PMX154 when incubated at 4°C over a period of four months. Data show melting temperature 1 (Tm1), aggregating temperature measured at 266nm (Tagg 266nm) the average molecular diameter (Z AVG diam) and the polydispersity index (PDI).

Table 11: Treatment regime of dogs in the single dose antigen recall dog study.

Table 12: Histological findings in non-injected skin areas from dogs in the single dose antigen recall study.

Table 13: Histological findings in KLH-injected skin areas from dogs in the single dose antigen recall study.

Detailed description

OX40 and its binding partner OX40L are part of the TNF superfamily, and OX40 signalling is a co-stimulatory pathway in promoting T cell activation. OX40 (the receptor) is expressed on the surface of T-cells, and OX40L on both the surface of T-cells and antigen presenting cells such as B cells and macrophages. Neither OX40 nor OX40L are constitutively expressed, but increase 24 – 72 hours following activation of their respective cells. OX40L binding to OX40 receptors on T-cells promote T cell

survival, proliferation and cytokine production. OX40 therefore has a critical role in establishing, maintaining and modulating an immune response.

In humans, both the density of OX40L and the number of OX40 positive cells is significantly greater in the lesional dermis than in the healthy-looking dermis in atopic dermatitis, and blockade of OX40/OX40L signalling modulates several pro-inflammatory responses. OX40L also controls the response of dendritic cells to thymic stromal lymphopoietin (TSLP), which results in IL-21 and CXCL13 production. The OX40/OX40L axis consequently offers the possibility of modulating multiple pro-inflammatory responses, as its co-stimulatory signal sits upstream of several cellular processes that release pro-inflammatory cytokines.

OX40 signalling has been linked to various diseases such as allergy, asthma, and diseases associated with autoimmunity and inflammation, which includes multiple sclerosis, rheumatoid arthritis, inflammatory bowel disease, graft-versus-host disease, experimental autoimmune encephalomyelitis (EAE), experimental leishmaniasis, collagen-induced arthritis, colitis (such as ulcerative colitis), contact hypersensitivity reactions, diabetes, Crohn's Disease, and Grave's Disease. Evidence in humans suggests that disruption of the OX40/OX40L axis reduces proliferative responses, such as immune cells, and could be used to prevent, treat or ameliorate the symptoms of a number of diseases, including atopic dermatitis, diabetes and cancer. Antibodies to either OX40 or OX40L could be used to achieve this disruption.

However, the role of antibody treatments for OX40/OX40L mediated diseases in companion animals, such as atopic dermatitis, e.g. in dogs, has not been investigated previously.

Thus, in a first aspect, the invention relates to an antibody or fragment thereof that specifically binds to companion animal OX40L or to companion animal OX40.

Companion animals of the invention are suitably selected from dogs, cats, horses, birds, rabbits, goats, reptiles, fish and amphibians. A dog is a preferred companion animal of the invention. A cat is a preferred companion animal of the invention. A horse is a preferred companion animal of the invention. For the avoidance of doubt, a human is not a companion animal.

In one aspect, the companion animal is a dog.

In one aspect, the companion animal is a cat.

In one aspect, the companion animal is a horse.

In one embodiment, antibodies and fragments described herein bind specifically to wild type canine OX40L. The amino acid sequence (SEQ ID No.1) and nucleotide sequences for wild type canine OX40L are shown in Table 2 (SEQ ID No. 2). Antibodies and fragments described herein bind specifically to

SEQ ID No.1. In one embodiment, antibodies and fragments described herein bind specifically to variants of SEQ ID No.1.

In one embodiment, antibodies and fragments described herein bind specifically to wild type canine OX40. The amino acid sequence (SEQ ID Nos. 4 and 6) and nucleotide sequences for wild type canine OX40 are shown in table 2 (SEQ ID Nos. 3 and 5). As explained in the examples, two different splice variants were identified. Antibodies and fragments described herein bind specifically to proteins codified by SEQ ID No. 3 and/or 5. In one embodiment, antibodies and fragments described herein bind specifically to proteins codified by variants of SEQ ID No. 3 and/or 5 (SEQ ID Nos. 4 and 6).

Variants of the sequences described above may have at least 75%, 80%, 85%, 90% or 95% sequence identity to the sequences shown above.

As used herein, the terms "homology" or “identity” generally refers to the percentage of amino acid residues in a sequence that are identical with the residues of the reference polypeptide with which it is compared, after aligning the sequences and in some embodiments after introducing gaps, if necessary, to achieve the maximum percent homology, and in some embodiments not considering any conservative substitutions as part of the sequence identity. Thus, the percent homology between two amino acid sequences is equivalent to the percent identity between the two sequences. Neither N- or C-terminal extensions, tags or insertions shall be construed as reducing identity or homology. Methods and computer programs for the alignment are well known. The percentage identity between two amino acid sequences can be determined using well known mathematical algorithms. As used herein the term “sequence similarity” generally refers to the percentage of amino acid residues in a sequence that are identical and/or comprise conservative amino acid substitutions, where the substituted amino acid has similar physicochemical properties. For example, where a positively charged amino acid has been replaced by a different positively charged amino acid. Percentage similarity may be calculated using tools such as “EMBOSS Needle” which implements the Needleman-Wunch algorithm for the pairwise percent identities or similarities, amino acids may be considered similar if they have a positive score in the BLOSUM62 matrix. In an embodiment, where the term “sequence identity” is used herein it may be replaced by the term “sequence similarity”.

Unless otherwise specified, the term OX40L as used herein refers to a companion animal OX40L, e.g. dog or cat OX40L. OX40L is also known as “OX40 Antigen Ligand”, “OX40 Ligand”, “CD252”, “TNFSF4” and “CD134 Ligand”. In one embodiment, the antibody or fragment thereof binds to dog OX40L. In one embodiment, the antibody or fragment thereof binds to cat OX40L.

Unless otherwise specified, the term OX40 as used herein refers to a companion animal OX40, e.g. dog or cat OX40. OX40 is also known as “TNFR Superfamily Member 4”, “TNFRSF4”, “OX40 Antigen” and “CD134”. In one embodiment, the antibody or fragment thereof binds to dog OX40L. In one embodiment, the antibody or fragment thereof binds does not bind to cat OX40L. In one embodiment, the antibody or fragment thereof is not 7D6 as disclosed in Willett et al.

The terms "OX40L binding molecule/protein/polypeptide/agent/moiety", "OX40L antigen binding molecule molecule/protein/polypeptide/agent/moiety", “anti- OX40L antibody”, “anti- OX40L antibody fragment” all refer to a molecule capable of specifically binding to the companion animal OX40L, e.g. dog or cat OX40L antigen. The binding reaction may be shown by standard methods, for example with reference to a negative control test using an antibody of unrelated specificity.

The terms "OX40 binding molecule/protein/polypeptide/agent/moiety", "OX40 antigen binding molecule molecule/protein/polypeptide/agent/moiety", “anti- OX40 antibody”, “anti- OX40 antibody fragment” all refer to a molecule capable of specifically binding to the companion animal OX40, e.g. dog or cat OX40 antigen. The binding reaction may be shown by standard methods, for example with reference to a negative control test using an antibody of unrelated specificity.

In some embodiments, the antibody or fragment provided herein binds to an OX40L epitope that is a three-dimensional surface feature of a OX40L polypeptide. In some embodiments, the antibody or fragment provided herein binds to an epitope comprising a polypeptide from a single subunit, or a conformational epitope arising from a multimeric form, (e.g., an epitope in a monomeric or trimeric form of an OX40L polypeptide). A region of an OX40L polypeptide contributing to an epitope may be contiguous amino acids of the polypeptide or the epitope may come together from two or more non-contiguous regions of the polypeptide. A OX40L epitope may be present in (a) the trimeric form ("a trimeric OX40L epitope") of OX40L, (b) the monomeric form ("a monomeric OX40L epitope") of OX40L, (c) both the trimeric and monomeric form of OX40L, (d) the trimeric form, but not the monomeric form of OX40L, or (e) the monomeric form, but not the trimeric form of OX40L

For example, in some embodiments, the epitope is only present or available for binding in the trimeric form, but is not present or available for binding in the monomeric form by an anti-OX40L antibody. In other embodiments, the OX40L epitope is linear feature of the OX40L polypeptide (e.g., in a trimeric form or monomeric form of the OX40L polypeptide). Antibodies provided herein may specifically bind to (a) an epitope of the monomeric form of OX40L, (b) an epitope of the trimeric form of OX40L, (c) an epitope of the monomeric but not the trimeric form of OX40L, (d) an epitope of the trimeric but not the monomeric form of OX40L, or (e) both the monomeric form and the trimeric form of OX40L. In some embodiments, the antibodies provided herein specifically bind to an epitope of the trimeric form of OX40L but do not specifically bind to an epitope the monomeric form of OX40L. In some embodiments, the antibodies provided herein bind to an epitope of the monomeric form of OX40L and may or may not bind to the trimeric form.

An antibody or fragment thereof "which binds" or is “capable of binding” an antigen of interest, e.g. companion animal OX40L or companion animal OX40 respectively, is one that binds the antigen with sufficient affinity such that the antibody or fragment is useful as a therapeutic agent in targeting a cell or tissue expressing the antigen OX40 or OX40L respectively as described herein.

Antibodies and fragments thereof as described herein bind specifically to the target companion animal OX40L or the target companion animal OX40 respectively. For example, in one embodiment, antibodies and fragments thereof as described herein bind specifically to canine OX40L. In another embodiment, antibodies and fragments thereof as described herein bind specifically to feline OX40L. For example, in one embodiment, antibodies and fragments thereof as described herein bind specifically to canine OX40. In another embodiment, antibodies and fragments thereof as described herein bind specifically to feline OX40. The term "specifically" in the context of antibody binding, refers to high avidity and/or high affinity binding of an antibody to a specific antigen, i.e., a polypeptide, or epitope. In many embodiments, the specific antigen is an antigen (or a fragment or subfraction of an antigen) used to immunize the animal host from which the antibody-producing cells were isolated.

In other words, binding to the OX40L or OX40 antigen is stronger than binding of the same antibody to other antigens, i.e. measurably different from a non-specific interaction. Thus, in one embodiment, the antibodies or fragments of the invention do not cross react with mouse or human OX40L or OX40 antigen.

The term "specific binding" or "specifically binds to" or is "specific for" a particular polypeptide or an epitope on a particular polypeptide target as used herein can be exhibited, for example, by a molecule having a KD (K_d) for the target of at least about 10^{-6} M, alternatively at least about 10^{-7} M, alternatively at least about 10^{-8} M, alternatively at least about 10^{-9} M, alternatively at least about 10^{-10} M, alternatively at least about 10^{-11} M, alternatively at least about 10^{-12} M, or lower. In one embodiment, the KD (K_d) is 10^{-9} M or lower. In a preferred embodiment the KD (K_d) is 10^{-9} M or lower, for example 10^{-10} M. In an embodiment the antibodies of the invention have a KD (K_d) for the target of about 10^{-6} M to 10^{-12} M, or about 10^{-7} M to 10^{-12} M, or about 10^{-8} M to 10^{-12} M, or about 10^{-9} M to 10^{-12} M, or about 10^{-10} M to 10^{-12} M, or about 10^{-11} M to 10^{-12} M. In one embodiment, the term "specific binding" refers to binding where a molecule binds to a particular polypeptide or epitope on a particular polypeptide without substantially binding to any other polypeptide or polypeptide epitope.

In one embodiment, antibodies of the invention are antagonistic antibodies that bind specifically to companion animal OX40L, for example canine OX40L.

As used herein, an "antagonist" or "inhibitor" of OX40L /OX40 refers to a ligand (e.g., antibody or fragment) that is capable of inhibiting or otherwise decreasing one or more of the biological activities of OX40L/OX40, such as in a cell expressing OX40L/OX40 or in a cell expressing an OX40L/OX40 ligand. For example, in certain embodiments, antibodies of the invention are antagonist antibodies that inhibit or otherwise decrease secretion of a cytokine from a cell having a cell surface-expressed OX40L/OX40 when said antibody is contacted with said cell. In some embodiments, an antagonist of OX40L (e.g., an antagonistic antibody of the invention) may, for example, act by inhibiting or otherwise decreasing the activation and/or cell signalling pathways of the cell expressing OX40L/OX40, thereby inhibiting a OX40L/OX40-mediated biological activity of the cell the relative to the OX40L/OX40-mediated biological

activity in the absence of antagonist. In certain embodiments, the antibodies provided herein are fully canine, antagonistic anti-OX40L/OX40 antibodies, preferably fully canine, monoclonal, antagonistic anti-OX40L/OX40 antibodies.

The term "antibody" as used herein broadly refers to any immunoglobulin (Ig) molecule, or antigen binding portion thereof, comprised of four polypeptide chains, two heavy (H) chains and two light (L) chains, or any functional fragment, mutant, variant, or derivation thereof, which retains the essential epitope binding features of an Ig molecule.

In a full-length antibody, each heavy chain is comprised of a heavy chain variable region or domain (abbreviated herein as HCVR) and a heavy chain constant region. The heavy chain constant region is comprised of three domains, C_H1, C_H2 and C_H3. Each light chain is comprised of a light chain variable region or domain (abbreviated herein as LCVR) and a light chain constant region. The light chain constant region is comprised of one domain, C_L.

The heavy chain and light chain variable regions can be further subdivided into regions of hypervariability, termed complementarity determining regions (CDR), interspersed with regions that are more conserved, termed framework regions (FR). Each heavy chain and light chain variable region is composed of three CDRs and four FRs, arranged from amino-terminus to carboxy-terminus in the following order: FR1, CDR1, FR2, CDR2, FR3, CDR3, FR4.

Immunoglobulin molecules can be of any type, class or subclass (e.g., for dogs IgG, IgE, IgM, IgD, IgA and IgY; e.g. canine IgG subtype, for example IgG-A, IgG-B, IgG-C, and IgG-D). In canine, there are four IgG heavy chains referred to as A, B, C, and D. These heavy chains represent four different subclasses of dog IgG, which are referred to as IgGA, IgGB, IgGC and IgGD. The DNA and amino acid sequences of these four heavy chains were first identified by Tang et al. (Vet. Immunol. Immunopathol. 80: 259-270 (2001)). Exemplary amino acid and DNA sequences for these heavy chains are also available from the GenBank data bases (IgGA: accession number AAL35301.1, IgGB: accession number AAL35302.1, IgGC: accession number AAL35303.1, IgGD: accession number AAL35304.1). Canine antibodies also contain two types of light chains, kappa and lambda (GenBank accession number kappa light chain amino acid sequence ABY 57289.1, GenBank accession number ABY 55569.1). Amino acid sequences for IgG-A, IgG-B, IgG-C and IgG-D as used by the inventors and according to the aspects and embodiments of the invention are shown in Table 2.

The term "CDR" refers to the complementarity-determining region within antibody variable sequences. There are three CDRs in each of the variable regions of the heavy chain and the light chain, which are designated CDR1, CDR2 and CDR3, for each of the variable regions. The term "CDR set" refers to a group of three CDRs that occur in a single variable region capable of binding the antigen. The exact boundaries of these CDRs can be defined differently according to different systems known in the art.

The Kabat Complementarity Determining Regions (CDRs) are based on sequence variability and are the most commonly used (Kabat et al., (1971) Ann. NY Acad. Sci. 190:382-391 and Kabat, et al., (1991) Sequences of Proteins of Immunological Interest, Fifth Edition, U.S. Department of Health and Human Services, NIH Publication No. 91-3242). Chothia refers instead to the location of the structural loops (Chothia and Lesk J. Mol. Biol. 196:901 -917 (1987)). The Kabat numbering system is generally used when referring to a residue in the variable domain (approximately residues 1-107 of the light chain and residues 1 -113 of the heavy chain). Another system is the ImMunoGeneTics (IMGT) numbering scheme. The IMGT numbering scheme is described in Lefranc et al., Dev. Comp. Immunol., 29, 185-203 (2005). These terms, which are recognized in the art, refer to a system of numbering amino acid residues which are more variable (i.e., hypervariable) than other amino acid residues in the heavy and light chain variable regions of an antibody, or an antigen binding portion.

The IMGT numbering scheme is used herein unless otherwise specified.

The antibody to OX40L or OX40 according to the invention may be a canine, humanized, feline, chimeric antibody, felinized or caninized antibody.

A “chimeric antibody” is a recombinant protein that contains the variable domains including the complementarity determining regions (CDRs) of an antibody derived from one species, while the constant domains of the antibody molecule are derived from those of another species, e.g., a canine antibody. An exemplary chimeric antibody is a chimeric human – canine antibody.

A “humanized antibody” is a recombinant protein in which the CDRs from an antibody from one species; e.g., a rodent, canine, feline antibody, are transferred from the heavy and light variable chains of the rodent, canine or feline antibody into human heavy and light variable domains (e.g., framework region sequences). The constant domains of the antibody molecule are derived from those of a human antibody. In certain embodiments, a limited number of framework region amino acid residues from the parent (e.g., rodent, canine or feline) antibody may be substituted into the human antibody framework region sequences. In an embodiment the CDRs disclosed herein may be transferred from the heavy and light variable chains of the antibody disclosed herein into the heavy and light variable domains (e.g., framework region sequences) of a different species.

As used herein, the term "caninized antibody" refers to forms of recombinant antibodies that contain sequences from both canine and non-canine (e.g., murine) antibodies. In general, the caninized antibody will comprise substantially all of at least one or more typically, two variable domains in which all or substantially all of the hypervariable loops correspond to those of a non-canine immunoglobulin, and all or substantially all of the framework (FR) regions (and typically all or substantially all of the remaining frame) are those of a canine immunoglobulin sequence. A caninized antibody may comprise both the three heavy chain CDRs and the three light chain CDRS from a murine or human antibody together with a canine frame or a modified canine frame. A modified canine frame comprises one or more amino acids changes that can further optimize the effectiveness of the caninized antibody, e.g., to

increase its binding to its target. The non-canine sequences, e.g., of the hypervariable loops, may further be compared to canine sequences and as many residues changed to be as similar to authentic canine sequences as possible.

A “speciated” antibody (e.g. humanized, caninized, chimeric, felinized) is one which has been engineered to render it similar to antibodies of the target species. In one embodiment, a “speciated” antibody is greater than about 80%, 85% or 90% similar to antibodies of the target species.

In one embodiment, the antibody or antibody fragment is canine. By canine is meant fully canine. The terms fully canine and canine are used interchangeably herein.

In contrast to speciated antibodies, fully canine antibodies of the present invention have canine variable regions and do not include full or partial CDRs or FRs from another species. Advantageously, fully canine antibodies as described herein have been obtained from transgenic mice comprising canine immunoglobulin sequences. Antibodies produced in these immunised mice are developed through in vivo B cell signalling and development to allow for natural affinity maturation including *in vivo* V(D)J recombination, *in vivo* junctional diversification, *in vivo* pairing of heavy and light chains and *in vivo* hypermutation. Fully canine antibodies produced in this way generate antibodies with optimal properties for developability, minimizing lengthy lead optimization prior to production at scale. Advantageously, such fully canine antibodies present the lowest possible risk of immunogenicity when introduced into a patient animal which, in turn, facilitates a repeated dosing regimen. Adverse *in vivo* immunogenicity can be assessed, for example, by assays to identify the production of anti-drug antibodies (ADA), or a loss of efficacy over time *in vivo*. Given that *ex vivo* mAb engineering runs the risk of introducing development liabilities, immunogenicity, and reduced affinity (as outlined above), fully canine antibodies of the present invention are, therefore, most likely to be efficacious therapies in a clinical context.

As used herein, the term "felinized antibody" refers to forms of recombinant antibodies that contain sequences from both feline and non-feline (e.g., murine) antibodies. In general, the felinized antibody will comprise substantially all of at least one or more typically, two variable domains in which all or substantially all of the hypervariable loops correspond to those of a non-feline immunoglobulin, and all or substantially all of the framework (FR) regions (and typically all or substantially all of the remaining frame) are those of a feline immunoglobulin sequence. A felinized antibody may comprise both the three heavy chain CDRs and the three light chain CDRs from a murine or human antibody together with a feline frame or a modified feline frame. A modified feline frame comprises one or more amino acids changes that can further optimize the effectiveness of the felinized antibody, e.g., to increase its binding to its target. The non-feline sequences, e.g., of the hypervariable loops, may further be compared to feline sequences and as many residues changed to be as similar to authentic feline sequences as possible.

In one embodiment, the antibody or antibody fragment is feline. By feline is meant fully feline. The terms fully feline and feline are used interchangeably herein.

In contrast to speciated antibodies, fully feline antibodies of the present invention have feline variable regions and do not include full or partial CDRs or FRs from another species. Fully feline antibodies may be obtained from transgenic mice comprising feline immunoglobulin sequences. Antibodies produced in these immunised mice are developed through in vivo B cell signalling and development to allow for natural affinity maturation including in vivo V(D)J recombination, in vivo junctional diversification, in vivo pairing of heavy and light chains and in vivo hypermutation. Fully feline antibodies produced in this way generate antibodies with optimal properties for developability, minimizing lengthy lead optimization prior to production at scale. Advantageously, such fully feline antibodies present the lowest possible risk of immunogenicity when introduced into a patient animal which, in turn, facilitates a repeated dosing regimen. Adverse in vivo immunogenicity can be assessed, for example, by assays to identify the production of anti-drug antibodies (ADA), or a loss of efficacy over time in vivo. Ex vivo mAb engineering runs the risk of introducing development liabilities, immunogenicity, and reduced affinity (as outlined above), as such fully feline antibodies are, therefore, most likely to be efficacious therapies in a clinical context.

As used herein, the term "equinized antibody" refers to forms of recombinant antibodies that contain sequences from both equine and non-equine (e.g., murine) antibodies. In general, the equinized antibody will comprise substantially all of at least one or more typically, two variable domains in which all or substantially all of the hypervariable loops correspond to those of a non- equine immunoglobulin, and all or substantially all of the framework (FR) regions (and typically all or substantially all of the remaining frame) are those of an equine immunoglobulin sequence. An equinized antibody may comprise both the three heavy chain CDRs and the three light chain CDRS from a murine or human antibody together with a feline frame or a modified equine frame. A modified equine frame comprises one or more amino acids changes that can further optimize the effectiveness of the equinized antibody, e.g., to increase its binding to its target. The non- equine sequences, e.g., of the hypervariable loops, may further be compared to equine sequences and as many residues changed to be as similar to authentic equine sequences as possible.

In one embodiment, the antibody or antibody fragment is equine. By equine is meant fully equine. The terms fully equine and equine are used interchangeably herein.

The term "monoclonal antibody" as used herein refers to an antibody derived from a single B or plasma cell. All antibody molecules in a monoclonal antibody preparation are identical except for possible naturally occurring post-translation modifications (e.g., isomerizations, amidations, carbohydrate addition) that may be present in minor amounts. Monoclonal antibodies are highly specific, being directed against a single antigenic site. In contrast to polyclonal antibody preparations which typically include different antibodies directed against different determinants (epitopes), each monoclonal antibody is directed against a single determinant on the antigen.

The term “epitope” or “antigenic determinant” refers to a site on the surface of an antigen (to which an immunoglobulin, antibody or antibody fragment, specifically binds. Generally, an antigen has several or many different epitopes and reacts with many different antibodies. The term specifically includes linear epitopes and conformational epitopes. Epitopes within protein antigens can be formed both from contiguous amino acids (usually a linear epitope) or non-contiguous amino acids juxtaposed by tertiary folding of the protein (usually a conformational epitope). Epitopes formed from contiguous amino acids are typically, but not always, retained on exposure to denaturing solvents, whereas epitopes formed by tertiary folding are typically lost on treatment with denaturing solvents. An epitope typically includes at least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 or 15 amino acids in a unique spatial conformation. Methods for determining what epitopes are bound by a given antibody or antibody fragment (i.e., epitope mapping) are well known in the art and include, for example, immunoblotting and immunoprecipitation assays, wherein overlapping or contiguous peptides from are tested for reactivity with a given antibody or antibody fragment.

An antibody binds "essentially the same epitope" as a reference antibody, when the two antibodies recognize identical or sterically overlapping epitopes. The most widely used and rapid methods for determining whether two epitopes bind to identical or sterically overlapping epitopes are competition assays, which can be configured in different formats, using either labelled antigen or labelled antibody. The epitope may or may not be a three-dimensional surface feature of the antigen. In certain embodiments, an OX40L epitope is a three-dimensional surface feature of a OX40L polypeptide (e.g., in a trimeric form of a OX40L polypeptide). In other embodiments, a OX40L epitope is linear feature of a OX40L polypeptide (e.g., in a trimeric form or monomeric form of the OX40L polypeptide). Antibodies provided herein may specifically bind to an epitope of the monomeric form of OX40L, an epitope of the trimeric form of OX40L, or both the monomeric form and the trimeric form of OX40L. In specific embodiments, the antibodies provided herein specifically bind to an epitope of the trimeric form of OX40L but do not specifically bind the monomeric form of OX40L. In some embodiments, an antibody may, for example, bind to a monomer/single subunit and block formation of an active trimeric form. Suitably the antibodies bind to the extracellular domain of OX40L.

The term "antigen binding site" refers to the part of the antibody or antibody fragment that comprises the area that specifically binds to an antigen. An antigen binding site may be provided by one or more antibody variable domains. An antigen binding site is typically comprised within the associated V_H and V_L of an antibody or antibody fragment.

The term antibody as used herein also includes antibody fragments. Specifically, the invention also extends to antibody fragments. An antibody fragment is a portion of an antibody, for example a F(ab')2, Fab, Fv, scFv, heavy chain, light chain, variable heavy (V_H), variable light (V_L) chain, CDR region, single V_H or V_L domain, maxibodies, minibodies, intrabodies, diabodies, triabodies, tetrabodies, and bis-scFv, and polypeptides that contain at least a portion of an immunoglobulin that is sufficient to confer specific

antigen binding to the polypeptide. Therefore, an antibody fragment comprises an antigen binding portion.

Antibody fragments are functional fragments of a full-length antibody, that is they retain the target specificity of a full antibody. Recombinant functional antibody fragments, such as Fab (Fragment, antibody), scFv (single chain variable chain fragments) and single domain antibodies (dAbs) have therefore been used to develop therapeutics as an alternative to therapeutics based on mAbs.

An “Fv" is the minimum antibody fragment which contains a complete antigen- recognition and -binding site. This fragment consists of a dimer of one heavy- and one light-chain variable region domain in tight, non-covalent association. From the folding of these two domains emanate six hypervariable loops (3 loops each from the H and L chain) that contribute the amino acid residues for antigen binding and confer antigen binding specificity to the antibody. However, even a single variable domain (or half of an Fv comprising only three HVRs specific for an antigen) has the ability to recognize and bind antigen, although at a lower affinity than the entire binding site. "Single-chain Fv" also abbreviated as "sFv" or "scFv" are antibody fragments that comprise the VH and VL antibody domains connected into a single polypeptide chain.

scFv fragments (~25kDa) consist of the two variable domains, V_H and V_L. Naturally, V_H and V_L domain are non-covalently associated via hydrophobic interaction and tend to dissociate. However, stable fragments can be engineered by linking the domains with a hydrophilic flexible linker to create a single chain Fv (scFv).

The smallest antigen binding fragment is the single variable fragment, namely the variable heavy (V_H) or variable light (V_L) chain domain. V_H and V_L domains respectively are capable of binding to an antigen. Binding to a light chain/heavy chain partner respectively or indeed the presence of other parts of the full antibody is not required for target binding. The antigen-binding entity of an antibody, reduced in size to one single domain (corresponding to the V_H or V_L domain), is generally referred to as a “single domain antibody” or “immunoglobulin single variable domain”. A single domain antibody (~12 to 15 kDa) has thus either the V_H or V_L domain.

Thus, in one embodiment, the fragment is selected from a F(ab')2, Fab, Fv, scFv, heavy chain, light chain, variable heavy (V_H), variable light (V_L) chain, CDR region, single V_H or V_L domain, maxibodies, minibodies, intrabodies, diabodies, triabodies, tetrabodies, and bis-scFv, and polypeptides that contain at least a portion of an immunoglobulin that is sufficient to confer specific antigen binding to the polypeptide.

In one embodiment, the invention does not relate to an immunoglobulin domain, e.g. an Fc domain, fused to a companion animal, e.g. canine, OX40L extracellular domain polypeptide fragment or biological equivalent thereof.

The antibodies and antibody fragments of the invention are isolated. The term "isolated" as used herein refers to a moiety that is isolated from its natural environment. For example, the term "isolated" refers to a single domain antibody that is substantially free of other single domain antibodies, antibodies or antibody fragments. Moreover, an isolated single domain antibody may be substantially free of other cellular material and/or chemicals.

In one aspect, the invention relates to an antibody or fragment thereof that binds specifically to companion animal, such as canine, OX40L wherein said antibody blocks binding of OX40L to OX40 and/or inhibits one or more functions associated with binding of OX40L to OX40. Suitably the antibody reduces, inhibits or neutralises OX40 activity in the companion animal. In one embodiment, the antibody or fragment thereof exhibits one or more of the following properties:

a) Is capable of modifying secretion of a cytokine in the cell or animal, and/or
b) Is capable of decreasing proliferation of leukocytes in the companion animal, such as dog.

“Modifying” refers to increasing or decreasing the amount of a compound in the presence of an antibody compared to a control. "Decreasing" or "decreases" as used herein refers to a reduction and the decrease may be at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95% or more.

For example, the antibody or fragment is capable of

a) Decreasing secretion of inflammatory cytokine in the companion animal or in a cell of the companion animal and/or
b) Decreasing secretion of an inflammatory chemokine or chemokine receptor in the companion animal or in a cell of the companion animal and/or
c) Increasing the secretion of suppressive cytokine(s) in the companion animal or in a cell of the companion animal and/or
d) Increasing the secretion of suppressive chemokines(s) or chemokine receptors in the companion animal or in a cell of the companion animal and/or
e) Decreasing proliferation of leukocytes in the companion animal.

The cytokine may be selected from TNF alpha, IL-2, IL-3, IL-4, IL-5, IL-6, IL-8, IL-9, IL-10, IL-13, IL-17, RANTES, GM-CSF, TGF-β and interferon gamma (IFN-ɣ). In an embodiment the antibody acts to decrease the secretion of the inflammatory cytokine in the companion animal or in a cell of the companion animal compared to where no antibody is present. In a preferred embodiment the inflammatory cytokine is IFN-ɣ.

The antibody may act to decrease the secretion of the inflammatory cytokine in the companion animal or in a cell of the companion animal by more than 30%, more than 40%, more than 50%, more than 60%, more than 70%, more than 80%, more than 90% compared to where no antibody is present. The antibody may act to decrease the secretion of the inflammatory cytokine in the companion animal or in

a cell of the companion animal by 30% to 100%, 40% to 100%, 50% to 100%, 60% to 100%, 70% to 100%, 80% to 100%, 90% to 100% compared to where no antibody is present. The decrease in secretion of the inflammatory cytokine may be determined using a cell signalling inhibition assay such as that described herein in Example 7 i.e., aPBMC activation assay.

An "inflammatory" compound is one that is involved in promoting inflammation, whereas a "suppressive" compound is one that is involved in suppressing or regulating inflammation. Inflammatory cytokines include interleukin-1 (IL-1), IL-12, and IL-18, TNF alpha, interferon gamma (IFNγ) and GM-CSF. Suppressive or anti-inflammatory cytokines or receptors include IL-4, IL-10, IL-11, IL-13 and TGF-β. The cytokine may be a chemokine. In one embodiment, the chemokine may be selected from CXCL13, CXCR5, for example. The antibody in accordance with the invention may also modify cytokine or chemokine receptor expression.

Assays may be carried out *in vitro* (e.g. using a cell, cells or tissue) or *in vivo*.

In one embodiment, binding of OX40L to OX40 in the presence of an antibody in accordance with the invention may be determined in an SPR (surface plasmon resonance) assay, for example. Other methods for determining inhibition of an OX40L/OX40 interaction are described, for example in WO2016/139482 or WO2013/008171 and include, for example, flow cytometry monitoring of antibody binding to recombinant OX40L-expressing cells.

In one embodiment, the ability of an antibody to OX40L to block binding of OX40L to OX40 can be measured by measuring an inhibition of NFkB activity. Suitable assays for measuring NFkB activity include the HEK-blue assay described herein. Accordingly, in one embodiment, the antibody or fragment thereof that binds specifically to companion animal, such as canine, OX40L reduces, inhibits or neutralises OX40R-mediated NFkB activity in a cell-based assay.

In one embodiment, the assay is a heterologous assay in which a companion animal (e.g. dog) OX40 is used in a cell line derived from a different species, e.g. a human cell line such as HEK, substantially as described in Example 7 herein.

In one embodiment, the ability of an antibody to OX40L to block binding of OX40L to OX40 can be measured by measuring a decreased secretion of a cytokine in a cell compared to that observed in the absence of the antibody. In one embodiment, the ability of an antibody to OX40L to block binding of OX40L to OX40 can be measured by measuring an inhibition of IL-2 or INF-gamma secretion from PBMCs. Accordingly, in one embodiment, the antibody or fragment thereof that binds specifically to companion animal, such as canine, OX40L reduces, inhibits or neutralises OX40R-mediated IL-2 or INF-gamma (INFγ) secretion from PBMCs. In another embodiment, the ability of an antibody to OX40L to block binding of OX40L to OX40 can be measured by measuring an inhibition of IL-13 secretion from

PBMCs. It will be understood that the ability of an antibody to OX40 to block binding of OX40L to OX40 can be measured in a similar manner.

The antibody or fragment is capable of effecting a decrease of the proliferation of leukocytes (e.g., mononuclear cells) in an *in vitro* assay wherein the antibody or fragment antagonises OX40L/OX40L receptor interaction.

As is known in the art, the term "leukocytes" includes, for example, one or more of lymphocytes, polymorphonuclear leukocyte and monocytes. As is also readily apparent to the skilled person the term "monocytes" includes, for example, peripheral blood mononuclear cells (PBMCs) or monocyte derived cells, e.g., dendritic cells (DCs).

Leukocyte proliferation may be measured, for example in a Mixed Lymphocyte Reaction (MLR) as described herein. The ability of an antibody in accordance with the invention to decrease proliferation may be measured by comparison to proliferation in the absence of the antibody.

The proliferation of leukocytes, e.g., lamina propria lymphocytes (LPLs), can be assessed using tissue biopsy, staining and histology, as will be apparent to the skilled person. Hematoxylin and eosin stain (H&E stain or HE stain) is, for example, commonly used in histology to look for infiltrating lymphocytes a whole range of human tissue and is one of the principal stains in histology. It is the most widely used stain in medical diagnosis and is often the gold standard, and as such can be used to assess proliferation of leukocytes as per the invention. For example, GI tract tissue (e.g., gut tissue) from a companion animal that is suffering from or at risk of a OX40L-mediated disease or condition can be obtained, stained and assessed for the extent of infiltration of LPLs.

Comparison can be made between such tissue from a companion animal that has received an antibody of the invention compared to the extent of infiltration in tissue obtained from the same animal prior to administration of antibody or from another companion animal that has not received treatment and is at risk of or suffering from the disease or condition. For example, the comparison is between companion animal gut tissues taken from the same (or different) companion animals suffering from e.g. IBD. The anti-OX40L antibody binds to OX40L and regulates cytokine and cellular receptor expression resulting in cytokine levels characteristic of non-disease states. The anti-OX40 antibody binds to OX40 and regulates cytokine and cellular receptor expression resulting in cytokine levels characteristic of non-disease states.

Cytokines are indispensable signals of the mucosa -associated immune system for maintaining normal gut homeostasis. An imbalance of their profile in favour of inflammation initiation may lead to disease states, such as that is observed in inflammatory bowel diseases (IBD), e.g., Crohn's disease (CD) and ulcerative colitis (UC). The role of pro-inflammatory cytokines such as IL-la, IL-Iβ, IL-2, - 6, -8, -12, -17, -23, IFN-gamma, or TNF alpha in IBD is associated with the initiation and progression of UC and CD. CD is often described as a prototype of T-helper (Th) 1-mediated diseases because the primary

inflammatory mediators are the Thl cytokines such as interleukin (IL)-12, interferon (IFN)-y, and tumour necrosis factor (TNF)-α. The cytokine or cytokine receptor may be selected from TNF alpha, IL-2, IL-3, IL-4, IL-5, IL-6, IL-8, IL-9, IL-10, IL-13, IL-17, RANTES, GM-CSF, TGF-β and interferon gamma.

Further information on suitable assays to assess properties of the antibodies is provided in the examples.

The antibodies disclosed herein can be grouped into different groups i.e., families based on the pairs of V genes that have been used to generate the antibodies. Family 1 comprises antibodies generated from heavy chain V-gene IGHV3-5 and light chain V-gene IGLV3-14. Examples of antibodies in Family 1 include antibodies designated PMX025, PMX026, PMX027, PMX089, PMX090, PMX091, PMX092, PMX093, the sequences of these antibodies are set out in Table 2.

Family 2 comprises antibodies generated from heavy chain V-gene IGHV3-5 and light chain V-gene IGLV3-21. Examples of antibodies in Family 2 include antibodies designated PMX028, PMX029, PMX032, PMX033, PMX034, PMX036, PMX038, PMX042, PMX045, PMX064, PMX082, PMX083 the sequences of these antibodies are set out in Table 2.

Family 3 comprises antibodies generated from heavy chain V-gene IGHV3-5 and light chain V-gene IGLV3-24. Examples of antibodies in Family 3 include antibodies designated PMX030, PMX031the sequences of these antibodies are set out in Table 2.

Family 4 comprises antibodies generated from heavy chain V-gene IGHV3-8 and light chain V-gene IGLV3-24. Examples of antibodies in Family 4 include antibodies designated PMX035, PMX037, PMX040, PMX048, PMX049, PMX065 the sequences of these antibodies are set out in Table 2.

Family 5 comprises antibodies generated from heavy chain V-gene IGHV3-18 and light chain V-gene IGLV3-3. Examples of antibodies in Family 5 include antibodies designated PMX039, PMX041, PMX043, PMX044, PMX046, PMX050 PMX055, PMX056, PMX057, PMX058, PMX059, PMX062, PMX085 the sequences of these antibodies are set out in Table 2.

Family 6 comprises antibodies generated from heavy chain V-gene IGHV3-19 and light chain V-gene IGKV2-5. Examples of antibodies in Family 6 include antibodies designated PMX047 and PMX053, the sequences of these antibodies are set out in Table 2.

Family 7 comprises antibodies generated from heavy chain V-gene IGHV3-44 and light chain V-gene IGLV3-8. Examples of antibodies in Family 7 include antibodies designated PMX051, PMX088, the sequences of these antibodies are set out in Table 2.

Family 8 comprises antibodies generated from heavy chain V-gene IGHV3-19 and light chain V-gene IGKV2-4. Examples of antibodies in Family 8 include antibodies designated PMX052, the sequences of these antibodies are set out in Table 2.

Family 9 comprises antibodies generated from heavy chain V-gene IGHV3-5 and light chain V-gene IGLV3-3. Examples of antibodies in Family 9 include antibodies designated PMX060, PMX061, the sequences of these antibodies are set out in Table 2.

Family 10 comprises antibodies generated from heavy chain V-gene IGHV3-5 and light chain V-gene IGLV3-8. Examples of antibodies in Family 10 include antibodies designated PMX063, PMX086, PMX087, PMX094, PMX095, PMX096, PMX097, PMX098, PMX099, PMX100, PMX101, PMX102, PMX 103, PMX104, PMX105, PMX107, PMX108, PMX109, PMX110, PMX111, the sequences of these antibodies are set out in Table 2.

Family 11 comprises antibodies generated from heavy chain V-gene IGHV3-5 and light chain V-gene IGKV2-4. Examples of antibodies in Family 11 include antibodies designated PMX106, the sequences of these antibodies are set out in Table 2.

Family 12 comprises antibodies generated from heavy chain V-gene IGHV3-18 and light chain V-gene IGLV3-24. Examples of antibodies in Family 12 include antibodies designated PMX054, PMX084, PMX154, PMX293, PMX294 the sequences of these antibodies are set out in Table 2.

Family 13 comprises antibodies generated from heavy chain V-gene IGHV3-19 and light chain V-gene IGLV3-21. Examples of antibodies in Family 13 include antibodies designated PMX155, PMX156, the sequences of these antibodies are set out in Table 2.

Family 14 comprises antibodies generated from heavy chain V-gene IGHV3-41 and light chain V-gene IGLV3-24. Examples of antibodies in Family 14 include antibodies designated PMX291, PMX292, the sequences of these antibodies are set out in Table 2.

In one embodiment, the antibody or fragment may be selected from an antibody as shown in any of Families 1 to 14 or an antibody with at least 80% sequence identity thereto.

In one embodiment the antibody or fragment thereof comprises an antibody comprising a Family 1 sequence or a variant thereof. In one embodiment the antibody or fragment thereof comprises an antibody comprising a Family 2 sequence or a variant thereof. In one embodiment the antibody or fragment thereof comprises an antibody comprising a Family 3 sequence or a variant thereof. In one embodiment the antibody or fragment thereof comprises an antibody comprising a Family 4 sequence or a variant thereof. In one embodiment the antibody or fragment thereof comprises an antibody comprising a Family 5 sequence or a variant thereof. In one embodiment the antibody or fragment thereof comprises an antibody comprising a Family 6 sequence or a variant thereof. In one embodiment the antibody or fragment thereof comprises an antibody comprising a Family 7 sequence or a variant thereof. In one embodiment the antibody or fragment thereof comprises an antibody comprising a Family 8 sequence or a variant thereof. In one embodiment the antibody or fragment thereof comprises an antibody comprising a Family 9 sequence or a variant thereof. In one embodiment the antibody or

fragment thereof comprises an antibody comprising a Family 10 sequence or a variant thereof. In one embodiment the antibody or fragment thereof comprises an antibody comprising a Family 11 sequence or a variant thereof. In one embodiment the antibody or fragment thereof comprises an antibody comprising a Family 12 sequence or a variant thereof. In one embodiment the antibody or fragment thereof comprises an antibody comprising a Family 13 sequence or a variant thereof. In one embodiment the antibody or fragment thereof comprises an antibody comprising a Family 14 sequence or a variant thereof.

In one embodiment the antibody that binds canine OX40L may be selected from one of the following antibodies

An antibody comprising a Family 1 sequence or a variant thereof, for example an antibody comprising a HC CDR1 comprising SEQ ID No: 15 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 16 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 17 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 18 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 19 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 20 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto;

An antibody comprising a Family 2 sequence or a variant thereof, for example an antibody comprising a HC CDR1 comprising SEQ ID No: 45 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 46 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 47 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 48 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 49 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 50 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto;

An antibody comprising a Family 3 sequence or a variant thereof, for example an antibody comprising a HC CDR1 comprising SEQ ID No: 65 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 66 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 67 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 68 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 69 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 70 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto;

An antibody comprising a Family 4 sequence or a variant thereof, for example an antibody comprising a HC CDR1 comprising SEQ ID No: 115 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 116 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 117 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 118 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 119 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 120 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto;

An antibody comprising a Family 5 sequence or a variant thereof, for example an antibody comprising a HC CDR1 comprising SEQ ID No: 155 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 156 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 157 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 158 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 159 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 160 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto;

An antibody comprising a Family 6 sequence or a variant thereof, for example an antibody comprising a HC CDR1 comprising SEQ ID No: 235 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 236 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 237 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 238 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 239 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 240 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto;

An antibody comprising a Family 7 sequence or a variant thereof, for example an antibody comprising a HC CDR1 comprising SEQ ID No: 275 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 276 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 277 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 278 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 279 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 280 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto;

An antibody comprising a Family 8 sequence or a variant thereof, for example an antibody comprising a HC CDR1 comprising SEQ ID No: 285 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 286 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 287 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 288 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 289 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 290 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto;

An antibody comprising a Family 9 sequence or a variant thereof, for example an antibody comprising a HC CDR1 comprising SEQ ID No: 365 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 366 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 367 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 368 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 369 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 370 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto;

An antibody comprising a Family 10 sequence or a variant thereof, for example an antibody comprising a HC CDR1 comprising SEQ ID No: 575 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 576 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 577 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 578 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 579 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 580 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto;

An antibody comprising a Family 10 sequence or a variant thereof, for example an antibody comprising a HC CDR1 comprising SEQ ID No: 395 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 396 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 397 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 398 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 399 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 400 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto;

An antibody comprising a Family 11 sequence or a variant thereof, for example an antibody comprising a HC CDR1 comprising SEQ ID No: 665 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 666 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 667 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 668 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 669 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 670 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto.

An antibody comprising a Family 12 sequence or a variant thereof, for example an antibody comprising a HC CDR1 comprising SEQ ID No: 741 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 742 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 743 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 744 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 745 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 746 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto.

An antibody comprising a Family 13 sequence or a variant thereof, for example an antibody comprising a HC CDR1 comprising SEQ ID No: 751 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 752 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 753 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 754 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 755 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 756 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto.

An antibody comprising a Family 14 sequence or a variant thereof, for example an antibody comprising a HC CDR1 comprising SEQ ID No: 771 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 772 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 773 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 774 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 775 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 776 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto.

In one embodiment, the antibody that binds canine OX40L may be selected from one of the following antibodies:

An antibody comprising a HC CDR1 comprising SEQ ID No: 15 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 16 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 17 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 18 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 19 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 20 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 25 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 26 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 27 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 28 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 29 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 30 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 35 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 36 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 37 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 38 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 39 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 40 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 45 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 46 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 47 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 48 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 49 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 50 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 55 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 56 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 57, or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 58 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 59 or a sequence with at least 80%

sequence identity thereto and a LC CDR3 comprising SEQ ID No: 60 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 65 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 66 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 67 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 68 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 69 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 70 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 75 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 76 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 77 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 78 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 79 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 80 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 85 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 86 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 87 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 88 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 89 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 90 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 95 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 96 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 97 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 98 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 99 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 100 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 105 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 106 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 107 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 108 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 109 or a sequence with at least 80%

sequence identity thereto and a LC CDR3 comprising SEQ ID No: 110 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 115 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 116 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 117 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 118 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 119 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 120 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 125 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 126 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 127 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 128 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 129 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 130 or a sequence with at least 80% sequence identity thereto; or

An antibody comprising a HC CDR1 comprising SEQ ID No: 135 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 136 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 137 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 138 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 139 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 140 or a sequence with at least 80% sequence identity thereto.

An antibody comprising a HC CDR1 comprising SEQ ID No: 145 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 146 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 147 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 148 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 149 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 150 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 155 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 156 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 157 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 158 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 159 or a sequence with at least 80%

sequence identity thereto and a LC CDR3 comprising SEQ ID No: 160 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 165 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 166 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 167 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 168 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 169 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 170 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 175 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 176 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 177 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 178 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 179 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 180 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 185 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 186 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 187 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 188 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 189 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 190 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 195 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 196 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 197 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 198 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 199 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 200 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 205 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 206 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 207 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 208 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 209 or a sequence with at least 80%

sequence identity thereto and a LC CDR3 comprising SEQ ID No: 210 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 215 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 216 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 217 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 218 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 219 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 220 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 225 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 226 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 227 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 228 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 229 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 230 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 235 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 236 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 237 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 238 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 239 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 240 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 245 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 246 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 247 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 248 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 249 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 250 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 255 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 256 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 257 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 258 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 259 or a sequence with at least 80%

sequence identity thereto and a LC CDR3 comprising SEQ ID No: 260 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 265 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 266 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 267 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 268 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 269 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 270 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 275 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 276 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 277 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 278 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 279 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 280 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 285 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 286 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 287 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 288 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 289 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 290 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 295 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 296 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 297 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 298 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 299 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 300 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 305 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 306 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 307 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 308 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 309 or a sequence with at least 80%

sequence identity thereto and a LC CDR3 comprising SEQ ID No: 310 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 315 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 316 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 317 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 318 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 319 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 320 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 325 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 326 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 327 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 328 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 329 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 330 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 335 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 336 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 337 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 338 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 339 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 340 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 345 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 346 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 347 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 348 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 349 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 350 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 355 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 356 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 357 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 358 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 359 or a sequence with at least 80%

sequence identity thereto and a LC CDR3 comprising SEQ ID No: 360 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 365 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 366 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 367 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 368 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 369 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 370 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 375 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 376 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 377 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 378 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 379 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 380 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 385 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 386 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 387 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 388 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 389 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 390 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 395 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 396 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 397 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 398 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 399 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 400 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 405 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 406 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 407 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 408 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 409 or a sequence with at least 80%

sequence identity thereto and a LC CDR3 comprising SEQ ID No: 410 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 415 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 416 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 417 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 418 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 419 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 420 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 425 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 426 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 427 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 428 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 429 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 430 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 435 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 436 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 437 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 438 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 439 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 440 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 445 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 446 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 447 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 448 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 449 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 440 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 455 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 456 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 457 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 458 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 459 or a sequence with at least 80%

sequence identity thereto and a LC CDR3 comprising SEQ ID No: 460 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 465 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 466 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 467 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 468 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 469 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 470 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 475 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 476 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 477 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 478 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 479 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 480 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 485 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 486 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 487 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 488 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 489 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 490 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 495 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 496 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 497 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 498 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 499 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 500 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 505 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 506 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 507 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 508 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 509 or a sequence with at least 80%

sequence identity thereto and a LC CDR3 comprising SEQ ID No: 510 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 515 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 516 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 517 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 518 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 519 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 520 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 525 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 526 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 527 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 528 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 529 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 530 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 535 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 536 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 537 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 538 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 539 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 540 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 545 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 546 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 547 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 548 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 549 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 550 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 555 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 556 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 557 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 558 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 559 or a sequence with at least 80%

sequence identity thereto and a LC CDR3 comprising SEQ ID No: 560 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 565 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 566 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 567 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 568 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 569 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 570 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 575 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 576 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 577 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 578 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 579 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 580 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 585 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 586 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 587 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 588 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 589 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 590 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 595 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 596 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 597 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 598 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 599 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 600 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 605 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 606 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 607 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 608 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 609 or a sequence with at least 80%

sequence identity thereto and a LC CDR3 comprising SEQ ID No: 610 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 615 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 616 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 617 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 618 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 619 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 620 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 625 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 626 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 627 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 628 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 629 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 630 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 635 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 636 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 637 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 638 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 639 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 640 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 645 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 646 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 647 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 648 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 649 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 650 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 655 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 656 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 657 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 658 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 659 or a sequence with at least 80%

sequence identity thereto and a LC CDR3 comprising SEQ ID No: 660 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 665 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 666 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 667 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 668 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 669 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 670 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 675 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 676 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 677 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 678 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 679 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 680 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 685 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 686 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 687 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 688 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 689 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 690 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 695 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 696 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 697 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 698 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 699 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 700 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC CDR1 comprising SEQ ID No: 705 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 706 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 707 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 708 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 709 or a sequence with at least 80%

sequence identity thereto and a LC CDR3 comprising SEQ ID No: 710 or a sequence with at least 80% sequence identity thereto; or

An antibody comprising a HC CDR1 comprising SEQ ID No: 715 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 716 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 717 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 718 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 719 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 720 or a sequence with at least 80% sequence identity thereto.

An antibody comprising a HC CDR1 comprising SEQ ID No: 741 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 742 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 743 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 744 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 745 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 746 or a sequence with at least 80% sequence identity thereto.

An antibody comprising a HC CDR1 comprising SEQ ID No: 751 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 752 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 753 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 754 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 755 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 756 or a sequence with at least 80% sequence identity thereto.

An antibody comprising a HC CDR1 comprising SEQ ID No: 761 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 762 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 763 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 764 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 765 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 766 or a sequence with at least 80% sequence identity thereto.

An antibody comprising a HC CDR1 comprising SEQ ID No: 771 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 772 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 773 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 774 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 775 or a sequence with at least 80%

sequence identity thereto and a LC CDR3 comprising SEQ ID No: 776 or a sequence with at least 80% sequence identity thereto.

An antibody comprising a HC CDR1 comprising SEQ ID No: 781 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 782 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 783 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 784 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 785 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 786 or a sequence with at least 80% sequence identity thereto.

An antibody comprising a HC CDR1 comprising SEQ ID No: 791 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 792 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 793 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 794 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 795 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 796 or a sequence with at least 80% sequence identity thereto.

An antibody comprising a HC CDR1 comprising SEQ ID No: 801 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 802 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 803 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 804 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 805 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 806 or a sequence with at least 80% sequence identity thereto.

In an embodiment the antibody is selected from one of those recited above but comprises a sequence identity of 85%, 90%, 95%, 96%, 97%, 98% or 99% identity to the HC and/or LC CDR1, 2 and/or CDR3 sequences that are listed.

An antibody comprising a HC CDR1 comprising SEQ ID No: 741 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 742 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 743 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 744 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 745 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 746 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto.

An antibody comprising a HC CDR1 comprising SEQ ID No: 751 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 752 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 753 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 754 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 755 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 756 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto.

An antibody comprising a HC CDR1 comprising SEQ ID No: 761 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 762 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 763 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 764 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 765 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 766 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto.

An antibody comprising a HC CDR1 comprising SEQ ID No: 771 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 772 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 773 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 774 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 775 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 776 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto.

An antibody comprising a HC CDR1 comprising SEQ ID No: 781 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 782 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 783 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 784 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 785 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 786 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto.

An antibody comprising a HC CDR1 comprising SEQ ID No: 791 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 792 or a sequence

with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 793 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 794 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 795 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 796 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto.

An antibody comprising a HC CDR1 comprising SEQ ID No: 801 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 802 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 803 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 804 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 805 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 806 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto.

In an embodiment the antibody is selected from one of those recited above but comprises a sequence identity of 85%, 90%, 95%, 96%, 97%, 98% or 99% identity to the HC and/or LC CDR1, 2 and/or CDR3 sequences that are listed.

In one embodiment the antibody is selected from one of those recited above, but comprises one or more HC and/or LC CDR1, 2 and/or CDR3 sequences with 1, 2, 3, 4 or 5 amino acid substitutions compared to the sequences defined in the SEQ ID Nos. above.

In a preferred embodiment the antibody comprises a HC CDR1 comprising SEQ ID No: 575 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 576 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 577 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 578 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 579 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 580 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto; or

a HC CDR1 comprising SEQ ID No: 741 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 742 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 743 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 744 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 745 or a sequence with at least 60%, 70%, 80%, 90% or 95%

sequence identity thereto and a LC CDR3 comprising SEQ ID No: 746 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto; or

a HC CDR1 comprising SEQ ID No: 275 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 276 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 277 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 278 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 279 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 280 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto; or

a HC CDR1 comprising SEQ ID No: 395 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 396 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 397 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 398 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 399 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 400 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto.

Fragments of the antibodies listed above are also provided and within the scope of the invention.

In one embodiment, the antibody may be selected from one of the following antibodies:

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 12 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 14 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 22 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 24 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 32 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 34 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 42 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 44 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 52 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 54 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 62 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 64 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 72 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 74 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 82 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 84 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 92 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 94 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 102 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 104 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 112 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 114 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 122 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 124 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 132 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 134 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 142 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 144 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 152 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 154 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 162 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 164 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 172 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 174 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 182 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 184 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 192 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 194 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 202 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 204 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 212 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 214 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 222 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 224 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 232 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 234 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 242 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 244 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 252 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 254 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 262 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 264 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 272 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 274 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 282 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 284 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 292 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 294 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 302 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 304 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 312 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 314 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 322 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 324 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 332 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 334 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 342 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 344 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 352 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 354 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 362 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 364 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 372 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 374 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 382 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 384 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 392 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 394 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 402 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 404 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 412 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 414 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 422 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 424 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 432 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 434 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 442 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 444 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 452 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 454 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 462 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 464 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 472 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 474 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 482 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 484 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 492 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 494 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 502 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 504 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 512 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 514 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 522 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 524 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 532 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 534 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 542 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 544 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 552 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 554 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 562 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 564 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 572 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 574 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 582 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 584 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 592 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 594 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 602 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 604 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 612 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 614 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 622 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 624 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 632 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 634 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 642 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 644 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 652 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 654 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 662 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 664 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 672 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 674 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 682 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 684 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 692 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 694 or a sequence with at least 80% sequence identity thereto;

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 702 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 704 or a sequence with at least 80% sequence identity thereto; or

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 712 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 714 or a sequence with at least 80% sequence identity thereto.

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 738 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 740 or a sequence with at least 80% sequence identity thereto.

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 748 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 750 or a sequence with at least 80% sequence identity thereto.

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 758 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 760 or a sequence with at least 80% sequence identity thereto.

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 768 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 770 or a sequence with at least 80% sequence identity thereto.

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 778 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 780 or a sequence with at least 80% sequence identity thereto.

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 788 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 790 or a sequence with at least 80% sequence identity thereto.

An antibody comprising a HC variable region comprising or consisting of SEQ ID No. 798 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 800 or a sequence with at least 80% sequence identity thereto.

In an embodiment the antibody is selected from one of those recited above but comprises a sequence identity of 85%, 90%, 95%, 96%, 97%, 98% or 99% identity to the HC and/or LC variable region sequences that are listed.

In one embodiment the antibody is selected from one of those recited above and comprises HC variable region and/or LC variable region which comprises 1 to 20, e.g. 1 to 10, e.g., 2, 3, 4 or 5 amino acid substitutions compared to the sequences as defined by the SEQ ID Nos above.

In a preferred embodiment the antibody comprises a HC variable region comprising or consisting of SEQ ID No. 572 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 574 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto; or

a HC variable region comprising or consisting of SEQ ID No. 738 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 740 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto; or

a HC variable region comprising or consisting of SEQ ID No. 272 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 274 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto; or

a HC variable region comprising or consisting of SEQ ID No. 392 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 394 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto.

Fragments of the antibodies listed above are also provided.

The amino acid sequences of the VH and VL regions of the antibodies are shown in Table 2. An antibody or fragment may therefore be selected from an antibody comprising or consisting of a sequence shown in Table 2. In one embodiment, the antibody is selected from PMX025, PMX026, PMX027, PMX028, PMX029, PMX030, PMX031, PMX032, PMX033, PMX034, PMX035, PMX036, PMX037, PMX038, PMX039, PMX040, PMX041, PMX042, PMX043, PMX044, PMX045, PMX046, PMX047, PMX048, PMX049, PMX050, PMX051, PMX052, PMX053, PMX054, PMX055, PMX056, PMX057, PMX058, PMX059, PMX060, PMX061, PMX062, PMX063, PMX064, PMX065, PMX082, PMX083, PMX084, PMX085, PMX086, PMX087, PMX088, PMX089, PMX090, PMX091, PMX092, PMX093, PMX094, PMX095, PMX096, PMX097, PMX098, PMX099, PMX100, PMX101, PMX102, PMX103, PMX104, PMX105, PMX106, PMX107, PMX108, PMX109, PMX110, PMX111 PMX154, PMX155, PMX 156, PMX291, PMX292, PMX293, or PMX294 as set out in Table 2. In one embodiment, the antibody is PMX051 or PMX063. Sequences are also shown in Table 2. In one embodiment, the antibody is selected from PMX051, PMX63, PMX97 or PMX154.

All sequences for antibody and antibody fragments designated as PMX as shown in the figures herein and in Table 2 are within the scope of the invention.

Sequence identity as described in the various embodiments above is at least 80%. In one embodiment, sequence identity is at least 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99%. In one embodiment, said sequence identity is at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99%. The embodiments described herein also cover sequences with sequence similarity of at least 80%. In one embodiment, sequence similarity is at least 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99%. In one embodiment, said sequence similarity is at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99%.

As described above, the antibody or fragment defined by reference to the sequence may comprise one or more amino acid substitutions. In one embodiment, the modification is a conservative sequence modification. As used herein, the term "conservative sequence modifications" is intended to refer to amino acid modifications that do not significantly affect or alter the binding characteristics of the antibody containing the amino acid sequence. Such conservative modifications include amino acid substitutions, additions and deletions. Modifications can be introduced into an antibody of the invention by standard techniques known in the art, such as site-directed mutagenesis and PCR-mediated mutagenesis. Conservative amino acid substitutions are ones in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (e.g., lysine, arginine, histidine), acidic side chains (e.g., aspartic acid, glutamic acid), uncharged polar side chains (e.g., glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine, tryptophan), nonpolar side chains (e.g., alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine), beta-branched side chains (e.g., threonine, valine, isoleucine) and aromatic side chains (e.g., tyrosine, phenylalanine,

tryptophan, histidine). Thus, one or more amino acid residues within one or more the CDR region and/or one or more framework region the antibody or fragment of the invention can be replaced with other amino acid residues from the same side chain family and the altered antibody can be tested for retained function (using the functional assays described herein or known in the art.

Thus, these amino acid changes can typically be made without altering the biological activity, function, or other desired property of the polypeptide, such as its affinity or its specificity for antigen. In general, single amino acid substitutions in nonessential regions of a polypeptide do not substantially alter biological activity. Furthermore, substitutions of amino acids that are similar in structure or function are less likely to disrupt the polypeptides' biological activity. Abbreviations for the amino acid residues of the polypeptides and peptides described herein, and conservative substitutions for these amino acid residues are shown in Table 1 below.

Table 1. Amino Acid Residues and Examples of Conservative Amino Acid Substitutions

Original residue **Three letter code, single letter code**	**Conservative substitution**
Alanine, Ala, A	Gly, Ser
Arginine, Arg, R	Lys, His
Asparagine, Asn, N	Gln, His
Aspartic acid Asp, D	Glu, Asn
Cysteine, Cys, C	Ser, Ala
Glutamine, Gln, Q	Asn
Glutamic acid, Glu, E	Asp, Gln
Glycine, Gly, G	Ala
Histidein, His, H	Asn, Gln
Isoleucine, Ile, I	Leu, Val
Leucine, Leu, L	Ile, Val
Lysine, lys, K	Ar, His

Methionine, Met, M	Leu, Ile, Tyr
Phenylalanine, Phe, F	Tyr, Met, Leu
Proline, Pro, P	Ala
Serine, Ser, S	Thr
Threonine, Thr, T	Ser
Tryptophan, Trp, W	Tyr, Phe
Tyrosine, Tyr, Y	Try, Phe
Valine, Val, V	Ile, Leu

Antibodies described herein may comprise suitable Fc regions. In one embodiment, the antibody or antigen-binding portion thereof comprises an Fc region, for example a canine Fc region, for example a canine IgGB Fc region. In one embodiment, the Fc portion of the antibody may be modified. For example, modifications may be made to the Fc region to improve certain properties, e.g. to provide reduced complement- and FcγR- mediated effector functions.

Exemplary modified Fc regions for canine antibodies of the invention based on a canine IgG-B Fc region are provided in SEQ ID Nos 722 to 730 which show the IgG-B constant region, including the Fc region. These sequences comprise modifications compared to wild type Fc IgG-B regions. The modified Fc regions reduce or abolish canine IgG-B effector function when compared to the same polypeptide comprising a wild-type IgG-B Fc domain. This is shown in the examples. The amino acid substitutions reside in the lower hinge, proline sandwich region and SHED region. Thus, an antibody of the invention may include a modified Fc region having the modifications as shown in SEQ ID Nos 722 to 730. Modifications are with reference to the wt sequence as shown in SEQ ID NO. 721.

Thus, with reference to the wild type residue in canine IgG-B constant region (SEQ ID NO: 721), the antibodies may have the following amino acid substitutions at the following positions in the Fc domain:

E119G;

M120S or A;

L121A;

D153G;

P154R;

D156N;

N211H;

K212I;

A213G;

P215G and/or

P217S.

In one embodiment, the Fc region comprises

a) an amino acid substitution at position 120 of SEQ ID NO: 721 to S and

b) an amino acid substitution at position 211 of SEQ ID NO: 721 to H, an amino acid substitution at position 212 of SEQ ID NO: 721 to I and an amino acid substitution at position 213 of SEQ ID NO: 721 to G.

In one embodiment, the Fc region comprises

a) an amino acid substitution at position 120 of SEQ ID NO: 721 to S;

b) an amino acid substitution at position 153 of SEQ ID NO: 721 to G and an amino acid substitution at position 154 of SEQ ID NO: 721 to R and

c) an amino acid substitution at position 211 of SEQ ID NO: 721 to H, an amino acid substitution at position 212 of SEQ ID NO: 721 to I and an amino acid substitution at position 213 of SEQ ID NO: 721to G.

In one embodiment, the Fc region comprises

a) an amino acid substitution at position 120 of SEQ ID NO: 721 to S;

b) an amino acid substitution at position 153 of SEQ ID NO: 721 to G and an amino acid substitution at position 154 of SEQ ID NO: 721 to R and

c) an amino acid substitution at position 211 of SEQ ID NO: 721 to H, an amino acid substitution at position 212 of SEQ ID NO: 721 to I and an amino acid substitution at position 213 of SEQ ID NO: 721to G and an amino acid substitution at position 217 of SEQ ID NO: 721 to S.

In one embodiment, the Fc region comprises

a) an amino acid substitution at position 120 of SEQ ID NO: 721 to S;

b) an amino acid substitution at position 153 of SEQ ID NO: 721 to G and an amino acid substitution at position 154 of SEQ ID NO: 721 to R and

c) an amino acid substitution at position 211 of SEQ ID NO: 721 to H, an amino acid substitution at position 212 of SEQ ID NO: 721 to I and an amino acid substitution at position 213 of SEQ ID NO: 141 to G and an amino acid substitution at position 215 of SEQ ID NO: 721 to G.

In one embodiment, the Fc region comprises an amino acid substitution at position 120 of SEQ ID NO: 721 to A and at position 121 to A.

In one embodiment, the Fc region comprises

a) an amino acid substitution at position 120 of SEQ ID NO: 721 to A and at position 121 to A and

b) an amino acid substitution at position 217 of SEQ ID NO: 721 to S.

In one embodiment, the Fc region comprises

a) an amino acid substitution at position 120 of SEQ ID NO: 721 to A and at position 121 to A and

b) an amino acid substitution at position 215 of SEQ ID NO: 721 to G.

In one embodiment, the Fc region comprises

a) an amino acid substitution at position 119 of SEQ ID NO: 721 to G and

b) an amino acid substitution at position 156 of SEQ ID NO: 721 to N.

In one embodiment, the Fc region comprises

a) an amino acid substitution at position 120 of SEQ ID NO: 721 to A and at position 121 to A;

b) an amino acid substitution at position 156 of SEQ ID NO: 721 to N and

c) an amino acid substitution at position 217 of SEQ ID NO: 721 to S.

In another aspect, there are provided binding molecules, e.g. antibodies, antibody fragments or antibody mimetics that bind at or near the same epitope or an overlapping epitope on the companion animal OX40L or OX40 respectively (e.g. dog OX40 or OX40L) as any of the OX40L / OX40 antibodies of the invention (i.e., antibodies that have the ability to cross-compete for binding to OX40L / OX40 with an antibody of the invention). The antibodies of the invention can thus be used as a reference antibody.

Such cross-competing antibodies can be identified based on their ability to cross-compete with an antibody described herein in standard OX40L / OX40 binding assays. For example, SPR analysis such

as BIAcore® analysis, BLI analysis such as FortBio Octet®, ELISA assays or flow cytometry may be used to demonstrate cross-competition with the antibodies.

In one embodiment, there is provided a binding agent capable of binding companion animal OX40L or OX40 respectively (e.g. dog OX40 or OX40L) wherein an antibody of the invention displaces the binding agent in a competitive assay.

Included within the scope of this invention are antibody derivatives. A "derivative" of an antibody contains additional chemical moieties not normally a part of the protein. Covalent modifications of the protein are included within the scope of this invention. Such modifications may be introduced into the molecule by reacting targeted amino acid residues of the antibody with an organic derivatizing agent that is capable of reacting with selected side chains or terminal residues. For example, derivatization with bifunctional agents, well-known in the art, is useful for cross-linking the antibody or fragment to a water-insoluble support matrix or to other macromolecular carriers.

The antibody or fragment thereof as described herein can be used as a building block in a multispecific, for example bispecific or trispecific, binding agent that provides dual targeting of a companion animal OX40L or OX40 respectively (e.g. dog OX40 or OX40L) expressing cell. Thus, the antibody or fragment thereof as described herein is linked to another therapeutic entity that targets a different antigen. This other therapeutic entity is for example selected from an antibody or antibody fragment (e.g., a Fab, F(ab')2, Fv, a single chain Fv fragment (scFv) or single domain antibody, for example a VH or VHH domain), CDR region or antibody mimetic protein. Suitable non-immunogenic linker peptides are known in the art, for example, linkers that include G and/or S residues, (G4S)n, (SG4)n or G4(SG4)n peptide linkers, wherein "n" is generally a number between 1 and 10.

In another embodiment, the antibody or fragment thereof according to the invention is linked to a further moiety that may serve to prolong the half-life of the molecule. The further moiety may comprise a protein, for example an antibody, or part thereof that binds a serum albumin, e.g., dog or cat serum albumin. Other modifications that prolong half-life are also known and include, for example, modification by PEG or by incorporation in a liposome.

In one embodiment, the antibody or fragment thereof according to the invention is labelled with a detectable or functional label. A label can be any molecule that produces or can be induced to produce a signal, including but not limited to fluorophores, fluorescers, radiolabels, enzymes, chemiluminescers, a nuclear magnetic resonance active label or photosensitizers. Thus, the binding may be detected and/or measured by detecting fluorescence or luminescence, radioactivity, enzyme activity or light absorbance.

In still other embodiments, the antibody or fragment thereof according to the invention is coupled to a toxin. In one embodiment, the therapeutic moiety is a toxin, for example a cytotoxic radionuclide, chemical toxin or protein toxin.

The term "half-life" as used herein refers to the time taken for the serum concentration of the amino acid sequence, compound or polypeptide to be reduced by 50%, in vivo, for example due to degradation of the sequence or compound and/or clearance or sequestration of the sequence or compound by natural mechanisms. Half-life may be increased by at least 1.5 times, preferably at least 2 times, such as at least 5 times, for example at least 10 times or more than 20 times, greater than the half-life of the corresponding antibodies of the invention. For example, increased half-life may be more than 1 hours, preferably more than 2 hours, more preferably more than 6 hours, such as more than 12 hours, or even more than 24, 48 or 72 hours, compared to the corresponding antibodies of the invention. The in vivo half-life of an amino acid sequence, compound or polypeptide of the invention can be determined in any manner known per se, such as by pharmacokinetic analysis. Suitable techniques will be clear to the person skilled in the art. Half-life can for example be expressed using parameters such as the t1/2-alpha t1/2-beta and the area under the curve (AUC).

The antibodies and fragments of the invention may also be used in cell therapy, for example chimeric antigen receptor T-cell (CAR-T) therapy.

Nucleic acids

In another aspect, the invention relates to a nucleic acid sequence encoding an amino acid sequence of an antibody or antibody fragment as described herein.

In one embodiment, the nucleic acid encodes a HC variable region which comprises or consists of a sequence selected from SEQ ID No. 11, SEQ ID No. 21, SEQ ID No. 31, SEQ ID No. 41, SEQ ID No. 51, SEQ ID No. 61, SEQ ID No. 71, SEQ ID No. 81, SEQ ID No. 91, SEQ ID No. 101, SEQ ID No. 111, SEQ ID No. 121, SEQ ID No. 131, SEQ ID No.141, SEQ ID No. 151, SEQ ID No.161, SEQ ID No.171, SEQ ID No.181, SEQ ID No.191, SEQ ID No. 201, SEQ ID No. 211, SEQ ID No. 221, SEQ ID No. 231, SEQ ID No. 241, SEQ ID No. 251, SEQ ID No. 261, SEQ ID No. 271, SEQ ID No. 281, SEQ ID No. 291, SEQ ID No.301, SEQ ID No. 311, SEQ ID No. 321, SEQ ID No. 331, SEQ ID No. 341, SEQ ID No. 351, SEQ ID No. 361, SEQ ID No. 371, SEQ ID No. 381, SEQ ID No.391, SEQ ID No.401, SEQ ID No. 411, SEQ ID No.421, SEQ ID No. 431, SEQ ID No. 441, SEQ ID No. 451, SEQ ID No. 461, SEQ ID No. 471, SEQ ID No. 481, SEQ ID No. 491, SEQ ID No. 501, SEQ ID No. 511, SEQ ID No. 521, SEQ ID No. 531, SEQ ID No. 541, SEQ ID No. 551, SEQ ID No. 561, SEQ ID No. 571, SEQ ID No. 581, SEQ ID No. 591, SEQ ID No. 601, SEQ ID No. 611, SEQ ID No. 621, SEQ ID No. 631, SEQ ID No. 641, SEQ ID No. 651, SEQ ID No. 661, SEQ ID No. 671, SEQ ID No. 681, SEQ ID No. 691, SEQ ID No.701, SEQ ID No. 711, SEQ ID No. 737, SEQ ID No. 747, SEQ ID No. 757, SEQ ID No. 767. SEQ ID No. 777. SEQ ID No. 787. SEQ ID No. 797.

In one embodiment, the nucleic acid encodes a LC variable region which comprises or consists of a sequence selected from SEQ ID No. 13, SEQ ID No. 23, SEQ ID No. 33, SEQ ID No. 43, SEQ ID No. 53, SEQ ID No. 63, SEQ ID No. 73, SEQ ID No. 83, SEQ ID No. 93, SEQ ID No. 103, SEQ ID No. 113, SEQ ID No. 123, SEQ ID No. 133, SEQ ID No. 143, SEQ ID No.153, SEQ ID No. 163, SEQ ID No.173,

SEQ ID No.183, SEQ ID No.193, SEQ ID No. 203, SEQ ID No. 213, SEQ ID No. 223, SEQ ID No. 233, SEQ ID No. 243, SEQ ID No. 253, SEQ ID No. 263, SEQ ID No. 273, SEQ ID No. 283, SEQ ID No. 293, SEQ ID No.303, SEQ ID No. 313, SEQ ID No. 323, SEQ ID No. 343, SEQ ID No. 353, SEQ ID No. 363, SEQ ID No. 373, SEQ ID No. 383, SEQ ID No. 393, SEQ ID No. 403, SEQ ID No. 413, SEQ ID No. 423, SEQ ID No. 433, SEQ ID No. 443, SEQ ID No. 453, SEQ ID No. 463, SEQ ID No. 473, SEQ ID No. 483, SEQ ID No. 493, SEQ ID No.503, SEQ ID No. 513, SEQ ID No. 523, SEQ ID No. 533, SEQ ID No. 543, SEQ ID No. 553, SEQ ID No. 563, SEQ ID No. 573, SEQ ID No. 583, SEQ ID No. 593, SEQ ID No. 603, SEQ ID No. 613, SEQ ID No. 623, SEQ ID No. 633, SEQ ID No. 643, SEQ ID No. 653, SEQ ID No. 663, SEQ ID No.673, SEQ ID No. 683, SEQ ID No. 693, SEQ ID No. 703, SEQ ID No. 713, SEQ ID No. 739, SEQ ID No. 749, SEQ ID No. 759, SEQ ID No. 769, SEQ ID No. 779, SEQ ID No. 789 or SEQ ID No. 799.

Exemplary methods for making the antibody

An antibody or fragment described herein can be obtained from a mammal, for example a rodent, for example a transgenic animal, that expresses antibodies upon stimulation with an OX40L or OX40 antigen of the target companion animal, e.g. dog or cat OX40L or OX40. Suitably companion animal antibody genes have been introduced such that companion animal antibodies are generated. The transgenic rodent, for example a mouse, preferably has a reduced capacity to express endogenous antibody genes. Thus, in one embodiment, the rodent has a reduced capacity to express endogenous light and/or heavy chain antibody genes. The rodent, for example a mouse, may therefore comprise modifications to disrupt expression of endogenous kappa and lambda light and/or heavy chain antibody genes so that no functional mouse light and/or heavy chains are produced, for example as further explained below. Such transgenic rodents are described in the art and this is further explained in the examples below.

Other methods may involve speciation of a mouse monoclonal typically following the steps of immunising a mouse with an OX40L or OX40 antigen of the target companion animal, isolating B cells and fusing them to a fusion partner cell line, isolating mouse monoclonal antibodies by selection. Speciation is then carried out by chimerization and/or further informatic-guided speciation. Strategies for speciation, such as strategies for caninization or felinization, are described, for example, in WO2013/011407, see Example 5.

In other methods, a set, collection or library of amino acid sequences may be displayed on a phage, phagemid, ribosome or suitable micro-organism (such as yeast), such as to facilitate screening. Suitable methods, techniques and host organisms for displaying and screening (a set, collection or library of) amino acid sequences will be clear to the person skilled in the art (see for example Phage Display of Peptides and Proteins: A Laboratory Manual, Academic Press; 1st edition (October 28, 1996) Brian K. Kay, Jill Winter, John McCafferty).

It is also possible to generate libraries, for example phage libraries, by isolating a cell or tissue expressing an antigen-specific, heavy chain-only antibody, cloning the sequence encoding the V_H domain(s) from mRNA derived from the isolated cell or tissue and displaying the encoded protein using a library. The antibody or fragment can be expressed in bacterial, yeast or other expression systems.

Exemplary therapeutic applications

In one aspect, we provide an antibody or fragment as described herein for use in the treatment of disease.

In another aspect, there is provided a pharmaceutical composition comprising an antibody or fragment as described herein and optionally a pharmaceutically acceptable carrier. The term pharmaceutical composition as used herein refers to a composition that is used to treat a companion animal, that is for veterinary use, i.e. a veterinary composition. In preferred embodiments the animal that is treated is a dog or a cat.

An antibody or fragment thereof as described herein or the pharmaceutical composition of the invention can be administered by any convenient route, including but not limited to oral, topical, parenteral, sublingual, rectal, vaginal, ocular, intranasal, pulmonary, intradermal, intravitreal, intramuscular, intraperitoneal, intravenous, subcutaneous, intracerebral, transdermal, transmucosal, by inhalation, or topical, particularly to the ears, nose, eyes, or skin or by inhalation.

In one embodiment, administration is subcutaneous. The concentration of the antibody or antibody fragment may be 10 to 50 mg/ml, e.g. 10, 20, 30, 40 or 50mg/ml. In one embodiment, the concentration is 25 to 35mg/ml, for example about 30mg/ml. In one embodiment, the antibody is provided as a dose in 1ml of solution.

Parenteral administration includes, for example, intravenous, intramuscular, intraarterial, intraperitoneal, intranasal, rectal, intravesical, intradermal, topical or subcutaneous administration. Preferably, the compositions are administered parenterally.

The pharmaceutically acceptable carrier or vehicle can be particulate, so that the compositions are, for example, in tablet or powder form. The term "carrier" refers to a diluent, adjuvant or excipient, with which a drug antibody conjugate of the present invention is administered. Such pharmaceutical carriers can be liquids, such as water and oils, including those of petroleum, animal, vegetable or synthetic origin, such as peanut oil, soybean oil, mineral oil, sesame oil and the like. The carriers can be saline, gum acacia, gelatin, starch paste, talc, keratin, colloidal silica, urea, and the like. In addition, auxiliary, stabilizing, thickening, lubricating and coloring agents can be used. In one embodiment, when administered to an animal, the antibody or fragment thereof of the present invention or compositions and pharmaceutically acceptable carriers are sterile. Water is a preferred carrier when the drug antibody conjugates of the present invention are administered intravenously. Saline solutions and aqueous

dextrose and glycerol solutions can also be employed as liquid carriers, particularly for injectable solutions. Suitable pharmaceutical carriers also include excipients such as starch, glucose, lactose, sucrose, gelatin, malt, rice, flour, chalk, silica gel, sodium stearate, glycerol monostearate, talc, sodium chloride, dried skim milk, glycerol, propylene, glycol, water, ethanol and the like. The present compositions, if desired, can also contain minor amounts of wetting or emulsifying agents, or pH buffering agents.

The pharmaceutical composition of the invention can be in the form of a liquid, *e.g.*, a solution, emulsion or suspension. The liquid can be useful for delivery by injection, infusion (*e.g.*, IV infusion) or subcutaneously.

When intended for oral administration, the composition is preferably in solid or liquid form, where semi-solid, semi-liquid, suspension and gel forms are included within the forms considered herein as either solid or liquid.

As a solid composition for oral administration, the composition can be formulated into a powder, granule, compressed tablet, pill, capsule, chewing gum, wafer or the like form. Such a solid composition typically contains one or more inert diluents. In addition, one or more of the following can be present: binders such as carboxymethylcellulose, ethyl cellulose, microcrystalline cellulose, or gelatin; excipients such as starch, lactose or dextrins, disintegrating agents such as alginic acid, sodium alginate, corn starch and the like; lubricants such as magnesium stearate; glidants such as colloidal silicon dioxide; sweetening agents such as sucrose or saccharin; a flavoring agent such as peppermint, methyl salicylate or orange flavoring; and a coloring agent. When the composition is in the form of a capsule (e. g. a gelatin capsule), it can contain, in addition to materials of the above type, a liquid carrier such as polyethylene glycol, cyclodextrin or a fatty oil.

The composition can be in the form of a liquid, e. g. an elixir, syrup, solution, emulsion or suspension. The liquid can be useful for oral administration or for delivery by injection. When intended for oral administration, a composition can comprise one or more of a sweetening agent, preservatives, dye/colorant and flavor enhancer. In a composition for administration by injection, one or more of a surfactant, preservative, wetting agent, dispersing agent, suspending agent, buffer, stabilizer and isotonic agent can also be included.

Compositions can take the form of one or more dosage units.

In specific embodiments, it can be desirable to administer the composition locally to the area in need of treatment, or by injection, intravenous injection or infusion.

The amount of the therapeutic that is effective/active in the treatment of a particular disorder or condition will depend on the nature of the disorder or condition and the animal to be treated and can be determined by standard clinical techniques. In addition, *in vitro* or *in vivo* assays can optionally be employed to help

identify optimal dosage ranges. The precise dose to be employed in the compositions will also depend on the route of administration, and the seriousness of the disease or disorder, and should be decided according to the judgment of the practitioner and each subject's circumstances. Factors like age, body weight, sex, diet, time of administration, rate of excretion, condition of the host, drug combinations, reaction sensitivities and severity of the disease shall be taken into account.

Typically, the amount is at least about 0.01% of an antibody of the present invention by weight of the composition. When intended for oral administration, this amount can be varied to range from about 0.1 % to about 80% by weight of the composition. Preferred oral compositions can comprise from about 4% to about 50% of the antibody of the present invention by weight of the composition.

Preferred compositions of the present invention are prepared so that a parenteral dosage unit contains from about 0.01 % to about 2% by weight of the antibody of the present invention.

For administration by injection, the composition can comprise from about typically about 0.1 mg/kg to about 250 mg/kg of the subject’s body weight, preferably, between about 0.1 mg/kg and about 20 mg/kg of the animal's body weight, and more preferably about 1 mg/kg to about 10 mg/kg of the animal's body weight. In one embodiment, the composition is administered at a dose of about 1 to 30 mg/kg, e.g., about 5 to 25 mg/kg, about 10 to 20 mg/kg, about 1 to 5 mg/kg, or about 3 mg/kg. The dosing schedule can vary from e.g., once a week to once every 2, 3, 4, 5, 6, 7, 8 or more weeks.

In one embodiment, post-treatment, the subject has at least 7 days, or at least 14 days, or at least 21 days, or at least 28 days, or at least 40 days, or at least 50 days, or at least 60 days disease progression-free.

In one embodiment, the number of days of survival, the number of disease-free days, or the number of disease-progression free days is at least 2 months, or at least 3 months, or at least 4 months, e.g. at least 5 months, such as at least 6 months.

In one embodiment, the number of days of survival, the number of disease-free days, or the number of disease-progression free days is at least 9 months, or at least one year. The invention provides methods of treating or preventing OX40L/OX40-mediated diseases or disorders in a companion animal, e.g., a dog, cat or horse, comprising administering an effective amount of an antibody or fragment of the present invention to the animal in need thereof.

As used herein, "treat", "treating" or "treatment" means inhibiting or relieving a disease or disorder. For example, treatment can include a postponement of development of the symptoms associated with a disease or disorder, and/or a reduction in the severity of such symptoms that will, or are expected, to develop with said disease. The terms include ameliorating existing symptoms, preventing additional symptoms, and ameliorating or preventing the underlying causes of such symptoms. Thus, the terms denote that a beneficial result is being conferred on at least some of the mammals, e.g., companion

animal patients, being treated. Many medical treatments are effective for some, but not all, patients that undergo the treatment.

Suitably, for treating a condition such as atopic dermatitis, post-treatment, a reduction in pruritus score is observed. Suitable methods for measuring pruritus score will be known to those skilled in the art.

In one embodiment, an antagonistic antibody in accordance with the invention, or fragment thereof, suppresses a GVHD reaction in a xenogenic graft versus host reaction such as described in WO2013/0008171. In an embodiment the antibody in accordance with the invention or a fragment thereof shows activity in an antigen recall study similar to what set out in Saghari M. et al, Clin Pharmacol Ther. 2022 Jan 29. doi: 10.1002/cpt.2539 or a house dust mites canine model as set out in Marsella R. et al, Vet. Dermatol 2006 Feb;17(1):24-35. doi: 10.1111/j.1365-3164.2005.00496.x.

The term "subject" or "patient" refers to a companion animal which is the object of treatment, observation, or experiment. By way of example only, a subject includes, but is not limited to, a dog, cat or horse. For the avoidance of doubt, the treatment of humans is excluded.

In one embodiment, a “patient” is one which is non-responsive to Cytopoint or Apoquel.

As used herein, the term "effective amount" means an amount of an anti-OX40L/OX40 antibody, that when administered alone or in combination with an additional therapeutic agent to a cell, tissue, or subject, is effective to achieve the desired therapeutic or prophylactic effect under the conditions of administration

In another aspect, the invention relates to the use of an antibody or fragment as described herein, or pharmaceutical composition of the invention in the manufacture of a medicament for the treatment or prevention of a disease as defined herein.

As mentioned above, the antibody or fragment according to the invention is useful in the treatment or prevention of an OX40L/OX40 mediated disease.

The term OX40L/OX40 mediated disease refers to any disease or disorder that is mediated by the OX40L/OX40 signalling pathway and which can be treated/alleviated by targeting the OX40L/OX40 antigen. An OX40L-mediated disease and OX40-mediated disease refer to any disease or condition that is completely or partially caused by or is the result of OX40L or OX40 respectively. In certain embodiments, OX40L or OX40 is aberrantly (e.g., highly) expressed on the surface of a cell. In some embodiments, OX40L or OX40 may be aberrantly upregulated on a particular cell type. In other embodiments, normal, aberrant or excessive cell signalling is caused by binding of OX40 to OX40L.

Evidence in humans suggests that disruption of the OX40/OX40L axis reduces T cell activation, proliferation and memory T cell establishment, and as such an anti-OX40L/OX40 antibody could be

used to prevent, treat or ameliorate the symptoms of a number of diseases, including atopic dermatitis, type 1 diabetes, Chron's disease, ulcerative colitis and other autoimmune diseases.

In one embodiment the anti-OX40L/OX40 antibody is used to prevent treat or ameliorate symptoms of a disease. In one embodiment, the disease such is selected from allergy, asthma, and diseases associated with autoimmunity and inflammation, which includes multiple sclerosis, rheumatoid arthritis, inflammatory bowel disease, graft-versus-host disease, experimental autoimmune encephalomyelitis (EAE), experimental leishmaniasis, collagen-induced arthritis, colitis (such as ulcerative colitis), contact hypersensitivity reactions, type 1 diabetes, Crohn's Disease, and Grave's Disease. In one embodiment the disease is an inflammatory condition which refers to pathological states resulting in inflammation or an autoimmune disease. In particular, the disease is selected from the following non-limiting list: inflammatory skin diseases, including atopic dermatitis (atopy), allergic dermatitis, pruritus, psoriasis, scleroderma, or eczema; responses associated with inflammatory bowel disease (such as Crohn's disease and ulcerative colitis); type 1 diabetes; ischemic reperfusion; adult respiratory distress syndrome; asthma; meningitis; encephalitis; uveitis; autoimmune diseases such as rheumatoid arthritis, Sjorgen's syndrome, vasculitis; diseases involving leukocyte diapedesis; central nervous system (CNS) inflammatory disorder, multiple organ injury syndrome secondary to septicaemia or trauma;, bacterial pneumonia, antigen-antibody complex mediated diseases; inflammations of the lung, including pleurisy, alveolitis, vasculitis, pneumonia, chronic bronchitis, bronchiectasis, and cystic fibrosis; etc. Other diseases include equine indications such as sweet itch, summer recurrent dermatitis or equine insect bite hypersensitivity.

Exemplary combinations with other agents

The antibodies, antibody fragments or pharmaceutical composition of the invention may be administered as the sole active ingredient or in combination with one or more other therapeutic agent. A therapeutic agent is a compound or molecule which is useful in the treatment of a disease.

Examples of therapeutic agents include antibodies, antibody fragments, drugs, toxins, nucleases, hormones, an anti-inflammatory agent, immunomodulators, pro-apoptotic agents, anti-angiogenic agents, boron compounds, photoactive agents or dyes and radioisotopes. An antibody molecule includes a full antibody or fragment thereof (e.g., a Fab, F(ab')2, Fv, a single chain Fv fragment (scFv) or a single domain antibody, for example a V_H domain, or antibody mimetic protein.

In one embodiment, the antibody or antibody fragment or the pharmaceutical composition described herein is used in combination with an existing therapy or therapeutic agent. Thus, in another aspect, the invention also relates to a combination therapy comprising administration of the antibody or antibody fragment or the pharmaceutical composition described herein and another therapy.

In one embodiment, the therapeutic agent is selected from the following non-limiting list: rapamycin (sirolimus), tacrolimus, cyclosporin, corticosteroids (e.g. methylprednisolone), methotrexate,

mycophenolate mofetil, anti-CD28 antibodies, anti-IL12/IL-23 antibodies, anti-CD20 antibodies, anti-CD30 antibodies, CTLA4-Fc molecules, CCR5 receptor antagonists, anti-CD40L antibodies, anti-VI_A4 antibodies, anti-LFA1 antibodies, fludarabine, anti-CD52 antibodies, anti-CD45 antibodies, cyclophosphamide, anti-thymocyte globulins, anti-complement C5 antibodies, anti-a4b7 integrin antibodies, anti-IL6 antibodies, anti-IL6-R antibodies, anti-IL2R antibodies, anti-CD25 antibodies, anti-TNFa / TNFa-Fc molecules , HDAC inhibitors, JAK inhibitors, such as JAK-1 and JAK-3 inhibitors, anti-IL-31 antibodies, SYK inhibitors, anti-IL-4Ra antibodies, anti-IL-13 antibodies, anti-TSLP antibodies, and PDE4 inhibitors lokietmab (Cytopoint®), cyclosporin (Atopica®) and oclacitinib (Apoquel®).In some embodiments, the antibody or antibody fragment or the pharmaceutical composition described herein may be administered with two or more therapeutic agents.

The antibody or antibody fragment or the pharmaceutical composition described herein may be administered at the same time or at a different time as the other therapy or therapeutic compound or therapy, e.g., simultaneously, separately or sequentially.

Exemplary kits

In another aspect, the invention provides a kit for the treatment or prevention of a disease for example as listed herein and/or for detecting OX40L/OX40 for diagnosis, prognosis or monitoring disease comprising an antibody or fragment of the invention. Such a kit may contain other components, packaging, instructions, or material to aid in the detection of OX40L/OX40 protein. The kit may include a labelled antibody that binds to OX40L/OX40 or a binding molecule comprising an antibody that binds to OX40L/OX40 and one or more compounds for detecting the label.

The invention in another aspect provides an antibody or fragment thereof that binds to OX40L/OX40, or pharmaceutical composition described herein packaged in lyophilized form, or packaged in an aqueous medium.

Exemplary non therapeutic applications

In another aspect, an antibody or fragment that binds to OX40L/OX40 as described herein is used for non-therapeutic purposes, such as diagnostic tests and assays. A method for detecting the presence of a companion animal OX40L/OX40 in a test sample comprises contacting said sample with an antibody or fragment thereof as described herein and at least one detectable label and detecting binding of said antibody to a companion animal OX40L/OX40.

Modifications of antibodies for diagnostic purposes are well known in the art. For example, antibodies may be modified with a ligand group such as biotin, or a detectable marker group such as a fluorescent group, a radioisotope, or an enzyme. Compounds of the invention can be used for diagnostic purposes and e.g. labelled using conventional techniques. Suitable detectable labels include but are not limited

to fluorophores, chromophores, radioactive atoms, electron-dense reagents, enzymes, and ligands having specific binding partners.

In some embodiments, the binding of antigen to antibody is detected without the use of a solid support. For example, the binding of antigen to antibody can be detected in a liquid format.

In other embodiments, an antibody or fragment can, for example, be fixed to nitrocellulose, or another solid support which is capable of immobilizing cells, cell particles or soluble proteins. The support can then be washed with suitable buffers followed by treatment with the detectably labelled antibody. The solid phase support can then be washed with the buffer a second time to remove unbound peptide or antibody. The amount of bound label on the solid support can then be detected by known method steps. "Solid phase support" or "carrier" refers to any support capable of binding peptide, antigen, or antibody. Well-known supports or carriers, include glass, polystyrene, polypropylene, polyethylene, polyvinylidenefluoride (PVDF), dextran, nylon, amylases, natural and modified celluloses, polyacrylamides, agaroses, and magnetite. The nature of the carrier can be either soluble to some extent or insoluble for the purposes of the present invention. The support material can have virtually any possible structural configuration so long as the coupled molecule is capable of binding to OX40L/OX40 or an anti- OX40L/OX40 antibody. Thus, the support configuration can be spherical, as in a bead, or cylindrical, as in the inside surface of a test tube, or the external surface of a rod. Alternatively, the surface can be flat, such as a sheet, culture dish, test strip, etc. For example, supports may include polystyrene beads. Those skilled in the art will know many other suitable carriers for binding antibody, peptide or antigen, or can ascertain the same by routine experimentation. Well known method steps can determine binding activity of a given lot of anti- OX40L/OX40 antibody. Those skilled in the art can determine operative and optimal assay conditions by routine experimentation.

For the purposes of the present invention, the OX40L/OX40 which is detected by the above assays can be present in a biological test sample. Any sample containing OX40L/OX40 may be used. For example, the sample is a biological fluid such as, for example, blood, serum, lymph, urine, feces, inflammatory exudate, cerebrospinal fluid, amniotic fluid, a tissue extract or homogenate, and the like.

Nucleic acid construct and hosts cells

Furthermore, the invention relates to a nucleic acid construct comprising at least one nucleic acid as defined herein, i.e. nucleic acid molecules encoding antibodies of the invention or nucleic acid molecules encoding an OX40 protein. The construct may be in the form of a plasmid, vector, transcription or expression cassette.

An expression vector can be, for example, a plasmid, such as pBR322, pUC, or Co1E1, or an adenovirus vector, such as an adenovirus Type 2 vector or Type 5 vector. Vectors suitable for use in the present invention include, for example, bacterial vectors, mammalian vectors, viral vectors (such as retroviral, adenoviral, adeno-associated viral, herpes virus, simian virus 40 (SV40), and bovine papilloma virus

vectors) and baculovirus-derived vectors for use in insect cells. Polynucleotides in such vectors are preferably operably linked to a promoter, which is selected based on, e.g., the cell type in which expression is sought.

The expression vector can be transferred to a host cell by conventional techniques and the transfected cells are then cultured by conventional techniques to produce an antibody of the invention. The invention includes host cells containing polynucleotides encoding an antibody of the invention (e.g., whole antibody, a heavy or light chain thereof, or portion thereof, or a single chain antibody of the invention, or a fragment or variant thereof), operably linked to a heterologous promoter. For the expression of entire antibody molecules, vectors encoding both the heavy and light chains may be co-expressed in the host cell for expression of the entire immunoglobulin molecule. In one embodiment, the expression vector is one which enables heterologous expression e.g. expression in a host organism from different species.

The invention also relates to an isolated recombinant host cell comprising one or more nucleic acid construct as described herein, i.e. nucleic acid molecules encoding antibodies of the invention or nucleic acid molecules encoding an OX40 protein. Host cells useful in the present invention are prokaryotic, yeast, or higher eukaryotic cells and include but are not limited to microorganisms such as bacteria (e.g., E. coli, B. subtilis) transformed with recombinant bacteriophage DNA, plasmid DNA or cosmid DNA expression vectors containing antibody coding sequences; yeast (e.g., Saccharomyces, Pichia) transformed with recombinant yeast expression vectors containing antibody coding sequences; insect cell systems infected with recombinant virus expression vectors (e.g. Baculovirus) containing antibody coding sequences; plant cell systems infected with recombinant virus expression vectors (e.g., cauliflower mosaic virus, CaMV; tobacco mosaic virus, TMV) or transformed with recombinant plasmid expression vectors (e.g., Ti plasmid) containing antibody coding sequences; or mammalian cell systems (e.g., COS, CHO, BHK, 293, 3T3 cells) harboring recombinant expression constructs containing promoters derived from the genome of mammalian cells (e.g., metallothionein promoter) or from mammalian viruses (e.g., the adenovirus late promoter; the vaccinia virus 7.5K promoter).

Prokaryotes useful as host cells in the present invention include gram negative or gram-positive organisms such as E. coli, B. subtilis, Enterobacter, Erwinia, Klebsiella, Proteus, Salmonella, Serratia, and Shigella, as well as Bacilli, Pseudomonas, and Streptomyces. One preferred E. coli cloning host is E. coli 294 (ATCC 31,446), although other strains such as E. coli B, E. coli X1776 (ATCC 31,537), and E. coli W3110 (ATCC 27,325) are suitable. These examples are illustrative rather than limiting. In one embodiment, a method of making an anti- OX40 antibody as described herein is provided, wherein the method comprises culturing the host cell under conditions suitable for expression of the polynucleotide encoding the antibody and isolating the antibody.

In some embodiments, the nucleic acid may also comprise a leader sequence. Any suitable leader sequences may be used, including the native immunoglobulin germline leader sequence, or others,

such as the Campath leader sequence (see US 8,362,208B2), may be chosen to enhance protein expression.

Assays and expression systems

The invention also relates to a heterologous assay or expression system comprising a companion animal (e.g. dog) OX40 and a cell line derived from a different species, e.g. a human cell line such as HEK.

The assay comprises contacting a companion animal (e.g. dog) OX40 with a cell line derived from a different species, e.g. a cell line from a different mammal, e.g. a rodent cell line or a human cell line such as HEK. For example, the cell line is transfected with companion animal (e.g. dog) OX40 such that it expresses companion animal (e.g. dog) OX40 in a stable or transient manner.

The cell line may comprise a reporter gene and activation of OX40 by OX40L can be assessed using the reporter gene, e.g. by quantification of reporter gene expression. Suitable reporter genes are known to the skilled person and may include fluorescent markers or alkaline phosphatase (SEAP).

It will be understood that particular embodiments described herein are shown by way of illustration and not as limitations of the invention. The principal features of this invention can be employed in various embodiments without departing from the scope of the invention. Those skilled in the art will recognize, or be able to ascertain using no more than routine study, numerous equivalents to the specific procedures described herein. Such equivalents are considered to be within the scope of this invention and are covered by the claims. All publications and patent applications mentioned in the specification are indicative of the level of skill of those skilled in the art to which this invention pertains. All publications and patent applications are herein incorporated by reference to the same extent as if each individual publication or patent application was specifically and individually indicated to be incorporated by reference. The use of the word "a" or "an" when used in conjunction with the term "comprising" in the claims and/or the specification may mean "one," but it is also consistent with the meaning of "one or more," "at least one," and "one or more than one." The use of the term "or" in the claims is used to mean "and/or" unless explicitly indicated to refer to alternatives only or the alternatives are mutually exclusive, although the disclosure supports a definition that refers to only alternatives and "and/or." Throughout this application, the term "about" is used to indicate that a value includes the inherent variation of error for the device, the method being employed to determine the value, or the variation that exists among the study subjects.

As used in this specification and claim(s), the words "comprising" (and any form of comprising, such as "comprise" and "comprises"), "having" (and any form of having, such as "have" and "has"), "including" (and any form of including, such as "includes" and "include") or "containing" (and any form of containing, such as "contains" and "contain") are inclusive or open-ended and do not exclude additional, unrecited elements or method steps

The term "or combinations thereof" as used herein refers to all permutations and combinations of the listed items preceding the term. For example, "A, B, C, or combinations thereof" is intended to include at least one of: A, B, C, AB, AC, BC, or ABC, and if order is important in a particular context, also BA, CA, CB, CBA, BCA, ACB, BAC, or CAB. Continuing with this example, expressly included are combinations that contain repeats of one or more item or term, such as BB, AAA, ABAB, BBC, AAABCCCC, CBBAAA, CABABB, and so forth. The skilled artisan will understand that typically there is no limit on the number of items or terms in any combination, unless otherwise apparent from the context.

Any part of this disclosure may be read in combination with any other part of the disclosure, unless otherwise apparent from the context.

All of the compositions and/or methods disclosed and claimed herein can be made and executed without undue experimentation in light of the present disclosure. While the compositions and methods of this invention have been described in terms of preferred embodiments, it will be apparent to those of skill in the art that variations may be applied to the compositions and/or methods and in the steps or in the sequence of steps of the method described herein without departing from the concept, spirit and scope of the invention. All such similar substitutes and modifications apparent to those skilled in the art are deemed to be within the spirit, scope and concept of the invention as defined by the appended claims.

The present invention is described in more detail in the following non-limiting examples.

Examples

Example 1: Cloning canine OX40L and OX40

OX40L Sequence Prediction

The nucleotide sequence and gene structure for canine OX40L was predicted based on human OX40L nucleotide sequence alignment to canine CamFam3.1 genome assembly from the UCSC Genome Browser (University of Santa Cruz). This gave 3 predicted exons (Figure 1A). Unlike many transmembrane proteins which consist of a 5' terminus followed by the extracellular domain, OX40L protein structure is reversed (see Figure 1B).

OX40 sequence prediction

The nucleotide sequence for canine OX40 was predicted based on nucleotide sequence homology alignment of human OX40 to the canine reference genome. This gave 7 predicted exons with extracellular domain at the N terminus (Figure 1A).

OX40L and OX40 Cloning

The sequence for both OX40L and OX40 were confirmed by cloning from PBMCs isolated from beagle blood using standard protocols. Beagle whole blood was supplied by Envigo RMS (Alconbury, Huntingdon, UK) and PBMCs were isolated using a Ficoll gradient. Briefly, 10 ml whole blood was diluted with 25 ml phosphate buffered saline (PBS) and layered onto 15 ml Ficoll Paque Plus (Sigma Aldrich) before centrifuging at 800rcf for 10 min at room temperature, with slow acceleration and no brake. The interphase disk, which represents the PBMC fraction was collected into PBS. The PBMCs were counted and resuspended at 10^6 cells ml^{-1} in RPMI media (Sigma Aldrich) supplemented with 1 µg ml^{-1} canine IL-2.

To stimulate OX40 and OX40L expression, 5 mg ml^{-1} Phytohaemagglutinin-L (PHA-L; Fisher Scientific) was added, and PBMC's were harvested 1 and 4 days later. Total RNA was isolated from activated PBMC's with the QIAGEN RNeasy Mini Kit (Qiagen, Hilden, DE), yielding 160 µg – 440 µg RNA following an on-column DNAse digestion. Specific cDNA amplification of OX40 and OX40L was undertaken using the SuperScript IV One-Step RT-PCR kit (ThermoFisher, Massachusetts, US) with 3' and 5' terminal primers generated from predicted OX40 and OX40L nucleotides sequences. Primer sequences are shown in Table 2 (SEQ ID NO: 7 to 10).

OX40 and OX40L RT-PCR products were subcloned into pJET using the CloneJET PCR Cloning Kit (ThermoFisher), before being transferred to pcDNA3.1 for mammalian expression.

The nucleotide and amino acid sequence for canine OX40L (sequence of cloned OX40L/Full length membrane form for cellular expression is shown in Table 2 (SEQ ID NO:1 and 2).

For OX40, the presence of potential splice variants in the RT-PCR products was observed. To isolate the individual splice variant transcripts, the RT-PCR products were subcloned and two different transcripts were identified with sequences as shown in Table 2 (nucleotide, amino acid translation), the short and the long variant (SEQ ID NO:3 to 6).

Figure 2 shows an alignment of these splice variants. The long splice variant of OX40 consists of exons arranged in the sequence 1-2-3-4-5-6-7. The short splice variant does not contain exon 6, and has the arrangement 1-2-3-4-5-7

The relative abundance of OX40 splice-variants were assessed using a single-step PCR of pJET-OX40 colonies. Briefly, single colonies were picked from LB-amp plates into 10 µl OneTaq Quick-Load PCR mix (NEB) and amplified with the following PCR cycle: 1 cycle of 94°C for 30s; 30 cycles of 94°C for 30s, 61°C for 30s, 68°C for 2min; 1 cycle of 68°C for 5 min. The abundance of the two splice variants was determined by assessing the relative lengths of the resultant PCR products (Figure 3). The short splice variant codes for a truncated product. As this product lacks the transmembrane region in its entirety, it seems most likely that the resultant short variant would be secreted.

Example 2: Generation of canine OX40 and OX40L stably expressing cells

Human embryonic kidney (HEK) 293 cells were grown on 90 mm round tissue culture plates as monolayers in DMEM / F12 (Life Technologies, California, US) supplemented with 10% fetal bovine serum (FBS; Sigma Aldrich) at 37°C in a moist atmosphere containing 5% CO_2. HEK293 cells were transfected with plasmids encoding either OX40 (SEQ. ID 5) or OX40L (SEQ. ID 2) cDNA using polyethyleneimine (PEI MAX: 40 kDa, Polysciences Inc., Eppelheim, Germany). 30 µl of PEI MAX (1 mg ml^{-1}), 5 µg cDNA and 1 ml DMEM/ F12 were incubated for 10 min at room temperature, added dropwise to a 90mm plate of 70 - 80% confluent HEK293 cells, and incubated for 2-3 days. Stably transfected cells were selected 48hrs later using a suitable antibiotic.

Mouse embryonic fibroblasts (MEF) were grown on 90 mm round tissue culture plates as monolayers in DMEM-high glucose (Life Technologies) supplemented with 10% FBS, 10% β-mercaptoethanol and 10% non-essential amino acids at 37°C in a moist atmosphere and 5% CO_2. Cells were transfected with plasmids encoding OX40L cDNA (SEQ. ID 2) using Lipofectamine LTX (ThermoFisher Scientific, Waltham, MA, USA) according to the manufacturer's recommended instructions. Stably transfected cells were selected 48hrs later using a suitable antibiotic.

Example 3: Canine OX40L Immunisation using Ky9™ transgenic platform

Ky9™ mice, substantially as described in WO2018/189520 and WO2020/074874, for example, were immunised with OX40L expression DNA construct or MEFs with OX40L stably expressed. The transgenic mice have been modified compared to wild type mice by insertion of immunoglobulin heavy (IGH) chain and light chain (IGL) variable (V) region genes, IGH D region genes and IGH and IGL J region genes from a dog into a mouse allowing the production of antibody heavy chains that comprise a variable antibody region originating from the expression of canine DNA in the mouse, in combination with a constant region. The constant region may be the rodent immunoglobulin (IG) constant region, resulting in production of chimeric heavy chains having canine variable region and a rodent constant region. Information concerning, or the nucleic acid comprising, the variable region of such chimeric antibody chains may be used to generate fully canine antibodies, for therapeutic use in dogs for example. The rodent containing the canine DNA may also serve as an animal model for understanding of disease and testing of medicines.

For DNA immunisation, a prime and boost regime using hydrodynamic tail vein injection (HTVI) was performed and tissues harvested.

For cell-based immunisation, a prime and boost regime using MEF cells stably expressing OX40L was performed and tissues harvested.

A further immunisation regime was performed using HTVI DNA immunisation for the prime combined with OX40L-expressing MEF cell boosts.

Determination of serum titres:

Mice were bled prior to immunisation and 10 days after each subsequent boost. Serum and red blood cells were separated using microvette 200 Z-gel tubes (Starstedt AG & Co. KG, Germany). Post-immunisation serum was serially diluted in FACS buffer (PBS + 3 % FBS) and added to either 10^5 wild type cells or 10^5 of the same cells stably-expressing OX40L. Mouse antibodies were detected with $^1/_{200}$ dilution of BB700 conjugated 2° monoclonal antibodies against isotypes IgG1, IgG2a, IgG2b (BD OptiBuild™, Becton Dickinson). Stained cells were analysed by flow cytometry using a BD Accuri C6 Flow Cytometer (Becton Dickinson, NJ, USA) or Beckman Coulter's CytoFLEX S. Pre-immunisation serum was used as control (Figure 4).

Example 4: Isolation of OX40-L-specific antibody producing cells

Tissue isolation:

Spleens, lymph nodes and bone marrow were harvested from mice immunised with canine OX40L as described above. Splenocytes were prepared by cutting the spleen into pieces and forcing these through a 45 µm cell strainer (Falcon) while rinsing with RPMI-1640 (Lonza, Basel, CH) + 10 % FBS on ice. A similar process was used for lymphocytes from lymph nodes. Bone marrow was collected from femur and tibia and flushing the marrow with RPMI-1640 using a 21-gauge needle, through a 45 µm cell strainer pre-wetted with RPMI-1640. All cell types were pelleted at 300g for 5 min, before either being directly used for flow sorting or resuspended in FBS + 10 % dimethyl sulfoxide (DMSO) and being frozen at -150°C.

Cell Sorting:

Antigen-specific cells can be captured by fluorescent labelled VLPs or antigen protein probes. VLPs are generated from HEK cells stably transfected with OX40L, and subsequently transiently transfected with the retrovirus gag protein, and fluorescently labelled MA (gag matrix fragment p15-GFP fusion protein); the gag expression enables VLP budding from cells, and MA labels the VLPs for fluorescence-detection.

Antigen-specific B cells can also be captured by labelled antigen protein probes. Monomeric OX40L protein containing canine OX40L extra cellular domain (ECD), or trimeric soluble canine OX40L extra cellular domain probes (shown in the schematic in Figure 5 and with reference to Willett et al. Mol Immunol. 2009, 46(6); 1020-1030) were synthesised in expression vectors and expressed in CHO cells. Fc tagged probes were purified from culture supernatant using Mab select SuRe protein A resin (Cytiva) or by AKTA using Mab Select SuRe columns (Cytiva). HIS tagged trimeric canine OX40L protein was purified using HIS-Pur Ni-NTA resin (ThermoFisher).

Conjugation of OX40L ECD TNCc HIS (MW=62.143 kDa; trimeric, Seq ID 811) to Alexa Fluor 647 was carried out using the Microscale Protein Labeling Kit (Molecular Probes – Invitrogen catalogue number A30009) according to the manufacturer's protocol. Degree of labelling was determined using a NanoDrop spectrophotometer.

Similarly, the conjugation of monomeric dOX40L-mvhfc (MW=40.435 kDa) (Seq ID 807) and canine OX40L ECD TNCc Fc (MW=280.980 kDa; hexameric, Seq ID 809) to Alexa Fluor 647 was carried out using the Alexa Fluor 647 Antibody labelling kit (Molecular Probes – Invitrogen catalog number A20186) following manufacturer's protocol for antibody labelling. Degree of labelling was determined using a NanoDrop spectrophotometer.

Probe specificity was determined on splenocytes from OX40L immunised or irrelevant antigen immunised mice. The optimal probe concentration was also determined based on maximum signal in relevant immunisation and minimally staining on irrelevant immunisation.

Sorted B cells are prepared using the 10XGenomics Chromium Single Cell Immune Profiling system and the V(D)J Kit (10XGenomics) according to the manufacturer's instructions. Nucleotide sequences of expressed antibodies are determined by Illumina MiSeq sequencing with 600 cycles (2x300 cycles) or by Ilumina iSeq, Miseq, MiniSeq, Nextseq, Hiseq 4000 or Novaseq sequencing with 2x150 cycles. The sequences are analysed using custom tools based on the pRESTO /Change-O (Yale University) / IgBlast (NCBI, USA) software to identify paired VH and VL sequences and a clonal lineage information is also constructed based on the identities of the heavy chain V, D, J and light chain V, J genes.

An example of the analysis of antibody sequences of sorted Ag-specific single B-cells is shown in Figure 5 of WO2015/040401, and shows antibody sequences that are arranged by heavy-chain V-gene family usage, and clustered to generate the displayed phylogenetic trees. From phylogenetic trees such as these, candidate clones are selected. The nucleic acid and amino acid sequences of candidate clones VH and VL and their corresponding CDRs are given in the Sequences Table 2 below.

For instance, anti-canine OX40L mAbs PMX025-027 are all encoded by the same heavy chain V-gene (clGHV3-5) and light chain V-gene (clGLV3-14), anti-canine OX40L mAbs PMX039, 041, 043, 044, 046, 050 are all encoded by the same heavy chain V-gene (clGHV3-18) and light chain V-gene (clGLV3-3) (Table 3).

PMX025-065, PMX082-111, PMX154-156 and PMX291-294 have the sequences set out in Table 2 below.

Example 5: Generation of monoclonal antibodies from single cells

In some examples, the heavy chain and light chain V(D)J sequence of selected candidate clones are synthesised and cloned into expression vectors containing the Fc regions, such as human IgG4, canine IgGB for the heavy chain, and human IgGK or canine IGK or IGL constant regions for the light chain. In some examples the IgGB constant region includes mutations that render the constant region effector

deficient. Suitable sequences for these mutated Fc regions are given in the Sequence table below (Seq ID 723 to 730).

DNA encoding for canine heavy chain variable regions selected as described above are cloned in expression vectors upstream constant regions (CH1-hinge-CH2-CH3) of canine IgGB Def2 (SEQ ID NO:723). DNA encoding for canine light chain variable regions are cloned in expression vectors upstream constant regions of canine kappa or lambda light chains.

The expression vectors encoding the heavy chain and light chain are co-transfected into a suitable mammalian cell line such as CHO cells to obtain stable or transient expression.

For antibody production, 6×10^6 selected stably transfected CHO cells are seeded in 3 ml culture media and incubated at 32°C, 5% CO_2 with shaking at 200 rpm. 4 % HyClone Cell Boost 7a supplement + 0.4 % HyClone Cell Boost 7b supplement + 1 % glucose is added to the media on days 1, 4, 7 and 10. Culture supernatants are collected on day 12 and the IgG concentration determined on a protein A chip using surface plasmon resonance (Biacore 8K, Cytiva Life Sciences).

Example 6: Binding assays of OX40L candidate antibodies

Binding assays: binding of OX40L candidate antibodies to cell surface expressed canine OX40L proteins.

CHO supernatants diluted in FACS buffer (PBS containing 3% FBS) at 1, 5 or 10 µg/ml were used to screen for their binding capacity to canine OX40L using a cell-based assay. In brief, HEK293 or MEF cells (or any other commonly used cell lines) expressing canine OX40L at the cell surface are incubated with 100µll of FACS buffer containing the candidate antibody for 30' on ice. Cells are washed with 150 µl FACS buffer followed by centrifugation at 300g for 3min. The cell pellet is resuspended in FACS buffer containing a 1:1000 dilution of a fluorescently labelled secondary antibody recognising the canine Fc region of the test antibody for 30min in the dark, followed by washing with 150µl FACS buffer. Cells are resuspended in FACS buffer and flow cytometry performed using either a Cytoflex (Beckton Dickinson) or an Accuri (Beckman Coulter) cytometer, followed by data analysis using FlowJo (Figure 6 and Table 4).

Example 7: Functional assays for OX40 and OX40L activity of candidate antibodies

HEK-Blue - NF_KB functional assay:

Cell-based signalling inhibition using HEK-Blue - NF_KB assay:

In order to quantify the signalling activation of OX40 and OX40L, a cell-based reporter assay was developed. Since OX40 signals via the NF_KB signalling pathway, canine OX40 (long form) (Seq ID 5

and 6) was stably transfected into HEK-Blue™ Null1-v cells (HEK blue OX40 cells). HEK-Blue™ Null1-v cells express a secreted embryonic alkaline phosphatase (SEAP) reporter gene under the control of the IFN-β minimal promoter fused to five NF-κB and AP-1 binding sites. Therefore, stimulation of canine OX40 expressing HEK-Blue™ Null1-v cells induces production and secretion of SEAP, the activity of which can be detected using the QuantiBlue detection kit (Invivogen, San Diego, USA). To provide the signalling molecule for canine OX40, canine OX40L (Seq ID 1 and 2) was transfected into wild type HEK cells (HEK OX40L cells). Co-culturing of HEK blue OX40 cells with HEK OX40L cells with 1:1 ratio results in NF_KB signalling activation (Figure 7).

Prior to the assay, candidate antibodies were batch purified from CHO supernatant using protein A resin (MabSelect SuRe LX, Cytiva). In brief, MabSelect SuRe LX resin is washed in PBS and diluted to a 10% slurry. An appropriate volume of the 10% slurry is added to the supernatant and incubated 5-10' at RT before being loaded into a filter column. After 3 washes with PBS, the antibodies are eluted using IgG elute buffer (Pierce) directly into neutralisation buffer (10mM TRIS pH8.0) with 8:1 IgG elute: neutralisation buffer ratio. Antibody concentrations are quantified by measuring absorbance at 280 nm, using Nanodrop One (Thermo Fisher).

To determine the inhibitory effect of candidate antibodies on OX40L-OX40 signalling, 5,000 HEK-blue-OX40 cells and 5,000 HEK-OX40L cells are seeded in a 96 well plate in presence of protein A purified anti-OX40L antibodies at a fixed concentration of 6.6 nM. After 24h incubation at 37°C, 20µl of supernatant is collected and the presence of SEAP is assessed by the addition of 180µl of QuantiBlue reagent and a further 4hr incubation at 37 °C, followed by measuring absorbance at 630nm with a ClarioStar plate reader (BMG Labtech). Data is analysed using the dedicated MARS software version 3.40 R2 (BMG Labtech) and GraphPad Prism version 9.1. Data are shown in Figure 8 and Table 5.

Ex vivo PBMC activation assay.

PBMCs are isolated from freshly drawn canine whole blood, with sodium heparin anticoagulant, using Ficoll-Paque plus (Cytiva, GE17-1440-02) density gradient centrifugation. In brief, canine blood is diluted 1:1 with phosphate buffer saline (PBS) and carefully layered on top of Ficoll-paque plus, centrifugated at 800rcf for 20' with slow acceleration and no break at the end. The top layer and interphase disk are diluted with PBS and centrifuged at 1300rpm for 10' to collect PBMCs. Pelleted PBMC is washed for a second time with PBS to remove all remnants of Ficoll. After a second centrifugation, PBMCs are resuspended in media (PBMC media = RPMI + 10% heat inactivated foetal bovine serum + 1% penicillin-streptomycin + 1% non-essential amino acids + 1% L-glutamine + 1% sodium pyruvate + 1% HEPES) before use or freezing.

Freshly isolated or thawed PBMCs are seeded in a 96 well plate in 200 µl/well of PBMC media supplemented with PHA (Sigma Aldrich) or ConA (ThermoFisher) and cultured with or without purified anti-OX40L antibodies at specified concentrations at 37^0C, 5% CO_2. Supernatant is then collected at

day 3-5 for cytokine quantification. IFN-γ is measured by ELISA (MABtech) according to manufacturer's recommendations.

Alternatively, freshly isolated or thawed PBMCs are seeded in a 96 well plate precoated with a combination of anti-canine CD3 (Biorad) and CD28 (eBioscience) antibodies and cultured with or without additional canine OX40L trimeric protein or HEK cells expressing canine OX40L, and/or purified anti-OX40L antibodies at different concentrations at 37^0C, 5% CO_2. Supernatant is then collected at day 3-5 for cytokines quantification. IFN-γ is measured by ELISA (MABtech) according to manufacturer's recommendations.

Table 6 and 7 show raw and normalised IFN-γ levels obtained from PBMCs cultured for 3 days in a 96 well plate (1 to 2 x 10^5 PBMC per well) precoated with a combination of anti-canine CD3 (Biorad) and CD28 (eBioscience) antibodies and cultured with 5000 HEK cells expressing canine OX40L (or 5000 wild type HEK cells as control), and the indicated anti-OX40L antibodies at 66, 6.6 or 0.66 nM. Table 6 show the calculated IFN-γ levels in supernatant. As levels of secreted IFN-γ varies greatly between experiments due to the usage of different PBMC donors, we normalised the level of secreted IFN-γ in wells with PBMC activated with CD3-CD28 in presence of HEK cells expressing OX40L and anti-OX40L antibodies for the level of secreted IFN-γ in wells with PBMCs activated with CD3-CD28 (0%) and PBMC activated with CD3-CD28 in presence of HEK cells expressing OX40L but no anti-OX40L antibodies (100%) in the same experiment (Table 7).

Example 8: Affinity determination of anti-OX40L antibodies candidates

Determination of antibody affinity by surface plasmon resonance (SPR)

Affinity (K_d) of OX40L antibodies is measured by SPR, using a recombinant canine OX40L ECD-TNCc-HIS protein (Seq ID 811) as the capturing agent (Figure 5B).

OX40L ECD-TNCc-HIS protein is purified from CHO supernatant using HIS-Pur Ni NTA resin (ThermoFisher). In brief, CHO supernatant is buffer exchanged into PBS pH 8.0 containing 10mM imidazole, using PD10 desalting columns (Cytiva). The buffer exchanged supernatant is then incubated 1h at 4°C with HIS-Pur Ni NTA resin in rotation. Resin is applied to a gravity filter column and washed 3 times with PBS pH 8.0 containing 10mM imidazole before elution with 2.5ml of PBS pH 8.0 containing 500mM imidazole and buffer exchange to PBS pH7.4 using PD10 desalting columns.

Functional affinity is determined using a Biakore 8K (Cytiva). in brief, purified OX40L ECD-TNCc-HIS protein is covalently bound at low density to the surface of a CM5 sensor chip (Cytiva) by amine coupling, using the manufacturer's recommended protocol. Candidate antibodies are subsequently passed across the chip surface at a range of concentrations and affinity determined using the dedicated software (Biacore Insight Evaluation Software). Curves were fitted using a bivalent analyte binding model. Results are summarised in Table 8.

Example 9: Determination of candidate anti-OX40L antibodies stability

After protein A purification, anti-OX40L antibodies were eluted using IgG elution buffer (Pierce) and buffer acidity was neutralised using 1M TRIS pH 8.0. Candidates' stability was assessed in such buffer or after buffer exchange into sodium acetate buffer pH 5.5 (20mM Sodium acetate 100mM NaCl pH 5.5).

The tendency of candidates to form aggregates or fragments was first assessed by high performance liquid chromatography-size exclusion chromatography (HPLC-SEC). In brief, HPLC-SEC chromatography (column: BioResolve SEC mAb 200A, 2.5um column WATERS) was performed using ACQUITY H-class Bio (WATERS) using PBS as mobile phase with isocratic 0.575mL/min flow rate. 10uL of each sample have been injected in H-SEC using the above protocol. Percentage of monomeric species and Area (indicative of antibody concentration) was determined for each molecule by manual integration on the chromatogram (Figure 9 and Table 9).

Candidate stability, fragmentation and aggregation propensity was further assessed by evaluating melting temperature (Tm1), aggregation temperature (Tagg266) and initial diameter by static light scattering (SLS) and dynamic light scattering (DLS) using UNcle (Unchained lab). In brief, 3 x 9 µL of each sample was loaded into the Uni. The data from individual experiments were analysed and outliers discarded, and the remaining data averaged. Thermal ramp stability measurements were taken over 25 to 95°C at a ramp rate of 0.3 °C/ min with an incubation period of 120s, while 10 DLS measurements per sample was recorded at the start and the finish. DLS measurements (size distribution and polydispersity) were calculated with the UNcle software (version 5.03) correlation function. For SLS the intensity of scattered light was measured at 266 nm and was used to calculate the aggregation temperature (Tagg) with UNcle software (version 5.03). The intrinsic fluorescence emission was measured at 473 nm and the barycentric mean (BCM) was used to calculate the melting temperature (Tm) using the same software. Data are summarised in Table 9 and an example of the profile showing PMX051 and PMX063 are shown in Figure 10.

Example 10: Sequence analysis and candidate clustering.

To expand on existing identified candidates with desirable properties, we searched paired B cell receptor sequences derived from canine OX40L immunisation. Given a query CDR3H peptide, we searched for candidate sequences with a CDR3H of the same length but allowing up to two amino acid variations. Using PMX051 and PMX063 as the lead sequence, 26 new antibodies (PMX086-PMX111) are identified (Table 2).

The 78 anti-OX40L antibodies were subsequently sub-grouped into 14 family groups by V-gene pair.

Example 11 Fc variants

Fc variants construction

For antibody production, DNA constructs were generated to encode chimeric antibodies comprising selected canine IgG constant regions fused to the variable regions of anti-human CD20 antibodies, Rituximab (see US 5,736,137) or Ofatumumab (sequence available on Drugbank https://go.drugbank.com/drugs/DB06650).

The canine IgG-B mutant variants (Def 1 to 9, Seq ID 722 to 730) were generated by site directed mutagenesis. Specifically, human Ofatumumab or Rituximab variable region and canine IgG-B mutant variants are PCR amplified using Q5 high fidelity DNA polymerase and assembled into a mammalian expression vector upstream sequences encoding for either canine IgGB WT or Def 1 to 9 (Seq ID 721 to 730) using NEBuilder HIFI DNA Assembly (New England Biolabs). Ofa-VH-cIgGB WT Ofatumumab sequence is shown in SEQ ID NO. 731. In the expression vector, the heavy chain and the antibiotic resistant gene expression units are flanked by DNA transposon *piggyBac* terminal inverted repeats to mediate stable integration into host cells in the presence of piggyBac transposase. The expression vectors encoding the heavy chain and light chain are co-transfected into a suitable mammalian cell line such as CHO cells together with PiggyBac transposase to obtain stable expression. For antibody production, 3×10^6 selected CHO cells are seeded in 3 ml culture media and incubated at 32°C, 5% CO_2 with shaking at 200 rpm. 4 % HyClone Cell Boost 7a supplement + 0.4 % HyClone Cell Boost 7b supplement + 1 % glucose is added to the media on days 1, 4, 7 and 10. Culture supernatants are collected on day 12 and the IgG concentration determined using surface plasmon resonance using protein A chip (Biacore 8K, Cytiva Life Sciences).

Complement Dependent Cytotoxicity (CDC) Activity

Canine lymphoid tumour cell lines such as CLBL1 (University of Veterinary Medicine Vienna) or CLC (Umeki S. et al J. Vet. Med. Sci., 75:467-474 (2013) PubMed=23196801; DOI=10.1292/jvms.12-0448) may be used as target cells. These cells are stably transfected or nucleofected with an expression construct encoding for the human CD20 protein (Seq ID 732) to generate hCD20-expressing cells. The expression constructs were generated using the same method as described above for antibody expression.

Transfected cells were selected for puromycin resistance and $hCD20^{high}$ (top 5%) cells were FACS sorted by staining for hCD20 expression using anti-human CD20 antibody (clone: 2H7, BioLegend).

To assess CDC activity, untransfected (wild type) target lymphoid cells or equivalent hCD20-expressing cells were used in a cell killing assay in which 5000 target cells per well of 96-well plate were incubated with anti-human CD20 canine Fc chimeric antibody as described above and canine complement preserved serum (BioIVT) at a final dilution of 1:12, for 2 hours at 37°C, 5% CO_2. The assay was set up using media (RPMI + 1% L-glutamine + 20% fetal bovine serum for CLBL-1 cells made using heat inactivated serum so that canine complement preserved serum would be the only source of complement.

Live cells were then quantified using CellTitre-Glo® Luminescent Cell Viability Assay (Promega) following the assay protocol. This assay uses the ATP content of live cells as an indication of cell viability. Luminescence was measured on a CLARIOstar (BMG Labtech). Data was analyzed using MARS software (BMG Labtech) and the number of live cells remaining was used to calculate the percentage of killing in the presence of antibodies using Microsoft Excel. Background signal was obtained from a sample of cells treated with 1 % triton (where no cells were left alive) and subtracted from the signal obtained from each test samples. Max signal (0% killing) was obtained from a sample of cells treated identically but where antibodies were omitted. Graphs were plotted in Microsoft Excel or GraphPad Prism. Exemplary CDC assays were performed using hCD20 expressing CLBL1 cells and WT CLBL1 cells and a titration of IgGB WT or Def mutant antibodies with Ofatumumab variable regions. Antibodies were used at serial 1:3 dilutions ranging from 10µg/ml to 0.01 10µg/ml.

All Def mutants tested (Def1, 2, 3, 5, 6, 7, 8, 9) completely abrogated the ability of canine IgGB WT to kill hCD20 CLBL1 cells by complement dependent cytotoxicity (data not shown).

Antibody Dependent Cellular Cytotoxicity (ADCC) Activity

Canine cell lines, such as MDCK II cells (ATCC) were stably transfected or nucleofected with a construct encoding for the human CD20 protein and a construct expressing a fluorescent protein (i.e. GFP), as described above. Wild type MDCK II cells expressing GFP were used as a control. Canine peripheral blood mononuclear cells (PBMCs, Envigo) were used as a source of effector cells. PBMCs were isolated from freshly drawn whole blood, with sodium heparin anticoagulant, using Ficoll-Paque plus (Cytiva, GE17-1440-02) density gradient centrifugation. In brief, 10ml blood was diluted 1:1 with phosphate buffer saline (PBS) and carefully layered on top of 15 ml of Ficoll-paque plus, centrifugated at 800rcf for 20' with slow acceleration and no break at the end. The top layer and interphase disk were diluted with PBS and centrifuged at 1300rpm for 10' to collect PBMC in the pellet which was washed a second time in PBS to remove all remnants of Ficoll. After a second centrifugation, PBMCs were resuspended in media (PBMC media = RPMI + 10% heat inactivated foetal bovine serum + 1% penicillin-streptomycin + 1% non-essential amino acids + 1% L-glutamine + 1% sodium pyruvate + 1% HEPES) supplemented with 50ng/ml recombinant canine IL-2 (R&D systems) and incubated for 24h at 37^0C, 5% CO_2 before use in the ADCC assay.

To assess ADCC activity of Def mutants antibodies, MDCK II cells wild type or expressing hCD20, both expressing GFP, were co-cultured with PBMCs at an effector: target ratio of 50:1 or 100:1 and a titration of IgGB WT or Def mutant antibodies with Ofatumumab variable regions for 24 h at 37^0C, 5% CO_2, in a 1:1 mix of MDCK II media (DMEM + 1% L-glutamine + 10% fetal bovine serum) and PBMC media.

GFP signal, which is proportional to the number of live cells per well, was used as a measure of the number of live cells remaining in the well at the end of the 24h incubation. GFP signal was measured on a CLARIOstar (BMG Labtech). Data was analysed using MARS (BMG Labtech) and percentage of killing in the presence of antibodies was calculated using Microsoft Excel. Background signal was

obtained from a sample of cells treated with 1 % triton (where no cells were left alive) and subtracted from the signal obtained from each test samples. Max signal (0% killing) was obtained from a sample of cells treated identically but where antibodies were omitted. Graphs were plotted in Microsoft Excel or GraphPad Prism.

Def mutants 2, 3 and 7 were the best at reducing canine IgGB ADCC activity and strongly reduced canine IgGB ADCC activity at up to 10μg/ml (data not shown).

Example 12 Long term stability and thermal stability

After protein A purification, anti-OX40L antibodies were eluted using IgG elution buffer (Pierce) and buffer acidity was neutralised using 1M TRIS pH 8.0. Candidates' stability was assessed in such buffer or after buffer exchange into sodium acetate buffer pH 5.5 or glycine buffer. After buffer exchange the candidate antibodies were concentrated to 5mg/ml before proceeding with analysis or incubation at 4ºC or 37ºC.

For long term stability, candidate antibodies were incubated at 4°C for up to 4 months. For thermal stability assessment, candidate antibodies were incubated at 37°C for up to 28 days.

Candidate stability, denaturation and aggregation propensity was further assessed by evaluating melting temperature (Tm1), aggregation temperature (Tagg 266 and Tagg 473) and initial diameter by static light scattering (SLS) and dynamic light scattering (DLS) using UNcle (Unchained lab). In brief, 3 x 9 µL of each sample was loaded into the Uni. The data from individual experiments were analysed and outliers discarded, and the remaining data averaged. Thermal ramp stability measurements were taken over 25 to 95°C at a ramp rate of 0.3 °C/ min with an incubation period of 120s, while 10 DLS measurements per sample was recorded at the start and the finish. DLS measurements (size distribution and polydispersity) were calculated with the UNcle software (version 5.03) correlation function. For SLS the intensity of scattered light was measured at 266 nm or 473 nm and was used to calculate the aggregation temperature (Tagg 266 and Tagg 473, respectively) with UNcle software (version 5.03). The intrinsic fluorescence emission was measured at 473 nm and the barycentric mean (BCM) was used to calculate the melting temperature (Tm) using the same software. Data for thermal stability at 37°C for PMX051, PMX063, PMX097, PMX098 and PMX154 are shown in figures 11 and 12. Data for long term stability at 4°C for PMX097 and PMX154 are summarised in Table 10.

Example 13 Pharmacokinetic profile

To determine the pharmacokinetic profile of anti-OX40L antibodies, laboratory beagle dogs were injected intravenously with 3.0 mg/kg of either PMX097 or PMX154. Blood samples were collected the day before injection and after 2 hours, 6 hours, 24 hours, 48 hours, 4 days, 8 days, 15 days, 21 days, 29 days, and 35 days. After coagulation, blood was centrifuged at 7000 g for 5 minutes to separate the serum which was then stored at -80ºC.

After collection of all time points the pharmacokinetic profile was determined by enzyme-linked immunosorbent assay (ELISA). Briefly, ELISA plates were coated overnight at 4°C with HIS tagged trimeric OX40L protein (0.2µg/ml in PBS, Seq ID 811). The next day plates are blocked for 2 hours with blocking buffer (PBS containing 0.05% tween 20 and 1% bovine serum albumin fraction V (BSA)) before washing 5 times with PBS containing 0.05% tween 20. Before application, sera are diluted 1 in 2000 in blocking buffer. Serial dilutions (one in two dilutions) of PMX097 or PMX154 were prepared in canine serum from a top concentration of 50 µg/ml. The standard dilutions were also diluted 1 in 2000 in blocking buffer before applying to the ELISA plates. After incubating sera and standard for 2 hours the plates were washed 5 times and incubated 1 hour with a secondary antibody anti dog IgG conjugated with biotin (Merck) diluted 1 in 100.000 in blocking buffer. After 5 more washes plates are incubated with streptavidin-HRP (Biolegends) diluted 1 in 5000 in blocking buffer, then washed again before adding TMB substrate (Pierce) and stopping the reaction with 0.2N sulphuric acid right before data acquisition. Absorbance at 450 nm and 650 nm was quantified using a plate reader (CLARIOstar, BMB Labtech). Data were analysed using the integrated MARS software (BMG Labtech). Concentration of samples in serum is determined by the MARS software using the standard curve generated from the serial dilution of PMX097 or PMX154, plotted as a four-parameter logistic curve fitting algorithm. Data shown in Figure 13 were plotted using Prism and the half-life was calculated fitting the points with a two-phase decay curve fitting.

Example 14 Pharmacodynamic profile

The ability of PMX097 and PMX157 to suppress T cell activation in vivo was assessed in laboratory beagle dogs. To induce T cell activation, we immunised the dogs with keyhole limpet hemocyanin (KLH). The schedule of the procedures is listed in table 11. Briefly, 20 dogs were divided in five groups that received a different treatment regime (Table 11). A single dose of 3 mg/kg or 0.5 mg/kg of PMX097 or PMX154, or vehicle control, was infused intravenously on day 0. The day following antibodies injection, all dogs received a first KLH injection. A second, intradermal, KLH injection was performed 3 weeks later and, two days after that, two full thickness skin biopsies (punch biopsies) were collected: one at the KLH injection site and one in a non-injected area, as control.

For serum preparation, blood samples were collected the day before injection and after 2 hours, 6 hours, 24 hours, 48 hours, 4 days, 8 days, 15 days, 21 days, 29 days, and 35 days. After coagulation, blood was centrifuged at 7000 g for 5 minutes to separate the serum which was then frozen. For PBMC isolation, whole blood was collected in tubes containing sodium heparin the day before antibody injection and after 8 days, 15 days, 21 days, 29 days, and 35 days. PBMC were isolated from whole blood on the same day of collection using lymphocyte separation medium (Corning) and frozen right after for long term storage in liquid nitrogen. In brief, canine blood is diluted 1:1 with phosphate buffer saline (PBS) and carefully layered on top of lymphocyte separation medium, centrifugated at 800 rcf for 20' with slow acceleration and no break at the end. The top layer and interphase disk are diluted with PBS and centrifuged at 400 rcf for 10' to collect PBMCs. Pelleted PBMC is washed for a second time with PBS

to remove all remnants of lymphocyte separation medium. After a second centrifugation, PBMCs are resuspended in media (PBMC media = RPMI + 10% heat inactivated foetal bovine serum + 1% penicillin-streptomycin + 1% non-essential amino acids + 1% L-glutamine + 1% sodium pyruvate + 1% HEPES) and diluted 1 to 1 with cold freezing medium (80% heat inactivated FBS, 20% DMSO) before freezing.

Determination of T cell activation by interferon gamma ELISpot

The number of activated T cells in response to KLH stimulation was determined by interferon gamma (IFNY) enzyme-linked immunosorbent spot (ELISpot) sing the canine IFNY ELISpot flex ALP kit (Mabtech).

Frozen PBMC were thawed and rested to eliminate dying cells by culturing in PBMC medium in low adhesion polypropylene tubes in a humidified incubator at 37°C with 5% CO_2 for between 18 hours and 48 hours. The day before setting up the experiment, ELISpot plates (Millipore) were activated by adding 15µl of 35% ethanol per well, immediately followed by 5 washes with sterile distilled water. After activation plates were coated by incubating overnight at 4°C with anti-canine IFNY antibody (MT13) diluted to 15 µg/ml in PBS. The next day plates were washed 5 times with PBS and blocked for at least 30 minutes with PBMC medium. After blocking 50µl of PBMC medium alone (for no stimulation control) or containing KLH (Merk) at 100µg/ml (2x) was added to each well. As positive control, 50µl of PBMC medium containing Phytohemagglutinine-L (PHA) (sigma-Aldrich) at 20µg/ml (2x) was added to the correspondent wells.

Before seeding onto ELISpot plates, PBMC were counted using an automated CellDrop (DeNovix) cell counter with primary AO/PI settings. Briefly, PBMC were resuspended and 10µl of PBMC were mixed with 10µl of acridine orange/propidium iodine (AO/PI) working solution to discriminate between live and dead cells before loading onto a CellDrop automated cell counter. After centrifugation to remove dead cells and debris, PBMC were then resuspended at 4.4 x 10^6 cells per ml of PBMC medium and 50µl of the cell suspension was added to the plates on top of the stimuli and incubated in a humidified incubator at 37°C with 5% CO_2 for 20 hours.

The next days the cells are discarded, and plates washed 5 times with PBS before incubating 1 hour with the detection antibody (MT166-biotin) diluted to 0.5 µg/ml in PBS with 0.5% FBS. Following 5 more washes with PBS, plates are then incubated 1 hours with streptavidin-ALP diluted 1 in 1000 in PBS with 0.5% FBS and washed another 5 times with PBS before adding BCIP/NBT plus substrate (Mabtech) till the spots become apparent. After stopping the reaction by washing with water, plates were air dried. Spots were quantified using an ELISpot counter (Immunospot). After quality control using the ELISpot counter integrated software, data were plotted using Prism. Data are presented in figure 14 and show a strong reduction of the number of KLH-responsive circulating T cells in dogs treated with PMX097 and PMX154 at all time points analysed. These data demonstrate the ability of both PMX097 and PMX154 to suppress T cell activation in vivo for up to 35 days, both when administered at 3.0 mg/ml and 0.5 mg/ml.

Determination of anti-KLH IgM and IgG serum titre

B cell activation and antibody secretion is also dependent upon helper T cells stimulation. Therefore, a reduced T cell activation should translate in a reduce humoral response. To evaluate the ability of PMX097 and PMX154 to reduce T cell-dependent antibody response (TCDAR) following KLH immunisation (Kawai R., Aida T. et al, The Journal of Toxicological Sciences, Vol.38, No.4, 571-579, 2013; Saghari M, Gal P, et al, Clinical Pharmacology & Therapeutics, Vol 111, N 5, May 2022), anti-KLH IgM and IgG serum titre was quantified by ELISA.

ELISA plates were coated overnight at 4°C with KLH protein diluted to 1 µg/ml in PBS. The next day plates are blocked for 2 hours with blocking buffer (PBS containing 0.05% tween 20 and 1% bovine serum albumin fraction V (BSA)) before washing 5 times with PBS containing 0.05% tween 20. Before application sera are diluted 1 in 6000 or 1 in 15000 in blocking buffer, for anti-KLH IgM or IgG detection, respectively. After incubating sera and standard for 2 hours the plates were washed 5 times and incubated 1 hour with a secondary antibody: anti dog IgG conjugated with biotin (Merck) or goat anti dog IgM diluted 1 in 5000 or 1 in 500 in blocking buffer, respectively. After 5 more washes plates are incubated with either streptavidin-HRP (Biolegends) or an anti-goat HRP conjugated antibody diluted 1 in 5000 or 1 in 10000 in blocking buffer, respectively, then washed again before adding TMB substrate (Pierce) and stopping the reaction with 0.2N sulphuric acid right before data acquisition. Absorbance at 450 nm and 650 nm was quantified using a plate reader (CLARIOstar, BMB Labtech). Data were analysed using the integrated MARS software (BMG Labtech). Due to the unavailability of a standard, data are presented as blank corrected difference of absorbance (Abs) at 450 nm minus blank corrected Abs at 650 nm (Figure 15 A and C) and as normalised to vehicle control treated samples (Figure 14 B and D). Data shown in Figure 15 were plotted using Prism and show the ability of both PMX097 and PMX154 to reduce both anti-KLH IgM and IgG serum titre for up to 98 days post administration.

Effect of PMX097 and PMX154 on local inflammation in the skin.

To evaluate the ability of PMX097 and PMX154 to reduce local inflammation in the skin, the second KLH immunisation was administered intradermally. This allowed collection of skin biopsies and histological analysis of the injection site. As control each dog also produced a skin biopsy from a non-injected site. Skin biopsies were fixed overnight in 10% normal buffered formalin and then moved into 70% ethanol the next day. After complete dehydration through incubation in ethanol 95% and then ethanol absolute for 1 hour each, biopsies were moved into xylene and then embedded in paraffin before cutting into 5 µm thick sections. Skin sections were then stained with haematoxylin and eosin and imaged using a wide field microscope (Nikon). Figure 16 shows representative images that illustrate the severe reduction in immune infiltrates in the subcutaneous fat near KLH injection sites of dogs treated with PMX097 and PMX154.

To obtain an objective assessment of the phenotype, we next submitted haematoxylin and eosin-stained slides to histopathological evaluation. Microscopic changes were graded as to severity utilizing a

standard grading system whereby 0 = no significant change, 1 = minimal, 2 = mild, 3 = moderate, and 4 = marked. International Harmonization of Nomenclature and Diagnostic (INHAND) Criteria standards are used as the basis of evaluation--https://www.toxpath.org/inhand.asp. All tissue sections contained portions of epidermis and dermis, but deeper subcutaneous adipose tissue and muscular layer are variably present. When the subcutaneous adipose tissue or muscular layer were absent in a tissue section, the findings associated with those layers were excluded from analysis and represented by a "-" symbol in the tables. Use of numerical grades allows a mechanism to calculate a total score lesion score which can be used to assess prevalence and severity of tissue changes within and between groups. Results of histopathological analysis are summarised in Table 12 and 13.

Treatment with PMX097 and PMX154 at both 3.0 mg/kg and 0.5 mg/kg reduced the severity of immune infiltrates in KLH injected areas.

Example 15 Safety profile of PMX097 and PMX154 in laboratory beagle dogs.

The safety profile of PMX097 and PMX154 was assessed in laboratory beagle dogs, after intravenous injection of the two compounds at either 3.0mg/kg or 0.5mg/kg (Table 11). During and after antibody injection dogs were regularly monitored. To determine the effect of PMX097 and PMX154 on the animal health, complete blood chemistry and blood cellular count was performed on each dog at 3 time points: right before (pre-bleed), 24 hours and 15 days after antibody injection.

Regular monitoring did not reveal any abnormality. All animals in all groups tolerated well the administration and did not show any visible side effects for the entire duration of the study. Blood cell count and biochemistry parameters were mostly within range at all time points and there was no indication of toxicity in all treatment groups.

Table 2 SEQUENCES All sequence for antibody and antibody fragments designated as "PMX" followed by a number and shown below are within the scope of the invention.

SEQ ID NO:	Description	Sequence
1	Wild type canine OX40L amino acid	MEGVQPLDQNVGNTPGRRFQKNKVLLVAAIIQGLGLLLCFTYI CLHFYASQVPPQYPPIQSIRVQFTRCENEKGCIITSPSKDETM KVQDNSIIINCDGFYLISLKGYFSEELSLSLYYRKGRGPLFSLS KVTSVDSIGVAYLAFKDKVYFNVTTHSTSYKDIQVNGGELILIH QNPGGFCAY

2	Wild type canine OX40L nucleic acid	ATGGAAGGGGTCCAACCCCTGGACCAGAATGTGGGAAACA CACCAGGGCGAAGATTCCAGAAGAACAAGGTATTGCTGGT GGCAGCCATAATTCAGGGGCTGGGTCTGCTCCTGTGTTTC ACCTACATCTGCCTGCACTTCTATGCTTCTCAGGTGCCGCC TCAGTATCCTCCAATTCAAAGTATCAGAGTACAATTTACCA GGTGTGAGAATGAGAAAGGTTGCATCATCACATCCCCAAG CAAGGATGAAACTATGAAGGTGCAAGACAACTCAATCATCA TTAACTGTGATGGGTTTTATCTCATCTCCCTGAAGGGTTAC TTCTCTGAGGAGCTCAGCCTCAGCCTTTATTACCGAAAGG GTCGGGGACCCCTCTTCTCTCTGAGCAAGGTCACATCTGT TGACTCCATTGGAGTGGCCTATCTGGCTTTCAAGGACAAA GTCTACTTTAATGTGACCACTCACAGTACCTCCTACAAAGA CATCCAGGTGAATGGTGGGGAATTGATTCTCATTCATCAAA ATCCTGGTGGCTTCTGTGCCTACTGA
3	Canine OX40 splice short variant nucleic acid	ATGAGGATGTTCGTGGAGTCCCTGCGGCTCAGCGGTCCTC ACTCAGCCCTCCTGCTCCTGGGGCTTGTGCTGGGTGCCGT AGCTGAGCACAACTGTTTCGGGAACACCTACCCCAAAGAC GGCAAGTGCTGCAATGACTGCCCACCAGGTTATGGAATGG AGAGCCGCTGCAGTAGGAGCCATGACACCAAATGTCATCA GTGTCCATCTGGCTTCTACAATGAGGCTACAAATTACGAAC CCTGCAAGCCCTGCACTCAGTGCAATCAGAGAAGTGGGAG TGAACCCAAGAGGAGATGCACACCCACGCAGGACACCATC TGCAGCTGTAAGCCAGGCACAGAGCCCCGGGACGGCTAC AAGCGTGGAGTCGACTGTGCCCCATGCCCACCCGGACACT TCTCCCCAGGGGATGACCAGGCCTGCAAGCCCTGGACCA ACTGTACCtTGATGggAAGGCGTACAATGCAGCCGGCCAGC AAGAGCTCAGACGCTGTCTGTGAGGACAGGAGCCTCCCC GCCACACTGCCATGGGAGACCCAGAGCCCCCTGACCCGG CCCCCTACCCCTCAGCCCACTATGGCCTGGCCCAGGACCT CGCAGGGGCCCTTCACACCCCCTACGGAGCCCCCCAGGG GTGGAAATAGCTTCCGGACCCCCATCCAAGAGGAGCATGC TGACGCCAACTCCACCCTGGCCAAGATCTGA
4	Canine OX40 splice short variant amino acid	MRMFVESLRLSGPHSALLLLGLVLGAVAEHNCFGNTYPKDGK CCNDCPPGYGMESRCSRSHDTKCHQCPSGFYNEATNYEPC KPCTQCNQRSGSEPKRRCTPTQDTICSCKPGTEPRDGYKRG VDCAPCPPGHFSPGDDQACKPWTNCTLMGRRTMQPASKSS

		DAVCEDRSLPATLPWETQSPLTRPPTPQPTMAWPRTSQGPF TPPTEPPRGGNSFRTPIQEEHADANSTLAKI
5	Canine OX40 splice long variant nucleic acid	ATGAGGATGTTCGTGGAGTCCCTGCGGCTCAGCGGTCCTC ACTCAGCCCTCCTGCTCCTGGGGCTTGTGCTGGGTGCCGT AGCTGAGCACAACTGTTTCGGGAACACCTACCCCAAAGAC GGCAAGTGCTGCAATGACTGCCCACCAGGTTATGGAATGG AGAGCCGCTGCAGTAGGAGCCATGACACCAAATGTCATCA GTGTCCATCTGGCTTCTACAATGAGGCTACAAATTACGAAC CCTGCAAGCCCTGCACTCAGTGCAATCAGAGAAGTGGGAG TGAACCCAAGAGGAGATGCACACCCACGCAGGACACCATC TGCAGCTGTAAGCCAGGCACAGAGCCCCGGGACGGCTAC AAGCGTGGAGTCGACTGTGCCCCATGCCCACCCGGACACT TCTCCCCAGGGGATGACCAGGCCTGCAAGCCCTGGACCA ACTGTACCtTGATGggAAGGCGTACAATGCAGCCGGCCAGC AAGAGCTCAGACGCTGTCTGTGAGGACAGGAGCCTCCCC GCCACACTGCCATGGGAGACCCAGAGCCCCCTGACCCGG CCCCCTACCCCTCAGCCCACTATGGCCTGGCCCAGGACCT CGCAGGGGCCCTTCACACCCCCTACGGAGCCCCCCAGGG GCCCCCAGCTGGCTGCTGTCCTGGGCTTGGGCCTAGGCT TGCTGGCCCCCGTGGCAGCCGCACTGGCCTTGCTCCTGC ACCACAGAGCCTGGCGGCTGCCCCCCGGTGGAAATAGCT TCCGGACCCCCATCCAAGAGGAGCATGCTGACGCCAACTC CACCCTGGCCAAGATCTGA
6	Canine OX40 splice long variant amino acid	MRMFVESLRLSGPHSALLLLGLVLGAVAEHNCFGNTYPKDGK CCNDCPPGYGMESRCSRSHDTKCHQCPSGFYNEATNYEPC KPCTQCNQRSGSEPKRRCTPTQDTICSCKPGTEPRDGYKRG VDCAPCPPGHFSPGDDQACKPWTNCTLMGRRTMQPASKSS DAVCEDRSLPATLPWETQSPLTRPPTPQPTMAWPRTSQGPF TPPTEPPRGPQLAAVLGLGLGLLAPVAAALALLLHHRAWRLP PGGNSFRTPIQEEHADANSTLAKI
7	OX40 Forward primer	GGCAGAGATGAGGATGTTCG
8	OX40 Reverse primer	CACTGGCTGCTCAGATCTTGG
9	OX40L Forward	GCCACAGTTTTCATCTCCCT

10	OX40L Reverse	GCTTGGCTTAGGTGCAGC
11	PMX025 Heavy chain variable region nucleic acid sequence	GAGGTGCACCTGGTGGAGTCTGGGGGAGACCTGGTGAAG CCTGGGGGGTCCCTGAGACTTTCCTGTGTGGCCTCTGGAT TCACCTTCAGTAGCTACCACATGAGTTGGGTCCGCCAGGC TCCAGGGAAGGGACTTCAGTGGGTCGCATTCATTAACGCT GGTGAAATTAGCACAAACTATGCAGACGCTGTGAAGGGCC GATTCACCATCTCCAGAGACAACGCCAAGAATATATTGTAT CTTCAGATGAACAGCCTGAGAGCCGAGGACACGGCCGTGT ATTACTGTGCGAGTGGACATATTTGGATACGTCCCTTTGAC TACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
12	PMX025 Heavy chain variable region amino acid sequence	EVHLVESGGDLVKPGGSLRLSCVASGFTFSSYHMSWVRQAP GKGLQWVAFINAGEISTNYADAVKGRFTISRDNAKNILYLQMN SLRAEDTAVYYCASGHIWIRPFDYWGQGTLVTVSS
13	PMX025 light chain variable region nucleotide sequence	TCCTATGTGCTGACACAGCTGCCATCCATGAGTGTGACCC TGAGGCAGACGGCCCGCATCACCTGTGAGGGAGACAGCA TTGGAAGGAAAAGAGTTAACTGGTACCAGCAGAAGTTGGG CCAGGTCCCTGTACTAATTATTTATGATGATGACAGCAGGC CGTCAGGGATCCCTGAGCGATTCTCCGGCGCCAACTCGG GGAACACAGCCACCCTGACCATCAGCGGGGCCCTGGCCG AGGACGAGGCTGAATATTACTGCCAGGTGTGGGACAGCAG TAATAATTGGGTATTCGGTGAGGGGACCCAGCTGACCGTC CTCG
14	PMX025 light chain variable region amino acid sequence	SYVLTQLPSMSVTLRQTARITCEGDSIGRKRVNWYQQKLGQV PVLIIYDDDSRPSGIPERFSGANSGNTATLTISGALAEDEAEYY CQVWDSSNNWVFGEGTQLTVL
15	PMX025 heavy chain CDR1	GFTFSSY
16	PMX025 heavy chain CDR2	NAGEIS
17	PMX025 heavy chain CDR3	CASGHIWIRPFDYW

18	PMX025 light chain CDR1	EGDSIGRKRVN
19	PMX025 light chain CDR2	DDDSRPS
20	PMX025 light chain CDR3	CQVWDSSNNWVF
21	PMX026 Heavy chain variable region nucleic acid sequence	GAGGTGCACCTGGTGGAGTCTGGGGGAGACCTGGTGAAG CCTGGGGGGTCCCTGAGACTTTCCTGTGTGGCCTCTGGAT TCACCTTCAGTAGCTACCACATGAGTTGGGTCCGCCAGGC TCCAGGGAAGGGACTTCAGTGGGTCGCATTCATTAACGCT GGTGAAATTAGCACAAACTATGCAGACGCTGTGAAGGGCC GATTCACCATCTCCAGAGACAACGCCAAGAATATATTGTAT CTTCAGATGAACAGCCTGAGAGCCGAGGACACGGCCGTGT ATTACTGTGCGAGTGGACATATTTGGATACGTCCCTTTGAC TACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
22	PMX026 Heavy chain variable region amino acid sequence	EVHLVESGGDLVKPGGSLRLSCVASGFTFSSYHMSWVRQAP GKGLQWVAFINAGEISTNYADAVKGRFTISRDNAKNILYLQMN SLRAEDTAVYYCASGHIWIRPFDYWGQGTLVTVSS
23	PMX026 light chain variable region nucleotide sequence	TCCTATGTGCTGACACAGCTGCCATCCATGAGTGTGACCC TGAGGCAGACGGCCCGCATCACCTGTGAGGGAGACAGCA TTGGAAGGAAAAGAGTTAACTGGTACCAGCAGAAGTTGGG CCAGGTCCCTGTACTAATTATTTATGATGATGACAGCAGGC CGTCAGGGATCCCTGAGCGATTCTCCGGCGCCAACTCGG GGAACACAGCCACCCTGACCATCAGCGGGGCCCTGGCCG AGGACGAGGCTGAATATTACTGCCAGGTGTGGGACAGCAG TAATAATTGGGTATTCGGTGAGGGGACCCAGCTGACCGTC CTCG
24	PMX026 light chain variable region amino acid sequence	SYVLTQLPSMSVTLRQTARITCEGDSIGRKRVNWYQQKLGQV PVLIIYDDDSRPSGIPERFSGANSGNTATLTISGALAEDEAEYY CQVWDSSNNWVFGEGTQLTVL
25	PMX026 heavy chain CDR1	GFTFSSY

26	PMX026 heavy chain CDR2	NAGEIS
27	PMX026 heavy chain CDR3	CASGHIWIRPFDYW
28	PMX026 light chain CDR1	EGDSIGRKRVN
29	PMX026 light chain CDR2	DDDSRPS
30	PMX026 light chain CDR3	CQVWDSSNNWVF
31	PMX027 Heavy chain variable region nucleic acid sequence	GAGGTGCACCTGGTGGAGTCTGGGGGAGACCTGGTGAAG CCTGGGGGGTCCCTGAGACTTTCCTGTGTGGCCTCTGGAT TCACCTTCAGTACCTACCACATGAGTTGGGTCCGCCAGGC TCCAGGGAAGGGACTTCAGTGGGTCGCATTCATTAACGCT GGTGAAATTAGCACAAACTATGCAGACGCTGTGAAGGGCC GATTCACCATCTCCAGAGACAACGCCAAGAATATATTCTAT CTTCAGATGAACAGCCTGAGAGCCGAGGACACGGCCGTGT ATTACTGTGCGACTGGACATATTTGGATACGTCCCTTTGAC TACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
32	PMX027 Heavy chain variable region amino acid sequence	EVHLVESGGDLVKPGGSLRLSCVASGFTFSTYHMSWVRQAP GKGLQWVAFINAGEISTNYADAVKGRFTISRDNAKNIFYLQMN SLRAEDTAVYYCATGHIWIRPFDYWGQGTLVTVSS
33	PMX027 light chain variable region nucleotide sequence	TCCTATGTACTGACACAGCTGCCATCCATGAGTGTGACCCT GAGGCAGACGGCCCGCATCACCTGTGAGGGAAACAGCAT TGGAAGGAAAAGAGTTAACTGGTACCAGCAGAAGTTGGGC CAGGTCCCTGTACTAATTATTTATGATGATGACAGCAGGCC GTCAGGGATCCCTGAGCGATTCTCCGGCGCCAACTCGGG GAACACAGCCACCCTGACCATCAGCGGGGCCCTGGCCGA GGACGAGGCTGAATATTACTGCCAGGTGTGGGACAGCAGT AATAATTGGGTATTCGGTGAGGGGACCCAGCTGACCGTCC TCG

34	PMX027 light chain variable region amino acid sequence	SYVLTQLPSMSVTLRQTARITCEGNSIGRKRVNWYQQKLGQV PVLIIYDDDSRPSGIPERFSGANSGNTATLTISGALAEDEAEYY CQVWDSSNNWVFGEGTQLTVL
35	PMX027 heavy chain CDR1	GFTFSTY
36	PMX027 heavy chain CDR2	NAGEIS
37	PMX027 heavy chain CDR3	CATGHIWIRPFDYW
38	PMX027 light chain CDR1	EGNSIGRKRVN
39	PMX027 light chain CDR2	DDDSRPS
40	PMX027 light chain CDR3	CQVWDSSNNWVF
41	PMX028 Heavy chain variable region nucleic acid sequence	GAGGTGCAGATGGTGGAGTCTGGGGGAGACCTGGTGAAG CCTGGGGGGTCCCTGAGACTTTCCTGTGTGGCCTCTGGAT TCACCTTCAGTGACTACCACATGAGCTGGGTCCGCCAGGC TCCAGGGAAGGGACTTCAGTGGGTCGCATACATTACCAGT GGTGGAAGTAGCACAAGCTATGCAGACGCTGTGAAGGGC CGATTCACCATCTCCAGAGACAACGCCAAGAACACGCTGT ATCTTCAGATGAACAGCCTGAGAGCCGAGGACACGGCCGT GTATTATTGTGCGAGTGATCTAGTTCTAGTAGTTGGCGGGG GGGTCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCT CAG
42	PMX028 Heavy chain variable region amino acid sequence	EVQMVESGGDLVKPGGSLRLSCVASGFTFSDYHMSWVRQA PGKGLQWVAYITSGGSSTSYADAVKGRFTISRDNAKNTLYLQ MNSLRAEDTAVYYCASDLVLVVGGGVYWGQGTLVTVSS
43	PMX028 light chain variable region nucleotide sequence	TCCTATGAACTGACTCAGCCACCATCCGTGAATGTGACCCT GAGGGAGACGGCCCACATCACCTGTGGGGGAGACAGCAT TGGAAGTAAATATGTTCAATGGATCCAGCAGAATCCAGGCC AGGCCCCCGTGGTGATTATCTATAAAGATAGCAACAGGCC

		GACAGGGATCCCTGAGCGATTCTCTGGCGCCAACTCAGGG AACACGGCTACCCTGACCATCAGTGGGGCCCTGGCCGAA GACGAGGCTGACTATTACTGCCAGGTGGGGGACAGTGGTA CTAAGGCGGTATTCGGTGAAGGGACCCAGCTGACCGTCCT CG
44	PMX028 light chain variable region amino acid sequence	SYELTQPPSVNVTLRETAHITCGGDSIGSKYVQWIQQNPGQA PVVIIYKDSNRPTGIPERFSGANSGNTATLTISGALAEDEADYY CQVGDSGTKAVFGEGTQLTVL
45	PMX028 heavy chain CDR1	GFTFSDY
46	PMX028 heavy chain CDR2	TSGGSS
47	PMX028 heavy chain CDR3	CASDLVLVVGGGVYW
48	PMX028 light chain CDR1	GGDSIGSKYVQ
49	PMX028 light chain CDR2	KDSNRPT
50	PMX028 light chain CDR3	CQVGDSGTKAVF
51	PMX029 Heavy chain variable region nucleic acid sequence	GAGGTGCAGCTGGTGGAGTCTGGGGGAGACCTGGTGAAG CCTGGGGGGTCCCTGAGACTTTCCTGTGTGGCCTCTGGAT TCACCTTCAGTTCCTACCACATGAACTGGGTCCGCCAGGC TCCAGGGAAGGGGCTTCAGTGGGTCGCATACATTAACACT GGTGGAAGTCGCACAAGCTATGCAGACGCTGTGAAGGGC CGATTCACCATCTCCAGAGACAACGCCAAGAACACGTTGT ATCTTCAGATGAACAGCCTGAGAGCCGAGGACACGGCCGT GTATTACTGTGCGAATAACTACTGGGATAATTTTGACTCCT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
52	PMX029 Heavy chain variable region amino acid sequence	EVQLVESGGDLVKPGGSLRLSCVASGFTFSSYHMNWVRQAP GKGLQWVAYINTGGSRTSYADAVKGRFTISRDNAKNTLYLQM NSLRAEDTAVYYCANNYWDNFDSWGQGTLVTVSS

53	PMX029 light chain variable region nucleotide sequence	TCCTATGAGCTGACTCAGCCACCATCCGTGAATGTGACCC TGAGGGAGACGGCCCACATCACCTGTGGGGGAGACAGCA TTGGAAGTAAATATGTTCAATGGATCCAGCAGAATCCAGGC CAGGCCCCCGTGGTGATTATCTATAAAGATACCAACAGGC CGACAGGGATCCCTGAGCGATTCTCTGGCGCCAACTCAGG GAACACGGCTACCCTGACCATCAGTGGGGCCCTGGCCGA AGACGAGGCTGACTATTACTGCCAGGTGGGGGACAGTGGT ACTAAGGCTAGTGTGTTCGGCGGAGGCACCCATCTGACCG TCCTCG
54	PMX029 light chain variable region amino acid sequence	SYELTQPPSVNVTLRETAHITCGGDSIGSKYVQWIQQNPGQA PVVIIYKDTNRPTGIPERFSGANSGNTATLTISGALAEDEADYY CQVGDSGTKASVFGGGTHLTVL
55	PMX029 heavy chain CDR1	GFTFSSY
56	PMX029 heavy chain CDR2	NTGGSR
57	PMX029 heavy chain CDR3	CANNYWDNFDSW
58	PMX029 light chain CDR1	GGDSIGSKYVQ
59	PMX029 light chain CDR2	KDTNRPT
60	PMX029 light chain CDR3	CQVGDSGTKASVF
61	PMX030 Heavy chain variable region nucleic acid sequence	GAGGTGCAGCTGGTGGAGTCTGGGGGAGACCTGGTGAAG CCTGGGGGGTCCCTGAGACTTTCCTGTGTGGCCTCTGGAT TCACCTTCAGTAACTACCACATGAACTGGGTCCGCCAGGC TCCAGGGAAGGGACTTCAGTGGGTCGCATACGTTGTCAGT GGTGGAAGTACCACAAGCTATGCAGACGCTGTGAAGGGCC GATTCACCATCTCCAGAGACAACGCCAAGAACACACTGTAT CTTCAGATGAACAGCCTGAGAGCCGAGGACACGGCCGTGT ATTACTGTGCGAAGGGGACTAGTAGTTGGGGGGTTCCTAT

		GGACTACTGGGGCCATGGCACCTCACTCTTCGTGTCCTCA G
62	PMX030 Heavy chain variable region amino acid sequence	EVQLVESGGDLVKPGGSLRLSCVASGFTFSNYHMNWVRQAP GKGLQWVAYVVSGGSTTSYADAVKGRFTISRDNAKNTLYLQ MNSLRAEDTAVYYCAKGTSSWGVPMDYWGHGTSLFVSS
63	PMX030 light chain variable region nucleotide sequence	TCCTATGTGCTGACACAGCTGCCATCCGTGAGTGTGACCC TGAGGCAGACGGCCCGCATCACCTGTGGGGGAGACAGCA TTAGAAGTAAAAATGTTTACTGGTACCAGCAGAAGCTGGGC CAGGCCCCTGTACTGATTATCTATGATGATAGCAGCAGGC CGTCAGGGATCCCTGAGCGATTCTCCGGCGCCAACTCGG GGAACACGGCCACCCTGACCATCAGCGGGGCCCTGGCCG AGGATGAGGCTGACTATTACTGCCAGGTGTGGGACAGCAG TACTAGTGTGTTCGGCGGAGGCACCCATCTGACCGTCCTC G
64	PMX030 light chain variable region amino acid sequence	SYVLTQLPSVSVTLRQTARITCGGDSIRSKNVYWYQQKLGQA PVLIIYDDSSRPSGIPERFSGANSGNTATLTISGALAEDEADYY CQVWDSSTSVFGGGTHLTVL
65	PMX030 heavy chain CDR1	GFTFSNY
66	PMX030 heavy chain CDR2	VSGGST
67	PMX030 heavy chain CDR3	CAKGTSSWGVPMDYW
68	PMX030 light chain CDR1	GGDSIRSKNVY
69	PMX030 light chain CDR2	DDSSRPS
70	PMX030 light chain CDR3	CQVWDSSTSVF

71	PMX031 Heavy chain variable region nucleic acid sequence	GAGGTGCAGCTGGTGGAGTCTGGGGGAGACCTGGTGAAG CCTGGGGGGTCCCTGAGACTTTCCTGTGTGGCCTCTGGAT TCACCTTCAGTAACTACCACATGAACTGGGTCCGCCAGGC TCCAGGGAAGGGACTTCAGTGGGTCGCATACGTTGTCAGT GGTGGAACTACCACGACCTATGCAGACGCTGTGAAGGGCC GATTCACCATCTCCAGAGACAACGCCAAGAACACACTGTAT CTTCAGATGAACAGCCTGAGAGCCGAGGACACGGCCGTGT ATTACTGTGCGAAGGGGACTAGTACTTGGGGGGTTCCTAT GGACTACTGGGGCCATGGCACCTCACTCTTCGTGTCCTCA G
72	PMX031 Heavy chain variable region amino acid sequence	EVQLVESGGDLVKPGGSLRLSCVASGFTFSNYHMNWVRQAP GKGLQWVAYVVSGGTTTTYADAVKGRFTISRDNAKNTLYLQ MNSLRAEDTAVYYCAKGTSTWGVPMDYWGHGTSLFVSS
73	PMX031 light chain variable region nucleotide sequence	TCCTATGTGCTGACACAGCTGCCATCCGTGAGTGTGACCC TGAGGCAGACGGCCCGCATCACCTGTGGGGGAGACAGCA TTAGAAGTAAAAATGTTTACTGGTACCAGAAGAAGCTGGGC CAGGCCCCTGTACTGATTATCTATGATGATAGCAGCAGGC CGTCAGGGATCCCTGAGCGATTCTCCGGCGCCAACTCGG GGAACACGGCCACCCTGACCATCAGCGGGGCCCTGGCCG AGGATGAGGCTGACTATTACTGCCAGGTGTGGGACAGCAG TACTAGTGTGTTCGGCGGAGGCACCCATCTGACCGTCCTC G
74	PMX031 light chain variable region amino acid sequence	SYVLTQLPSVSVTLRQTARITCGGDSIRSKNVYWYQKKLGQA PVLIIYDDSSRPSGIPERFSGANSGNTATLTISGALAEDEADYY CQVWDSSTSVFGGGTHLTVL
75	PMX031 heavy chain CDR1	GFTFSNY
76	PMX031 heavy chain CDR2	VSGGTT
77	PMX031 heavy chain CDR3	CAKGTSTWGVPMDYW
78	PMX031 light chain CDR1	GGDSIRSKNVY

79	PMX031 light chain CDR2	DDSSRPS
80	PMX031 light chain CDR3	CQVWDSSTSVF
81	PMX032 Heavy chain variable region nucleic acid sequence	GAGGTGCAGCTGGTGGAGTCTGGGGGAGACCTGGTGAAG CCGGGGGGGTCCCTGAGACTTTCCTGTGTGGCCTCTGGAT TCACCTTCAGCAGTTATCACATGAGCTGGGTCCGCCAGGC TCCAGGGAAGGGGCTTCAGTGGGTCGCATACATTACCAGT GGTGGAAGAACCACAAGCTATGCAGACGCTGTGAAGGGC CGATTCATCATCTCCAGAGACAACGCCAAGAACACGTTGTA TCTTCAGATGAACAGCCTGAGAGCCGAGGACACGGCCGTG TATTACTGTGCGAGTGATCTGGTTCTAATATTAGGGGGGGC TGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA G
82	PMX032 Heavy chain variable region amino acid sequence	EVQLVESGGDLVKPGGSLRLSCVASGFTFSSYHMSWVRQAP GKGLQWVAYITSGGRTTSYADAVKGRFIISRDNAKNTLYLQM NSLRAEDTAVYYCASDLVLILGGADYWGQGTLVTVSS
83	PMX032 light chain variable region nucleotide sequence	TCCTATGAGCTGACTCAGCCACCATCCGTGAATGTGACCC TGAGGGAGACGGCCCACATCACCTGTGGGGGAGACAGCA TTGGAAGGAAATATGTTCAATGGATCCAGCAGAATCCAGG CCAGGCCCCCGTGGTGATTATCTATAAAGATAACAACAGG CCGACAGGGATCCCTGAGCGATTCTCTGGCGCCAACTCAG GGAACACGGCTACCCTGACCATCAGTGGGGCCCTGGCCG AAGACGAGGCTGACTATTACTGCCAGGTGGGGGACAGTG GTTCTAAGGCTGTGTTCGGCGGAGGCACCCACCTGACCGT CCTCG
84	PMX032 light chain variable region amino acid sequence	SYELTQPPSVNVTLRETAHITCGGDSIGRKYVQWIQQNPGQA PVVIIYKDNNRPTGIPERFSGANSGNTATLTISGALAEDEADYY CQVGDSGSKAVFGGGTHLTVL
85	PMX032 heavy chain CDR1	GFTFSSY
86	PMX032 heavy chain CDR2	TSGGRT

87	PMX032 heavy chain CDR3	CASDLVLILGGADYW
88	PMX032 light chain CDR1	GGDSIGRKYVQ
89	PMX032 light chain CDR2	KDNNRPT
90	PMX032 light chain CDR3	CQVGDSGSKAVF
91	PMX033 Heavy chain variable region nucleic acid sequence	GAGGTGCAGCTGGTGGAGTCTGGGGGAGACCTGGTGAAG CCTGGGGGGTCCCTGAGACTTTCCTGTGTGGCCTCTGGAT TCACCTTCAGTAGTTATCACATGAGCTGGGTCCGCCAGGC TCCAGGGAAGGGGCTTCAGTGGGTCGCATACATTACCAGT GGTGGAAGAACCACAAGCTATGCAGACGCTGTGAAGGGC CGATTCACCATCTCCAGAGACAATGCCAAGAACACGTTGTA TCTTCAGATGAAAAGCCTGAGAGCCGAGGACACGGCCGTG TATTACTGTGCGAGTGATCTGGTTCTAGTATTAGGGGGGG CTGAGTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTC AG
92	PMX033 Heavy chain variable region amino acid sequence	EVQLVESGGDLVKPGGSLRLSCVASGFTFSSYHMSWVRQAP GKGLQWVAYITSGGRTTSYADAVKGRFTISRDNAKNTLYLQM KSLRAEDTAVYYCASDLVLVLGGAEYWGQGTLVTVSS
93	PMX033 light chain variable region nucleotide sequence	TCCTATGAGCTGACTCAGCCACCATCCGTGAATGTGACCC TGAGGGAGACGGCCCACATCACCTGTGGGGGAGACAGCA TTGGAAGGAAATATGTTCAATGGATCCAGCAGAATCCAGG CCAGGCCCCCGTCGTGATTATCTATAAAGATAGCAACAGG CCGACAGGGATCCCTGAGCGATTCTCTGGCGCCAACTCAG GGAACACGGCTACCCTGACCATCAGTGGGGCCCTGGCCG AAGACGAGGCTGACTATTACTGCCAGGTGGGGGACAGTG GTTCTAAGGCTGTGTTCGGCGGAGGCACCCACCTGACCGT CCTCG

94	PMX033 light chain variable region amino acid sequence	SYELTQPPSVNVTLRETAHITCGGDSIGRKYVQWIQQNPGQA PVVIIYKDSNRPTGIPERFSGANSGNTATLTISGALAEDEADYY CQVGDSGSKAVFGGGTHLTVL
95	PMX033 heavy chain CDR1	GFTFSSY
96	PMX033 heavy chain CDR2	TSGGRT
97	PMX033 heavy chain CDR3	CASDLVLVLGGAEYW
98	PMX033 light chain CDR1	GGDSIGRKYVQ
99	PMX033 light chain CDR2	KDSNRPT
100	PMX033 light chain CDR3	CQVGDSGSKAVF
101	PMX034 Heavy chain variable region nucleic acid sequence	GAGGTGCAGCTGGTGGAGTCTGGGGGAGACCTGGTGAAG CCTGGGGGGTCCCTGAGACTTTCCTGTGTGGCCTCTGGAT TCACCTTCAGTAATTATCACATGAGCTGGGTCCGCCAGGCT CCAGGGAAGGGGCTTCAGTGGGTCGCATACATTGTCAGTG GTGGAAGTAGCACAACCTATGCAGACGCTGTGAAGGGCCG ATTCACCATCTCCAGAGACAACGCCAAGAACACGCTGTATC TTCAGATGACCAGCCTACGAGCCGAGGATACGGCCGTGTA TTACTGTGCGAGTGATCTGGTTCTACTAGTAGGGGGGGCT GACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
102	PMX034 Heavy chain variable region amino acid sequence	EVQLVESGGDLVKPGGSLRLSCVASGFTFSNYHMSWVRQAP GKGLQWVAYIVSGGSSTTYADAVKGRFTISRDNAKNTLYLQM TSLRAEDTAVYYCASDLVLLVGGADYWGQGTLVTVSS
103	PMX034 light chain variable region nucleotide sequence	TCCTATGAGCTGACTCAGCCACCATCCGTGAATGTGACCC TGAGGGAGACGGCCCACATCACCTGTGGGGGAGACAGCA TTGGAAGTAAATATGTTCAATGGATCCAGCAGAATCCAGGC CAGGCCCCCGTGGTGATTATCTATAAAGATAGCAACAGGC CGACAGGGATCCCTGAGCGATTCTCTGGCGCCAACTCAGG

		GAACACGGCTACCCTGACCATCAGTGGGGCCCTGGCCGA AGACGAGGCTGACTATTACTGCCAGGTGGGGGACAGTGGT ACTAAGGCTGTGTTCGGCGGAGGCACCCACCTGACCGTCC TCG
104	PMX034 light chain variable region amino acid sequence	SYELTQPPSVNVTLRETAHITCGGDSIGSKYVQWIQQNPGQA PVVIIYKDSNRPTGIPERFSGANSGNTATLTISGALAEDEADYY CQVGDSGTKAVFGGGTHLTVL
105	PMX034 heavy chain CDR1	GFTFSNY
106	PMX034 heavy chain CDR2	VSGGSS
107	PMX034 heavy chain CDR3	CASDLVLLVGGADYW
108	PMX034 light chain CDR1	GGDSIGSKYVQ
109	PMX034 light chain CDR2	KDSNRPT
110	PMX034 light chain CDR3	CQVGDSGTKAVF
111	PMX035 Heavy chain variable region nucleic acid sequence	GAGGTGCAGCTGGTGGAGTCTGGGGGAGACCTGGTGAAG CCTGGGGGGTCCCTGAGACTCTCCTGTGTGGCCTCTGGAT TCACCTTCAGTAACTTCGAAATGTACTGGGTCCGCCAGGCT CCAGGGAAAGGGCTGGAGTGGGTCGCAAGGATTTATAAGA GTGGAAGTACCACATACCATTCAGAACGTGTAAAGGGCCG ATTCACCATCTCCAAAGACAGCGCCACGAACATGGCGTTT CTGCAGATGAACAGCCTGAGAGCCGAGGACACGGCCGTA TATTACTGTACGAGTGCTAGTTCTACTGGTTGGCGTTTTGA CTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
112	PMX035 Heavy chain variable region amino acid sequence	EVQLVESGGDLVKPGGSLRLSCVASGFTFSNFEMYWVRQAP GKGLEWVARIYKSGSTTYHSERVKGRFTISKDSATNMAFLQM NSLRAEDTAVYYCTSASSTGWRFDYWGQGTLVTVSS

113	PMX035 light chain variable region nucleotide sequence	TCCTATGTGCTGACACAGTTGCCATCCGTGAGTGTGACCC TGAGGCAGACGGCCCGCATCACCTGTGGGGGAGACAGCA TTGGAAGAAAAAATGTTTGCTGGTTCCAGCAGAAGCTGGG CCAGGCCCCTGTACTGATTATCTATGATGATAACAGCAGGC CGTCAGGGATCCCTGAGCGATTCTCCGGCGCCAACTCGG GGAACACGGCCACCCTGACCATCAGCGGGGCCCTGGCCG AGGATGAGGCTGACTATTACTGCCAGGTGTGGGACAGCAG TACTGGTATATTCGGCGGAGGCACCCATCTGACCGTCCTC G
114	PMX035 light chain variable region amino acid sequence	SYVLTQLPSVSVTLRQTARITCGGDSIGRKNVCWFQQKLGQA PVLIIYDDNSRPSGIPERFSGANSGNTATLTISGALAEDEADYY CQVWDSSTGIFGGGTHLTVL
115	PMX035 heavy chain CDR1	GFTFSNF
116	PMX035 heavy chain CDR2	YKSGST
117	PMX035 heavy chain CDR3	CTSASSTGWRFDYW
118	PMX035 light chain CDR1	GGDSIGRKNVC
119	PMX035 light chain CDR2	DDNSRPS
120	PMX035 light chain CDR3	CQVWDSSTGIF
121	PMX036 Heavy chain variable region nucleic acid sequence	GAGGTGCAGTTGGTGGAGTCTGGGGGAGACCTGGTGAAG CCTGGGGGGTCCCTGAGACTTTCCTGTGTGGCCTCTGGAT TCACCTTCAGTAGTTATCACATGAGCTGGGTCCGCCAGGC TCCAGGGAAGGGGCTTCAGTGGGTCGCATACATTACCAGT GGTGGAAGAACCACAAGCTATGCAGACGCTGTGAAGGGC CGATTCACCATCTCCAGAGACAACGCCAAGAACACGCTGT ATCTTCAGATGAACAGCCTGAGAGCCGAGGACACGGCCGT GTATTACTGTGCGAGTGATCTGGTTCTAGTATTAGGGGGG

		GCTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCT CAG
122	PMX036 Heavy chain variable region amino acid sequence	EVQLVESGGDLVKPGGSLRLSCVASGFTFSSYHMSWVRQAP GKGLQWVAYITSGGRTTSYADAVKGRFTISRDNAKNTLYLQM NSLRAEDTAVYYCASDLVLVLGGADYWGQGTLVTVSS
123	PMX036 light chain variable region nucleotide sequence	TCCTATGAGCTGACTCAGCCACCATCCGTGAATGTGACCC TGAGGGAGACGGCCCACATCACCTGTGGGGGAGACAGCA TTGGAAGGAAATATGTTCAATGGATCCAGCAGAATCCAGG CCAGGCCCCCGTGGTGATTATCTATAAAGATACCAACAGG CCGACAGGGATCCCTGAGCGATTCTCTGGCGCCAACTCAG GGAACACGGCTACCCTGACCATCAGTGGGGCCCTGGCCG AAGACGAGGCTGACTATTACTGCCAGGTGGGGGACAGTG GTACTAAGGCTGTGTTCGGCGGAGGCACCCACCTGACCGT CCTCG
124	PMX036 light chain variable region amino acid sequence	SYELTQPPSVNVTLRETAHITCGGDSIGRKYVQWIQQNPGQA PVVIIYKDTNRPTGIPERFSGANSGNTATLTISGALAEDEADYY CQVGDSGTKAVFGGGTHLTVL
125	PMX036 heavy chain CDR1	GFTFSSY
126	PMX036 heavy chain CDR2	TSGGRT
127	PMX036 heavy chain CDR3	CASDLVLVLGGADYW
128	PMX036 light chain CDR1	GGDSIGRKYVQ
129	PMX036 light chain CDR2	KDTNRPT
130	PMX036 light chain CDR3	CQVGDSGTKAVF

131	PMX037 Heavy chain variable region nucleic acid sequence	GAGGTGCAGCTGCTGGAGTCTGGGGGAGACCTGGTGAAG CCTGGGGGGTCCCTGAGACTCTCCTGTGTGGCCTCTGGAT TCACCTTCAGTAACTACGAAATGTACTGGGTCCGCCAGGC TCCAGGGAAAGGGCTGGAGTGGGTCGCAAGGTTTTATGAG AGTGGAAGTACCACATACTCTGCAGAAGCTGTTCCGGGCC GATTCACCATCTCCAGAGACAACGCCAAGAACATGGCCTA TCTGCAGATGAACAGCCTGAGAGCCGAGGACACGGCCGT ATATTACTGTGCGAGTGCTAGTTCTAGTTCTTGGCGTTTTG ACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
132	PMX037 Heavy chain variable region amino acid sequence	EVQLLESGGDLVKPGGSLRLSCVASGFTFSNYEMYWVRQAP GKGLEWVARFYESGSTTYSAEAVPGRFTISRDNAKNMAYLQ MNSLRAEDTAVYYCASASSSSWRFDYWGQGTLVTVSS
133	PMX037 light chain variable region nucleotide sequence	TCCTATGTGCTGACACAGCTGCCATCCGTGAGTGTGACCC TGGGGCAGACGGCCCGCATCACCTGTGGGGGAGACAGCA TTGGAAGTAAAAATGTTTACTGGTTCCAGCAGAAGCTGGGC CAGGCCCCTGTACTGATTATCTATGATGATCGCAGCAGGC CGTCAGGGATCCCTGAGCGATTCTCCGGCGCCAACTCGG GGAACACGGCCACCCTGACCATCAGCGGGGCCCTGGCCG AGGATGAGGCTGACTATTACTGCCAGGTGTGGGACAGCAG TACTGGTGTGTTCGGCGGAGGCACCCATCTGACCGTCCTC G
134	PMX037 light chain variable region amino acid sequence	SYVLTQLPSVSVTLGQTARITCGGDSIGSKNVYWFQQKLGQA PVLIIYDDRSRPSGIPERFSGANSGNTATLTISGALAEDEADYY CQVWDSSTGVFGGGTHLTVL
135	PMX037 heavy chain CDR1	GFTFSNY
136	PMX037 heavy chain CDR2	YESGST
137	PMX037 heavy chain CDR3	CASASSSSWRFDYW
138	PMX037 light chain CDR1	GGDSIGSKNVY

139	PMX037 light chain CDR2	DDRSRPS
140	PMX037 light chain CDR3	CQVWDSSTGVF
141	PMX038 Heavy chain variable region nucleic acid sequence	GAGGTGCAGCTGGTGGAGTCTGGGGGAGACCTGGTGAAG CCTGGGGGGTCCCTGAGACTTTCCTGTGTGGCCTCTGGAT TCACCTTCAGTAGTTATCACATGAGCTGGGTCCGCCAGGC TCCAGGGAAGGGGCTTCAGTGGGTCGCATACATTACCAGT GGTGGAAGAACCACAAGCTATGCAGACGCTGTGAAGGGC CGATTCACCATCTCCAGAGACAATGCCAAGAACACGTTGTA TCTTCAGATGAAAAGCCTGAGAGCCGAGGACACGGCCGTG TATTACTGTGCGAGGGATCTGGTTCTAGTATTAGGGGGGG CTGAGTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTC AG
142	PMX038 Heavy chain variable region amino acid sequence	EVQLVESGGDLVKPGGSLRLSCVASGFTFSSYHMSWVRQAP GKGLQWVAYITSGGRTTSYADAVKGRFTISRDNAKNTLYLQM KSLRAEDTAVYYCARDLVLVLGGAEYWGQGTLVTVSS
143	PMX038 light chain variable region nucleotide sequence	TCCTATGAGCTGACTCAGCCACCATCCGTGAATGTGACCC TGAGGGAGACGGCCCACATCACCTGTGGGGGAGACAGCA TTGGAAGGAAATATGTTCAATGGATCCAGCAGAATCCAGG CCAGGCCCCCGTCGTGATTATCTATAAAGATAGCAACAGG CCGACAGGGATCCCTGAGCGATTCTCTGGCGCCAACTCAG GGAACACGGCTACCCTGACCATCAGTGGGGCCCTGGCCG AAGACGAGGCTGACTATTACTGCCAGGTGGGGGACAGTG GTTCTAAGGCTGTGTTCGGCGGAGGCACCCACCTGACCGT CCTCG
144	PMX038 light chain variable region amino acid sequence	SYELTQPPSVNVTLRETAHITCGGDSIGRKYVQWIQQNPGQA PVVIIYKDSNRPTGIPERFSGANSGNTATLTISGALAEDEADYY CQVGDSGSKAVFGGGTHLTVL
145	PMX038 heavy chain CDR1	GFTFSSY
146	PMX038 heavy chain CDR2	TSGGRT

147	PMX038 heavy chain CDR3	CARDLVLVLGGAEYW
148	PMX038 light chain CDR1	GGDSIGRKYVQ
149	PMX038 light chain CDR2	KDSNRPT
150	PMX038 light chain CDR3	CQVGDSGSKAVF
151	PMX039 Heavy chain variable region nucleic acid sequence	GAGGTGCAGCTGGTGGAGTCTGGGGGAGACCTTGTGAAA CCTGAGGGGTCCCTGAGACTCTCCTGTGTGGTCTCTGGCT TCACCTTCATTACCAACGACATGAGCTGGGTCCGCCAGGC TCCAGGGAAGGGGCTGCAGTGGGTCGCATACATTACCAAT GATGGAAGGTACACAAGTTACACAGACGCTGTGAAGGGCC GATTCACCATCTCCAGAGACAATGCCAAGAACACGCTGTAT CTGCAGATGAACAGCCTGAGAACTGAGGACACAGCCGTTT ATTACTGTGCGAAGCATAGTAGCAACTACTACAGGGGGAG GTTTGGTATGGACTACTGGGGCCATGGCACCTCACTCTTC GTGTCCTCAG
152	PMX039 Heavy chain variable region amino acid sequence	EVQLVESGGDLVKPEGSLRLSCVVSGFTFITNDMSWVRQAP GKGLQWVAYITNDGRYTSYTDAVKGRFTISRDNAKNTLYLQM NSLRTEDTAVYYCAKHSSNYYRGRFGMDYWGHGTSLFVSS
153	PMX039 light chain variable region nucleotide sequence	TCCTATGTGCTGACACAGCTGCCATCCAAAAATGTGACCCT GAAGCAGCCGGCCCACATCACCTGTGGGGGAGACAACATT GGAAGTAAAAGTGTTCACTGGTACCAGCAGAAGCTGGGCC AGGCCCCTGTACTGATTATCTATTATGATAGCACCAGGCCG ACAGGGATCCCTGAGCGATTCTCCGGCGCCAACTCGGGG AACACGGCCACCCTGACCATCAGCGGGGCCCTGGCCGAG GACGAGGCTGACTATTACTGCCAGGTGTGGGACAGCAGTG CTAGTGTGTTCGGCGGAGGCACCCATCTGACCGTCCTCG
154	PMX039 light chain variable region amino acid sequence	SYVLTQLPSKNVTLKQPAHITCGGDNIGSKSVHWYQQKLGQA PVLIIYYDSTRPTGIPERFSGANSGNTATLTISGALAEDEADYY CQVWDSSASVFGGGTHLTVL

155	PMX039 heavy chain CDR1	GFTFITN
156	PMX039 heavy chain CDR2	TNDGRY
157	PMX039 heavy chain CDR3	CAKHSSNYYRGRFGMDYW
158	PMX039 light chain CDR1	GGDNIGSKSVH
159	PMX039 light chain CDR2	YDSTRPT
160	PMX039 light chain CDR3	CQVWDSSASVF
161	PMX040 Heavy chain variable region nucleic acid sequence	GAGGTGCAGCTGGTGGAGTCTGGGGGAGACCTGGTGAAG CCTGGGGGGTCCCTGAGACTCTCCTGTGTGGCCTCTGGAT TCACCTTCAGTAACTTCGAAATGTACTGGGTCCGCCAGGCT CCAGGGAAAGGGCTGGAGTGGGTCGCAAGGATTTATGAG AGTGGAACTACCACATACCATGCAGAAGGTGTAAAGGGCC GATTCACCATTTCCAAAGACAACGTCAAGAACATGGCGTAT CTGCAGATGAACAGCCTGAGAGCCGAGGACACGGCCGTA TATTACTGTACGAGTGCTAGTTCTAGTAGTTGGCGTTTTGA CTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
162	PMX040 Heavy chain variable region amino acid sequence	EVQLVESGGDLVKPGGSLRLSCVASGFTFSNFEMYWVRQAP GKGLEWVARIYESGTTTYHAEGVKGRFTISKDNVKNMAYLQM NSLRAEDTAVYYCTSASSSSWRFDYWGQGTLVTVSS
163	PMX040 light chain variable region nucleotide sequence	TCCTATGTGCTGACACAGCTGCCATCCGTGAGTGTGACCC TGAGGCAGACGGCCCGCATCACCTGTGGGGGAGACAGCA TTGGAAGAAAAAATGTTTGCTGGTTCCAGCAGAAGCTGGG CCAGGCCCCTATACTGATTATCTATGATGATAGCAGCAGGC CGTCAGGGATCCCTGAGCGATTCTCCGGCGCCAACTCGG GGAACACGGCCACCCTGACCATCAGCGGGGCCCTGGCCG AGGATGAGGCTGACTATTACTGCCAGGTGTGGGACAGCAG

		TACTGGTATATTCGGCGGAGGCACCCATCTGACCGTCCTC G
164	PMX040 light chain variable region amino acid sequence	SYVLTQLPSVSVTLRQTARITCGGDSIGRKNVCWFQQKLGQA PILIIYDDSSRPSGIPERFSGANSGNTATLTISGALAEDEADYY CQVWDSSTGIFGGGTHLTVL
165	PMX040 heavy chain CDR1	GFTFSNF
166	PMX040 heavy chain CDR2	YESGTT
167	PMX040 heavy chain CDR3	CTSASSSSWRFDYW
168	PMX040 light chain CDR1	GGDSIGRKNVC
169	PMX040 light chain CDR2	DDSSRPS
170	PMX040 light chain CDR3	CQVWDSSTGIF
171	PMX041 Heavy chain variable region nucleic acid sequence	GAGGTGCATCTGGTGGAGTCTGGGGGAGACCTTGTGAAAC CTGAGGGGTCCCTGAGACTCTCCTGTGTGGTCTCTGGCTT CACCTTCACTACTAACGACATGAGCTGGGTCCGCCAGGCT CCAGGGAAGGGGCTGCAGTGGGTCGCATACATTACCAGT GATGGAAGGATCACAACTTACACAGACGCTGTGAAGGGCC GATTCACCATCTCCAGAGACAATGCCAAGAACACGCTGTAT CTGCAGATGAACAGCCTGAGAACTGAGGACACAGCCGTGT ATTATTGTGCGAAACATAGTAGTAACTGGTCCAGGGGGAG GTTTGGTTTGGACTACTGGGGCCATGGCACCTCACTCTTC GTGTCCTCAG
172	PMX041 Heavy chain variable region amino acid sequence	EVHLVESGGDLVKPEGSLRLSCVVSGFTFTTNDMSWVRQAP GKGLQWVAYITSDGRITTYTDAVKGRFTISRDNAKNTLYLQMN SLRTEDTAVYYCAKHSSNWSRGRFGLDYWGHGTSLFVSS

173	PMX041 light chain variable region nucleotide sequence	TCCTATGTGCTGACACAGCTGCCATCCAAAAATGTGACCCT GAAGCAGCCGGCCCACATCACCTGTGGGGGAGACAACATT GGAAGTAAAAGTGTTCACTGGTACCAGCAGAAGCTGGGCC AGGCCCCTGTACTGATTATCTATTATGATAGCAGCAGGCCG ACAGGGATCCCTGAGCGATTCTCCGGCGCCAACTCGGGG AACACGGCCACCCTGACCATCAGCGGGGCCCTGGCCGAG GACGAGGCTGACTATTACTGCCAGGTGTGGGACAACAGTG CTAGTGTGTTCGGCGGAGGCACCCATCTGACCGTCCTCG
174	PMX041 light chain variable region amino acid sequence	SYVLTQLPSKNVTLKQPAHITCGGDNIGSKSVHWYQQKLGQA PVLIIYYDSSRPTGIPERFSGANSGNTATLTISGALAEDEADYY CQVWDNSASVFGGGTHLTVL
175	PMX041 heavy chain CDR1	GFTFTTN
176	PMX041 heavy chain CDR2	TSDGRI
177	PMX041 heavy chain CDR3	CAKHSSNWSRGRFGLDYW
178	PMX041 light chain CDR1	GGDNIGSKSVH
179	PMX041 light chain CDR2	YDSSRPT
180	PMX041 light chain CDR3	CQVWDNSASVF
181	PMX042 Heavy chain variable region nucleic acid sequence	GAAGTGCAGCTGGTGGAGTCTGGGGGAGACCTCGTGAAG CCTGGGGGGTCCCTGAGACTTTCCTGTGTGGCCTCTGGAT TCACCTTCAGTAGTTATCACATGAGCTGGGTCCGCCAGGC TCCAGGGAAGGGGCTTCAGTGGGTCGCATACATTACCAGT GGTGGAAGTACCACAAGCTATGCAGACGCTGTGAAGGGCC GATTCACCATCTCCAGAGACAACGCCAAGAACACGCTGTA TCTTCAGATGGACAGCCTGAGAGCCGACGACACGGCCGT GTATTACTGTGCGAGTGATCTGGTTCTGCTATTAGGGGGG

		GCTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCT CAG
182	PMX042 Heavy chain variable region amino acid sequence	EVQLVESGGDLVKPGGSLRLSCVASGFTFSSYHMSWVRQAP GKGLQWVAYITSGGSTTSYADAVKGRFTISRDNAKNTLYLQM DSLRADDTAVYYCASDLVLLLGGADYWGQGTLVTVSS
183	PMX042 light chain variable region nucleotide sequence	TCCTATGAGCTGACTCAGCCACCATCCGTGAATGTGACCC TGAGGGAGACGGCCCACATCACCTGTGGGGGAGACAGCA TTGGAAGGAAATATGTTCAATGGATCCAGCAGCATCCAGG CCAGGCCCCCGTGGTGATTATCTATAAAGATTACAACAGG CCGACAGGGATCCCTGAGCGATTCTCTGGCGCCAACTCAG GGAACACGGCTACCCTGACCATCAGTGGGGCCCTGGCCG AAGACGAGGCTGACTATTACTGCCAGGTGGGGGACAGTG GTACTAAGGCTGTGTTCGGCGGAGGCACCCACCTGACCGT CCTCG
184	PMX042 light chain variable region amino acid sequence	SYELTQPPSVNVTLRETAHITCGGDSIGRKYVQWIQQHPGQA PVVIIYKDYNRPTGIPERFSGANSGNTATLTISGALAEDEADYY CQVGDSGTKAVFGGGTHLTVL
185	PMX042 heavy chain CDR1	GFTFSSY
186	PMX042 heavy chain CDR2	TSGGST
187	PMX042 heavy chain CDR3	CASDLVLLLGGADYW
188	PMX042 light chain CDR1	GGDSIGRKYVQ
189	PMX042 light chain CDR2	KDYNRPT
190	PMX042 light chain CDR3	CQVGDSGTKAVF

191	PMX043 Heavy chain variable region nucleic acid sequence	GAGGTGCAGCTGGTGGAGTCTGGGGGAGACCTTGTGAAA CCTGAGGGGTCCCTGAGACTCTCCTGTGTGGTCTCTGGCT TCACCTTCAGTAGCTACGACATGAGCTGGGTCCGCCAGGC TCCAGGGAAGGGGCTGCAGTGGGTCGCATACATCACCAAT GACGGAAGGTACACAAGTTACACAGACGCTGTGAAGGGCC GATTCACCATCTCCAGAGACAATGCCAAGAACACGCTGTAT CTGCAGATGAACAGCCTGAGAACTGAGGACACAGCCATCT ATTACTGTGCGAAGCATGGTAGCAGCTGGTCCAGGGGGAG ATTTGCTATGGACTACTGGGGCCAAGGCACCTCACTCTTC GTGTCCTCAG
192	PMX043 Heavy chain variable region amino acid sequence	EVQLVESGGDLVKPEGSLRLSCVVSGFTFSSYDMSWVRQAP GKGLQWVAYITNDGRYTSYTDAVKGRFTISRDNAKNTLYLQM NSLRTEDTAIYYCAKHGSSWSRGRFAMDYWGQGTSLFVSS
193	PMX043 light chain variable region nucleotide sequence	TCCTATGTGCTGACACAGCTGCCATCCAAAAATGTGACCCT GAACCAGCCGGCCCACATCACCTGTGGGGGAGACAGCAT TGGAACTAAAAGTGTTCACTGGTACCAGCAGAAGCTGGGC CAGGCCCCTGTCCTGATTATCTTTTATGATAGCAGCAGGCC GACAGGGATCCCTGAGCGATTCTCCGGCGCCAACTCGGG GAACACGGCCACCCTGACCATCAGCGGGGCCCTGGCCGA GGACGAGGCTGACTATTACTGCCAGGTGTGGGACAGCAAT GCTAGTGTGTTCGGCGGAGGCACCCATCTGACCGTCCTCG
194	PMX043 light chain variable region amino acid sequence	SYVLTQLPSKNVTLNQPAHITCGGDSIGTKSVHWYQQKLGQA PVLIIFYDSSRPTGIPERFSGANSGNTATLTISGALAEDEADYY CQVWDSNASVFGGGTHLTVL
195	PMX043 heavy chain CDR1	GFTFSSY
196	PMX043 heavy chain CDR2	TNDGRY
197	PMX043 heavy chain CDR3	CAKHGSSWSRGRFAMDYW
198	PMX043 light chain CDR1	GGDSIGTKSVH

199	PMX043 light chain CDR2	YDSSRPT
200	PMX043 light chain CDR3	CQVWDSNASVF
201	PMX044 Heavy chain variable region nucleic acid sequence	GAGGTGCAGCTGGTGGAGTCTGGGGGAGACCCTGTGAAA CCTGAGGGGTCCCAGAGACTCTCCTGTGTGGTCTCTGGCT TCACCTTCAGTAGCTACGACATGAGCTGGGTCCGCCAGGC TCCAGGGAAGGGGCTGCAGTGGGTCGCATACATTACCAGT GATGGAAGGAGCACAAGTTACACAGACGCTGTGAAGGGCC GATTCACCATCTCCAGAGACAATGCCAGGAACACGCTGTTT CTGCAGATGAACAGCCTGAGAACTGAGGACACAGCCGTGT ATTACTGTGCGAGGCATAGTAGCAGCTGGTCCAGGGGGAG GTTTGGTATGGACTACTGGGGCCATGGCACCTCGCTCTTC GTGTCCTCAG
202	PMX044 Heavy chain variable region amino acid sequence	EVQLVESGGDPVKPEGSQRLSCVVSGFTFSSYDMSWVRQA PGKGLQWVAYITSDGRSTSYTDAVKGRFTISRDNARNTLFLQ MNSLRTEDTAVYYCARHSSSWSRGRFGMDYWGHGTSLFVS S
203	PMX044 light chain variable region nucleotide sequence	TCCTATGTGCTGACACAGCTGCCATCCAAAAATGTGACCCT GAAGCAGCCGGCCCACATCACCTGTGGGGGAGACAACATT GGAAGTAAAAGTGTTCACTGGTACCAGCAGAAGCTGGGCC AGGCCCCTGTACTGATTATCTATTATGATAGCAGCAGGCCG ACAGGGATCCCTGAGCGATTCTCCGGCGCCAACTCGGGG AACACGGCCACCCTGACCATCAGCGGGGCCCTGGCCGAG GACGAGGCTGACTATTACTGCCAGGTGTGGGACAGCAGTG CTGGTGTGTTCGGCGGAGGCACCCATCTGACCGTCCTCG
204	PMX044 light chain variable region amino acid sequence	SYVLTQLPSKNVTLKQPAHITCGGDNIGSKSVHWYQQKLGQA PVLIIYYDSSRPTGIPERFSGANSGNTATLTISGALAEDEADYY CQVWDSSAGVFGGGTHLTVL
205	PMX044 heavy chain CDR1	GFTFSSY
206	PMX044 heavy chain CDR2	TSDGRS

207	PMX044 heavy chain CDR3	CARHSSSWSRGRFGMDYW
208	PMX044 light chain CDR1	GGDNIGSKSVH
209	PMX044 light chain CDR2	YDSSRPT
210	PMX044 light chain CDR3	CQVWDSSAGVF
211	PMX045 Heavy chain variable region nucleic acid sequence	GAGGTGCAGCTGGTGGAGTCTGGGGGAGACCTGGTGAAG CCTGGGGGGTCCCTGAGACTTTCCTGTGTGGCCTCTGGAT TCACCTTCAGTAGTTATCACATGACCTGGGTCCGCCAGGC TCCAGGGAAGGGGCTTCAGTGGGTCGCATACATTACCAGT GGTGGAATTACCACAAGCTATGCAGACGCTGTGAAGGGCC GATTCACCATCTCCAGAGACAACGCCAAGAACACGCTGTA TCTTCAGATGAGCAGCCTGAGAGCCGAGGACACGGCCATG TATTACTGTGCGAGGGATCTGGTTCTACTATTAGGGGGGG CTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTC AG
212	PMX045 Heavy chain variable region amino acid sequence	EVQLVESGGDLVKPGGSLRLSCVASGFTFSSYHMTWVRQAP GKGLQWVAYITSGGITTSYADAVKGRFTISRDNAKNTLYLQMS SLRAEDTAMYYCARDLVLLLGGADYWGQGTLVTVSS
213	PMX045 light chain variable region nucleotide sequence	TCCTATGAGCTGACTCAGCCACCATCCGTGAATGTGACCC TGAGGGAGACGGCCCACATCACCTGTGGGGGAGACAGCA TTGGAAGGAAATATGTTCAATGGATCCAGCAGAATCCAGG CCAGGCCCCCGTGGTGATTATCTATAAAGATAGCAACAGG CCGACAGGGATCCCTGAGCGATTCTCTGGCGCCAACTCAG GGAACACGGCTACCCTGACCATCAGTGGGGCCCTGGCCG AAGACGAGGCTGACTATTACTGCCAGGTGGGGGACAGTG GTACTAAGGCTGTGTTCGGCGGAGGCACCCACCTGACCGT CCTCG
214	PMX045 light chain variable region amino acid sequence	SYELTQPPSVNVTLRETAHITCGGDSIGRKYVQWIQQNPGQA PVVIIYKDSNRPTGIPERFSGANSGNTATLTISGALAEDEADYY CQVGDSGTKAVFGGGTHLTVL

215	PMX045 heavy chain CDR1	GFTFSSY
216	PMX045 heavy chain CDR2	TSGGIT
217	PMX045 heavy chain CDR3	CARDLVLLLGGADYW
218	PMX045 light chain CDR1	GGDSIGRKYVQ
219	PMX045 light chain CDR2	KDSNRPT
220	PMX045 light chain CDR3	CQVGDSGTKAVF
221	PMX046 Heavy chain variable region nucleic acid sequence	GAGGTGCAGCTGGTGGAGTCTGGGGGAGACCTTGTGAAA CCTGAGGGGTCCCTGAGACTCTCCTGTGTGGTCGCTGGCT TCACCTTCAATAGCTACGACATGAGCTGGGTCCGCCAGGC TCCAGGGAAGGGGCTGCAGTGGGTCGCATACATTACCAGT GATGGAAGGTTCACAAGTTACACAGACGCTGTGAAGGGCC GATTCACCATCTCCAGAGACAATGCCAAGAACACGCTCTAT CTGCAGATGAGCAGCCTGAGAACTGAGGACACAGCCGTGT ATTACTGTGCGAGACATAGTAGCAGCTGGTACAGGGGGAG GTTTGGTATGGACTTCTGGGGCCATGGCACCTCACTCTTC GTGTCCTCAG
222	PMX046 Heavy chain variable region amino acid sequence	EVQLVESGGDLVKPEGSLRLSCVVAGFTFNSYDMSWVRQAP GKGLQWVAYITSDGRFTSYTDAVKGRFTISRDNAKNTLYLQM SSLRTEDTAVYYCARHSSSWYRGRFGMDFWGHGTSLFVSS
223	PMX046 light chain variable region nucleotide sequence	TCCTATGTGCTGACACAGCTGCCATCCAAAAATGTGACCCT GAAGCAGCCGGCCCACATCACCTGTGGGGGAGACAACATT GGAAGTAAAAGTGTTCACTGGTACCAGCAGAAGCTGGGCC AGGCCCCTATACTGATTATCTATTATGATAGCAGCAGGCCG ACAGGGATCCCTGAGCGATTCTCCGGCGCCAACTCGGGG AACACGGCCACCCTGACCATCAGCGGGGCCCTGGCCGAG

		GACGAGGCTGACTATTACTGCCAGGTGTGGGACAGCAGTG CTAGTGTGTTCGGCGGAGGCACCCATCTGACCGTCCTCG
224	PMX046 light chain variable region amino acid sequence	SYVLTQLPSKNVTLKQPAHITCGGDNIGSKSVHWYQQKLGQA PILIIYYDSSRPTGIPERFSGANSGNTATLTISGALAEDEADYYC QVWDSSASVFGGGTHLTVL
225	PMX046 heavy chain CDR1	GFTFNSY
226	PMX046 heavy chain CDR2	TSDGRF
227	PMX046 heavy chain CDR3	CARHSSSWYRGRFGMDFW
228	PMX046 light chain CDR1	GGDNIGSKSVH
229	PMX046 light chain CDR2	YDSSRPT
230	PMX046 light chain CDR3	CQVWDSSASVF
231	PMX047 Heavy chain variable region nucleic acid sequence	GAGGTGCAGCTGGTGGAGTCTGGGGGAGACCTGGTGAAG CCTGGGGGGTCCCTGAGACTGTCCTGTGTGGCCTCTGGAT TCATCTTCAGTAGCTACAGCATGAGCTGGGTCCGCCAGGC TCCTGAGAAGGGGCTGCAGTTGGTCGCAGGTATTAACAGC GCTGGAAGTAGCACGTACTACACAGACGCTGTGAAGGGCC GATTCACCATCTCCAGAGACAACGCCAAGAACACAGTGTAT CTGCAGATGAACAGCCTGAGAGCCGAGGACACGGCCATTT ATTACTGTGCAAAGCGTTGGGTTTTTGACTTCTGGGGCCAG GGAACCCTGGTCACCGTCTCCTCAG
232	PMX047 Heavy chain variable region amino acid sequence	EVQLVESGGDLVKPGGSLRLSCVASGFIFSSYSMSWVRQAP EKGLQLVAGINSAGSSTYYTDAVKGRFTISRDNAKNTVYLQM NSLRAEDTAIYYCAKRWVFDFWGQGTLVTVSS

233	PMX047 light chain variable region nucleotide sequence	CATATTGTCATGACACAGACCCCACTGTCCCTGTCCGTCAG CCCTGGAGAGCCGGCCTCCATCTCCTGCAAGGCCAGTCA GAGCCTCCTGCTCAGTTATGGAAACACCTATTTGTATTGGT TCCGACAGAAGCCAGGCCAGTCTCCACAGCGTTTGATCTA TAAGGTCTCCAACAGAGACCCTGGGGTCCCAGACAGGTTC AGTGGCAGCGGGTCAGGGACAGATTTCACCCTGAGAATCA GCAGAGTGGAGGCTGATGATGCTGGAGTTTATTACTGCGG GCAAGGTATACAAGATCCGTTCACTTTTGGCCAAGGGACC AAACTGGAGATCAAAC
234	PMX047 light chain variable region amino acid sequence	HIVMTQTPLSLSVSPGEPASISCKASQSLLLSYGNTYLYWFRQ KPGQSPQRLIYKVSNRDPGVPDRFSGSGSGTDFTLRISRVEA DDAGVYYCGQGIQDPFTFGQGTKLEIK
235	PMX047 heavy chain CDR1	GFIFSSY
236	PMX047 heavy chain CDR2	NSAGSS
237	PMX047 heavy chain CDR3	CAKRWVFDFW
238	PMX047 light chain CDR1	KASQSLLLSYGNTYLY
239	PMX047 light chain CDR2	KVSNRDP
240	PMX047 light chain CDR3	CGQGIQDPFTF
241	PMX048 Heavy chain variable region nucleic acid sequence	GAGGTGCAGCTGGTGGAGTCTGGGGGAGACCTGGTGAAG CCTGGGGGGTCCCTGAGACTCTCCTGTGTGGCCTCTGGAT TCACCTTCAATAACTACGAAATGTACTGGGTCCGCCAGGCT CCAGGGAAAGGGCTGGAGTGGGTCGCAAGGATTTATGAG AGTGGAACAACCACATATTCTGCAGAAGCTGATACGGGCC GATTCACCATCTCCAGAGACAACGCCAAGAACATGGTTTTT CTGCAGATGAACAGCCTGAGAGCCGAGGACACGGCCGTC

		TATTACTGTGCGAGTGCTAGTTCTAGTACTTGGCGTTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
242	PMX048 Heavy chain variable region amino acid sequence	EVQLVESGGDLVKPGGSLRLSCVASGFTFNNYEMYWVRQAPGKGLEWVARIYESGTTTYSAEADTGRFTISRDNAKNMVFLQMNSLRAEDTAVYYCASASSSTWRFDYWGQGTLVTVSS
243	PMX048 light chain variable region nucleotide sequence	TCCTATGTGCTGACACAATTGCCTTCCGTGAGTGTGACCCTGGGGCAGACGGCCCGCATCACCTGTGGGGGAGACAGCATTGGAAGAAAAAATGTTTACTGGTTCCAGCAGAAGCTGGGCCAGGCCCCTGTACTGATTATCTATGATGATCGCAGCAGGCCGTCAGGGATCCCTGAGCGATTCTCCGGCGCCAACTCGGGGAACACGGCCACCCTGACCATCAGCGGGGCCCTGGCCGAGGATGAGGCTGACTATTACTGCCAGGTGTGGGACAGCAGTACTGGTGTGTTCGGCGGAGGCACCCATCTGACCGTCCTCG
244	PMX048 light chain variable region amino acid sequence	SYVLTQLPSVSVTLGQTARITCGGDSIGRKNVYWFQQKLGQAPVLIIYDDRSRPSGIPERFSGANSGNTATLTISGALAEDEADYYCQVWDSSTGVFGGGTHLTVL
245	PMX048 heavy chain CDR1	GFTFNNY
246	PMX048 heavy chain CDR2	YESGTT
247	PMX048 heavy chain CDR3	CASASSSTWRFDYW
248	PMX048 light chain CDR1	GGDSIGRKNVY
249	PMX048 light chain CDR2	DDRSRPS
250	PMX048 light chain CDR3	CQVWDSSTGVF

251	PMX049 Heavy chain variable region nucleic acid sequence	GAGGTGCAGCTGGTGGAGTCTGGGGGAGACCTGGTGAAG CCTGGGGGGTCCCTGAGACTCTCCTGTGTGGCCTCTGGAT TCACCTTCAATAACTACGAAATGTACTGGGTCCGCCAGGCT CCAGGGAAAGGGCTGGAGTGGGTCGCAAGGATTTATGAG AGTGGAAGTACCACTTTTTCTGCAGAAGCTGTTACGGGCC GATTCACCATCTCCAGAGACAACGCCAAGAACATGGTGTAT CTGCAGATGAACAGCCTGAGAGCCGAGGACACGGCCGTG TATTACTGTGCGAGTGCTAGTTCTAGTTCTTGGCGTTTTGA CTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
252	PMX049 Heavy chain variable region amino acid sequence	EVQLVESGGDLVKPGGSLRLSCVASGFTFNNYEMYWVRQAP GKGLEWVARIYESGSTTFSAEAVTGRFTISRDNAKNMVYLQM NSLRAEDTAVYYCASASSSSWRFDYWGQGTLVTVSS
253	PMX049 light chain variable region nucleotide sequence	TCCTATGTGCTGACACAGCTGCCATCCGTGAGTGTGACCC TGGGGCAGACGGCCCGCATCACCTGTGGGGGAGACAGCA TTGGGCGAAAAAATGTTTGCTGGTTCCAGCAGAGGCTGGG CCAGGCCCCTGAACTGATTATCTATGATGATCGCAGCAGG CCGTCAGGGATCCCTGAGCGATTCTCCGGCGCCAACTCG GGGAACACGGCCACCCTGACCATCAGCGGGGCCCTGGCC GAGGATGAGGCTGACTATTACTGCCAGGTGTGGGACAGCA GTACTGGTGTGTTCGGCGGAGGCACCCATCTGACCGTCCT CG
254	PMX049 light chain variable region amino acid sequence	SYVLTQLPSVSVTLGQTARITCGGDSIGRKNVCWFQQRLGQA PELIIYDDRSRPSGIPERFSGANSGNTATLTISGALAEDEADYY CQVWDSSTGVFGGGTHLTVL
255	PMX049 heavy chain CDR1	GFTFNNY
256	PMX049 heavy chain CDR2	YESGST
257	PMX049 heavy chain CDR3	CASASSSSWRFDYW
258	PMX049 light chain CDR1	GGDSIGRKNVC

259	PMX049 light chain CDR2	DDRSRPS
260	PMX049 light chain CDR3	CQVWDSSTGVF
261	PMX050 Heavy chain variable region nucleic acid sequence	GAGGTGCAGCTGGTGGAGTCTGGGGGAGACCTTGTGAAA CCTGAGGGGTCCCTGAGACTCTCCTGTGTGGTCTCTGGCT TCACCTTCACTACTTACGACATGAGCTGGGTCCGCCAGGC TCCAGGGAAGGGGCTGCAGTGGGTCGCATACATTACCAAT GATGGAAGGATCACAACTTACACAGACGCTGTGAAGGGCC GATTCACCATCTCCAGAGACAATGCCAAGAACACGCTGTAT CTGCAGATGAACAGCCTGAGAACTGTTGACACAGGCGTGT ATTATTGTGCGAGGCATAGTAGCAGCTGGTCCAGGGGGAG GTTTGGTTTGGACTACTGGGGCCATGGTACTTCAGTCTTCG TGTCCTCAG
262	PMX050 Heavy chain variable region amino acid sequence	EVQLVESGGDLVKPEGSLRLSCVVSGFTFTTYDMSWVRQAP GKGLQWVAYITNDGRITTYTDAVKGRFTISRDNAKNTLYLQM NSLRTVDTGVYYCARHSSSWSRGRFGLDYWGHGTSVFVSS
263	PMX050 light chain variable region nucleotide sequence	TCCTATGTGCTGACACAGTTGCCATCCAAAAATGTGACCCT GAAGCAGCCGGCCCACATCACCTGTGGGGGAGACAACATT GGAAGGAAAGGTGTTCACTGGTACCAGCAGAAGCTGGGC CAGGCCCCTGTATTGATTATCTATTATGATAGCAGCAGGCC GACAGGGATCCCTGAGCGATTCTCCGGCGCCAACTCGGG GAACACGGCCACCCTGACCATCAGCGGGGCCCTGGCCGA GGACGAGGCTGACTATTACTGCCAGGTGTGGGACAACAGT GCTAGTGTGTTCGGCGGAGGCACCCATCTGACCGTCCTCG
264	PMX050 light chain variable region amino acid sequence	SYVLTQLPSKNVTLKQPAHITCGGDNIGRKGVHWYQQKLGQA PVLIIYYDSSRPTGIPERFSGANSGNTATLTISGALAEDEADYY CQVWDNSASVFGGGTHLTVL
265	PMX050 heavy chain CDR1	GFTFTTY
266	PMX050 heavy chain CDR2	TNDGRI

267	PMX050 heavy chain CDR3	CARHSSSWSRGRFGLDYW
268	PMX050 light chain CDR1	GGDNIGRKGVH
269	PMX050 light chain CDR2	YDSSRPT
270	PMX050 light chain CDR3	CQVWDNSASVF
271	PMX051 Heavy chain variable region nucleic acid sequence	GAGGTACAGTTGGTGGAGTCTGGGGGAGACCTGGTGAAG CCGGGGGGGTCCCTGAGACTTTCCTGTGTGGCCTCTGGAT TCTCCTTCAATACCTACCACATGAACTGGGTCCGCCAGGCT CCAGGGAAGGGGCTTCACTGGGTCGCATTCATTAACAGCG ATGGGGGTGGCACAAGTTATGCAGACACTGTGAAGGGCC GATTCACCATCTCCAGAGACTACGCCAAGAATACACTCTAT CTTCAGATGAATAGTCTGAGAGCCGAAGACACGGCCGTTT ATTATTGTGTGAGTGGATCTATATGGACTCATTTTGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
272	PMX051 Heavy chain variable region amino acid sequence	EVQLVESGGDLVKPGGSLRLSCVASGFSFNTYHMNWVRQAP GKGLHWVAFINSDGGGTSYADTVKGRFTISRDYAKNTLYLQM NSLRAEDTAVYYCVSGSIWTHFDYWGQGTLVTVSS
273	PMX051 light chain variable region nucleotide sequence	TCCTATGTGCTGACACAGCTGCCATCCGTGAGTATGACCC TGAGGCAGACGGCCCACATCACCTGTGGGGGAGACATCAT TGGAAGTAAAAGTGTTTATTGGTACCAGCAGAAGCTGGGC CAGGCCCCTGTACTGATTATTTATAGAGATACCAACAGGCC GACAGGGATCCCTGAGCGATTCTCTGGCGCCAGCTCGGG GAACACGGCCACCCTGACCATCAGCGGGGCCCTGGCCGA GGACGAGGCTGACTATTACTGCCAGGTTTGGGACAGCAGT ACTCAGGCTGTGTTCGGCGGAGGCACCCATCTGACCGTCC TCG
274	PMX051 light chain variable region amino acid sequence	SYVLTQLPSVSMTLRQTAHITCGGDIIGSKSVYWYQQKLGQA PVLIIYRDTNRPTGIPERFSGASSGNTATLTISGALAEDEADYY CQVWDSSTQAVFGGGTHLTVL

275	PMX051 heavy chain CDR1	GFSFNTY
276	PMX051 heavy chain CDR2	NSDGGG
277	PMX051 heavy chain CDR3	CVSGSIWTHFDYW
278	PMX051 light chain CDR1	GGDIIGSKSVY
279	PMX051 light chain CDR2	RDTNRPT
280	PMX051 light chain CDR3	CQVWDSSTQAVF
281	PMX052 Heavy chain variable region nucleic acid sequence	GAGGTGCAGCTGGTGGAGTCTGGGGGAGACCTGGTGAAG CCTGCGGGGTCCCTGAGACTGTCCTGTGTGGCCTCTGGAT TCACCTTCAGTAGCTACAGCATGAGCTGGGTCCGCCAGGC TCCTGAGAAGGGGCTGCAGTTGGTCGCAGGTATTAGCGGC GGTGGAAGTCGCACATACTACTCAGACGCTGTGAAGGGCC GATTCACCATCTCCAGAGACAACGCCAAGAACACAGTGTAT CTGCAGATGAACAGCCTGAGAGCCGAGGACACGGCCATTT ATTACTGTGCAAAGGATGGTGGCAGCTGGGCGGGATATAA TTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCC TCAG
282	PMX052 Heavy chain variable region amino acid sequence	EVQLVESGGDLVKPAGSLRLSCVASGFTFSSYSMSWVRQAP EKGLQLVAGISGGGSRTYYSDAVKGRFTISRDNAKNTVYLQM NSLRAEDTAIYYCAKDGGSWAGYNFDYWGQGTLVTVSS
283	PMX052 light chain variable region nucleotide sequence	GATATTGTCATGACACAGACGCCACCGTCCCTGTCTGTCA GCCCTAGAGAGACGGCCTCCATCTCCTGCAAGGCCAGTCA GAGCCTCCTGCACAGTGATGGAAGCACCTATTTGGATTGG TACCTGCAAAAGCCAGGCCAGTCTCCACAGCTTCTGATATA CTTGGGTTCCAACCGCTTCACTGGCGTGTCAGACAGGTTC AGTGGCAGCGGGTCAGGGACAGAATTCACCCTGAGAATCA GCAGAGTGGAGGCTAACGATACTGGAGTTTATTACTGCGG

		GCAAGGTACACAGCTTCCTTATACTTTCGGCCAGGGAACC GAGCTGGAGATAAAAC
284	PMX052 light chain variable region amino acid sequence	DIVMTQTPPSLSVSPRETASISCKASQSLLHSDGSTYLDWYLQ KPGQSPQLLIYLGSNRFTGVSDRFSGSGSGTEFTLRISRVEAN DTGVYYCGQGTQLPYTFGQGTELEIK
285	PMX052 heavy chain CDR1	GFTFSSY
286	PMX052 heavy chain CDR2	SGGGSR
287	PMX052 heavy chain CDR3	CAKDGGSWAGYNFDYW
288	PMX052 light chain CDR1	KASQSLLHSDGSTYLD
289	PMX052 light chain CDR2	LGSNRFT
290	PMX052 light chain CDR3	CGQGTQLPYTF
291	PMX053 Heavy chain variable region nucleic acid sequence	GAGGTGCAGCTGGTGGAGTCTGGGGGAGACCTGGTGAAG CCTGCGGGGTCCCTAAGACTGTCCTGTGTGGCCTCTGGTT TCACCTTCAGTAGCTACAGCATGAGCTGGGTCCGCCAGGC TCCTGAGAAGGGGCTGCAGTTGGTCGCAGGTATTAACAGC GCTGGAAGTAGCACATACTACACAGACGCTGTGAAGGGCC GATTCACCATATCCAGAGACAACGCCAAGAACACAGTGTAT TTGCAGATGAACAGCCTGAGAGCCGAGGACACGGCCATTT ATTACTGTGCAAAGCGTTGGGTTTTTGACTACTGGGGCCA GGGAACCCTGGTCACCGTCTCCTCAG
292	PMX053 Heavy chain variable region amino acid sequence	EVQLVESGGDLVKPAGSLRLSCVASGFTFSSYSMSWVRQAP EKGLQLVAGINSAGSSTYYTDAVKGRFTISRDNAKNTVYLQM NSLRAEDTAIYYCAKRWVFDYWGQGTLVTVSS

293	PMX053 light chain variable region nucleotide sequence	GATATTGTCATGACACAGACCCCACTGTCCCTGTCCGTCA GCCCTGGAGAGCCGGCCTCCATCTCCTGCAAGGCCAGTC AGAGCCTCCCGCACAGTCTTGGGAACACCTATTTATACTG GTTCCGACAGAAGCCAGGCCAGTCTCCACAGCGTTTGATC TATAAGGTCTCCAACAGAGACCCTGGGGTCCCAGACAGGT TCAGTGGCAGCGGGTCAGGGACAGATTTCACCCTGAGAAT CAGCAGAGTGGAGGCTGATGATGCTGGAATTTATTACTGC GGGCAAGGTATACAAGATCCGTTCACTTTTGGCCAAGGGA CCAAACTGGAGATCAAAC
294	PMX053 light chain variable region amino acid sequence	DIVMTQTPLSLSVSPGEPASISCKASQSLPHSLGNTYLYWFRQ KPGQSPQRLIYKVSNRDPGVPDRFSGSGSGTDFTLRISRVEA DDAGIYYCGQGIQDPFTFGQGTKLEIK
295	PMX053 heavy chain CDR1	GFTFSSY
296	PMX053 heavy chain CDR2	NSAGSS
297	PMX053 heavy chain CDR3	CAKRWVFDYW
298	PMX053 light chain CDR1	KASQSLPHSLGNTYLY
299	PMX053 light chain CDR2	KVSNRDP
300	PMX053 light chain CDR3	CGQGIQDPFTF
301	PMX054 Heavy chain variable region nucleic acid sequence	GAGGTGCACCTGGTGGAGTCTGGGGGAGACCTTGTGAAA CCTGAGGGGTCCCTGAGACTCTCCTGTGTGGTCTCTGGCT TCACCTTCAGTAGCTACGACATGAGCTGGGTCCGCCAGGC TCCAGGGAAGGGGCTGCAGTGGGTCGCATACATTAGCAGT GATGGAAGGAGCACAGGTTACACAGACGCTGTGAAGGGC CGATTCACCATCTCCAGAGACAATGCCAAGAAAACGCTGTA TCTGCAGATGAACAGCCTGAGAAGTGAGGACACAGCCGTT

		TATTACTGTGCGAAGGAGACGCCTAGGTGGGGCTTTGACT ACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
302	PMX054 Heavy chain variable region amino acid sequence	EVHLVESGGDLVKPEGSLRLSCVVSGFTFSSYDMSWVRQAP GKGLQWVAYISSDGRSTGYTDAVKGRFTISRDNAKKTLYLQM NSLRSEDTAVYYCAKETPRWGFDYWGQGTLVTVSS
303	PMX054 light chain variable region nucleotide sequence	TCCTATGTGCTGACACAGCTGCCATCCGTGAGTGTGACCC TGAGGCAGACGGCCCGCATCACCTGTGGGGGAGCCAGTA TTGGAAGTAAAAATGTTTACTGGCACCAGCAGAAGCTGGG CCAGGCCCCTTTACTGATTATCTATGATGATAGCAGCAGGC CGTCAGGGATCCCTGAGCGATTCTCCGGCGCCAACTCGG GGAACACGGCCACCCTGACCATCAGCGGGGCCCTGGCCG AAGATGAGGCTGACTATTACTGCCAGGTGTGGGACAGCAG TACTAGTGTGTTCGGCGGAGGCACCCATCTGACCGTCCTC G
304	PMX054 light chain variable region amino acid sequence	SYVLTQLPSVSVTLRQTARITCGGASIGSKNVYWHQQKLGQA PLLIIYDDSSRPSGIPERFSGANSGNTATLTISGALAEDEADYY CQVWDSSTSVFGGGTHLTVL
305	PMX054 heavy chain CDR1	GFTFSSY
306	PMX054 heavy chain CDR2	SSDGRS
307	PMX054 heavy chain CDR3	CAKETPRWGFDYW
308	PMX054 light chain CDR1	GGASIGSKNVY
309	PMX054 light chain CDR2	DDSSRPS
310	PMX054 light chain CDR3	CQVWDSSTSVF

311	PMX055 Heavy chain variable region nucleic acid sequence	GAGGTGCAGCTGGAGGAGTCTGGGGGAGACCTTGTGAAA CCTGAGGGGTCCCTGAGACTCTCCTGTGTGGTCTCTGGCT TCACCCTCAGTACCTTCGGCATGAGCTGGGTCCGCCAGGC TCCAGGGAAGGGGCTGCAGTGGGTCGCATACATTAGCAGT GATGGAAGGAGCACAAGTTACACAGACGCTGTGAAGGGCC GATTCACCATCTCCAGAGACAATGCCAAGAACACGCTGTAT CTGCAGATGAACAGCCTGCGAACTGACGACACAGCCGTGT ATTACTGTGTCCAGTTGGGCCGGGGATTTGGTATAGACTA CTGGGGCCATGGCACCTCACTCTTCGTGTCCTCAG
312	PMX055 Heavy chain variable region amino acid sequence	EVQLEESGGDLVKPEGSLRLSCVVSGFTLSTFGMSWVRQAP GKGLQWVAYISSDGRSTSYTDAVKGRFTISRDNAKNTLYLQM NSLRTDDTAVYYCVQLGRGFGIDYWGHGTSLFVSS
313	PMX055 light chain variable region nucleotide sequence	TCCTATGTGCTGACACAGCTGCCATCCAAAAATGTGACCCT GAGGCAGCCGGCCCACATCCCCTGTGGGGGAGACAACAT TGGAAGTAAAAGTGTTCACTGGTACCAGCAGAAGCTGGGC CAGGCCCCTGTACTGATTATCTATTATGATACCAGCAGGCC GACAGGGATCCCTGAGCGATTCTCCGGCGCCAACTCGGG GAACACGGCCACCCTGACCATCAGCGGGGCCCTGGCCGA GGACGAGGCTGACTATTACTGCCAGGTGTGGGACAGCAGT GCTGCTGTGTTCGGCGGAGGCACCCACCTGACCGTCCTC G
314	PMX055 light chain variable region amino acid sequence	SYVLTQLPSKNVTLRQPAHIPCGGDNIGSKSVHWYQQKLGQA PVLIIYYDTSRPTGIPERFSGANSGNTATLTISGALAEDEADYY CQVWDSSAAVFGGGTHLTVL
315	PMX055 heavy chain CDR1	GFTLSTF
316	PMX055 heavy chain CDR2	SSDGRS
317	PMX055 heavy chain CDR3	CVQLGRGFGIDYW
318	PMX055 light chain CDR1	GGDNIGSKSVH

319	PMX055 light chain CDR2	YDTSRPT
320	PMX055 light chain CDR3	CQVWDSSAAVF
321	PMX056 Heavy chain variable region nucleic acid sequence	GAGGTGCAGCTGGTGGAGTCTGGGGGAGACCTTGTGAAA CCTGAGGGGTCCCTGAGACTCTCCTGTGTGGTCTCTGGCT TCACCTTGAGTAGCTACGGCATGAGCTGGGTCCGCCAGGC TCCAGGGAGGGGGCTGCAGTGGGTCGCATACATTAGCAG TGATGGAAGGAGCACAAGTTACACAGACGCTGTGAAGGGC CGATTCACCATCTCCAGAGACAATGCCAAGAACACGCTGT ATCTGCAGATGAACAGCCTGAGAAGTGAGGACACAGCCGT GTATTACTGTGTCCAGTTGGGCCGGGGCTTTGGCATGGAC TATTGGGGCCATGGCACCTCACTCTTCGTGTCCTCAG
322	PMX056 Heavy chain variable region amino acid sequence	EVQLVESGGDLVKPEGSLRLSCVVSGFTLSSYGMSWVRQAP GRGLQWVAYISSDGRSTSYTDAVKGRFTISRDNAKNTLYLQM NSLRSEDTAVYYCVQLGRGFGMDYWGHGTSLFVSS
323	PMX056 light chain variable region nucleotide sequence	TCCTATGTGCTGACACAGCTGCCATCCAAAAATGTGACCCT GAAGCAGCCGGCCCACATCACCTGTGGGGGAGACAACATT GGAAGTAAAAGCGTTCACTGGTACCAGCAGAAGCTGGGCC AGGCCCCTGTAGTGATTATCTATTATGATAGTACCAGGCCG ACAGGGATCCCTGAGCGATTCTCCGGCGCCAACTCGGGG AACACGGCCACCCTGACCATCAGCGGGGCCCTGGCCGAG GACGAGGCTGACTATTACTGCCAGGTGTGGGACAGCAGTG CTGCTGTGTTCGGCGGAGGCACCCACCTGACCGTCCTCG
324	PMX056 light chain variable region amino acid sequence	SYVLTQLPSKNVTLKQPAHITCGGDNIGSKSVHWYQQKLGQA PVVIIYYDSTRPTGIPERFSGANSGNTATLTISGALAEDEADYY CQVWDSSAAVFGGGTHLTVL
325	PMX056 heavy chain CDR1	GFTLSSY
326	PMX056 heavy chain CDR2	SSDGRS

327	PMX056 heavy chain CDR3	CVQLGRGFGMDYW
328	PMX056 light chain CDR1	GGDNIGSKSVH
329	PMX056 light chain CDR2	YDSTRPT
330	PMX056 light chain CDR3	CQVWDSSAAVF
331	PMX057 Heavy chain variable region nucleic acid sequence	GAGGTGCAACTGGTGGAGTCTGGGGGAGACCTTGTGAAA CCTGAGGGGTCCCTGAGACTCTCCTGTGTGGTCTCTGGCT TCACCTTCAATAACTACGGCATGAGTTGGGTCCGCCAGGC TCCAGGGAAGGGGCTGCAGTGGGTCGCATACATTAGTATT GATGGAAGGAGCACAAGTTACACAGACGCTGTGAAGGGCC GATTCACCATCTCCAGAGACAATGCCAAGAACACGCTGTAT CTGCATATAAACAGCCTGAGAACTGAGGACACAGCCGTGT ATTACTGTACGAAGTTGGGGAGGGGGTTCACTTTTGGTTAC TGGGGCCAGGGCACCCTGGTCACTGTCTCCTCAG
332	PMX057 Heavy chain variable region amino acid sequence	EVQLVESGGDLVKPEGSLRLSCVVSGFTFNNYGMSWVRQAP GKGLQWVAYISIDGRSTSYTDAVKGRFTISRDNAKNTLYLHIN SLRTEDTAVYYCTKLGRGFTFGYWGQGTLVTVSS
333	PMX057 light chain variable region nucleotide sequence	TCCTATGTGCTGACACAGCTGCCATCCAAAAATGTGACCCT GAAGCAGCCGGCCCACATCACCTGTGGGGGAGACAACATT GGAAGTAAAAGTGTTCACTGGTACCAGCAGAAGCTGGGCC AGGCCCCTGCACTGATTATCTATTATGATAGCAGCAGGCC GACAGGGATCCCTGAGCGATTCTCCGGCGCCAACTCGGG GAACACGGCCACCCTGACCATCAGCGGGGCCCTGGCCGA GGACGAGGCTGACTATTACTGCCAGGTGTGGGACAGCAGT GTTAGTGTGTTCGGCGGAGGCACCCATCTGACCGTCCTCG
334	PMX057 light chain variable region amino acid sequence	SYVLTQLPSKNVTLKQPAHITCGGDNIGSKSVHWYQQKLGQA PALIIYYDSSRPTGIPERFSGANSGNTATLTISGALAEDEADYY CQVWDSSVSVFGGGTHLTVL

335	PMX057 heavy chain CDR1	GFTFNNY
336	PMX057 heavy chain CDR2	SIDGRS
337	PMX057 heavy chain CDR3	CTKLGRGFTFGYW
338	PMX057 light chain CDR1	GGDNIGSKSVH
339	PMX057 light chain CDR2	YDSSRPT
340	PMX057 light chain CDR3	CQVWDSSVSVF
341	PMX058 Heavy chain variable region nucleic acid sequence	GAGGTGCAGCTGGTGGAGTCTGGGGGAGACCTTGTGAAA CCTGAGGGGTCCCTGAGACTCTCCTGTGTGGTCTCTGACT TCACCTTCGGTAGCTACGGCATGAGCTGGGTCCGCCAGGC TCCAGGGAAGGGGCTGCAGTGGGTCGCATACATTAGCAGT GATGGAAGGAGCACAAGTTACACAGACGCTGTGAAGGGCC GATTCACCATCTCCAGAGACAATGCCAAGAACACGCTACAT CTGCAGATGAACAGCCTGAGAACTGAGGACACAGCCGTGT ATTACTGTGCGAAGTTGGGGAGGGGGTTTGCTTTTGGTTA CTGGGGCCAGGGCACCCTGGTCACTGTCTCCTCAG
342	PMX058 Heavy chain variable region amino acid sequence	EVQLVESGGDLVKPEGSLRLSCVVSDFTFGSYGMSWVRQAP GKGLQWVAYISSDGRSTSYTDAVKGRFTISRDNAKNTLHLQM NSLRTEDTAVYYCAKLGRGFAFGYWGQGTLVTVSS
343	PMX058 light chain variable region nucleotide sequence	TCCTATGTGCTGACACAGCTGCCATCCAAAAATGTGACCCT GAAGCAGCCGGCCCACATCACCTGTGGGGGAGACAACATT GGAAGTAAAAGTGTTCACTGGTACCAGCAGAAGCTGGGCC AGGCCCCTGTACTGATTATCTATTATGATAGCAACAGGCCG ACAGGGATCCCTGAGCGATTCTCCGGCGCCAACTCGGGG AACACGGCCACCCTGACCATCAGCGGGGCCCTGGCCGAG GACGAGGCTGACTATTACTGCCAGGTGTGGGACAGCAGTG CTAGTGTGTTCGGCGGAGGCACCCATCTGACCGTCCTCG

344	PMX058 light chain variable region amino acid sequence	SYVLTQLPSKNVTLKQPAHITCGGDNIGSKSVHWYQQKLGQA PVLIIYYDSNRPTGIPERFSGANSGNTATLTISGALAEDEADYY CQVWDSSASVFGGGTHLTVL
345	PMX058 heavy chain CDR1	DFTFGSY
346	PMX058 heavy chain CDR2	SSDGRS
347	PMX058 heavy chain CDR3	CAKLGRGFAFGYW
348	PMX058 light chain CDR1	GGDNIGSKSVH
349	PMX058 light chain CDR2	YDSNRPT
350	PMX058 light chain CDR3	CQVWDSSASVF
351	PMX059 Heavy chain variable region nucleic acid sequence	GAGGTTCACCTGGTGGAGTCTGGGGGAGACCTTGTGAAAC CTGAGGGGTCCCTGAGACTCTCCTGTGTGGTCTCTGGCTT CACCTTCAGTAACTACGTCATGAACTGGGTCCGCCAGGCT CCAGGGAAGGGGCTGCAGTGGGTCGCATTCATTAGCGGT GATGGAAGGAGCACAACTTACACAGACGCTGTGAAGAGCC GATTCACCATCTCCAGAGACAATGCCAAGAACACGCTGTAT CTGCAGATGAGCAGCCTGAGAACTGAGGACACAGCCATAT ACTTCTGTGCGAAGGAGAAATATAGTAGCGGCTGGTCTTTT GAGTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA G
352	PMX059 Heavy chain variable region amino acid sequence	EVHLVESGGDLVKPEGSLRLSCVVSGFTFSNYVMNWVRQAP GKGLQWVAFISGDGRSTTYTDAVKSRFTISRDNAKNTLYLQM SSLRTEDTAIYFCAKEKYSSGWSFEYWGQGTLVTVSS
353	PMX059 light chain variable region nucleotide sequence	TCCTATGTGCTGACACAGCTGCCATCCAAAAATGTGACCCT GAAGCAGCCGGCCCACATCACCTGTGGGGGAGACAACATT GGAAGTAAAAGTGTTCACTGGTACCAGCAGAAGCTGGGCC AGGCCCCTGTATTGATTATCTATTATGACAGCAGCAGGCCG

		ACAGGGATCCCTGAGCGATTCTCCGGCGCCAACTCGGGG AACACGGCCACCCTGACCATCAGCGGGGCCCTGGCCGAG GACGAGGCTGACTATTACTGCCAGGTGTGGGACAGCAGTG CTAGTGTGTTCGGCGGAGGCACCCATCTGACCGTCCTCG
354	PMX059 light chain variable region amino acid sequence	SYVLTQLPSKNVTLKQPAHITCGGDNIGSKSVHWYQQKLGQA PVLIIYYDSSRPTGIPERFSGANSGNTATLTISGALAEDEADYY CQVWDSSASVFGGGTHLTVL
355	PMX059 heavy chain CDR1	GFTFSNY
356	PMX059 heavy chain CDR2	SGDGRS
357	PMX059 heavy chain CDR3	CAKEKYSSGWSFEYW
358	PMX059 light chain CDR1	GGDNIGSKSVH
359	PMX059 light chain CDR2	YDSSRPT
360	PMX059 light chain CDR3	CQVWDSSASVF
361	PMX060 Heavy chain variable region nucleic acid sequence	GAGGTGCAGCTGGTGGAGTCTGGGGGAGACCTGATGAAG CCTGGGGGGTCCCTGAGACTTTCCTGTGTGGCCTCTGGAT TCACCTTCAGTAGCTTCCCCATGAGTTGGGTCCGCCAGGC TCCAGGGAAGGGGCTTCAGTGGGTCGCATACATTCACAGT GGTGGAAGTAGCACAAGCTATGCAGACGCTGTGAAGGGC CGATTCACCATCTCCAGAGACAACGCCAAGAATACGCTGT ATCTTCAGATGAACAGCCTGCGAGCCGAGGACACGGCCAT ATATTACTGTGCGCGTACCTTCCCTACGGTAGCTGCTGACA ACTGGTTCTACTACTGGGGCCAAGGGACCCTGGTCACTGT GTCCTCAG
362	PMX060 Heavy chain variable region amino acid sequence	EVQLVESGGDLMKPGGSLRLSCVASGFTFSSFPMSWVRQAP GKGLQWVAYIHSGGSSTSYADAVKGRFTISRDNAKNTLYLQM NSLRAEDTAIYYCARTFPTVAADNWFYYWGQGTLVTVSS

363	PMX060 light chain variable region nucleotide sequence	TCCTATGTGCTGACACAGCTGCCATCCAAAAATGTGACCCT GAAGCAGGCGGCCCACATCACCTGTGGGGGAGACAACAT TGGAAGTAAAAGTGTTCACTGGTACCAGCAGAAGCTGGGC CAGGCCCCTGTACTGATTATCTATTATGATAGCAGCAGGCC GACAGGGATCCCTGAGCGATTCTCCGGCGCCAACTCGGG GAACACGGCCACCCTGACCATCAGCGGGGCCCTGGCCGA GGACGAGGCTGACTATTACTGCCAGGTGTGGGACAGCAGT GCTAAGTGGGTATTCGGTGAAGGGACCCAGCTGACCGTCC TCG
364	PMX060 light chain variable region amino acid sequence	SYVLTQLPSKNVTLKQAAHITCGGDNIGSKSVHWYQQKLGQA PVLIIYYDSSRPTGIPERFSGANSGNTATLTISGALAEDEADYY CQVWDSSAKWVFGEGTQLTVL
365	PMX060 heavy chain CDR1	GFTFSSF
366	PMX060 heavy chain CDR2	HSGGSS
367	PMX060 heavy chain CDR3	CARTFPTVAADNWFYYW
368	PMX060 light chain CDR1	GGDNIGSKSVH
369	PMX060 light chain CDR2	YDSSRPT
370	PMX060 light chain CDR3	CQVWDSSAKWVF
371	PMX061 Heavy chain variable region nucleic acid sequence	GAGGTGCAGCTGGTGGAGTCTGGGGGAGACCTGGTGAAG CCTGGGGGGTCCCTGAGACTTTCCTGTGTGGCCTCTGGAT TCACCTTCAGTAGTTTCCCCATGAGCTGGGTCCGCCAGGC TCCAGGGAAGGGGCTTCAGTGGGTCGCATACATTAACAGT GGTGGAAGTAGCACAAGTTATGCAGACGTTGTGAAGGGCC GATTCACCATCTCCAGAGACAACGCCAAGAACACGCTGTA TCTTCAGATGAACAGCCTGAGAGCCGACGACACGGCCGTA TATTACTGTGCGCGTACCTTCCCTACGGTAGCTACTGACAA

		CTGGTTCTACTACTGGGGCCAAGGGACCCTGGTCACTGTG TCCTCAG
372	PMX061 Heavy chain variable region amino acid sequence	EVQLVESGGDLVKPGGSLRLSCVASGFTFSSFPMSWVRQAP GKGLQWVAYINSGGSSTSYADVVKGRFTISRDNAKNTLYLQM NSLRADDTAVYYCARTFPTVATDNWFYYWGQGTLVTVSS
373	PMX061 light chain variable region nucleotide sequence	TCCTATGTGCTGACACAGCTGCCATCCAAAAATGTGACCCT GAAGCAGGCGGCCCACATCACCTGTGGGGGAGACAACAT TGGAAGTAAAAGTGTTCACTGGTACCAGCAGAAGCTGGGC CAGGCCCCTGTACTGATTATCTATTATGATAGCAGCAGGCC GACAGGGATCCCTGAGCGATTCTCCGGCGCCAACTCGGG GAACACGGCCACCCTGACCATCAGCGGGGCCCTGGCCGA GGACGAGGCTGACTATTACTGCCAGGTGTGGGACAGCAGT GCTAAGTGGGTATTCGGTGAAGGGACCCAGCTGACCGTCC TCG
374	PMX061 light chain variable region amino acid sequence	SYVLTQLPSKNVTLKQAAHITCGGDNIGSKSVHWYQQKLGQA PVLIIYYDSSRPTGIPERFSGANSGNTATLTISGALAEDEADYY CQVWDSSAKWVFGEGTQLTVL
375	PMX061 heavy chain CDR1	GFTFSSF
376	PMX061 heavy chain CDR2	NSGGSS
377	PMX061 heavy chain CDR3	CARTFPTVATDNWFYYW
378	PMX061 light chain CDR1	GGDNIGSKSVH
379	PMX061 light chain CDR2	YDSSRPT
380	PMX061 light chain CDR3	CQVWDSSAKWVF

381	PMX062 Heavy chain variable region nucleic acid sequence	GAGGTGCAGTTGGTGGAGTCTGGGGGAGACCTTGTGAAA CCTGAGGGGTCCCTGAGACTCTCCTGTGTGGTCTCTGGCT TCACCTTCAGTAGTTATGACATGAGCTGGGTCCGCCAGGC TCCAGGGAAGGGGCTGCAGTGGGTCGCATACATTAGCTTT GATGGAAGGAGCACAAGTTACACAGACGTTGTGAAGGGCC GATTCACCATCTCCAGAGACAATGCCAAGACCACGCTGTAT CTGCAGATGAACACCCTGAGAATTGAGGACACAGCCGTGT ATTACTGTGCGAAGTTAAGTTCTAGTGGTTGGAGTATGGAC TATTGGGGCCATGGCACCTCACTCTTCGTGTCCTCAG
382	PMX062 Heavy chain variable region amino acid sequence	EVQLVESGGDLVKPEGSLRLSCVVSGFTFSSYDMSWVRQAP GKGLQWVAYISFDGRSTSYTDVVKGRFTISRDNAKTTLYLQM NTLRIEDTAVYYCAKLSSSGWSMDYWGHGTSLFVSS
383	PMX062 light chain variable region nucleotide sequence	TCCTATGTGCTGACACAGCTGCCATCCAAAAATGTGACCCT GAAGCAGCCGGCCCACATCACCTGTGGGGGAGACAACATT GGAAGTAAAAGTGTTCACTGGTACCAGCAGAAGCTGGGCC AGGCCCCTGTACTGATTATCTATTATGATAGCAGCAGGCCG ACAGGGATCCCTGAGCGATTCTCCGGCGCCAACTCGGGG AACACGGCCACCCTGACCATCAGCGGGGCCCTGGCCGAG GACGAGGCTGACTATTACTGCCAGGTGTGGGACAGCAGTG CTAGTGTGTTCGGCGGAGGCACCCATCTGACCGTCCTCG
384	PMX062 light chain variable region amino acid sequence	SYVLTQLPSKNVTLKQPAHITCGGDNIGSKSVHWYQQKLGQA PVLIIYYDSSRPTGIPERFSGANSGNTATLTISGALAEDEADYY CQVWDSSASVFGGGTHLTVL
385	PMX062 heavy chain CDR1	GFTFSSY
386	PMX062 heavy chain CDR2	SFDGRS
387	PMX062 heavy chain CDR3	CAKLSSSGWSMDYW
388	PMX062 light chain CDR1	GGDNIGSKSVH

389	PMX062 light chain CDR2	YDSSRPT
390	PMX062 light chain CDR3	CQVWDSSASVF
391	PMX063 Heavy chain variable region nucleic acid sequence	GAGGTACAACTGGTGGAGTCTGGGGGAGACCTGGTGAGG CCTGGGGGGTCCCTGAGACTTTCCTGTGTGGCCTCTGGAT TCACCTTCAATAATTACCACATGAGCTGGGTCCGCCAGGCT CCTGGGAAGGGGCTTCAGTGGGTCGCATTCATTAACAGTG GTGGAAGTGGTACAACCTTTGCAGACGTTGTGAGGGGCCG ATTCACCATCTCCAGAGACTACGCCAAAAACGCCCTGTATC TTCAGATGAACAGCCTGAGAGCCGAGGACACGGCCGTATA TTATTGTGCGAGTGGATCTATATGGACTCATTTTGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
392	PMX063 Heavy chain variable region amino acid sequence	EVQLVESGGDLVRPGGSLRLSCVASGFTFNNYHMSWVRQAP GKGLQWVAFINSGGSGTTFADVVRGRFTISRDYAKNALYLQM NSLRAEDTAVYYCASGSIWTHFDYWGQGTLVTVSS
393	PMX063 light chain variable region nucleotide sequence	TCCTTTGTGCTGACACAGCTGCCATCCGTGAGTGTGACCC TGAGGCAGACGGCCCGCATCACCTGTGGGGGAGACATCA TTGGAAGTAAAAATGTTTACTGGTACCAGCAGAGGCTGGG CCAGGCCCCTGTATTGATTATCTATAGAGATAACAACAGGC CGACAGGGATCCCTGAGCGATTCTCTGGCGCCAGCTCGG GGAACACGGCCACCCTGACCATCAGCGGGGCCCTGGCCG AGGACGAGGCTGACTATTACTGCCAGGTGTGGGACAACAG TAATAAGGCTATGTTCGGCGGAGGCACCCATCTGACCGTC CTCG
394	PMX063 light chain variable region amino acid sequence	SFVLTQLPSVSVTLRQTARITCGGDIIGSKNVYWYQQRLGQAP VLIIYRDNNRPTGIPERFSGASSGNTATLTISGALAEDEADYYC QVWDNSNKAMFGGGTHLTVL
395	PMX063 heavy chain CDR1	GFTFNNY
396	PMX063 heavy chain CDR2	NSGGSG

397	PMX063 heavy chain CDR3	CASGSIWTHFDYW
398	PMX063 light chain CDR1	GGDIIGSKNVY
399	PMX063 light chain CDR2	RDNNRPT
400	PMX063 light chain CDR3	CQVWDNSNKAMF
401	PMX064 Heavy chain variable region nucleic acid sequence	GAGGTGCAGCTGGTGGAGTCTGGGGGAGACCTGGTGAAG CCTGGGGGGTCCCTGAGACTTTCCTGTGTGGCCTCTGGAT TCACCTTCAGTAGTTATCACATGAGCTGGGTCCGCCAGGC TCCAGGGAAGGGGCTTCAGTGGGTCGCATATATTACCAGT GGTGGGATTACCACAAGCTATGCAGACGCTGTGAAGGGCC GATTCACCATCTCCAGAGACAACGCCAAGAACACGCTGTA TCTTCAGATGAACAGCCTGAGAGCCGAGGACACGGCCGTG TATTACTGTGCGAGTGATCTGGTTCTAATATTAGGGGGGGC TGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA G
402	PMX064 Heavy chain variable region amino acid sequence	EVQLVESGGDLVKPGGSLRLSCVASGFTFSSYHMSWVRQAP GKGLQWVAYITSGGITTSYADAVKGRFTISRDNAKNTLYLQM NSLRAEDTAVYYCASDLVLILGGADYWGQGTLVTVSS
403	PMX064 light chain variable region nucleotide sequence	TCCTATGAGCTGACTCAGCCACCATCCGTGAATGTGACCC TGAGTGAGACGGCCCACATCACCTGTGGGGGAGACAGCA TTGGAAGGAAATATGTTCAATGGATCCAGCAGAATCCAGG CCAGGCCCCCGTGGTGATTATCTATAAAGATAGCAACAGG CCGACAGGGATCCCTGAGCGCTTCTCTGGCGCCAACTCAG GGAACACGGCTACCCTGACCATCAGTGGGGCCCTGGCCG AAGACGAGGCTGACTATTACTGCCAGGTGGGGGACAGTG GTACTAAGGCTGTGTTCGGCGGAGGCACCCACCTGACCGT CCTCG
404	PMX064 light chain variable region amino acid sequence	SYELTQPPSVNVTLSETAHITCGGDSIGRKYVQWIQQNPGQA PVVIIYKDSNRPTGIPERFSGANSGNTATLTISGALAEDEADYY CQVGDSGTKAVFGGGTHLTVL

405	PMX064 heavy chain CDR1	GFTFSSY
406	PMX064 heavy chain CDR2	TSGGIT
407	PMX064 heavy chain CDR3	CASDLVLILGGADYW
408	PMX064 light chain CDR1	GGDSIGRKYVQ
409	PMX064 light chain CDR2	KDSNRPT
410	PMX064 light chain CDR3	CQVGDSGTKAVF
411	PMX065 Heavy chain variable region nucleic acid sequence	GAGGTGCAGCTGGTGGAGTCTGGGGGAGACCTGGTGAAG CCTGGGGGGTCCCTGAGACTCTCCTGTGTGGCCTCTGGAT TCACCTTCAATAACTACGAAATGTACTGGGTCCGCCAGGCT CCAGGGAAAGGGCTGGAGTGGGTCGCAAGGATTTATGAG AGTGGAAGTACCACTTTTTCTGCAGAAGCTGTTACGGGCC GATTCACCATCTCCAGAGACAACGCCAAGAACATGGTGTAT CTGCAGATGAACAGCCTGAGAGCCGAGGACACGGCCGTG TATTACTGTGCGAGTGCTAGTTCTAGTTCTTGGCGTTTTGA CTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
412	PMX065 Heavy chain variable region amino acid sequence	EVQLVESGGDLVKPGGSLRLSCVASGFTFNNYEMYWVRQAP GKGLEWVARIYESGSTTFSAEAVTGRFTISRDNAKNMVYLQM NSLRAEDTAVYYCASASSSSWRFDYWGQGTLVTVSS
413	PMX065 light chain variable region nucleotide sequence	TCCTATGTGCTGACACAGCTGCCATCCGTGAGTGTGACCC TGGGGCAGACGGCCCGCATCACCTGTGGGGGAGACAGCA TTGGGCGAAAAAATGTTTGCTGGTTCCAGCAGAGGCTGGG CCAGGCCCCTGAACTGATTATCTATGATGATCGCAGCAGG CCGTCAGGGATCCCTGAGCGATTCTCCGGCGCCAACTCG GGGAACACGGCCACCCTGACCATCAGCGGGGCCCTGGCC GAGGATGAGGCTGACTATTACTGCCAGGTGTGGGACAGCA

		GTACTGGTGTGTTCGGCGGAGGCACCCATCTGACCGTCCTCG
414	PMX065 light chain variable region amino acid sequence	SYVLTQLPSVSVTLGQTARITCGGDSIGRKNVCWFQQRLGQAPELIIYDDRSRPSGIPERFSGANSGNTATLTISGALAEDEADYYCQVWDSSTGVFGGGTHLTVL
415	PMX065 heavy chain CDR1	GFTFNNY
416	PMX065 heavy chain CDR2	YESGST
417	PMX065 heavy chain CDR3	CASASSSSWRFDYW
418	PMX065 light chain CDR1	GGDSIGRKNVC
419	PMX065 light chain CDR2	DDRSRPS
420	PMX065 light chain CDR3	CQVWDSSTGVF
421	PMX082 Heavy chain variable region nucleic acid sequence	GAGGTGCAGCTGGTGGAGTCTGGGGGAGACCTGGTGAAGCCTGGGGGGTCCCTGAGACTTTCCTGTGTGGCCTCTGGATTCACCTTCAGTAGCCACCACATGACCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTTCAGTGGGTCGCATATATTGTCAGTGGTGGAACTAACACTAACTATGCAGACGCTGTGAAGGGCCGGTTCACCATCTCCAGAGACAACGCCAAGAACACGCTGTATCTTCAGATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGTGATCTAGTTCTAGCAGTTGGGGCTCCTTTCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
422	PMX082 Heavy chain variable region amino acid sequence	EVQLVESGGDLVKPGGSLRLSCVASGFTFSSHHMTWVRQAPGKGLQWVAYIVSGGTNTNYADAVKGRFTISRDNAKNTLYLQMNSLRAEDTAVYYCASDLVLAVGAPFYWGQGTLVTVSS

423	PMX082 light chain variable region nucleotide sequence	TCCTATGAGCTGACTCAGCCACCATCCGTGAATGTGACCC TGAGGGAGACGGCCCACATCACCTGTGGGGGAGACAGCA TTGGAAGAAAATATGTTCAATGGATCCAGCAGAATCCAGGC CAGGCCCCCGTGGTAATTATCTATAAAGACATCAACAGGC CGACAGGGATCCCTGAGCGATTCTCTGGCGCCAACTCAGG GAACACGGCTACCCTGACCATCAGTGGGGCCCTGGCCGA AGACGAGGCTGACTATTACTGCCAGGTGGGGGACAGTGGT ACTAAGGCGGTATTCGGTGAAGGGACCCAGCTGACCGTCC TCG
424	PMX082 light chain variable region amino acid sequence	SYELTQPPSVNVTLRETAHITCGGDSIGRKYVQWIQQNPGQA PVVIIYKDINRPTGIPERFSGANSGNTATLTISGALAEDEADYY CQVGDSGTKAVFGEGTQLTVL
425	PMX082 heavy chain CDR1	GFTFSSH
426	PMX082 heavy chain CDR2	VSGGTN
427	PMX082 heavy chain CDR3	CASDLVLAVGAPFYW
428	PMX082 light chain CDR1	GGDSIGRKYVQ
429	PMX082 light chain CDR2	KDINRPT
430	PMX082 light chain CDR3	CQVGDSGTKAVF
431	PMX083 Heavy chain variable region nucleic acid sequence	GAGGTGCAACTGGTGGAGTCTGGGGGAGACCTGGTGAAG CCTGGGGGGTCCCTGAGACTTTCCTGTGTGGCCTCTGGAT TCACCTTCAGAACCTACCACATGAGCTGGGTCCGCCAGGC TCCAGGGAAGGGGCTTCAGTGGGTCGCATACATTACCCGT GATGGAATTAGCACAACCTATACAGACGCTGTGAAGGGCC GATTCACCATCTCCAGAGACAACGCCAAGAACACTCTGTTT CTTCAGATGAACAGCCTGAGAGCCGATGACACGGCCGTGT

		ATTACTGTGCGAGTGATCTAGTTCTAGTACTTGGGGCTCCT TTCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
432	PMX083 Heavy chain variable region amino acid sequence	EVQLVESGGDLVKPGGSLRLSCVASGFTFRTYHMSWVRQAP GKGLQWVAYITRDGISTTYTDAVKGRFTISRDNAKNTLFLQMN SLRADDTAVYYCASDLVLVLGAPFYWGQGTLVTVSS
433	PMX083 light chain variable region nucleotide sequence	TCCTATGAGCTGACTCAGCCACCATCCGTGAATGTGACCC TGGGGGAGACGGCCCACATCACCTGTGGGGGAGACAGCA TTGGAAGAAAATATGTTCAATGGATCCAGCAGAATCCAGGC CAGGCCCCCGTGGTGATTATCTATAAAGATAGCAACAGGC CGACAGGGATCCCTGAGCGATTCTCTGGCGCCAACTCAGG GAACACGGCTACCCTGACCATCAGTGGGGCCCTGGCCGA AGACGAGGCTGACTATTACTGCCAGGTGGGGGACAGTGGT ACTAAGGCGGTATTCGGTGAAGGGACCCAGCTGACCGTCC TCG
434	PMX083 light chain variable region amino acid sequence	SYELTQPPSVNVTLGETAHITCGGDSIGRKYVQWIQQNPGQA PVVIIYKDSNRPTGIPERFSGANSGNTATLTISGALAEDEADYY CQVGDSGTKAVFGEGTQLTVL
435	PMX083 heavy chain CDR1	GFTFRTY
436	PMX083 heavy chain CDR2	TRDGIS
437	PMX083 heavy chain CDR3	CASDLVLVLGAPFYW
438	PMX083 light chain CDR1	GGDSIGRKYVQ
439	PMX083 light chain CDR2	KDSNRPT
440	PMX083 light chain CDR3	CQVGDSGTKAVF

441	PMX084 Heavy chain variable region nucleic acid sequence	GAGGTGCAGCTGGTGGAGTCTGGGGGAGACCTTGTGAAA CCTGAGGGGTCCCTGAGACTCTCCTGTGTGGTCTCTGGCT TCACTTTCAGTAATTACGACATGAGCTGGGTCCGCCAGGC TCCAGGGAAGGGGCTGCAGTGGGTCGCATTCATTAGCAAT GATGGGAGGATCACAGGTTACACAGACGCTGTGGAGGGC CGATTCACCATCTCCAGAGACAACGCCAAGAACACGCTGT ATCTGCAGATGAACAGCCTGAGAACTGAGGACACAGCCGT GTATTACTGTGCGAAGGAGACTAGTCGTTGGGGGTTTGAC TACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
442	PMX084 Heavy chain variable region amino acid sequence	EVQLVESGGDLVKPEGSLRLSCVVSGFTFSNYDMSWVRQAP GKGLQWVAFISNDGRITGYTDAVEGRFTISRDNAKNTLYLQM NSLRTEDTAVYYCAKETSRWGFDYWGQGTLVTVSS
443	PMX084 light chain variable region nucleotide sequence	TCCTATGTGCTGACACAGCTGCCATCCGTGAGTGTGACCC TGAGGCAGACGGCCCGCATCACCTGTGGGGGAGACAGCA TTGGAAGTAAAAATGTTTACTGGCACCAGCAGAAGCTGGG CCAGGCCCCTGTACTGATTATCTATGATGATAGCAGCAGG CCGTCAGGGATCCCTGAGCGATTCTCCGGCGCCAATTCGG GGAATACGGCCACCCTGACCATCAGCGGGGCCCTGGCCG AGGATGAGGCTGACTATTACTGTCAGGTGTGGGACAGTAG TACTAGTGTGTTCGGCGGAGGCACCCATCTGACCGTCCTC G
444	PMX084 light chain variable region amino acid sequence	SYVLTQLPSVSVTLRQTARITCGGDSIGSKNVYWHQQKLGQA PVLIIYDDSSRPSGIPERFSGANSGNTATLTISGALAEDEADYY CQVWDSSTSVFGGGTHLTVL
445	PMX084 heavy chain CDR1	GFTFSNY
446	PMX084 heavy chain CDR2	SNDGRI
447	PMX084 heavy chain CDR3	CAKETSRWGFDYW
448	PMX084 light chain CDR1	GGDSIGSKNVY

449	PMX084 light chain CDR2	DDSSRPS
450	PMX084 light chain CDR3	CQVWDSSTSVF
451	PMX085 Heavy chain variable region nucleic acid sequence	GAGGTTAAGCTGGTGGAGTCTGGGGGAGACCTTGTGAAAC CTGAGGGGTCCCTGAGACTCTCCTGTGTGGTCTCTGGCTT CACCTTTAGTAGGTACGGCATGAGCTGGGTCCGCCAGGCT CCAGGGAAGGGGCTGCAGTGGGTCGCGTACATTAGCAGT GATGGAAGGAGCTCAAGTTACACAGACGCTGTGCAGGGCC GATTCACCATCTCCAGCGACAATGCCAAGAACACGCTGTAT CTGCAGATGAACAGCCTGACAACTGAGGACACAGCCGTGT ATTACTGTGCGAAGTTGGGGCGCGGATTTAATTTTAACTTC TGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
452	PMX085 Heavy chain variable region amino acid sequence	EVKLVESGGDLVKPEGSLRLSCVVSGFTFSRYGMSWVRQAP GKGLQWVAYISSDGRSSSYTDAVQGRFTISSDNAKNTLYLQM NSLTTEDTAVYYCAKLGRGFNFNFWGQGTLVTVSS
453	PMX085 light chain variable region nucleotide sequence	TCCTATGTGCTGACACAGCTGCCATCCAAAAATGTGACCCT GAAGCAGCCGGCCCACATCACCTGTGGGGGAGACAACATT GGAAGTAAAAGTGTTCACTGGTACCAGCAGAAGCTGGGCC AGGCCCCTGTACTGATTATCTATTATGATAGCAGCAGGCCG ACAGGGATCCCTGAGCGATTCTCCGGCGCCAACTCGGGG AACACGGCCACCCTGACCATCAGCGGGGCCCTGGCCGAG GACGAGGCTGACTATTACTGCCAGGTGTGGGACAGCAGTG CTAGTGTGTTCGGCGGAGGCACCCATCTGACCGTCCTCG
454	PMX085 light chain variable region amino acid sequence	SYVLTQLPSKNVTLKQPAHITCGGDNIGSKSVHWYQQKLGQA PVLIIYYDSSRPTGIPERFSGANSGNTATLTISGALAEDEADYY CQVWDSSASVFGGGTHLTVL
455	PMX085 heavy chain CDR1	GFTFSRY
456	PMX085 heavy chain CDR2	SSDGRS

457	PMX085 heavy chain CDR3	CAKLGRGFNFNFW
458	PMX085 light chain CDR1	GGDNIGSKSVH
459	PMX085 light chain CDR2	YDSSRPT
460	PMX085 light chain CDR3	CQVWDSSASVF
461	PMX086 Heavy chain variable region nucleic acid sequence	GAGGTGCAGCTGGTGGAGTCTGGGGGAGACCTGGTGAAG CCTGGGGGGTCCCTGAGACTTTCCTGTGTGGCCTCTGGAT TCACCTTCAGTAGCTACCACATGAGCTGGGTCCGCCAGGC TCCAGGGAAGGGACTTCAGTGGGTCGCATTCATTAACAGT GCTGAAAGTAGCACAACCTATGCAGACGCTGTGAAGGGCC GATTCACCATCTCCAGAGACAACGCCAAGAACACGCTGTA TCTTCAGATGAACAGCCTGAGAGCCGAGGACACGGCCGTA TATTACTGTGCGGGTGGATATATATGGACCCATTTTGACTA CTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
462	PMX086 Heavy chain variable region amino acid sequence	EVQLVESGGDLVKPGGSLRLSCVASGFTFSSYHMSWVRQAP GKGLQWVAFINSAESSTTYADAVKGRFTISRDNAKNTLYLQM NSLRAEDTAVYYCAGGYIWTHFDYWGQGTLVTVSS
463	PMX086 light chain variable region nucleotide sequence	TCCTATGTGCTGACACAGCTGCCATCCGTGAGTGTGACCC TGAGGCAGACGGCCCGCATCACCTGTGGGGGAGACATCA TTGGAAGTAAAAGTGTTTACTGGTACCAGCAGAATCTGGGC CAGGCCCCTGTACTGATTATCTATAGAGATACCAACAGGCC GACAGGGATCCCTGAGCGATTCTCTGGCGCCAGCTCGGG GAACACGGCCACCCTGACCATCAGCGGGGCCCTGGCCGA GGACGAGGCTGACTATTACTGCCAGGTGTGGGACAGCAGT ACTAGTGTGTTCGGCGGAGGCACCCATCTGACCGTCCTCG
464	PMX086 light chain variable region amino acid sequence	SYVLTQLPSVSVTLRQTARITCGGDIIGSKSVYWYQQNLGQAP VLIIYRDTNRPTGIPERFSGASSGNTATLTISGALAEDEADYYC QVWDSSTSVFGGGTHLTVL

465	PMX086 heavy chain CDR1	GFTFSSY
466	PMX086 heavy chain CDR2	NSAESS
467	PMX086 heavy chain CDR3	CAGGYIWTHFDYW
468	PMX086 light chain CDR1	GGDIIGSKSVY
469	PMX086 light chain CDR2	RDTNRPT
470	PMX086 light chain CDR3	CQVWDSSTSVF
471	PMX087 Heavy chain variable region nucleic acid sequence	GAGGTGCACCTGGTGGAGTCTGGGGGAGACCTGGTGAAG CCTGGGGGGTCCCTGAGACTTTCCTGTGTGGCCTCTGGAT TCACCTTCAGTAACTACCACATGAGCTGGGTCCGCCAGGC TCCAGGGAAGGGGCTTCAGTGGGTCGCATTCATTAACAGT GGTGGAAGTGGCACAAGCTATGCAGACGCTGTGAAGGGC CGATTCACCATCTCCAGAGACTACGCCAAGAGCACGCTAT ATCTTCAGATGAACAGCCTGAGAGCCGAGGACACGGCCGT CTATTACTGTGCGAGTGGATATATATGGACCCATTTTGACT ACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
472	PMX087 Heavy chain variable region amino acid sequence	EVHLVESGGDLVKPGGSLRLSCVASGFTFSNYHMSWVRQAP GKGLQWVAFINSGGSGTSYADAVKGRFTISRDYAKSTLYLQM NSLRAEDTAVYYCASGYIWTHFDYWGQGTLVTVSS
473	PMX087 light chain variable region nucleotide sequence	TCCTATGTGCTGACACAGCTGCCATCCGTGAGTGTGACCC TGAGGCAGACGGCCCGCATCACCTGTGGGGGAGACATCA TTGGAAGTAAAAATGTTTACTGGTACCAGCAGAAGCTGGG CCAGGCCCCTATACTGATTATCTATAGAGATAGCAACAGGC CGACAGGGATCCCTGAGCGATTCTCTGGCGCCAGCTCGG GGAACACGGCCACCCTGACCATCAGCGGGGCCCTGGCCG AGGACGAGGCTGACTATTACTGCCAGGTGTGGGACAGCAG

		TACTAGTGTGTTCGGCGGAGGCACCCATCTGACCGTCCTC G
474	PMX087 light chain variable region amino acid sequence	SYVLTQLPSVSVTLRQTARITCGGDIIGSKNVYWYQQKLGQAP ILIIYRDSNRPTGIPERFSGASSGNTATLTISGALAEDEADYYC QVWDSSTSVFGGGTHLTVL
475	PMX087 heavy chain CDR1	GFTFSNY
476	PMX087 heavy chain CDR2	NSGGSG
477	PMX087 heavy chain CDR3	CASGYIWTHFDYW
478	PMX087 light chain CDR1	GGDIIGSKNVY
479	PMX087 light chain CDR2	RDSNRPT
480	PMX087 light chain CDR3	CQVWDSSTSVF
481	PMX088 Heavy chain variable region nucleic acid sequence	GAGGTGCAGTTGGTGGAGTCTGGGGGAGACCTGGTGAAG CCTGGGGGGTCCCTGAGACTTTCCTGTGTGGCCTCTGGAT TCACCTTCAATACCTACCACATGAACTGGGTCCGCCAGGC TCCAGGGAAGGGGCTTCACTGGGTCGCATTCATTAACAGC GGTGGGACTGGCACAGGCTATTCAGACACTGTGAAGGGC CGATTCACCATCTCCAGAGACTACGCCAAGAATACACTCTA TCTTCAGATGAATAGTCTGAGAGCCGAAGACACGGCCGTT TATTATTGTGTGAGTGGATCTATATGGACTCATTTTGACTAC TGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
482	PMX088 Heavy chain variable region amino acid sequence	EVQLVESGGDLVKPGGSLRLSCVASGFTFNTYHMNWVRQAP GKGLHWVAFINSGGTGTGYSDTVKGRFTISRDYAKNTLYLQM NSLRAEDTAVYYCVSGSIWTHFDYWGQGTLVTVSS

483	PMX088 light chain variable region nucleotide sequence	TCCTATGTGCTGACACAGCTGCCATCCGTGAGTATGACCC TGAGGCAGACGGCCCACATCACCTGTGGGGGAGACATCAT TGGAAGTAAAAGTGTTTACTGGTACCAGCAGAAGCTGGGC CAGGCCCCTGTACTGATTATTTATAGAGATACCAACAGGCC GACAGGGATCCCTGAGCGATTCTCTGGCGCCAGCTCGGG GAACACGGCCACCCTGACCATCAGCGGGGCCCTGGCCGA GGACGAGGCTGACTATTACTGCCAGGTTTGGGACAGCAAT ACTCAGGCTGTGTTCGGCGGAGGCACCCATCTGACCGTCC TCG
484	PMX088 light chain variable region amino acid sequence	SYVLTQLPSVSMTLRQTAHITCGGDIIGSKSVYWYQQKLGQA PVLIIYRDTNRPTGIPERFSGASSGNTATLTISGALAEDEADYY CQVWDSNTQAVFGGGTHLTVL
485	PMX088 heavy chain CDR1	GFTFNTY
486	PMX088 heavy chain CDR2	NSGGTG
487	PMX088 heavy chain CDR3	CVSGSIWTHFDYW
488	PMX088 light chain CDR1	GGDIIGSKSVY
489	PMX088 light chain CDR2	RDTNRPT
490	PMX088 light chain CDR3	CQVWDSNTQAVF
491	PMX089 Heavy chain variable region nucleic acid sequence	GAGGTGCAGCTGGTGGAGTCTGGGGGAGACCTGGTGAAG CCTGGGGGGTCCCTGAGACTTTCCTGTGTGGCCTCTGGAT TCACCTTCAATAACTTCCACATGAGTTGGGTCCGCCAGGCT CCAGGGAAGGGGCTTCAGTGGGTCGCATTCATTAACAGTG ATGGAGGTAATAGAAACTATGCAGACGTTGTGAAGGGCCG AGTCACCATCTCCAGAGACTACGCCAAGAATACGCTGTATC TTCAGATAAACAGTCTGAGAGCCGAGGACACGGCCGTGTA

		TTACTGTGCGGGTGGATCTATATGGACTCACTTTGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
492	PMX089 Heavy chain variable region amino acid sequence	EVQLVESGGDLVKPGGSLRLSCVASGFTFNNFHMSWVRQAP GKGLQWVAFINSDGGNRNYADVVKGRVTISRDYAKNTLYLQI NSLRAEDTAVYYCAGGSIWTHFDYWGQGTLVTVSS
493	PMX089 light chain variable region nucleotide sequence	TCCTATGTGTTGACACAGCTGCCATCCATGAGTGTGACCCT GAGGCAGACGGCCCGCATCACCTGTGAGGGAGACATCATT GCAAGTAAAAGAATTTACTGGTACCAACAGAAGCTGGGCC AGGTCCCTGTACTGCTTATCTATGCTGATAGCAGCAGGCC GTCAGGGATCCCTGAACGATTCTCCGGCGCCAGCTCGGG GAACACAGCCACCCTGACCATCAGCGGGGCCCTGGCCGA GGACGAGGCTGACTATTACTGCCAGGTGTGGGACAACAAT GCTAATAGTGTGTTCGGCGGAGGCACCCATCTGACCGTCC TCG
494	PMX089 light chain variable region amino acid sequence	SYVLTQLPSMSVTLRQTARITCEGDIIASKRIYWYQQKLGQVP VLLIYADSSRPSGIPERFSGASSGNTATLTISGALAEDEADYYC QVWDNNANSVFGGGTHLTVL
495	PMX089 heavy chain CDR1	GFTFNNF
496	PMX089 heavy chain CDR2	NSDGGN
497	PMX089 heavy chain CDR3	CAGGSIWTHFDYW
498	PMX089 light chain CDR1	EGDIIASKRIY
499	PMX089 light chain CDR2	ADSSRPS
500	PMX089 light chain CDR3	CQVWDNNANSVF

501	PMX090 Heavy chain variable region nucleic acid sequence	GAGGTACAGTTGGTGGAATCTGGGGGAGACCTGGTGAAG CCTGGGGGGTCCCTGAGACTTTCCTGTGTGGCCTCTGGAT TCACCTTCAATACCTACCACATGAACTGGGTCCGCCAGGC TCCAGGGAAGGGACTTCACTGGGTCGCATTCATTAACAGC GGTGGAGGTGGCACAAGCTATGCAGACACTGTGCAGGGC CGATTCACCATCTCCAGAGACTACGCCAAGAACGCACTCT ATCTTCAGATGAACAGCCTGAGAGCCGAGGACACGGCCGT TTATTACTGTGCGAGTGGATCTATATGGACTCATTTTGACTA CTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
502	PMX090 Heavy chain variable region amino acid sequence	EVQLVESGGDLVKPGGSLRLSCVASGFTFNTYHMNWVRQAP GKGLHWVAFINSGGGGTSYADTVQGRFTISRDYAKNALYLQ MNSLRAEDTAVYYCASGSIWTHFDYWGQGTLVTVSS
503	PMX090 light chain variable region nucleotide sequence	TCCTATGTGCTGACACAGCTGCCATTCATGCGTGTGACCCT GAGTCAGACGGCCCGCATCACCTGTGAGGGAGACAACATT GGAAGTAAAAGAGTTTTCTGGTACCAGCAGAAGCCGGGCC AGGTCCCTGTAGTGATTATTCATGATGATAGCAGCAGGCC GTCAGGGATCCCTGAGCGATTCTCCGGCGCCAATTCGGG GAACACAGCCACCCTGACCATCAGCGGGGCCCTGGCCGA GGACGAGGCTGCCTATTACTGCCAGGTGTGGGACAGCAGT ACTAATAGTGTGTTCGGCGGGGGCACCCATCTGACCGTCC TCG
504	PMX090 light chain variable region amino acid sequence	SYVLTQLPFMRVTLSQTARITCEGDNIGSKRVFWYQQKPGQV PVVIIHDDSSRPSGIPERFSGANSGNTATLTISGALAEDEAAYY CQVWDSSTNSVFGGGTHLTVL
505	PMX090 heavy chain CDR1	GFTFNTY
506	PMX090 heavy chain CDR2	NSGGGG
507	PMX090 heavy chain CDR3	CASGSIWTHFDYW
508	PMX090 light chain CDR1	EGDNIGSKRVF

509	PMX090 light chain CDR2	DDSSRPS
510	PMX090 light chain CDR3	CQVWDSSTNSVF
511	PMX091 Heavy chain variable region nucleic acid sequence	GAGGTGCAGCTGGTGGAGTCTGGGGGAGACCTGGTGAGG CCTGGGGGGTCCCTGAGACTTTCCTGTGTGGCCTCTGGAT TCACCTTCAGTAACTACCACATGAATTGGGTCCGCCAGGCT CCAGGGAAGGGGCTTCAGTGGGTCGCATTCATTAACAGTG GTGGAGGTGGCACATCCTATGCAGACGTTGTGAGGGGCC GATTCACCATCTCCAGAGACTACGCCAAAAACACATTGTAT CTTCAGATGAACAGCCTGAGCGCCGAGGACACGGCCGTAT ATTACTGTGCGAGTGGATCTATATGGACTCATTTTGACTAC TGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
512	PMX091 Heavy chain variable region amino acid sequence	EVQLVESGGDLVRPGGSLRLSCVASGFTFSNYHMNWVRQAP GKGLQWVAFINSGGGGTSYADVVRGRFTISRDYAKNTLYLQ MNSLSAEDTAVYYCASGSIWTHFDYWGQGTLVTVSS
513	PMX091 light chain variable region nucleotide sequence	TCCTATGTGCTGACACAGCTGACATCCATGAGTGTGACCCT GAGGCAGGCGGCCCGCTTCACCTGTGAGAGAGACACCAT TGGAAGTAAAAGAGTTTACTGGTACCAGCAGAGGCTGGGC CAGGTCCCTGTCCTGATTATCTATGATTATAACATCAGGCC GTCAGGGATCCCTGAGCGACTCTCCGGCGCCTATTCGGG GAACACAGCCGCCCTGACCATCAGCGGGGCCCTGGCCGA GGACGAGGCTGACTATTTCTGCCAGGTGTGGGACAGCAGT GCTAATAGTGTGTTCGGCGGAGGCACCCATCTGACCGTCC TCG
514	PMX091 light chain variable region amino acid sequence	SYVLTQLTSMSVTLRQAARFTCERDTIGSKRVYWYQQRLGQ VPVLIIYDYNIRPSGIPERLSGAYSGNTAALTISGALAEDEADYF CQVWDSSANSVFGGGTHLTVL
515	PMX091 heavy chain CDR1	GFTFSNY
516	PMX091 heavy chain CDR2	NSGGGG

517	PMX091 heavy chain CDR3	CASGSIWTHFDYW
518	PMX091 light chain CDR1	ERDTIGSKRVY
519	PMX091 light chain CDR2	DYNIRPS
520	PMX091 light chain CDR3	CQVWDSSANSVF
521	PMX092 Heavy chain variable region nucleic acid sequence	GAGGTGCAGTTGGTGGAGTCTGGGGGAGACCTGGTGAAG CCGGGGGGGTCCCTGAGACTTTCCTGTGTGGCCTCTGGAT TCACCTTCAATAACCTCCACATGAGTTGGGTCCGCCAGGC TCCAGGGAAGGGGCTTCAGTGGGTCGCATTCATTAACAGT GATGGACGTAATAGAAACTATGCAGACGCTGTGAAGGGCC GAGTCACCATCTCCAGAGACTACGCCAAGAATACGCTGTA TCTTCAGATAAACAGTCTGAGAGCCGAAGACACGGCCGTG TATTACTGTACGGGTGGATCTATATGGACTCACTTTGACTA CTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
522	PMX092 Heavy chain variable region amino acid sequence	EVQLVESGGDLVKPGGSLRLSCVASGFTFNNLHMSWVRQAP GKGLQWVAFINSDGRNRNYADAVKGRVTISRDYAKNTLYLQI NSLRAEDTAVYYCTGGSIWTHFDYWGQGTLVTVSS
523	PMX092 light chain variable region nucleotide sequence	TCCTATGTGTTGACACAGCTGCCATCCATGAGTGTGACCCT GAGGCAGACGGCCCGCATCACCTGTGAGGGAGACATCATT GCAAGTAAAAGAGTTTACTGGTACCAACAGAAGCTGGGCC AGGTCCCTGTACTGTTTATCTATGCTGATAACAGCAGGCCG TCAGGGATCCCTGAACGATTCTCCGGCGCCAGCTCGGGG AACACAGCCACCCTGACCATCAGCGGGGCCCTGGCCGAG GACGAGGCTGACTATTACTGCCAGGTGTGGGACAGCAATG CTAATAGTGTGTTCGGCGGAGGCACCCATCTGACCGTCCT CG
524	PMX092 light chain variable region amino acid sequence	SYVLTQLPSMSVTLRQTARITCEGDIIASKRVYWYQQKLGQVP VLFIYADNSRPSGIPERFSGASSGNTATLTISGALAEDEADYY CQVWDSNANSVFGGGTHLTVL

525	PMX092 heavy chain CDR1	GFTFNNL
526	PMX092 heavy chain CDR2	NSDGRN
527	PMX092 heavy chain CDR3	CTGGSIWTHFDYW
528	PMX092 light chain CDR1	EGDIIASKRVY
529	PMX092 light chain CDR2	ADNSRPS
530	PMX092 light chain CDR3	CQVWDSNANSVF
531	PMX093 Heavy chain variable region nucleic acid sequence	GAGGTGCAGCTGGTGGAGTCTGGGGGAGACCTGGTGAAG CCTGGGGGGTCCCTGAGACTTTCCTGTGTGGCCTCTGGAT TCACCTTCAGTAGCTACCACATGAGCTGGGTCCGCCAGGC TCCAGGGAAGGGGCTTCAGTGGGTCGCATTCATTAACAGT GGTGGAGGTGGCACAAACTATGCAGACGCTGTGAAGGGC CGATTCACCATCTCCAGAGACTACGCCAAGAATACGCTGTA TCTTCAGATGAACAGCCTGAGAGCCGAGGACACGGCCGTG TATTACTGTGTGGGTGGATCTATATGGACTCATTTTGACTA CTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
532	PMX093 Heavy chain variable region amino acid sequence	EVQLVESGGDLVKPGGSLRLSCVASGFTFSSYHMSWVRQAP GKGLQWVAFINSGGGGTNYADAVKGRFTISRDYAKNTLYLQ MNSLRAEDTAVYYCVGGSIWTHFDYWGQGTLVTVSS
533	PMX093 light chain variable region nucleotide sequence	TCCTATGTGCTGACACAGCTGCCATCCATGAGTGTGACCC TGAGGCAGACGGCCCGCATCACCTGTGAGGGAGACATCAT TGCAAGTAAAAGAGTTTACTGGTACCAACAGAAGCTGGGC CAGGTCCCTGTACTGCTTATCTATGGTGATAGCAGCAGGC CGTCAGGGATCCCTGAGCGATTCTCCGGCGCCAACTCGG GGAACACAGCCACCCTGACCATCAGCGGGGCCCTGGCCG AGGACGAGGCTGACTATTACTGCCAGGTGTGGGACAGCG

		GTACTAATAGTGTGTTCGGCGGAGGCACCCATCTGACCGT CCTCG
534	PMX093 light chain variable region amino acid sequence	SYVLTQLPSMSVTLRQTARITCEGDIIASKRVYWYQQKLGQVP VLLIYGDSSRPSGIPERFSGANSGNTATLTISGALAEDEADYY CQVWDSGTNSVFGGGTHLTVL
535	PMX093 heavy chain CDR1	GFTFSSY
536	PMX093 heavy chain CDR2	NSGGGG
547	PMX093 heavy chain CDR3	CVGGSIWTHFDYW
538	PMX093 light chain CDR1	EGDIIASKRVY
539	PMX093 light chain CDR2	GDSSRPS
540	PMX093 light chain CDR3	CQVWDSGTNSVF
541	PMX094 Heavy chain variable region nucleic acid sequence	GACATACATCTGGTGGAGTCTGGGGGAGACCTGGTGAGG CCTGGGGGGTCCCTGAGACTTTCCTGTGTGGCCTCTGGAT TCACCTTCAGTAACCTCCACATGAACTGGGTCCGCCAGGC TCCAGGGAAGGGGCTTCAGTGGGTCGCATTCATTAACAGT GGTGGAAGTGGCACAACCTATGCAGACGTTGTGAGGGGC CGATTCACCATCTCCAGAGACTACGCCAAAAACACACTGTA TCTTCAGATGAATAGCCTGAGAGCCGACGACACGGCCGTA TATTACTGTGCGAGTGGATCTATATGGACTCATTTTGACTA CTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
542	PMX094 Heavy chain variable region amino acid sequence	DIHLVESGGDLVRPGGSLRLSCVASGFTFSNLHMNWVRQAP GKGLQWVAFINSGGSGTTYADVVRGRFTISRDYAKNTLYLQM NSLRADDTAVYYCASGSIWTHFDYWGQGTLVTVSS

543	PMX094 light chain variable region nucleotide sequence	TCCTTTGTGTTGACACAGCTGCCATCCGTGAGTGTGACCCT GAGGCAGACGGCCCGCATCACCTGTGGGGGAGACAGTAT TGGAAGTAAAAGTGTTTACTGGTACCAGCAGAAGTTGGGC CAGGCCCCTGTACTGATTATCTATAGAGATAGCAACAGGC CGACAGGGATCCCTGAGCGAATCTCTGGCGCCAGCTCGG GGAACACGGCCACCCTGACCATCAGCGGGGCCCTGGCCG AGGACGAGGCTGACTATTACTGCCAGGTGTGGGACAGCAG TAATAAGGCTATGTTCGGCGGAGGCACCCATCTGACCGTC CTCG
544	PMX094 light chain variable region amino acid sequence	SFVLTQLPSVSVTLRQTARITCGGDSIGSKSVYWYQQKLGQA PVLIIYRDSNRPTGIPERISGASSGNTATLTISGALAEDEADYY CQVWDSSNKAMFGGGTHLTVL
545	PMX094 heavy chain CDR1	GFTFSNL
546	PMX094 heavy chain CDR2	NSGGSG
547	PMX094 heavy chain CDR3	CASGSIWTHFDYW
548	PMX094 light chain CDR1	GGDSIGSKSVY
549	PMX094 light chain CDR2	RDSNRPT
550	PMX094 light chain CDR3	CQVWDSSNKAMF
551	PMX095 Heavy chain variable region nucleic acid sequence	GCGGTGCAGCTGGTGGAGTCTGGGGGAGACCTGGTGAGG CCTGGGGGGTCCCTGAGACTTTCCTGTGTGGCCTCTGGAT TCACCTTCAGTAGTTACCACATGAACTGGGTCCGCCAGGC TCCTGGGAAGGGGCTTCAGTGGGTCGCATTCATTAACAGT GGAGGAAGTAGTACAACCTATGCAGACGTTGTCAGGGGCC GATTCACCATCTCCAGAGACTACGCCAAAAACACGCTATTT CTTCAGATGAACAGCCTGAGAGCCGAGGACACGGCCGTGT

		ATTATTGTGCGATTGGATCTATATGGACACATTTTGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
552	PMX095 Heavy chain variable region amino acid sequence	AVQLVESGGDLVRPGGSLRLSCVASGFTFSSYHMNWVRQAP GKGLQWVAFINSGGSSTTYADVVRGRFTISRDYAKNTLFLQM NSLRAEDTAVYYCAIGSIWTHFDYWGQGTLVTVSS
553	PMX095 light chain variable region nucleotide sequence	TCCTTTGTGCTGACACAGCTGCCATCCGTGAGTGTGACCC TGAGGCAGACGGCCCGCATCACCTGTGGGGGAGACATCA TTGGAAGTAAAAATGTTTACTGGTACCAGCAGAGGCTGGG CCAGGCCCCTGTATTGATTCTCTATAGAGATACCAACAGGC CGACAGGGATCCCTGAGCGATTCTCTGGCGCCAGCTCGG GGAACACGGCCACCCTGACCATCAGCGGGGCCCTGGCCG AGGACGAGGCTGACTATTACTGCCAGGTGTGGGACAACAG TAATAAGGCTATGTTCGGCGGAGGCACCCATCTGACCGTC CTCG
554	PMX095 light chain variable region amino acid sequence	SFVLTQLPSVSVTLRQTARITCGGDIIGSKNVYWYQQRLGQAP VLILYRDTNRPTGIPERFSGASSGNTATLTISGALAEDEADYYC QVWDNSNKAMFGGGTHLTVL
555	PMX095 heavy chain CDR1	GFTFSSY
556	PMX095 heavy chain CDR2	NSGGSS
557	PMX095 heavy chain CDR3	CAIGSIWTHFDYW
558	PMX095 light chain CDR1	GGDIIGSKNVY
559	PMX095 light chain CDR2	RDTNRPT
560	PMX095 light chain CDR3	CQVWDNSNKAMF

561	PMX096 Heavy chain variable region nucleic acid sequence	GAGGTACAGTTGGTGGAGTCTGGGGGAGACCTGGTGAAG CCTGGGGGGTCCCTGAGACTTTCCTGTGTGGCCTCTGGAT TCACCTTCAATACTTACCACATGAACTGGGTCCGCCAGGCT CCAGGGAAGGGGCTTCACTGGGTCGCATTTATTAACAGCG GTGGAAGTGACACAAGCTATGCAGACACTGTGCAGGGCCG GTTCACCATCTCCAGAGACTACGCCAAGAACACACTCTATC TTCAGATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTA TTACTGTGCGAGTGGATATATATGGACTCATTTTGACTACT GGGGCCAGGGAACCCTAGTCACCGTCTCCTCAG
562	PMX096 Heavy chain variable region amino acid sequence	EVQLVESGGDLVKPGGSLRLSCVASGFTFNTYHMNWVRQAP GKGLHWVAFINSGGSDTSYADTVQGRFTISRDYAKNTLYLQM NSLRAEDTAVYYCASGYIWTHFDYWGQGTLVTVSS
563	PMX096 light chain variable region nucleotide sequence	TCCTATGTGCTGACACAGCTGCCATCCGTGAGTGTGACCC TGAGGCAGACGGCCCACATCACCTGTGGGGGAGACATCAT TGGAAGTAAAAGTGTTTACTGGTACCAGCAGAAGCTGGGC CAGGCCCCTGTAATGATTATCTATAGAGATAACAACAGGCC GACAGGGATCCCTGAGCGATTCTCTGGCGCCAGCTCGGG GAACACGGCCACCCTGACCATCAGCGGGTCCCTGGCCGA GGACGAGGCTGACTATTACTGCCAGGTTTGGGACAGCAGG ACTCAGGCTTTGTTCGGCGGAGGCACCCATCTGACCGTCC TCG
564	PMX096 light chain variable region amino acid sequence	SYVLTQLPSVSVTLRQTAHITCGGDIIGSKSVYWYQQKLGQAP VMIIYRDNNRPTGIPERFSGASSGNTATLTISGSLAEDEADYY CQVWDSRTQALFGGGTHLTVL
565	PMX096 heavy chain CDR1	GFTFNTY
566	PMX096 heavy chain CDR2	NSGGSD
567	PMX096 heavy chain CDR3	CASGYIWTHFDYW
568	PMX096 light chain CDR1	GGDIIGSKSVY

569	PMX096 light chain CDR2	RDNNRPT
570	PMX096 light chain CDR3	CQVWDSRTQALF
571	PMX097 Heavy chain variable region nucleic acid sequence	GAGGTGCAGCTGGTGGAGTCTGGGGGAGACCTGGTGAGG CCTGGGGGGTCCCTGAGACTTTCCTGTGTGGCCTCTGGAA TCACCTTCAGTAGTTACCACATGAGTTGGGTCCGCCAGGC TCCTGGGAAGGGGCTTCAGTGGGTCGCACTCATAAACAGT GGTGGAAGTAGTATAACCTATGCAGACGTTGTGAGGGGCC GATTCACCATCTCCAGAGACTACGCCAAAAACACGCTGTAT CTTCAGATGAACAGCCTGAGAGCCGAGGACACGGCCGTGT ATTATTGTGCGAGTGGATCTATATGGACTCATTTTGACTATT GGGGCCAGGGGACCCGGGTCACCGTCTCCTCAG
572	PMX097 Heavy chain variable region amino acid sequence	EVQLVESGGDLVRPGGSLRLSCVASGITFSSYHMSWVRQAP GKGLQWVALINSGGSSITYADVVRGRFTISRDYAKNTLYLQM NSLRAEDTAVYYCASGSIWTHFDYWGQGTRVTVSS
573	PMX097 light chain variable region nucleotide sequence	TCCTTTGTGCTGACACAGCTGCCATCCGTGAGTGTGACCC TGAGGCAGACGGCCCGCATCACCTGTGGGGGAGACATCA TTGGAAGTAAAAATGTTTACTGGTATCAACAGAGGCTGGGC CAGGCCCCTGTATTGATTATCTATAGAGATAGCAACAGGCC GACAGGGATCCCTGAGCGATTCTCTGGCGCCAGCTCGGG GAACACGGCCACCCTGACCATCAGCGGGGCCCTGGCCGA GGACGAGGCTGACTATTACTGCCAGGTGTGGGACAACAGT AATAAGGCTATGTTCGGCGGAGGCACCCATCTGACCGTCC TCG
574	PMX097 light chain variable region amino acid sequence	SFVLTQLPSVSVTLRQTARITCGGDIIGSKNVYWYQQRLGQAP VLIIYRDSNRPTGIPERFSGASSGNTATLTISGALAEDEADYYC QVWDNSNKAMFGGGTHLTVL
575	PMX097 heavy chain CDR1	GITFSSY
576	PMX097 heavy chain CDR2	NSGGSS

577	PMX097 heavy chain CDR3	CASGSIWTHFDYW
578	PMX097 light chain CDR1	GGDIIGSKNVY
579	PMX097 light chain CDR2	RDSNRPT
580	PMX097 light chain CDR3	CQVWDNSNKAMF
581	PMX098 Heavy chain variable region nucleic acid sequence	GAGGTGCAATTGGTGGAGTCTGGGGGAGACCTGGTGAAG CCTGGGGGGTCCCTGAGACTTTCCTGTGTGGCCTCTGGAT TCACCTTCAATACCTACCACATGAACTGGGTCCGCCAGGC TCCAGGGAAGGGGCTTCACTGGGTCGCATTCATTAACAGC GGTGGAAGTGGCACAAGCTATGCAGACACTGTGAAGGGC CGATTCACCATCTCCAGAGACTACGCCAAGAACACACTCTA TCTTCAGATGAACAGCCTGAGAGCCGAGGACACGGCCGTG TATTACTGTGCGAGTGGATCTATATGGACTCATTTTGACTA CTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
582	PMX098 Heavy chain variable region amino acid sequence	EVQLVESGGDLVKPGGSLRLSCVASGFTFNTYHMNWVRQAP GKGLHWVAFINSGGSGTSYADTVKGRFTISRDYAKNTLYLQM NSLRAEDTAVYYCASGSIWTHFDYWGQGTLVTVSS
583	PMX098 light chain variable region nucleotide sequence	TCCTATGTGCTGACACAGCTGCCATCCGTGAGTTTGACCCT GAGGCAGACGGCCCACATCACCTGTGGGGGAGACATCATT GGAAGTAAAAGTGTTTACTGGTACCAGCAGAAGCTGGGCC AGGCCCCTGTATTGATTATCTATAGAGATAACAACAGGCCG ACAGGGATCCCTGAGCGATTCTCTGGCGCCAGCTCGGGG AACACGGCCACCCTGACCATCAGCGGGGCCCTGGCCGAG GACGAGGCTGACTATTACTGCCAGGTTTGGGACAGCAGTA CTCAGGCTATGTTCGGCGGAGGCACCCATCTGACCGTCCT CG
584	PMX098 light chain variable region amino acid sequence	SYVLTQLPSVSLTLRQTAHITCGGDIIGSKSVYWYQQKLGQAP VLIIYRDNNRPTGIPERFSGASSGNTATLTISGALAEDEADYYC QVWDSSTQAMFGGGTHLTVL

585	PMX098 heavy chain CDR1	GFTFNTY
586	PMX098 heavy chain CDR2	NSGGSG
587	PMX098 heavy chain CDR3	CASGSIWTHFDYW
588	PMX098 light chain CDR1	GGDIIGSKSVY
589	PMX098 light chain CDR2	RDNNRPT
590	PMX098 light chain CDR3	CQVWDSSTQAMF
591	PMX099 Heavy chain variable region nucleic acid sequence	GAGGTGCAGCTGGTGGAGTCTGGGGGAGACCTGGTGAGG CCTGGGGGGTCCCTGAGACTTTCCTGTGTGGCCTCTGGAT TCACCTTCAGTAGCTACCACATGAACTGGGTCCGCCAGGC TCCAGGGAAGGGGCTTCAGTGGGTCGCATTCATTAACAGT GGTGGAAGTAGCACAACCTATGCAGACGTTGTGAGGGGCC GATTCACCATCTCCAGAGACTACGCCAAAAACACGCTGTAT CTTCAGATGAACAGCCTGAGAGCCGAGGACACGGCCGTGT ATTACTGTGCGAGTGGATCTATATGGACTCATTTTGACTAC TGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
592	PMX099 Heavy chain variable region amino acid sequence	EVQLVESGGDLVRPGGSLRLSCVASGFTFSSYHMNWVRQAP GKGLQWVAFINSGGSSTTYADVVRGRFTISRDYAKNTLYLQM NSLRAEDTAVYYCASGSIWTHFDYWGQGTLVTVSS
593	PMX099 light chain variable region nucleotide sequence	TCCTTTGTGCTGACACAGCTGCCATCCGTAAGTGTGACCCT GAGGCAGACGGCCCGCATCACCTGTGGGGGAGACAGCAT TGGAACTAAGAGTGTTTACTGGTACCAGCAGAAGCTGGGC CAGGCCCCTGTATTGATTATCTATAGAGATAGCAACAGGCC GACAGGGATCCCTGAGCGATTCTCTGGCGCCAGCTCGGG GAACACGGCCACCCTGACCATCAGCGGGGCCCTGGCCGA GGACGAGGCTGACTATTACTGCCAGGTGTGGGACAGCAGT

		AATAAGGCTATGTTCGGCGGAGGCACCCATCTGACCGTCC TCG
594	PMX099 light chain variable region amino acid sequence	SFVLTQLPSVSVTLRQTARITCGGDSIGTKSVYWYQQKLGQA PVLIIYRDSNRPTGIPERFSGASSGNTATLTISGALAEDEADYY CQVWDSSNKAMFGGGTHLTVL
595	PMX099 heavy chain CDR1	GFTFSSY
596	PMX099 heavy chain CDR2	NSGGSS
597	PMX099 heavy chain CDR3	CASGSIWTHFDYW
598	PMX099 light chain CDR1	GGDSIGTKSVY
599	PMX099 light chain CDR2	RDSNRPT
600	PMX099 light chain CDR3	CQVWDSSNKAMF
601	PMX100 Heavy chain variable region nucleic acid sequence	GAGGTGCAGCTGGTGGAGTCTGGGGGAGACCTGGTGAGG CCTGGGGGGTCCCTGAGACTTTCCTGTGTGGCCTCTGGAT TCACCTTCAGTAGTTACCACATGAGCTGGGTCCGCCAGGC TCCTGGGAAGGGGCTTCAGTGGGTCGCATTCATTAACAGT GGTGGAAGTAGTACAACCTATGCAGACGTTGTGAGGGGCC GATTCACCATCTCCAGAGACTACGCCAAAAACACGCTGTAT CTTCAGATGAACAGCCTGAGAGCCGAGGACACGGCCGTGT ATTATTGTGCGAGTGGATCTATATGGACTCATTTTGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
602	PMX100 Heavy chain variable region amino acid sequence	EVQLVESGGDLVRPGGSLRLSCVASGFTFSSYHMSWVRQAP GKGLQWVAFINSGGSSTTYADVVRGRFTISRDYAKNTLYLQM NSLRAEDTAVYYCASGSIWTHFDYWGQGTLVTVSS

603	PMX100 light chain variable region nucleotide sequence	TCCTTTGTGCTGACACAGCTGCCATCCGTGAGTGTGACCC TGAGGCAGACGGCCCGCATCACCTGTGGGGGAGACAGCA TTGGAAGTAAAAGTGTTTACTGGTACCAGCAGAGGCTGGG CCAGGCCCCTGTATTGATTATCTATAGAGATAGCAACAGGC CGACAGGGATCCCTGAGCGATTCTCTGGCGCCAGCTCGG GGAACACGGCCACCCTGACCATCAGCGGGGCCCTGGCCG AGGACGAGGCTGACTATTACTGCCAGGTGTGGGACAACAG TAATAAGGCTATGTTCGGCGGAGGCACCCATCTGACCGTC CTCG
604	PMX100 light chain variable region amino acid sequence	SFVLTQLPSVSVTLRQTARITCGGDSIGSKSVYWYQQRLGQA PVLIIYRDSNRPTGIPERFSGASSGNTATLTISGALAEDEADYY CQVWDNSNKAMFGGGTHLTVL
605	PMX100 heavy chain CDR1	GFTFSSY
606	PMX100 heavy chain CDR2	NSGGSS
607	PMX100 heavy chain CDR3	CASGSIWTHFDYW
608	PMX100 light chain CDR1	GGDSIGSKSVY
609	PMX100 light chain CDR2	RDSNRPT
610	PMX100 light chain CDR3	CQVWDNSNKAMF
611	PMX101 Heavy chain variable region nucleic acid sequence	GAGGTGCAGCTGGTGGAGTCTGGGGGAGACCTGGTGAGG CCTGGGGGGTCCCTGAGACTTTCCTGTGTGGCCTCTGGAT TCACCTTCAGTAACTACCACATGAGCTGGGTCCGCCAGGC TCCAGGGAAGGGGCTTCAGTGGGTCGCATTCATTAACAGT GGTGGAAGTAGCACAAGCTATGCAGACGCTGTGAGGGGC CGATTCACCATCTCCAGAGACTACGCCAAGAACACGCTGT ATCTTCAGATGAACAGCCTGAGAGCCGAGGACACGGCCGT

		CTATTACTGTGCGAGTGGATCTATATGGACTCATTTTGACT ATTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
612	PMX101 Heavy chain variable region amino acid sequence	EVQLVESGGDLVRPGGSLRLSCVASGFTFSNYHMSWVRQAP GKGLQWVAFINSGGSSTSYADAVRGRFTISRDYAKNTLYLQM NSLRAEDTAVYYCASGSIWTHFDYWGQGTLVTVSS
613	PMX101 light chain variable region nucleotide sequence	TCCTTTGTGCTGACACAGCTGCCATCCGTGAGTGTGACCC TGAGGCAGACGGCCCGCATCACCTGTGGGGGAGACATCA TTGGAAGTAAAAGTGTTTACTGGTTCCAGCAGAAGCTGGG CCAGGCCCCTATACTGATTATCTATAGAGATGACAACAGGC CGACAGGGATCCCTGAGCGATTCTCTGGCGCCAGCTCGG GGAACACGGCCACCCTGATCATCAGCGGGGCCCTGGCCG AGGACGAGGCTCACTATTACTGCCAGGTGTGGGACAGCAG TTCTAAGGCCATGTTCGGCGGAGGCACCCATCTGACCGTC CTCG
614	PMX101 light chain variable region amino acid sequence	SFVLTQLPSVSVTLRQTARITCGGDIIGSKSVYWFQQKLGQAP ILIIYRDDNRPTGIPERFSGASSGNTATLIISGALAEDEAHYYCQ VWDSSSKAMFGGGTHLTVL
615	PMX101 heavy chain CDR1	GFTFSNY
616	PMX101 heavy chain CDR2	NSGGSS
617	PMX101 heavy chain CDR3	CASGSIWTHFDYW
618	PMX101 light chain CDR1	GGDIIGSKSVY
619	PMX101 light chain CDR2	RDDNRPT
620	PMX101 light chain CDR3	CQVWDSSSKAMF

621	PMX102 Heavy chain variable region nucleic acid sequence	GAGGTACAACTGGTGGAGTCTGGGGGAGACCTGGTGAGG CCTGGGGGGTCCCTGAGACTTTCCTGTGTGGCCTCTGGAT TCACCTTCAATAATTACCACATGAGCTGGGTCCGCCAGGCT CCTGGGAAGGGGCTTCAGTGGGTCGCATACATTAACAGTG GTGGAAGTAGCACAAGTTATGCAGACGCTGTGAAGGGCCG ATTCACCATCTCCAGAGACAACGCCAAGAACACGCTGTATC TTCAGATGAACAGCCTGAGAGCCGAGGACACGGCCTTATA TTATTGTGCGAGTGGATCTATATGGACTCATTTTGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
622	PMX102 Heavy chain variable region amino acid sequence	EVQLVESGGDLVRPGGSLRLSCVASGFTFNNYHMSWVRQAP GKGLQWVAYINSGGSSTSYADAVKGRFTISRDNAKNTLYLQM NSLRAEDTALYYCASGSIWTHFDYWGQGTLVTVSS
623	PMX102 light chain variable region nucleotide sequence	TCCTTTGTGCTGACACAGCTGCCATCCGTGAGTGTGACCC TGAGGCAGACGGCCCGCATCACCTGTGGGGGAGACATCA TTGGAAGTAAAAATGTTTACTGGTACCAGCAGAGGCTGGG CCAGGCCCCTGTATTGATTATCTATAGAGATAGTAACAGGC CGACAGGGATCCCTGAGCGATTCTCTGGCGCCAGCTCGG GGAACACGGCCACCCTGACCATCAGCGGGGCCCTGGCCG AGGACGAGGGTGACTATTACTGCCAGGTGTGGGACAACAG TAATAAGGCTATATTCGGCGGAGGCACCCATCTGACCGTC CTCG
624	PMX102 light chain variable region amino acid sequence	SFVLTQLPSVSVTLRQTARITCGGDIIGSKNVYWYQQRLGQAP VLIIYRDSNRPTGIPERFSGASSGNTATLTISGALAEDEGDYYC QVWDNSNKAIFGGGTHLTVL
625	PMX102 heavy chain CDR1	GFTFNNY
626	PMX102 heavy chain CDR2	NSGGSS
627	PMX102 heavy chain CDR3	CASGSIWTHFDYW
628	PMX102 light chain CDR1	GGDIIGSKNVY

629	PMX102 light chain CDR2	RDSNRPT
630	PMX102 light chain CDR3	CQVWDNSNKAIF
631	PMX103 Heavy chain variable region nucleic acid sequence	GAGGTACAGCTGGTGGAGTCTGGGGGAGACCTGGTGAGG CCTGGGGGGTCCCTGAGACTCTCCTGTGTGGCCTCTGGAT TCACCTTCAGTAACCTCCACATGAATTGGGTCCGCCAGGC TCCAGGGAAGGGGCTTCAGTGGGTCGCATTCATTAACAGT GGTGGAAGTGGCACAACCTATGCAGACGTTGTGAGGGGC CGATTCACCATCTCCAGGGACTACGCCAAAAACACACTGA ATCTTCAGATGACTAGCCTGAGAGCCGAGGACACGGCCGT ATATTATTGTGCGACTGGATCTATATGGACTCATTTTGACTA TTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
632	PMX103 Heavy chain variable region amino acid sequence	EVQLVESGGDLVRPGGSLRLSCVASGFTFSNLHMNWVRQAP GKGLQWVAFINSGGSGTTYADVVRGRFTISRDYAKNTLNLQM TSLRAEDTAVYYCATGSIWTHFDYWGQGTLVTVSS
633	PMX103 light chain variable region nucleotide sequence	TCCTTTGTGTTGACACAGCTGCCATCCGTGAGTGTGACCCT GAGGCAGACGGCCCGCATCACCTGTGGGGGAGACAGTAT TGGAAGTAAAAGTGTTTACTGGTACCAGCAGAAGTTGGGC CAGGCCCCTGTATTGATTATCTATAGAGATAGCAACAGGCC GACAGGGATCCCTGAGCGAATCTCTGGCGCCAGCTCGGG GAACACGGCCACCCTGACCATCAGCGGGGCCCTGGCCGA GGACGAGGCTGACTATTACTGCCAGGTGTGGGACAGCAGT AATAAGGCTATGTTCGGCGGAGGCACCCATCTGACCGTCC TCG
634	PMX103 light chain variable region amino acid sequence	SFVLTQLPSVSVTLRQTARITCGGDSIGSKSVYWYQQKLGQA PVLIIYRDSNRPTGIPERISGASSGNTATLTISGALAEDEADYY CQVWDSSNKAMFGGGTHLTVL
635	PMX103 heavy chain CDR1	GFTFSNL
636	PMX103 heavy chain CDR2	NSGGSG

637	PMX103 heavy chain CDR3	CATGSIWTHFDYW
638	PMX103 light chain CDR1	GGDSIGSKSVY
639	PMX103 light chain CDR2	RDSNRPT
640	PMX103 light chain CDR3	CQVWDSSNKAMF
641	PMX104 Heavy chain variable region nucleic acid sequence	GAGGTGCAGCTGGTGGAGTCTGGGGGAGACCTGGTGAGG CCTGGGGGGTCCCTGAGACTTTCCTGTGTGGCCTCTGGAT TCACCTTCAGTAACTACCACATGAGCTGGGTCCGCCAGGC TCCAGGGAAGGGGCTTCAGTGGGTCGCATTCATTAACAGT GGTGGAACTAGTACAACCTATGCAGACGCTGTGAGGGGCC GATTCACCACCTCCAGAGACTACGCCAAGAACACGCTGTA TCTTCAGATGAACAGCCTGAGAGCCGAGGACACGGCCGTC TATTACTGTACGAGTGGATCTATATGGACTCATTTTGACTAT TGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
642	PMX104 Heavy chain variable region amino acid sequence	EVQLVESGGDLVRPGGSLRLSCVASGFTFSNYHMSWVRQAP GKGLQWVAFINSGGTSTTYADAVRGRFTTSRDYAKNTLYLQ MNSLRAEDTAVYYCTSGSIWTHFDYWGQGTLVTVSS
643	PMX104 light chain variable region nucleotide sequence	TCCTTTGTGCTGACACAGCTGCCATCCGTGAGTGTGACCC TGAGGCAGACGGCCCGCATCACCTGTGGGGGAGACATCA TTGGAAGTAAAAGTGTTTACTGGTTCCAGCAGAAGCTGGG CCAGGCCCCTATACTGATTATCTATAGAGATGACAACAGGC CGACAGGGATCCCTGAGCGATTCTCTGGCGCCAGCTCGG GGAACACGGCCACCCTGATCATCAGCGGGGCCCTGGCCG AGGACGAGGCTCACTATTACTGCCAGGTGTGGGACAGCAG TTCTAAGGCCATGTTCGGCGGAGGCACCCATCTGACCGTC CTCG
644	PMX104 light chain variable region amino acid sequence	SFVLTQLPSVSVTLRQTARITCGGDIIGSKSVYWFQQKLGQAP ILIIYRDDNRPTGIPERFSGASSGNTATLIISGALAEDEAHYYCQ VWDSSSKAMFGGGTHLTVL

645	PMX104 heavy chain CDR1	GFTFSNY
646	PMX104 heavy chain CDR2	NSGGTS
647	PMX104 heavy chain CDR3	CTSGSIWTHFDYW
648	PMX104 light chain CDR1	GGDIIGSKSVY
649	PMX104 light chain CDR2	RDDNRPT
650	PMX104 light chain CDR3	CQVWDSSSKAMF
651	PMX105 Heavy chain variable region nucleic acid sequence	GAGGTGCAATTGGTGGAGTCTGGTGGAGACCTGGTGAAG CCTGGGGGGTCCCTGAGACTTTCCTGTGTGGCCTCTGGAT TCACCTTCAATACCTACCACATGAACTGGGTCCGCCAGGC TCCAGGGAAGGGGCTTCACTGGGTCGCATTCATTAACAGC GGTGGAAGTGGCACAAGCTATGAAGACACTGTGCAGGGC CGATTCACCATCTCCAGAGACTACGCCAAGAACACACTCTA TCTTCAGATGAACAGCCTGAGAGCCGAGGACACGGCCGTA TATTACTGTGCGTGTGGATCTATATGGACTCATTTTGACTA CTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
652	PMX105 Heavy chain variable region amino acid sequence	EVQLVESGGDLVKPGGSLRLSCVASGFTFNTYHMNWVRQAP GKGLHWVAFINSGGSGTSYEDTVQGRFTISRDYAKNTLYLQM NSLRAEDTAVYYCACGSIWTHFDYWGQGTLVTVSS
653	PMX105 light chain variable region nucleotide sequence	TCCTATGTGCTGACACAGCTGCCATCCGTGAGTGTGACCC TGAGGCAGACGGCCCACATCACCTGTGGGGGAGACATCAT TGGAAGTAAAAGTGTTTACTGGTACCAGCAGAAGCTGGGC CAGGCCCCTGTAATGATTATCTATAGAGATAACAACAGGCC GACAGGGATCCCTGAGCGATTCTCTGGCGCCAGCTCGGG GAACACGGCCACCCTGACCATCAGCGGGTCCCTGGCCGA GGACGAGGCTGACTATTACTGCCAGGTTTGGGACAGCAGG

		ACTCAGGCTTTGTTCGGCGGAGGCACCCATCTGACCGTCC TCG
654	PMX105 light chain variable region amino acid sequence	SYVLTQLPSVSVTLRQTAHITCGGDIIGSKSVYWYQQKLGQAP VMIIYRDNNRPTGIPERFSGASSGNTATLTISGSLAEDEADYY CQVWDSRTQALFGGGTHLTVL
655	PMX105 heavy chain CDR1	GFTFNTY
656	PMX105 heavy chain CDR2	NSGGSG
657	PMX105 heavy chain CDR3	CACGSIWTHFDYW
658	PMX105 light chain CDR1	GGDIIGSKSVY
659	PMX105 light chain CDR2	RDNNRPT
660	PMX105 light chain CDR3	CQVWDSRTQALF
661	PMX106 Heavy chain variable region nucleic acid sequence	GAGGTGCAGCTGGTGGAGTCTGGGGGAGACCTGGTGAAG CCTGGGGGGTCCCTGAGACTTTCCTGTGTGGCCTCTGGAT TCACCTTCAGTAGCTACCACATGAGCTGGGTCCGCCAGGC TCCAGGGAAGGGGCTTCAGTGGGTCGCATACATTAACAGT GGTGGAAGTAGCACAAGCTATGCAGACGCTGTGAAGGGC CGATTCACCATCTCCAGAGACAACGCCAAGAACACGCTGT ATCTTCAGATGAACAGCCTGAGAGCCGAGGACACGGCCGT GTATTACTGTGCGGGCTTTATATGGACTCATTTTGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
662	PMX106 Heavy chain variable region amino acid sequence	EVQLVESGGDLVKPGGSLRLSCVASGFTFSSYHMSWVRQAP GKGLQWVAYINSGGSSTSYADAVKGRFTISRDNAKNTLYLQM NSLRAEDTAVYYCAGFIWTHFDYWGQGTLVTVSS

663	PMX106 light chain variable region nucleotide sequence	GATATTGTCATGACACAGACGCCACCGTCCCTGTCTGTCA GCCCTAGAGAGACGGCCTCCATCTCCTGCAAGGCCAGTCA GAGCCTCCTGCACAGTGATGGAAACACCTATTTGGATTGG TACCTGCAAAAGCCAGGCCAGTCTCCACAGCTTCTGATCTA CTTGGTTTCCAACCGCTTCACTGGCGTGTCAGACAGGTTC AGTGGCAGCGGGTCAGGGACAGATTTCACCCTGAGAATCA GCAGAGTGGAGGCTAACGATACTGGAGTTTATTACTGCGG GCAAGGTACACAGCTGTGGACGTTCGGAGCAGGAACCAA GGTGGAGCTCAAAC
664	PMX106 light chain variable region amino acid sequence	DIVMTQTPPSLSVSPRETASISCKASQSLLHSDGNTYLDWYLQ KPGQSPQLLIYLVSNRFTGVSDRFSGSGSGTDFTLRISRVEAN DTGVYYCGQGTQLWTFGAGTKVELK
665	PMX106 heavy chain CDR1	GFTFSSY
666	PMX106 heavy chain CDR2	NSGGSS
667	PMX106 heavy chain CDR3	CAGFIWTHFDYW
668	PMX106 light chain CDR1	KASQSLLHSDGNTYLD
669	PMX106 light chain CDR2	LVSNRFT
670	PMX106 light chain CDR3	CGQGTQLWTF
671	PMX107 Heavy chain variable region nucleic acid sequence	GCGGTGCAGCTGGTGGAGTCTGGGGGAGACCTGGTGAGG CCTGGGGGGTCCCTGAGACTTTCCTGTGTGGCCTCTGGAT TCACCTTCAGTAGTTACCACATGAACTGGGTCCGCCAGGC TCCTGGGAAGGGGCTTCAGTGGGTCGCATTCATTAACAGT GGAGGAAGTAGTACAACCTATGCAGACGTTGTCAGGGGCC GATTCACCATCTCCAGAGACTACGCCAAAAACACGCTATTT CTTCAGATGAACAGCCTGAGAGCCGAGGACACGGCCGTGT

		ATTATTGTGCGATTGTATCTATATGGACACATTTTGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
672	PMX107 Heavy chain variable region amino acid sequence	AVQLVESGGDLVRPGGSLRLSCVASGFTFSSYHMNWVRQAP GKGLQWVAFINSGGSSTTYADVVRGRFTISRDYAKNTLFLQM NSLRAEDTAVYYCAIVSIWTHFDYWGQGTLVTVSS
673	PMX107 light chain variable region nucleotide sequence	TCCTTTGTGCTGACACAGCTGCCATCCGTGAGTGTGACCC TGAGGCAGACGGCCCGCATCACCTGTGGGGGAGACATCA TTGGAAGTAAAAATGTTTACTGGTACCAGCAGAGGCTGGG CCAGGCCCCTGTATTGATTCTCTATAGAGATACCAACAGGC CGACAGGGATCCCTGAGCGATTCTCTGGCGCCAGCTCGG GGAACACGGCCACCCTGACCATCAGCGGGGCCCTGGCCG AGGACGAGGCTGACTATTACTGCCAGGTGTGGGACAACAG TAATAAGGCTATGTTCGGCGGAGGCACCCATCTGACCGTC CTCG
674	PMX107 light chain variable region amino acid sequence	SFVLTQLPSVSVTLRQTARITCGGDIIGSKNVYWYQQRLGQAP VLILYRDTNRPTGIPERFSGASSGNTATLTISGALAEDEADYYC QVWDNSNKAMFGGGTHLTVL
675	PMX107 heavy chain CDR1	GFTFSSY
676	PMX107 heavy chain CDR2	NSGGSS
677	PMX107 heavy chain CDR3	CAIVSIWTHFDYW
678	PMX107 light chain CDR1	GGDIIGSKNVY
679	PMX107 light chain CDR2	RDTNRPT
680	PMX107 light chain CDR3	CQVWDNSNKAMF

681	PMX108 Heavy chain variable region nucleic acid sequence	GAGGTGCAGCTGGTGGAGTCTGGGGGAGACCTGGTGAGG CCGGGGGGGTCCCTGAGACTTTCCTGTGTGGCCTCTGGAT TCACCTTCACTAACTACCACATGAGCTGGGTCCGCCAGGC TCCAGGGAAGGGGCTTCAGTGGGTCGCATTCATTAACAGT GGTGGAAGTAGCACAACCTATACAGACGTTGTGAGGGGCC GATTCACCATCTCCAGAGACTACGCCAAAAACACGCTGTAT CTTCAGATGAACAGCCTGACAGCCGAGGACACGGCCGTGT ATTACTGTGCGAGTGGAGCTATATGGACTCATTTTGACCAC TGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
682	PMX108 Heavy chain variable region amino acid sequence	EVQLVESGGDLVRPGGSLRLSCVASGFTFTNYHMSWVRQAP GKGLQWVAFINSGGSSTTYTDVVRGRFTISRDYAKNTLYLQM NSLTAEDTAVYYCASGAIWTHFDHWGQGTLVTVSS
683	PMX108 light chain variable region nucleotide sequence	TCCTTTGTACTGACACAGCTGCCATCCGTGAGTGTGACCCT GAGGCAGACGGCCCGCATCACCTGTGGGGGAGACAGCGT TGGAAGTAAAAGTGTTTACTGGTACCAGCAGAAGCTGGGC CAGGCCCCTGTACTGATTATCTATAGAGATAGCAACAGGC CGACAGGGATCCCTGAGCGATTCTCTGGCGCCAGCTCGG GGAACACGGCCACCCTGACCATCAGCGGGGCCCTGGCCG AGGACGAGGCTGACTATTACTGCCAGGTGTGGGACAACAG TAATAAGGCTATATTCGGCGGAGGCACCCATCTGACCGTC CTCG
684	PMX108 light chain variable region amino acid sequence	SFVLTQLPSVSVTLRQTARITCGGDSVGSKSVYWYQQKLGQA PVLIIYRDSNRPTGIPERFSGASSGNTATLTISGALAEDEADYY CQVWDNSNKAIFGGGTHLTVL
685	PMX108 heavy chain CDR1	GFTFTNY
686	PMX108 heavy chain CDR2	NSGGSS
687	PMX108 heavy chain CDR3	CASGAIWTHFDHW
688	PMX108 light chain CDR1	GGDSVGSKSVY

689	PMX108 light chain CDR2	RDSNRPT
690	PMX108 light chain CDR3	CQVWDNSNKAIF
691	PMX109 Heavy chain variable region nucleic acid sequence	GAGGTGCAGCTGGTGGAGTCTGGGGGAGACCTGGTGAGG CCGGGGGGGTCCCTGAGACTTTCCTGTGTGGCCTCTGGAT TCACCTTCACTAACTACCACATGAGCTGGGTCCGCCAGGC TCCAGGGAAGGGGCTTCAGTGGGTCGCATTCATTAACAGT GGTGGAAGTAGCACAACCTATACAGACGTTGTGAGGGGCC GATTCACCATCTCCAGAGACTACGCCAAAAACACGCTGTAT CTTCAGATGAACAGCCTGACAGCCGAGGACACGGCCGTGT ATTACTGTGCGAGTGGATCTATATGGACTCATTTTGACCAC TGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
692	PMX109 Heavy chain variable region amino acid sequence	EVQLVESGGDLVRPGGSLRLSCVASGFTFTNYHMSWVRQAP GKGLQWVAFINSGGSSTTYTDVVRGRFTISRDYAKNTLYLQM NSLTAEDTAVYYCASGSIWTHFDHWGQGTLVTVSS
693	PMX109 light chain variable region nucleotide sequence	TCCTTTGTACTGACACAGCTGCCATCCGTGAGTGTGACCCT GAGGCAGACGGCCCGCATCACCTGTGGGGGAGACAGCGT TGGAAGTAAAAGTGTTTACTGGTACCAGCAGAAGCTGGGC CAGGCCCCTGTACTGATTATCTATAGAGATAGCAACAGGC CGACAGGGATCCCTGAGCGATTCTCTGGCGCCAGCTCGG GGAACACGGCCACCCTGACCATCAGCGGGGCCCTGGCCG AGGACGAGGCTGACTATTACTGCCAGGTGTGGGACAACAG TAATAAGGCTATATTCGGCGGAGGCACCCATCTGACCGTC CTCG
694	PMX109 light chain variable region amino acid sequence	SFVLTQLPSVSVTLRQTARITCGGDSVGSKSVYWYQQKLGQA PVLIIYRDSNRPTGIPERFSGASSGNTATLTISGALAEDEADYY CQVWDNSNKAIFGGGTHLTVL
695	PMX109 heavy chain CDR1	GFTFTNY
696	PMX109 heavy chain CDR2	NSGGSS

697	PMX109 heavy chain CDR3	CASGSIWTHFDHW
698	PMX109 light chain CDR1	GGDSVGSKSVY
699	PMX109 light chain CDR2	RDSNRPT
700	PMX109 light chain CDR3	CQVWDNSNKAIF
701	PMX110 Heavy chain variable region nucleic acid sequence	GAGGTGCAGCTGGTGGAGTCTGGGGGAGACCTGGTGAGG CCTGGGGGGTCCCTGAGACTTTCCTGTGTGGCCTCTGGAT TCACCTTCAGTAGCTACCACATGAGCTGGGTCCGCCAGGC TCCAGGGAAGGGGCTTCAGTGGGTCGCATTCATTAACAGT GGTGGAAGTAGCACAACCTATGCAGACGTTGTGAGGGGCC GATTCACCATCTCCAGAGACTACGCCAAAAACACGCTGTAT CTTCAGATGAACAGCCTGAGAGCCGAGGACACGGCCGTGT ATTACTGTGCGAGTGGATCTATATTGACTCATTTTGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
702	PMX110 Heavy chain variable region amino acid sequence	EVQLVESGGDLVRPGGSLRLSCVASGFTFSSYHMSWVRQAP GKGLQWVAFINSGGSSTTYADVVRGRFTISRDYAKNTLYLQM NSLRAEDTAVYYCASGSILTHFDYWGQGTLVTVSS
703	PMX110 light chain variable region nucleotide sequence	TCCTTTGTGCTGACACAGCTGCCATCCGTGAGTGTGACCC TGAGGCAGACGGCCCGCATCACCTGTGGGGGAGACAGCG TTGGAAGTAAAAGTGTTTACTGGTACCAGCAGAAGCTGGG CCAGGCCCCTGTACTGATTATCTATAGAGATAGCAACAGG CCGACAGGGATCCCTGAGCGATTCTCTGGCGCCAGCTCG GGGAACACGGCCACCCTGACCATCAGCGGGGCCCTGGCC GAGGACGAGGCTGACTATTACTGCCAGGTGTGGGACAACA GTAATAAGGCTATGTTCGGCGGAGGCACCCATCTGACCGT CCTCG
704	PMX110 light chain variable region amino acid sequence	SFVLTQLPSVSVTLRQTARITCGGDSVGSKSVYWYQQKLGQA PVLIIYRDSNRPTGIPERFSGASSGNTATLTISGALAEDEADYY CQVWDNSNKAMFGGGTHLTVL

705	PMX110 heavy chain CDR1	GFTFSSY
706	PMX110 heavy chain CDR2	NSGGSS
707	PMX110 heavy chain CDR3	CASGSILTHFDYW
708	PMX110 light chain CDR1	GGDSVGSKSVY
709	PMX110 light chain CDR2	RDSNRPT
710	PMX110 light chain CDR3	CQVWDNSNKAMF
711	PMX111 Heavy chain variable region nucleic acid sequence	GAGGTGCAGCTGGTGGAGTCTGGGGGAGACCTGGTGAGG CCGGGGGGGTCCCTGAGACTTTCCTGTGTGGCCTCTGGAT TCACCTTCAGTAGCTACCACATGAACTGGGTCCGCCAGGC TCCAGGGAAGGGGCTTCAGTGGGTCGCATTCATTAATAGT GGAGCAAGTAGCGCAACCTATGCAGACGTTGTGAGGGGC CGATTCACCATCTCCAGAGACTACGCCAAAAACACGCTGTA TCTTCAGATGAACAGCCTGAGAGCCGAGGACACGGCCGTG TATTATTGTGCGAGTGGATCTATTTGGACTCATTTTGACTTC TGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
712	PMX111 Heavy chain variable region amino acid sequence	EVQLVESGGDLVRPGGSLRLSCVASGFTFSSYHMNWVRQAP GKGLQWVAFINSGASSATYADVVRGRFTISRDYAKNTLYLQM NSLRAEDTAVYYCASGSIWTHFDFWGQGTLVTVSS
713	PMX111 light chain variable region nucleotide sequence	TCCTTTGTGCTGACACAGCTGCCATCCGTGAGTGTGACCC TGAGGCAGACGGCCCGCATCACCTGTGGGGGAGACAGCG TTGGAAGTAAAAGTGTTTACTGGTACCAGCAGAAGCTGGG CCAGGCCCCTGTACTGATTATCTATAGAGATAGCAACAGG CCGACAGGGATCCCTGAGCGATTCTCTGGCGCCAGCTCG GGGAACACGGCCACCCTGACCATCAGCGGGGCCCTGGCC GAGGACGAGGCTGACTATTACTGCCAGGTGTGGGACAACA

		GTAATAAGGCTATGTTCGGCGGAGGCACCCATCTGACCGTCCTCG
714	PMX111 light chain variable region amino acid sequence	SFVLTQLPSVSVTLRQTARITCGGDSVGSKSVYWYQQKLGQAPVLIIYRDSNRPTGIPERFSGASSGNTATLTISGALAEDEADYYCQVWDNSNKAMFGGGTHLTVL
715	PMX111 heavy chain CDR1	GFTFSSY
716	PMX111 heavy chain CDR2	NSGASS
717	PMX111 heavy chain CDR3	CASGSIWTHFDFW
718	PMX111 light chain CDR1	GGDSVGSKSVY
719	PMX111 light chain CDR2	RDSNRPT
720	PMX111 light chain CDR3	CQVWDNSNKAMF
721	WT IgGB Constant region	ASTTAPSVFPLAPSCGSTSGSTVALACLVSGYFPEPVTVSWNSGSLTSGVHTFPSVLQSSGLYSLSSMVTVPSSRWPSETFTCNVAHPASKTKVDKPVPKRENGRVPRPPDCPKCPAPEMLGGPSVFIFPPKPKDTLLIARTPEVTCVVVDLDPEDPEVQISWFVDGKQMQTAKTQPREEQFNGTYRVVSVLPIGHQDWLKGKQFTCKVNNKALPSPIERTISKARGQAHQPSVYVLPPSREELSKNTVSLTCLIKDFFPPDIDVEWQSNGQQEPESKYRTTPPQLDEDGSYFLYSKLSVDKSRWQRGDTFICAVMHEALHNHYTQKSLSHSPGK
722	Def 1 IgGB Constant region	ASTTAPSVFPLAPSCGSTSGSTVALACLVSGYFPEPVTVSWNSGSLTSGVHTFPSVLQSSGLYSLSSMVTVPSSRWPSETFTCNVAHPASKTKVDKPVPKRENGRVPRPPDCPKCPAPESLGGPSVFIFPPKPKDTLLIARTPEVTCVVVDLDPEDPEVQISWFVDGKQMQTAKTQPREEQFNGTYRVVSVLPIGHQDWLKGKQFTCKVNHIGLPSPIERTISKARGQAHQPSVYVLPPSREELSKNTVSLT

		CLIKDFFPPDIDVEWQSNGQQEPESKYRTTPPQLDEDGSYFL YSKLSVDKSRWQRGDTFICAVMHEALHNHYTQKSLSHSPGK
723	Def 2 IgGB Constant region	ASTTAPSVFPLAPSCGSTSGSTVALACLVSGYFPEPVTVSWN SGSLTSGVHTFPSVLQSSGLYSLSSMVTVPSSRWPSETFTCN VAHPASKTKVDKPVPKRENGRVPRPPDCPKCPAPESLGGPS VFIFPPKPKDTLLIARTPEVTCVVVDLGREDPEVQISWFVDGK QMQTAKTQPREEQFNGTYRVVSVLPIGHQDWLKGKQFTCKV NHIGLPSPIERTISKARGQAHQPSVYVLPPSREELSKNTVSLT CLIKDFFPPDIDVEWQSNGQQEPESKYRTTPPQLDEDGSYFL YSKLSVDKSRWQRGDTFICAVMHEALHNHYTQKSLSHSPGK
724	Def 3 IgGB Constant region	ASTTAPSVFPLAPSCGSTSGSTVALACLVSGYFPEPVTVSWN SGSLTSGVHTFPSVLQSSGLYSLSSMVTVPSSRWPSETFTCN VAHPASKTKVDKPVPKRENGRVPRPPDCPKCPAPESLGGPS VFIFPPKPKDTLLIARTPEVTCVVVDLGREDPEVQISWFVDGK QMQTAKTQPREEQFNGTYRVVSVLPIGHQDWLKGKQFTCKV NHIGLPSSIERTISKARGQAHQPSVYVLPPSREELSKNTVSLT CLIKDFFPPDIDVEWQSNGQQEPESKYRTTPPQLDEDGSYFL YSKLSVDKSRWQRGDTFICAVMHEALHNHYTQKSLSHSPGK
725	Def 4 IgGB Constant region	ASTTAPSVFPLAPSCGSTSGSTVALACLVSGYFPEPVTVSWN SGSLTSGVHTFPSVLQSSGLYSLSSMVTVPSSRWPSETFTCN VAHPASKTKVDKPVPKRENGRVPRPPDCPKCPAPESLGGPS VFIFPPKPKDTLLIARTPEVTCVVVDLGREDPEVQISWFVDGK QMQTAKTQPREEQFNGTYRVVSVLPIGHQDWLKGKQFTCKV NHIGLGSPIERTISKARGQAHQPSVYVLPPSREELSKNTVSLT CLIKDFFPPDIDVEWQSNGQQEPESKYRTTPPQLDEDGSYFL YSKLSVDKSRWQRGDTFICAVMHEALHNHYTQKSLSHSPGK
726	Def 5 IgGB Constant region	ASTTAPSVFPLAPSCGSTSGSTVALACLVSGYFPEPVTVSWN SGSLTSGVHTFPSVLQSSGLYSLSSMVTVPSSRWPSETFTCN VAHPASKTKVDKPVPKRENGRVPRPPDCPKCPAPEAAGGPS VFIFPPKPKDTLLIARTPEVTCVVVDLDPEDPEVQISWFVDGK QMQTAKTQPREEQFNGTYRVVSVLPIGHQDWLKGKQFTCKV NNKALPSPIERTISKARGQAHQPSVYVLPPSREELSKNTVSLT

		CLIKDFFPPDIDVEWQSNGQQEPESKYRTTPPQLDEDGSYFL YSKLSVDKSRWQRGDTFICAVMHEALHNHYTQKSLSHSPGK
727	Def 6 IgGB Constant region	ASTTAPSVFPLAPSCGSTSGSTVALACLVSGYFPEPVTVSWN SGSLTSGVHTFPSVLQSSGLYSLSSMVTVPSSRWPSETFTCN VAHPASKTKVDKPVPKRENGRVPRPPDCPKCPAPEAAGGPS VFIFPPKPKDTLLIARTPEVTCVVVDLDPEDPEVQISWFVDGK QMQTAKTQPREEQFNGTYRVVSVLPIGHQDWLKGKQFTCKV NNKALPSSIERTISKARGQAHQPSVYVLPPSREELSKNTVSLT CLIKDFFPPDIDVEWQSNGQQEPESKYRTTPPQLDEDGSYFL YSKLSVDKSRWQRGDTFICAVMHEALHNHYTQKSLSHSPGK
728	Def 7 IgGB Constant region	ASTTAPSVFPLAPSCGSTSGSTVALACLVSGYFPEPVTVSWN SGSLTSGVHTFPSVLQSSGLYSLSSMVTVPSSRWPSETFTCN VAHPASKTKVDKPVPKRENGRVPRPPDCPKCPAPEAAGGPS VFIFPPKPKDTLLIARTPEVTCVVVDLDPEDPEVQISWFVDGK QMQTAKTQPREEQFNGTYRVVSVLPIGHQDWLKGKQFTCKV NNKALGSPIERTISKARGQAHQPSVYVLPPSREELSKNTVSLT CLIKDFFPPDIDVEWQSNGQQEPESKYRTTPPQLDEDGSYFL YSKLSVDKSRWQRGDTFICAVMHEALHNHYTQKSLSHSPGK
729	Def 8 IgGB Constant region	ASTTAPSVFPLAPSCGSTSGSTVALACLVSGYFPEPVTVSWN SGSLTSGVHTFPSVLQSSGLYSLSSMVTVPSSRWPSETFTCN VAHPASKTKVDKPVPKRENGRVPRPPDCPKCPAPGMLGGPS VFIFPPKPKDTLLIARTPEVTCVVVDLDPENPEVQISWFVDGK QMQTAKTQPREEQFNGTYRVVSVLPIGHQDWLKGKQFTCKV NNKALPSPIERTISKARGQAHQPSVYVLPPSREELSKNTVSLT CLIKDFFPPDIDVEWQSNGQQEPESKYRTTPPQLDEDGSYFL YSKLSVDKSRWQRGDTFICAVMHEALHNHYTQKSLSHSPGK
730	Def 9 IgGB Constant region	ASTTAPSVFPLAPSCGSTSGSTVALACLVSGYFPEPVTVSWN SGSLTSGVHTFPSVLQSSGLYSLSSMVTVPSSRWPSETFTCN VAHPASKTKVDKPVPKRENGRVPRPPDCPKCPAPEAAGGPS VFIFPPKPKDTLLIARTPEVTCVVVDLDPENPEVQISWFVDGK QMQTAKTQPREEQFNGTYRVVSVLPIGHQDWLKGKQFTCKV NNKALPSSIERTISKARGQAHQPSVYVLPPSREELSKNTVSLT CLIKDFFPPDIDVEWQSNGQQEPESKYRTTPPQLDEDGSYFL YSKLSVDKSRWQRGDTFICAVMHEALHNHYTQKSLSHSPGK

731	Ofa-VH-clgGB WT	MELGLSWIFLLAILKGVQCEVQLVESGGGLVQPGRSLRLSCA ASGFTFNDYAMHWVRQAPGKGLEWVSTISWNSGSIGYADSV KGRFTISRDNAKKSLYLQMNSLRAEDTALYYCAKDIQYGNYY YGMDVWGQGTTVTVSSASTTAPSVFPLAPSCGSTSGSTVAL ACLVSGYFPEPVTVSWNSGSLTSGVHTFPSVLQSSGLYSLSS MVTVPSSRWPSETFTCNVAHPASKTKVDKPVPKRENGRVPR PPDCPKCPAPEMLGGPSVFIFPPKPKDTLLIARTPEVTCVVVD LDPEDPEVQISWFVDGKQMQTAKTQPREEQFNGTYRVVSVL PIGHQDWLKGKQFTCKVNNKALPSPIERTISKARGQAHQPSV YVLPPSREELSKNTVSLTCLIKDFFPPDIDVEWQSNGQQEPES KYRTTPPQLDEDGSYFLYSKLSVDKSRWQRGDTFICAVMHEA LHNHYTQKSLSHSPGK
732	hCD20 DNA sequence used for generation of target cells:	5'ATGACAACACCCAGAAATTCAGTAAATGGGACTTTCCCG GCAGAGCCAATGAAAGGCCCTATTGCTATGCAATCTGGTC CAAAACCACTCTTCAGGAGGATGTCTTCACTGGTGGGCCC CACGCAAAGCTTCTTCATGAGGGAATCTAAGACTTTGGGG GCTGTCCAGATTATGAATGGGCTCTTCCACATTGCCCTGG GGGGTCTTCTGATGATCCCAGCAGGGATCTATGCACCCAT CTGTGTGACTGTGTGGTACCCTCTCTGGGGAGGCATTATG TATATTATTTCCGGATCACTCCTGGCAGCAACGGAGAAAAA CTCCAGGAAGTGTTTGGTCAAAGGAAAAATGATAATGAATT CATTGAGCCTCTTTGCTGCCATTTCTGGAATGATTCTTTCAA TCATGGACATACTTAATATTAAAATTTCCCATTTTTTAAAAAT GGAGAGTCTGAATTTTATTAGAGCTCACACACCATATATTA ACATATACAACTGTGAACCAGCTAATCCCTCTGAGAAAAAC TCCCCATCTACCCAATACTGTTACAGCATACAATCTCTGTT CTTGGGCATTTTGTCAGTGATGCTGATCTTTGCCTTCTTCC AGGAACTTGTAATAGCTGGCATCGTTGAGAATGAATGGAAA AGAACGTGCTCCAGACCCAAATCTAACATAGTTCTCCTGTC AGCAGAAGAAAAAAAAGAACAGACTATTGAAATAAAAGAAG AAGTGGTTGGGCTAACTGAAACATCTTCCCAACCAAAGAAT GAAGAAGACATTGAAATTATTCCAATCCAAGAAGAGGAAGA AGAAGAAACAGAGACGAACTTTCCAGAACCTCCCCAAGAT CAGGAATCCTCACCAATAGAAAATGACAGCTCTCCTTAA3'
733	IgG-B	MEFVLGWVFLVAILQGVQGEVQLVESGGDLVKPAGSLRLSCV ASGFTFSNNAMNWVRQAPGKGLQWVAGINSGGSTASADAV

		KGRFTISRDNAKNTVYLQMNSLTAEDTAVYYCAKVIGNWIATS DLDYWGQGTLVIVSSASTTAPSVFPLAPSCGSTSGSTVALAC LVSGYFPEPVTVSWNSGSLTSGVHTFPSVLQSSGLYSLSSMV TVPSSRWPSETFTCNVAHPASKTKVDKPVPKRENGRVPRPP DCPKCPAPEMLGGPSVFIFPPKPKDTLLIARTPEVTCVVVDLD PEDPEVQISWFVDGKQMQTAKTQPREEQFNGTYRVVSVLPI GHQDWLKGKQFTCKVNNKALPSPIERTISKARGQAHQPSVYV LPPSREELSKNTVSLTCLIKDFFPPDIDVEWQSNGQQEPESKY RTTPPQLDEDGSYFLYSKLSVDKSRWQRGDTFICAVMHEALH NHYTQKSLSHSPGK
734	IgG-A	MEFVLGWVFLVAILQGVQGEVQLVESGGDLVKPAGSLRLSCV ASGFTFSNNAMNWVRQAPGKGLQWVAGINSGGSTASADAV KGRFTISRDNAKNTVYLQMNSLTAEDTAVYYCAKVIGNWIATS DLDYWGQGTLVIVSSASTTAPSVFPLAPSCGSTSGSTVALAC LVSGYFPEPVTVSWNSGSLTSGVHTFPSVLQSSGLYSLSSMV TVPSSRWPSETFTCNVVHPASNTKVDKPVFNECRCTDTPPC PVPEPLGGPSVLIFPPKPKDILRITRTPEVTCVVLDLGREDPEV QISWFVDGKEVHTAKTQSREQQFNGTYRVVSVLPIEHQDWLT GKEFKCRVNHIDLPSPIERTISKARGRAHKPSVYVLPPSPKEL SSSDTVSITCLIKDFYPPDIDVEWQSNGQQEPERKHRMTPPQ LDEDGSYFLYSKLSVDKSRWQQGDPFTCAVMHETLQNHYTD LSLSHSPGK
735	IgG-C	MEFVLGWVFLVAILQGVQGEVQLVESGGDLVKPAGSLRLSCV ASGFTFSNNAMNWVRQAPGKGLQWVAGINSGGSTASADAV KGRFTISRDNAKNTVYLQMNSLTAEDTAVYYCAKVIGNWIATS DLDYWGQGTLVIVSSASTTAPSVFPLAPSCGSQSGSTVALAC LVSGYIPEPVTVSWNSGSLTSGVHTFPSILQSSGLYSLSSMVT VPSSRWPSETFTCNVAHPATNTKVDKPVVKECECKCNCNNC PCPGCGLLGGPSVFIFPPKPKDILVTARTPTVTCVVVDLDPEN PEVQISWFVDSKQVQTANTQPREEQSNGTYRVVSVLPIGHQ DWLSGKQFKCKVNNKALPSPIEEIISKTPGQAHQPNVYVLPPS RDEMSKNTVTLTCLVKDFFPPEIDVEWQSNGQQEPESKYRM TPPQLDEDGSYFLYSKLSVDKSRWQRGDTFICAVMHEALHN HYTQKSLSHSPGK

736	IgG-D	MEFVLGWVFLVAILQGVQGEVQLVESGGDLVKPAGSLRLSCV ASGFTFSNNAMNWVRQAPGKGLQWVAGINSGGSTASADAV KGRFTISRDNAKNTVYLQMNSLTAEDTAVYYCAKVIGNWIATS DLDYWGQGTLVIVSSASSTAPSVFPLAPSCGSTSGSTVALAC LVSGYFPEPVTVSWNSGSLTSGVHTFPSVLKSSGLYSLSSMV TVPSSRLPSETFTCNVVHPATNTKVDKPVPKESTCKCISPCPV PESLGGPSVFIFPPKPKDILRITRTPEVTCVVLDLGREDPEVQI SWFVDGKEVHTAKTQPREQQFNSTYRVVSVLPIEHQDWLTG KEFKCRVNHIGLPSPIERTISKARGQAHQPGVYVLPPSPKELS SSDTVTLTCLIKDFFPPEIDVEWQSNGQPEPESKYHTTAPQLD EDGSYFLYSKLSVDKSRWQQGDPFTCAVMHEALQNHYTDLS LSHSPGK
737	PMX154 Heavy chain variable region nucleic acid sequence	GAGGTGCAGTTGGTGGAGTCTGGGGGAGACCTTGTGAAA CCTGAGGGGTCCCTGAGACTCTCCTGTGTGGTCTCTGGCT TCACCTTCAGTGGCTTCGACATGAGCTGGGTCCGCCAGGC TCCAGGGAAGGGGCTGCAGTGGGTCGCATACATTAGTACT GATGGAAGGAGCACAGGTTACACAGACGCTGTGAAGGGC CGATTCACCATCTCCAGAGACAATGTCAAGAACACGCTGTA TCTGCAGATGAACAGCCTGAGAACTGAGGACACAGCCGTG TATTACTGTGCGAAGGAAACTCGTCATTGGGGCTTTGACTA CTGGGGCCAGGGAACCCTAGTCATCGTCTCCTCAG
738	PMX154 Heavy chain variable region amino acid sequence	EVQLVESGGDLVKPEGSLRLSCVVSGFTFSGFDMSWVRQAP GKGLQWVAYISTDGRSTGYTDAVKGRFTISRDNVKNTLYLQM NSLRTEDTAVYYCAKETRHWGFDYWGQGTLVIVSS
739	PMX154 light chain variable region nucleotide sequence	TCCTATGTGTTGACACAGCTGTCATCCGTGAGTGTGAGCCT GAGGCAGACGGCCCACATCACCTGTGGGGGAGACAGCAT TGGACGTAAAAATGTTTACTGGCACCAGCAGAAGCTGGGC CGGGCCCCTATACTGATTATCTATGATGATAGCAGCAGGC CGTCAGGGATCCCTGAGCGATTCTCCGGCGCCAACTCGG GGAACACGGCCACCCTGACCATCAGCGGGGCCCTGGCCG AGGATGAGGCTGCCTATTACTGCCAGGTGTGGGACAGCAG TACTAGTGTGTTCGGCGGAGGCACCCATCTGACCGTCCTC G

740	PMX154 light chain variable region amino acid sequence	SYVLTQLSSVSVSLRQTAHITCGGDSIGRKNVYWHQQKLGRA PILIIYDDSSRPSGIPERFSGANSGNTATLTISGALAEDEAAYYC QVWDSSTSVFGGGTHLTVL
741	PMX154 heavy chain CDR1	GFTFSGF
742	PMX154 heavy chain CDR2	STDGRS
743	PMX154 heavy chain CDR3	CAKETRHWGFDYW
744	PMX154 light chain CDR1	GGDSIGRKNVY
745	PMX154 light chain CDR2	DDSSRPS
746	PMX154 light chain CDR3	CQVWDSSTSVF
747	PMX155 Heavy chain variable region nucleic acid sequence	GAGTTGCACCTAGTGGAGTCTGGGGGAGACCTGGTGAAG CCTGCGGGGTCCCTGAGACTGTCCTGTGTGGCCTCTGGAT TCACCTTCAGTAGCTTCAGAATGAGTTGGGTCCGCCAGTCT CCTGGGAAGGGACTGCAATTTGTCGCAGGTATCAACAGCG ATGGATATAACACACAGTACAGAGACGATGTGAAGGGTCG ATTCACCATCTCCAGAGACAACACCGAAAAGACACTATATC TACAGATGAACAACCTGAGAGTCGAGGACACGGCCATGTA TTACTGTGTAAAGGATCAGGGAAGTTGGGGAGGAAATTTT GACTTCTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
748	PMX155 Heavy chain variable region amino acid sequence	ELHLVESGGDLVKPAGSLRLSCVASGFTFSSFRMSWVRQSP GKGLQFVAGINSDGYNTQYRDDVKGRFTISRDNTEKTLYLQM NNLRVEDTAMYYCVKDQGSWGGNFDFWGQGTLVTVSS
749	PMX155 light chain variable region nucleotide sequence	TCCTATGGCCTGACTCAGCCACCATCCGTGAATGTGACCC TGAGGGAGACGGCCCACATCACCTGTGGGGGAGACAGCA TTGGAAGTAAATATGTTCAATGGATCCAGCAGATTCCAGGC CAGGCCCCCGTAGTGATTATCTATAAAGATAGGAACAGGC CGACAGGGATCCCTGAGCGATTCTCTGGCGCCAACTCAGG

		GAACACGGCTACCCTGACCATCAGTGGGGCCCTGGCCGA AGACGAGGCTGACTATTACTGCCAGGTGGGGGACAGTGGT ACTAGTGTGTTCGGCGGAGGCACCCATCTGACCGTCCTCG
750	PMX155 light chain variable region amino acid sequence	SYGLTQPPSVNVTLRETAHITCGGDSIGSKYVQWIQQIPGQAP VVIIYKDRNRPTGIPERFSGANSGNTATLTISGALAEDEADYYC QVGDSGTSVFGGGTHLTVL
751	PMX155 heavy chain CDR1	GFTFSSF
752	PMX155 heavy chain CDR2	NSDGYN
753	PMX155 heavy chain CDR3	CVKDQGSWGGNFDFW
754	PMX155 light chain CDR1	GGDSIGSKYVQ
755	PMX155 light chain CDR2	KDRNRPT
756	PMX155 light chain CDR3	CQVGDSGTSVF
757	PMX156 Heavy chain variable region nucleic acid sequence	GAGTTGCAGCTGGTGGAGTCTGGGGGAGACCTGGTGAAG CCTGCGGGGTCCCTGAGACTGTCCTGTGTGGCCTCTGGAT TCACCTTCAGTAACTTCAGAATGAGTTGGGTCCGCCAGGC TCCTGGGAAGGGACTGCAATTTGTCGCAGGTATCAACAGC GATGGATATAGCACACAGTACAGAGACGATGTGAAGGGTC GATTCACCATCTCCAGAGACAACACCGAAAAGACACTATAT CTACAGATGAACAACCTGAGAGTCGAGGACACGGCCATGT ATTACTGTGTAAAGGATCAGGGAAGTTGGGGAGGAAATTTT GACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
758	PMX156 Heavy chain variable region amino acid sequence	ELQLVESGGDLVKPAGSLRLSCVASGFTFSNFRMSWVRQAP GKGLQFVAGINSDGYSTQYRDDVKGRFTISRDNTEKTLYLQM NNLRVEDTAMYYCVKDQGSWGGNFDYWGQGTLVTVSS

759	PMX156 light chain variable region nucleotide sequence	TCCTATGGCCTGACTCAGCCACCATCCGTGAATGTGACCC TGAGGGAGACGGCCCACATCACCTGTGGGGGAGACAGCA TTGGAAGTAAATATGTTCAATGGATCCAGCAGATTCCAGGC CAGGCCCCCGTAGTGATTATCTATAAAGATAGGAACAGGC CGACAGGGATCCCTGAGCGATTCTCTGGCGCCAACTCAGG GAACACGGCTACCCTGACCATCAGTGGGGCCCTGGCCGA AGACGAGGCTGACTATTACTGCCAGGTGGGGGACAGTGGT ACTAGTGTGTTCGGCGGAGGCACCCATCTGACCGTCCTCG
760	PMX156 light chain variable region amino acid sequence	SYGLTQPPSVNVTLRETAHITCGGDSIGSKYVQWIQQIPGQAP VVIIYKDRNRPTGIPERFSGANSGNTATLTISGALAEDEADYYC QVGDSGTSVFGGGTHLTVL
761	PMX156 heavy chain CDR1	GFTFSNF
762	PMX156 heavy chain CDR2	NSDGYS
763	PMX156 heavy chain CDR3	CVKDQGSWGGNFDYW
764	PMX156 light chain CDR1	GGDSIGSKYVQ
765	PMX155 light chain CDR2	KDRNRPT
766	PMX156 light chain CDR3	CQVGDSGTSVF
767	PMX291 Heavy chain variable region nucleic acid sequence	GAGGTGCAGCTGGTGGAGTCTGGGGGAGACCTGTTGAAG CCTGGGGGGTCCCTGAGACTCTCCTGTGTAGCCTCTGGAT TCCCCTTCAGGAACTACGACATGACCTGGGTCCGCCAGGC TCCTGGGAAGGGGCTGCAGTGGGTCGCCGCTATTCACTAT GATGGAAGTAACACATACTACACTGACGCTGTGAAGGGCC GATTCACCATTTCCAGAGACAACGCCAGGAACACAGTGTTT CTGCAGATGAACAGCCTGAGAGCCGAGGACACGGCTGTG TATTACTGTGCGAAGAAATTTAATAATTACCGTCCTTTTGAT TACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG

768	PMX291 Heavy chain variable region amino acid sequence	EVQLVESGGDLLKPGGSLRLSCVASGFPFRNYDMTWVRQAP GKGLQWVAAIHYDGSNTYYTDAVKGRFTISRDNARNTVFLQM NSLRAEDTAVYYCAKKFNNYRPFDYWGQGTLVTVSS
769	PMX291 light chain variable region nucleotide sequence	GATATTGTCATGACACAGACGCCACCGTCCCTGTCTGTCA GCCCTAGAGAGACGCCCTCCATCTCCTGCAAGGCCAGTCA GAGCCTCCTGCGCAGTGATGGAAACACCTATTTGGAATGG TACCTGCAAAAGCCCGGCCAGTCTCCACAGCTTCTGATCT ACTTGGTTTCCAACCGCTTCACTGGCGTGTCAGACAGGTT CAGTGGCAGCGGGTCAGGGACAGATTTCACCCTGAGAATC AGCAGAGTGGAGGCTAACGATGCTGGAGTTTATTACTGCG GGCAAGGTACACAGCTTCCGTGGACGTTCGGAGCAGGAA CCAAGGTGGAGCTCAAAC
770	PMX291 light chain variable region amino acid sequence	DIVMTQTPPSLSVSPRETPSISCKASQSLLRSDGNTYLEWYLQ KPGQSPQLLIYLVSNRFTGVSDRFSGSGSGTDFTLRISRVEAN DAGVYYCGQGTQLPWTFGAGTKVELK
771	PMX291 heavy chain CDR1	GFPFRNY
772	PMX291 heavy chain CDR2	HYDGSN
773	PMX291 heavy chain CDR3	CAKKFNNYRPFDYW
774	PMX291 light chain CDR1	KASQSLLRSDGNTYLE
775	PMX291 light chain CDR2	LVSNRFT
776	PMX291 light chain CDR3	CGQGTQLPWTF
777	PMX292 Heavy chain variable region nucleic acid sequence	GCGGTGCAGCTGGTGGAGTCTGGGGGAGACCTGGTGAGG CCGGGGGGGTCCCTGAGACTCTCCTGTGTAGCCTCTGGAT TCACCTTCAGTAACTTCGACATGTACTGGGTCCGCCAGGC TCCTGGGAGGGGGCTGCAGTGGGTCGCAACTATTTCCTAT GATGGATTTAACACATACTCCACTGACACTGTGCGGGGCC

		GATTCACCATCTCCAGAGACAACGCCAGGAACACAGTGTA TCTGCAGATGAACAGTCTCAGAGTCGAGGACACGGCTGTT TTTTACTGTACGGCTAGGAGGTTTGGACTTGGGTACTGGG GCCAGGGAACCCTGGTCACCGTCTCCTCAG
778	PMX292 Heavy chain variable region amino acid sequence	AVQLVESGGDLVRPGGSLRLSCVASGFTFSNFDMYWVRQAP GRGLQWVATISYDGFNTYSTDTVRGRFTISRDNARNTVYLQM NSLRVEDTAVFYCTARRFGLGYWGQGTLVTVSS
779	PMX292 light chain variable region nucleotide sequence	GATATTTTCATGGCACAGACGCCACCGTCCCTGTCTGTCA GCCCTAGAGAGACGGCCTCCATCTCCTGTAAGGCCAGTCA GAGCCTCCTGCACAGTGATGGAAACACCTATTTGGATTGG TACCTGCAAAAGCCAGGCCAGTCTCCACAGCTTCTGATCTA CTTGGTTTCCAACCGCTTCCCTGGCGTGTCAGACAGGTTC AGTGGCAGCGGGTCAGGGACAGGTTTCACCCTGAGAATCA GCAGAGTGGAGGCTAGTGATACTGGAGTTTATTACTGCGG GCAAGGTACACAGCTTCCTTATACCTTCAGCCAGGGAACC AAGCTGGAGATAAAAC
780	PMX292 light chain variable region amino acid sequence	DIFMAQTPPSLSVSPRETASISCKASQSLLHSDGNTYLDWYLQ KPGQSPQLLIYLVSNRFPGVSDRFSGSGSGTGFTLRISRVEAS DTGVYYCGQGTQLPYTFSQGTKLEIK
781	PMX292 heavy chain CDR1	GFTFSNF
782	PMX292 heavy chain CDR2	SYDGFN
783	PMX292 heavy chain CDR3	CTARRFGLGYW
784	PMX292 light chain CDR1	KASQSLLHSDGNTYLD
785	PMX292 light chain CDR2	LVSNRFP
786	PMX292 light chain CDR3	CGQGTQLPYTF

787	PMX293 Heavy chain variable region nucleic acid sequence	GAGGTGCGACTGCTGGAGTCTGGGGGAGACCTTGTGAAA CCTGCGGGGTCCCTGAGACTCTCCTGTGCGGTTTCTGGCT TCACCTTCAGTACCTACGACATGAGTTGGGTCCGCCAGGC TCCAGGGAAGGGGCTGCAGTGGGTCGCATACATTACCTAT GATGGAAGGACCACAAGTTACACAGACACTGTGAAGGGCC GATTCACCGTCTCCAGAGACAATGCCAAGAACATGCTGTAT CTGAAGATGAACAGCCTGAGAAGTGAGGACGCAGCCGTTT ATTACTGTGCGAAGGCCCATAGGGGGTGGTTTTTTGACCA CTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
788	PMX293 Heavy chain variable region amino acid sequence	EVRLLESGGDLVKPAGSLRLSCAVSGFTFSTYDMSWVRQAP GKGLQWVAYITYDGRTTSYTDTVKGRFTVSRDNAKNMLYLK MNSLRSEDAAVYYCAKAHRGWFFDHWGQGTLVTVSS
789	PMX293 light chain variable region nucleotide sequence	TCCTATGTGCTGACACAGCTGCCATCCGTGAGTGTGACCC TGAGGCAGACGGCCCGCATCACCTGTGGGGGAGACAGTA TTGGAAGTAAAAATGTTTACTGGTACCAACAGAAACTGGGC CAGGCCCCTGTATTGATTATCTATGATGATACCAGCAGGCC GTCAGGGATCCCTGAGCGATTCTCCGGCGCCAATTCGGG GACCACGGCCACCCTGACCATCAGCGGGGCCCTGGCCGA GGATGAGGCTGACTATTACTGCCAGGTGTGGGACAGCAGT ACTGGTGTGTTCGGCGGAGGCACCCACCTGACCGTCCTC G
790	PMX293 light chain variable region amino acid sequence	SYVLTQLPSVSVTLRQTARITCGGDSIGSKNVYWYQQKLGQA PVLIIYDDTSRPSGIPERFSGANSGTTATLTISGALAEDEADYY CQVWDSSTGVFGGGTHLTVL
791	PMX293 heavy chain CDR1	GFTFSTY
792	PMX293 heavy chain CDR2	TYDGRT
793	PMX293 heavy chain CDR3	CAKAHRGWFFDHW
794	PMX293 light chain CDR1	GGDSIGSKNVY

795	PMX293 light chain CDR2	DDTSRPS
796	PMX293 light chain CDR3	CQVWDSSTGVF
797	PMX294 Heavy chain variable region nucleic acid sequence	GAGGTGCAGCTGGTGGAGTCTGGGGGAGACCTTGTGAAA CCTGAGGGGTCCCTGAGACTCTCCTGTGCGGTCTCTGGCT TCACCTTCAGTAGTAACGACATGAGTTGGGTCCGCCAGGC TCCAGGGAAGGGGCTGCAGTGGGTCGCATACATTACCTAT GATGGAAGGAGCACAAGTTACACAGACATTGTGAAGGGCC GATTCACCGTCTCCAGAGACAATGCCAAGAACACGCTGTA TCTGCAGATGAATAGCCTGAGAAGTGAGGACGCAGCCGTG TACTACTGTGCGAAGGCCCAGAGGGGGTGGTTTTTTGACT ACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
798	PMX294 Heavy chain variable region amino acid sequence	EVQLVESGGDLVKPEGSLRLSCAVSGFTFSSNDMSWVRQAP GKGLQWVAYITYDGRSTSYTDIVKGRFTVSRDNAKNTLYLQM NSLRSEDAAVYYCAKAQRGWFFDYWGQGTLVTVSS
799	PMX294 light chain variable region nucleotide sequence	TCCTATGTGCTGACACAGCTGCCATCCGTGAGTGTGACCC TGAGGCAGACGGCCCGCATCACCTGTGGGGGAGACAGTA TTGGAAGTAAAAATGTTTACTGGTACCAACAGAAACTGGGC CAGGCCCCTGTACTGATTATCTATGATGATGACAGCAGGC CGTCAGGGATCCCTGAGCGAATCTCCGGCGCCAATTCGG GGAACACGGCCACCCTGACCATCAGCGGGGCCCTGGCCG AGGATGAGGCTGACTATTACTGCCAGGTGTGGGACAGCAG TACTGGTGTGTTCGGCGGAGGCACCCACCTGACCGTCCTC G
800	PMX294 light chain variable region amino acid sequence	SYVLTQLPSVSVTLRQTARITCGGDSIGSKNVYWYQQKLGQA PVLIIYDDDSRPSGIPERISGANSGNTATLTISGALAEDEADYY CQVWDSSTGVFGGGTHLTVL
801	PMX294 heavy chain CDR1	GFTFSSN
802	PMX294 heavy chain CDR2	TYDGRS

803	PMX294 heavy chain CDR3	CAKAQRGWFFDYW
804	PMX294 light chain CDR1	GGDSIGSKNVY
805	PMX294 light chain CDR2	DDDSRPS
806	PMX294 light chain CDR3	CQVWDSSTGVF

Table 3: VH and VL gene usage

PMX number	VH_name	VL_name	Family
PMX025	IGHV3-5cf	IGLV3-14cf	Family 1
PMX026	IGHV3-5cf	IGLV3-14cf	Family 1
PMX027	IGHV3-5cf	IGLV3-14cf	Family 1
PMX028	IGHV3-5cf	IGLV3-21cf	Family 2
PMX029	IGHV3-5cf	IGLV3-21cf	Family 2
PMX030	IGHV3-5cf	IGLV3-24cf	Family 3
PMX031	IGHV3-5cf	IGLV3-24cf	Family 3
PMX032	IGHV3-5cf	IGLV3-21cf	Family 2
PMX033	IGHV3-5cf	IGLV3-21cf	Family 2
PMX034	IGHV3-5cf	IGLV3-21cf	Family 2
PMX035	IGHV3-8cf	IGLV3-24cf	Family 4
PMX036	IGHV3-5cf	IGLV3-21cf	Family 2
PMX037	IGHV3-8cf	IGLV3-24cf	Family 4

PMX038	IGHV3-5cf	IGLV3-21cf	Family 2
PMX039	IGHV3-18cf	IGLV3-3cf	Family 5
PMX040	IGHV3-8cf	IGLV3-24cf	Family 4
PMX041	IGHV3-18cf	IGLV3-3cf	Family 5
PMX042	IGHV3-5cf	IGLV3-21cf	Family 2
PMX043	IGHV3-18cf	IGLV3-3cf	Family 5
PMX044	IGHV3-18cf	IGLV3-3cf	Family 5
PMX045	IGHV3-5cf	IGLV3-21cf	Family 2
PMX046	IGHV3-18cf	IGLV3-3cf	Family 5
PMX047	IGHV3-19cf	IGKV2-5cf	Family 6
PMX048	IGHV3-8cf	IGLV3-24cf	Family 4
PMX049	IGHV3-8cf	IGLV3-24cf	Family 4
PMX050	IGHV3-18cf	IGLV3-3cf	Family 5
PMX051	IGHV3-44cf	IGLV3-8cf	Family 7
PMX052	IGHV3-19cf	IGKV2-4cf	Family 8
PMX053	IGHV3-19cf	IGKV2-5cf	Family 6
PMX054	IGHV3-18cf	IGLV3-24cf	Family 12
PMX055	IGHV3-18cf	IGLV3-3cf	Family 5
PMX056	IGHV3-18cf	IGLV3-3cf	Family 5
PMX057	IGHV3-18cf	IGLV3-3cf	Family 5
PMX058	IGHV3-18cf	IGLV3-3cf	Family 5
PMX059	IGHV3-18cf	IGLV3-3cf	Family 5

PMX060	IGHV3-5cf	IGLV3-3cf	Family 9
PMX061	IGHV3-5cf	IGLV3-3cf	Family 9
PMX062	IGHV3-18cf	IGLV3-3cf	Family 5
PMX063	IGHV3-5cf	IGLV3-8cf	Family 10
PMX064	IGHV3-5cf	IGLV3-21cf	Family 2
PMX065	IGHV3-8cf	IGLV3-24cf	Family 4
PMX082	IGHV3-5cf	IGLV3-21cf	Family 2
PMX083	IGHV3-5cf	IGLV3-21cf	Family 2
PMX084	IGHV3-18cf	IGLV3-24cf	Family 12
PMX085	IGHV3-18cf	IGLV3-3cf	Family 5
PMX086	IGHV3-5cf	IGLV3-8cf	Family 10
PMX087	IGHV3-5cf	IGLV3-8cf	Family 10
PMX088	IGHV3-44cf	IGLV3-8cf	Family 7
PMX089	IGHV3-5cf	IGLV3-14cf	Family 1
PMX090	IGHV3-5cf	IGLV3-14cf	Family 1
PMX091	IGHV3-5cf	IGLV3-14cf	Family 1
PMX092	IGHV3-5cf	IGLV3-14cf	Family 1
PMX093	IGHV3-5cf	IGLV3-14cf	Family 1
PMX094	IGHV3-5cf	IGLV3-8cf	Family 10
PMX095	IGHV3-5cf	IGLV3-8cf	Family 10
PMX096	IGHV3-5cf	IGLV3-8cf	Family 10
PMX097	IGHV3-5cf	IGLV3-8cf	Family 10

PMX098	IGHV3-5cf	IGLV3-8cf	Family 10
PMX099	IGHV3-5cf	IGLV3-8cf	Family 10
PMX100	IGHV3-5cf	IGLV3-8cf	Family 10
PMX101	IGHV3-5cf	IGLV3-8cf	Family 10
PMX102	IGHV3-5cf	IGLV3-8cf	Family 10
PMX103	IGHV3-5cf	IGLV3-8cf	Family 10
PMX104	IGHV3-5cf	IGLV3-8cf	Family 10
PMX105	IGHV3-5cf	IGLV3-8cf	Family 10
PMX106	IGHV3-5cf	IGKV2-4cf	Family 11
PMX107	IGHV3-5cf	IGLV3-8cf	Family 10
PMX108	IGHV3-5cf	IGLV3-8cf	Family 10
PMX109	IGHV3-5cf	IGLV3-8cf	Family 10
PMX110	IGHV3-5cf	IGLV3-8cf	Family 10
PMX111	IGHV3-5cf	IGLV3-8cf	Family 10
PMX154	IGHV3-18cf	IGLV3-24cf	Family 12
PMX155	IGHV3-19cf	IGLV3-21cf	Family 13
PMX156	IGHV3-19cf	IGLV3-21cf	Family 13
PMX291	IGHV3-41cf	IGKV2-4cf	Family 14
PMX292	IGHV3-41cf	IGKV2-4cf	Family 14
PMX293	IGHV3-18cf	IGLV3-24cf	Family 12
PMX294	IGHV3-18cf	IGLV3-24cf	Family 12

Table 4. Geomeans obtained from cell binding assay

Antibody	GEO mean OX40L expressing HEK	GEO mean WT HEK	GEO mean difference
PMX025	2830000	18587	2811413
PMX026	1390000	26716	1363284
PMX027	1650000	33774	1616226
PMX028	1050000	30825	1019175
PMX029	1090000	28348	1061652
PMX030	1420000	29779	1390221
PMX031	1550000	39212	1510788
PMX032	1450000	28489	1421511
PMX033	1460000	28385	1431615
PMX034	1390000	27398	1362602
PMX035	1410000	26814	1383186
PMX036	1310000	30928	1279072
PMX037	1420000	27618	1392382
PMX038	1560000	27561	1532439
PMX039	1520000	29268	1490732
PMX040	1180000	27194	1152806
PMX041	1560000	28620	1531380
PMX042	1510000	28750	1481250
PMX043	1280000	33769	1246231
PMX044	1530000	28856	1501144
PMX045	1470000	28564	1441436
PMX046	1250000	28149	1221851
PMX047	1950000	28632	1921368
PMX048	3920000	23672	3896328
PMX049	3500000	24403	3475597
PMX050	3080000	23859	3056141
PMX051	3940000	24704	3915296
PMX052	765000	30802	734198
PMX053	3030000	30828	2999172
PMX054	3270000	30515	3239485
PMX055	3260000	30461	3229539
PMX056	3160000	31120	3128880
PMX057	3320000	29889	3290111
PMX058	3340000	29794	3310206
PMX059	3140000	29668	3110332
PMX060	3100000	29772	3070228
PMX061	3290000	29916	3260084
PMX062	2810000	29671	2780329
PMX063	3180000	30351	3149649

PMX064	3450000	29540	3420460
PMX065	3550000	29783	3520217
PMX082	544000	12535	531465
PMX083	701000	11438	689562
PMX084	622000	12275	609725
PMX085	839000	12581	826419
PMX086	857000	7973	849027
PMX087	1050000	7984	1042016
PMX088	783000	8225	774775
PMX105	584000	3533	580467
PMX106	7759	3656	4103
PMX107	58797	3625	55172
PMX108	611000	3520	607480
PMX109	633000	3599	629401
PMX110	31927	3525	28402
PMX111	647000	3572	643428
PMX154	789000	8196	780804
PMX155	738000	7995	730005
PMX156	680000	7941	672059
PMX291	463000	3826	459174
PMX292	471000	3757	467243
PMX293	602000	3571	598429
PMX294	595000	3543	591457
neg CTR	19634	24019	-4385

Table 5. Normalised HEK blue assay results, showing the percentage of OX40 signal inhibition.

	% Signal Inhibition				
Ab	Rep1	Rep2	Rep3	Average	SD
PMX25	87.86279683	61.7414248	68.33773087	72.6473175	13.58347974
PMX26	67.6056338	65.14084507	68.66197183	67.13615023	1.806901915
PMX27	72.17741935	83.46774194	85.48387097	80.37634409	7.171678264
PMX28	61.69354839	75.40322581	62.09677419	66.39784946	7.801490248
PMX29	75.80645161	76.20967742	56.0483871	69.35483871	11.52548865
PMX30	70.56451613	83.87096774	42.33870968	65.59139785	21.20804197
PMX31	83.45070423	89.08450704	62.67605634	78.40375587	13.90882213
PMX32	76.76056338	57.3943662	75.70422535	69.95305164	10.8889576
PMX33	55.81395349	69.76744186	55.42635659	60.33591731	8.170238632
PMX34	76.35658915	64.72868217	51.5503876	64.2118863	12.41117308
PMX35	85.27131783	67.44186047	67.82945736	73.51421189	10.18379659
PMX36	87.59689922	79.06976744	65.50387597	77.39018088	11.14186598
PMX37	85.65891473	79.84496124	69.76744186	78.42377261	8.04049503

PMX38	79.83870968	75	50.80645161	68.5483871	15.55427542
PMX39	81.69014085	86.61971831	73.5915493	80.63380282	6.578007638
PMX40	75.35211268	84.15492958	71.83098592	77.11267606	6.347801541
PMX41	86.36990852	78.19287576	75.63755302	80.0667791	5.606201827
PMX42	77.82258065	87.5	70.96774194	78.76344086	8.306190621
PMX43	69.15888	77.33333	96.052632	80.84828067	13.78711836
PMX44	75.70093	66	83.55263	75.08452	8.79253524
PMX45	79.92957746	81.69014085	66.1971831	75.93896714	8.482432613
PMX46	84.83671488	69.50477845	100.1686513	84.83671488	15.33193642
PMX47	49.3485391	73.12009148	62.28748533	61.58537197	11.90131917
PMX48	57.47664	69.33333	82.89474	69.90157	12.71857399
PMX49	84.57944	79.33333	90.131579	84.68144967	5.399847206
PMX50	68.69159	83.33333	77.63158	76.55216667	7.380310794
PMX51	82.24299	75.33333	94.736842	84.10438733	9.834768401
PMX52	15.6626506	29.18340027	21.68674699	22.17759929	6.773726438
PMX53	24.49799197	45.78313253	48.86211513	39.71441321	13.26742778
PMX54	21.01740295	32.7978581	42.03480589	31.95002231	10.53432133
PMX55	48.32663989	57.69745649	52.34270415	52.78893351	4.701318051
PMX56	27.30923695	57.02811245	48.4605087	44.2659527	15.29701328
PMX57	52.07496653	72.02141901	73.89558233	65.99732262	12.09347433
PMX58	12.4497992	35.34136546	39.49129853	29.0941544	14.56301501
PMX59	51.13788487	64.25702811	57.96519411	57.78670237	6.561392711
PMX60	58.90227577	68.40696118	71.08433735	66.13119143	6.401952986
PMX61	51.00401606	61.57965194	55.68942436	56.09103079	5.299243752
PMX62	4.149933066	22.08835341	18.7416332	14.99330656	9.538563602
PMX63	68.27309237	82.99866131	72.02141901	74.43105756	7.652801032
PMX64	88.88888889	94.77911647	89.69210174	91.1200357	3.194204403
PMX65	62.65060241	85.27443106	69.87951807	72.60151718	11.55492817
PMX82	72.78911565	71.88208617	72.10884354	72.26001512	0.4720331065
PMX83	65.98639456	65.75963719	81.63265306	71.12622827	9.09953714
PMX84	47.16553288	66.89342404	68.02721088	60.69538927	11.73090485
PMX85	43.76417234	56.23582766	40.81632653	46.93877551	8.185281473
PMX154	62.57309942	77.19298246	51.4619883	63.74269006	12.90530789
PMX155	19.88304094	37.42690058	40.93567251	32.74853801	11.2791237
PMX156	21.6374269	34.50292398	49.12280702	35.0877193	13.75201873
PMX086	5.847953216	35.0877193	14.03508772	18.32358674	15.08424337
PMX087	29.8245614	46.19883041	21.6374269	32.55360624	12.50605453
PMX088	16.95906433	3.50877193	1.169590643	7.212475634	8.521439764
PMX089	43.2748538	49.70760234	49.12280702	47.36842105	3.55717107
PMX092	33.33333333	39.18128655	31.57894737	34.69785575	3.980619465
PMX093	0	-0.5847953216	16.95906433	5.458089669	9.964427227
PMX094	38.59649123	54.97076023	42.69005848	45.41910331	8.521439764

PMX095	40.93567251	52.63157895	57.30994152	50.29239766	8.434038071
PMX096	36.84210526	59.06432749	54.38596491	50.09746589	11.71538339
PMX097	56.14035088	73.0994152	53.21637427	60.81871345	10.73541506
PMX098	40.35087719	54.97076023	39.76608187	45.02923977	8.614573019
PMX099	25.14619883	32.74853801	16.37426901	24.75633528	8.194093395
PMX100	49.12280702	28.07017544	19.88304094	32.35867446	15.08424337
PMX101	62.57309942	50.29239766	44.44444444	52.43664717	9.252588137
PMX103	57.30994152	26.31578947	59.06432749	47.56335283	18.42182615
PMX104	30.99415205	28.07017544	33.91812865	30.99415205	2.923976608
PMX105	85.43956044	94.78021978	72.52747253	84.24908425	11.17403755
PMX106	-9.89010989	-4.120879121	-37.63736264	-17.21611722	17.91902493
PMX107	7.142857143	20.87912088	-43.95604396	-5.311355311	34.16475092
PMX108	95.6043956	89.83516484	61.26373626	82.23443223	18.38881652
PMX109	67.85714286	69.50549451	22.52747253	53.2967033	26.65967812
PMX110	55.21978022	43.13186813	13.73626374	37.36263736	21.33503112
PMX111	44.23076923	37.36263736	35.16483516	38.91941392	4.729212943
PMX291	95.87912088	70.32967033	53.57142857	73.26007326	21.30553104
PMX292	97.52747253	54.3956044	62.91208791	71.61172161	22.84408527
PMX293	81.59340659	77.47252747	62.08791209	73.71794872	10.28050219
PMX294	93.95604396	88.73626374	53.02197802	78.57142857	22.27986409

Table 6. Calculated IFN-γ levels in supernatant from PBMC activated with CD3 and CD28 antibodies in presence of HEK cells expressing OX40L and the indicated anti-OX40L antibody.

		mean			SD		
Exp	**Antibody**	IFNg at 10ug/ml	IFNg at 1ug/ml	IFNg at 0.1ug/ml	IFNg at 10ug/ml	IFNg at 1ug/ml	IFNg at 0.1ug/ml
1	PMX26	1814.78	3433.28	5414.20	45.21	1375.01	3356.63
	PMX27	1990.07	3288.97	4044.77	208.16	588.51	722.95
	PMX28	3747.50	4167.48		1137.43	1708.61	
	PMX29	4098.23	4809.27		255.24	1688.96	
	PMX30	3576.96	3853.98	5362.51	532.12	264.01	780.97

	PMX31	2912.32	3002.01	4036.50	347.72	287.54	1033.25
	PMX32	2024.93	3618.68	4223.01	767.06	1546.09	2435.17
	PMX33	2531.64	3951.58	4723.81	906.87	1184.23	1455.97
	PMX34	2556.40	5339.85	7042.10	1272.17	3076.37	4007.35
	PMX35	4176.35	3976.67	4495.16	956.20	709.57	419.94
	PMX36	2326.33	4754.37	5649.25	1129.18	2516.11	1417.65
	PMX37	2461.41	3790.18	4648.46	1804.94	1137.25	1786.08
	PMX38	2442.77	4449.14	4525.85	1295.10	1040.33	1710.84
	PMX39	2933.59	3249.37	4135.69	806.02	493.70	852.67
	PMX40	3645.35	3412.83	3715.94	91.46	195.43	339.31
	PMX41	2723.49	4487.53	5710.89	2252.21	1492.53	3591.86
	PMX42	2905.62	3655.92	3704.68	191.37	272.16	398.88
	PMX43	2528.79	3085.59	3545.46	379.45	345.11	759.76
	PMX44	4019.73	5116.65	6095.48	2087.93	2502.78	3813.82
	PMX45	3053.12	3325.59	3590.83	215.13	161.04	260.98
	PMX46	2645.25	3882.33	3866.09	716.92	1161.45	1534.08
	PMX48	2652.66	3832.05	4265.84	713.49	1120.59	1425.55
	PMX49	2470.91	4239.59	4974.37	1049.96	1745.68	2370.81
	PMX50	1899.51	4270.99	5333.26	659.02	1613.99	1699.31

	PMX51	1596.68	3469.98	4544.13	1006.82	1168.05	180.60
					mean	sd	
				Activated PBMC only	885.59	184.72	
				Activated PBMC plus HEK WT	2459.88	365.80	
				Activated PBMC plus HEK OX40L	3407.36	865.71	
2	PMX25	2770.11	3057.09	3805.02	1045.67	681.15	1274.56
	PMX47	2768.58	4677.64	5507.66	769.44	2263.08	3049.61
					mean	sd	
				Activated PBMC only	386.55	168.92	
				Activated PBMC plus HEK WT	1817.34	250.69	
				Activated PBMC plus HEK OX40L	4212.20	968.56	
3	PMX52	1315.32	3054.47	4681.29	269.15	526.97	217.93
	PMX53	1737.69	2811.98	3777.63	399.51	690.91	302.86
	PMX54	1368.39	2407.42	4081.28	374.45	209.24	918.24
	PMX55	882.63	2862.91	3709.13	442.93	210.87	331.55
	PMX56	1323.43	2611.83	3784.45	475.85	267.59	580.60
	PMX57	1050.92	2394.91	3696.83	189.37	322.04	349.06
	PMX58	1341.49	2542.25	4250.69	197.27	159.80	1123.55

	PMX59	1317.75	3125.89	3563.65	243.01	812.81	1050.36
	PMX60	1115.59	2097.85	3075.43	274.87	185.73	459.90
	PMX61	1192.01	2321.95	3470.64	631.57	401.53	608.19
	PMX62	1701.95	3331.77	4447.21	563.04	576.85	810.82
	PMX63	731.17	2591.77	3520.33	35.02	345.75	1022.69
	PMX64	1409.13	2188.59	3356.51	217.58	115.17	1339.26
	PMX65	1961.45	2775.70	3712.55	221.52	173.26	947.67
					mean	sd	
				Activated PBMC only	403.44	273.42	
				Activated PBMC plus HEK WT	1936.31	591.88	
				Activated PBMC plus HEK OX40L	3340.52	596.95	
4	PMX82	651.66	1484.65	1743.93	556.18	199.46	67.16
	PMX83	772.03	1318.61	1512.28	100.81	164.38	62.11
	PMX84	805.25	1338.86	1732.75	130.18	274.27	225.94
	PMX85	492.34	1303.38	1752.97	121.61	168.09	173.12
					mean	sd	
				Activated PBMC only	285.11	92.85	
				Activated PBMC plus HEK WT	1019.26	60.26	
				Activated PBMC plus HEK OX40L	1817.28	174.80	

5	PMX025	1359.97	2746.66	3081.29	413.02	634.79	621.45
	PMX033	1340.55	2058.00	2654.86	166.80	667.24	428.35
	PMX034	1016.67	1326.64	2383.32	320.74	254.87	622.78
	PMX036	1198.65	1464.58	1900.32	17.46	219.68	539.28
	PMX037	1670.23	1755.54	1974.41	352.94	323.52	510.13
	PMX041	1674.07	2323.12	2114.73	445.58	665.34	125.76
	PMX044	1224.32	2098.99	2491.96	334.83	488.84	573.10
	PMX046	1639.40	2471.90	3456.61	454.11	541.02	386.48
	PMX048	1544.70	1904.61	2996.43	136.77	117.45	395.65
	PMX049	1582.82	1922.43	2551.69	316.23	175.51	277.21
	PMX050	1497.70	2481.89	2723.57	270.41	303.37	315.16
	PMX051	958.94	1635.98	2861.09	139.68	162.57	68.92
	PMX053	1545.71	3434.39	3427.15	80.61	634.34	311.61
	PMX063	1112.67	2394.40	2979.97	81.81	215.38	576.27
					mean	sd	
				Activated PBMC only	742.35	45.45	
				Activated PBMC plus HEK WT	1481.56	161.15	
				Activated PBMC plus HEK OX40L	2144.71	523.58	

Table 6 - Experiment 6

	mean			SD		
Antibody	IFNg at 10ug/ml	IFNg at 1ug/ml	IFNg at 0.1ug/ml	IFNg at 10ug/ml	IFNg at 1ug/ml	IFNg at 0.1ug/ml
PMX044	1722.38	1759.58	2329	278.952	187.664	224.124
PMX050	1245.66	1719.77	2531.82	42.7925	219.931	113.751
PMX051	1305.74	1354.63	2365.89	252.408	324.315	46.1784
PMX063	1102.77	1113.98	2113.32	205.53	654.097	132.529
PMX097	1336.77	1383.23	2310.45	588.363	174.174	48.2587
PMX098	1362.69	1461.92	2362.47	238.854	199.5	109.641
PMX154	1345.93	1273.41	2521.93	549.126	249.381	340.828
PMX155	987.95	1199.91	1899.39	217.595	326.565	485.313
				mean	sd	
			Activated PBMC only	1178.41	117.19	
			Activated PBMC plus HEK WT	1887.27	556.10	
			Activated PBMC plus HEK OX40L	2498.20	149.14	

Table 6 - Experiment 7

	mean			SD		
Antibody	IFNg at 10ug/ml	IFNg at 1ug/ml	IFNg at 0.1ug/ml	IFNg at 10ug/ml	IFNg at 1ug/ml	IFNg at 0.1ug/ml
PMX051	1536.3	1815.21	1875.8	96.6475	592.227	627.987
PMX063	1738	2020.37	2575.4	73.6416	280.029	371.363
PMX097	1318.61	1561.57	1557.5	227.078	276.753	149.508
PMX154	1764.41	2285.1	2407.64	143.011	402.333	443.682
PMX155	1192.73	1475.6	1518.13	210.448	124.464	281.658
PMX156	1350.71	1418.98	1626.17	592.994	693.986	1140.91
				mean	sd	
			Activated PBMC only	2494.90	343.44	
			Activated PBMC plus HEK WT	1732.29	594.21	
			Activated PBMC plus HEK OX40L	2522.38	681.991	

Table 6 - Experiment 8

Antibody	IFNg at 10ug/ml	IFNg at 1ug/ml	IFNg at 0.1ug/ml	IFNg at 10ug/ml	IFNg at 1ug/ml	IFNg at 0.1ug/ml
PMX155	357.9	913.51	992.1	152.3108213	277.3656686	113.2125951
PMX156	356.41	1040.08	911.54	44.25830092	353.2083203	263.9567016
PMX154	298.13	553.2	908.56	119.0447945	133.027378	31.03897389
PMX086	603.78	629.04	796.25	115.4089823	269.0244727	35.34964215
PMX087	486.52	778.08	959.18	159.0133985	47.25368557	330.1825272
PMX088	548.81	511.83	797.76	174.4212418	110.5179031	153.3083628
PMX089	392.55	597.97	628.25	113.3400596	48.49787727	160.525939
PMX099	456.31	475.78	389.09	74.26587305	107.6157177	191.4946819
PMX100	466.78	419.54	437.56	152.4082006	117.8966615	59.98653099
PMX101	439.32	373.57	482.51	190.5790206	81.896249	99.86248995
PMX092	428.95	482.03	414.24	64.19260004	116.2632276	164.677411
PMX093	185.73	308.17		134.5765626	10.13415512	
PMX097	207.72	523.94		19.93420427	107.4632384	
PMX098	232.29	284.08	389.82	69.03847406	11.403802	206.5741751
					mean	sd
				Activated PBMC only	165.552	47.70432339
				Activated PBMC plus HEK WT	453.67	98.27820267
				Activated PBMC plus HEK OX40L	682.185	87.44989348

Table 6 - Experiment 9

Antibody	IFNg at 10ug/ml	IFNg at 1ug/ml	IFNg at 0.1ug/ml	IFNg at 10ug/ml	IFNg at 1ug/ml	IFNg at 0.1ug/ml
PMX097	951.94	1177.41	1335.68	145.4115267	251.8712832	80.03178181
PMX063	870.03	1500.67	1455.14	178.699512	127.4849685	189.0959383
PMX105	1104.64	1115.07	1326.7	399.3461607	180.9313431	193.302486
PMX294	932.35	1308.39	1646.86	74.29910094	56.79637048	144.9110255
PMX293	1034.17	1230.16	1651.52	125.7269374	179.1317669	250.3058343
PMX291	983.92	1364.04	1442.19	169.5388902	261.9525531	176.134747
PMX292	962.85	1316.63	1258.25	210.8505326	329.8375541	234.001241
					mean	sd
				Activated PBMC only	498.05	26.86289076
				Activated PBMC plus HEK WT	396.12	103.2492266
				Activated PBMC plus HEK OX40L	1683.16	23.41211866

Table 6 - Experiment 10

Antibody	IFNg at 10ug/ml	IFNg at 1ug/ml	IFNg at 0.1ug/ml	IFNg at 10ug/ml	IFNg at 1ug/ml	IFNg at 0.1ug/ml
PMX105	193.7766667	302.6883333	652.1316667	35.68407535	128.4039884	73.91448054
PMX108	413.9133333	534.4916667	687.6116667	23.13906779	51.02767248	132.1214445
PMX109	402.9333333	483.9466667	512.375	2.1185923	149.3776638	208.7832167
PMX111	589.9716667	417.425	525.77	196.7615302	4.422943025	49.29426361
					mean	sd
				Activated PBMC only	133.3694444	63.04364532
				Activated PBMC plus HEK WT	254.0545833	110.5967559
				Activated PBMC plus HEK OX40L	781.07125	211.8972647

Table 7. Normalised IFN-γ levels in supernatant from PBMC activated with CD3 and CD28 antibodies in presence of HEK cells expressing OX40L and the indicated anti-OX40L antibody.

		mean			SD		
Exp	**Antibody**	**Relative IFNg at 10ug/ml (%)**	**Relative IFNg at 1ug/ml (%)**	**Relative IFNg at 0.1ug/ml (%)**	**Relative IFNg at 10ug/ml (%)**	**Relative IFNg at 1ug/ml (%)**	**Relative IFNg at 0.1ug/ml (%)**
1	PMX26	36.85	101.03	103.12	1.79	54.53	18.89
	PMX27	43.80	95.31	125.28	8.25	23.34	28.67
	PMX28	113.49	130.14		45.10	67.75	
	PMX29	127.40	155.59		10.12	66.98	
	PMX30	106.73	117.71	177.53	21.10	10.47	30.97
	PMX31	80.37	83.93	124.95	13.79	11.40	40.97
	PMX32	45.18	108.38	132.34	30.42	61.31	96.57
	PMX33	65.27	121.58	152.20	35.96	46.96	57.74
	PMX34	66.26	176.63	244.13	50.45	121.99	158.91
	PMX35	130.49	122.58	143.14	37.92	28.14	16.65
	PMX36	57.13	153.42	188.90	44.78	99.78	56.22
	PMX37	62.49	115.18	149.22	71.57	45.10	70.83
	PMX38	61.75	141.31	144.35	51.36	41.25	67.84
	PMX39	81.21	93.74	128.88	31.96	19.58	33.81

	PMX40	109.44	100.22	112.24	3.63	7.75	13.46
	PMX41	72.88	142.83	191.35	89.31	59.19	142.43
	PMX42	80.10	109.86	111.79	7.59	10.79	15.82
	PMX43	65.16	87.24	105.48	15.05	13.69	30.13
	PMX44	124.28	167.78	206.60	82.80	99.25	151.24
	PMX45	85.95	96.76	107.28	8.53	6.39	10.35
	PMX46	69.78	118.83	118.19	28.43	46.06	60.83
	PMX48	70.07	116.84	134.04	28.29	44.44	56.53
	PMX49	62.87	133.00	162.14	41.64	69.22	94.01
	PMX50	40.21	134.25	176.37	26.13	64.00	67.39
	PMX51	28.20	102.48	145.08	39.93	46.32	7.16
2	PMX25	57.57	66.01	88.02	30.77	20.04	37.50
	PMX47	57.52	113.69	138.12	22.64	66.59	89.73
3	PMX52	31.05	90.26	145.65	9.16	17.94	7.42
	PMX53	45.43	82.00	114.88	13.60	23.52	10.31
	PMX54	32.85	68.23	125.22	12.75	7.12	31.26
	PMX55	16.32	83.74	112.55	15.08	7.18	11.29
	PMX56	31.32	75.19	115.11	16.20	9.11	19.77
	PMX57	22.05	67.80	112.13	6.45	10.96	11.88
	PMX58	31.94	72.82	130.99	6.72	5.44	38.25
	PMX59	31.13	92.69	107.60	8.27	27.67	35.76
	PMX60	24.25	57.69	90.97	9.36	6.32	15.66
	PMX61	26.85	65.32	104.43	21.50	13.67	20.71
	PMX62	44.21	99.70	137.68	19.17	19.64	27.61
	PMX63	11.16	74.51	106.12	1.19	11.77	34.82
	PMX64	34.24	60.78	100.54	7.41	3.92	45.60
	PMX65	53.05	80.77	112.67	7.54	5.90	32.27
4	PMX82	23.92	78.29	95.21	36.30	13.02	4.38
	PMX83	31.78	67.45	80.09	6.58	10.73	4.05
	PMX84	33.95	68.78	94.48	8.50	17.90	14.75
	PMX85	13.53	66.46	95.80	7.94	10.97	11.30
5	PMX025	44.04	142.92	166.79	29.45	45.27	44.31
	PMX033	42.66	93.82	136.38	11.89	47.58	30.54
	PMX034	19.56	41.66	117.01	22.87	18.17	44.41
	PMX036	32.54	51.50	82.57	1.25	15.66	38.46
	PMX037	66.17	72.25	87.86	25.17	23.07	36.38
	PMX041	66.44	112.72	97.86	31.77	47.44	8.97
	PMX044	34.37	96.74	124.76	23.88	34.86	40.87

	PMX046	63.97	123.33	193.55	32.38	38.58	27.56
	PMX048	57.21	82.88	160.73	9.75	8.38	28.21
	PMX049	59.93	84.15	129.02	22.55	12.52	19.77
	PMX050	53.86	124.04	141.28	19.28	21.63	22.47
	PMX051	15.44	63.72	151.08	9.96	11.59	4.91
	PMX053	57.29	191.96	191.45	5.75	45.23	22.22
	PMX063	26.41	117.80	159.56	5.83	15.36	41.09
6	PMX044	41.22	44.04	87.18	21.14	14.22	16.98
	PMX050	5.10	41.02	102.55	3.24	16.66	8.62
	PMX051	9.65	13.35	89.97	19.12	24.57	3.50
	PMX063	-5.73	-4.88	70.84	15.57	49.56	10.04
	PMX097	12.00	15.52	85.77	44.58	13.20	3.66
	PMX098	13.96	21.48	89.72	18.10	15.12	8.31
	PMX154	12.69	7.20	101.80	41.61	18.90	25.82
	PMX155	-14.43	1.63	54.63	16.49	24.74	36.77

Table 7 - Experiment 8

	mean			SD		
Antibody	**Relative IFNg at 10ug/ml (%)**	**Relative IFNg at 1ug/ml (%)**	**Relative IFNg at 0.1ug/ml (%)**	**Relative IFNg at 10ug/ml (%)**	**Relative IFNg at 1ug/ml (%)**	**Relative IFNg at 0.1ug/ml (%)**
PMX155	37.23107119	144.7754983	159.9874572	29.48143486	53.68717611	21.9135431
PMX156	36.9426653	169.274514	144.3941831	8.566680974	68.3673556	51.09172305
PMX154	25.66193023	75.03353444	143.8173713	23.04242944	25.74891229	6.007934818
PMX086	84.82384981	89.71320067	122.0785354	22.338678	52.0726459	6.842312076
PMX087	62.12688698	118.5615321	153.6154291	30.77879239	9.146470622	63.91046008
PMX088	74.18380165	67.02591588	122.3708125	33.76114995	21.39195581	29.67451998
PMX089	43.93795983	83.6992604	89.56028748	21.93821524	9.387297612	31.07156125
PMX099	56.27940917	60.04804184	43.26823877	14.37497664	20.83020591	37.06590208
PMX100	58.30599284	49.16217121	52.65014043	29.50028368	22.82019568	11.61105291
PMX101	52.99080779	40.26417205	61.35070737	36.88866577	15.85191983	19.3294834
PMX092	50.98358022	61.25779809	48.13629791	12.42518384	22.50402658	31.87512432
PMX093	3.905673854	27.60528267		26.048774	1.961577197	
PMX097	8.162080239	69.36993959		3.858484509	20.80069186	
PMX098	12.917874	22.94239818	43.4095383	13.36315606	2.207331316	39.98470385

Table 7 - Experiment 9

	mean			SD		
Antibody	**Relative IFNg at 10ug/ml (%)**	**Relative IFNg at 1ug/ml (%)**	**Relative IFNg at 0.1ug/ml (%)**	**Relative IFNg at 10ug/ml (%)**	**Relative IFNg at 1ug/ml (%)**	**Relative IFNg at 0.1ug/ml (%)**
PMX097	38.29939837	57.32463653	70.67951498	12.26987594	21.25298776	6.753109991
PMX063	31.38780366	84.6014294	80.75959194	15.07872788	10.75722663	15.95598201
PMX105	51.18427825	52.06436533	69.92177941	33.69696996	15.26705057	16.31093198
PMX294	36.64638726	68.37677515	96.93699319	6.269384356	4.792497784	12.22764346
PMX293	45.23799479	61.77570015	97.33020563	10.60888335	15.1152017	21.12089463
PMX291	40.99788205	73.07254179	79.66686637	14.30575138	22.10364887	14.86231211
PMX292	39.21998802	69.07206926	64.14594426	17.79164235	27.83180921	19.74510729

Table 7 - Experiment 10

	mean			SD		
Antibody	**Relative IFNg at 10ug/ml (%)**	**Relative IFNg at 1ug/ml (%)**	**Relative IFNg at 0.1ug/ml (%)**	**Relative IFNg at 10ug/ml (%)**	**Relative IFNg at 1ug/ml (%)**	**Relative IFNg at 0.1ug/ml (%)**
PMX105	9.326399485	26.14149091	80.09275049	5.509336216	19.82455021	11.41180542
PMX108	43.31374253	61.93007411	85.5705791	3.57248725	7.878265059	20.39849575
PMX109	41.61851823	54.12632982	58.51543743	0.3270937294	23.06271817	32.23446105
PMX111	70.49574297	43.85591582	60.58351844	30.37840868	0.6828670758	7.610640576

Table 8. Functional affinity of anti OX40L antibodies for trimeric canine OX40L determined by surface plasmon resonance (SPR).

PMX number	SPR KD1	SPR Koff (kd1)	SPR Koff (kd2)
PMX25	1.95E-07	1.29E-02	1.69E-03
PMX26	9.03E-07	1.91E-03	1.31E-03
PMX27	3.16E-07	1.61E-02	5.05E-04
PMX28	1.70E-08	9.35E-03	6.27E-04
PMX29	5.16E-08	2.94E-02	7.79E-04

PMX30	1.14E-07	2.83E-02	9.24E-04
PMX31	1.54E-07	1.24E-02	6.06E-04
PMX32	7.20E-09	5.86E-03	1.71E-05
PMX33	3.64E-08	1.03E-02	1.01E-03
PMX34	7.23E-06	1.35E-01	2.52E-04
PMX35	2.69E-07	3.11E-02	4.98E-04
PMX36	2.16E-08	1.66E-03	5.22E-02
PMX37	3.08E-07	1.83E-02	8.62E-04
PMX38	1.00E-07	1.05E-02	7.96E-04
PMX39	4.64E-08	1.28E-02	1.39E-03
PMX40	1.26E-09	7.48E-04	4.36E-01
PMX41	1.59E-06	1.34E-02	4.09E-04
PMX42	2.74E-07	2.92E-02	5.60E-04
PMX43	1.70E-08	2.49E-03	2.20E-03
PMX44	8.23E-09	1.71E-04	5.98E-02
PMX45	1.04E-08	4.84E-03	5.54E-04
PMX46	4.04E-08	1.01E-03	2.02E-05
PMX47	1.25E-08	4.51E-04	1.50E-05
PMX48	1.22E-08	4.85E-03	2.10E+01
PMX49	1.56E-08	2.11E-03	2.20E+01
PMX50	1.31E-09	5.25E-04	1.61E-01
PMX51	7.92E-09	1.19E-03	4.81E+00

PMX52	1.20E-08	2.76E-03	7.25E-02
PMX53	3.40E-09	5.87E-04	5.65E-01
PMX54	5.76E-09	3.45E-02	8.48E-02
PMX55	5.43E-09	3.66E-03	4.01E-01
PMX56	6.10E-08	1.48E-02	6.24E-04
PMX57	1.29E-09	4.72E-03	2.20E-01
PMX58	8.46E-09	1.44E-02	3.23E-01
PMX59	1.00E-08	7.37E-03	7.37E-03
PMX60	7.09E-08	9.33E-03	9.25E-04
PMX61	8.96E-08	7.46E-03	7.29E-04
PMX62	N/D	N/D	N/D
PMX63	2.71E-10	9.05E-05	5.21E+00
PMX64	1.45E-07	3.52E-02	9.21E-04
PMX65	1.07E-07	1.25E-02	4.12E-01
PMX097	4.92E-10	7.16E-05	7.44E-01
PMX098	1.41E-08	1.47E-03	1.03E+00
PMX154	1.56E-08	3.84E-03	6.94E+00
PMX155	9.06E-08	3.20E-02	2.94E-04
PMX156	1.98E-06	1.02E-01	2.38E-04
PMX105	1.76E-08	1.74E-03	1.23E+00
PMX294	1.44E-08	1.55E-03	2.69E+00
PMX293	1.00E-09	3.87E-04	1.45E+02
PMX104	1.76E-08	1.74E-03	1.23E+00

Table 9. Stability determination of OX40L antibodies.

Antibody	Tm1	Tagg266	Initial diameter	% monomer (SEC)
PMX25				91.01
PMX26		67.40	9.85	97.37
PMX27		68.00	9.79	97.90
PMX28	60.10	63.10	9.99	97.74
PMX29	61.50	62.50	10.07	95.28
PMX30	60.90	59.00	12.60	93.17
PMX31	58.9	57.4	10.84	94.07
PMX32	60.2	61.7	10.13	97.11
PMX33	62.50	62.40	10.52	32.73
PMX34	57.70	58.70	10.76	97.07
PMX35		51.1	14.20	94.89
PMX36	61	62.30	10.13	95.33
PMX37		55.90	11.00	97.87
PMX38	58.2	59.1	10.41	89.30
PMX39	59.6	59.9	12.09	
PMX40		54.5	24.88	97.75
PMX41	60.00	60.00	11.70	94.88
PMX42	62.9	64.1		96.90
PMX43	66.90	69.10	11.19	96.06
PMX44	62.30	62.90	12.39	88.77
PMX45	57.8	58.6	11.88	93.19

PMX46	62.30	62.90	12.39	95.25
PMX47				75.43
PMX48	64.6	61.4	9.97	97.22
PMX49	64.6	61.4	9.97	97.32
PMX50	64.9	65.9	42.33	89.26
PMX51	63	62.5	10.24	96.68
PMX53	61.2	58.4	9.72	93.21
PMX63	63	61	9.74	94.58
PMX097	65.8	66.7	10.1	99.28
PMX098	62.2	60.6	14.66	97.5
PMX154	67.2	68.8	10.04	99.19
PMX155	62.5	62.1	10.6	99.43
PMX156	63.4	62.7	10.33	99.63

Table 10. Long term stability of PMX097 and PMX154 at 4°C

PMX097	**After purification 5mg/ml**	**4 months at 4C 5mg/ml**
Tm	65.8 ± 0.17	69.4 ± 0.85
Tagg 266nm	66.7 ± 0.23	64.7 ± 0.94
Z AVG diam	10.1	9.92 ± 0.08
PDI	0.05	0.061 ± 0.018

PMX154	After purification 5mg/ml	4 months at 4C 5mg/ml
Tm	67.2 ± 0.21	66.71 ± 0.35 (N=2)
Tagg 266nm	68.8 ± 0.23	61.4 ± 3.5
Z AVG diam	10.04	10.23 ± 0.20
PDI	0.03	0.060 ± 0.016

Table 11 Treatment regime of dogs in the single dose antigen recall dog study

Group	Test substance (Day 0)	1st immunisation (day 1)	2nd immunisation (day 21)	Skin biopsies (day 23)	3rd immunisation (day 63)
1	Vehicle control	100µg KLH+100 µg alhydrogel intramuscular injection	10µg KLH intradermal	2 biopsies per dog, one in KLH injected area, one in control area	100µg KLH intramuscular
2	PMX154 at 3.0 mg/kg				
3	PMX154 at 0.5 mg/kg				
4	PMX097 at 3.0 mg/kg				
5	PMX097 at 0.5 mg/kg				

Table 12 Histological findings in non-injected skin areas from dogs in the single dose antigen recall study.

	Group 1		Group 2		Group 3	
	Non injected area		Non injected area		Non injected area	
	N of dogs with abnormalities	Mean score	N of dogs with abnormalities	Mean score	N of dogs with abnormalities	Mean score
Hyperkeratosis	0	0	0	0	0	0
Infiltrate, lymphocytic, dermal	0	0	0	0	0	0
Infiltrate, histiocytic/macrophagic, dermal	0	0	0	0	0	0
Infiltrate, neutrophilic, dermal	0	0	0	0	0	0
Infiltrate, lymphocytic, subcutaneous/muscular	0	0	0	0	0	0
Infiltrate, histiocytic/macrophagic, subcutaneous/muscular	0	0	0	0	0	0
Infiltrate, neutrophilic, subcutaneous/muscular	0	0	0	0	0	0
Fibroplasia, subcutaneous	0	0	0	0	0	0
Hemorrhage, subcutaneous	0	0	0	0	0	0
Myofiber loss	-	-	-	-	0	0
Myofiber degeneration	-	-	-	-	0	0
Artifact	4	1	4	1	4	1
Sum score	0	0	0	0	0	0
No Significant findings	4		4		4	

	Group 4		Group 5	
	Non injected area		Non injected area	
	N of dogs with abnormalities	Mean score	N of dogs with abnormalities	Mean score
Hyperkeratosis	0	0	0	0
Infiltrate, lymphocytic, dermal	0	0	0	0
Infiltrate, histiocytic/macrophagic, dermal	0	0	0	0
Infiltrate, neutrophilic, dermal	0	0	0	0
Infiltrate, lymphocytic, subcutaneous/muscular	0	0	0	0

Infiltrate, histiocytic/macrophagic, subcutaneous/muscular	0	0	0	0
Infiltrate, neutrophilic, subcutaneous/muscular	0	0	0	0
Fibroplasia, subcutaneous	0	0	0	0
Hemorrhage, subcutaneous	0	0	0	0
Myofiber loss	0	0	-	-
Myofiber degeneration	0	0	-	-
Artifact	4	1	4	1
Sum score	0	0	0	0
No Significant findings	4		4	

Table 13 Histological findings in KLH-injected skin areas from dogs in the single dose antigen recall study.

	Group 1		Group 2		Group 3	
	KLH injected area		KLH injected area		KLH injected area	
	N of dogs with abnormalities	Mean score	N of dogs with abnormalities	Mean score	N of dogs with abnormalities	Mean score
Hyperkeratosis	1	0.3	0	0	0	0
Infiltrate, lymphocytic, dermal	4	1.3	3	1.3	0	0
Infiltrate, histiocytic/macrophagic, dermal	2	0.5	0	0	0	0
Infiltrate, neutrophilic, dermal	2	0.5	0	0	0	0
Infiltrate, lymphocytic, subcutaneous/muscular	3	2	4	1.3	0	0
Infiltrate, histiocytic/macrophagic, subcutaneous/muscular	3	2.7	4	1	0	0
Infiltrate, neutrophilic, subcutaneous/muscular	3	2.3	4	1.3	0	0
Fibroplasia, subcutaneous	3	1.3	1	0.3	0	0
Hemorrhage, subcutaneous	3	1	3	0.8	1	0.5
Myofiber loss	1	1	1	1	-	-
Myofiber degeneration	0	0	1	1	-	-
Artifact	3	0.8	4	1	4	1
Sum score	25	12.8	21	7.8	1	0.5
N. of dogs with No Significant findings	0		0		3	

	Group 4		Group 5	
	KLH injected area		KLH injected area	
	N of dogs with abnormalities	Mean score	N of dogs with abnormalities	Mean score
Hyperkeratosis	0	0	0	0
Infiltrate, lymphocytic, dermal	3	1.8	2	1
Infiltrate, histiocytic/macrophagic, dermal	2	1	2	1
Infiltrate, neutrophilic, dermal	2	0.8	2	1
Infiltrate, lymphocytic, subcutaneous/muscular	2	1.3	3	1.7
Infiltrate, histiocytic/macrophagic, subcutaneous/muscular	2	1	3	2
Infiltrate, neutrophilic, subcutaneous/muscular	2	1	3	2
Fibroplasia, subcutaneous	1	0.7	0	0
Hemorrhage, subcutaneous	1	0.7	1	0.3
Myofiber loss	0	0	0	0
Myofiber degeneration	0	0	0	0
Artifact	4	1	0	0
Sum score	15	8.2	16	9
N. of dogs with No Significant findings	1		0	

Sequences Used in Experimental

SEQ ID NO. 807

Monomeric OX40L probe amino acid sequence

NGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVNLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLNSTLTVDKSRWQQGNVFSCSVMHEALHNH
YTQKSLSLSHHHHHHENLYFQGQVPPQYPPIQSIRVQFTRCENEKGCIITSPSKDETMKVQDNSIIINC
DGFYLISLKGYFSEELSLSLYYRKGRGPLFSLSKVTSVDSIGVAYLAFKDKVYFNVTTHSTSYKDIQVN
GGELILIHQNPGGFCAY

SEQ ID NO. 808

Trimeric OX40L probe (hIgG1 Fc fusion) DNA sequence

gacaaaactcacacatgcccaccgtgcccagcacctgaactcctgggggggaccgtcagtcttcctcttccccccaaaacccaaggacaccct
catgatctcccggaccccctgaggtcacatgcgtggtggtggacgtgagccacgaagaccctgaggtcaagttcaactggtacgtggacggcgt
ggaggtgcataatgccaagacaaagccgcgggaggagcagtacaacagcacgtaccgtgtggtcagcgtcctcaccgtcctgcaccagga
ctggctgaatggcaaggagtacaagtgcaaggtctccaacaaagccctcccagccccatcgagaaaaccatctccaaagccaaagggc
agccccgagaaccacaggtgtacaccctgccccatcccgggatgagctgaccaagaaccaggtcagcctgacctgcctggtcaaaggctt
ctatcccagcgacatcgccgtggagtgggagagcaatgggcagccggagaacaactacaagaccacgcctcccgtgctggactccgacg
gctccttcttcctctacagcaagctcaccgtggacaagagcaggtggcagcaggggaacgtcttctcatgctccgtgatgcatgaggctctgca
caaccactacacacagaagagcctctccctgtctccgggtaaaAGGAGCCCCCAGCCCCAGCCCAAGCCCCAGCCC
AAGCCCGAGCCCGAGGGCAGCCTGCACGCCTGCGGCTGCGCCGCCGCCCCCGACATCAAGGA
CCTGCTGAGCAGGCTGGAGGAGCTGGAGGGCCTGGTGAGCAGCCTGAGGGAGCAGGGCACCG
GCGGCGGCAGCGGCGGCAGGGGCCTGCAGCAGGTGCCGCCTCAGTATCCTCCAATTCAAAGTA
TCAGAGTACAATTTACCAGGTGTGAGAATGAGAAAGGTTGCATCATCACATCCCCAAGCAAGGAT
GAAACTATGAAGGTGCAAGACAACTCAATCATCATTAACTGTGATGGGTTTTATCTCATCTCCCTG
AAGGGTTACTTCTCTGAGGAGCTCAGCCTCAGCCTTTATTACCGAAAGGGTCGGGGACCCCTCTT
CTCTCTGAGCAAGGTCACATCTGTTGACTCCATTGGAGTGGCCTATCTGGCTTTCAAGGACAAAG
TCTACTTTAATGTGACCACTCACAGTACCTCCTACAAAGACATCCAGGTGAATGGTGGGGAATTG
ATTCTCATTCATCAAAATCCTGGTGGCTTCTGTGCCTAC

SEQ ID NO. 809

Trimeric OX40L probe (hIgG1 Fc fusion) amino acid sequence

DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA
KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR
DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV
FSCSVMHEALHNHYTQKSLSLSPGKRSPQPQPKPQPKPEPEGSLHACGCAAAPDIKDLLSRLEELEG
LVSSLREQGTGGGSGGRGLQQVPPQYPPIQSIRVQFTRCENEKGCIITSPSKDETMKVQDNSIIINCDG
FYLISLKGYFSEELSLSLYYRKGRGPLFSLSKVTSVDSIGVAYLAFKDKVYFNVTTHSTSYKDIQVNGGE
LILIHQNPGGFCAY

SEQ ID NO. 810

Trimeric OX40L probe (HIS tag) DNA sequence

CACCATCACcatcaccatGGCCCCGGCCAGGTGCAGCTGCACGCCTGCGGCTGCGCCGCCGCCCC
CGACATCAAGGACCTGCTGAGCAGGCTGGAGGAGCTGGAGGGCCTGGTGAGCAGCCTGAGGGA
GCAGGGCACCGGCGGCGGCAGCGGCGGCAGGGGCCTGCAGCAGGTGCCGCCTCAGTATCCTC
CAATTCAAAGTATCAGAGTACAATTTACCAGGTGTGAGAATGAGAAAGGTTGCATCATCACATCCC
CAAGCAAGGATGAAACTATGAAGGTGCAAGACAACTCAATCATCATTAACTGTGATGGGTTTTATC
TCATCTCCCTGAAGGGTTACTTCTCTGAGGAGCTCAGCCTCAGCCTTTATTACCGAAAGGGTCGG
GGACCCCTCTTCTCTCTGAGCAAGGTCACATCTGTTGACTCCATTGGAGTGGCCTATCTGGCTTT
CAAGGACAAAGTCTACTTTAATGTGACCACTCACAGTACCTCCTACAAAGACATCCAGGTGAATG
GTGGGGAATTGATTCTCATTCATCAAAATCCTGGTGGCTTCTGTGCCTAC

SEQ ID NO. 811

Trimeric OX40L probe (HIS tag) amino acid sequence

HHHHHHGPGQVQLHACGCAAAPDIKDLLSRLEELEGLVSSLREQGTGGGSGGRGLQQVPPQYPPIQ
SIRVQFTRCENEKGCIITSPSKDETMKVQDNSIIINCDGFYLISLKGYFSEELSLSLYYRKGRGPLFSLSK
VTSVDSIGVAYLAFKDKVYFNVTTHSTSYKDIQVNGGELILIHQNPGGFCAY

Claims

1. An antibody or fragment thereof that specifically binds to companion animal OX40L, wherein the antibody is selected from one of the following antibodies:

an antibody comprising a HC CDR1 comprising SEQ ID No: 575 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 576 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 577 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 578 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 579 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 580 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto;

a HC CDR1 comprising SEQ ID No: 741 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 742 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 743 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 744 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 745 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 746 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto; or

an antibody comprising a HC CDR1 comprising SEQ ID No: 275 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 276 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 277 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 278 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 279 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 280 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 395 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 396 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 397 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 398 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 399 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 400 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 15 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 16 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 17 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 18 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 19 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 20 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto.

an antibody comprising a HC CDR1 comprising SEQ ID No: 45 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 46 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 47 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 48 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 49 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 50 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto

an antibody comprising a HC CDR1 comprising SEQ ID No: 65 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 66 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 67 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 68 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 69 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 70 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 115 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 116 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 117 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 118 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 119 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 120 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 155 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 156 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC

CDR3 comprising SEQ ID No: 157 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 158 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 159 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 160 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 235 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 236 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 237 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 238 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 239 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 240 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 285 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 286 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 287 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 288 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 289 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 290 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 365 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 366 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 367 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 368 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 369 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 370 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 665 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 666 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 667 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 668 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR2 comprising SEQ ID No:

669 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 670 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, or;

an antibody comprising a HC CDR1 comprising SEQ ID No: 751 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 752 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 753 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 754 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 755 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 756 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, or;

an antibody comprising a HC CDR1 comprising SEQ ID No: 771 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 772 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 773 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 774 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 775 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 776 or a sequence with at least 60%, 70%, 80%, 90% or 95% sequence identity thereto.

2. An antibody or fragment thereof that specifically binds to companion animal OX40L, wherein the antibody is selected from one of the following antibodies:

an antibody comprising a HC CDR1 comprising SEQ ID No: 575 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 576 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 577 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 578 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 579 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 580 or a sequence with at least 80% sequence identity thereto;

a HC CDR1 comprising SEQ ID No: 741 or a sequence with at least 80%, sequence identity thereto, a HC CDR2 comprising SEQ ID No: 742 or a sequence with at least 80%, sequence identity thereto, a HC CDR3 comprising SEQ ID No: 743 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 744 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 745 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 746 or a sequence with at least 80% sequence identity thereto; or

an antibody comprising a HC CDR1 comprising SEQ ID No: 275 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 276 or a sequence with at

least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 277 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 278 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 279 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 280 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 395 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 396 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 397 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 398 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 399 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 400 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 15 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 16 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 17 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 18 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 19 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 20 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 25 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 26 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 27 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 28 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 29 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 30 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 35 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 36 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 37 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 38 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 39 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 40 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 45 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 46 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 47 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 48 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 49 or a sequence

with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 50 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 55 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 56 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 57, or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 58 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 59 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 60 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 65 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 66 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 67 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 68 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 69 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 70 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 75 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 76 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 77 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 78 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 79 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 80 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 85 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 86 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 87 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 88 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 89 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 90 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 95 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 96 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 97 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 98 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 99 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 100 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 105 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 106 or a sequence with at

least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 107 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 108 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 109 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 110 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 115 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 116 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 117 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 118 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 119 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 120 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 125 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 126 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 127 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 128 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 129 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 130 or a sequence with at least 80% sequence identity thereto; or

an antibody comprising a HC CDR1 comprising SEQ ID No: 135 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 136 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 137 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 138 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 139 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 140 or a sequence with at least 80% sequence identity thereto.

an antibody comprising a HC CDR1 comprising SEQ ID No: 145 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 146 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 147 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 148 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 149 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 150 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 155 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 156 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 157 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 158 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 159

or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 160 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 165 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 166 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 167 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 168 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 169 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 170 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 175 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 176 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 177 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 178 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 179 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 180 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 185 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 186 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 187 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 188 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 189 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 190 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 195 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 196 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 197 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 198 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 199 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 200 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 205 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 206 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 207 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 208 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 209 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 210 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 215 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 216 or a sequence with at

least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 217 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 218 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 219 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 220 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 225 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 226 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 227 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 228 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 229 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 230 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 235 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 236 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 237 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 238 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 239 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 240 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 245 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 246 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 247 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 248 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 249 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 250 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 255 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 256 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 257 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 258 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 259 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 260 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 265 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 266 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 267 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 268 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 269

or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 270 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 285 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 286 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 287 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 288 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 289 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 290 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 295 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 296 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 297 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 298 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 299 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 300 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 305 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 306 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 307 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 308 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 309 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 310 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 315 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 316 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 317 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 318 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 319 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 320 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 325 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 326 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 327 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 328 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 329 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 330 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 335 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 336 or a sequence with at

least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 337 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 338 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 339 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 340 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 345 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 346 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 347 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 348 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 349 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 350 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 355 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 356 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 357 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 358 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 359 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 360 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 365 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 366 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 367 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 368 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 369 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 370 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 375 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 376 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 377 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 378 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 379 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 380 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 385 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 386 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 387 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 388 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 389

or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 390 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 405 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 406 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 407 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 408 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 409 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 410 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 415 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 416 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 417 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 418 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 419 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 420 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 425 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 426 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 427 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 428 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 429 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 430 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 435 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 436 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 437 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 438 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 439 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 440 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 445 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 446 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 447 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 448 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 449 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 440 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 455 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 456 or a sequence with at

least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 457 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 458 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 459 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 460 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 465 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 466 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 467 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 468 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 469 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 470 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 475 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 476 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 477 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 478 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 479 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 480 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 485 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 486 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 487 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 488 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 489 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 490 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 495 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 496 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 497 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 498 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 499 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 500 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 505 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 506 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 507 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 508 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 509

or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 510 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 515 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 516 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 517 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 518 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 519 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 520 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 525 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 526 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 527 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 528 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 529 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 530 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 535 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 536 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 537 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 538 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 539 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 540 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 545 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 546 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 547 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 548 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 549 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 550 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 555 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 556 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 557 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 558 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 559 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 560 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 565 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 566 or a sequence with at

least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 567 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 568 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 569 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 570 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 585 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 586 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 587 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 588 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 589 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 590 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 595 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 596 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 597 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 598 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 599 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 600 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 605 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 606 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 607 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 608 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 609 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 610 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 615 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 616 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 617 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 618 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 619 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 620 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 625 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 626 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 627 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 628 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 629

or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 630 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 635 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 636 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 637 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 638 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 639 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 640 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 645 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 646 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 647 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 648 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 649 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 650 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 655 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 656 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 657 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 658 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 659 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 660 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 665 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 666 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 667 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 668 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 669 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 670 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 675 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 676 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 677 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 678 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 679 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 680 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 685 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 686 or a sequence with at

least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 687 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 688 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 689 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 690 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 695 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 696 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 697 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 698 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 699 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 700 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 705 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 706 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 707 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 708 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 709 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 710 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 715 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 716 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 717 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 718 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 719 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 720 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 751 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 752 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 753 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 754 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 755 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 756 or a sequence with at least 80%sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 761 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 762 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 763 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 764 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 765

or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 766 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 771 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 772 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 773 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 774 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 775 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 776 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 781 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 782 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 783 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 784 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 785 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 786 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC CDR1 comprising SEQ ID No: 791 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 792 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 793 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 794 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 795 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 796 or a sequence with at least 80% sequence identity thereto, or;

An antibody comprising a HC CDR1 comprising SEQ ID No: 801 or a sequence with at least 80% sequence identity thereto, a HC CDR2 comprising SEQ ID No: 802 or a sequence with at least 80% sequence identity thereto, a HC CDR3 comprising SEQ ID No: 803 or a sequence with at least 80% sequence identity thereto, a LC CDR1 comprising SEQ ID No: 804 or a sequence with at least 80% sequence identity thereto, a LC CDR2 comprising SEQ ID No: 805 or a sequence with at least 80% sequence identity thereto and a LC CDR3 comprising SEQ ID No: 806 or a sequence with at least 80% sequence identity thereto.

3. The antibody or fragment according to any of claims 1 to 2 wherein said companion animal is a dog or a cat.
4. The antibody or fragment according to any of claims 1 to 2 wherein the antibody or fragment binds to canine OX40L.
5. The antibody or fragment according to claim 4 wherein said antibody or fragment is capable of
    a) reducing, inhibiting or neutralising OX40 activity or activation in the companion animal or in a cell of the companion animal;
    b) modifying secretion of a cytokine in the companion animal or in a cell of the companion animal and/or

c) decreasing proliferation of leukocytes in the companion animal.

6. The antibody or fragment according to a preceding claim wherein the antibody is a canine or caninized antibody.

7. The antibody or antibody fragment according to a preceding claim wherein the antibody is selected from one of the following antibodies:

an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 12 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 14 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 22 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 24 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 32 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 34 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 42 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 44 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 52 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 54 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 62 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 64 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 72 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 74 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 82 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 84 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 92 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 94 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 102 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 104 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 112 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 114 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 122 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 124 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 132 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 134 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 142 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 144 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 152 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 154 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 162 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 164 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 172 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 174 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 182 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 184 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 192 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 194 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 202 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 204 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 212 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 214 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 222 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 224 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 232 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 234 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 242 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 244 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 252 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 254 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 262 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 264 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 272 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 274 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 282 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 284 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 292 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 294 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 302 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 304 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 312 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 314 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 322 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 324 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 332 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 334 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 342 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 344 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 352 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 354 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 362 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 364 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 372 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 374 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 382 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 384 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 392 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 394 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 402 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 404 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 412 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 414 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 422 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 424 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 432 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 434 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 442 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 444 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 452 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 454 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 462 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 464 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 472 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 474 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 482 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 484 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 492 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 494 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 502 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 504 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 512 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 514 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 522 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 524 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 532 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 534 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 542 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 544 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 552 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 554 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 562 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 564 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 572 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 574 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 582 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 584 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 592 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 594 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 602 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 604 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 612 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 614 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 622 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 624 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 632 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 634 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 642 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 644 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 652 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 654 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 662 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 664 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 672 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 674 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 682 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 684 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 692 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 694 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 702 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 704 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 712 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 714 or a sequence with at least 80% sequence identity thereto or an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 738 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 740 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 748 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 750 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 758 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 760 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 768 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 770 or a sequence with at least 80% sequence identity thereto;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 778 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 780 or a sequence with at least 80% sequence identity thereto;

an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 788 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 790 or a sequence with at least 80% sequence identity thereto, or;
an antibody comprising a HC variable region comprising or consisting of SEQ ID No. 798 or a sequence with at least 80% sequence identity thereto and a LC variable region comprising or consisting of SEQ ID No. 800 or a sequence with at least 80% sequence identity thereto.

8. The antibody or fragment according to a preceding claim wherein said fragment is selected from a F(ab')2, Fab, Fv, scFv, heavy chain, light chain, variable heavy (VH), variable light (VL) chain, CDR region, single VH or VL domain, maxibodies, minibodies, intrabodies, diabodies, triabodies, tetrabodies, and bis-scFv, and polypeptides that contain at least a portion of an immunoglobulin that is sufficient to confer specific antigen binding to the polypeptide.
9. The antibody or fragment according to a preceding claim wherein said antibody or fragment is conjugated to another moiety.
10. The antibody or fragment according to a preceding claim comprising a therapeutic moiety, half life extending moiety or label.
11. A binding molecule comprising an antibody or fragment according to a preceding claim.
12. The antibody or fragment according to any of claims 1 to 10 or the binding molecule of claim 11 for use in the treatment of a disease.
13. A pharmaceutical composition comprising an antibody or fragment thereof according to any of claims 1 to 10 or the binding molecule of claim 11.
14. An antibody or fragment thereof according to any of claims 1 to 10, the binding molecule of claim 11 or a pharmaceutical composition according to claim 13 for use in the treatment of an OX40 or OX40L-mediated disease.
15. A method of treating or preventing an OX40 or OX40L-mediated disease comprising administering to a subject in need thereof an antibody or fragment according to any of claims 1 to 10, the binding molecule of claim 11 or the pharmaceutical composition according to claim 13.
16. The antibody or fragment, binding molecule or pharmaceutical composition according claim 14 or the method of claim 15 wherein said disease is selected from an inflammatory or autoimmune disease.
17. The antibody or fragment, binding molecule, pharmaceutical composition or method according claim 16 wherein said disease is selected from an inflammatory skin diseases, including atopic dermatitis, allergic dermatitis, pruritus, psoriasis, scleroderma, or eczema; responses associated with inflammatory bowel disease (such as Crohn's disease and ulcerative colitis); ischemic reperfusion; adult respiratory distress syndrome; asthma; meningitis; encephalitis; uveitis; autoimmune diseases such as rheumatoid arthritis, Sjorgen's syndrome, vasculitis; diseases involving leukocyte diapedesis; central nervous system (CNS) inflammatory disorder, multiple organ injury syndrome secondary to septicaemia or trauma, bacterial pneumonia,

antigen-antibody complex mediated diseases; inflammations of the lung, including pleurisy, alveolitis, vasculitis, pneumonia, chronic bronchitis, bronchiectasis, and cystic fibrosis.

18. The antibody or fragment, binding molecule, pharmaceutical composition according to any of claims 14, 16 or 17 or the method according to any of claims 15 to 17 wherein said antibody or fragment is administered together with one or more therapeutic agent.
19. The antibody or fragment, binding molecule, pharmaceutical composition or method according claim 18 wherein said one or more therapeutic agent is selected from rapamycin (sirolimus), tacrolimus, cyclosporine (e.g. Atopica®), corticosteroids (e.g. methylprednisolone), methotrexate, mycophenolate mofetil, anti-CD28 antibodies, anti-IL12/IL-23 antibodies, anti-CD20 antibodies, anti-CD30 antibodies, CTLA4-Fc molecules, CCR5 receptor antagonists, anti-CD40L antibodies, anti-Vl_A4 antibodies, anti-LFA1 antibodies, fludarabine, anti-CD52 antibodies, anti-CD45 antibodies, cyclophosphamide, anti-thymocyte globulins, anti-complement C5 antibodies, anti-a4b7 integrin antibodies, anti-IL6 antibodies, anti-IL6-R antibodies, anti-IL2R antibodies, anti-CD25 antibodies, anti-TNFa / TNFa-Fc molecules, HDAC inhibitors, JAK inhibitors, such as JAK-1 and JAK-3 inhibitors, anti-IL-31 antibodies, SYK inhibitors, anti-IL-4Ra antibodies, anti-IL-13 antibodies, anti-TSLP antibodies, PDE4 inhibitors, lokietmab (Cytopoint®), and oclacitinib (Apoquel®).
20. A method of decreasing the secretion of cytokines comprising administering to a subject in need thereof an antibody or fragment according to any of claims 1 to 10, a binding molecule of claim 11 or a pharmaceutical composition of claim 13.
21. A multispecific binding agent comprising an antibody or fragment thereof according to any of claims 1 to 10 or a binding molecule of claim 11.
22. A combination therapy comprising antibody or fragment according to any of claims 1 to 10, a binding molecule of claim 11 or a pharmaceutical composition of claim 13.
23. An immunoconjugate comprising an antibody or fragment according to any of claims 1 to 10 or a binding molecule of claim 11.
24. A kit comprising an antibody or fragment thereof according to any of claims 1 to 10, the binding molecule of claim 11 or a pharmaceutical composition according to claim 13.
25. A method for detecting OX40L or OX40 in a companion animal comprising contacting a test sample with an antibody or fragment according to any of claims 1 to 10 or a binding molecule of claim 11.

Figure 1

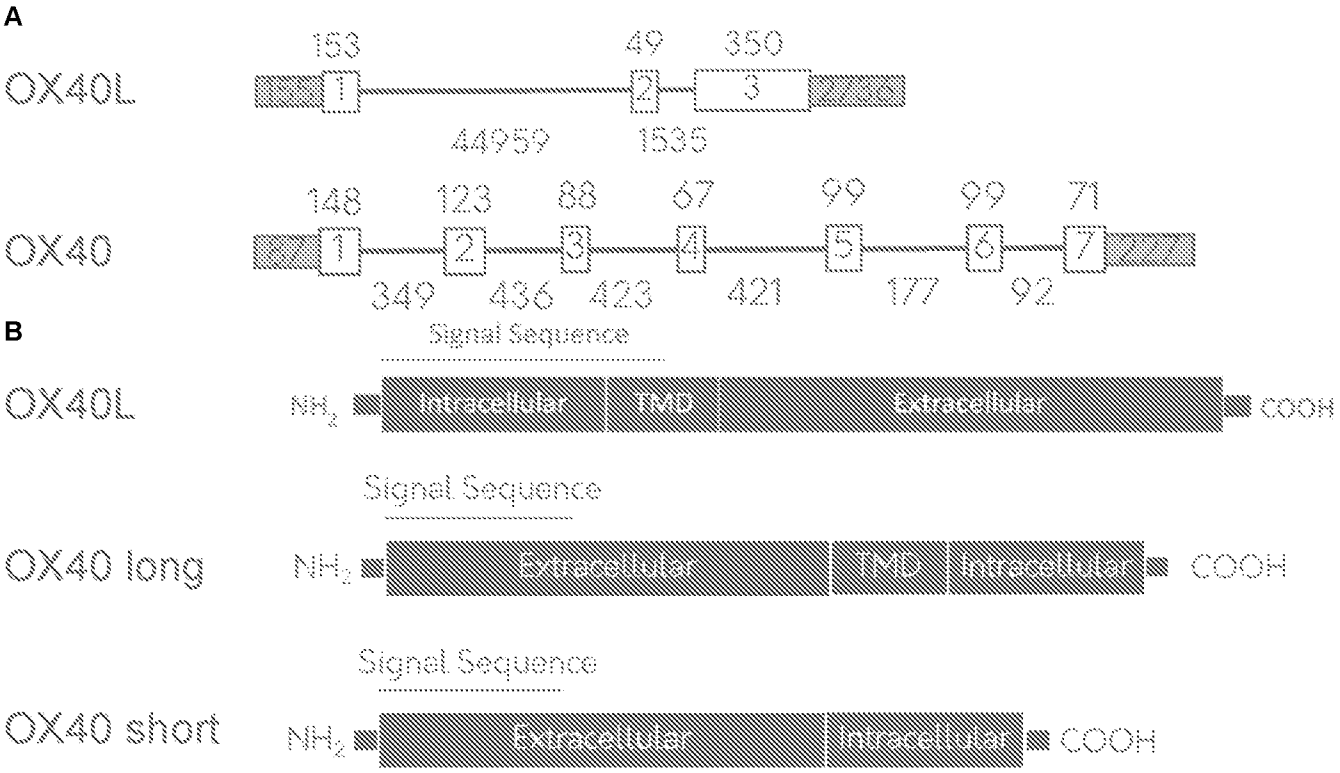


Figure 2

```
Short    MRMFVESLRLSGPHSALLLLGLVLGAVAEHNCFGNTYPKDGKCCNDCPPGYGMESRCSRS
Long     MRMFVESLRLSGPHSALLLLGLVLGAVAEHNCFGNTYPKDGKCCNDCPPGYGMESRCSRS
         ************************************************************

Short    HDTKCHQCPSGFYNEATNYEPCKPCTQCNQRSGSEPKRRCTPTQDTICSCKPGTEPRDGY
Long     HDTKCHQCPSGFYNEATNYEPCKPCTQCNQRSGSEPKRRCTPTQDTICSCKPGTEPRDGY
         ************************************************************

Short    KRGVDCAPCPPGHFSPGDDQACKPWTNCTLMGRRTMQPASKSSDAVCEDRSLPATLPWET
Long     KRGVDCAPCPPGHFSPGDDQACKPWTNCTLMGRRTMQPASKSSDAVCEDRSLPATLPWET
         ************************************************************

Short    QSPLTRPPTPQPTMAWPRTSQGPFTPPTEPPRG-------------------------
Long     QSPLTRPPTPQPTMAWPRTSQGPFTPPTEPPRGPQLAAVLGLGLGLLAPVAAALALLLHH
         *********************************

Short    --------GNSFRTPIQEEHADANSTLAKI
Long     RAWRLPPGGNSFRTPIQEEHADANSTLAKI
                ********************
```

Figure 3

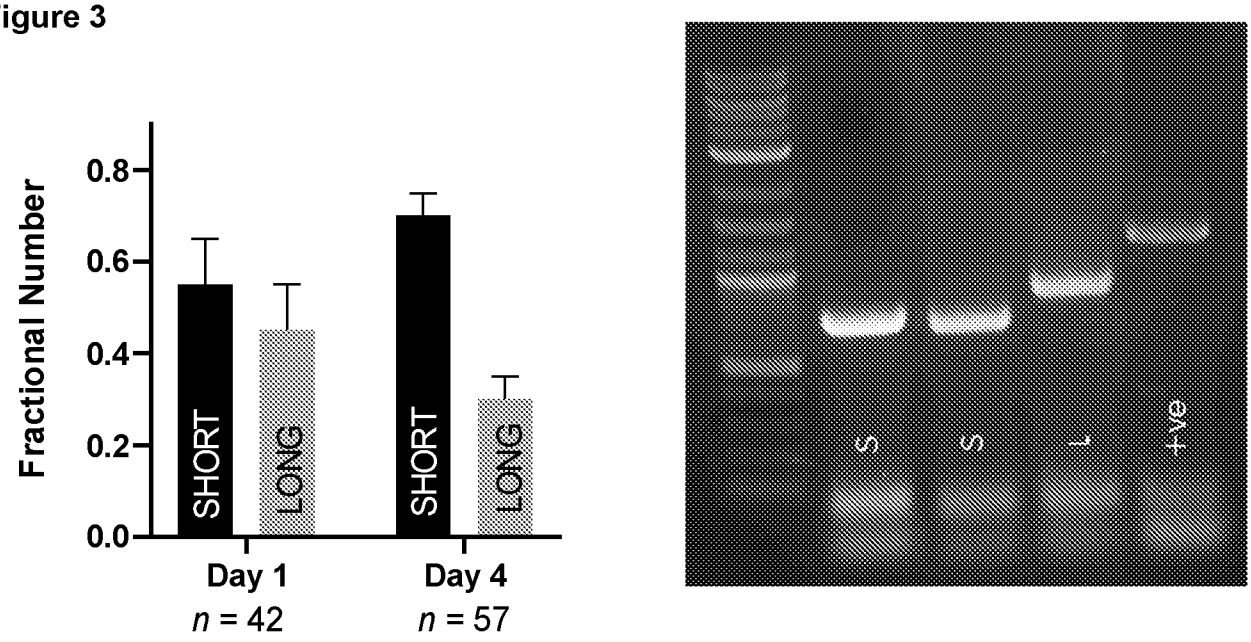
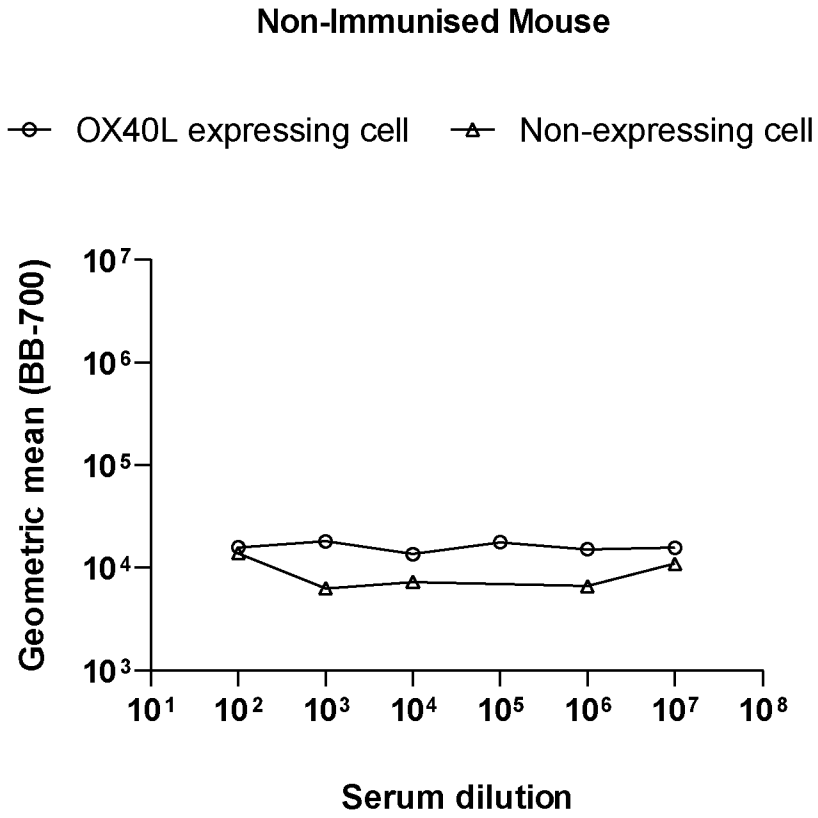


Figure 4

A



B

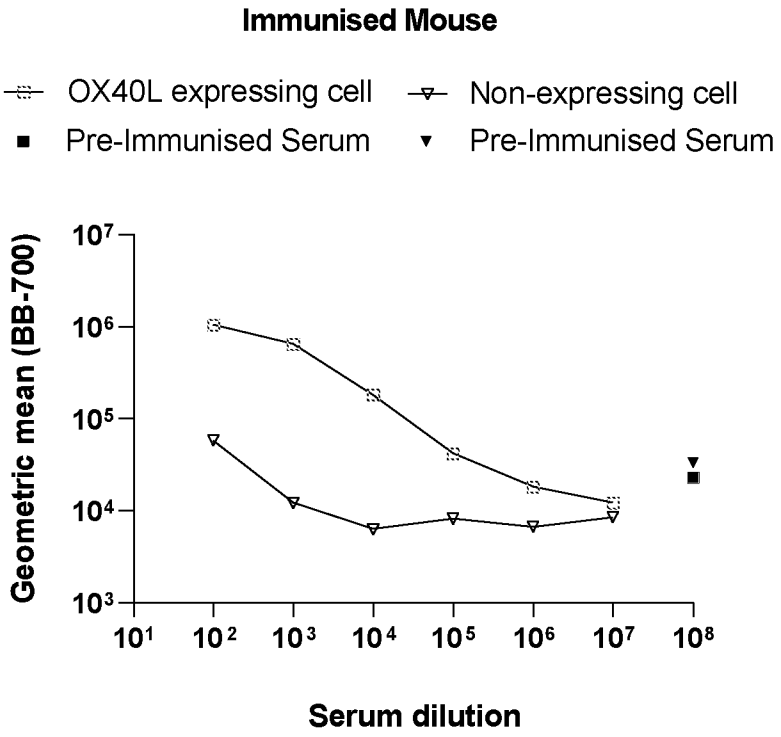

Immunised Mouse
OX40L expressing cell
Non-expressing cell
Pre-Immunised Serum
Pre-Immunised Serum
Geometric mean (BB-700)
10^7
10^6
10^5
10^4
10^3
10^1
10^2
10^3
10^4
10^5
10^6
10^7
10^8
Serum dilution

Figure 5

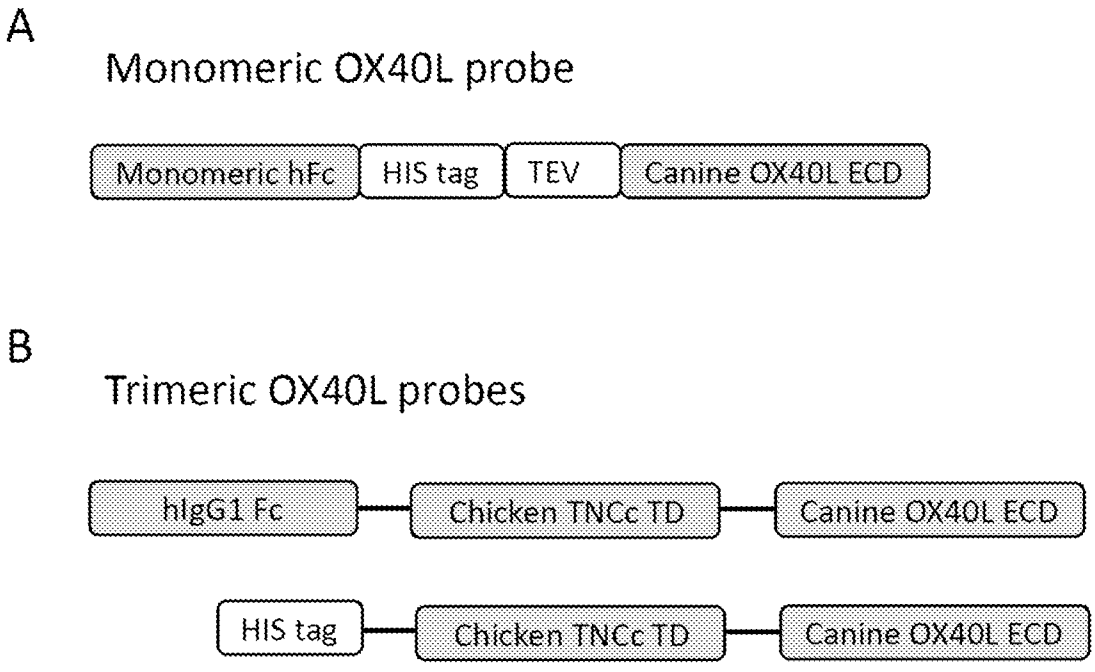

A
Monomeric OX40L probe
Monomeric hFc
HIS tag
TEV
Canine OX40L ECD
B
Trimeric OX40L probes
hIgG1 Fc
Chicken TNCc TD
Canine OX40L ECD
HIS tag
Chicken TNCc TD
Canine OX40L ECD

Figure 6

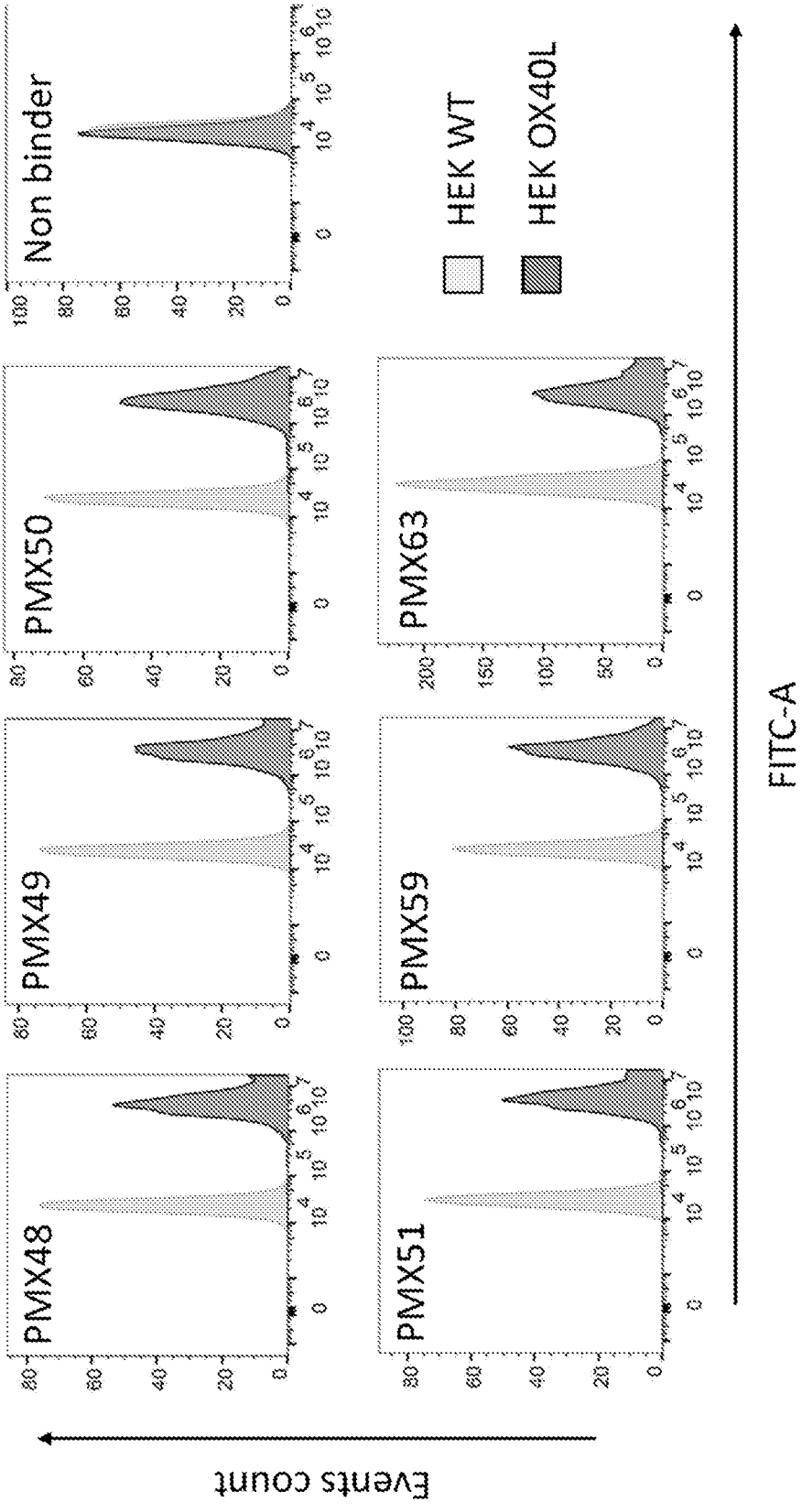

Non binder
PMX50
PMX49
PMX48
PMX63
PMX59
PMX51
HEK WT
HEK OX40L
FITC-A
Events count

Figure 7

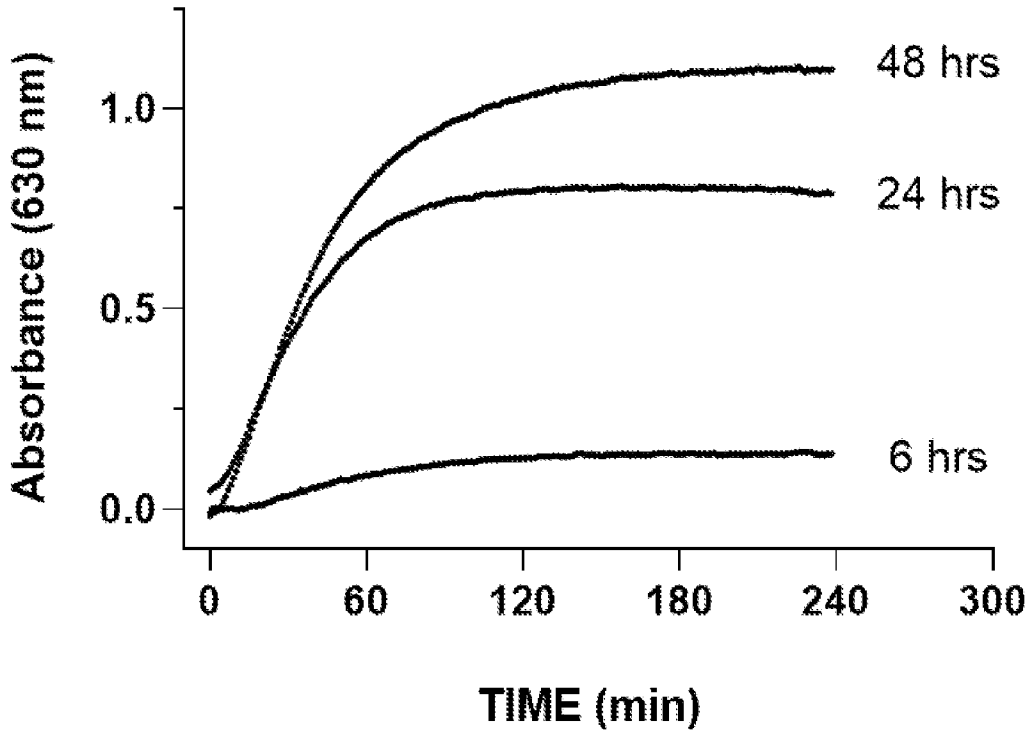

Absorbance (630 nm)
1.0
0.5
0.0
0
60
120
180
240
300
TIME (min)
48 hrs
24 hrs
6 hrs

Figure 8

A

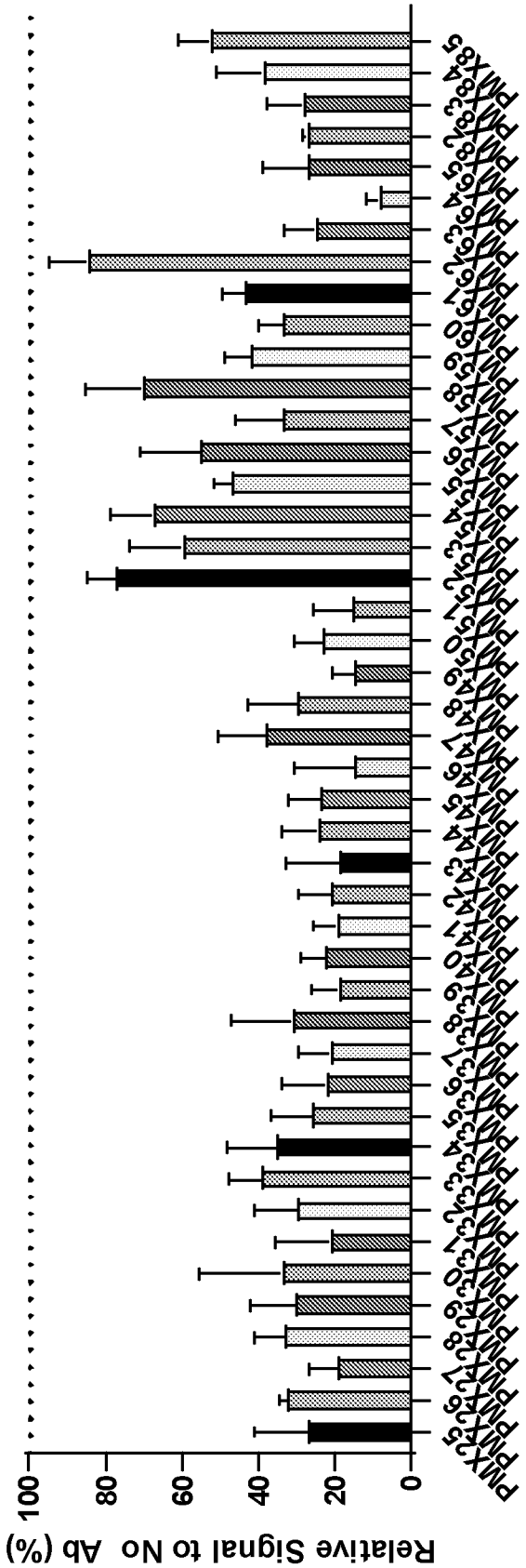

Relative Signal to No Ab (%)
0
20
40
60
80
100
pMX25
pMX26
pMX27
pMX28
pMX29
pMX30
pMX31
pMX32
pMX33
pMX34
pMX35
pMX36
pMX37
pMX38
pMX39
pMX40
pMX41
pMX42
pMX43
pMX44
pMX45
pMX46
pMX47
pMX48
pMX49
pMX50
pMX51
pMX52
pMX53
pMX54
pMX55
pMX56
pMX57
pMX58
pMX59
pMX60
pMX61
pMX62
pMX63
pMX64
pMX65
pMX66
pMX67
pMX68
pMX69
pMX70
pMX71
pMX72
pMX73
pMX74
pMX75
pMX76
pMX77
pMX78
pMX79
pMX80
pMX81
pMX82
pMX83
pMX84
pMX85

Figure 8 continued

B

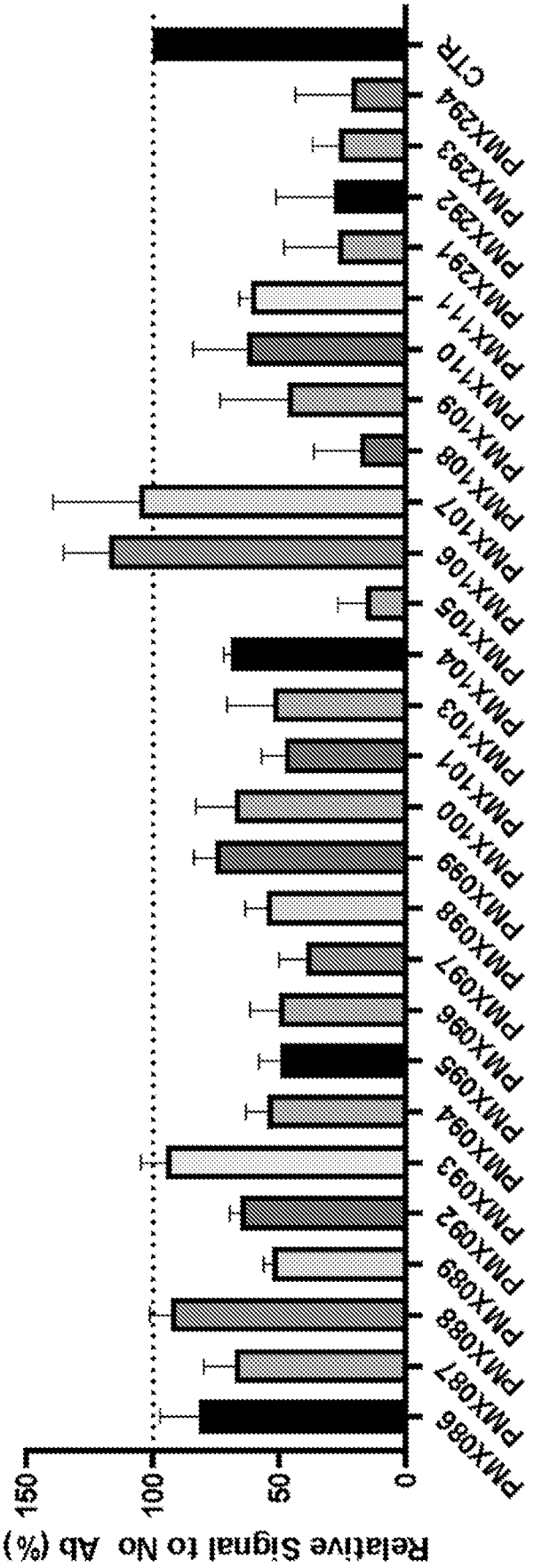


Figure 9

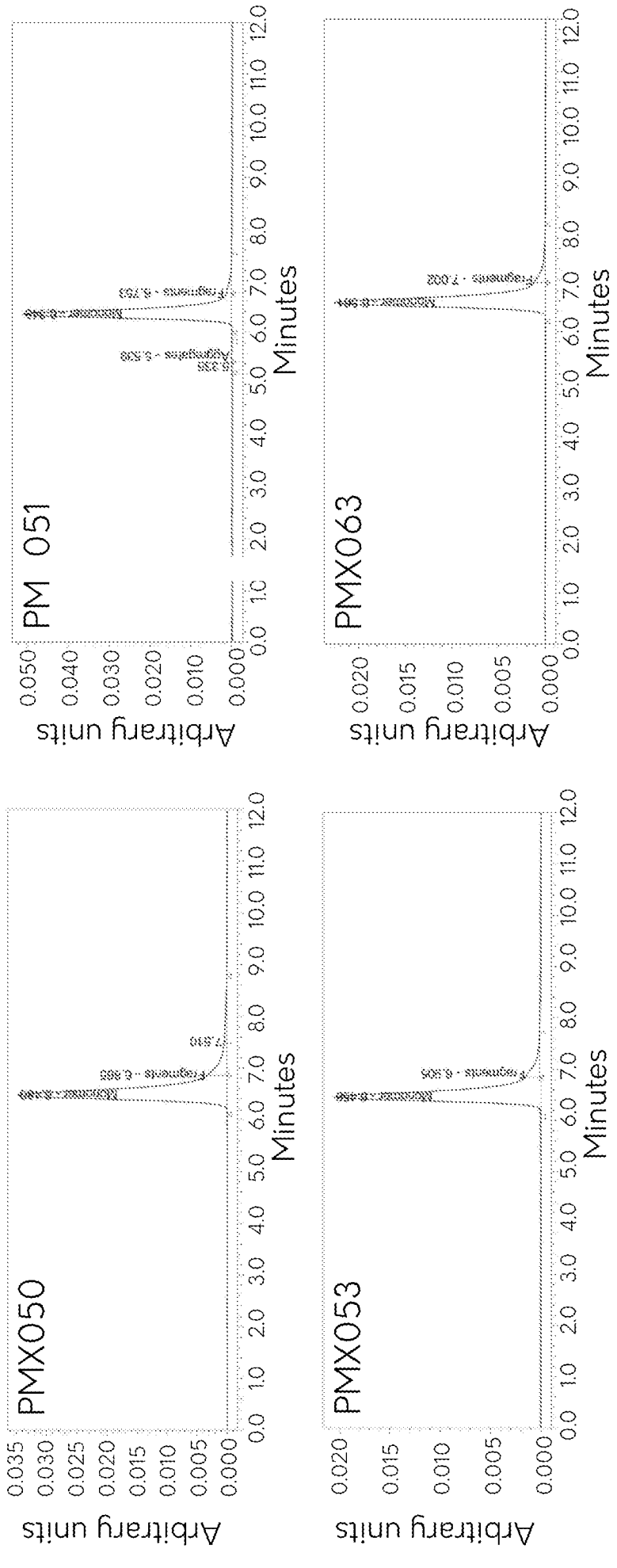


Figure 10

A

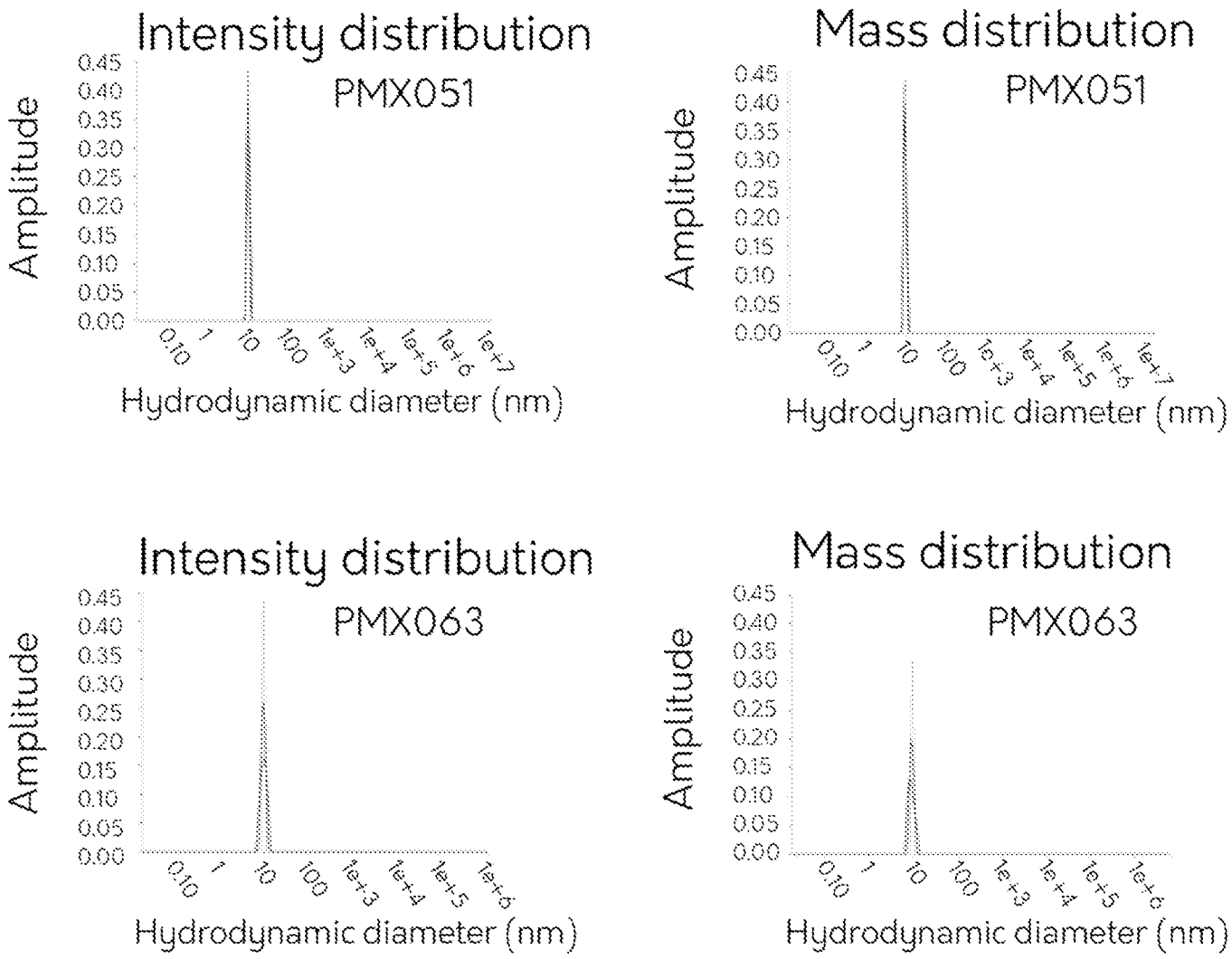

Intensity distribution
PMX051
Amplitude
0.45
0.40
0.35
0.30
0.25
0.20
0.15
0.10
0.05
0.00
0.10
1
10
100
1e+3
1e+4
1e+5
1e+6
1e+7
Hydrodynamic diameter (nm)
Mass distribution
PMX051
Amplitude
Hydrodynamic diameter (nm)
Intensity distribution
PMX063
Amplitude
Hydrodynamic diameter (nm)
Mass distribution
PMX063
Amplitude
Hydrodynamic diameter (nm)

Figure 10

B

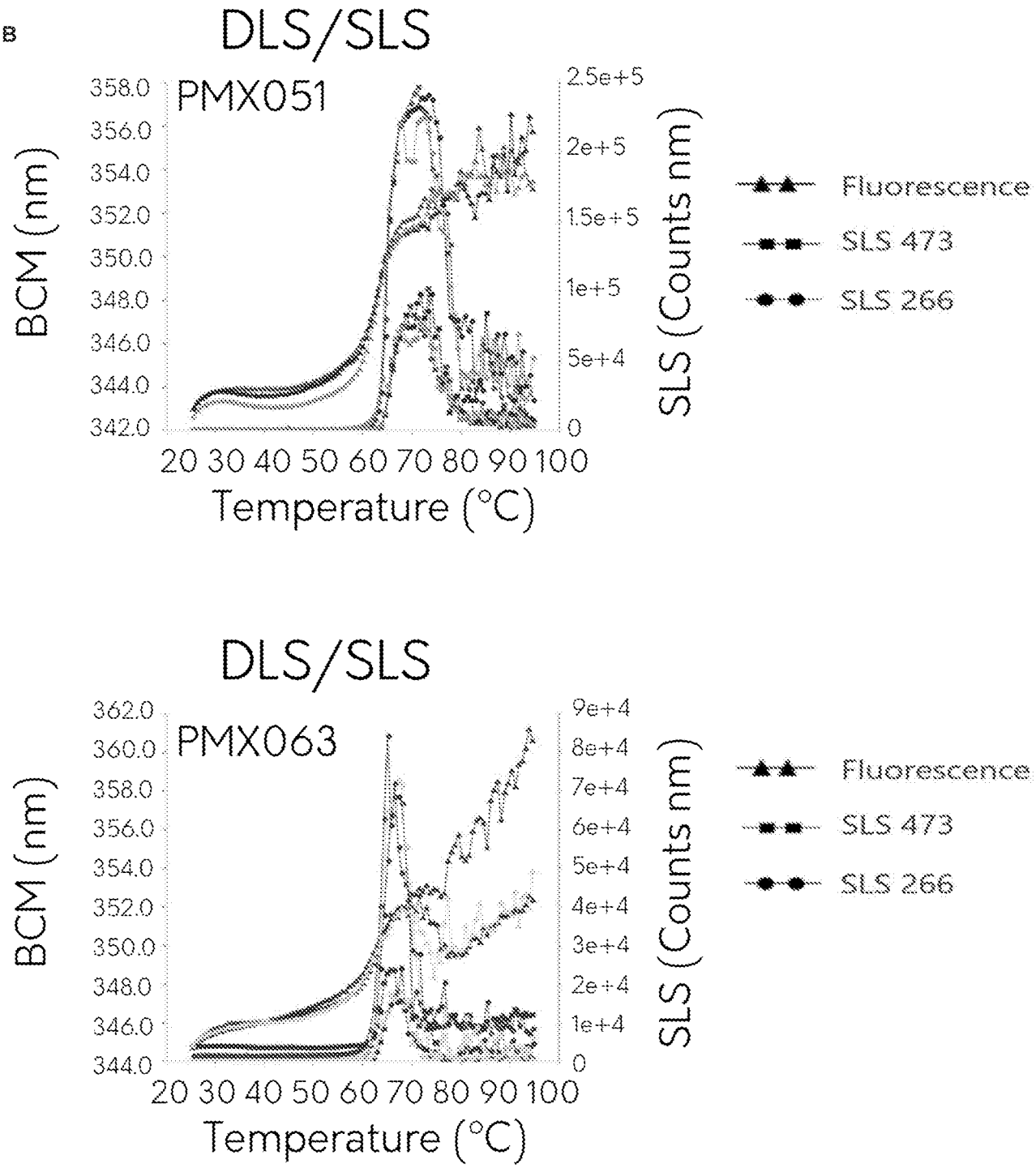

DLS/SLS
PMX051
BCM (nm)
358.0
356.0
354.0
352.0
350.0
348.0
346.0
344.0
342.0
2.5e+5
2e+5
1.5e+5
1e+5
5e+4
0
SLS (Counts nm)
20 30 40 50 60 70 80 90 100
Temperature (°C)
Fluorescence
SLS 473
SLS 266
DLS/SLS
PMX063
BCM (nm)
362.0
360.0
358.0
356.0
354.0
352.0
350.0
348.0
346.0
344.0
9e+4
8e+4
7e+4
6e+4
5e+4
4e+4
3e+4
2e+4
1e+4
0
SLS (Counts nm)
20 30 40 50 60 70 80 90 100
Temperature (°C)
Fluorescence
SLS 473
SLS 266

Figure 11

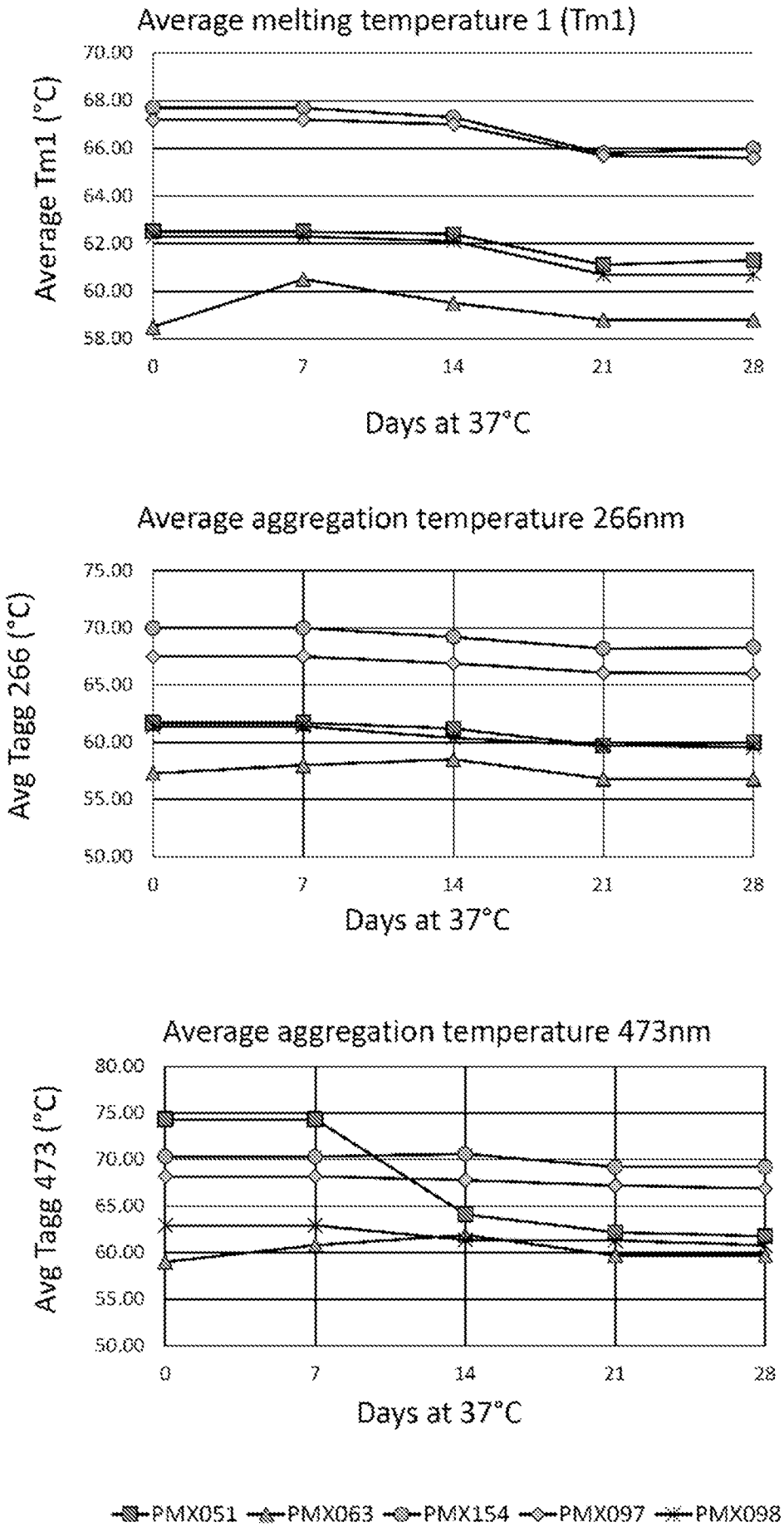

Average melting temperature 1 (Tm1)
Average Tm1 (°C)
70.00
68.00
66.00
64.00
62.00
60.00
58.00
0
7
14
21
28
Days at 37°C
Average aggregation temperature 266nm
Avg Tagg 266 (°C)
75.00
70.00
65.00
60.00
55.00
50.00
0
7
14
21
28
Days at 37°C
Average aggregation temperature 473nm
Avg Tagg 473 (°C)
80.00
75.00
70.00
65.00
60.00
55.00
50.00
0
7
14
21
28
Days at 37°C
PMX051
PMX063
PMX154
PMX097
PMX098

Figure 12

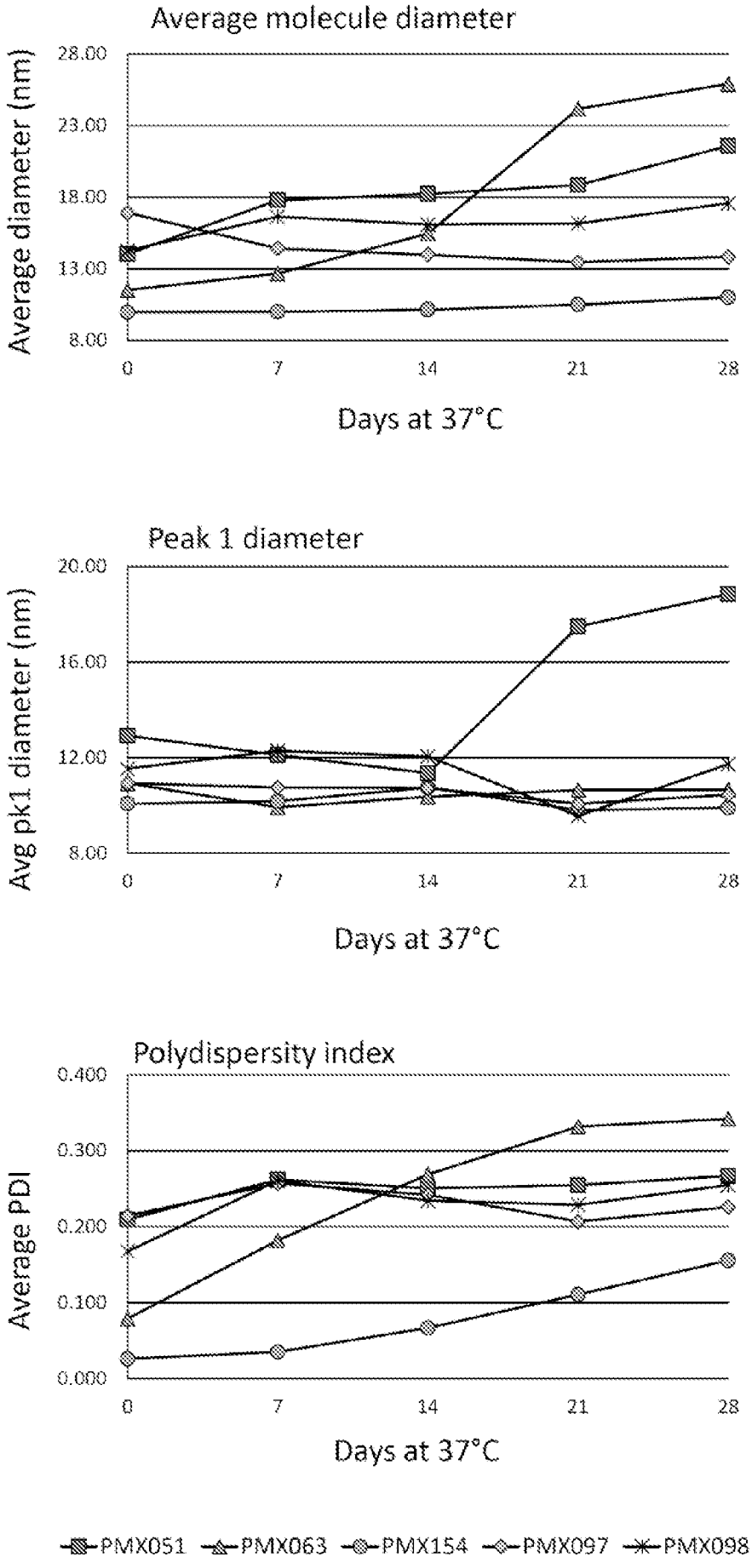

Average molecule diameter
Average diameter (nm)
28.00
23.00
18.00
13.00
8.00
0
7
14
21
28
Days at 37°C
Peak 1 diameter
Avg pk1 diameter (nm)
20.00
16.00
12.00
8.00
0
7
14
21
28
Days at 37°C
Polydispersity index
Average PDI
0.400
0.300
0.200
0.100
0.000
0
7
14
21
28
Days at 37°C
PMX051
PMX063
PMX154
PMX097
PMX098

Figure 13

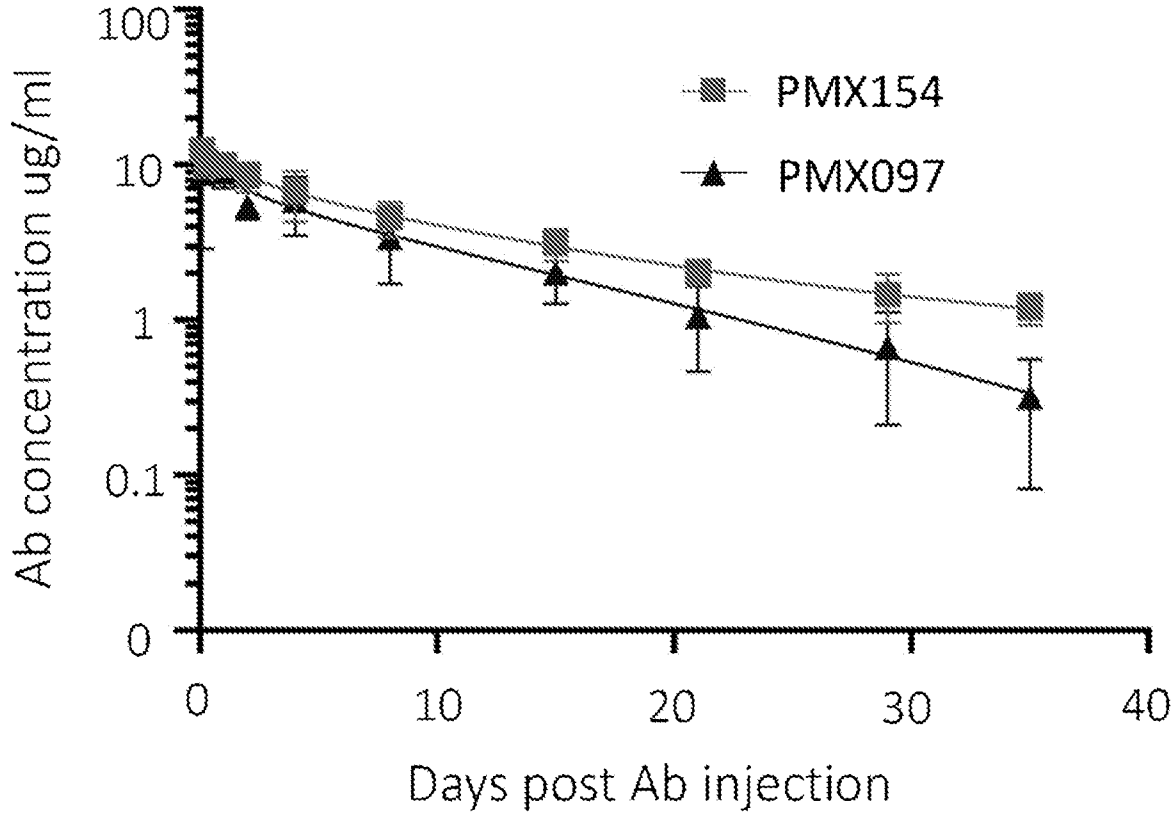

100
10
1
0.1
0
Ab concentration ug/ml
PMX154
PMX097
0
10
20
30
40
Days post Ab injection

Figure 14

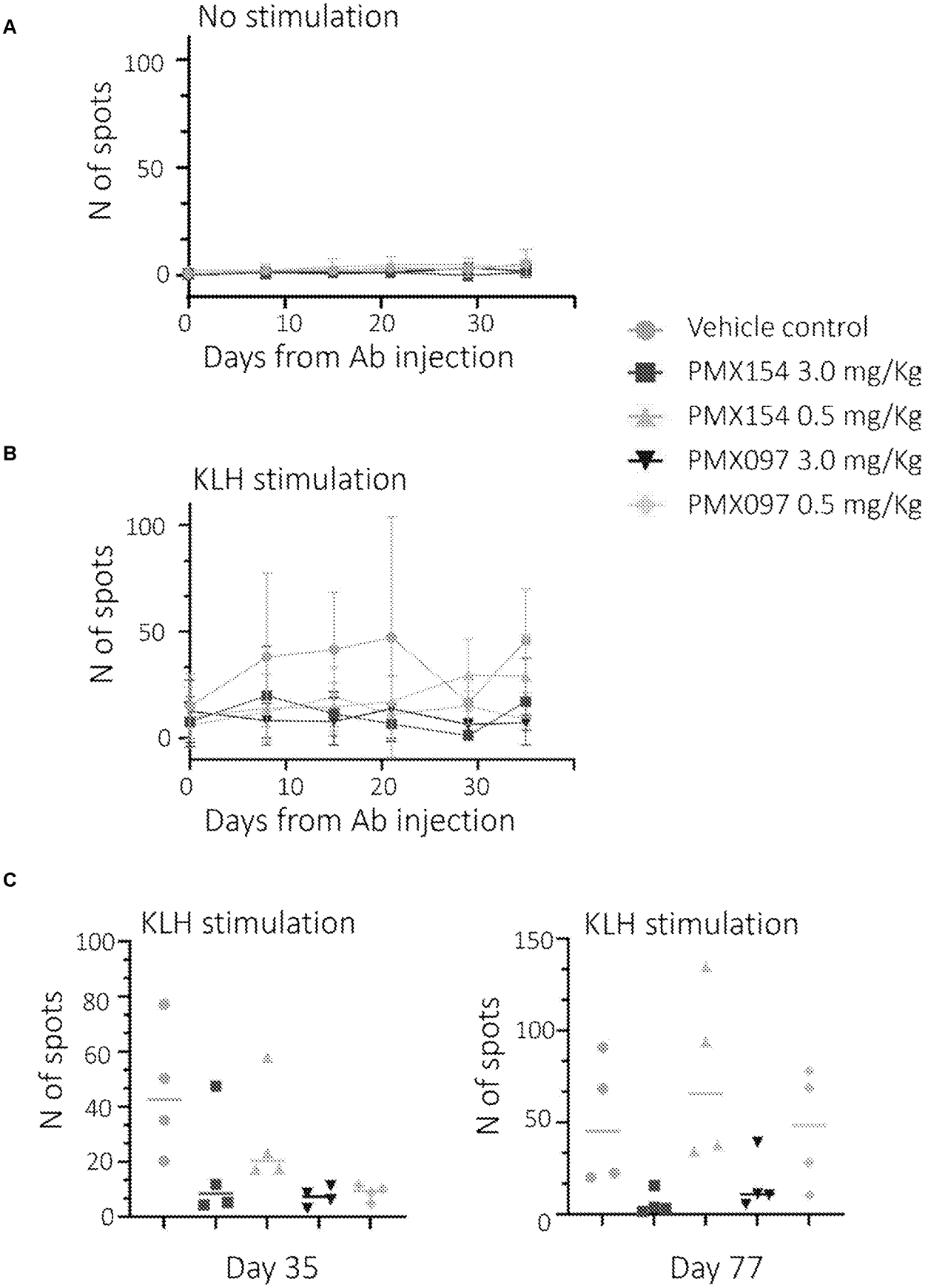
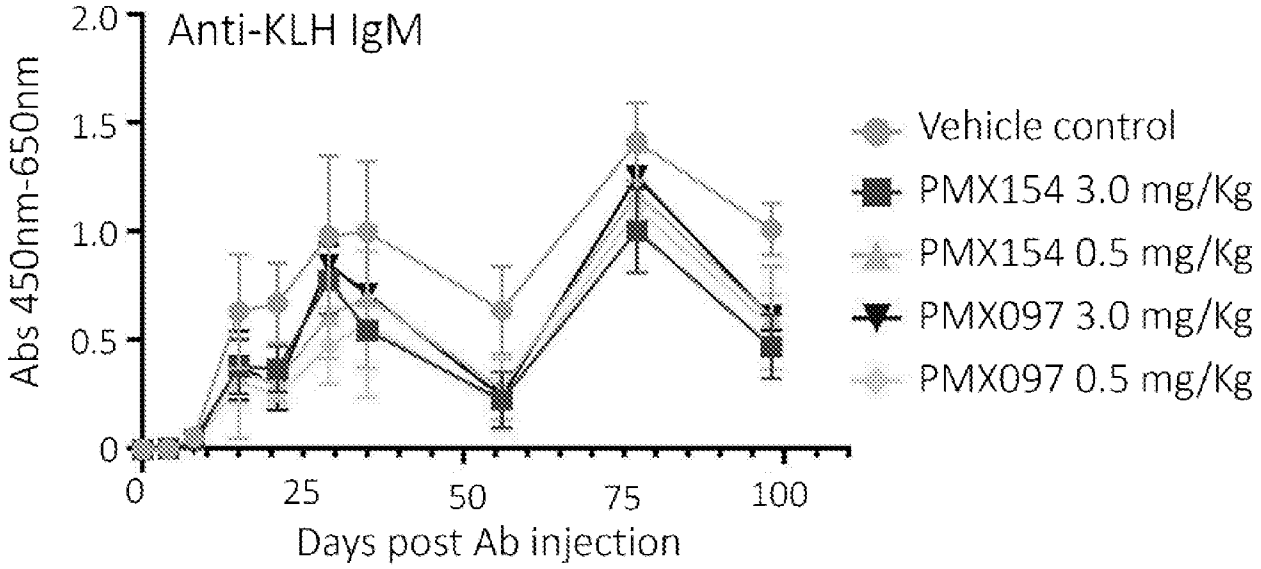
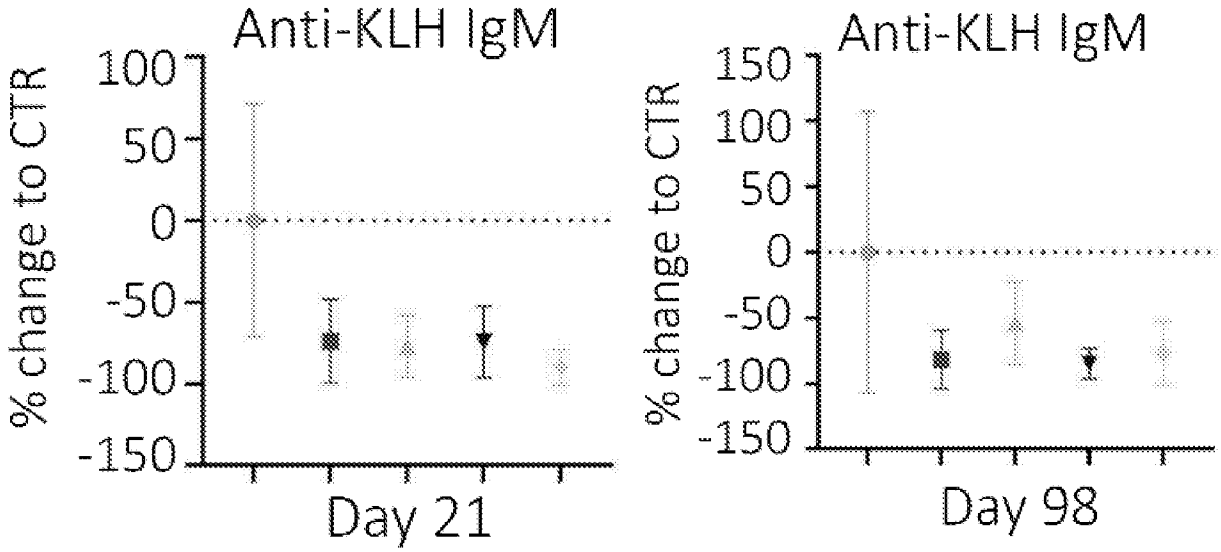

A
No stimulation
N of spots
100
50
0
0
10
20
30
Days from Ab injection
Vehicle control
PMX154 3.0 mg/Kg
PMX154 0.5 mg/Kg
PMX097 3.0 mg/Kg
PMX097 0.5 mg/Kg
B
KLH stimulation
N of spots
100
50
0
0
10
20
30
Days from Ab injection
C
KLH stimulation
N of spots
100
80
60
40
20
0
Day 35
KLH stimulation
N of spots
150
100
50
0
Day 77

Figure 15

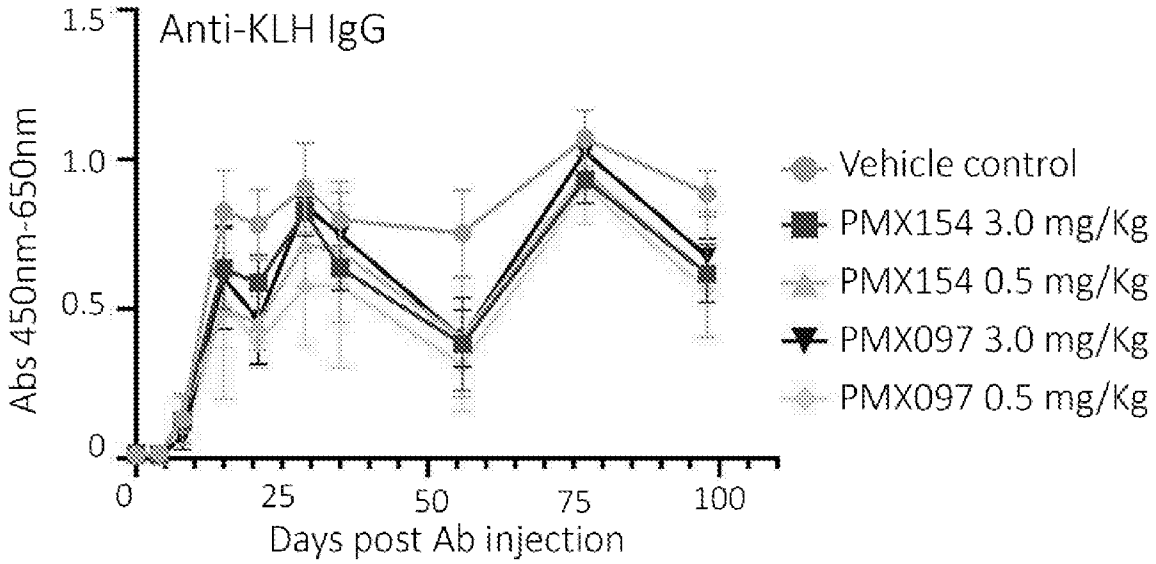
A


Anti-KLH IgM
Abs 450nm-650nm
2.0
1.5
1.0
0.5
0
0
25
50
75
100
Days post Ab injection
Vehicle control
PMX154 3.0 mg/Kg
PMX154 0.5 mg/Kg
PMX097 3.0 mg/Kg
PMX097 0.5 mg/Kg

B


Anti-KLH IgM
% change to CTR
100
50
0
-50
-100
-150
Day 21
Anti-KLH IgM
% change to CTR
150
100
50
0
-50
-100
-150
Day 98

C


Anti-KLH IgG
Abs 450nm-650nm
1.5
1.0
0.5
0
0
25
50
75
100
Days post Ab injection
Vehicle control
PMX154 3.0 mg/Kg
PMX154 0.5 mg/Kg
PMX097 3.0 mg/Kg
PMX097 0.5 mg/Kg

D

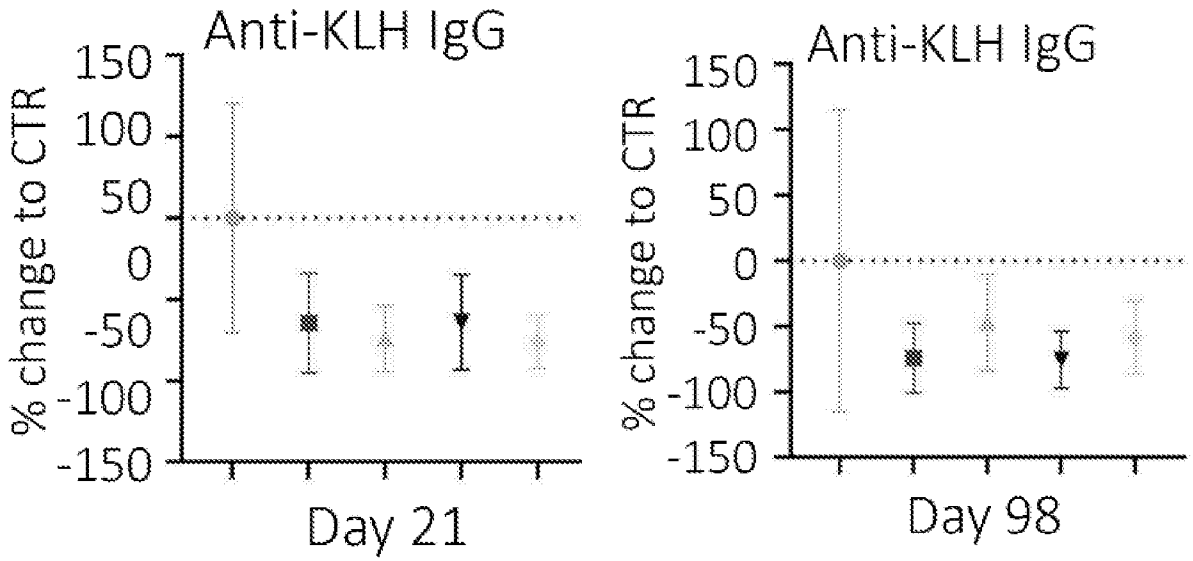
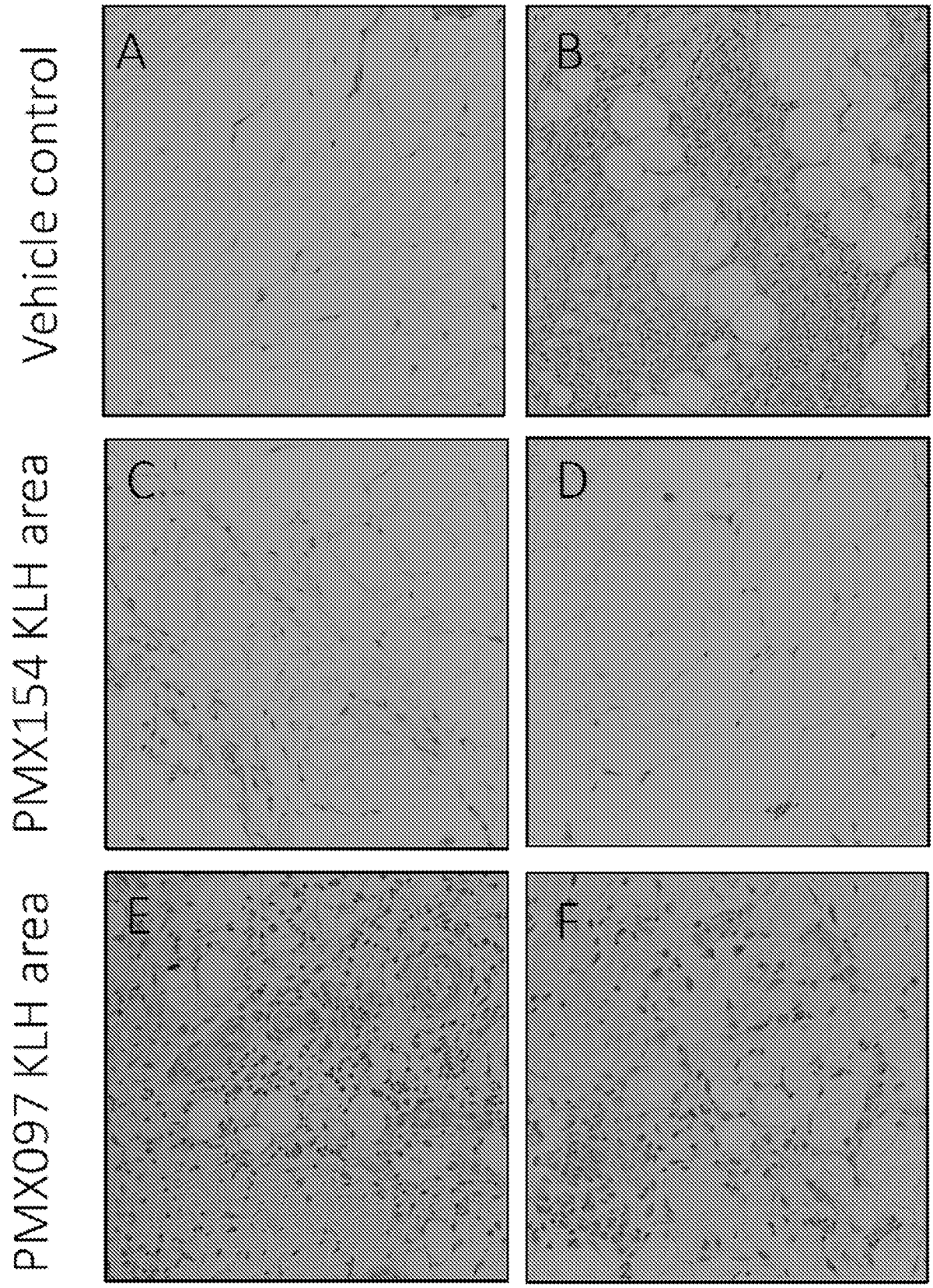

Anti-KLH IgG
% change to CTR
150
100
50
0
-50
-100
-150
Day 21
Anti-KLH IgG
% change to CTR
150
100
50
0
-50
-100
-150
Day 98

Figure 16



INTERNATIONAL SEARCH REPORT

International application No
PCT/GB2023/050281

A. CLASSIFICATION OF SUBJECT MATTER
INV. C07K16/28 A61P37/06 A61P29/00
ADD.

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

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
C07K A61K A61P

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

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
EPO-Internal, WPI Data

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 2007/133290 A2 (GENENTECH INC [US]; MARTIN FLAVIUS [US]) 22 November 2007 (2007-11-22) page 2, line 7 - page 5, line 32 page 6, line 27 - page 11, line 27 page 12, line 5 - line 21 page 13, line 12 - line 38 page 23, line 26 - line 37 page 27, line 6 - line 10 page 43, line 20 - page 45, line 2 page 52, line 33 - page 54, line 19 page 61, line 3 - page 62, line 2 examples 1-8 ----- -/--	1-25

[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 application or patent but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

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

"Y" document of particular relevance;; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
19 April 2023	23/06/2023

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	Stein, Annette

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Form PCT/ISA/210 (second sheet) (April 2005)

INTERNATIONAL SEARCH REPORT

International application No
PCT/GB2023/050281

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 2005/094879 A2 (AMGEN INC [US]; ABGENIX INC [US] ET AL.) 13 October 2005 (2005-10-13) the whole document; in particular examples 1-7; paragraphs 174, 175, 179-184, 187-196	1-25
A	US 2013/209511 A1 (MEBATSION TESHOME [US] ET AL) 15 August 2013 (2013-08-15) paragraphs [0018], [0060], [0078]; figure 16; examples 2, 6; sequence 12	1-25
A	WO 2020/074874 A1 (GENOME RES LTD [GB]) 16 April 2020 (2020-04-16) cited in the application the whole document, in particular examples 1-3	1-25
A	WO 2018/189520 A1 (GENOME RES LTD [GB]) 18 October 2018 (2018-10-18) cited in the application the whole document	1-25
X,P	WO 2022/029447 A1 (PETMEDIX LTD [GB]) 10 February 2022 (2022-02-10) the whole document, in particular examples 1-8	1-25

1

INTERNATIONAL SEARCH REPORT

International application No.
PCT/GB2023/050281

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

1. With regard to any nucleotide and/or amino acid sequence disclosed in the international application, the international search was carried out on the basis of a sequence listing:

   a. [X] forming part of the international application as filed.

   b. [ ] furnished subsequent to the international filing date for the purposes of international search (Rule 13*ter*.1(a)).

      [ ] accompanied by a statement to the effect that the sequence listing does not go beyond the disclosure in the international application as filed.

2. [ ] With regard to any nucleotide and/or amino acid sequence disclosed in the international application, this report has been established to the extent that a meaningful search could be carried out without a WIPO Standard ST.26 compliant sequence listing.

3. Additional comments:

INTERNATIONAL SEARCH REPORT

International application No.
PCT/GB2023/050281

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☒ Claims Nos.: 1-25 (partially)
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
see FURTHER INFORMATION sheet PCT/ISA/210

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fees, this Authority did not invite payment of additional fees.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims;; it is covered by claims Nos.:
1-25 (partially)

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.

☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.

☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. claims: 1-25(partially)

An antibody or fragment thereof that specifically binds to companion animal OX40L, wherein the antibody is selected from one of the following antibodies designated PMX097, PMX063, PMX086, PMX087, PMX094, PMX095, PMX096, PMX098, PMX099, PMX100, PMX101, PMX102, PMX103, PMX104, PMX105, PMX107, PMX108, PMX109, PMX110 or PMX111, which are characterized by at least all of their six CDR sequences as disclosed in table 2; and related subject-matter.

---

2. claims: 1-25(partially)

An antibody or fragment thereof that specifically binds to companion animal OX40L, wherein the antibody is selected from one of the following antibodies designated PMX154, PMX054, PMX084, PMX293 or PMX294, which are characterized by at least all of their six CDR sequences as disclosed in table 2; and related subject-matter.

---

3. claims: 1-25(partially)

An antibody or fragment thereof that specifically binds to companion animal OX40L, wherein the antibody is selected from one of the following antibodies designated PMX051 or PMX088, which are characterized by at least all of their six CDR sequences as disclosed in table 2; and related subject-matter.

---

4. claims: 1-25(partially)

An antibody or fragment thereof that specifically binds to companion animal OX40L, wherein the antibody is selected from one of the following antibodies designated PMX025, PMX026, PMX027, PMX089, PMX090, PMX091, PMX092 or PMX093, which are characterized by at least all of their six CDR sequences as disclosed in table 2; and related subject-matter.

---

5. claims: 1-25(partially)

An antibody or fragment thereof that specifically binds to companion animal OX40L, wherein the antibody is selected from one of the following antibodies designated PMX028, PMX029, PMX032, PMX033, PMX034, PMX035, PMX036, PMX038, PMX042, PMX045, PMX064, PMX082 or PMX083, which are characterized by at least all of their six CDR sequences as disclosed in table 2; and related subject-matter.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

---

6. claims: 1-25(partially)

An antibody or fragment thereof that specifically binds to companion animal OX40L, wherein the antibody is selected from one of the following antibodies designated PMX030 or PMX031, which are characterized by at least all of their six CDR sequences as disclosed in table 2; and related subject-matter.

---

7. claims: 1-25(partially)

An antibody or fragment thereof that specifically binds to companion animal OX40L, wherein the antibody is selected from one of the following antibodies designated PMX035, PMX037, PMX040, PMX048, PMX049 or PMX065, which are characterized by at least all of their six CDR sequences as disclosed in table 2; and related subject-matter.

---

8. claims: 1-25(partially)

An antibody or fragment thereof that specifically binds to companion animal OX40L, wherein the antibody is selected from one of the following antibodies designated PMX039, PMX041, PMX043, PMX044, PMX046, PMX050, PMX055, PMX056, PMX057, PMX058, PMX059, PMX062 or PMX085, which are characterized by at least all of their six CDR sequences as disclosed in table 2; and related subject-matter.

---

9. claims: 1-25(partially)

An antibody or fragment thereof that specifically binds to companion animal OX40L, wherein the antibody is selected from one of the following antibodies designated PMX047 or PMX053, which are characterized by at least all of their six CDR sequences as disclosed in table 2; and related subject-matter.

---

10. claims: 1-25(partially)

An antibody or fragment thereof that specifically binds to companion animal OX40L, wherein the antibody is the antibody designated PMX052, which is characterized by at least all of its six CDR sequences as disclosed in table 2; and related subject-matter.

---

11. claims: 1-25(partially)

An antibody or fragment thereof that specifically binds to

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

companion animal OX40L, wherein the antibody is selected from one of the following antibodies designated PMX060 or PMX061, which are characterized by at least all of their six CDR sequences as disclosed in table 2; and related subject-matter.

---

12. claims: 1-25(partially)

An antibody or fragment thereof that specifically binds to companion animal OX40L, wherein the antibody is the following antibody designated PMX106, which is characterized by at least all of its six CDR sequences as disclosed in table 2; and related subject-matter.

---

13. claims: 1-25(partially)

An antibody or fragment thereof that specifically binds to companion animal OX40L, wherein the antibody is selected from one of the following antibodies designated PMX054, PMX084, PMX293 or PMX294, which are characterized by at least all of their six CDR sequences as disclosed in table 2; and related subject-matter.

---

14. claims: 1-25(partially)

An antibody or fragment thereof that specifically binds to companion animal OX40L, wherein the antibody is selected from one of the following antibodies designated PMX155 or PMX156, which are characterized by at least all of their six CDR sequences as disclosed in table 2; and related subject-matter.

---

15. claims: 1-25(partially)

An antibody or fragment thereof that specifically binds to companion animal OX40L, wherein the antibody is selected from one of the following antibodies designated PMX291 or PMX292, which are characterized by at least all of their six CDR sequences as disclosed in table 2; and related subject-matter.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box II.2

Claims Nos.: 1-25(partially)

Present claims 1-8 (as well as claims 9-25 dependent thereon) relate to an extremely large number of possible antibodies. Support and disclosure in the sense of Article 6 and 5 PCT is to be found however for only a very small proportion of the antibodies claimed, see the antibodies defined by at least all of their six specific CDR sequences in the right order and according to a clear definition disclosed and supported by the present application in table 2 on pages 90-188. In this regard it is noted that the characterization of an antibody by at least all of its six CDR sequences is essential to its definition for the reason that antibodies functional properties depend (at least) on these sequences. The non-compliance with the substantive provisions is to such an extent, that the search was performed taking into consideration the non-compliance in determining the extent of the search of these claims (PCT Guidelines 9.19 and 9.23).The search of claims 1-8 (as well as claims 9-25 dependent thereon) was restricted to those claimed antibodies which appear to be supported (see sequences of CDRs, VH/VL in table 2 on pages 90-188) taking also into consideration the lack of unity of invention.

The applicant's attention is drawn to the fact that claims relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure. If the application proceeds into the regional phase before the EPO, the applicant is reminded that a search may be carried out during examination before the EPO (see EPO Guidelines C-IV, 7.2), should the problems which led to the Article 17(2) PCT declaration be overcome.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No
PCT/GB2023/050281

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 2007133290 A2	22-11-2007	AR 057253 A1	21-11-2007
		AU 2006343459 A1	22-11-2007
		BR PI0621065 A2	29-11-2011
		CA 2633602 A1	22-11-2007
		CN 101374865 A	25-02-2009
		CR 10069 A	10-10-2008
		EC SP088543 A	30-07-2008
		EP 1973949 A2	01-10-2008
		JP 2009519718 A	21-05-2009
		KR 20080080639 A	04-09-2008
		MA 30153 B1	02-01-2009
		TW 200732349 A	01-09-2007
		US 2009053230 A1	26-02-2009
		US 2010272738 A1	28-10-2010
		WO 2007133290 A2	22-11-2007
		ZA 200804868 B	28-10-2009
WO 2005094879 A2	13-10-2005	AU 2005229009 A1	13-10-2005
		CA 2560889 A1	13-10-2005
		EP 1740208 A2	10-01-2007
		JP 2007530045 A	01-11-2007
		US 2006002929 A1	05-01-2006
		WO 2005094879 A2	13-10-2005
US 2013209511 A1	15-08-2013	AU 2013221502 A1	28-08-2014
		BR 112014020019 A2	04-07-2017
		CA 2864119 A1	22-08-2013
		CN 104203271 A	10-12-2014
		EA 201400912 A1	30-01-2015
		EP 2814506 A1	24-12-2014
		EP 3466443 A1	10-04-2019
		ES 2723273 T3	23-08-2019
		ES 2866108 T3	19-10-2021
		HK 1200327 A1	07-08-2015
		JP 6260972 B2	17-01-2018
		JP 2015511948 A	23-04-2015
		MX 360415 B	31-10-2018
		NZ 628270 A	30-09-2016
		NZ 722700 A	22-12-2017
		US 2013209511 A1	15-08-2013
		US 2017137843 A1	18-05-2017
		WO 2013123242 A1	22-08-2013
WO 2020074874 A1	16-04-2020	CA 3114502 A1	16-04-2020
		CN 113544147 A	22-10-2021
		EP 3864038 A1	18-08-2021
		GB 2578867 A	03-06-2020
		JP 2022512638 A	07-02-2022
		US 2021388117 A1	16-12-2021
		WO 2020074874 A1	16-04-2020
WO 2018189520 A1	18-10-2018	BR 112019021252 A2	12-05-2020
		CA 3059513 A1	18-10-2018
		CN 111031789 A	17-04-2020
		EP 3609319 A1	19-02-2020
		GB 2561352 A	17-10-2018
		JP 2020512840 A	30-04-2020
		US 2020056202 A1	20-02-2020

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No
PCT/GB2023/050281

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
		WO 2018189520 A1	18-10-2018
WO 2022029447 A1	10-02-2022	AU 2021319941 A1	16-02-2023
		CA 3186391 A1	10-02-2022
		CN 116249710 A	09-06-2023
		EP 4192867 A1	14-06-2023
		WO 2022029447 A1	10-02-2022