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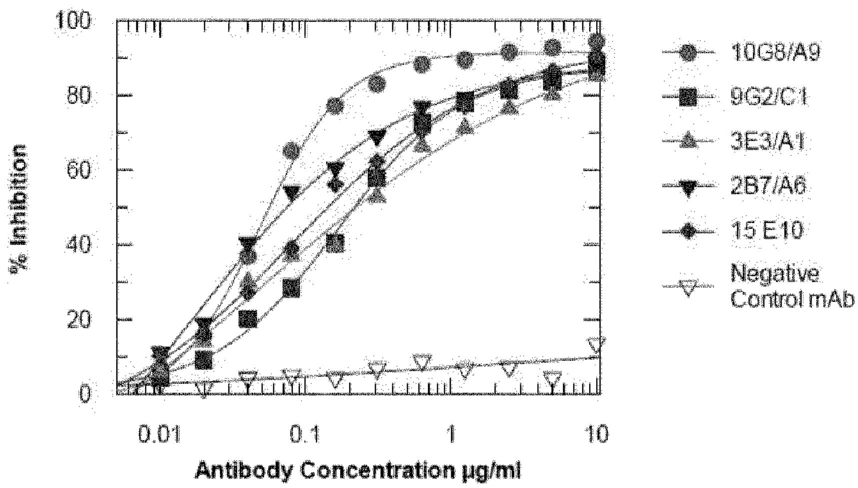
[Continued on next page]

(54) Title: ANTIGEN BINDING PROTEINS

Figure 1: Human gp130 ELISA



(57) Abstract: The present invention concerns antigen binding proteins and fragments thereof which specifically bind Oncostatin M (OSM), particularly human OSM (hOSM) and which inhibit the binding of OSM to the gp130 receptor but does not directly interact with site II residues. The invention also concerns a method of humanising antibodies. Further disclosed are pharmaceutical compositions, screening and medical treatment methods.

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Antigen Binding Proteins

Field of the invention

The present invention relates to immunoglobulins that specifically bind Oncostatin M (OSM) and in particular human OSM (hOSM).
The present invention also concerns methods of treating diseases or disorders with said immunoglobulins, pharmaceutical compositions comprising said immunoglobulins and methods of manufacture. Other embodiments of the present invention will be apparent from the description below.

Background of the invention

Oncostatin M is a 28 KDa glycoprotein that belongs to the interleukin 6 (IL-6) family of cytokines which includes IL-6, Leukaemia Inhibitory Factor (LIF), ciliary neurotrophic factor (CNTF), cardiotropin-1 (CT-1) and cardiotrophin-1 like cytokine (See Kishimoto T et al (1995) Blood 86: 1243-1254), which share the gp130 transmembrane signalling receptor (See Taga T and Kishimoto T (1997) Annu. Rev. Immunol. 15: 797-819). OSM was originally discovered by its ability to inhibit the growth of the melanoma cell line A375 (See Malik N (1989) et al Mol Cell Biol 9: 2847-2853). Subsequently, more effects were discovered and it was found to be a multifunctional mediator like other members of the IL-6 family. OSM is produced in a variety of cell types including macrophages, activated T cells (See Zarling JM (1986) PNAS (USA) 83: 9739-9743), polymorphonuclear neutrophils (See Grenier A et al (1999) Blood 93:1413-1421), eosinophils (See Tamura S et al (2002) Dev. Dyn. 225: 327-31), dendritic cells (See Suda T et al (2002) Cytokine 17:335-340). It is also expressed in pancreas, kidney, testes, spleen stomach and brain (See Znoyko I et al (2005) Anat Rec A Discov Mol Cell Evol Biol 283: 182-186), and bone marrow (See Psenak O et al (2003) Acta Haematol 109: 68-75) Its principle biological effects include activation of endothelium (See Brown TJ et al (1993) Blood 82: 33-7), activation of the acute phase response (See Benigni F et al (1996) Blood 87: 1851-1854), induction of cellular proliferation or differentiation, modulation of inflammatory mediator release and haematopoesis (See Tanaka M et al (2003) 102: 3154-3162), re-modelling of bone (See de Hooge ASK (2002) Am J Pathol 160: 1733-1743) and, promotion of angiogenesis (See Vasse M et al (1999) Arterioscler Thromb Vasc Biol 19:1835-1842) and wound healing.

Receptors for OSM (OSM receptor β, "OSMRβ") are expressed on a wide range of cells including epithelial cells, chondrocytes, fibroblasts (See Langdon C et al (2003) J Immunol 170: 548-555), neuronal smooth muscle, lymph node, bone, heart,small intestine, lung and kidney (See Tamura S et al (2002) Mech Dev 115: 127-131) and endothelial cells. Several lines of evidence suggest that endothelial cells are a primary target for OSM. These cells express 10 to 20 fold higher numbers of both high and low affinity receptors and exhibit profound and prolonged alterations in phenotype following stimulation with OSM (See Modur V et al (1997) J Clin Invest 100: 158-168). In addition, OSM is a major autocrine growth factor for Kaposi's sarcoma cells, which are thought to be of endothelial origin (See Murakami-Mori K et al (1995) J Clin Invest 96:1319-1327).

In common with other IL-6 family cytokines, OSM binds to the transmembrane signal transducing glycoprotein gp130. A key feature of the gp130 cytokines is the formation of oligomeric receptor complexes that comprise gp130 and one or more co-receptors depending on the ligand (Reviewed in Heinrich PC et al (2003) Biochem J. 374: 1-20). As a result, these cytokines can mediate both the shared and unique biological activities *in vitro* and *in vivo* depending on the composition of the receptor complex formed. Human OSM (hOSM) differs from the other IL-6 cytokines in that it can form complexes with gp130 and either one of the two co-receptors, LIFR or the oncostatin receptor (OSMR). Figure 27 illustrates the interaction between hOSM and gp130, LIFR and OSMR. The crystal structure of hOSM has been solved and shown to comprise a four α helical bundle with two potential glycosylation sites. Two separate ligand binding sites have been identified by site-directed mutagenesis on the hOSM molecule (See Deller MC et al (2000) Structural Fold Des. 8:863-874). The first, called Site II (sometimes “site 2”) interacts with gp130 and the second site, called Site III (sometimes “site 3”), at the opposite end of the molecule interacts with either LIFR or OSMR. Mutagenesis experiments have shown that the binding sites for LIFR and OSMR are almost identical but that a single amino acid mutation can discriminate between the two.

There is increasing evidence to support the hypothesis that modulating OSM-gp130 interaction may be of benefit in the treatment of RA and other diseases and disorders, particularly chronic inflammatory diseases and disorders such as osteoarthritis, idiopathic pulmonary fibrosis, pain, inflammatory lung disease, cardiovascular disease and psoriasis.

OSM is found in the SF of human RA patients (See Hui W et al (1997) 56: 184-7). These levels correlate with; the number of neutrophils in SF, levels of TNF alpha (sometimes “TNF”) in SF, and markers of cartilage destruction (Manicourt DH et al (2000) Arthritis Rheum 43: 281-288). Furthermore, the synovial tissue from RA patients secretes OSM spontaneously ex vivo (See Okamoto H et al (1997) Arthritis and Rheumatism 40: 1096-1105). It has also been demonstrated that OSM is present in synovial macrophages (Cawston TE et al (1998) Arthritis Rheum 41: 1760-1771) and as discussed earlier, OSM receptors and gp130 are expressed on endothelial cells, synovial fibroblasts, chonodrocytes and osteoblasts. Adenoviral expression of murine OSM (mOSM) in the joints of normal mice results in a severe inflammatory and erosive arthritis (See Langdon C et al (2000) Am J Pathol 157: 1187-1196). Similarly aggressive disease is seen in knockout mice lacking TNF, IL-1, IL-6 and iNOS following adenoviral mOSM delivery (See de Hooge ASK et al (2003) Arthritis and Rheumatism 48:1750-1761), demonstrating that OSM can mediate all embodiments of arthritis pathology. Mouse OSM expression using an adenovirally expressed mOSM vector causes damage to the growth plate typical of Juvenile Idiopathic Arthritis (See de Hooge ASK et al (2003) Arthritis and Rheumatism 48:1750-1761). In an experimental model of collagen induced arthritis, an anti-OSM antibody administered therapeutically to mice prevented all further progression of disease.

Similar results were seen when anti-OSM was administered prophylatically to mice with pristane induced arthritis, a relapsing/remitting model reminiscient of the human disease (See Plater-Zyberk C et al (2001) Arthritis and Rheumatism 44:

Osteoarthritis is a condition that affects the joints. There are three characteristics of osteoarthritis. It causes damage to cartilage - the strong, smooth surface that lines the bones and allows joints to move easily and without friction. It results in bony growths developing around the edge of the joints, and it causes mild inflammation of the tissues around the joints (synovitis). OSM has been demonstrated to play an important role in cartilage breakdown, inflammation and bone turnover and therefore blockade of this cytokine could play a role in the key aspects of disease pathogenesis. OSM acts synergistically with either IL-1 or TNF to induce collagenolysis in human nasal cartilage, involving loss of proteoglycans (PG) and collagen, the latter correlating with induction of MMP-1 and MMP-13. OSM with IL-1 will also induce PG loss from human articular cartilage, but the increase in collagen loss was not significant. (Morgan et al 2006) A number of studies using adenoviral vectors to increase joint cytokine concentrations have shown that OSM over-expression will induce inflammation, pannus formation, cartilage destruction and bone erosion. (Langdon et al 2000). Overall the literature suggests that OSM, particularly when combined with other cytokines, induces proteases that are involved in proteoglycan and collagen breakdown resulting in cartilage degradation and bone erosion.

Information from the literature suggests that OSM molecule may have some involvement in the inflammatory process associated with psoriasis. Work by Boifati et al (1998) has shown that spontaneous release of OSM is increased in organ cultures of psoriatic lesions, compared with non-lesional psoriatic skin and normal skin. (Kunsfeild et al 2004) Keratinocytes express the receptor for this molecule and in response to the ligand this causes keratinocyte migration and increases the thickness of reconstituted epidermis. Microarray analysis comparing the gene modulating effects of OSM with 33 different cytokines indicate that it is a potent keratinocyte activator and can act in synergy with pro-inflammatory cytokines in the induction of molecules such as S100A7 and β-defensin 2 expression, characteristic of psoriatic skin. (Gazel et al 2006)

A role for OSM in inflammatory lung disease such as asthma and pulmonary fibrosis is also suggested from the literature. These diseases are characterized by an increased deposition of extracellular matrix (ECM), concomitant with proliferation and activation of sub-epithelial fibroblasts. OSM has been detected in the bronchoaveolar lavage fluid of patients during acute lung injury, particularly in cases of pneumonia (Grenier et al 2001).

OSM has been detected in the brains of MS patients, where it localises to microglia, astrocytes and infiltrating leukocytes (Ruprecht et al 2001). In addition, PBMCs isolated from MS patients spontaneously release more cytokines, including OSM, than cells from healthy controls and MS patients show a trend towards increased sera [OSM] (Ensoli et al 2002).

In addition to promoting inflammation in the brain, OSM may directly contribute to neurodegeneration, a feature of Alzhiemer's disease, MS and of a subset of HIV patients. Monocyte supernatants from HIV patients' cause profound neuroblast growth inhibition and neuronal cell death. These effects were mediated by Oncostatin M in the culture supernatant (Ensoli et al 1999). Since many HIV patients suffer from brain atrophy caused by neuronal cell loss, OSM may be one mediator of this pathology.

Work by Tamura et al suggests that OSM may be involved in the development and maintenance of neuropathic pain (2003). Their studies revealed a subset of nociceptive sensory neurons that express the OSMβ receptor. All the OSMβR +ve neurons also expressed VR1 and P2X3 receptors, which have been shown to be crucial for development of both neuropathic and inflammatory pain (Jarvis et al 2002, Walker et al 2003). It has also been shown that the OSM -/- mouse showed reduced noxious responses to chemical, thermal, visceral and mechanical pain (Morikawa et al 2004). Interestingly, these animals have a deficit in VR1+, P2X3+ small sized neurons, but otherwise the animals appear normal.

A role supporting OSM in modulating the biology of cancer cells has also been suggested from the literature. OSM has been reported as having both growth stimulating and growth inhibitory properties in studies using tumour cell lines (Grant and Begly 1999). It is a potent mitogen for Kaposi's sarcoma derived cells (Miles et al 1992) and for myeloma cell lines (Zhang et al 1994). OSM decreases growth rates and increases differentiation in a number of tumour cell lines, including breast (Douglas et al 1998), and lung (McKormick et al 2000). However, whilst OSM may inhibit growth, at least in some breast carcinoma cell lines, it increases cell detachment and enhances the metatastic potential (Holzer et al 2004, Jorcyk et al 2006). OSM also upregulates expression and activation state of the hyaluronan receptor CD44, in some tumour cell lines (Cichy et al 2000), which is associated with tumour growth and metastasis (Yu et al 1997). In addition, the angiogenic properties of OSM and its ability to induce other angiogenic factors in some tumour cells (Repovic et al 2003), suggest that it could contribute to tumour angiogenesis in those tumours expressing OSM. The scientific literature suggests the OSM involvement in tumour biology but indicate the complexity. It is possible that OSM neutralisation could beneficial for treatment of some tumours. On the other hand, like TNF and IL-6 neutralisation, it carries some potential risk in others.

Evidence from literature suggests a potential role for OSM in cardiovascular disease. OSM is found in tissue macrophages in atherosclerotic lesions (Modur et al 1997) and as an angiogenic factor (Vasse et al 1999) may promote the neo-vascularisation characteristic of atherosclerotic plaques thought to contribute to vessel wall fragility. However, OSM also induces expression other angiogenic factors in endothelial cells; VEGF (Wijelah et al 1997) and bFGF (Bernard et al 1999). Interestingly, human endothelial cells have about 10-20 fold greater OSM receptor density than other cells (Brown et al 1991).

It is therefore an object of the present invention to provide a therapeutic approach to the treatment of RA and other diseases and disorders, particularly chronic inflammatory diseases and disorders such as osteoarthritis, idiopathic pulmonary fibrosis, cancer, asthma, pain, cardiovascular and psoriasis. In particular it is an object of the present invention to provide immunoglobulins, especially antibodies that specifically bind OSM (e.g. hOSM, particularly Site II thereof) and modulate (i.e. inhibit or block) the interaction between OSM and gp130 in the treatment of diseases and disorders responsive to modulation of that interaction.

In WO99/48523, we disclose the use of OSM antagonists in the treatment of inflammatory diseases and disorders. This disclosure used an anti-mouse OSM antibody in a murine model of arthritis.

All patent and literature references disclosed within the present specification are expressly and entirely incorporated herein by reference.

Brief Description of Figures

Figure 1: Human gp130 ELISA - Inhibition of Human OSM binding to human gp130 by 10G8, 9G2, 3E3 & 2B7. A non-competitive anti-OSM mouse antibody (15E10) was added for comparison purposes. A tool antibody was used as a negative control. Data shown are representative of one of four assay repeats.

Figure 2: KB Cell Assay- Inhibition of Human OSM by 10G8, 9G2, 3E3 & 2B7. A non-competitive anti-OSM mouse antibody (15E10) was added for comparison purposes. A tool antibody was used as a negative control. Data shown are representative of one of three assay repeats.

Figure 3: KB Cell Assay- Inhibition of Human OSM in the Presence of 25% Human AB Serum by 10G8, 9G2, 3E3 & 2B7. A non-competitive anti-OSM mouse antibody (15E10) was added for comparison purposes. A tool antibody was used as a negative control. Data shown are representative of one of two assay repeats.

Figure 4: Endogenous OSM Human gp130 Assay- Inhibition of Endogenous Human OSM Binding to Human gp130 by 10G8, 9G2, 3E3 & 2B7 antibodies. A non-competitive anti-OSM mouse antibody (110) was added for comparison purposes. A tool antibody was used as a negative control. Data shown are representative of one of two donors.

Figure 5: KB Cell Assay- Lack of Inhibition of Human LIF by 10G8, 9G2, 3E3 & 2B7. A non-competitive anti-OSM mouse antibody (15E10) was added for comparison purposes. A commercial anti-Human LIF mAb (R&D Systems, MAB250) was used as a positive control. A tool antibody was used as a negative control.

Figure 6: KB Cell Assay- Inhibition of Marmoset OSM by 10G8, 9G2, 3E3 & 2B7. A non-competitive anti-OSM mouse antibody (15E10) was added for comparison purposes. A tool antibody was used as a negative control. Data shown are representative of one of two assay repeats.

Figure 7: Comparison of the VH sequences of the 2B7, 3E3, 9G2 and 10G8 hybridomas. Small boxed residues represent a difference from the majority. Large boxes across sequences represent the CDR'S.

Figure 8: Comparison of the VL sequences of the 2B7, 3E3, 9G2 and 10G8 hybridomas. Small boxed residues represent a difference from the majority. Large boxes across sequences represent the CDR'S.

Figure 9: Sequence Analysis of the Variable Light Chains - of 10G8, 9G2, 3E3 and 2B7 compared with a non-competitive anti-OSM mouse parental antibody 15E10.

Figure 10: Sequence Analysis of the Variable Heavy Chains - of 10G8, 9G2, 3E3 and 2B7 compared with a non-competitive anti-OSM mouse parental antibody 15E10.

Figure 11: Direct Human OSM Binding ELISA- Comparison of human OSM binding of 10G8 and 9G2 chimaeras with 15E10 chimaera (15E10c).

Figure 12: Human gp130 ELISA- Inhibition of Human OSM binding to human gp130 by 10G8, 10G8 Chimaera, 9G2 & 9G2 Chimaera. A non-competitive anti-OSM mouse antibody (15E10) was added for comparison purposes. A tool antibody was used as a negative control. Data shown are representative of one of three assay repeats.

Figure 13: KB Cell Assay- Inhibition of Human OSM by 10G8, 10G8 Chimaera, 9G2 & 9G2 Chimaera. A non-competitive anti-OSM mouse antibody (15E10) was added for comparison purposes. A tool antibody was used as a negative control. Data shown are representative of one of three assay repeats.

Figure 14: KB Cell Assay- Inhibition of Human OSM in the Presence of 25% Human AB Serum by 10G8, 10G8 Chimaera, 9G2 & 9G2 Chimaera. A non-competitive anti-OSM mouse antibody (15E10) was added for comparison purposes. A tool antibody was used as a negative control. Data shown are representative of one of three assay repeats.

Figure 15: Endogenous OSM Human gp130 Assay- Inhibition of Endogenous Human OSM Binding to Human gp130 by 10G8, 10G8 Chimaera, 9G2 & 9G2 Chimaera antibodies. A non-competitive anti-OSM mouse antibody (15E10) was added for comparison purposes. A tool antibody was used as a negative control. Data shown are representative of one of two donors.

Figure 16: Human LIF KB Cell Assay- No Inhibition of Human LIF by 10G8, 10G8 Chimaera, 9G2 & 9G2 Chimaera. A non-competitive anti-OSM mouse antibody (15E10) was added for comparison purposes. An anti-Human LIF antibody (MAB250, R&D Systems) was used as a positive control. A tool antibody was used as a negative control. Data shown are representative of one of three assay repeats.

Figure 17: KB Cell Assay- Inhibition of Human OSM by Humanised 10G8 L1 and L4 Variants. 15E10h was added for comparison. Data shown are representative of one of three assay repeats.

Figure 18: Human gp130 ELISA- Inhibition of Human OSM binding to human gp130 by Humanised 10G8 H0L1, H1L1 and H2L1 variants. 15E10h was added for comparison. A tool antibody was used as a negative control. Data shown are representative of one of two assay repeats.

Figure 19: Human OSM-10G8 mAb Binding Complex- Binding of human OSM with 10G8 mAb light chain and heavy chain. The OSM receptor binding sites are shown (Site II and Site III). The amino acid residues important in the receptor binding regions are listed for each site.

Figure 20: KB Cell Assay- Inhibition of Human OSM by Humanised 10G8 H0L1 CDRH1 and CDRL2 variant antibodies. 15E10h was added for comparison. A tool antibody was used as a negative control. Data shown are representative of one of three assay repeats.

Figure 21: Human gp130 ELISA- Inhibition of Human OSM binding to human gp130 by the 10G8 mouse parental, 10G8 Chimera, the Humanised 10G8 H0L1 parent (H0L1) and H0(huCDRH1)L1. 15E10h was added for comparison. A tool antibody was used as a negative control. Data shown are representative of one of three assay repeats.

Figure 22: KB Cell Assay- Inhibition of Human OSM by the 10G8 mouse parental, 10G8 Chimera, the Humanised 10G8 H0L1 parent (H0L1) and H0(huCDRH1)L1. 15E10h was added for comparison. Data shown are representative of one of three assay repeats

Figure 23: KB Cell Assay- Inhibition of Human OSM in the Presence of 25% Human AB Serum by the 10G8 mouse parental, 10G8 Chimera, the Humanised 10G8 H0L1 parent (H0L1) and H0(H1)L1. 15E10h was added for comparison. A tool antibody was used as a negative control. Data shown are representative of one of two assay repeats.

Figure 24: Endogenous OSM Human gp130 Assay- Inhibition of Endogenous Human OSM Binding to Human gp130 by the 10G8 mouse parental, 10G8 Chimera, the Humanised 10G8 H0L1 parent (H0L1) and H0(huCDRH1)L1. 15E10h was added for comparison. A tool antibody was used as a negative control. Data shown are representative of one of four donors.

Figure 25: Human LIF KB Cell Assay- No Inhibition of Human LIF by the 10G8 mouse parental, 10G8 Chimaera, the Humanised 10G8 H0L1 parent (H0L1), H0(huCDRH1)L1 . 15E10h was added for comparison. An anti-Human LIF antibody (MAB250, R&D Systems) was used as a positive control. A tool antibody was used as a negative control. Data shown are representative of one of three assay repeats.

Figure 26: Human Primary Hepatocyte Assay- Inhibition of Serum Amyloid A (SAA) release by H0(huCDRH1)L1 from human hepatocytes stimulated with (A) 3ng/ml and (B) 10ng/ml human OSM. Humanised 15E10 was added for comparison purposes. Data shown are representative of one of three hepatocyte donors.

Figure 27: Human Primary Hepatocyte Assay- Inhibition of C-Reactive Protein (CRP) release by H0(huCDRH1)L1 from human hepatocytes stimulated with (A) 3ng/ml and (B) 10ng/ml human OSM. Humanised 15E10 was added for comparison purposes. Data shown are representative of one of three hepatocyte donors.

Figure 28: Human RA Fibroblast-Like Assay- Inhibition of IL-6 release by H0(huCDRH1)L1 from human RA fibroblast-like synoviocyte (HFLS-RA) cells stimulated with (A) 0.3ng/ml and (B) 3ng/ml of human OSM. Humanised 15E10 was added for comparison purposes. Data shown are representative of one of three HFLS-RA donors.

Figure 29: Human RA Fibroblast-Like Assay- Inhibition of MCP-1 release by H0(huCDRH1)L1 from human RA fibroblast-like synoviocyte (HFLS-RA) cells stimulated with (A) 0.3ng/ml and (B) 3ng/ml of human OSM. Humanised 15E10 was added for comparison purposes. Data shown are representative of one of three HFLS-RA donors.

Figure 30: Human Umbilical Vein Endothelial Cell Assay- Inhibition of IL-6 release by H0(huCDRH1)L1 from human umbilical vein endothelial cells stimulated with (A) 30ng/ml and (B) 100ng/ml of human OSM. Humanised 15E10 was added for comparison purposes. Data shown are representative of one of three assay repeats.

Figure 31: Human Lung Fibroblast Assay- Inhibition of MCP-1 release by H0(huCDRH1)L1 from human lung fibroblast stimulated with human OSM. Humanised 15E10 was added for comparison purposes. Data shown are representative of (A) one healthy and (B) one IPF donor.

Figure 32: Human Lung Fibroblast Assay- Inhibition of IL-6 release by H0(huCDRH1)L1 from human lung fibroblast stimulated with human OSM. Humanised 15E10 (labelled Antibody X) was added for comparison purposes. Data shown are representative of (A) one healthy and (B) one IPF donor.

Figure 33: CDRH3 variant binding data – Alanine scanning was performed on the residues found in CDRH3. The data provided shows how binding affinity is affected by a change is such a residue.

Figure 34: Illustration of the interaction between hOSM and gp130, LIFR and OSMR.

Nomenclature of antibodies - For the avoidance of doubt 15E10h and humanised 15E10 relate to the same antibody and are labelled Antibody X in some figures. Also 10G8/A9 and 10G8 relate to the same antibody.

Summary of the Invention

The present invention provides antigen binding proteins which are capable of binding to OSM, for example antibodies which specifically bind to OSM and which inhibit the binding of OSM to the gp130 receptor but do not directly interact with site II residues.

The OSM antibodies of the present invention are related to, or derived from a murine mAb 10G8. The 10G8 murine heavy chain variable region amino acid sequence is provided as SEQ ID NO. 26 and the 10G8 murine light chain variable region amino acid sequence is provided as SEQ ID NO. 28.

The heavy chain variable regions (VH) of the present invention may comprise the following CDRs or variants of these CDR's (as defined by Kabat (Kabat et al; Sequences of proteins of Immunological Interest NIH, 1987)):

CDRH1 of SEQ ID NO. 1 or SEQ ID NO 77
CDRH2 of SEQ ID NO. 2
CDRH3 of SEQ ID NO. 3

The light chain variable regions (VL) of the present invention may comprise the following CDRs or variants of these CDR's (as defined by Kabat (Kabat et al; Sequences of proteins of Immunological Interest NIH, 1987)):

CDRL1 of SEQ ID NO. 4
CDRL2 of SEQ ID NO. 5 or SEQ ID NO 78
CDRL3 of SEQ ID NO. 6

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

The invention also provides a recombinant transformed or transfected host cell comprising one or more polynucleotides encoding a heavy chain and or a light chain of any of the antigen-binding proteins described herein.

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

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

In a further aspect, the present invention provides a method of treatment or prophylaxis of a disease or disorder responsive to modulation of the interaction between hOSM and gp130 which method comprises the step of administering to said patient a therapeutically effective amount of the antigen binding protein thereof as described herein.

It is therefore an object of the present invention to provide a therapeutic approach to the treatment of RA and other diseases and disorders, particularly chronic inflammatory diseases and disorders such as osteoarthritis, idiopathic pulmonary fibrosis, pain, inflammatory lung disease, cardiovascular disease and psoriasis. In particular it is an object of the present invention to provide immunoglobulins, especially antibodies that specifically bind OSM (e.g. hOSM, particularly Site II thereof) and modulate (i.e. inhibit or block) the interaction between OSM and gp130 in the treatment of diseases and disorders responsive to modulation of that interaction.

In another aspect of the present invention there is provided a method of treating a human patient afflicted with an inflammatory disease or disorder which method comprises the step of administering to said patient a therapeutically effective amount of the antigen binding protein as described herein.

In another aspect of the present invention there is provided a method of humanising an antibody which method comprises the steps of: obtaining a non-human antibody which binds to a target antigen, obtaining the crystallographic structure of the antibody-antigen co crystal, determining to about 2-5Å from the crystal structure the residues of the non-human antibody involved directly in binding to the antigen, mutating one or more of the residues not involved in binding to a residue derived from a human sequence and recovering said antibody.

Detailed Description of the Invention

The present invention provides an antigen binding protein which specifically binds to OSM, for example which specifically binds human OSM (hOSM) and which inhibits the binding of OSM to the gp130 receptor but does not directly interact with site II residues.

In a further aspect of the invention as herein described the antigen binding protein does not directly bind to residues Q20, G120, Q16, N124.

In a further aspect of the invention as herein described there is provided an antigen binding protein which specifically binds to OSM, for example which specifically binds human OSM (hOSM) and which inhibits the binding of OSM to the gp130 receptor and which interacts with one or more of residues 82, 83, 84, 90, 94, 112,115, 122, 123, 152 of hu OSM.

In one such aspect the invention provides an antigen binding protein which specifically binds to OSM, for example which specifically binds human OSM (hOSM) and which inhibits the binding of OSM to the gp130 receptor but does not directly interact with site II residues and which does not compete with an antibody which has a heavy chain of SEQ ID NO.79 and a light chain of SEQ ID NO. 80 in a competition ELISA assay.

In one such aspect the invention provides an antigen binding protein which competes with the antigen binding protein as described herein for binding to OSM for example to human OSM.

In another aspect the antigen binding protein binds to human OSM with high affinity for example when measured by Biacore the antigen binding protein binds to human OSM with an affinity of 500pM or less or an affinity of 400pM or less, or 300pM or less, or 250pM or less, or 200pM or less, or for example 140pM or less. In a further embodiment the antigen binding protein binds to human OSM when measured by Biacore of between about 100pM and about 500pM or between about 100pM and about 300pM, or between about 100pM and about 250pM, or between about 100pM and about 200pM. In one embodiment of the present invention the antigen binding protein binds OSM with an affinity of less than 250pm. In a further embodiment of the present invention the antigen binding protein binds OSM with an affinity of less than 140pm.
In one such embodiment, this is measured by Biacore, for example as set out in Example 2.5.1.

In another aspect the antigen binding protein binds to human OSM with high affinity for example when measured by the solution based Kinexa method the antigen binding protein binds to human OSM with an affinity of 200pM or less or an affinity of 150pM or less, or 100pM or less, or 50pM or less or for

example 40pM or less. In a further embodiment the antigen binding protein binds to human OSM when measured by Kinexa of between about 10pM and about 200pM or between about 10pM and about 150pM, or between about 10pM and about 100pM, or between about 10pM and about 70pM or between about 10pM and about 40pM. In one embodiment of the present invention the antigen binding protein binds OSM with an affinity of less than 70pm. In a further embodiment of the present invention the antigen binding protein binds OSM with an affinity of less than 40pm.
In one such embodiment, this is measured by Kinexa, for example as set out in Example 2.5.1

In another aspect the antigen binding protein binds to human OSM and neutralises OSM in a cell neutralisation assay wherein the antigen binding protein has an IC50 of between about 10pM and about 200pM, or between about 10pM and about 150pM, or between about 10pM and about 100pM, or between about 20pM and about 100pM, or between about 20pM and about 100pM. In a further embodiment of the present invention the antigen binding protein binds OSM and neutralises OSM in a cell neutralisation assay wherein the antigen binding protein has an IC50 of about 20pM with an affinity of less than 140pm.

In one such embodiment, this is measured by a cell neutralisation assay, for example as set out in Example 2 section 2.2.1.

In one aspect the present invention further provides that the antigen binding protein comprises CDRH3 of SEQ ID NO. 3 or a variant of SEQ ID NO. 3 wherein CDRH3 is substituted by the alternative amino acids set out below at one or more of the following positions (using Kabat numbering):
Position 95 is substituted for Ala, Glu, Gly, His, Leu, Met, Pro, Gln, Ser, Thr, or Val
Position 96 is substituted for Ala, Cys, Phe, Gly, His, Lys, Leu, Ser, Thr, Trp or Tyr
Position 97 is substituted for Ala, Cys, Phe, Met or Ser
Position 98 is substituted for Ala, Asp, Phe, Gly, Leu, Pro, Gln or Trp
Position 99 is substituted for Ala, Cys, Pro, Ser, Val or Tyr
Position 100B is substituted for Glu
Position 100C is substituted for Ala, Glu, Phe, Gly, Val or Trp
Position 100D is substituted for Ala, Cys, Asp, Glu, Gly, Leu, Ser, Thr, Val, Trp or Tyr
Position 101 is substituted for Glu, Gly, Ser, Thr or Val
Position 102 is substituted for Ala, Phe, Gly, Leu, Pro, Gln, Arg, Ser Tyr, His, Ile, Asp or Trp

In a further aspect of the invention the antigen binding protein comprises:
i) CDRH3 as set out in SEQ ID NO. 3 or a variant of SEQ ID NO. 3 wherein Val 102 is substituted for Tyr, His, Ile, Ser, Asp or Gly
ii) CDRH2 as set out in SEQ ID NO. 2 or a variant of SEQ ID NO. 2 wherein Thr50 is substituted for Gly, Tyr, Phe, Ile, Glu or Val and/or Ile51 is substituted for Leu, Val, Thr, Ser or Asn and/or Ser52 is substituted for Phe, Trp or His and/or Gly53 is substituted for Asp, Ser or Asn and/orGly54 is

substituted for Ser and/or Phe56 is substituted for Ser, Tyr, Thr, Asn, Asp or Arg and/or Tyr58 is substituted for Gly, His, Phe, Asp or Asn.

iii) CDRL1 as set out in SEQ ID NO. 4 or a variant of SEQ ID NO. 4 wherein Ser27A is substituted for Asn, Asp, Thr or Glu and/or Ser 27C is substituted for Asp, Leu, Tyr, Val, Ile, Asn, Phe, His, Gly or Thr and/or Asn 31 is substituted for Ser, Thr, Lys or Gly and/or Phe32 is substituted for Tyr, Asn, Ala, His, Ser or Arg and/or Met 33 is substituted for Leu, Val, Ile or Phe.

iv) CDRL3 as set out in SEQ ID NO. 6 or a variant of SEQ ID NO. 6 wherein Leu89 is substituted for Gln, Ser, Gly or Phe and/or His90 is substituted for Gln or Asn, Ser 91 is substituted for Asn, Phe, Gly, Arg, Asp, His, Thr, Tyr or Val and/or Arg92 is substituted for Asn, Tyr, Trp, Thr, Ser, Gln, His, ala or Asp and/or Glu93 is substituted for Asn, Gly, His, Thr, Ser, Ar or Ala and/or Phe96 is substituted for Pro, Leu, Tyr, Arg, Ile,or Trp.

In yet a further aspect the antigen binding protein further comprises:

v) CDRL2 as set out in SEQ ID NO. 5 or SEQ ID NO. 78

In yet a further aspect the antigen binding protein further comprises:

vi) CDRH1 as set out in SEQ ID NO. 1 or SEQ ID NO. 77 or a variant of SEQ ID NO. 1 or SEQ ID NO. 77 wherein Tyr 32 is substituted for Ile, His, Phe, Thr, Asn, Cys, Glu or Asp and/or Ala 33 is substituted for Tyr, Trp, Gly, Thr, Leu or Val and/or Met 34 is substituted for Ile, Val or Trp and/or Ser 35 is substituted for His, Glu, Asn, Gln, Tyr or Thr.

The variant CDR sequences for CDR's L1, L2, L3, H1 and H2 have been determined using mutagenesis and or canonical technology. The complementarity determining regions (CDRs) L1, L2, L3, H1 and H2 tend to structurally exhibit one of a finite number of main chain conformations. The particular canonical structure class of a CDR is defined by both the length of the CDR and by the loop packing, determined by residues located at key positions in both the CDRs and the framework regions (structurally determining residues or SDRs). Martin and Thornton (1996; J Mol Biol 263:800-815) have generated an automatic method to define the "key residue" canonical templates. Cluster analysis is used to define the canonical classes for sets of CDRs, and canonical templates are then identified by analysing buried hydrophobics, hydrogen-bonding residues, and conserved glycines and prolines. The CDRs of antibody sequences can be assigned to canonical classes by comparing the sequences to the key residue templates and scoring each template using identity or similarity matrices.

In one aspect the invention provides an antigen binding protein which comprises CDR H3 of SEQ. ID. NO: 3: CDRH2: SEQ. ID. NO: 2: CDRL1: SEQ. ID. NO: 4 and CDRL3: SEQ. ID. NO: 6 and may further comprise CDR H1 of SEQ. ID. NO: 1 or SEQ ID NO 77 and CDRL2: SEQ. ID. NO: 5 or SEQ ID NO. 78

In another aspect the antigen binding protein comprises CDR H3 of SEQ. ID. NO: 3: CDRH2: SEQ. ID. NO: 2: CDRL1: SEQ. ID. NO: 4: CDRL2: SEQ. ID. NO: 5 and CDRL3: SEQ. ID. NO: 6.

In yet another aspect the antigen binding protein comprises CDR H3 of SEQ. ID. NO: 3: CDRH2: SEQ. ID. NO: 2: CDR H1 of SEQ. ID. NO: 1: CDRL1: SEQ. ID. NO: 4: CDRL2: SEQ. ID. NO: 5 and CDRL3: SEQ. ID. NO: 6.

In yet another aspect the antigen binding protein comprises CDR H3 of SEQ. ID. NO: 3: CDRH2: SEQ. ID. NO: 2: CDR H1 of SEQ. ID. NO: 1: CDRL1: SEQ. ID. NO: 4: CDRL2: SEQ. ID. NO: 78 and CDRL3: SEQ. ID. NO: 6.

In yet another aspect the antigen binding protein comprises CDR H3 of SEQ. ID. NO: 3: CDRH2: SEQ. ID. NO: 2: CDR H1 of SEQ. ID. NO: 77: CDRL1: SEQ. ID. NO: 4: CDRL2: SEQ. ID. NO: 5 and CDRL3: SEQ. ID. NO: 6.

In yet another aspect the antigen binding protein comprises CDR H3 of SEQ. ID. NO: 3: CDRH2: SEQ. ID. NO: 2: CDR H1 of SEQ. ID. NO: 77: CDRL1: SEQ. ID. NO: 4: CDRL2: SEQ. ID. NO: 78 and CDRL3: SEQ. ID. NO: 6.

In one aspect of the present invention the antigen binding protein does not interact directly via CDR H1 with OSM.

In one aspect the antigen binding protein does not interact directly via CDR H1 or CDR L2 with OSM.

The antigen binding proteins of the invention may comprise heavy chain variable regions and light chain variable regions of the invention which may be formatted into the structure of a natural antibody or functional fragment or equivalent thereof. An antigen binding protein of the invention may therefore comprise the VH regions of the invention formatted into a full length antibody, a (Fab')2 fragment, a Fab fragment, or equivalent thereof (such as scFV, bi- tri- or tetra-bodies, Tandabs etc.), when paired with an appropriate light chain. The antibody may be an IgG1, IgG2, IgG3, or IgG4; or IgM; IgA, IgE or IgD or a modified variant thereof. The constant domain of the antibody heavy chain may be selected accordingly. The light chain constant domain may be a kappa or lambda constant domain. Furthermore, the antigen binding protein may comprise modifications of all classes e.g. IgG dimers, Fc mutants that no longer bind Fc receptors or mediate C1q binding. The antigen binding protein may also be a chimeric antibody of the type described in WO86/01533 which comprises an antigen binding region and a non-immunoglobulin region.
The constant region is selected according to any functionality required. An IgG1 may demonstrate lytic ability through binding to complement and/or will mediate ADCC (antibody dependent cell cytotoxicity). An IgG4 can be used if a non-cytotoxic blocking antibody is required. However, IgG4 antibodies can demonstrate instability in production and therefore an alternative is to modify the generally more stable IgG1. Suggested modifications are described in EP0307434, for example

mutations at positions 235 and 237. The invention therefore provides a lytic or a non-lytic form of an antigen binding protein, for example an antibody according to the invention.
In certain forms the antibody of the invention is a full length (e.g. H2L2 tetramer) lytic or non-lytic IgG1 antibody having any of the heavy chain variable regions described herein.

The antigen binding proteins of the present invention are derived from the murine antibody having the variable regions as described in SEQ ID NO:26 and SEQ ID NO:28 or non-murine equivalents thereof, such as rat, human, chimeric or humanised variants thereof, for example they are derived from the humanised antibody having the heavy and light chains as described in SEQ ID NO:54 and SEQ ID NO:62.

In one aspect of the invention there is provided an antigen binding protein comprising an isolated heavy chain variable domain selected from any on the following: SEQ ID NO 54, SEQ ID NO 56, SEQ ID NO.58 or SEQ ID NO: 74.
In another aspect of the invention there is provided an antigen binding protein comprising an isolated light chain variable domain selected from any on the following: SEQ ID NO 62, SEQ ID NO 64, SEQ ID NO.66 or SEQ ID NO.68.
In a further aspect of the invention there is provided an antigen binding protein comprising an isolated heavy chain variable domain selected from any on the following: SEQ ID NO 54, SEQ ID NO 56, SEQ ID NO.58 or SEQ ID NO: 74 and a an isolated light chain variable domain selected from any on the following: SEQ ID NO 62, SEQ ID NO 64, SEQ ID NO.66 or SEQ ID NO.68.

In a further embodiment of the invention there is provided an antigen binding protein comprising an isolated heavy chain variable domain of SEQ ID NO 54 and an isolated light chain variable domain of SEQ ID NO 62. In a further embodiment the antigen binding protein comprises a heavy chain variable region of SEQ. ID. NO:74 and a light chain variable region of SEQ. ID. NO:62.

In one aspect the antigen binding protein of the present invention comprises a heavy chain variable region encoded by SEQ. ID. NO:53 and a light chain variable region encoded by SEQ. ID. NO:61
In one aspect the antigen binding protein of the present invention comprises a heavy chain variable region encoded by SEQ. ID. NO:73 and a light chain variable region encoded by SEQ. ID. NO:61.

In one aspect there is provided a polynucleotide encoding an isolated variable heavy chain said polynucleotide comprising SEQ. ID. NO. 53, or SEQ. ID. NO. 55, or SEQ. ID. NO. 57, or SEQ. ID. NO. 73.
In one aspect there is provided a polynucleotide encoding an isolated variable light chain said polynucleotide comprising SEQ. ID. NO. 61, or SEQ. ID. NO. 63, or SEQ. ID. NO. 65, or SEQ. ID. NO. 67.
In a further aspect there is provided a polynucleotide encoding an isolated variable heavy chain said polynucleotide comprising SEQ. ID. NO. 53, or SEQ. ID. NO. 73 and a polynucleotide encoding an

isolated variable light chain said polynucleotide comprising SEQ. ID. NO. 61, or SEQ. ID. NO. 63, or SEQ. ID. NO. 65, or SEQ. ID. NO. 67. In yet a further aspect there is provided a polynucleotide encoding an isolated variable heavy chain said polynucleotide comprising SEQ. ID. NO. 53 or SEQ. ID. NO. 73 and a polynucleotide encoding an isolated variable light chain said polynucleotide comprising SEQ. ID. NO. 61.

In a further aspect the antigen binding protein may comprise any one of the variable heavy chains as described herein in combination with any one of the light chains as described herein.

In one aspect the antigen binding protein is an antibody or antigen binding fragment thereof comprising one or more CDR's according to the invention described herein, or one or both of the heavy or light chain variable domains according to the invention described herein. In one embodiment the antigen binding protein binds primate OSM. In one such embodiment the antigen binding protein additionally binds non-human primate OSM, for example cynomolgus macaque monkey OSM. In another embodiment the antigen binding protein binds marmoset OSM.

In one aspect there is provided an antigen binding protein which binds to both Marmoset and human OSM with an affinity stronger than 1nM when measured by Biacore or Kinexa.

The ability of these antibodies to neutralise marmoset OSM provides a unique means to assess the role of OSM in marmoset disease models, such as the EAE model of MS, for additional indications

In another aspect the antigen binding protein is selected from the group consisting of a dAb, Fab, Fab', $F(ab')_2$, Fv, diabody, triabody, tetrabody, miniantibody, and a minibody,.

In one aspect of the present invention the antigen binding protein is a humanised or chimaeric antibody, in a further aspect the antibody is humanised.

In one aspect the antibody is a monoclonal antibody.

The present invention further provides that in one aspect the antigen binding protein comprises:
i) CDRH3 as set out in SEQ ID NO. 3 or a variant of SEQ ID NO. 3 wherein CDRH3 is substituted by the alternative amino acids set out below at one or more of the following positions (using Kabat numbering):
Position 95 is substituted for Ala, Glu, Gly, His, Leu, Met, Pro, Gln, Ser, Thr, or Val
Position 96 is substituted for Ala, Cys, Phe, Gly, His, Lys, Leu, Ser, Thr, Trp or Tyr
Position 97 is substituted for Ala, Cys, Phe, Met or Ser
Position 98 is substituted for Ala, Asp, Phe, Gly, Leu, Pro, Gln or Trp
Position 99 is substituted for Ala, Cys, Pro, Ser, Val or Tyr
Position 100B is substituted for Glu

Position 100C is substituted for Ala, Glu, Phe, Gly, Val or Trp

Position 100D is substituted for Ala, Cys, Asp, Glu, Gly, Leu, Ser, Thr, Val, Trp or Tyr

Position 101 is substituted for Glu, Gly, Ser, Thr or Val

Position 102 is substituted for Ala, Phe, Gly, Leu, Pro, Gln, Arg, Ser Tyr, His, Ile, Asp or Trp

ii) CDRH1 as set out in SEQ ID NO. 1 or SEQ ID NO. 77 or a variant of SEQ ID NO. 1 or SEQ ID NO. 77 wherein Tyr 32 is substituted for Ile, His, Phe, Thr, Asn, Cys, Glu or Asp and/or Ala 33 is substituted for Tyr, Trp, Gly, Thr, Leu or Val and/or Met 34 is substituted for Ile, Val or Trp and/or Ser 35 is substituted for His, Glu, Asn, Gln, Tyr or Thr.

iii) CDRH2 as set out in SEQ ID NO. 2 or a variant of SEQ ID NO. 2 wherein Thr50 is substituted for Gly, Tyr, Phe, Ile, Glu or Val and/or Ile51 is substituted for Leu, Val, Thr, Ser or Asn and/or Ser52 is substituted for Phe, Trp or His and/or Gly53 is substituted for Asp, Ser or Asn and/orGly54 is substituted for Ser and/or Phe56 is substituted for Ser, Tyr, Thr, Asn, Asp or Arg and/or Tyr58 is substituted for Gly, His, Phe, Asp or Asn.

iv) CDRL1 as set out in SEQ ID NO. 4 or a variant of SEQ ID NO. 4 wherein Ser27A is substituted for Asn, Asp, Thr or Glu and/or Ser 27C is substituted for Asp, Leu, Tyr, Val, Ile, Asn, Phe, His, Gly or Thr and/or Asn 31 is substituted for Ser, Thr, Lys or Gly and/or Phe32 is substituted for Tyr, Asn, Ala, His, Ser or Arg and/or Met 33 is substituted for Leu, Val, Ile or Phe.

v) CDRL2 as set out in SEQ ID NO. 5 or SEQ ID NO. 78

vi) CDRL3 as set out in SEQ ID NO. 6 or a variant of SEQ ID NO. 6 wherein Leu89 is substituted for Gln, Ser, Gly or Phe and/or His90 is substituted for Gln or Asn, Ser 91 is substituted for Asn, Phe, Gly, Arg, Asp, His, Thr, Tyr or Val and/or Arg92 is substituted for Asn, Tyr, Trp, Thr, Ser, Gln, His, ala or Asp and/or Glu93 is substituted for Asn, Gly, His, Thr, Ser, Ar or Ala and/or Phe96 is substituted for Pro, Leu, Tyr, Arg, Ile,or Trp.

vii) the heavy chain framework comprises the following residues:

Position 2 Val, Ile or Gly,

Position 4 Leu or Val

Position 20 Leu, Ile, Met or Val

Position 22 Cys

Position 24 Thr, Ala, Val, Gly or Ser

Position 26 Gly

Position 29 Ile, Phe, Leu or Ser

Position 36 Trp

Position 47 Trp

Position 48 Ile, met, Val or Leu

Position 69 Ile, Leu, Phe, Met or Val

Position 71 Arg

Position 78 Ala, Leu, Val, Tyr or Phe

Position 80 Leu, Met,

Position 90 Tyr or Phe

Position 92 Cys

Position 94 Arg, Lys, Gly, Ser, His or Asn

The present invention further provides that in one aspect the antigen binding protein comprises:

i) CDRH3 as set out in SEQ ID NO. 3

ii) CDRH1 as set out in SEQ ID NO. 1 or SEQ ID NO. 77

iii) CDRH2 as set out in SEQ ID NO. 2

iv) CDRL1 as set out in SEQ ID NO. 4

v) CDRL2 as set out in SEQ ID NO. 5 or SEQ ID NO. 78

vi) CDRL3 as set out in SEQ ID NO. 6

vii) the heavy chain framework comprises the following residues:

Position 2 Val, Ile or Gly,

Position 4 Leu or Val

Position 20 Leu, Ile, Met or Val

Position 22 Cys

Position 24 Thr, Ala, Val, Gly or Ser

Position 26 Gly

Position 29 Ile, Phe, Leu or Ser

Position 36 Trp

Position 47 Trp

Position 48 Ile, met, Val or Leu

Position 69 Ile, Leu, Phe, Met or Val

Position 71 Arg

Position 78 Ala, Leu, Val, Tyr or Phe

Position 80 Leu, Met,

Position 90 Tyr or Phe

Position 92 Cys

Position 94 Arg, Lys, Gly, Ser, His or Asn

The present invention further provides that in one aspect the antigen binding protein comprises:

i) CDRH3 as set out in SEQ ID NO. 3

ii) CDRH1 as set out in SEQ ID NO. 1 or SEQ ID NO. 77

iii) CDRH2 as set out in SEQ ID NO. 2

iv) CDRL1 as set out in SEQ ID NO. 4

v) CDRL2 as set out in SEQ ID NO. 5 or SEQ ID NO. 78

vi) CDRL3 as set out in SEQ ID NO. 6

vii) the heavy chain framework comprises the following residues:

Position 2 Val

Position 4 Leu

Position 20 Leu

Position 22 Cys

Position 24 Ala

Position 26 Gly
Position 29 Phe
Position 36 Trp
Position 47 Trp
Position 48 Val
Position 69 Ile
Position 71 Arg
Position 78 Leu
Position 80 Leu
Position 90 Tyr
Position 92 Cys
Position 94 Arg

The present invention further provides that in one aspect the antigen binding protein comprises:

i) CDRH3 as set out in SEQ ID NO. 3
ii) CDRH1 as set out in SEQ ID NO. 1 or SEQ ID NO. 77
iii) CDRH2 as set out in SEQ ID NO. 2
iv) CDRL1 as set out in SEQ ID NO. 4
v) CDRL2 as set out in SEQ ID NO. 5 or SEQ ID NO. 78
vi) CDRL3 as set out in SEQ ID NO. 6
vii) the heavy chain framework comprises the following residues:

Position 2 Val
Position 4 Leu
Position 20 Leu
Position 22 Cys
Position 24 Ala
Position 26 Gly
Position 29 Phe
Position 36 Trp
Position 47 Trp
Position 48 Leu
Position 69 Ile, Leu, Phe, Met or Val
Position 71 Arg
Position 78 Ala
Position 80 Leu, Met,
Position 90 Tyr or Phe
Position 92 Cys
Position 94 Arg, Lys, Gly, Ser, His or Asn

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

A selected host cell is co-transfected by conventional techniques with both the first and second vectors (or simply transfected by a single vector) to create the transfected host cell of the invention comprising both the recombinant or synthetic light and heavy chains. The transfected cell is then cultured by conventional techniques to produce the engineered antigen binding protein of the invention. The antigen binding protein which includes the association of both the recombinant heavy chain and/or light chain is screened from culture by appropriate assay, such as ELISA or RIA. Similar conventional techniques may be employed to construct other antigen binding proteins.

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

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

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

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

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

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

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

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

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

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

In accordance with the present invention there is provided a method of producing an anti-OSM antibody of the present invention which binds to and neutralises the activity of human OSM which method comprises the steps of;

(a) providing a first vector encoding a heavy chain of the antibody;

(b) providing a second vector encoding a light chain of the antibody;

(c) transforming a mammalian host cell (e.g. CHO) with said first and second vectors;

(d) culturing the host cell of step (c) under conditions conducive to the secretion of the antibody from said host cell into said culture media;

(e) recovering the secreted antibody of step (d).

Once expressed by the desired method, the antibody is then examined for in vitro activity by use of an appropriate assay. Presently conventional ELISA assay formats are employed to assess qualitative and quantitative binding of the antibody to OSM. Additionally, other in vitro assays may also be used to verify neutralizing efficacy prior to subsequent human clinical studies performed to evaluate the persistence of the antibody in the body despite the usual clearance mechanisms.
The dose and duration of treatment relates to the relative duration of the molecules of the present invention in the human circulation, and can be adjusted by one of skill in the art depending upon the condition being treated and the general health of the patient. It is envisaged that repeated dosing (e.g. once a week or once every two weeks) over an extended time period (e.g. four to six months) maybe required to achieve maximal therapeutic efficacy.

In one embodiment of the present invention there is provided a recombinant transformed, transfected or transduced host cell comprising at least one expression cassette, for example where the expression cassette comprises a polynucleotide encoding a heavy chain of an antigen binding protein according to the invention described herein and further comprises a polynucleotide encoding a light chain of an antigen binding protein according to the invention described herein or where there are two expression cassettes and the 1st encodes the light chain and the second encodes the heavy chain. For example in one embodiment the first expression cassette comprises a polynucleotide encoding a heavy chain of an antigen binding protein comprising a constant region or antigen binding fragment thereof which is linked to a constant region according to the invention described herein and further comprises a second cassette comprising a polynucleotide encoding a light chain of an antigen binding protein comprising a constant region or antigen binding fragment thereof which is linked to a constant region according to the invention described herein for example the first expression cassette comprises a polynucleotide encoding a heavy chain selected from SEQ. ID. NO: 70, or SEQ. ID. NO: 76 and a second expression cassette comprising a polynucleotide encoding a light chain selected from SEQ. ID. NO: 72.

It will be understood that the sequences described herein (SEQ ID NO.25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 83) include sequences which are substantially identical, for example sequences which are at least 90% identical, for example which are

at least 91%, or at least 92%, or at least 93%, or at least 94% or at least 95%, or at least 96%, or at least 97% or at least 98%, or at least 99% identical to the sequences described herein.
For nucleic acids, the term “substantial identity” indicates that two nucleic acids, or designated sequences thereof, when optimally aligned and compared, are identical, with appropriate nucleotide insertions or deletions, in at least about 80% of the nucleotides, at least about 90% to about 95%, or at least about 98% to about 99.5% of the nucleotides. Alternatively, substantial identity exists when the segments will hybridize under selective hybridization conditions, to the complement of the strand.

For nucleotide and amino acid sequences, the term “identical" indicates the degree of identity between two nucleic acid or amino acid sequences when optimally aligned and compared with appropriate insertions or deletions. Alternatively, substantial identity exists when the DNA segments will hybridize under selective hybridization conditions, to the complement of the strand.
In another embodiment of the invention there is provided a stably transformed host cell comprising a vector comprising one or more expression cassettes encoding a heavy chain and/or a light chain of the antibody comprising a constant region or antigen binding fragment thereof which is linked to a constant region as described herein. For example such host cells may comprise a first vector encoding the light chain and a second vector encoding the heavy chain, for example the first vector encodes a heavy chain selected from SEQ. ID. NO: 70, or SEQ. ID. NO: 76 and a second vector encoding a light chain for example the light chain of SEQ ID NO: 72.

In another embodiment of the present invention there is provided a host cell according to the invention described herein wherein the cell is eukaryotic, for example where the cell is mammalian. Examples of such cell lines include CHO or NS0.

In another embodiment of the present invention there is provided a method for the production of an antibody comprising a constant region or antigen binding fragment thereof which is linked to a constant region according to the invention described herein which method comprises the step of culturing a host cell in a culture media, for example serum- free culture media.

In another embodiment of the present invention there is provided a method according to the invention described herein wherein said antibody is further purified to at least 95% or greater (e.g. 98% or greater) with respect to said antibody containing serum- free culture media.

In yet another embodiment there is provided a pharmaceutical composition comprising an antigen binding protein and a pharmaceutically acceptable carrier.

In another embodiment of the present invention there is provided a kit-of-parts comprising the composition according to the invention described herein described together with instructions for use.

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

Therapeutic agents of the invention may be prepared as pharmaceutical compositions containing an effective amount of the antigen binding protein of the invention as an active ingredient in a pharmaceutically acceptable carrier. In one embodiment the prophylactic agent of the invention is an aqueous suspension or solution containing the antigen binding proteinin a form ready for injection. In one embodiment the suspension or solution is buffered at physiological pH. In one embodiment the compositions for parenteral administration will comprise a solution of the antigen binding protein of the invention or a cocktail thereof dissolved in a pharmaceutically acceptable carrier. In one embodiment the carrier is an aqueous carrier. A variety of aqueous carriers may be employed, e.g., 0.9% saline, 0.3% glycine, and the like. These solutions may be made sterile and generally free of particulate matter. These solutions may be sterilized by conventional, well known sterilization techniques (e.g., filtration). The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, etc. The concentration of the antigen binding protein of the invention in such pharmaceutical formulation can vary widely, i.e., from less than about 0.5%, usually at or at least about 1% to as much as about 15 or 20% by weight and will be selected primarily based on fluid volumes, viscosities, etc., according to the particular mode of administration selected.
Thus, a pharmaceutical composition of the invention for intramuscular injection could be prepared to contain about 1 mL sterile buffered water, and between about 1 ng to about 100 mg, e.g. about 50 ng to about 30 mg or about 5 mg to about 25 mg, of an antigen binding protein, for example an antibody of the invention. Similarly, a pharmaceutical composition of the invention for intravenous infusion could be made up to contain about 250 ml of sterile Ringer's solution, and about 1 to about 30 or 5 mg to about 25 mg of an antigen binding protein of the invention per ml of Ringer's solution. Actual methods for preparing parenterally administrable compositions are well known or will be apparent to those skilled in the art and are described in more detail in, for example, Remington's Pharmaceutical Science, 15th ed., Mack Publishing Company, Easton, Pennsylvania. For the preparation of intravenously administrable antigen binding protein formulations of the invention see Lasmar U and Parkins D "The formulation of Biopharmaceutical products", Pharma. Sci.Tech.today, page 129-137, Vol.3 (3rd April 2000); Wang, W "Instability, stabilisation and formulation of liquid protein pharmaceuticals", Int. J. Pharm 185 (1999) 129-188; Stability of Protein Pharmaceuticals Part A and B ed Ahern T.J., Manning M.C., New York, NY: Plenum Press (1992); Akers,M.J. "Excipient-Drug interactions in Parenteral Formulations", J.Pharm Sci 91 (2002) 2283-2300; Imamura, K et al "Effects of types of sugar on stabilization of Protein in the dried state", J Pharm Sci 92 (2003) 266-274; Izutsu, Kkojima, S. "Excipient crystalinity and its protein-structure-stabilizing effect during freeze-drying", J Pharm. Pharmacol, 54 (2002) 1033-1039; Johnson, R, "Mannitol-sucrose mixtures-versatile formulations for protein lyophilization", J. Pharm. Sci, 91 (2002) 914-922; and Ha,E Wang W, Wang

Y.j. “Peroxide formation in polysorbate 80 and protein stability”, J. Pharm Sci, 91, 2252-2264,(2002) the entire contents of which are incorporated herein by reference and to which the reader is specifically referred.

In one embodiment the therapeutic agent of the invention, when in a pharmaceutical preparation, is present in unit dose forms. The appropriate therapeutically effective dose will be determined readily by those of skill in the art. Suitable doses may be calculated for patients according to their weight, for example suitable doses may be in the range of about 0.1 to about 20mg/kg, for example about 1 to about 20mg/kg, for example about 10 to about 20mg/kg or for example about 1 to about 15mg/kg, for example about 10 to about 15mg/kg. To effectively treat conditions such as asthma or IPF in a human, suitable doses may be within the range of about 0.1 to about 1000 mg, for example about 0.1 to about 500mg, for example about 500mg, for example about 0.1 to about 100mg, or about 0.1 to about 80mg, or about 0.1 to about 60mg, or about 0.1 to about 40mg, or for example about 1 to about 100mg, or about 1 to about 50mg, of an antigen binding protein of this invention, which may be administered parenterally, for example subcutaneously, intravenously or intramuscularly. Such dose may, if necessary, be repeated at appropriate time intervals selected as appropriate by a physician.

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

In another aspect of the present invention there is provided a method of treating a human patient afflicted with an inflammatory arthropathy such as rheumatoid arthritis, juvenile onset arthritis, osteoarthritis, psoriatic arthritis and ankylosing spondylitis which method comprises the step of administering to said patient a therapeutically effective amount of the antigen binding protein as described herein.

In another aspect of the present invention there is provided a method of treating a human patient afflicted with a disease or disorder selected from type 1 diabetes, psoriasis, inflammatory bowel disease (IBD) including Crohn’s disease and ulcerative colitis (UC), systemic lupus erythematosus (SLE, Lupus), atopic dermatitis, allergic rhinitis, chronic obstructive pulmonary disease (COPD), pneumonia, eosinophilic esophagitis, Systemic sclerosis (SS) or Idiopathic Pulmonary Fibrosis (IPF), Sjögren's syndrome, scleroderma, vasculitides (including Takayasu arteritis, giant cell (temporal) arteritis, polyarteritis nodosa, Wegener's granulomatosis, Kawasaki disease, isolated CNS vasculitis, Churg-Strauss arteritis, microscopic polyarteritis/polyangiitis, hypersensitivity vasculitis (allergic vasculitis), Henoch-Schonlein purpura, and essential cryoglobulinemic vasculitis), undifferentiated spondyloarthropathy (USpA), ankylosing spondylitis (AS), graft-versus-host disease (GVHD), primary biliary cirrhosis (PBC), primary sclerosing cholangitis (PSC), idiopathic thrombocytopenic purpura (ITP), multiple sclerosis (MS), and asthma wherein said method comprises the step of administering to said patient a therapeutically effective amount of the antigen binding protein as described herein.

Any one or more of the aforementioned diseases may be the target disease for a method of treatment of the invention.

In a particular aspect, the disease or disorder is selected from the group consisting of Osteoarthrtits,(OA), Psoriasis, Idiopathic Pulmonary Fibrosis (IPF), Systemic sclerosis (SS Sjögren's syndrome, scleroderma, or Multiple Sclerosis (MS.

In one aspect of the present invention the autoimmune disease is Osteoarthritis.

In one aspect of the present invention the autoimmune disease is Psoriasis.

In one aspect of the present invention the autoimnmune disease or disorder is a fibrotic disease or disorder.

In one aspect of the present invention the autoimmune disease is Idiopathic Pulmonary Fibrosis (IPF).

In one aspect of the present invention the autoimmune disease is Systemic Sclerosis (SS).

In one aspect of the present invention the autoimmune disease is Sjögren's syndrome.

In one aspect of the present invention the autoimmune disease is Scleroderma.

In another aspect of the invention there is provided a method of reducing or preventing cartilage degradation in a human patient afflicted with (or suspectible to) such degradation which method comprises the step of administering a therapeutically effective amount of the antigen binding protein to said patient as described herein.

In another aspect of the present invention there is provided a method of reducing TNF alpha production in a patient afflicted with a disease or disorder responsive to TNF alpha reduction which method comprises administering to said patient a therapeutically effective amount of the antigen binding protein as described herein

In another aspect of the invention there is provided a method of treating the extra articular manifestations of an arthritic disease or disorder e.g. Feltys syndrome and/or treat the formation of atherosclerotic plaques which method comprises the step of administering a therapeutically effective amount of the antigen binding protein as described herein to the human patient afflicted with the extra articular manifestations of an arthritic disease or disorder.

In another aspect of the present invention there is provided a method of treating a human patient afflicted with a disease of endothelial cell origin which method comprises the steps of administering to said patient a therapeutically effective amount of the antigen binding protein as described herein.

In another aspect of the present invention there is provided a method of treating a human patient afflicted with fibrotic diseases or disorders such as idiopathic pulmonary fibrosis, progressive systemic sclerosis (scleroderma), hepatic fibrosis, hepatic granulomas, schistosomiasis, and leishmaniasis which method comprises the steps of administering to said patient a therapeutically effective amount of the antigen binding protein as described herein.

In another aspect of the present invention there is provided a method of treating a human patient afflicted with a disease or disorder of the central nervous system such as multiple sclerosis (MS), Alzheimer's disease (AD) and other dementias and furthermore concerns the use in the treatment of pain, particularly neuropathic and/or inflammatory pain wherein said method comprises the steps of administering to said patient a therapeutically effective amount of the antigen binding protein as described herein.

Use of the antigen binding protein as described herein in the manufacture of a medicament for the treatment of diseases and disorders as described herein is also provided.

For example in one aspect of the invention there is provided the use of the antigen binding protein as described herein for use in the treatment or prophylaxis of diseases and disorders responsive to modulation of the interaction between hOSM and gp130.

In another aspect of the invention there is provided the use of the antigen binding protein as described herein for use in the treatment or prophylaxis of an inflammatory arthropathy such as rheumatoid arthritis, juvenile onset arthritis, osteoarthritis, psoriatic arthritis and ankylosing spondylitis.

In yet another aspect of the invention there is provided the use of the antigen binding protein as described herein for use in the treatment or prophylaxis of a disease or disorder selected from type 1 diabetes, psoriasis, inflammatory bowel disease (IBD) including Crohn’s disease and ulcerative colitis (UC), systemic lupus erythematosus (SLE, Lupus), atopic dermatitis, allergic rhinitis, chronic obstructive pulmonary disease (COPD), pneumonia, eosinophilic esophagitis, Systemic sclerosis (SS) or Idiopathic Pulmonary Fibrosis (IPF), Sjögren's syndrome, scleroderma, vasculitides (including Takayasu arteritis, giant cell (temporal) arteritis, polyarteritis nodosa, Wegener's granulomatosis, Kawasaki disease, isolated CNS vasculitis, Churg-Strauss arteritis, microscopic polyarteritis/polyangiitis, hypersensitivity vasculitis (allergic vasculitis), Henoch-Schonlein purpura, and essential cryoglobulinemic vasculitis), undifferentiated spondyloarthropathy (USpA), ankylosing spondylitis (AS), graft-versus-host disease (GVHD), primary biliary cirrhosis (PBC), primary sclerosing cholangitis (PSC), idiopathic thrombocytopenic purpura (ITP), multiple sclerosis (MS), and asthma wherein said method comprises the step of administering to said patient a therapeutically effective amount of the antigen binding protein as described herein.

For example in a particular aspect, use of the antigen binding protein for use in the treatment or prophylaxis of Osteoarthrtits,(OA), Psoriasis, Idiopathic Pulmonary Fibrosis (IPF) or Multiple Sclerosis (MS) is provided.

Other aspects and advantages of the present invention are described further in the detailed description and the embodiments thereof.

In one aspect, the invention provides a pharmaceutical composition comprising an antigen binding protein of the present invention or a functional fragment thereof and a pharmaceutically acceptable carrier for treatment or prophylaxis of inflammatory diseases and or disorders for example, inflammatory arthropathy such as rheumatoid arthritis, juvenile onset arthritis, osteoarthritis, psoriatic arthritis and ankylosing spondylitis or selected from type 1 diabetes, psoriasis, inflammatory bowel disease (IBD) including Crohn's disease and ulcerative colitis (UC), systemic lupus erythematosus (SLE, Lupus), atopic dermatitis, allergic rhinitis, chronic obstructive pulmonary disease (COPD), pneumonia, eosinophilic esophagitis, Systemic sclerosis (SS) or Idiopathic Pulmonary Fibrosis (IPF), Sjögren's syndrome, scleroderma, vasculitides (including Takayasu arteritis, giant cell (temporal) arteritis, polyarteritis nodosa, Wegener's granulomatosis, Kawasaki disease, isolated CNS vasculitis, Churg-Strauss arteritis, microscopic polyarteritis/polyangiitis, hypersensitivity vasculitis (allergic vasculitis), Henoch-Schonlein purpura, and essential cryoglobulinemic vasculitis), undifferentiated spondyloarthropathy (USpA), ankylosing spondylitis (AS), graft-versus-host disease (GVHD), primary biliary cirrhosis (PBC), primary sclerosing cholangitis (PSC), idiopathic thrombocytopenic purpura (ITP), multiple sclerosis (MS), and asthma

In another embodiment of the present invention there is provided a method of treating a human patient afflicted with an inflammatory disorder or disease which method comprises the step of administering a therapeutically effective amount of the antigen binding protein according to the invention as described herein, for example there is provided a method of treating a human patient afflicted with an inflammatory disorder or disease which method comprises the step of administering a pharmaceutical composition comprising an antigen binding protein according to the invention herein in combination with a pharmaceutically acceptable carrier. In a further embodiment there is provided a method of treating a human patient afflicted with an inflammatory disorder or disease selected from for example, inflammatory arthropathy such as rheumatoid arthritis, juvenile onset arthritis, osteoarthritis, psoriatic arthritis and ankylosing spondylitis or selected from type 1 diabetes, psoriasis, inflammatory bowel disease (IBD) including Crohn's disease and ulcerative colitis (UC), systemic lupus erythematosus (SLE, Lupus), atopic dermatitis, allergic rhinitis, chronic obstructive pulmonary disease (COPD), pneumonia, eosinophilic esophagitis, Systemic sclerosis (SS) or Idiopathic Pulmonary Fibrosis (IPF), Sjögren's syndrome, scleroderma, vasculitides (including Takayasu arteritis, giant cell (temporal) arteritis, polyarteritis nodosa, Wegener's granulomatosis, Kawasaki disease, isolated CNS vasculitis, Churg-Strauss arteritis, microscopic polyarteritis/polyangiitis, hypersensitivity vasculitis (allergic vasculitis), Henoch-Schonlein purpura, and essential cryoglobulinemic vasculitis), undifferentiated spondyloarthropathy (USpA), ankylosing spondylitis (AS), graft-versus-host disease (GVHD), primary biliary cirrhosis (PBC), primary sclerosing cholangitis (PSC), idiopathic thrombocytopenic purpura (ITP), multiple sclerosis (MS), and asthma

In an alternative aspect of the invention there is provided a method for humanising a non-human antibody or antibody fragment thereof which method comprises the steps of:
a) incorporating one or more non-human CDR's onto a human acceptor framework to produce a chimeric or humanised antibody
b) binding the chimeric or humanised antibody to its antigen
c) determining the residues of the antibody involved directly in binding to the antigen
d) mutating one or more of the residues not involved in step (c) to human germline sequence;
e) recovering said antibody.

In a further aspect the residues of the antibody involved in binding to antigen may be determined by crystallography, homology modelling, protein docking, mutagenesis or linear peptide mapping.
For example in one such aspect of the invention as herein described the crystallographic structure of the antibody-antigen co crystal.is obtained and residues involved in binding are determined to be between about 2-5Å

The term non-human encompasses any antibody which can be mutated or substituted in some way as to bring it closer to a human germline sequence. In this way decreasing the likelihood of immunogenicity.

In one aspect at least one CDR is reverted to germline. In a further aspect at least two CDR's are reverted to germline. In yet a further aspect at least 5 residues are reverted to germline, for example at least 7 or at least 8 or at least 9 or at least 10 residues are reverted to germline.

Transfer of non-human monoclonal antibodies or fragments thereof onto a human acceptor often additionally rely on the introduction of changes within the framework to re-establish proper CDR region-antigen interactions these are often referred to as back mutations. In one embodiment of the present invention back mutations are required in order to re-establish proper CDR-region-antigen interactions.

In an alternative embodiment the human acceptor framework may be incorporated onto an antibody with one or more non-human CDR's to produce a chimeric antibody. In yet an alternative embodiment the sequence may be generated by oilgo-synthesis.
CDR's (or hypervariable region residues) of the non-human antibody are incorporated into the VL and/or VH human acceptor frameworks. For example, one may incorporate residues corresponding to

the Kabat CDR residues, the Chothia hypervariable loop residues, the Abm residues, and/or contact residues.

In one embodiment there is provided a method for humanising an antibody which method comprises the steps of:
a) obtaining a non-human antibody which binds to a target antigen
b) obtaining the crystallographic structure of the antibody-antigen co crystal
c) determining to about 2-5Å from the crystal structure the residues of the non-human antibody involved directly in binding to the antigen
e) mutating one or more of the residues not involved in step (c) to a residue derived from a human sequence;
f) recovering said antibody.

In a further embodiment of the methods described herein the antibody or antibody binding fragment retains binding to its antigen. For example the antibody or antibody binding fragment retains binding to its antigen as compared to the non-human antibody. For example the antibody of step f) has a binding affinity (KD) within or better than 10 fold of the non-human antibody of step a), for example the antibody of step f) has a binding affinity (KD) within or better than 3-5 fold of the non-human antibody of step a).
For example the antibody or antibody binding fragment retains binding to its antigen within 1000nM of the non-human antibody when measured by Biacore, or within 500nM of the non-human antibody when measured by Biacore, or within 100nM of the non-human antibody when measured by Biacore. For example the antibody or antibody binding fragment retains binding to its antigen within 500pM of the non-human antibody when measured by Biacore, or within 300pM of the non-human antibody when measured by Biacore, or within 100pM of the non-human antibody when measured by Biacore. For example the antibody of step f) binds to its antigen with an affinity (KD) that is equal to or less than 400pM or equal to or less than 300pM, or is equal to or less than 200pM or is equal to or less than 140pM.
In another embodiment of the methods described herein the antibody or antibody binding fragment retains the same canonical structures as the non-human antibody or antibody fragment.

In yet another embodiment the non-human antibody or antibody fragment thereof is from a non human animal, for example mouse, rat, rabbit, camelid or shark.
In a further embodiment the non-human antibody or antibody fragment thereof is from a mouse.

In yet another embodiment the non-human antibody or antibody fragment thereof is a monoclonal antibody, polyclonal antibody or multispecific antibody or this may be an immunoglobulin single variable domain for example a camelid or shark immunoglobulin single variable domain or it may be a domain which is a derivative of a non-human non antibody protein scaffold.

In yet a further embodiment the non-human antibody is a monoclonal antibody.

In one embodiment of the methods described herein at least 2 non-human CDR’s are incorporated into the human acceptor sequence, or at least 3 CDR’s or at least 4 CDR’s or at least 5’ CDR’s or all 6 CDR’s are incorporated to the human acceptor sequence.

In a further embodiment of the methods described herein the residues to be mutated to a residue derived from a human sequence which are not involved directly in binding antigen and are not already human, may be residues in the CDR’s or in the framework regions or in both. In a further embodiment at least 1 CDR is mutated to human germline sequence, or at least 2 CDR’s are mutated or at least 3 CDR’s are mutated, or at least 4 CDR’s are mutated.
In yet another embodiment at least 5 residues are mutated to human germline sequence, or at least 7 residues, or at least 10 residues or at least 15 residues or at least 20 residues or at least 40 residues or at least 60 residues are mutated to human germline sequence.

In yet another embodiment of the methods described herein the residues of the antibody involved directly with binding to the antigen are determined to between about 2-5Å, or between about 3-5Å or between about 3-4Å or at about 3.5Å.

In yet a further embodiment of the methods described herein there is provided an antibody obtainable by such a method.

Definitions

The term “antigen binding protein” as used herein refers to antibodies, antibody fragments and other protein constructs which are capable of binding to and neutralising human OSM.

The terms Fv, Fc, Fd, Fab, or F(ab)2 are used with their standard meanings (see, e.g., Harlow et al., Antibodies A Laboratory Manual, Cold Spring Harbor Laboratory, (1988)).

The term “antibody” is used herein in the broadest sense and specifically covers monoclonal antibodies (including full length monoclonal antibodies), polyclonal antibodies, multispecific antibodies (e.g. bispecific antibodies)

The term “monoclonal antibody” as used herein refers to an antibody obtained from a population of substantially homogenous antibodies i.e. the individual antibodies comprising the population are identical except for possible naturally occurring mutations that may be present in minor amounts. Monoclonal antibodies are highly specific being directed against a single antigenic binding site. Furthermore, 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.

A "chimeric antibody" refers to a type of engineered antibody in which a portion of the heavy and/ or light chain is identical with or homologous to corresponding sequences in antibodies derived from a particular donor antibody class or subclass, while the remainder of the chain(s) is identical with or homologous to corresponding sequences in antibodies derived from another species or belonging to another antibody class or subclass, as well as fragments of such antibodies, so long as they exhibit the desired biological activity (*US Patent No. 4, 816,567 and Morrison et al. Proc. Natl. Acad. Sci. USA 81:6851-6855) (1984)).*

A "humanised antibody" refers to a type of engineered antibody having its CDRs derived from a non-human donor immunoglobulin, the remaining immunoglobulin-derived parts of the molecule being derived from one (or more) human immunoglobulin(s). In addition, framework support residues may be altered to preserve binding affinity (see, e.g., Queen et al., Proc. Natl Acad Sci USA, 86:10029-10032 (1989), Hodgson et al., Bio/Technology, 9:421 (1991)). A suitable human acceptor antibody may be one selected from a conventional database, e.g., the KABAT® database, Los Alamos database, and Swiss Protein database, by homology to the nucleotide and amino acid sequences of the donor antibody. A human antibody characterized by a homology to the framework regions of the donor antibody (on an amino acid basis) may be suitable to provide a heavy chain constant region and/or a heavy chain variable framework region for insertion of the donor CDRs. A suitable acceptor antibody capable of donating light chain constant or variable framework regions may be selected in a similar manner. It should be noted that the acceptor antibody heavy and light chains are not required to originate from the same acceptor antibody. The prior art describes several ways of producing such humanised antibodies – see for example EP-A-0239400 and EP-A-054951.

"Identity," means, for polynucleotides and polypeptides, as the case may be, the comparison calculated using an algorithm provided in (1) and (2) below:

(1) Identity for polynucleotides is calculated by multiplying the total number of nucleotides in a given sequence by the integer defining the percent identity divided by 100 and then subtracting that product from said total number of nucleotides in said sequence, or:

$$n_n \leq x_n - (x_n \bullet y),$$

wherein nn is the number of nucleotide alterations, xn is the total number of nucleotides in a given sequence, y is 0.95 for 95%, 0.97 for 97% or 1.00 for 100%, and • is the symbol for the multiplication operator, and wherein any non-integer product of xn and y is rounded down to the nearest integer prior to subtracting it from xn. Alterations of a polynucleotide sequence encoding a polypeptide may create nonsense, missense or frameshift mutations in this coding sequence and thereby alter the polypeptide encoded by the polynucleotide following such alterations.

(2) Identity for polypeptides is calculated by multiplying the total number of amino acids by the integer defining the percent identity divided by 100 and then subtracting that product from said total number of amino acids, or:

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

wherein na is the number of amino acid alterations, xa is the total number of amino acids in the sequence, y is 0.95 for 95%, 0.97 for 97% or 1.00 for 100%, and • is the symbol for the multiplication operator, and wherein any non-integer product of xa and y is rounded down to the nearest integer prior to subtracting it from xa.

"Isolated" means altered "by the hand of man" from its natural state, has been changed or removed from its original environment, or both. For example, a polynucleotide or a polypeptide naturally present in a living organism is not “isolated,” but the same polynucleotide or polypeptide separated from the coexisting materials of its natural state is "isolated", including but not limited to when such polynucleotide or polypeptide is introduced back into a cell, even if the cell is of the same species or type as that from which the polynucleotide or polypeptide was separated.

Throughout the present specification and the accompanying claims the term “comprising” and “comprises” incorporates “consisting of” and “consists of”. That is, these words are intended to convey the possible inclusion of other elements or integers not specifically recited, where the context allows.

The term “specifically binds” as used throughout the present specification in relation to antigen binding proteins of the invention means that the antigen binding protein binds human OSM (hOSM) with no or insignificant binding to other human proteins. The term however does not exclude the fact that antigen binding proteins of the invention may also be cross-reactive with other forms of OSM, for example primate OSM.

The term “directly interact” as used throughout this specification in relation to antigen binding proteins of the invention means that when the antigen binding protein is bound to human OSM (hOSM) that specific residues on the antigen binding protein are within 3.5Å of specific residues on the hOSM.

The term inhibits as used throughout the present specification in relation to antigen binding proteins of the invention means that the biological activity of OSM is reduced in the presence of the antigen binding proteins of the present invention in comparison to the activity of OSM in the absence of such antigen binding proteins. Inhibition may be due but not limited to one or more of blocking ligand binding, preventing the ligand activating the receptor, down regulating the OSM or affecting effector functionality. The antibodies of the invention may neutralise OSM. Levels of neutralisation can be measured in several ways, for example by use of the assays as set out in the examples below, for example in 2.2.1 in a KB Cell Neutralisation Assay. OSM is able to induce Interleukin 6 release from KB cells via signalling through the Gp130/OSMR complex. The neutralisation of OSM in this assay is measured by assessing the ability of anti-OSM monoclonal antibodies to inhibit IL6 production.

If an antibody or antigen binding fragment thereof is capable of neutralisation then this is indicative of inhibition of the interaction between human OSM and its gp130 receptor. Antibodies which are considered to have neutralising activity against human OSM would have an IC50 of less than 10 micrograms/ml, or less than 5 micrograms/ml, or less than 2 micrograms/ml, or less than 1 micrograms/ml or less than 0.1 micrograms/ml in the KB cell neutralisation assay as set out in Example 2.2.1

"CDRs" are defined as the complementarity determining region amino acid sequences of an antibody which are the hypervariable domains of immunoglobulin heavy and light chains. There are three heavy chain and three light chain CDRs (or CDR regions) in the variable portion of an immunoglobulin. Thus, "CDRs" as used herein may refer to all three heavy chain CDRs, or all three light chain CDRs (or both all heavy and all light chain CDRs, if appropriate).

CDRs provide the majority of contact residues for the binding of the antibody to the antigen or epitope. CDRs of interest in this invention are derived from donor antibody variable heavy and light chain sequences, and include analogs of the naturally occurring CDRs, which analogs also share or retain the same antigen binding specificity and/or neutralizing ability as the donor antibody from which they were derived.
The CDR sequences of antibodies can be determined by the Kabat numbering system (Kabat et al; (Sequences of proteins of Immunological Interest NIH, 1987), alternatively they can be determined using the Chothia numbering system (Al-Lazikani et al., (1997) JMB 273,927-948), the contact definition method (MacCallum R.M., and Martin A.C.R. and Thornton J.M, (1996), Journal of Molecular Biology, 262 (5), 732-745) or any other established method for numbering the residues in an antibody and determining CDRs known to the skilled man in the art
Other numbering conventions for CDR sequences available to a skilled person include “AbM” (University of Bath) and “contact” (University College London) methods. The minimum overlapping region using at least two of the Kabat, Chothia, AbM and contact methods can be determined to provide the “minimum binding unit”. The minimum binding unit may be a sub-portion of a CDR.

Table 1 below represents one definition using each numbering convention for each CDR or binding unit. The Kabat numbering scheme is used in Table 1 to number the variable domain amino acid sequence. It should be noted that some of the CDR definitions may vary depending on the individual publication used.

	Kabat CDR	Chothia CDR	AbM CDR	Contact CDR	Minimum binding unit
H1	31-35/35A/35B	26-32/33/34	26-35/35A/35B	30-35/35A/35B	31-32
H2	50-65	52-56	50-58	47-58	52-56
H3	95-102	95-102	95-102	93-101	95-101
L1	24-34	24-34	24-34	30-36	30-34
L2	50-56	50-56	50-56	46-55	50-55

L3	89-97	89-97	89-97	89-96	89-96

.

Throughout this specification, amino acid residues in antibody sequences are numbered according to the Kabat scheme. Similarly, the terms "CDR", "CDRL1", "CDRL2", "CDRL3", "CDRH1", "CDRH2", "CDRH3" follow the Kabat numbering system as set forth in Kabat et al; Sequences of proteins of Immunological Interest NIH, 1987.

The terms “VH” and “VL” are used herein to refer to the heavy chain variable domain and light chain variable domain respectively of an antibody.

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

The phrase “immunoglobulin single variable domain” refers to an antibody variable domain (VH, VHH, VL) that specifically binds an antigen or epitope independently of a different V region or domain. An immunoglobulin single variable domain can be present in a format (e.g., homo- or hetero-multimer) with other, different variable regions or variable domains where the other regions or domains are not required for antigen binding by the single immunoglobulin variable domain (i.e., where the immunoglobulin single variable domain binds antigen independently of the additional variable domains). A “domain antibody” or “dAb” is the same as an “immunoglobulin single variable domain” which is capable of binding to an antigen as the term is used herein. An immunoglobulin single variable domain may be a human antibody variable domain, but also includes single antibody variable domains from other species such as rodent (for example, as disclosed in WO 00/29004), nurse shark and Camelid VHH dAbs. Camelid VHH are immunoglobulin single variable domain polypeptides that are derived from species including camel, llama, alpaca, dromedary, and guanaco, which produce heavy chain antibodies naturally devoid of light chains. Such VHH domains may be humanised according to standard techniques available in the art, and such domains are still considered to be “domain antibodies” according to the invention. As used herein “VH includes camelid VHH domains. NARV are another type of immunoglobulin single variable domain which were identified in cartilaginous fish including the nurse shark. These domains are also known as Novel Antigen Receptor variable region (commonly abbreviated to V(NAR) or NARV). For further details see Mol. Immunol. 44, 656-665 (2006) and US20050043519A.

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

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

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

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

Avimers are multidomain proteins derived from the A-domain scaffold family. The native domains of approximately 35 amino acids adopt a defined disulphide bonded structure. Diversity is generated by shuffling of the natural variation exhibited by the family of A-domains. For further details see Nature Biotechnology 23(12), 1556 - 1561 (2005) and Expert Opinion on Investigational Drugs 16(6), 909-917 (June 2007)

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

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

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

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

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

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

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

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

The term “antigen binding protein” as used herein refers to antibodies, antibody fragments for example a domain antibody (dAb), ScFv, FAb, FAb2, and other protein constructs. Antigen binding molecules may comprise at least one Ig variable domain, for example antibodies, domain antibodies (dAbs), Fab, Fab', F(ab')2, Fv, ScFv, diabodies, mAbdAbs, affibodies, heteroconjugate antibodies or bispecific antibodies. In one embodiment the antigen binding molecule is an antibody. In another embodiment the antigen binding molecule is a dAb, i.e. an immunoglobulin single variable domain such as a VH, VHH or VL that specifically binds an antigen or epitope independently of a different V region or domain. Antigen binding molecules may be capable of binding to two targets, i.e. they may be dual targeting proteins. Antigen binding molecules may be a combination of antibodies and antigen binding fragments such as for example, one or more domain antibodies and/or one or more ScFvs linked to a monoclonal antibody. Antigen binding molecules may also comprise a non-Ig domain for example a domain which is a derivative of a scaffold selected from the group consisting of CTLA-4 (Evibody); lipocalin; Protein A derived molecules such as Z-domain of Protein A (Affibody, SpA), A-domain (Avimer/Maxibody); Heat shock proteins such as GroEl and GroES; transferrin (trans-body); ankyrin repeat protein (DARPin); peptide aptamer; C-type lectin domain (Tetranectin); human γ-crystallin and human ubiquitin (affilins); PDZ domains; scorpion toxinkunitz type domains of human protease inhibitors; and fibronectin (adnectin); which has been subjected to protein engineering in order to obtain binding to OSM. As used herein “antigen binding protein” will be capable of antagonising and/or neutralising human OSM. In addition, an antigen binding protein may inhibit and or block OSM activity by binding to OSM and preventing a natural ligand from binding and/or activating the gp130 receptor.

The term “Effector Function” as used herein is meant to refer to one or more of Antibody dependant cell mediated cytotoxic activity (ADCC) , Complement–dependant cytotoxic activity (CDC) mediated responses, Fc-mediated phagocytosis and antibody recycling via the FcRn receptor. For IgG antibodies, effector functionalities including ADCC and ADCP are mediated by the interaction of the heavy chain constant region with a family of Fcγ receptors present on the surface of immune cells. In humans these include FcγRI (CD64), FcγRII (CD32) and FcγRIII (CD16). Interaction between the antigen binding protein bound to antigen and the formation of the Fc/ Fcγ complex induces a range of effects including cytotoxicity, immune cell activation, phagocytosis and release of inflammatory cytokines.
The interaction between the constant region of an antigen binding protein and various Fc receptors (FcR) is believed to mediate the effector functions of the antigen binding protein. Significant biological effects can be a consequence of effector functionality, in particular, antibody-dependent cellular cytotoxicity (ADCC), fixation of complement (complement dependent cytotoxicity or CDC), and half-life/clearance of the antigen binding protein. Usually, the ability to mediate effector function requires

binding of the antigen binding protein to an antigen and not all antigen binding proteins will mediate every effector function.

Effector function can be measured in a number of ways including for example via binding of the FcγRIII to Natural Killer cells or via FcγRI to monocytes/macrophages to measure for ADCC effector function. For example an antigen binding protein of the present invention can be assessed for ADCC effector function in a Natural Killer cell assay. Examples of such assays can be found in Shields et al, 2001 The Journal of Biological Chemistry, Vol. 276, p6591-6604; Chappel et al, 1993 The Journal of Biological Chemistry, Vol 268, p25124-25131; Lazar et al, 2006 PNAS, 103; 4005-4010.

Examples of assays to determine CDC function include that described in 1995 J Imm Meth 184:29-38.

Some isotypes of human constant regions, in particular IgG4 and IgG2 isotypes, essentially lack the functions of a) activation of complement by the classical pathway; and b) antibody-dependent cellular cytotoxicity. Various modifications to the heavy chain constant region of antigen binding proteins may be carried out depending on the desired effector property. IgG1 constant regions containing specific mutations have separately been described to reduce binding to Fc receptors and therefore reduce ADCC and CDC (Duncan et al. Nature 1988, 332; 563-564; Lund et al. J. Immunol. 1991, 147; 2657-2662; Chappel et al. PNAS 1991, 88; 9036-9040; Burton and Woof, Adv. Immunol. 1992, 51;1-84; Morgan et al., Immunology 1995, 86; 319-324; Hezareh et al., J. Virol. 2001, 75 (24); 12161-12168).

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

Human IgG1 constant regions containing specific mutations or altered glycosylation on residue Asn297 have also been described to enhance binding to Fc receptors. In some cases these mutations have also been shown to enhance ADCC and CDC(Lazar et al. PNAS 2006, 103; 4005-4010; Shields et al. J Biol Chem 2001, 276; 6591-6604; Nechansky et al. Mol Immunol, 2007, 44; 1815-1817).

In one embodiment of the present invention, such mutations are in one or more of positions selected from 239, 332 and 330 (IgG1), or the equivalent positions in other IgG isotypes. Examples of suitable mutations are S239D and I332E and A330L. In one embodiment the antigen binding protein of the invention herein described is mutated at positions 239 and 332, for example S239D and I332E or in a further embodiment it is mutated at three or more positions selected from 239 and 332 and 330, for example S239D and I332E and A330L. (EU index numbering).

In an alternative embodiment of the present invention, there is provided an antigen binding protein comprising a heavy chain constant region with an altered glycosylation profile such that the antigen binding protein has enhanced effector function. For example, wherein the antigen binding protein has enhanced ADCC or enhanced CDC or wherein it has both enhanced ADCC and CDC effector function. Examples of suitable methodologies to produce antigen binding proteins with an altered glycosylation profile are described in WO2003011878, WO2006014679 and EP1229125, all of which can be applied to the antigen binding proteins of the present invention.

The present invention also provides a method for the production of an antigen binding protein according to the invention comprising the steps of:
a) culturing a recombinant host cell comprising an expression vector comprising the isolated nucleic acid as described herein, wherein the FUT8 gene encoding alpha-1,6-fucosyltransferase has been inactivated in the recombinant host cell; and
b) recovering the antigen binding protein.
Such methods for the production of antigen binding proteins can be performed, for example, using the POTELLIGENT™ technology system available from BioWa, Inc. (Princeton, NJ) in which CHOK1SV cells lacking a functional copy of the FUT8 gene produce monoclonal antibodies having enhanced antibody dependent cell mediated cytotoxicity (ADCC) activity that is increased relative to an identical monoclonal antibody produced in a cell with a functional FUT8 gene. Aspects of the POTELLIGENT™ technology system are described in US7214775, US6946292, WO0061739 and WO0231240 all of which are incorporated herein by reference. Those of ordinary skill in the art will also recognize other appropriate systems.

In one embodiment of the present invention there is provided an antigen binding protein comprising a chimaeric heavy chain constant region for example an antigen binding protein comprising a chimaeric heavy chain constant region with at least one CH2 domain from IgG3 such that the antigen binding protein has enhanced effector function, for example wherein it has enhanced ADCC or enhanced CDC, or enhanced ADCC and CDC functions,. In one such embodiment, the antigen binding protein may comprise one CH2 domain from IgG3 or both CH2 domains may be from IgG3.

Also provided is a method of producing an antigen binding protein according to the invention comprising the steps of:
a) culturing a recombinant host cell comprising an expression vector comprising an isolated nucleic acid as described herein wherein the expression vector comprises a nucleic acid sequence encoding an Fc domain having both IgG1 and IgG3 Fc domain amino acid residues; and
b) recovering the antigen binding protein.
Such methods for the production of antigen binding proteins can be performed, for example, using the COMPLEGENT™ technology system available from BioWa, Inc. (Princeton, NJ) and Kyowa Hakko Kogyo (now, Kyowa Hakko Kirin Co., Ltd.) Co., Ltd. in which a recombinant host cell comprising an expression vector in which a nucleic acid sequence encoding a chimeric Fc domain having both IgG1 and IgG3 Fc domain amino acid residues is expressed to produce an antigen binding protein having enhanced complement dependent cytotoxicity (CDC) activity that is increased relative to an otherwise

identical antigen binding protein lacking such a chimeric Fc domain. Aspects of the COMPLEGENT™ technology system are described in WO2007011041 and US20070148165 each of which are incorporated herein by reference. In an alternative embodiment CDC activity may be increased by introducing sequence specific mutations into the Fc region of an IgG chain. Those of ordinary skill in the art will also recognize other appropriate systems.

It will be apparent to those skilled in the art that such modifications may not only be used alone but may be used in combination with each other in order to further enhance effector function. In one such embodiment of the present invention there is provided an antigen binding protein comprising a heavy chain constant region which comprises a mutated and chimaeric heavy chain constant region for example wherein an antigen binding protein comprising at least one CH2 domain from IgG3 and one CH2 domain from IgG1, wherein the IgG1 CH2 domain has one or more mutations at positions selected from 239 and 332 and 330 (for example the mutations may be selected from S239D and I332E and A330L) such that the antigen binding protein has enhanced effector function, for example wherein it has one or more of the following functions, enhanced ADCC or enhanced CDC, for example wherein it has enhanced ADCC and enhanced CDC. In one embodiment the IgG1 CH2 domain has the mutations S239D and I332E.

In an alternative embodiment of the present invention there is provided an antigen binding protein comprising a chimaeric heavy chain constant region and which has an altered glycosylation profile. In one such embodiment the heavy chain constant region comprises at least one CH2 domain from IgG3 and one CH2 domain from IgG1 and has an altered glycosylation profile such that the ratio of fucose to mannose is 0.8:3 or less, for example wherein the antigen binding protein is defucosylated so that said antigen binding protein has an enhanced effector function in comparison with an equivalent antigen binding protein with an immunoglobulin heavy chain constant region lacking said mutations and altered glycosylation profile, for example wherein it has one or more of the following functions, enhanced ADCC or enhanced CDC, for example wherein it has enhanced ADCC and enhanced CDC In an alternative embodiment the antigen binding protein has at least one IgG3 CH2 domain and at least one heavy chain constant domain from IgG1 wherein both IgG CH2 domains are mutated in accordance with the limitations described herein.

In one aspect of the invention there is provided a method of producing an antigen binding protein according to the invention described herein comprising the steps of:

a) culturing a recombinant host cell containing an expression vector containing an isolated nucleic acid as described herein, said expression vector further comprising a Fc nucleic acid sequence encoding a chimeric Fc domain having both IgG1 and IgG3 Fc domain amino acid residues, and wherein the FUT8 gene encoding alpha-1,6-fucosyltransferase has been inactivated in the recombinant host cell;and

b) recovering the antigen binding protein .

Such methods for the production of antigen binding proteins can be performed, for example, using the ACCRETAMAB™ technology system available from BioWa, Inc. (Princeton, NJ) which combines the POTELLIGENT™ and COMPLEGENT™ technology systems to produce an antigen binding protein having both ADCC and CDC enhanced activity that is increased relative to an otherwise identical monoclonal antibody lacking a chimeric Fc domain and which has fucose on the oligosaccharide

In yet another embodiment of the present invention there is an antigen binding protein comprising a mutated and chimeric heavy chain constant region wherein said antigen binding protein has an altered glycosylation profile such that the antigen binding protein has enhanced effector function, for example wherein it has one or more of the following functions, enhanced ADCC or enhanced CDC. In one embodiment the mutations are selected from positions 239 and 332 and 330, for example the mutations are selected from S239D and I332E and A330L. In a further embodiment the heavy chain constant region comprises at least one CH2 domain from IgG3 and one Ch2 domain from IgG1. In one embodiment the heavy chain constant region has an altered glycosylation profile such that the ratio of fucose to mannose is 0.8:3 or less for example the antigen binding protein is defucosylated, so that said antigen binding protein has an enhanced effector function in comparison with an equivalent non-chimaeric antigen binding protein or with an immunoglobulin heavy chain constant region lacking said mutations and altered glycosylation profile.

Another means of modifying antigen binding proteins of the present invention involves increasing the in-vivo half life of such proteins by modification of the immunoglobulin constant domain or FcRn (Fc receptor neonate) binding domain.

In adult mammals, FcRn, also known as the neonatal Fc receptor, plays a key role in maintaining serum antibody levels by acting as a protective receptor that binds and salvages antibodies of the IgG isotype from degradation. IgG molecules are endocytosed by endothelial cells, and if they bind to FcRn, are recycled out into circulation. In contrast, IgG molecules that do not bind to FcRn enter the cells and are targeted to the lysosomal pathway where they are degraded.

The neonatal FcRn receptor is believed to be involved in both antibody clearance and the transcytosis across tissues (see Junghans R.P (1997) Immunol.Res 16. 29-57 and Ghetie et al (2000) Annu.Rev.Immunol. 18, 739-766). Human IgG1 residues determined to interact directly with human FcRn includes Ile253, Ser254, Lys288, Thr307, Gln311, Asn434 and His435. Switches at any of these positions described in this section may enable increased serum half-life and/or altered effector properties of antigen binding proteins of the invention.

Antigen binding proteins of the present invention may have amino acid modifications that increase the affinity of the constant domain or fragment thereof for FcRn. Increasing the half-life of therapeutic and diagnostic IgG's and other bioactive molecules has many benefits including reducing the amount and/or frequency of dosing of these molecules. In one embodiment there is therefore provided an antigen binding according to the invention provided herein or a fusion protein comprising all or a portion (an FcRn binding portion) of an IgG constant domain having one or more of these amino acid modifications and a non-IgG protein or non-protein molecule conjugated to such a modified IgG constant domain, wherein the presence of the modified IgG constant domain increases the in vivo half life of the antigen binding protein.

PCT Publication No. WO 00/42072 discloses a polypeptide comprising a variant Fc region with altered FcRn binding affinity, which polypeptide comprises an amino acid modification at any one or more of amino acid positions 238, 252, 253, 254, 255, 256, 265, 272, 286, 288, 303, 305, 307, 309, 311, 312, 317, 340, 356, 360, 362, 376, 378, 380, 386,388, 400, 413, 415, 424,433, 434,435, 436, 439, and 447 of the Fc region, wherein the numbering of the residues in the Fc region is that of the EU index (Kabat et al).

PCT Publication No. WO 02/060919 A2 discloses a modified IgG comprising an IgG constant domain comprising one or more amino acid modifications relative to a wild-type IgG constant domain, wherein the modified IgG has an increased half-life compared to the half-life of an IgG having the wild-type IgG constant domain, and wherein the one or more amino acid modifications are at one or more of positions 251, 253, 255, 285-290, 308-314, 385-389, and 428-435.

Shields et al. (2001, J Biol Chem ; 276:6591-604) used alanine scanning mutagenesis to alter residues in the Fc region of a human IgG1 antibody and then assessed the binding to human FcRn. Positions that effectively abrogated binding to FcRn when changed to alanine include I253, S254, H435, and Y436. Other positions showed a less pronounced reduction in binding as follows: E233-G236, R255, K288, L309, S415, and H433. Several amino acid positions exhibited an improvement in FcRn binding when changed to alanine; notable among these are P238, T256, E272, V305, T307, Q311, D312, K317, D376, E380, E382, S424, and N434. Many other amino acid positions exhibited a slight improvement (D265, N286, V303, K360, Q362, and A378) or no change (S239, K246, K248, D249, M252, E258, T260, S267, H268, S269, D270, K274, N276, Y278, D280, V282, E283, H285, T289, K290, R292, E293, E294, Q295, Y296, N297, S298, R301, N315, E318, K320, K322, S324, K326, A327, P329, P331, E333, K334, T335, S337, K338, K340, Q342, R344, E345, Q345, Q347, R356, M358, T359, K360, N361, Y373, S375, S383, N384, Q386, E388, N389, N390, K392, L398, S400, D401, K414, R416, Q418, Q419, N421, V422, E430, T437, K439, S440, S442, S444, and K447) in FcRn binding.

The most pronounced effect was found for combination variants with improved binding to FcRn. At pH 6.0, the E380A/N434A variant showed over 8-fold better binding to FcRn, relative to native IgG1, compared with 2-fold for E380A and 3.5-fold for N434A. Adding T307A to this effected a 12-fold improvement in binding relative to native IgG1. In one embodiment the antigen binding protein of the invention comprises the E380A/N434A mutations and has increased binding to FcRn.

Dall'Acqua et al. (2002, J Immunol.;169:5171-80) described random mutagenesis and screening of human IgG1 hinge-Fc fragment phage display libraries against mouse FcRn. They disclosed random mutagenesis of positions 251, 252, 254-256, 308, 309, 311, 312, 314, 385-387, 389, 428, 433, 434, and 436. The major improvements in IgG1-human FcRn complex stability occur in substituting residues located in a band across the Fc-FcRn interface (M252, S254, T256, H433, N434, and Y436) and to lesser extend substitutions of residues at the periphery like V308, L309, Q311, G385, Q386, P387, and N389. The variant with the highest affinity to human FcRn was obtained by combining the M252Y/S254T/T256E and H433K/N434F/Y436H mutations and exhibited a 57-fold increase in affinity

relative to the wild-type IgG1. The in vivo behaviour of such a mutated human IgG1 exhibited a nearly 4-fold increase in serum half-life in cynomolgus monkey as compared to wild-type IgG1.
The present invention therefore provides a variant of an antigen binding protein with optimized binding to FcRn. In a preferred embodiment, the said variant of an antigen binding protein comprises at least one amino acid modification in the Fc region of said antigen binding protein, wherein said modification is selected from the group consisting of 226, 227, 228, 230, 231, 233, 234, 239, 241, 243, 246, 250, 252, 256, 259, 264, 265, 267, 269, 270, 276, 284, 285, 288, 289, 290, 291, 292, 294, 297, 298, 299, 301, 302, 303, 305, 307, 308, 309, 311, 315, 317, 320, 322, 325, 327, 330, 332, 334, 335, 338, 340, 342, 343, 345, 347, 350, 352, 354, 355, 356, 359, 360, 361, 362, 369, 370, 371, 375, 378, 380, 382, 384, 385, 386, 387, 389, 390, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401 403, 404, 408, 411, 412, 414, 415, 416, 418, 419, 420, 421, 422, 424, 426, 428, 433, 434, 438, 439, 440, 443, 444, 445, 446 and 447 of the Fc region as compared to said parent polypeptide, wherein the numbering of the amino acids in the Fc region is that of the EU index in Kabat.,
In a further aspect of the invention the modifications are M252Y/S254T/T256E.
Additionally, various publications describe methods for obtaining physiologically active molecules whose half-lives are modified either by introducing an FcRn-binding polypeptide into the molecules (WO 97/43316; U.S. Patent N° 5,869,046; U.S. Patent N° 5,747,035; WO 96/32478; WO 91/14438) or by fusing the molecules with antibodies whose FcRn-binding affinities are preserved but affinities for other Fc receptors have been greatly reduced (WO 99/43713) or fusing with FcRn binding domains of antibodies (WO 00/09560; U.S. Patent N°4,703,039).
Additionally, methods of producing an antigen binding protein with a decreased biological half-life are also provided. A variant IgG in which His435 is mutated to alanine results in the selective loss of FcRn binding and a significantly reduced serum half-life (Firan et al. 2001, International immunology 13:993). U.S. Pat. No. 6,165,745 discloses a method of producing an antigen binding protein with a decreased biological half-life by introducing a mutation into the DNA segment encoding the antigen binding protein. The mutation includes an amino acid substitution at position 253, 310, 311, 433, or 434 of the Fc-hinge domain.

The term “Non Human antibody or antibody fragment thereof” as used herein is meant to refer to antibodies or fragments thereof which originate from any species other than human wherein human includes chimeric antibodies.
The term "donor antibody" refers to an antibody (monoclonal, and/or recombinant) which contributes the amino acid sequences of its variable domains, CDRs, or other functional fragments or analogs thereof to a first immunoglobulin partner, so as to provide the altered immunoglobulin coding region and resulting expressed altered antibody with the antigenic specificity and neutralizing activity characteristic of the donor antibody.

The term "acceptor antibody" refers to an antibody (monoclonal and/or recombinant) heterologous to the donor antibody, which contributes all (or any portion, but preferably all) of the amino acid sequences encoding its heavy and/or light chain framework regions and/or its heavy and/or light chain constant regions to the first immunoglobulin partner. The human antibody is the acceptor antibody.

The term “Human acceptor sequence” as used herein is meant to refer to a framework of an antibody or antibody fragment thereof comprising the amino acid sequence of a VH or VL framework derived from a human antibody or antibody fragment thereof or a human consensus sequence framework into which CDR’s from a non-human species may be incorporated.

The term “incorporation” of CDR’s or hypervariable regions as used herein encompasses any means by which the non-human CDR’s are situated with the human acceptor framework. It will be appreciated that this can be achieved in various ways, for example, nucleic acids encoding the desired amino acid sequence can be generated by mutating nucleic acids encoding the non-human variable domain sequence so that the framework residues thereof are changed to human acceptor framework residues, or by mutating nucleic acid encoding the human variable domain sequence so that the CDR’s are changed to non-human residues, or by synthesizing nucleic acids encoding the desired sequence. In one embodiment the final sequence is generated in silico.

The present invention is now described by way of example only. The appended claims may include a generalisation of one of more of the following examples.

Examples

Example 1 Monoclonal Antibody Generation and Selection

1.1 Immunisation strategy

The anti human OSM mAb S168110G08(1)1A09 ("10G8") was identified from hybridomas derived from mice immunized with recombinant glycosylated human OSM (K598). Female SJL mice (n=2, Harlan, UK, HOST SP06-06031) were immunised conventionally using a total of 10µg protein intraperitoneally with AS02-like adjuvant. Booster immunisations were with 5µg protein. Test bleeds were taken following each booster and the mouse with the best response (168#4) was chosen for hybridoma fusion (R16092/177-198). The spleen was excised, disrupted and a PEG1500 induced somatic cell fusion performed with mouse myeloma cells X63 AG8 653.GFP.Bcl-2.11 (BioCat 112754; R17209/58). The fusion was plated out into 10 x 96 well plates and 5 Nunc Omnitrays in methylcellulose containing semi-solid medium. Colonies were picked from the semi-solid media into 5 x 96 well plates.

1.2 Screening strategy

1.2.1 Primary screen

The primary screen for the Anti-OSM back-up antibodies was based on selecting hybridoma material capable of binding human OSM and, in order to select for Anti-Site II molecules, inhibiting both human and cynomolgus OSM from binding the gp130 receptor. Positive hybridoma supernatants from these screens were analysed by BIACore off-rate kinetics to select the top binding hybridomas.

In excess of 3000 clones were recovered from fusions, 86 of which showed appreciable binding to human OSM by binding ELISA. Analysis for anti-Site II activity was performed on positive hybridomas by gp130 ELISA with human and cynomolgus OSM, Hybridoma clones which inhibited both human and cynomolgus OSM from binding to human gp13 were subjected to BIACore off-rate kinetic analysis.. The top four human OSM binders by off-rate analysis, 10G8, 9G2, 3E3 and 2B7, were monocloned and re-screened. There was no difference in BIACore and ELISA binding activity or gp130 inhibition between the monoclones from each hybridoma. The daughter clones: 10G8.A9, 9G2.C1, 2B7.A6 and 3E3.A1 were cryopreserved and used for serum free scale-up and purification. These were progressed into secondary screening.

1.2.2 Secondary screen

Secondary screening to rank the four daughter clones, 10G8/A9, 9G2/C1, 2B7/A6 and 3E3/A1, included BIACore kinetic analysis against human/ cynomolgus OSM; Human gp130 ELISA with human/ cynomolgus OSM; KB cell neutralisation assay with human/ cynomolgus OSM. In addition to this, the ability to neutralise endogenous, neutrophil-derived human OSM, retain neutralisation ability in 25% human AB serum and reactivity against human LIF was assessed.

BIACore Analysis:

BIACore analysis demonstrated that 10G8, 9G2, 3E3 and 2B7 had higher affinities for human OSM than an alternative non-competitive anti-OSM mouse antibody (15E10) (**Table 1**). 10G8 showed the greatest affinity for both human (~550pM) and cynomolgus (~310pM) OSM. Compared with 15E10, 10G8 had an 8-fold/ 0.9 log increased affinity for human and an 11-fold/ 1 log increased affinity for cynomolgus OSM. Both 10G8 and 9G2 exhibited an increased affinity for cynomolgus OSM over human OSM.

Table 1: BIACore Kinetics- Four anti-OSM back-up lead antibodies 10G8, 9G2, 3E3 and 2B7 compared with 15E10.

mAb	OSM	ka (on rate)	kd (off-rate)	KD nM
10G8	**Human**	1.12E+05	6.14E-05	**0.55**
	Cyno	9.69E+04	2.99E-05	**0.308**
9G2	**Human**	7.52E+04	1.21E-04	**1.60**
	Cyno	6.14E+04	4.76E-05	**0.75**
3E3	**Human**	1.95E+05	2.53E-04	**1.30**
	Cyno	1.71E+05	5.60E-04	**3.28**
2B7	**Human**	1.21E+05	2.54E-04	**2.09**
	Cyno	1.00E+05	9.33E-04	**9.31**
15E10	**Human**	1.94E+05	8.69E-04	**4.48**
	Cyno	1.77E+05	5.97E-04	**3.37**

Human gp130 ELISA:

The human gp130 ELISA uses relatively high levels of OSM (25ng/ml), reducing its ability to separate high affinity from lower affinity antibodies as the ligand is in excess. Following four repeats of this assay, 10G8 was shown to be the most potent antibody in blocking both human and cynomolgus OSM from binding to gp130 receptor in this assay (**Figure 1**; **Table 2**).

Table 2: Human gp130 ELISA- Summary of four repeats of the human gp130 ELISA to rank 10G8, 9G2, 3E3 and 2B7 activity against human and cynomolgus OSM. A non – competitive mouse antibody 15E10 and a negative control tool antibody were added for comparison purposes.

Human OSM Ranking	Antibody	Human OSM Mean IC50 µg/ml±SD	Cynomolgus OSM Mean IC50 µg/ml±SD (Cyno OSM ranking)
1	**10G8**	0.06±0.01 (400pM)	0.01± 0.00 (1) (40pM)
2	**2B7**	0.08±0.02 (533pM)	0.14±0.04 (6) (993pM)
3	**9G2**	0.16±0.04 (1.1nM)	0.03±0.04 (4) (200pM)
4	**15E10**	0.19±0.07 (1.3nM)	0.03±0.05 (3) (200pM)
5	**3E3**	0.19±0.04 (1.3nM)	0.06±0.07 (5) (400pM)

The human gp130 assay was repeated in the presence of 25% human AB serum. Two repeats of this assay showed that all four lead antibodies 10G8, 9G2, 3E3 and 2B7, along with 15E10, retained their ability to block human and cynomolgus OSM from binding to gp130 (Data not shown).

KB Cell Neutralisation Assay:

OSM induces IL-6 release from KB cells (a human epithelial cell line expressing mRNA for gp130 and OSM receptors). Breifly KB cells are stimulated with 1 ng/ml OSM +/- different antibody concentrations for 16-18 hours at 37^{O}C and IL6 release monitored by ELISA. The KB cell neutralisation assay uses a reduced amount of OSM compared with the gp130 assay (1ng/ml versus 25ng/ml). This makes it a more discriminating assay for separating high affinity from low affinity neutralisers. Compared with Antibody 15E10, 10G8 was 15-fold/ 1.2 log more potent against human OSM in the KB cell neutralisation assay. From three repeats of the assay, 10G8 ranked first in all repeats, giving a mean IC50 value of 8ng/ml against human OSM and 6ng/ml against cynomolgus (**Figure 2**; **Table 3**). 9G2 ranked second in this assay with an IC50 of 18ng/ml and 15ng/ml against human and cynomolgus OSM respectively.

Table 3: KB Cell Neutralisation Assay- Summary of three repeats of the KB cell neutralisation assay to rank 10G8, 9G2, 3E3 and 2B7 activity against human and cynomolgus OSM. Antibody 15E10 was added for comparison purposes. The tool antibody was used as a negative control.

Human OSM Ranking	Antibody	Human OSM Mean IC50 µg/ml±SD	Cynomolgus OSM Mean IC50 µg/ml±SD (Cyno OSM ranking)
1	**10G8**	0.008±0.003 (53pM)	0.006±0.002 (1) (40pM)
2	**9G2**	0.018±0.008 (120pM)	0.015±0.006 (2) (100pM)
3	**2B7**	0.049±0.003 (327pM)	0.344±0.186 (6) (2.3nM)
4	**3E3**	0.054±0.034 (360pM)	0.150±0.013 (5) (1nM)
6	**15E10**	0.279±0.161(1.9nM)	0.035±0.013 (4) (233pM)

In the presence of 25% human AB serum, 10G8, 9G2 and 3E3 retained their ability to neutralise both human and cynomolgus OSM (**Figure 3**). 15E10 and 2B7 failed to produce fitted curves of sufficient quality to calculate IC50 values. As with the non- human serum KB cell assay, the most potent antibody was 10G8 with 9G2 ranking second. Some drop-off in activity was seen in the presence of 25% AB serum. To some extent this may be due to the AB serum interfering with this assay readout. Higher IL-6 background levels were observed in this assay than in the non-human serum.

Endogenous Human OSM (gp130 Assay):

All four lead antibodies, 10G8, 9G2, 3E3 and 2B7, as well as Antibody 15E10, inhibited endogenous human OSM from four separate donors (**Figure 4**). This native OSM was generated from GM-CSF-stimulation of healthy human neutrophils.

Human LIF Reactivity (KB Cell Neutralisation Assay):

Human LIF is the closest related member of the IL-6 family to human OSM. Initial studies showed that there was no reactivity between 10G8, 9G2, 3E3 and 2B7 and human LIF, indicating that these antibodies are OSM-specific (**Figure 5**).

Marmoset OSM Reactivity (KB Cell Neutralisation Assay):

All four lead molecules 10G8, 9G2, 3E3 and 2B7 were shown to neutralise marmoset OSM in the KB cell neutralisation assay (**Figure 6**). 15E10 and a panel of three additional anti-human OSM antibodies, 10D3DLE, OM4.11.17 and OM4.11.31, also failed to neutralise marmoset OSM.

From two assay repeats, 10G8 was the most potent neutraliser of marmoset OSM, with 9G2 being ranked second.

1.2.3 Monoclonals selected for progression

From the four antibodies, 10G8 was chosen as the lead antibody for chimaerisation based on it ranking first in all of the assays listed above. 9G2 was also selected for chimaerisation as a back-up molecule in the case of difficulties in humanisation.

1.3 Antibody Engineering and Lead Antibody Series Selection

1.3.2 Variable region sequences

The variable genes for the four selected monoclonals, 2B7, 3E3, 9G2 and 10G8 were isolated and sequenced in parallel to allow generation of the corresponding chimaeric antibodies. Total RNA was extracted from the hybridoma cell pellets. Heavy and light chain V-gene coding sequences were amplified by either RT-PCR or 5'RACE and then TA cloned for sequence analysis. V-gene amplification was carried out in duplicate for each antibody to enable subsequent verification of the correct sequences from two independent reactions. Sequence of the variable heavy and variable light chains was obtained for all 4 hybridoma clones. Alignment of the protein sequences showed that the antibodies had a high degree of sequence identity in the both the variable heavy and light chain regions (**Figures 7 & 8**). The sequences of the heavy and light chain variable regions of these antibodies are set out in SEQ ID NO. 26-48. See Table A.

Sequence comparison between the four lead monoclonals and Antibody 15E10 show only 50-60% identity with either the light (**Figure 9**) or the heavy (**Figure 10**) chains. This indicates that these antibodies bind epitopes distinct from those recognised by Antibody 15E10.

1.3.3 Antibody Cloning

1.3.3.1 Construction of chimaera

Both 10G8 and 9G2 were generated as chimaeric antibodies by grafting the mouse VH and VL regions described above onto codon optimised human gamma 1 Fc wild type and human kappa constant regions respectively. The chimaeric antibodies are used to confirm functionality of the cloned mouse V-regions and were purified and used as a reference when testing humanized constructs. PCR primers were designed based on the 5' and 3' DNA sequences determined in 2.3.1 to include restriction sites required for cloning into the Rlx and pTT5 mammalian expression vectors. Primers were also designed to replace the native signal sequence with the Campath signal sequence. Hind III and Spe I sites were designed to frame the V_H domain and allow cloning into a modified Rld or pTT5 vector containing the human γ1 C region. The introduction of a Spe I site into the framework 4 sequence resulted in a single amino acid change in FR4 at position 108. For the 9G2 VH region, an internal SpeI site was present at the 5'-end of the DNA sequence, the PCR primer for the 9G2 chimera was designed to remove this internal SpeI site. Hind III and BsiWI sites were designed to frame the V_L domain and allow cloning into a modified RIn or pTT5 vector containing the human κ C region.

Clones with the correct V_H and V_L sequences were identified and plasmids prepared for expression in CHO or HEK cells.

1.3.3.2 Expression of chimaera

The RId and RIn plasmids encoding chimaeric 10G8 and 9G2 V_H and V_L domains, respectively were co-transfected into CHOE1A cells by electroporation and expressed in a polyclonal cell culture. The pTT plasmids encoding the chimaeric 10G8 and 9G2 V_H and V_L domains were co-transfected into HEK293 cells using lipid transfection methodology to allow transient episomal expression, transfection in the episomal expression system can potentially yield mg quantities of antibody. The chimaeric antibodies (10G8c and 9G2c) produced were purified from the cell culture supernatants by affinity chromatography on Protein A Sepharose. Purified antibodies were QCed by SDS-PAGE analysis and size exclusion chromatography.

1.3.3.3 Binding assay data

Human OSM Binding ELISA:

Both the 10G8 and 9G2 chimaeras successfully bound to human OSM, to a greater extent than 15E10chimera (15E10c) (**Figure 11**). This was a direct ELISA where human OSM was coated at 1μg/ml and bound antibodies detected using anti-human IgG.

BIACore Analysis:

BIACore analysis showed that there was little or no loss in human or cynomolgus OSM binding in the chimaeric 10G8 and 9G2 molecules compared with the mouse parental antibodies (**Table 4**). 10G8 chimaera ranks first (654pM), ahead of 9G2 chimaera (1.33nM). All antibodies exhibited an increased affinity for cynomolgus OSM over human OSM.

Table 4: BIACore Kinetics- Binding kinetics of 10G8, 10G8 Chimaera, 9G2 & 9G2 Chimaera antibodies.

	Cyno OSM			**Human OSM**		
	Ka (M-1.s-1)	Kd (s-1)	**KD (nM)**	Ka (M-1.s-1)	Kd (s-1)	**KD (nM)**
10G8 chimera	2.37E+5	1.14E-4	**0.480**	2.33E+5	1.52E-4	**0.654**
Mouse 10G8	9.69e+4	2.99e-5	**0.308**	1.12e+5	6.14e-5	**0.549**
9G2 chimera	1.27E+5	9.99E-5	**0.787**	1.26E+5	1.68E-4	**1.333**
Mouse 9G2	6.14e+4	4.76e-5	**0.775**	7.52e+4	1.21e-4	**1.60**

1.3.3.4 Functional assay data

Human gp130 ELISA:

The human gp130 ELISA uses relatively high levels of OSM (25ng/ml), reducing its ability to separate high affinity from lower affinity antibodies as the ligand is in excess. Following three repeats of this assay, the 10G8 chimaera was the most effective antibody at inhibiting both human and cynomolgus OSM from binding to gp130 receptor. Values for 10G8 mouse parental and 10G8 chimaera were very similar in this assay (**Figure 12**; **Table 5**). There was no significant difference between 9G2 and its chimaera.

Table 5: Human gp130 ELISA- Summary of three repeats of the human gp130 ELISA to rank 10G8, 10G8 Chimaera, 9G2 & 9G2 Chimaera activity against human and cynomolgus OSM. Antibody 15E10 was added for comparison purposes. A tool antibody was used as a negative control.

Human OSM Ranking	Antibody	Human OSM Mean IC50 µg/ml±SD	Cynomolgus OSM Mean IC50 µg/ml±SD (Cyno OSM ranking)
1	**10G8Chimaera**	0.037±0.035 (247pM)	0.016±0.015 (1) (107pM)
2	**9G2**	0.038±0.004 (253pM)	0.049±0.059 (5) (327pM)
3	**10G8**	0.044±0.034 (293pM)	0.017±0.013 (2) (113pM)
4	**9G2Chimaera**	0.078±0.102 (520pM)	0.028±0.033 (3) (187pM)
5	**15E10**	0.250±0.403 (1.7nM)	0.071±0.096 (6) (473pM)

The human gp130 assay was repeated in the presence of human AB serum for both human and cynomolgus OSM. All molecules retained their activity in 25% serum. Against human and cynomolgus OSM, 10G8 chimaera and 10G8 mouse parental ranked first and second respectively. IC50 values for these two antibodies were similar. No significant difference was observed between the 9G2 chimaera, ranked third, and its mouse parental (Data not shown).

KB Cell Neutralisation Assay:

The 10G8 mouse parental behaved similarly to the chimaera (**Figure 13**; **Table 6**). 9G2 mouse parental and chimaera ranked third and fourth, respectively, in this assay.

Table 6: KB Cell Neutralisation Assay- Summary of three repeats of the KB cell neutralisation assay to rank 10G8, 10G8 Chimaera, 9G2 & 9G2 Chimaera activity against human and cynomolgus OSM. Antibody 15E10 was added for comparison purposes. A tool antibody was used as a negative control.

Human OSM Ranking	Antibody	Human OSM Mean IC50 µg/ml±SD	Cynomolgus OSM Mean IC50 µg/ml±SD (Cyno OSM ranking)
1	**10G8Ch**	0.021±0.008 (140pM)	0.008±0.007 (1) (53pM)
2	**10G8**	0.054±0.066 (360pM)	0.034±0.047 (3) (227pM)
3	**9G2**	0.163±0.197 (1.1nM)	0.046±0.025 (4) (307pM)
4	**9G2Ch**	0.231±0.287 (1.5nM)	0.031±0.008 (2) (207pM)
5	**15E10**	Out of Range	0.057±0.036 (5) (380pM)

In the presence of 25% human AB serum, 10G8, 10G8 Chimaera, 9G2 & 9G2 Chimaera retained their ability to neutralise both human and cynomolgus OSM (**Figure 14**). Some drop-off in activity was seen in the presence of 25% AB serum. While IC50 values could not be calculated with a 1µg/ml antibody starting concentration, a clear titration neutralisation effect was seen for all antibodies except the unrelated negative control. This drop-off in activity may, to some extent, be due to the AB serum interfering with this assay readout. Higher IL-6 background levels were observed in this assay than in the non-human serum.

Endogenous Human OSM (gp130 Assay):

10G8, 10G8 Chimaera, 9G2 & 9G2 Chimaera, inhibited endogenous human OSM from two separate donors (**Figure 15**). For these two donors, 10G8 and 10G8 chimaera ranked joint first, while 9G2 and its chimaera ranked third and fourth respectively (**Table 7**). This native OSM was generated from GM-CSF-stimulation of healthy human neutrophils.

Table 7: Endogenous OSM Human gp130 Assay- Summary of two neutrophil donors in the gp130 ELISA to assess of 10G8, 10G8 Chimaera, 9G2 & 9G2 Chimaera activity against endogenous human OSM. A tool antibody was used as a negative control.

Ranking	mAb	IC50 µg/ml±SD
1=	**10G8**	0.009±0.001 (60pM)
1=	**10G8Ch**	0.009±0.000 (60pM)
3	**9G2Ch**	0.017±0.001 (113pM)
4	**9G2**	0.020±0.004 (133pM)

Human LIF Reactivity (KB Cell Neutralisation Assay):

Human LIF is the closest related member of the IL-6 family to human OSM. Three repeats of the Human LIF KB cell assay showed that 10G8, 10G8 chimaera, 9G2, and 9G2 chimaera did not neutralise human LIF. A commercially available anti-human LIF antibody did neutralise LIF in this assay (**Figure 16**). This proves that these antibodies are OSM-specific.

<u>Example 2: Humanisation</u>

2.1.1 Heavy chain Humanisation Strategy

Following a BLAST analysis of the human V gene germline databases, human germline IGHV3_7) which had 74% identity (including CDRs) with the mouse 10G8 variable heavy chain sequence was selected as the preferred acceptor framework for humanisation. The germline V region was combined in silico with a suitable FR4, in this case the JH2 minigene (Kabat Vol.II) based on sequence similarity. The first six residues of the JH2 minigene residues fall within the CDR3 region which is replaced by the incoming CDR from the donor antibody. Three humanised heavy chain variants were generated on the basis of sequence comparison and possible impact on antibody function. Construct H0 was a straight graft of mouse CDRs from 10G8 (using the Kabat definition) into the human acceptor framework selected above. Constructs H1 and H2 are based on H0, both incorporate one additional framework mutation which were different in each construct; positions 2 and 105 respectively.

2.1.2 Light Chain Humanisation

Following a BLAST analysis of the human V gene germline databases, human germline IGKV4_1) which had 64% identity (including CDRs) with the mouse 10G8 variable light chain sequence was selected as the preferred acceptor framework for humanisation. The germline V region was combined in silico with a suitable FR4, in this case the J-region kappa 4 minigene (Kabat Vol.II) based on sequence similarity. The first two residues of the JK-4 minigene residues fall within the CDR3 region and are identical to the last two residues in the mouse 10G8 light chain CDR3. Five humanised light chain variants were generated on the basis of sequence comparison and possible impact on antibody function. Construct L0 was a straight graft of mouse CDRs from 10G8 (using the Kabat definition) into the human acceptor framework selected above. Constructs L1, L2 and L3 are based on L0, each incorporates one additional framework mutation which were different in each construct; positions 46, 84 and 103 respectively. Construct L4 incorporates all three of the above back mutations.

2.1.3 Construction of humanised vectors

The DNA sequences of the humanised variable regions were sequence optimised using the LETO 1.0 software (Entelechon GmbH) and synthesised *de novo* by build up of overlapping oligonucleotide and PCR amplification. Primers included restriction sites for cloning into mammalian expression vectors and human immunoglobulin signal sequences for secretion. The humanised variable heavy regions H0-H2 were cloned into mammalian expression vectors containing the human gamma 1 constant region using HindIII and SpeI. In parallel, the humanised variable light regions L0-L4 were cloned into mammalian expression vectors containing the human kappa constant region using HindIII and BsiWI.

2.1.4 Initial screening of the panel of humanised variants

To screen and narrow the panel of humanised variants (3 heavy chain x 5 light chains = 15), the antibodies were expressed in HEK cells and assessed by BIACore, ELISAs and functional assays.

2.2 Humanised 10G8 Antibodies Bioassays: Chimaera to Humanised mAbs

2.2.1 Secondary screen

The secondary screening to rank the humanised 10G8 antibodies, listed in Table 9, included BIACore kinetic analysis against human OSM; human gp130 ELISA with human/ cynomolgus OSM; KB cell neutralisation assay with human/ cynomolgus OSM. In addition to this, the ability to block gp130 binding in 25% human AB serum was assessed.

<u>BIACore Analysis:</u>

Initial BIACore analysis on transfection supernatants demonstrated that L1 and L4 humanised variants had higher affinities for human OSM than L0, L2 and L3 humanised variants (**Table 8**). These light chain mutations improved affinity compared with the straight-graft alone (H0L0) and the 10G8 chimaera. The heavy chain variants, H1 and H2, had little impact on the affinity of the antibodies over the straight-graft, H0.

Analysis on the scaled-up purified L1 and L4 variants showed that there were very few differences between the affinities of these mAbs to both human and cyno OSM (**Table 9**).

Table 8: BIACore Kinetics- *Human OSM binding kinetics of fifteen anti-OSM back-up humanised 10G8 antibodies transfection supernatants compared with the 10G8 Chimæra.*

	Ka (M-1.s-1)	Kd (s-1)	**KD (nM)**
H0L0	3.69E+5	1.60E-4	**0.435**
H0L1	3.98E+5	9.95E-5	**0.250**
H0L2	3.65E+5	1.37E-4	**0.375**
H0L3	3.74E+5	1.45E-4	**0.388**
H0L4	4.13E+5	1.11E-4	**0.268**
H1L0	3.81E+5	1.62E-4	**0.425**
H1L1	4.00E+5	9.99E-5	**0.250**
H1L2	3.65E+5	1.63E-4	**0.445**
H1L3	3.71E+5	1.27E-4	**0.344**
H1L4	3.77E+5	1.30E-4	**0.344**
H2L0	3.63E+5	1.45E-4	**0.398**
H2L1	3.94E+5	1.13E-4	**0.286**
H2L2	3.68E+5	1.42E-4	**0.387**
H2L3	3.76E+5	1.50E-4	**0.398**
H2L4	4.48E+5	1.01E-4	**0.226**
10G8 Chimæra supernatant	2.52E+5	1.03E-4	0.407
10G8 Chimæra purified	2.57E+5	1.05E-4	0.407

Table 9: BIACore Kinetics- *Cynomolgus and Human OSM binding kinetics of the purified batches of anti-OSM humanised 10G8 L1 and L4 variant antibodies compared with the 10G8 Chimæra*

	Cyno OSM			**Human OSM**		
	Ka (M-1.s-1)	**Kd (s-1)**	**KD (nM)**	**Ka (M-1.s-1)**	**Kd (s-1)**	**KD (nM)**
H0L1	4.26E+5	1.07E-4	0.251	3.87E+5	1.37E-4	0.355
H1L1	4.28E+5	1.10E-4	0.258	3.75E+5	1.66E-4	0.443
H2L1	4.14E+5	1.24E-4	0.299	3.83E+5	1.40E-4	0.365
H0L4	4.18E+5	1.01E-4	0.242	3.74E+5	1.40E-4	0.374
H1L4	4.21E+5	1.11E-4	0.264	3.65E+5	1.35E-4	0.370
H2L4	4.41E+5	9.01E-5	0.205	3.80E+5	1.35E-4	0.356
10G8 chimera	2.53E+5	9.95E-5	0.394	2.41E+5	1.25E-4	0.518
15E10h	5.26E+5	3.10E-4	0.590	4.29E+5	6.15E-4	1.43

KB Cell Neutralisation Assay:

The KB cell neutralisation assay uses a reduced amount of OSM compared with the gp130 assay (1ng/ml versus 25ng/ml). This makes it a more discriminating assay for separating high affinity from low affinity neutralisers. A KB cell assay screen of the initial H0, H1, H2, L0, L1, L2, L3 and L4 variant constructs showed superiority in the L1 constructs (Data not shown). These, along with the L4 variants which performed well in the BIACore analysis, were produced in larger batches for further assays. From three repeats of the assay, Humanised 10G8 L1 variants ranked first, giving a mean IC50 value of 14ng/ml against human OSM and 10ng/ml against cynomolgus (**Figure 17**; **Table 10**).

Table 10: KB Cell Neutralisation Assay- *Summary of three repeats of the KB cell neutralisation assay to rank Humanised 10G8 L1 and L4 Variants activity against human and cynomolgus OSM.*

Human OSM Ranking	Antibody	Human OSM Mean IC50 µg/ml±SD	Cynomolgus OSM Mean IC50 µg/ml±SD (Cyno OSM ranking)
1	H1L1	0.013±0.001 (83pM)	0.010±0.002 (3) (67pM)
2	H2L1	0.014±0.007 (93pM)	0.013±0.003 (6) (14pM)
3	H0L1	0.015±0.009 (102pM)	0.007±0.002 (1) (21pM)
4	H1L4	0.016±0.015 (107pM)	0.011±0.007 (4) (10pM)
5	H0L4	0.018±0.012 (118pM)	0.012±0.009 (5) (49pM)
6	H2L4	0.022±0.015 (147pM)	0.016±0.015 (7) (58pM)
7	10G8 Chimaera	0.022±0.022 (144pM)	0.008±0.005 (2) (100pM)

The Humanised 10G8 L1 variants were selected for further testing as they showed greater biological activity in the KB cell assay compared with the L4 variants. The L4 variants had a very low production yield in the CHO-E1a system and this also ruled them out for further progression.

Human gp130 ELISA:

The human gp130 ELISA uses relatively high levels of OSM (25ng/ml), reducing its ability to separate high affinity from lower affinity antibodies, as the ligand is in excess. Following two repeats of this assay with the Humanised 10G8 L1 variants, all three variants were shown to be equipotent in blocking both human and cynomolgus OSM from binding to gp130 receptor in this assay (**Figure 18**). The human gp130 assay was also carried out in the presence of 25% human AB serum. Two repeats of this assay showed that all antibodies, Humanised 10G8 H0L1, H1L1 and H2L1 variants retained their ability to block human and cynomolgus OSM from binding to gp130 (Data not shown).

2.3 Isolation of Fab Fragments and Crystallisation of 10G8 mAb-OSM Complex

2.3.2 Generation of Fab Fragments

Fab fragments from the 10G8 parental antibody were generated by digestion with bead immobilized papain (Pierce 20341) for 20h at 37C in a buffer containing 20mM phosphate buffer pH 7, 10mM

EDTA and 10mM L-cysteine. Following digestion the beads were removed using a disposable plastic column, contaminating Fc fragments and undigested antibody were then removed from the Fab fragments using Protein A type chromatography (MabSelect, GE Healthcare 17-5438-03). The unbound fraction, containing the Fab fragments, were further purified using Superdex 200pg Size Exclusion Chromatography (SEC) (GE Healthcare 17-1069-01) using 25mM HEPES pH 7.7, 150mM NaCl buffer as the mobile phase. The complex was made by mixing 11.5mg purified Fabs (GRITS30249) with 5.75mg recombinant OSM (GRITS23122), a molar ratio of 1:1, for 1.5h at 4C. The complex was then purified from uncomplexed material using Superdex 200pg SEC. Resolved complex was concentrated to 44mg/ml total protein (yield 9.2mg) using a centrifugal concentration device fitted with a 10kmwco membrane (Vivaspin VS2002). Complex components were validated using N-terminal sequencing, mass spectrometry and SDS-PAGE. OSM functional binding activity of the Fab fragments was confirmed using the gp130 inhibition assay (data not shown).

2.3.2 10G8-OSM Complex Crystallisation

10G8 OSM Fab fragments were complexed with OSM, and this was crystallised at 20°C using PEG3500 as a precipitate. Crystallisation was optimised, sent for analysis at the European Synchrotron Radiation Facility (ESRF) and the structure solved at 3.5 Å. The 10G8 mAb bound helices B and C of OSM with good surface complimentarity and blocked OSM Site II from binding gp130 receptor purely by steric hindrance, with no direct interaction with any residues from Site II. The only residues directly involved in binding (distance of less than 5 Å)when resolved at 3.5 Å are illustrated in **Table 11** and **Figure 19**. The light chain was responsible for most of this blocking effect. Four CDRs bound helices B and C of OSM, CDRH2, H3 and CDRL1 and L3, either directly or through water mediation interactions. There was no significant distortion of the OSM molecule on binding 10G8 mAb. As two of the CDRs were non-binding, CDRH1 and L2, variants of the antibody were be made where one or both of these were reverted back to a human sequence. This may lead to a less immunogenic molecule than the straight humanised graft.

Table 11:

OSM residues	Resno(Type)	Atom	Antibody residues (L=light chain, H=heavy chain)	Resno(Type)	Atom	Distance In Angstroms
A	82(LEU)	C	H	104(THR)	CG2	3.45
A	82(LEU)	O	H	104(THR)	CG2	3.47
A	83(HIS).	CA	H	59(TYR)	OH	3.20
A	83(HIS).	CB	H	59(TYR)	OH	3.37
A	83(HIS).	CE1	H	103(THR).	CG2	3.43
A	83(HIS).	NE2	H	106(TRP).	CH2	3.44
A	83(HIS).	CD2	H	59(TYR).	OH	3.30
A	83(HIS).	C	H	59(TYR).	OH	3.26

A	83(HIS).	O	H	59(TYR).	OH	2.62
A	84(ARG).	NH1	H	57(PHE).	CE1	3.47
A	90(GLN).	OE1	H	60(TYR).	O	3.30
A	90(GLN).	NE2	H	65(ARG).	NH2	3.08
A	94(LYS).	NZ	H	62(ASP).	OD2	3.38
A	115(ARG).	NE	H	104(THR).	OG1	3.19
A	115(ARG).	NH2	H	105(PHE).	CD1	3.49
A	115(ARG).	NH2	H	105(PHE).	CE1	3.25
A	115(ARG).	NH2	H	104(THR).	O	3.21
A	122(ARG).	NH2	H	103(THR).	OG1	3.14
A	152(THR).	OG1	H	58(THR).	OG1	3.19
A	112(GLN).	O	L	96(ARG).	NH2	3.08
A	115(ARG).	NH2	L	96(ARG).	O	3.30
A	123(ASN).	CG	L	34(TYR).	OH	3.18
A	123(ASN).	ND2	L	34(TYR).	OH	2.56

2.3.3

2.3.4 Humanised 10G8 Antibody: Human CDR Substitutions

The in-house solved crystal structure of the anti-OSM 10G8 mAb complexed with OSM, identified CDRH1 and CDRL2 as not being directly involved in antigen binding. Suitable human germline CDRs were selected to replace these mouse germline CDRs. Two CDRH1 and two CDRL2 human germline sequences were tested for their effects on antigen binding. For both heavy and light chain CDRs the sequences from the original human germline acceptor framework were tested (IGHV3_7 and IGKV4_1 respectively) and also two further human germline sequences which were selected based on CDR and flanking framework homology (IGHV3_23 and IGKV1_5).The human germline CDRH1 and CDRL2 sequences were exchanged for the respective mouse CDRs in the humanized H0 and L1 V-regions. The new V-regions were synthesised *de novo* by build up of overlapping oligonucleotide and PCR amplification as in section 1.1.4.

2.4 Humanised 10G8 Antibodies Bioassays: Humanised 10G8 H0L1 mAb to Humanised 10G8 mAb with Humanised Non-Binding CDR

2.4.1 Secondary screen

<u>BIACore Analysis:</u>

BIACore analysis on transfection supernatants from the various humanised 10G8 H0L1 CDRH1 and CDRL2 constructs demonstrated that the only antibody to fully retain the human OSM affinity of the pre-candidate mAb was H0(IGHV3_23)L1 molecule (**Table 12**). This construct, along with two further molecules with the next best KD values, H0L1(IGKV4_1) and H0(IGHV3_23)L1(IGK4_1), were scaled-up and purified for further study.

Table 12: BIACore Kinetics- *Cynomolgus and Human OSM binding kinetics of the transfection supernatants of anti-OSM back-up humanised 10G8 H0L1 CDRH1 and CDRL2 variant antibodies compared with the 10G8 Chimæra.*

	Cyno OSM			Human OSM		
	Ka	Kd	KD	Ka	Kd	KD

	(M-1.s-1)	(s-1)	(nM)	(M-1.s-1)	(s-1)	(nM)
H0 IGHV3_7 +L1	**3.37E+7**	**0.8146**	24.2	**9.10E+4**	**9.67E-4**	10.6
H0 IGHV3_23 +L1	**3.52E+5**	**1.09E-4**	0.310	**3.61E+5**	**1.58E-4**	0.437
H0+L1 IGKV4_1	**1.50E+5**	**2.12E-4**	1.41	**1.61E+5**	**2.21E-4**	1.37
H0+L1 IGKV1_5	**6.75E+4**	**5.57E-4**	8.26	**6.87E+4**	**6.40E-4**	9.33
H0 IGHV3_7 +L1 IGKV4_1	**5.07E+4**	**1.77E-3**	34.9	**3.68E+4**	**1.63E-3**	44.4
H0 IGHV3_7 +L1 IGKV1_5	**low capture level**			**low capture level**		
H0 IGHV3_23 +L1 IGKV4_1	**1.52E+5**	**2.23E-4**	1.47	**1.59E+5**	**2.47E-4**	1.56
H0 IGHV3_23 +L1 IGKV1_5	**6.67E+4**	**5.93E-4**	8.89	**7.11E+4**	**6.60E-4**	9.27
H0+L1	**3.45E+5**	**1.04E-4**	0.301	**3.32E+5**	**1.53E-4**	0.461
H0L1 purified	**3.38E+5**	**1.15E-4**	0.341	**3.40E+5**	**1.51E-4**	0.445

KB Cell Neutralisation Assay:

The KB cell neutralisation assay demonstrated that the humanised 10G8 H0(IGHV3_23)L1 construct (labelled as H0('CDRH1)L1) shows very similar potency to the parent Humanised 10G8 H0L1 (labelled as H0L1) mAb. Any reversion of the non-binding CDRL2 to the human sequence showed a decrease in neutralisation activity, as seen from the data for the H0L1(IGKV4_1) (labelled H0L1(huCDRL2)) and H0(IGHV3_23)L1(IGK4_1) (Labelled H0(huCDRH1)L1(huCDRL2)) antibodies (**Figure 20, Table 13**).

Table 13: KB Cell Neutralisation Assay- *Summary of three repeats of the KB cell neutralisation assay to rank Humanised 10G8 H0L1 CDRH1 and CDRL2 Variants activity against human and cynomolgus OSM.*

Human OSM Ranking	**Antibody**	**Human OSM Mean IC50 µg/ml±SD**	**Cynomolgus OSM Mean IC50 µg/ml±SD (Cyno OSM ranking)**
1	**H0(huCDRH1)L1**	0.008±0.005 (53pM)	0.007±0.000 (1) (47pM)
2	**H0L1**	0.009±0.002 (60pM)	0.007±0.002 (2) (47pM)
3	**H0L1(huCDRL2)**	0.054±0.024 (360pM)	0.081±0.004 (4) (540pM)
4	**H0(huCDRH1)L1(huCDRL2)**	0.077±0.038 (513pM)	0.114±0.045 (5) (760pM)

From these data, the Humanised 10G8 H0(huCDRH1)L1 was chosen as the lead pre-candidate mAb for full characterisation.

2.5 Humanised 10G8 Antibodies Bioassays: Humanised 10G8 H0(IGHV3_23)L1 mAb

2.5.1 Secondary screen

BIACore Analysis:

BIACore analysis was carried out on purified H0(IGHV3_23)L1 mAb and ranked against the 10G8 chimaera and Humanised 10G8 H0L1 parent mAb. There was little or no difference between H0(IGHV3_23)L1 mAb and the parent H0L1 mAb in affinity for both human and cyno OSM (**Table 6**). H0(IGHV3_23)L1 mAb had a 6.5-fold (0.8 log) increased affinity for human OSM compared to an alternative non-competitive anti-OSM humanised antibody 15E10h A new batch of OSM was used for this study, resulting in lower KD values however, the differences between the humanised variants and the non-competitive antibody remained the same.

Table 14: BIACore Kinetics- *Cynomolgus and Human OSM binding kinetics of purified* H0(IGHV3_23)L1 mAb *compared with 10G8 Chimæra and* compared with the Humanised 10G8 H0L1 parent mAb and to an alternative non-competitive anti-OSM humanised antibody 15E10h.

	Cyno OSM			**Human OSM**		
	Ka (M-1.s-1)	**Kd (s-1)**	**KD (pM)**	**Ka (M-1.s-1)**	**Kd (s-1)**	**KD (pM)**
10G8 chimaera	2.50E+05	6.63E-05	**266**	4.27E+05	7.87E-05	**184**
H0 (CDRH1 IGHV3_23) L1	4.23E+05	8.39E-05	**199**	7.09E+05	9.65E-05	**136**
H0L1	4.27E+05	8.31E-05	**195**	7.12E+05	8.90E-05	**125**
15E10h	5.07E+05	3.24E-04	**640**	7.36E+05	6.49E-04	**882**

Kinexa Analysis

Kinexa (Sapidyne Instruments 3200) solution phase affinity was used to determine the overall affinity of anti-OSM antibody H0(huCDRH1)L1 and Humanised 15E10 (an unrelated OSM antibody) to human, cynomolgus macaque, rhesus macaque and marmoset OSM (**Table 15**). Humanised 15E10 was added for comparison purposes.

OSM beads were prepared either by adsorption (polymethylmethacrylate beads-PMMA) or amine coupling (NHS-activated sepharose beads). The range of OSM molecules studied necessitated the generation of beads coated with different concentrations of OSM. For the solution phase portion of the assay, a fixed concentration of antibody was incubated with a broad range of OSM concentrations and allowed to reach equilibrium by incubation at r.t. for at least 2 h before analysis proceeded. The OSM beads were then used to determine the amount of free antibody present in the solution phase samples, by means of the free antibody binding to the OSM bead matrix then detected using an appropriate secondary antibody (either anti-human or anti-mouse depending on the construct being tested) labelled with a fluorescent dye. The binding curves where fitted using the Kinexa Pro analysis software inherent to the machine. Multiple runs using varying starting concentrations of antibody were then compiled and analysed using the n-curve analysis software to give a more accurate determination of affinity.

H0(huCDRH1)L1 shows a higher affinity for human OSM as was previously assessed by Biacore analysis. Unlike Biacore where the antibody was bound to the chip surface, Kinexa uses free antibody and ligand in a fluid phase to assess affinity, which is more akin to the natural state

Table 15: Kinexa Kinetics- *Human, cynomolgus, rhesus and marmoset OSM binding kinetics of purified anti-OSM back-up antibody H0(huCDRH1)L1 and Humanised 15E10.*

Construct	**Antigen**	**KD (pM)**	**95% high (pM)**	**95% low (pM)**
H0(huCDRH1)L1	Human OSM	**38**	62	22
H0(huCDRH1)L1	Cyno OSM	**53**	82	31
H0(huCDRH1)L1	Marmoset OSM	**21**	31	14
H0(huCDRH1)L1	Rhesus OSM	**122**	161	90
Humanised 15E10	Human OSM	**727**	1000	499
Humanised 15E10	Cyno OSM	**102**	157	61
Humanised 15E10	Marmoset OSM	****6100**	468000	<22.5
Humanised 15E10	Rhesus OSM	**102**	181	52

** The affinity is very poor for marmoset OSM which means that for a receptor driven experiment more than 40nM of antibody would be needed to use uM amounts of OSM.

Overall conclusion is that the binding of 15E10 humanised to marmoset OSM is significantly poorer than it is to human OSM.

<u>Human gp130 ELISA:</u>

The human gp130 ELISA uses an excess of OSM (25ng/ml), thus reducing its ability to separate high affinity from lower affinity antibodies. Following three repeats of the gp130 assay, it was confirmed that the 10G8 mouse parental, the 10G8 Chimera, the Humanised 10G8 H0L1 parent (H0L1) and H0(huCDRH1)L1 were all potent in blocking both human and cynomolgus OSM from binding to gp130 receptor in this assay (**Figure 21**). Due to the high levels of antigen in this assay, there were no clear ranking could be discerned.

The human gp130 assay was repeated in the presence of 25% human AB serum and 25% human pooled synovial fluid. Three repeats of this assay for each matrix showed that all antibodies, the 10G8 mouse parental, the 10G8 Chimera, the Humanised 10G8 H0L1 parent (H0L1) and H0(huCDRH1)L1 along with 15E10h retained their ability to block human and cynomolgus OSM from binding to gp130 (Data not shown).

KB Cell Neutralisation Assay:

The KB cell neutralisation assay is a more discriminating assay for separating high affinity from low affinity neutralisers than the gp130 assay, due to the low (1ng/ml) levels of OSM used. From three repeats of the assay, (H0(huCDRH1)L1 gave a mean IC50 value of 30ng/ml against human OSM, 41ng/ ml against cynomolgus OSM and 36ng/ml against marmoset OSM (**Figure 22**; **Table 17**).

Table 17: KB Cell Neutralisation Assay- *Summary of three repeats of the KB cell neutralisation assay to rank H0(huCDRH1)L1 activity against human, cynomolgus and marmoset OSM. 15E10h was added for comparison purposes*

Human OSM Ranking	**Antibody**	**Human OSM Mean IC50 µg/ml±SD**	**Cynomolgus OSM Mean IC50 µg/ml±SD (Cyno OSM ranking)**	**Marmoset OSM Mean IC50 µg/ml±SD (Marm OSM ranking)**
1	**10G8**	0.0026±0.0009 (17pM)	0.0017±0.0006 (3) (11pM)	0.0017±0.0003 (1) (11pM)
2	**H0L1**	0.0028±0.0004 (19pM)	0.0014±0.0003 (2) (9pM)	0.0017±0.0008 (2) (11pM)
3	**(H0(huCDRH1)L1**	0.0030±0.0015 (20pM)	0.0041±0.0025 (4) (27pM)	0.0036±0.0024 (3) (24pM)
4	**10G8Ch**	0.0052±0.0064 (35pM)	0.0011±0.0004 (1) (7pM)	0.0271±0.0450 (4) (181pM)
5	**15E10h**	0.0391±0.0207 (261pM)	0.0054±0.0020 (5) (36pM)	No Neutralisation

In the presence of 25% human AB serum or 25% pooled human synovial fluid, (H0(huCDRH1)L1 and 15E10h retained their ability to neutralise both human and cynomolgus OSM (**Figure 23**). Some drop-off in activity was seen in the presence of either 25% AB serum or 25% pooled synovial fluid. This is most probably due to these matrices interfering with this assay readout. Higher IL-6 background levels were observed in this assay than in the normal assay.

Unlike 15E10h, H0(huCDRH1)L1 has been shown to neutralise marmoset OSM in the KB cell neutralisation assay. A panel of three additional anti-human OSM antibodies, 10D3DLE, OM4.11.17 and OM4.11.31, also failed to neutralise marmoset OSM.

Endogenous Human OSM gp130 Assay:

The 10G8 mouse parental, the 10G8 Chimaera, the Humanised 10G8 H0L1 parent (H0L1) and H0(huCDRH1)L1 as well as 15E10h inhibited endogenous human OSM from four separate donors (**Figure 24**). From the results of these four donors, there was very little difference between the H0L1 parent and the H0(huCDRH1)L1 mAbs; these ranked higher than the 10G8 mouse parental and its chimaera (**Table 18**). H0(huCDRH1)L1 had approximately 12-fold (1.09 log) increase in potency compared with 15E10h. The native OSM was generated from GM-CSF-stimulation of healthy human neutrophils.

Table 18: Endogenous OSM Human gp130 Assay- *Summary of four neutrophil donors in the gp130 ELISA to assess the 10G8 mouse parental, 10G8 Ch, the Humanised 10G8 H0L1 parent (H0L1) and H0(huCDRH1)L1 activity against endogenous human OSM. 15E10h* was added for comparison purposes. *An unrelated antibody was used as a negative control.*

Ranking	mAb	IC50 µg/ml±SD
1	**H0L1**	0.0058±0.0019 (39pM)
2	**H0(huCDRH1)L1**	0.0062±0.0023 (41pM)
3	**10G8**	0.0090±0.0020 (60pM)
4	**10G8Ch**	0.0091±0.0004 (61pM)
5	**15E10h**	0.0760±0.0181 (507pM)

Human LIF Reactivity (KB Cell Neutralisation Assay):

Human LIF is the closest related member of the IL-6 family to human OSM. Three repeats of the Human LIF KB cell assay showed that the 10G8 mouse parental, the 10G8 Chimaera, the Humanised 10G8 H0L1 parent (H0L1) and H0(huCDRH1)L1 or 15E10h did not neutralise human LIF.15E10h was added for comparison purposes. A commercially available anti-human LIF antibody did neutralise LIF in this assay (**Figure 25**). This proves that these antibodies are OSM-specific.

Primary Human Hepatocyte Assay:

Human primary hepatocytes are sensitive to OSM and release acute phase proteins, such as SAA and CRP, in response to OSM stimulation. H0(huCDRH1)L1 inhibited human OSM-induced SAA (**Figure 26**) and CRP (**Figure 27**) release in hepatocytes in a dose-dependent manner from three separate donors. Humanised 15E10 was added for comparison purposes.

Equivalent assays were carried out using other primary human cell types. These included human umbilical vein endothelial cells; human fibroblast like synoviocytes from rheumatoid arthritis patients; human lung fibroblasts from healthy and idiopathic lung fibrosis patients (data not shown). As with the previous assays, H0(huCDRH1)L1 shows superior neutralisation of OSM over humanised 15E10. The fold difference in the potency between H0(huCDRH1)L1 and humanised 15E10 varies depending on cell line and OSM concentration.

2.6 Biophysical Characterisation

A basic biophysical profile of H0(huCDRH1)L1 was carried out along with the Humanised 10G8 H0L1 parent mAb. The antibodies were subjected to environmental stresses, such as:

- Temperature, by incubation for 14 days at 4°C or 37°C;
- Five freeze-thaw cycles;
- Forced deamidation, by incubation with 1% ammonium bicarbonate at 37°C for 48 hours.

Neither antibody showed loss in biophysical alteration or loss in activity following the above mentioned stresses.

2.6 CDRH3 Variant Humanised Antibodies

2. 6.1 Construction of CDRH3 variant humanised antibodies

Substitution of each residue of CDRH3 (SEQ ID NO:3) to an alternative amino acid residue was carried out using the heavy chain H0 (IGHV3_23) full length sequence SEQ ID NO. 75 (variable sequence: SEQ ID NO: 74) on a pTT plasmid (National Research Council Canada, with a modified Multiple Cloning Site (MCS)) as a base molecule. The site-directed mutagenesis technique (SDM) was used whereby oligonucleotides are designed bearing the sequence NNK (N = A/T/G/C; K = G or T) at the amino acid substitution position. Polymerase chain reaction (PCR) was used to generate new plasmids containing the change, and DNA sequencing was used to identify clones with amino acid changes. In this way, variants were isolated having between 10 and 17 different amino acids at each of the 12 CDRH3 positions. CDRH3 variant antibodies were produced by co-transfecting pTT vectors comprising an H0 (IGHV3_23) variant with the L1 light chain (SEQ ID NO: 72) and testing supernatants for binding.

164 CDRH3 variants were generated and tested in the subsequent analysis (see 2.6.2 and 2.6.3).

2.6.2 CDRH3 variant expression in HEK 293 6E cells

pTT plasmids encoding the heavy chain (H0 (IGHV3_23)) CDRH3 variants and light chain L1 were transiently co-transfected into HEK 293 6E cells and expressed at small scale to produce antibody. Antibodies were assessed directly from the tissue culture supernatant.

2.6.3 Kinetic analysis of CDRH3-variant tissue Culture Supernatants

The initial kinetic analyses for the CDRH3 screen were carried out on the ProteOn XPR36 (Biorad Laboratories) and certain supernatants were selected for more accurate kinetic analysis on the BiaCore T100.

For the ProteOn analysis, anti-human IgG (GE Healthcare/Biacore BR-1008-39) was coupled to a GLM chip (Biorad Laboratories 176-5012) by primary amine coupling. The CDRH3 variants were captured directly on to this surface and recombinant human OSM was passed over the captured antibody surface at 256, 64, 16, 4 and 1nM, with a buffer injection alone (i.e. 0nM) used to double reference the binding curves. Following the OSM binding event, the capture surfaces were regenerated: with 3M $MgCl_2$ the regeneration removed the previously captured antibody ready for another cycle of capture and binding analysis. The data was then fitted to the 1:1 model (with mass transport) inherent to the ProteOn analysis software. The run was carried out using HBS-EP (Biacore/GE-Healthcare BR-1006-69) and the analysis temperature was 25°C.

A similar method was used for analysis of constructs using the Biacore T100, anti-human IgG (GE Healthcare/Biacore BR-1008-39) was coupled to a CM5 chip (GE Healthcare/Biacore BR-1006-68) by primary amine coupling, antibodies were captured on this surface and recombinant human OSM was passed over the captured antibody surface at 256, 64, 16, 4 and 1nM, with a buffer injection alone (i.e. 0nM) used to double reference the binding curves. Regeneration was by using pulses of 3M 3M $MgCl_2$ or 100mM phosphoric acid or using both reagents. The data was fitted to the 1:1 model

inherent to the Biacore T100 analysis software. The run was carried out using HBS-EP (Biacore/GE-Healthcare BR-1006-69) and the analysis temperature was 25°C.
See Figure 33 for binding data results.

Sequence Summary (Table A)

Description	Amino acid sequence	Polynucleotide sequence
10G8 CDRH1	SEQ.I.D.NO:1	n/a
10G8 CDRH2	SEQ.I.D.NO:2	n/a
10G8 CDRH3	SEQ.I.D.NO:3	n/a
10G8 CDRL1	SEQ.I.D.NO:4	n/a
10G8 CDRL2	SEQ.I.D.NO:5	n/a
10G8 CDRL3	SEQ.I.D.NO:6	n/a
3E3 CDRH1	SEQ.I.D.NO:7	n/a
3E3 CDRH2	SEQ.I.D.NO:8	n/a
3E3 CDRH3	SEQ.I.D.NO:9	n/a
3E3 CDRL1	SEQ.I.D.NO:10	n/a
3E3 CDRL2	SEQ.I.D.NO:11	n/a
3E3 CDRL3	SEQ.I.D.NO:12	n/a
2B7 CDRH1	SEQ.I.D.NO:13	n/a
2B7 CDRH2	SEQ.I.D.NO:14	n/a
2B7 CDRH3	SEQ.I.D.NO:15	n/a
2B7 CDRL1	SEQ.I.D.NO:16	n/a
2B7 CDRL2	SEQ.I.D.NO:17	n/a
2B7 CDRL3	SEQ.I.D.NO:18	n/a
9G2 CDRH1	SEQ.I.D.NO:19	n/a
9G2 CDRH2	SEQ.I.D.NO:20	n/a
9G2 CDRH3	SEQ.I.D.NO:21	n/a
9G2 CDRL1	SEQ.I.D.NO:22	n/a
9G2 CDRL2	SEQ.I.D.NO:23	n/a
9G2 CDRL3	SEQ.I.D.NO:24	n/a
10G8 V_H domain (murine)	SEQ.I.D.NO:26	SEQ.I.D.NO:25
10G8 V_L domain (murine)	SEQ.I.D.NO:28	SEQ.I.D.NO:27
3E3 V_H domain (murine)	SEQ.I.D.NO:30	SEQ.I.D.NO:29
3E3 V_L domain (murine)	SEQ.I.D.NO:32	SEQ.I.D.NO:31
2B7 V_H domain (murine)	SEQ.I.D.NO:34	SEQ.I.D.NO:33
2B7 V_L domain (murine)	SEQ.I.D.NO:36	SEQ.I.D.NO:35
9G2 V_H domain (murine)	SEQ.I.D.NO:38	SEQ.I.D.NO:37
9G2 V_L domain (murine)	SEQ.I.D.NO:40	SEQ.I.D.NO:39
10G8 V_H domain (chimera)	SEQ.I.D.NO:42	SEQ.I.D.NO:41
10G8 V_L domain (chimera)	SEQ.I.D. NO:44	SEQ.I.D.NO:43
9G2 V_H domain (chimera)	SEQ.I.D.NO:46	SEQ.I.D.NO:45
9G2 V_L domain (chimera)	SEQ.I.D. NO:48	SEQ.I.D.NO:47

IGHV3_7 human variable heavy chain germline acceptor nucleotide sequence	SEQ.I.D. NO:50	SEQ.I.D.NO:49
IGKV4_1 human variable light chain germline acceptor nucleotide sequence	SEQ.I.D. NO:52	SEQ.I.D.NO:51
10G8 Humanised V_H H0 (nucleotide sequence was leto codon optimised)	SEQ.I.D.NO:54	SEQ.I.D.NO:53
10G8 Humanised V_H H1 (nucleotide sequence was leto codon optimised)	SEQ.I.D.NO:56	SEQ.I.D.NO:55
10G8 Humanised V_H H2 (nucleotide sequence was leto codon optimised)	SEQ.I.D.NO:58	SEQ.I.D.NO:57
10G8 Humanised V_L L0 (nucleotide sequence was leto codon optimised)	SEQ.I.D. NO:60	SEQ.I.D.NO:59
10G8 Humanised V_L L1 (nucleotide sequence was leto codon optimised)	SEQ.I.D. NO:62	SEQ.I.D.NO:61
10G8 Humanised V_L L2 (nucleotide sequence was leto codon optimised)	SEQ.I.D. NO:64	SEQ.I.D.NO:63
10G8 Humanised V_L L3 (nucleotide sequence was leto codon optimised)	SEQ.I.D. NO:66	SEQ.I.D.NO:65
10G8 Humanised V_L L4 (nucleotide sequence was leto codon optimised)	SEQ.I.D. NO:68	SEQ.I.D.NO:67
Mature H0 heavy chain (nucleotide sequence was leto codon optimised)	SEQ.I.D. NO:70	SEQ.I.D.NO:69
Mature L1 light chain (nucleotide sequence was leto codon optimised)	SEQ.I.D. NO:72	SEQ.I.D.NO:71
Humanised VH variant H0 (IGHV3_23 CDRH1) (nucleotide sequence was leto codon optimised)	SEQ.I.D. NO:74	SEQ.I.D.NO:73
Mature H0 (IGHV3_23 CDRH1) heavy chain (nucleotide sequence was leto codon optimised)	SEQ.I.D. NO:76	SEQ.I.D.NO:75
Human heavy chain germline IGHV3_23 CDRH1	SEQ.I.D. NO:77	n/a
Human light chain germline IGKV1_5 CDRL2	SEQ.I.D. NO:78	n/a
15E10h Heavy chain	SEQ.I.D.NO:79	n/a

15E10h Light chain	SEQ.I.D.NO:80	n/a
15E10 Humanised VH B3	SEQ.I.D.NO:81	n/a
15E10 Humanised VL L2	SEQ.I.D.NO:82	n/a
Human OSM	SEQ.I.D.NO:84	SEQ.I.D.NO:83

Sequence Listing

SEQ ID NO: 1 10G8 CDRH1

NYAMS

SEQ ID NO: 2 10G8 CDRH2

TISDGGSFTYYLDNVRG

SEQ ID NO: 3 10G8 CDRH3

DVGHTTFWYFDV

SEQ ID NO: 4 10G8 CDRL1

RASKSVSAAGYNFMH

SEQ ID NO: 5 10G8 CDRL2

YASNLES

SEQ ID NO: 6 10G8 CDRL3

LHSREFPFT

SEQ ID NO: 7 3E3 CDRH1

SYAMS

SEQ ID NO: 8 3E3 CDRH2

TISDGGSFTYYFANIQG

SEQ ID NO: 9 3E3 CDRH3

DVGLTTFWYFDV

SEQ ID NO: 10 3E3 CDRL1

RASKSVSPSGYDFMH

SEQ ID NO: 11 3E3 CDRL2

YASELES

SEQ ID NO: 12 3E3 CDRL3

QHSREFPFT

SEQ ID NO: 13 2B7 CDRH1

NYAMS

SEQ ID NO: 14 2B7 CDRH2

TISDGGGYTYYLDNGQG

SEQ ID NO: 15 2B7 CDRH3

DVGLTTFWYFDV

SEQ ID NO: 16 2B7 CDRL1

RASKSVSPSSYNFMH

SEQ ID NO: 17 2B7 CDRL2

YASNLES

SEQ ID NO: 18 *2B7 CDRL3*

QHSREFPFT

SEQ ID NO: 19 *9G2 CDRH1*

NYAMS

SEQ ID NO: 20 *9G2 CDRH2*

TISDGGSFTYYLDNVKG

SEQ ID NO: 21 *9G2 CDRH3*

DVGHTTFWYFDV

SEQ ID NO: 22 *9G2 CDRL1*

RASKSVSASGYNFMH

SEQ ID NO: 23 *9G2 CDRL2*

YASNLES

SEQ ID NO: 24 *9G2 CDRL3*

QHSREFPFT

SEQ ID NO: 25 10G8 V_H nucleotide sequence

GAAATGCAACTGGTGGAGTCTGGGGAAGGCTTAGTGGAGCCTGGAGGGTCCCTGAAACTCTCC
TGTGCAGCCTCTGGATTCACTTTCAGTAACTATGCCATGTCTTGGGTTCGCCAGACTCCGGAAAA
GAGCCTGGAGTGGGTCGCAACCATTAGTGATGGTGGTAGTTTCACCTACTATCTAGACAATGTAA
GGGGCCGATTCACCATCTCCAGAGACAATGCCAAGAACAACCTGTATTTGCAAATGAGCCATTTG
AAGTCTGACGACACAGCCATGTATTACTGTGCAAGAGATGTGGGACATACTACCTTTTGGTACTT
CGATGTCTGGGGCTCAGGGACCGCGGTCACCGTCTCCTCA

SEQ ID NO: 26 10G8 V_H amino acid sequence

EMQLVESGEGLVEPGGSLKLSCAASGFTFSNYAMSWVRQTPEKSLEWVATISDGGSFTYYLDNVRG
RFTISRDNAKNNLYLQMSHLKSDDTAMYYCARDVGHTTFWYFDVWGSGTAVTVSS

SEQ ID NO: 27 10G8 V_L nucleotide sequence

GACATTGTGCTGACACAGTCTCCTGTTTTCTTAGTTGTATCTCTGGGGCAGAGGGCCACCATCTC
CTGTAGGGCCAGCAAAAGTGTCAGTGCAGCTGGCTATAATTTCATGCACTGGTACCAACAGAAA

CCAGGACAGCCGCCCAAAGTCCTCATCAAGTATGCATCCAACCTAGAATCTGGGGTCCCTGCCA
GGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCATCCTGTGGAGGAGGAGG
ATGCTGTAACATATTACTGTCTGCACAGTAGGGAGTTTCCGTTCACGTTCGGAGGGGGGACCAA
CCTGGAAATAAAA

SEQ ID NO: 28 10G8 V_L amino acid sequence

DIVLTQSPVFLVVSLGQRATISCRASKSVSAAGYNFMHWYQQKPGQPPKVLIKYASNLESGVPARFS
GSGSGTDFTLNIHPVEEEDAVTYYCLHSREFPFTFGGGTNLEIK

SEQ ID NO: 29 3E3 V_H nucleotide sequence

GAAGTGCAGCTGGTGGAGTCTGGGGGAGACTTAGTGAAACCTGGAGGGTCCCTGAAACTCTCC
TGTGTACCCTCTGGATTCACTTTCAGTAGTTATGCCATGTCTTGGGTTCGCCAGACTCCGGAAAA
GAGGCTGGAGTGGGTCGCAACCATTAGTGATGGTGGTAGTTTCACCTACTATTTTGCCAATATAC
AGGGCCGATTCACCATCTCCAGAGACAATACCAAGAACAACCTATACCTGCAAATGAACCATCTG
AAGTCTGAGGACGCAGGCATGTATTACTGTGCAAGAGATGTGGGCCTTACTACGTTTTGGTATTT
CGATGTCTGGGGCACAGGGACCACGGTCACCGTCTCCTCA

SEQ ID NO: 30 3E3 V_H amino acid sequence

EVQLVESGGDLVKPGGSLKLSCVPSGFTFSSYAMSWVRQTPEKRLEWVATISDGGSFTYYFANIQG
RFTISRDNTKNNLYLQMNHLKSEDAGMYYCARDVGLTTFWYFDVWGTGTTVTVSS

SEQ ID NO: 31 3E3 V_L nucleotide sequence

GACATTGTGCTGACACAGTCTCCTGCTTCCTTAACTATATCTCTGGGGCAGAGGGCCACCATCTC
CTGCAGGGCCAGCAAAAGTGTCAGTCCATCTGGCTATGATTTCATGCACTGGTATCAACAGAAG
CCAGGACAGCCGCCCAAACTCCTCATCAAGTATGCATCCGAACTAGAATCTGGGGTCCCTGGCA
GGTTCAGTGGCAGTGGGTCTGGGACAGATTTCACCCTCAACATCCATCCTGTGGAGGAAGAAGA
TGCTGCAACATATTTCTGTCAGCACAGTAGGGAGTTTCCGTTCACGTTCGGAGGGGGGACCAAG
CTGGAAATAAAA

SEQ ID NO: 32 3E3 V_L amino acid sequence

DIVLTQSPASLTISLGQRATISCRASKSVSPSGYDFMHWYQQKPGQPPKLLIKYASELESGVPGRFSG
SGSGTDFTLNIHPVEEEDAATYFCQHSREFPFTFGGGTKLEIK

SEQ ID NO: 33 2B7 V_H nucleotide sequence

GAAGTGCAGCTGGTGGAGTCTGGGGGAGGCTTAGTGAAACCTGGAGGGTCCCTGAAACTCTCC
TGTGCAGCCTCTGGATTCACTTTCAGTAACTATGCCATGTCTTGGGTTCGCCAGACTCCGGAAAA
GAGGCTGGAGTGGGTCGCGACCATTAGTGATGGTGGTGGTTACACCTACTATTTAGACAATGGA
CAGGGCCGATTCACCATCTCCAGAGACAATGCCAAGAACAACCTGTACCTGCAGATGAGCCATC
TGAAGTCTGAGGACACAGCCATGTATTACTGTGCAAGAGATGTGGGACTTACTACGTTTTGGTAC
TTCGATGTCTGGGGCACAGGGACCACGGTCACCGTCTCCTCA

SEQ ID NO: 34 2B7 V_H amino acid sequence

EVQLVESGGGLVKPGGSLKLSCAASGFTFSNYAMSWVRQTPEKRLEWVATISDGGGYTYYLDNGQ
GRFTISRDNAKNNLYLQMSHLKSEDTAMYYCARDVGLTTFWYFDVWGTGTTVTVSS

SEQ ID NO: 35 2B7 V_L nucleotide sequence

GACATTGTGCTGACACAGTCTCCTGTTTCCTTAGTTATATCTCTGGGGCAGAGGGCCACCATCTC
CTGCAGGGCCAGCAAAAGTGTCAGTCCATCTAGCTATAATTTCATGCACTGGTACCAACAGAGAC
CAGGACAGCCGCCCAAACTCCTCATCACGTATGCTTCCAACCTAGAATCTGGGGTCCCTGCCAG
GTTCAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCATCCTGTGGAGGAAGAGGAT
GCTGCAACATATTACTGTCAGCACAGTAGGGAGTTTCCGTTCACGTTCGGAGGGGGGACCAGGC
TGGAAATAAAA

SEQ ID NO: 36 2B7 V_L amino acid sequence

DIVLTQSPVSLVISLGQRATISCRASKSVSPSSYNFMHWYQQRPGQPPKLLITYASNLESGVPARFSG
SGSGTDFTLNIHPVEEEDAATYYCQHSREFPFTFGGGTRLEIK

SEQ ID NO: 37 9G2 V_H nucleotide sequence

GAAGTACAACTAGTGGAGTCTGGGGGAGGCTTAGTGGAGCCTGGAGGGTCCCTGAAACTCTCC
TGTGCAGCCTCTGGATTCACTTTCAGTAACTATGCCATGTCTTGGGTTCGCCAGACTCCGGAAAA
GAGGCTGGAGTGGGTCGCAACCATTAGTGATGGTGGTAGTTTCACCTACTATCTAGACAATGTAA
AGGGCCGATTCACCATCTCCAGAGACAATGCCAAGAACAACCTGTATTTGCAAATGAGCCATTTG
AAGTCTGACGACACAGCCATGTATTACTGTGCAAGAGATGTGGGACATACTACGTTTTGGTACTT
CGATGTCTGGGGCACAGGGACCACGGTCACCGTCTCCTCA

SEQ ID NO: 38 9G2 V_H amino acid sequence

EVQLVESGGGLVEPGGSLKLSCAASGFTFSNYAMSWVRQTPEKRLEWVATISDGGSFTYYLDNVKG
RFTISRDNAKNNLYLQMSHLKSDDTAMYYCARDVGHTTFWYFDVWGTGTTVTVSS

SEQ ID NO: 39 9G2 V_L nucleotide sequence

GACATTGTGCTGACACAGTCTCCTGTTTTCTTAGTTATATCTCTGGGGCAGAGGGCCACCATCTC
CTGCAGGGCCAGCAAAAGTGTCAGTGCATCTGGCTATAATTTCATGCACTGGTACCAACAGAAAC
CAGGACAGCCGCCCAAAGTCCTCATCAAGTATGCATCCAACCTAGAATCTGGGGTCCCTGCCAG
GTTCAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCATCCTGTGGAGGAGGAGGAT
GCTGTAACATATTACTGTCAGCACAGTAGGGAGTTTCCGTTCACGTTCGGAGGGGGGACCAAGC
TGGAAATAAAA

SEQ ID NO: 40 9G2 V_L amino acid sequence

DIVLTQSPVFLVISLGQRATISCRASKSVSASGYNFMHWYQQKPGQPPKVLIKYASNLESGVPARFSG
SGSGTDFTLNIHPVEEEDAVTYYCQHSREFPFTFGGGTKLEIK

SEQ ID NO:41 10G8 V_H chimera nucleotide sequence

GAAATGCAACTGGTGGAGTCTGGGGAAGGCTTAGTGGAGCCTGGAGGGTCCCTGAAACTCTCC
TGTGCAGCCTCTGGATTCACTTTCAGTAACTATGCCATGTCTTGGGTTCGCCAGACTCCGGAAAA
GAGCCTGGAGTGGGTCGCAACCATTAGTGATGGTGGTAGTTTCACCTACTATCTAGACAATGTAA
GGGGCCGATTCACCATCTCCAGAGACAATGCCAAGAACAACCTGTATTTGCAAATGAGCCATTTG
AAGTCTGACGACACAGCCATGTATTACTGTGCAAGAGATGTGGGACATACTACCTTTTGGTACTT
CGATGTCTGGGGCTCAGGGACACTAGTGACCGTGTCCAGCGCCAGCACCAAGGGCCCCAGCGT
GTTCCCCCTGGCCCCCAGCAGCAAGAGCACCAGCGGCGGCACAGCCGCCCTGGGCTGCCTGG
TGAAGGACTACTTCCCCGAACCGGTGACCGTGTCCTGGAACAGCGGAGCCCTGACCAGCGGCG
TGCACACCTTCCCCGCCGTGCTGCAGAGCAGCGGCCTGTACAGCCTGAGCAGCGTGGTGACCG
TGCCCAGCAGCAGCCTGGGCACCCAGACCTACATCTGTAACGTGAACCACAAGCCCAGCAACAC
CAAGGTGGACAAGAAGGTGGAGCCCAAGAGCTGTGACAAGACCCACACCTGCCCCCCCTGCCC
TGCCCCCGAGCTGCTGGGAGGCCCCAGCGTGTTCCTGTTCCCCCCCAAGCCTAAGGACACCCT
GATGATCAGCAGAACCCCCGAGGTGACCTGTGTGGTGGTGGATGTGAGCCACGAGGACCCTGA
GGTGAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCACAATGCCAAGACCAAGCCCAGGGA
GGAGCAGTACAACAGCACCTACCGGGTGGTGTCCGTGCTGACCGTGCTGCACCAGGATTGGCT
GAACGGCAAGGAGTACAAGTGTAAGGTGTCCAACAAGGCCCTGCCTGCCCCTATCGAGAAAACC
ATCAGCAAGGCCAAGGGCCAGCCCAGAGAGCCCCAGGTGTACACCCTGCCCCCTAGCAGAGAT
GAGCTGACCAAGAACCAGGTGTCCCTGACCTGCCTGGTGAAGGGCTTCTACCCCAGCGACATC
GCCGTGGAGTGGGAGAGCAACGGCCAGCCCGAGAACAACTACAAGACCACCCCCCCTGTGCTG
GACAGCGATGGCAGCTTCTTCCTGTACAGCAAGCTGACCGTGGACAAGAGCAGATGGCAGCAG
GGCAACGTGTTCAGCTGCTCCGTGATGCACGAGGCCCTGCACAATCACTACACCCAGAAGAGCC
TGAGCCTGTCCCCTGGCAAG

SEQ ID NO: 42 10G8 V_H chimera amino acid sequence

EMQLVESGEGLVEPGGSLKLSCAASGFTFSNYAMSWVRQTPEKSLEWVATISDGGSFTYYLDNVRG
RFTISRDNAKNNLYLQMSHLKSDDTAMYYCARDVGHTTFWYFDVWGSGTLVTVSSASTKGPSVFPL
APSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT
QTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV
VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL
PAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP
VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

SEQ ID NO: 43 10G8 V_L chimera nucleotide sequence

GACATTGTGCTGACACAGTCTCCTGTTTTCTTAGTTGTATCTCTGGGGCAGAGGGCCACCATCTC
CTGTAGGGCCAGCAAAAGTGTCAGTGCAGCTGGCTATAATTTCATGCACTGGTACCAACAGAAA
CCAGGACAGCCGCCCAAAGTCCTCATCAAGTATGCATCCAACCTAGAATCTGGGGTCCCTGCCA
GGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCATCCTGTGGAGGAGGAGG
ATGCTGTAACATATTACTGTCTGCACAGTAGGGAGTTTCCGTTCACGTTCGGAGGGGGGACCAA
CCTGGAAATAAAACGTACGGTGGCCGCCCCCAGCGTGTTCATCTTCCCCCCCAGCGATGAGCAG
CTGAAGAGCGGCACCGCCAGCGTGGTGTGTCTGCTGAACAACTTCTACCCCCGGGAGGCCAAG
GTGCAGTGGAAGGTGGACAATGCCCTGCAGAGCGGCAACAGCCAGGAGAGCGTGACCGAGCA
GGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCAAGGCCGACTACGA
GAAGCACAAGGTGTACGCCTGTGAGGTGACCCACCAGGGCCTGTCCAGCCCCGTGACCAAGAG
CTTCAACCGGGGCGAGTGC

SEQ ID NO: 44 10G8 V_L chimera amino acid sequence

DIVLTQSPVFLVVSLGQRATISCRASKSVSAAGYNFMHWYQQKPGQPPKVLIKYASNLESGVPARFS
GSGSGTDFTLNIHPVEEEDAVTYYCLHSREFPFTFGGGTNLEIKRTVAAPSVFIFPPSDEQLKSGTASV
VCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTH
QGLSSPVTKSFNRGEC

SEQ ID NO: 45 9G2 V_H chimera nucleotide sequence

GAAGTACAACTGGTGGAGTCTGGGGGAGGCTTAGTGGAGCCTGGAGGGTCCCTGAAACTCTCC
TGTGCAGCCTCTGGATTCACTTTCAGTAACTATGCCATGTCTTGGGTTCGCCAGACTCCGGAAAA
GAGGCTGGAGTGGGTCGCAACCATTAGTGATGGTGGTAGTTTCACCTACTATCTAGACAATGTAA
AGGGCCGATTCACCATCTCCAGAGACAATGCCAAGAACAACCTGTATTTGCAAATGAGCCATTTG
AAGTCTGACGACACAGCCATGTATTACTGTGCAAGAGATGTGGGACATACTACGTTTTGGTACTT
CGATGTCTGGGGCACAGGGACACTAGTGACCGTGTCCAGCGCCAGCACCAAGGGCCCCAGCGT
GTTCCCCCTGGCCCCCAGCAGCAAGAGCACCAGCGGCGGCACAGCCGCCCTGGGCTGCCTGG
TGAAGGACTACTTCCCCGAACCGGTGACCGTGTCCTGGAACAGCGGAGCCCTGACCAGCGGCG
TGCACACCTTCCCCGCCGTGCTGCAGAGCAGCGGCCTGTACAGCCTGAGCAGCGTGGTGACCG

TGCCCAGCAGCAGCCTGGGCACCCAGACCTACATCTGTAACGTGAACCACAAGCCCAGCAACAC
CAAGGTGGACAAGAAGGTGGAGCCCAAGAGCTGTGACAAGACCCACACCTGCCCCCCCTGCCC
TGCCCCCGAGCTGCTGGGAGGCCCCAGCGTGTTCCTGTTCCCCCCCAAGCCTAAGGACACCCT
GATGATCAGCAGAACCCCCGAGGTGACCTGTGTGGTGGTGGATGTGAGCCACGAGGACCCTGA
GGTGAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCACAATGCCAAGACCAAGCCCAGGGA
GGAGCAGTACAACAGCACCTACCGGGTGGTGTCCGTGCTGACCGTGCTGCACCAGGATTGGCT
GAACGGCAAGGAGTACAAGTGTAAGGTGTCCAACAAGGCCCTGCCTGCCCCTATCGAGAAAACC
ATCAGCAAGGCCAAGGGCCAGCCCAGAGAGCCCCAGGTGTACACCCTGCCCCCTAGCAGAGAT
GAGCTGACCAAGAACCAGGTGTCCCTGACCTGCCTGGTGAAGGGCTTCTACCCCAGCGACATC
GCCGTGGAGTGGGAGAGCAACGGCCAGCCCGAGAACAACTACAAGACCACCCCCCCTGTGCTG
GACAGCGATGGCAGCTTCTTCCTGTACAGCAAGCTGACCGTGGACAAGAGCAGATGGCAGCAG
GGCAACGTGTTCAGCTGCTCCGTGATGCACGAGGCCCTGCACAATCACTACACCCAGAAGAGCC
TGAGCCTGTCCCCTGGCAAG

SEQ ID NO: 46 9G2 V_H chimera amino acid sequence

EVQLVESGGGLVEPGGSLKLSCAASGFTFSNYAMSWVRQTPEKRLEWVATISDGGSFTYYLDNVKG
RFTISRDNAKNNLYLQMSHLKSDDTAMYYCARDVGHTTFWYFDVWGTGTLVTVSSASTKGPSVFPL
APSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT
QTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV
VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL
PAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP
VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

SEQ ID NO: 47 9G2 V_L chimera nucleotide sequence

GACATTGTGCTGACACAGTCTCCTGTTTTCTTAGTTATATCTCTGGGGCAGAGGGCCACCATCTC
CTGCAGGGCCAGCAAAAGTGTCAGTGCATCTGGCTATAATTTCATGCACTGGTACCAACAGAAAC
CAGGACAGCCGCCCAAAGTCCTCATCAAGTATGCATCCAACCTAGAATCTGGGGTCCCTGCCAG
GTTCAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCATCCTGTGGAGGAGGAGGAT
GCTGTAACATATTACTGTCAGCACAGTAGGGAGTTTCCGTTCACGTTCGGAGGGGGGACCAAGC
TGGAAATAAAACGTACGGTGGCCGCCCCCAGCGTGTTCATCTTCCCCCCCAGCGATGAGCAGCT
GAAGAGCGGCACCGCCAGCGTGGTGTGTCTGCTGAACAACTTCTACCCCCGGGAGGCCAAGGT
GCAGTGGAAGGTGGACAATGCCCTGCAGAGCGGCAACAGCCAGGAGAGCGTGACCGAGCAGG
ACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCAAGGCCGACTACGAGA
AGCACAAGGTGTACGCCTGTGAGGTGACCCACCAGGGCCTGTCCAGCCCCGTGACCAAGAGCT
TCAACCGGGGCGAGTGC

SEQ ID NO: 48 9G2 V_L chimera amino acid sequence

DIVLTQSPVFLVISLGQRATISCRASKSVSASGYNFMHWYQQKPGQPPKVLIKYASNLESGVPARFSG
SGSGTDFTLNIHPVEEEDAVTYYCQHSREFPFTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASV
VCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTH
QGLSSPVTKSFNRGEC

SEQ ID NO:49 IGHV3_7 human V_H germline acceptor nucleotide sequence

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTC
CTGTGCAGCCTCTGGATTCACCTTTAGTAGCTATTGGATGAGCTGGGTCCGCCAGGCTCCAGGG
AAGGGGCTGGAGTGGGTGGCCAACATAAAGCAAGATGGAAGTGAGAAATACTATGTGGACTCTG
TGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAACAG
CCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGA

SEQ ID NO:50 IGHV3_7 human V_H germline acceptor amino acid sequence

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYYVDSVK
GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR

SEQ ID NO:51 IGKV4_1 human V_L germline acceptor nucleotide sequence

GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCA
ACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCTTGGTACCAG
CAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC
CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGC
TGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT

SEQ ID NO:52 IGKV4_1 human V_L germline acceptor amino acid sequence

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTRESGVPDR
FSGSGSGTDFTLTISSLQAEDVAVYYCQQYYST

SEQ ID NO:53 10G8 Humanised V_H H0 nucleotide sequence -leto codon optimised

GAGGTGCAGCTGGTGGAAAGCGGCGGCGGCCTGGTCCAGCCCGGCGGGAGCCTGAGACTCTC
TTGCGCCGCTAGCGGCTTCACCTTCAGCAACTACGCCATGAGCTGGGTGAGGCAGGCCCCCGG
CAAGGGCCTGGAGTGGGTGGCCACCATCAGCGACGGCGGCAGCTTCACCTACTATCTGGACAA
CGTGAGGGGCAGGTTCACCATCAGCAGGGACAACGCCAAGAACAGCCTGTACCTGCAGATGAA
CAGCCTGAGGGCCGAGGATACCGCCGTGTACTACTGCGCCAGGGACGTCGGCCACACCACCTT
CTGGTACTTCGACGTCTGGGGCAGGGGCACACTAGTGACCGTGTCCAGC

SEQ ID NO:54 10G8 Humanised V_H H0 amino acid sequence

EVQLVESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVATISDGGSFTYYLDNVR
GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDVGHTTFWYFDVWGRGTLVTVSS

SEQ ID NO:55 10G8 Humanised V_H H1 nucleotide sequence -leto codon optimised

GAGATGCAGCTGGTGGAAAGCGGCGGCGGCCTGGTCCAGCCCGGCGGGAGCCTGAGACTCTC
TTGCGCCGCTAGCGGCTTCACCTTCAGCAACTACGCCATGAGCTGGGTGAGGCAGGCCCCCGG
CAAGGGCCTGGAGTGGGTGGCCACCATCAGCGACGGCGGCAGCTTCACCTACTATCTGGACAA
CGTGAGGGGCAGGTTCACCATCAGCAGGGACAACGCCAAGAACAGCCTGTACCTGCAGATGAA
CAGCCTGAGGGCCGAGGATACCGCCGTGTACTACTGCGCCAGGGACGTCGGCCACACCACCTT
CTGGTACTTCGACGTCTGGGGCAGGGGCACACTAGTGACCGTGTCCAGC

SEQ ID NO:56 10G8 Humanised V_H H1 amino acid sequence

EMQLVESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVATISDGGSFTYYLDNVR
GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDVGHTTFWYFDVWGRGTLVTVSS

SEQ ID NO:57 10G8 Humanised V_H H2 nucleotide sequence -leto codon optimised

GAGGTGCAGCTGGTGGAAAGCGGCGGCGGCCTGGTCCAGCCCGGCGGGAGCCTGAGACTCTC
TTGCGCCGCTAGCGGCTTCACCTTCAGCAACTACGCCATGAGCTGGGTGAGGCAGGCCCCCGG
CAAGGGCCTGGAGTGGGTGGCCACCATCAGCGACGGCGGCAGCTTCACCTACTATCTGGACAA
CGTGAGGGGCAGGTTCACCATCAGCAGGGACAACGCCAAGAACAGCCTGTACCTGCAGATGAA
CAGCCTGAGGGCCGAGGATACCGCCGTGTACTACTGCGCCAGGGACGTCGGCCACACCACCTT
CTGGTACTTCGACGTCTGGGGCTCCGGCACACTAGTGACCGTGTCCAGC

SEQ ID NO:58 10G8 Humanised V_H H2 amino acid sequence

EVQLVESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVATISDGGSFTYYLDNVR
GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDVGHTTFWYFDVWGSGTLVTVSS

SEQ ID NO:59 10G8 Humanised V_L L0 nucleotide sequence -leto codon optimised

GACATCGTGATGACTCAGAGCCCCGATAGCCTGGCCGTGAGCCTGGGCGAAAGGGCCACCATC
AACTGCAGGGCCAGCAAGAGCGTGAGCGCTGCCGGCTACAACTTCATGCACTGGTACCAGCAG
AAGCCCGGCCAGCCCCCCAAGCTGCTGATCTACTACGCCTCCAACCTGGAGAGCGGCGTGCCA

GACAGGTTCAGCGGATCTGGCAGCGGCACCGACTTCACCCTGACCATCTCAAGCCTGCAGGCC
GAGGACGTCGCCGTGTACTACTGCCTGCACAGCAGGGAGTTCCCCTTCACCTTTGGCGGCGGC
ACCAAGGTGGAGATCAAG

SEQ ID NO:60 10G8 Humanised V_L L0 amino acid sequence

DIVMTQSPDSLAVSLGERATINCRASKSVSAAGYNFMHWYQQKPGQPPKLLIYYASNLESGVPDRFS
GSGSGTDFTLTISSLQAEDVAVYYCLHSREFPFTFGGGTKVEIK

SEQ ID NO:61 10G8 Humanised V_L L1 nucleotide sequence -leto codon optimised

GACATCGTGATGACTCAGAGCCCCGATAGCCTGGCCGTGAGCCTGGGCGAAAGGGCCACCATC
AACTGCAGGGCCAGCAAGAGCGTGAGCGCTGCCGGCTACAACTTCATGCACTGGTACCAGCAG
AAGCCCGGCCAGCCCCCCAAGGTGCTGATCTACTACGCCTCCAACCTGGAGAGCGGCGTGCCA
GACAGGTTCAGCGGATCTGGCAGCGGCACCGACTTCACCCTGACCATCTCAAGCCTGCAGGCC
GAGGACGTCGCCGTGTACTACTGCCTGCACAGCAGGGAGTTCCCCTTCACCTTTGGCGGCGGC
ACCAAGGTGGAGATCAAG

SEQ ID NO:62 10G8 Humanised V_L L1 amino acid sequence

DIVMTQSPDSLAVSLGERATINCRASKSVSAAGYNFMHWYQQKPGQPPKVLIYYASNLESGVPDRFS
GSGSGTDFTLTISSLQAEDVAVYYCLHSREFPFTFGGGTKVEIK

SEQ ID NO:63 10G8 Humanised V_L L2 nucleotide sequence- leto codon optimised

GACATCGTGATGACTCAGAGCCCCGATAGCCTGGCCGTGAGCCTGGGCGAAAGGGCCACCATC
AACTGCAGGGCCAGCAAGAGCGTGAGCGCTGCCGGCTACAACTTCATGCACTGGTACCAGCAG
AAGCCCGGCCAGCCCCCCAAGCTGCTGATCTACTACGCCTCCAACCTGGAGAGCGGCGTGCCA
GACAGGTTCAGCGGATCTGGCAGCGGCACCGACTTCACCCTGACCATCTCAAGCCTGCAGGCC
GAGGACGTCGTGGTGTACTACTGCCTGCACAGCAGGGAGTTCCCCTTCACCTTTGGCGGCGGC
ACCAAGGTGGAGATCAAG

SEQ ID NO:64 10G8 Humanised V_L L2 amino acid sequence

DIVMTQSPDSLAVSLGERATINCRASKSVSAAGYNFMHWYQQKPGQPPKLLIYYASNLESGVPDRFS
GSGSGTDFTLTISSLQAEDVVVYYCLHSREFPFTFGGGTKVEIK

SEQ ID NO:65 10G8 Humanised V_L L3 nucleotide sequence - leto codon optimised

GACATCGTGATGACTCAGAGCCCCGATAGCCTGGCCGTGAGCCTGGGCGAAAGGGCCACCATC
AACTGCAGGGCCAGCAAGAGCGTGAGCGCTGCCGGCTACAACTTCATGCACTGGTACCAGCAG

AAGCCCGGCCAGCCCCCCAAGCTGCTGATCTACTACGCCTCCAACCTGGAGAGCGGCGTGCCA
GACAGGTTCAGCGGATCTGGCAGCGGCACCGACTTCACCCTGACCATCTCAAGCCTGCAGGCC
GAGGACGTCGCCGTGTACTACTGCCTGCACAGCAGGGAGTTCCCCTTCACCTTTGGCGGCGGC
ACCAACGTGGAGATCAAG

SEQ ID NO:66 10G8 Humanised V_L L3 amino acid sequence

DIVMTQSPDSLAVSLGERATINCRASKSVSAAGYNFMHWYQQKPGQPPKLLIYYASNLESGVPDRFS
GSGSGTDFTLTISSLQAEDVAVYYCLHSREFPFTFGGGTNVEIK

SEQ ID NO:67 10G8 Humanised V_L L4 nucleotide sequence -leto codon optimised

GACATCGTGATGACTCAGAGCCCCGATAGCCTGGCCGTGAGCCTGGGCGAAAGGGCCACCATC
AACTGCAGGGCCAGCAAGAGCGTGAGCGCTGCCGGCTACAACTTCATGCACTGGTACCAGCAG
AAGCCCGGCCAGCCCCCCAAGGTGCTGATCTACTACGCCTCCAACCTGGAGAGCGGCGTGCCA
GACAGGTTCAGCGGATCTGGCAGCGGCACCGACTTCACCCTGACCATCTCAAGCCTGCAGGCC
GAGGACGTCGTGGTGTACTACTGCCTGCACAGCAGGGAGTTCCCCTTCACCTTTGGCGGCGGC
ACCAACGTGGAGATCAAG

SEQ ID NO:68 10G8 Humanised V_L L4 amino acid sequence

DIVMTQSPDSLAVSLGERATINCRASKSVSAAGYNFMHWYQQKPGQPPKVLIYYASNLESGVPDRFS
GSGSGTDFTLTISSLQAEDVVVYYCLHSREFPFTFGGGTNVEIK

SEQ ID NO:69 Mature H0 heavy chain nucleotide sequence -leto codon optimised

GAGGTGCAGCTGGTGGAAAGCGGCGGCGGCCTGGTCCAGCCCGGCGGGAGCCTGAGACTCTC
TTGCGCCGCTAGCGGCTTCACCTTCAGCAACTACGCCATGAGCTGGGTGAGGCAGGCCCCCGG
CAAGGGCCTGGAGTGGGTGGCCACCATCAGCGACGGCGGCAGCTTCACCTACTATCTGGACAA
CGTGAGGGGCAGGTTCACCATCAGCAGGGACAACGCCAAGAACAGCCTGTACCTGCAGATGAA
CAGCCTGAGGGCCGAGGATACCGCCGTGTACTACTGCGCCAGGGACGTCGGCCACACCACCTT
CTGGTACTTCGACGTCTGGGGCAGGGGCACACTAGTGACCGTGTCCAGCGCCAGCACCAAGGG
CCCCAGCGTGTTCCCCCTGGCCCCCAGCAGCAAGAGCACCAGCGGCGGCACAGCCGCCCTGG
GCTGCCTGGTGAAGGACTACTTCCCCGAACCGGTGACCGTGTCCTGGAACAGCGGAGCCCTGA
CCAGCGGCGTGCACACCTTCCCCGCCGTGCTGCAGAGCAGCGGCCTGTACAGCCTGAGCAGC
GTGGTGACCGTGCCCAGCAGCAGCCTGGGCACCCAGACCTACATCTGTAACGTGAACCACAAG
CCCAGCAACACCAAGGTGGACAAGAAGGTGGAGCCCAAGAGCTGTGACAAGACCCACACCTGC
CCCCCCTGCCCTGCCCCCGAGCTGCTGGGAGGCCCCAGCGTGTTCCTGTTCCCCCCCAAGCCT
AAGGACACCCTGATGATCAGCAGAACCCCCGAGGTGACCTGTGTGGTGGTGGATGTGAGCCAC
GAGGACCCTGAGGTGAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCACAATGCCAAGACC

AAGCCCAGGGAGGAGCAGTACAACAGCACCTACCGGGTGGTGTCCGTGCTGACCGTGCTGCAC
CAGGATTGGCTGAACGGCAAGGAGTACAAGTGTAAGGTGTCCAACAAGGCCCTGCCTGCCCCTA
TCGAGAAAACCATCAGCAAGGCCAAGGGCCAGCCCAGAGAGCCCCAGGTGTACACCCTGCCCC
CTAGCAGAGATGAGCTGACCAAGAACCAGGTGTCCCTGACCTGCCTGGTGAAGGGCTTCTACCC
CAGCGACATCGCCGTGGAGTGGGAGAGCAACGGCCAGCCCGAGAACAACTACAAGACCACCCC
CCCTGTGCTGGACAGCGATGGCAGCTTCTTCCTGTACAGCAAGCTGACCGTGGACAAGAGCAGA
TGGCAGCAGGGCAACGTGTTCAGCTGCTCCGTGATGCACGAGGCCCTGCACAATCACTACACC
CAGAAGAGCCTGAGCCTGTCCCCTGGCAAG

SEQ ID NO:70 Mature H0 heavy chain amino acid sequence

EVQLVESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVATISDGGSFTYYLDNVR
GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDVGHTTFWYFDVWGRGTLVTVSSASTKGPSVFP
LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV
VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA
LPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

SEQ ID NO:71 Mature L1 light chain nucleotide sequence - leto codon optimised

GACATCGTGATGACTCAGAGCCCCGATAGCCTGGCCGTGAGCCTGGGCGAAAGGGCCACCATC
AACTGCAGGGCCAGCAAGAGCGTGAGCGCTGCCGGCTACAACTTCATGCACTGGTACCAGCAG
AAGCCCGGCCAGCCCCCCAAGGTGCTGATCTACTACGCCTCCAACCTGGAGAGCGGCGTGCCA
GACAGGTTCAGCGGATCTGGCAGCGGCACCGACTTCACCCTGACCATCTCAAGCCTGCAGGCC
GAGGACGTCGCCGTGTACTACTGCCTGCACAGCAGGGAGTTCCCCTTCACCTTTGGCGGCGGC
ACCAAGGTGGAGATCAAGCGTACGGTGGCCGCCCCCAGCGTGTTCATCTTCCCCCCCAGCGAT
GAGCAGCTGAAGAGCGGCACCGCCAGCGTGGTGTGTCTGCTGAACAACTTCTACCCCCGGGAG
GCCAAGGTGCAGTGGAAGGTGGACAATGCCCTGCAGAGCGGCAACAGCCAGGAGAGCGTGAC
CGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCAAGGCCGA
CTACGAGAAGCACAAGGTGTACGCCTGTGAGGTGACCCACCAGGGCCTGTCCAGCCCCGTGAC
CAAGAGCTTCAACCGGGGCGAGTGC

SEQ ID NO:72 Mature L1 light chain amino acid sequence

DIVMTQSPDSLAVSLGERATINCRASKSVSAAGYNFMHWYQQKPGQPPKVLIYYASNLESGVPDRFS
GSGSGTDFTLTISSLQAEDVAVYYCLHSREFPFTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASV
VCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTH
QGLSSPVTKSFNRGEC

SEQ ID NO:73 Humanised V_H variant H0 (IGHV3_23 CDRH1) nucleotide sequence- leto codon optimised

GAGGTGCAGCTGGTGGAAAGCGGCGGCGGCCTGGTCCAGCCCGGCGGGAGCCTGAGACTCTC
TTGCGCCGCTAGCGGCTTCACCTTCAGCAGCTACGCCATGAGCTGGGTGAGGCAGGCCCCCGG
CAAGGGCCTGGAGTGGGTGGCCACCATCAGCGACGGCGGCAGCTTCACCTACTATCTGGACAA
CGTGAGGGGCAGGTTCACCATCAGCAGGGACAACGCCAAGAACAGCCTGTACCTGCAGATGAA
CAGCCTGAGGGCCGAGGATACCGCCGTGTACTACTGCGCCAGGGACGTCGGCCACACCACCTT
CTGGTACTTCGACGTCTGGGGCAGGGGCACACTAGTGACCGTGTCCAGC

SEQ ID NO:74 Humanised V_H variant H0 (IGHV3_23 CDRH1) amino acid sequence

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVATISDGGSFTYYLDNVR
GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDVGHTTFWYFDVWGRGTLVTVSS

SEQ ID NO:75 Mature H0 (IGHV3_23 CDRH1) heavy chain nucleotide sequence - leto codon optimised

GAGGTGCAGCTGGTGGAAAGCGGCGGCGGCCTGGTCCAGCCCGGCGGGAGCCTGAGACTCTC
TTGCGCCGCTAGCGGCTTCACCTTCAGCAGCTACGCCATGAGCTGGGTGAGGCAGGCCCCCGG
CAAGGGCCTGGAGTGGGTGGCCACCATCAGCGACGGCGGCAGCTTCACCTACTATCTGGACAA
CGTGAGGGGCAGGTTCACCATCAGCAGGGACAACGCCAAGAACAGCCTGTACCTGCAGATGAA
CAGCCTGAGGGCCGAGGATACCGCCGTGTACTACTGCGCCAGGGACGTCGGCCACACCACCTT
CTGGTACTTCGACGTCTGGGGCAGGGGCACACTAGTGACCGTGTCCAGCGCCAGCACCAAGGG
CCCCAGCGTGTTCCCCCTGGCCCCCAGCAGCAAGAGCACCAGCGGCGGCACAGCCGCCCTGG
GCTGCCTGGTGAAGGACTACTTCCCCGAACCGGTGACCGTGTCCTGGAACAGCGGAGCCCTGA
CCAGCGGCGTGCACACCTTCCCCGCCGTGCTGCAGAGCAGCGGCCTGTACAGCCTGAGCAGC
GTGGTGACCGTGCCCAGCAGCAGCCTGGGCACCCAGACCTACATCTGTAACGTGAACCACAAG
CCCAGCAACACCAAGGTGGACAAGAAGGTGGAGCCCAAGAGCTGTGACAAGACCCACACCTGC
CCCCCCTGCCCTGCCCCCGAGCTGCTGGGAGGCCCCAGCGTGTTCCTGTTCCCCCCCAAGCCT
AAGGACACCCTGATGATCAGCAGAACCCCCGAGGTGACCTGTGTGGTGGTGGATGTGAGCCAC
GAGGACCCTGAGGTGAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCACAATGCCAAGACC
AAGCCCAGGGAGGAGCAGTACAACAGCACCTACCGGGTGGTGTCCGTGCTGACCGTGCTGCAC
CAGGATTGGCTGAACGGCAAGGAGTACAAGTGTAAGGTGTCCAACAAGGCCCTGCCTGCCCCTA
TCGAGAAAACCATCAGCAAGGCCAAGGGCCAGCCCAGAGAGCCCCAGGTGTACACCCTGCCCC
CTAGCAGAGATGAGCTGACCAAGAACCAGGTGTCCCTGACCTGCCTGGTGAAGGGCTTCTACCC
CAGCGACATCGCCGTGGAGTGGGAGAGCAACGGCCAGCCCGAGAACAACTACAAGACCACCCC
CCCTGTGCTGGACAGCGATGGCAGCTTCTTCCTGTACAGCAAGCTGACCGTGGACAAGAGCAGA
TGGCAGCAGGGCAACGTGTTCAGCTGCTCCGTGATGCACGAGGCCCTGCACAATCACTACACC
CAGAAGAGCCTGAGCCTGTCCCCTGGCAAG

SEQ ID NO:76 Mature H0 (IGHV3_23 CDRH1) heavy chain amino acid sequence

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVATISDGGSFTYYLDNVR
GRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDVGHTTFWYFDVWGRGTLVTVSSASTKGPSVFP
LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV
VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA
LPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

SEQ ID NO:77 Human heavy chain germline IGHV3_23 CDRH1

SYAMS

SEQ ID NO:78 Human light chain germline IGKV1_5 CDRL2

KASSLES

SEQ ID NO: 79 15E10 Humanised Heavy Chain Amino Acid Sequence:
QVQLVESGGGVVQPGRSLRLSCAASGFSLTNYGVHWVRQAPGKGLEWVAVIWRGGSTDYNAAFM
SRFTISKDNSKNTLYLQMNSLRAEDTAVYYCAKSPNSNFYWYFDVWGRGTLVTVSSASTKGPSVFPL
APSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT
QTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV
VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL
PAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP
VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 80 15E10 Humanised Light Chain Amino Acid Sequence:
EIVLTQSPATLSLSPGERATLSCSGSSSVSYMYWYQQKPGQAPRLLIEDTSNLASGIPARFSGSGSGT
DYTLTISNLEPEDFAVYYCQQWSSYPPTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLN
NFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSS
PVTKSFNRGEC
SEQ ID NO: 81 15E10 Humanised VH B3
QVQLVESGGGVVQPGRSLRLSCAASGFSLTNYGVHWVRQAPGKGLEWVAVIWRGGSTDYNAAFM
SRFTISKDNSKNTLYLQMNSLRAEDTAVYYCAKSPNSNFYWYFDVWGRGTLV (TVSS)

SEQ ID NO: 82 15E10 Humanised VL L2
EIVLTQSPATLSLSPGERATLSCSGSSSVSYMYWYQQKPGQAPRLLIEDTSNLASGIPARFSGSGSGT
DYTLTISNLEPEDFAVYYCQQWSSYPPTFGQGTKLEIK
SEQ ID NO: 83 Human OSM polynucleotide sequence

ATGGGGGTACTGCTCACACAGAGGACGCTGCTCAGTCTGGTCCTTGCACTC
CTGTTTCCAAGCATGGCGAGCATGGCGGCTATAGGCAGCTGCTCGAAAGAG
TACCGCGTGCTCCTTGGCCAGCTCCAGAAGCAGACAGATCTCATGCAGGAC
ACCAGCAGACTCCTGGACCCCTATATACGTATCCAAGGCCTGGATGTTCCT
AAACTGAGAGAGCACTGCAGGGAGCGCCCCGGGGCCTTCCCCAGTGAGGAG
ACCCTGAGGGGGCTGGGCAGGCGGGGCTTCCTGCAGACCCTCAATGCCACA
CTGGGCTGCGTCCTGCACAGACTGGCCGACTTAGAGCAGCGCCTCCCCAAG
GCCCAGGATTTGGAGAGGTCTGGGCTGAACATCGAGGACTTGGAGAAGCTG
CAGATGGCGAGGCCGAACATCCTCGGGCTCAGGAACAACATCTACTGCATG
GCCCAGCTGCTGGACAACTCAGACACGGCTGAGCCCACGAAGGCTGGCCGG
GGGGCCTCTCAGCCGCCCACCCCCACCCCTGCCTCGGATGCTTTTCAGCGC
AAGCTGGAGGGCTGCAGGTTCCTGCATGGCTACCATCGCTTCATGCACTCA
GTGGGGCGGGTCTTCAGCAAGTGGGGGGAGAGCCCGAACCGGAGCCGGAGA
CACAGCCCCCACCAGGCCCTGAGGAAGGGGGTGCGCAGGACCAGACCCTCC
AGGAAAGGCAAGAGACTCATGACCAGGGGACAGCTGCCCCGGTAG

SEQ ID NO: 84 Human OSM amino acid sequence

MGVLLTQRTLLSLVLALLFPSMASMAAIGSCSKEYRVLLG**Q**LQK**Q**TDLMQD
TSRLLDPYIRIQGLDVPKLREHCRERPGAFPSEETLRGLGRRGFLQTLNAT
LGCVLHRLADLEQRLPKAQDLERSGLNIEDLEKLQMARPNIL**G**LRN**N**IYCM
AQLLDNSDTAEPTKAGRGASQPPTPTPASDAFQRKLEGCRFLHGYHRFMHS
VGRVFSKWGESPNRSRRHSPHQALRKGVRRTRPSRKGKRLMTRGQLPR.

CLAIMS

1. An antigen binding protein which specifically binds to OSM and which inhibits the binding of OSM to the gp130 receptor but does not directly interact with site II residues.

2. An antigen binding protein according to claim 1 wherein the antigen binding protein does not directly bind to any one of residues Q20, G120, Q16, N124.

3. An antigen binding protein according to claim 1 which interacts with one or more of residues 82, 83, 84, 90, 94, 112,115, 122, 123, 152 of human OSM.

4. An antigen binding protein according to any one of claims 1-3 wherein the antigen binding protein comprises CDRH3 of SEQ ID NO. 3 or a variant of SEQ ID NO. 3 wherein the variant of SEQ ID NO. 3 comprises one or more of the following :
Position 95 is substituted for Ala, Glu, Gly, His, Leu, Met, Pro, Gln, Ser, Thr, or Val;
Position 96 is substituted for Ala, Cys, Phe, Gly, His, Lys, Leu, Ser, Thr, Trp or Tyr;
Position 97 is substituted for Ala, Cys, Phe, Met or Ser
Position 98 is substituted for Ala, Asp, Phe, Gly, Leu, Pro, Gln or Trp
Position 99 is substituted for Ala, Cys, Pro, Ser, Val or Tyr
Position 100B is substituted for Glu
Position 100C is substituted for Ala, Glu, Phe, Gly, Val or Trp
Position 100D is substituted for Ala, Cys, Asp, Glu, Gly, Leu, Ser, Thr, Val, Trp or Tyr
Position 101 is substituted for Glu, Gly, Ser, Thr or Val
Position 102 is substituted for Ala, Phe, Gly, Leu, Pro, Gln, Arg, Ser Tyr, His, Ile, Asp or Trp

5. An antigen binding protein according to any one of claims 1-3 wherein the antigen binding protein comprises:
i) CDRH3 as set out in SEQ ID NO. 3 or a variant of SEQ ID NO. 3 wherein Val 102 is substituted for Tyr, His, Ile, Ser, Asp or Gly
ii) CDRH2 as set out in SEQ ID NO. 2 or a variant of SEQ ID NO. 2 wherein Thr50 is substituted for Gly, Tyr, Phe, Ile, Glu or Val and/or Ile51 is substituted for Leu, Val, Thr, Ser or Asn and/or Ser52 is substituted for Phe, Trp or His and/or Gly53 is substituted for Asp, Ser or Asn and/orGly54 is substituted for Ser and/or Phe56 is substituted for Ser, Tyr, Thr, Asn, Asp or Arg and/or Tyr58 is substituted for Gly, His, Phe, Asp or Asn.
iii) CDRL1 as set out in SEQ ID NO. 4 or a variant of SEQ ID NO. 4 wherein Ser27A is substituted for Asn, Asp, Thr or Glu and/or Ser 27C is substituted for Asp, Leu, Tyr, Val, Ile, Asn, Phe, His, Gly or Thr and/or Asn 31 is substituted for Ser, Thr, Lys or Gly and/or Phe32 is substituted for Tyr, Asn, Ala, His, Ser or Arg and/or Met 33 is substituted for Leu, Val, Ile or Phe.
iv) CDRL3 as set out in SEQ ID NO. 6 or a variant of SEQ ID NO. 6 wherein Leu89 is substituted for Gln, Ser, Gly or Phe and/or His90 is substituted for Gln or Asn, Ser 91 is substituted for Asn, Phe, Gly, Arg, Asp, His, Thr, Tyr or Val and/or Arg92 is substituted for Asn, Tyr, Trp, Thr, Ser,

Gln, His, ala or Asp and/or Glu93 is substituted for Asn, Gly, His, Thr, Ser, Ar or Ala and/or Phe96 is substituted for Pro, Leu, Tyr, Arg, Ile,or Trp.

6. An antigen binding protein according to claim 5 wherein the antigen binding protein further comprises:

i) CDRH1 as set out in SEQ ID NO. 1 or a variant of SEQ ID NO. 1 wherein Tyr 32 is substituted for Ile, His, Phe, Thr, Asn, Cys, Glu or Asp and/or Ala 33 is substituted for Tyr, Trp, Gly, Thr, Leu or Val and/or Met 34 is substituted for Ile, Val or Trp and/or Ser 35 is substituted for His, Glu, Asn, Gln, Tyr or Thr.

ii) CDRL2 as set out in SEQ ID NO. 5

7. An antigen binding protein according to any preceding claim wherein the antigen binding protein comprises CDR H3 of SEQ. ID. NO: 3: CDRH2: SEQ. ID. NO: 2: CDRL1: SEQ. ID. NO: 4 and CDRL3: SEQ. ID. NO: 6

8. An antigen binding protein according to claim 7 wherein the antigen binding protein further comprises CDR H1 of SEQ. ID. NO: 1 and CDRL2: SEQ. ID. NO: 5

9. An antigen binding protein according to claim 8 wherein the antigen binding protein comprises:

i) CDRH3 as set out in SEQ ID NO. 3

ii) CDRH1 as set out in SEQ ID NO. 1

iii) CDRH2 as set out in SEQ ID NO. 2

iv) CDRL1 as set out in SEQ ID NO. 4

v) CDRL2 as set out in SEQ ID NO. 5

vi) CDRL3 as set out in SEQ ID NO. 6; and

vii) the heavy chain framework comprises the following residues:

Position 2 Val, Ile or Gly,

Position 4 Leu or Val

Position 20 Leu, Ile, Met or Val

Position 22 Cys

Position 24 Thr, Ala, Val, Gly or Ser

Position 26 Gly

Position 29 Ile, Phe, Leu or Ser

Position 36 Trp

Position 47 Trp

Position 48 Ile, met, Val or Leu

Position 69 Ile, Leu, Phe, Met or Val

Position 71 Arg

Position 78 Ala, Leu, Val, Tyr or Phe

Position 80 Leu, Met,

Position 90 Tyr or Phe
Position 92 Cys
Position 94 Arg, Lys, Gly, Ser, His or Asn

10. An. The antigen binding protein according to any preceding claim wherein the antigen binding protein does not interact directly via CDR H1 or CDR L2 with OSM.

11. An. The antigen binding protein according to any one of claims 1 to 3 and further comprising a heavy chain variable region encoded by SEQ. ID. NO:73 and a light chain variable region encoded by SEQ. ID. NO:71.

12. An. The antigen binding protein according to any one of claims 1 to 3 and further comprising a heavy chain variable region of SEQ. ID. NO:74 and a light chain variable region of SEQ. ID. NO:72.

13. An antigen binding protein according to any preceding claim wherein the antigen binding protein is a humanised antibody.

14. An antigen binding protein according to claim 13 wherein the antibody is IgG1.

15. An antigen binding protein according to any one of claims 13-15 wherein when bound to OSM the co crystal comprises a unit cell having dimensions of about a=168.525 A, b=81.614A, c=55.540 A and beta=106.60 degrees

16. An antigen binding protein comprising the CDR's of any one of claims 1 to 10 wherein the antigen binding protein is a fragment which is a Fab, Fab', $F(ab')_2$, Fv, diabody, triabody, tetrabody, miniantibody, minibody, isolated VH or isolated VL.

17. An antigen binding protein according to any preceding claim wherein the antigen binding protein additionally binds non-human primate OSM

18. An antigen binding protein according to any one of the preceding claims and wherein the antigen binding protein binds OSM with an affinity of less than 40pm.

19. An antigen binding protein according to any preceding claim wherein the antigen binding protein does not compete with an antibody which has a heavy chain of SEQ ID NO.79 and a light chain of SEQ ID NO. 80 in a competition ELISA assay.

20. An antigen binding protein which competes with the antigen binding protein of any preceding claim.

21. An antigen binding protein which binds to both Marmoset and human OSM with an affinity stronger than 1nM when measured by Biacore or kinexa.

22. A recombinant transformed, transfected or transduced host cell comprising at least one expression cassette, whereby said expression cassette comprises a polynucleotide encoding a heavy chain of an antigen binding protein according to claim 12 and further comprises a polynucleotide encoding a light chain of an antigen binding protein or according to claim 12

23. The host cell according to claim 22 wherein the cell is mammalian.

24. The host cell according to claim 23 wherein the cell is CHO or NSO.

25. A pharmaceutical composition comprising an antigen binding protein according to any preceding claim and a pharmaceutically acceptable carrier.

26. A method of treating a human patient afflicted with an inflammatory disorder or disease which method comprises the step of administering the composition of claim 25

27. Use of the composition of claim 25 in treating a human patient afflicted with an inflammatory arthropathy, rheumatoid arthritis, osteoarthritis, idiopathic pulmonary fibrosis (IPF), Systemic sclerosis, Sjogrens syndrome, Scleroderma and/or psoriasis.

28. A method for humanising a non-human antibody or antibody fragment thereof which method comprises the steps of:

a) incorporating one or more non-human CDR's onto a human acceptor framework to produce a chimeric or humanised antibody

b) binding the chimeric or humanised antibody to its antigen

c) determining the epitope/paratope structure of the bound antibody to antigen.

d) determining the residues of the antibody involved directly in binding to the antigen

e) mutating one or more of the residues not involved in step (d) to human germline sequence;

f) recovering said antibody.

29. An antibody obtainable by the method of claim 28.

Figures

Figure 1: Human gp130 ELISA

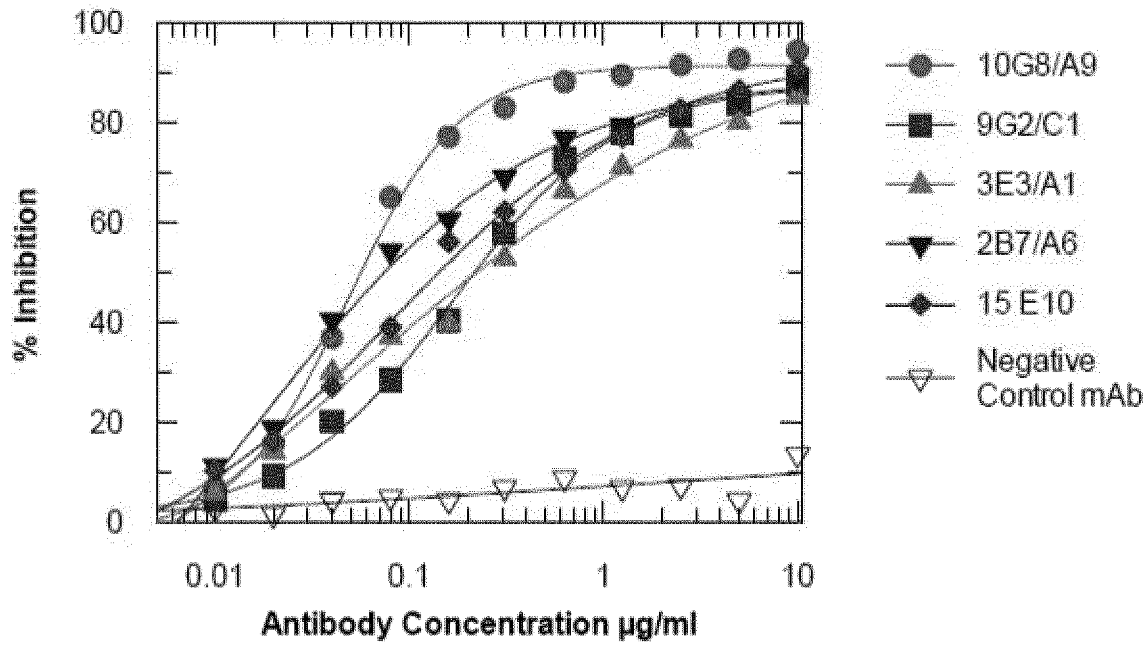


Figure 2: KB Cell Assay

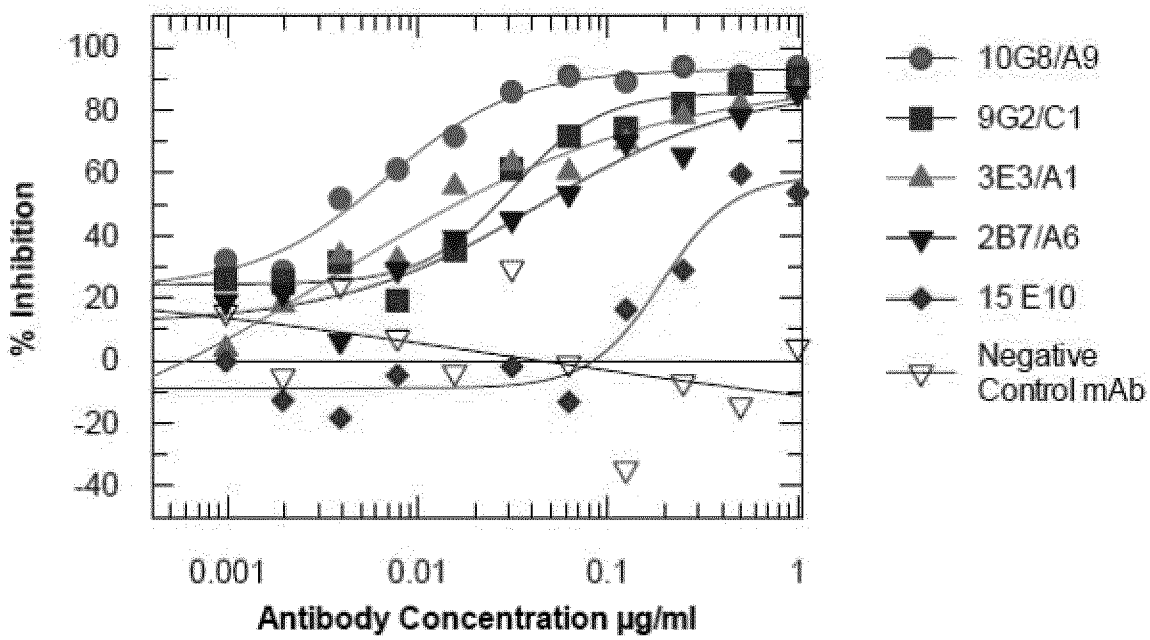


Figure 3: KB Cell Assay

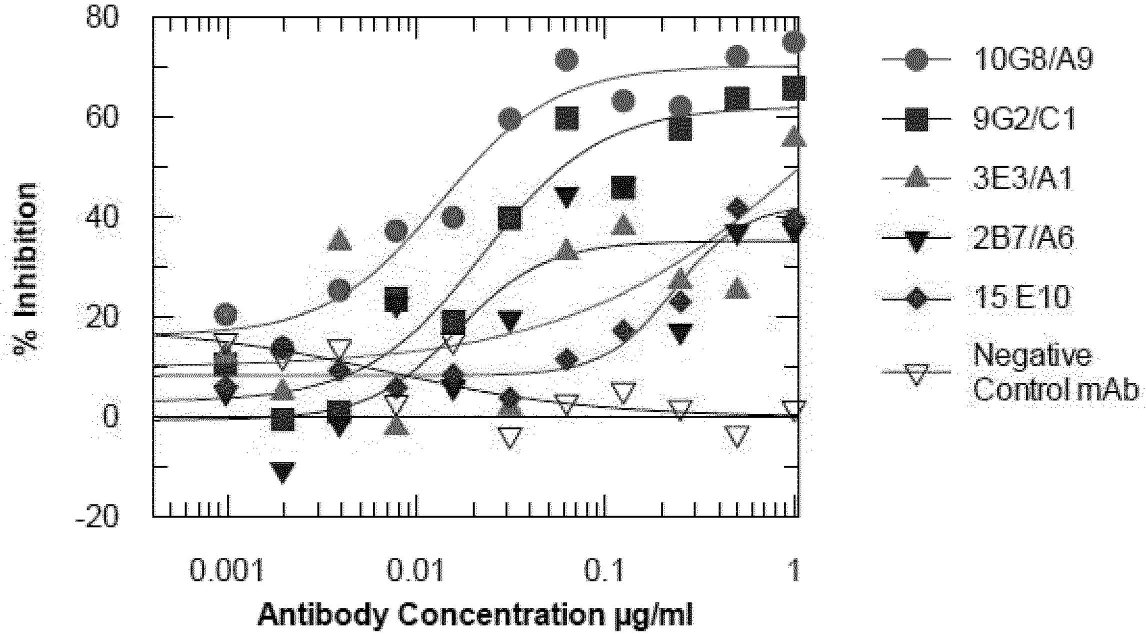


Figure 4: Endogenous OSM Human gp130 Assay

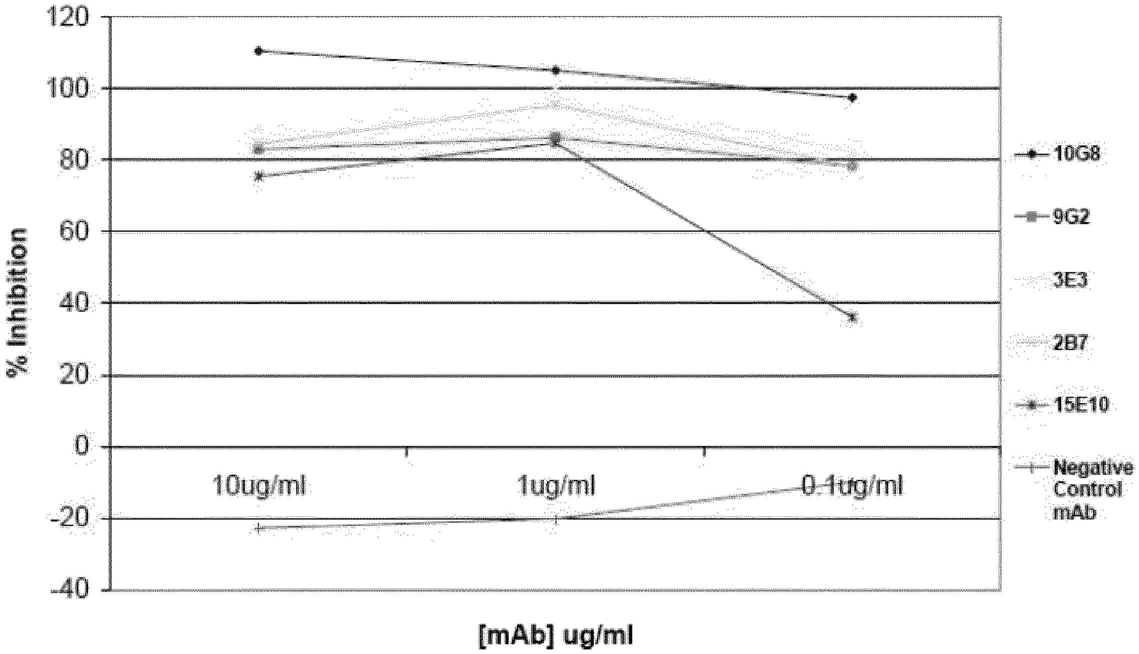


Figure 5: KB Cell Assay

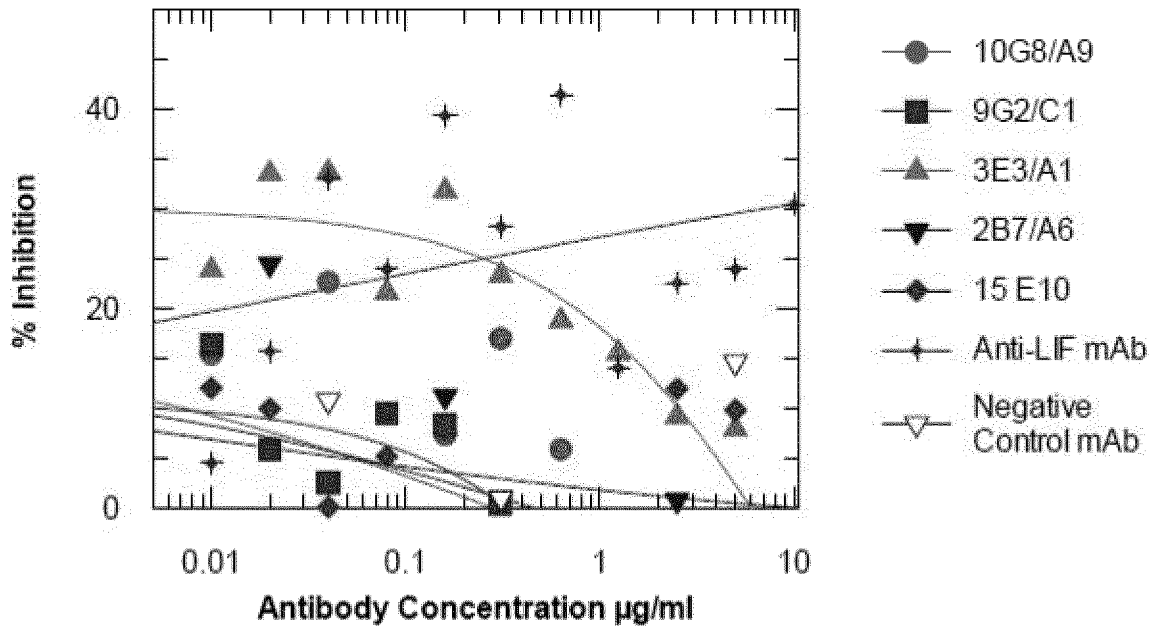


Figure 6: KB Cell Assay

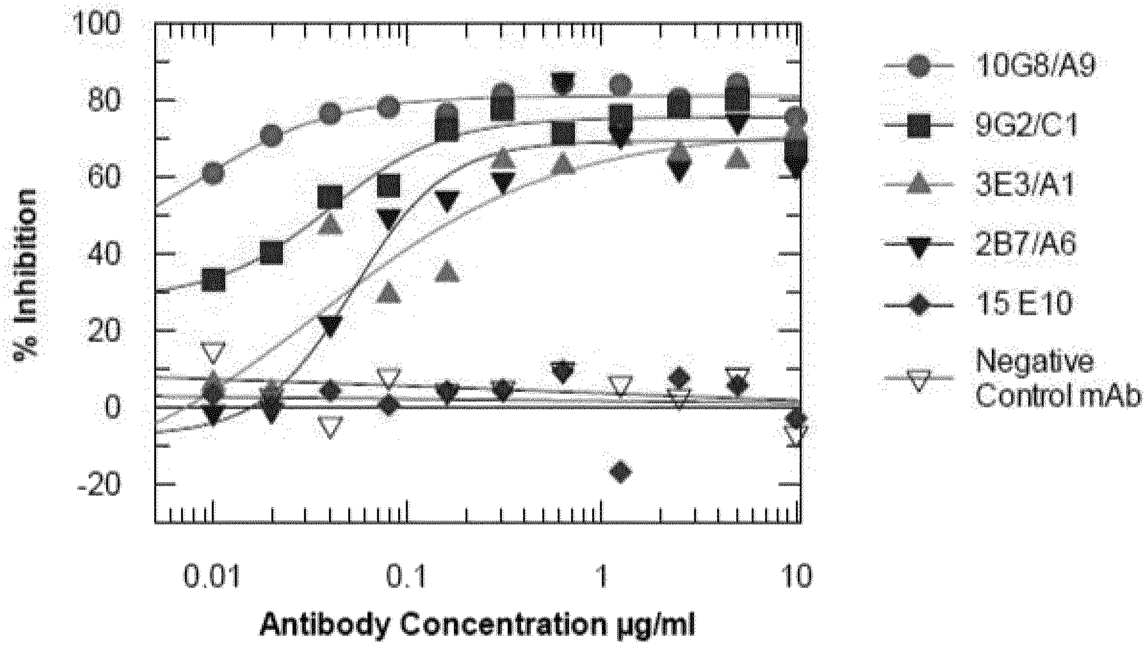


Figure 7

```
     E V Q L V E S G G G L V E P G G S L K L S C A A S G F T F S  Majority
                       10                  20                  30
1    E V Q L V E S G G G L V K P G G S L K L S C A A S G F T F S  2B7 VH protein
1    E V Q L V E S G G D L V K P G G S L K L S C V P S G F T F S  3E3 VH protein
1    E V Q L V E S G G G L V E P G G S L K L S C A A S G F T F S  9G2 VH protein
1    E M Q L V E S G E G L V E P G G S L K L S C A A S G F T F S  10G8 VH protei

     N Y A M S W V R Q T P E K R L E W V A T I S D G G S F T Y Y  Majority
                       40                  50                  60
31   N Y A M S W V R Q T P E K R L E W V A T I S D G G G Y T Y Y  2B7 VH protein
31   S Y A M S W V R Q T P E K R L E W V A T I S D G G S F T Y Y  3E3 VH protein
31   N Y A M S W V R Q T P E K R L E W V A T I S D G G S F T Y Y  9G2 VH protein
31   N Y A M S W V R Q T P E K S L E W V A T I S D G G S F T Y Y  10G8 VH protei

     L D N V Q G R F T I S R D N A K N N L Y L Q M S H L K S D D  Majority
                       70                  80                  90
61   L D N G Q G R F T I S R D N A K N N L Y L Q M S H L K S E D  2B7 VH protein
61   F A N I Q G R F T I S R D N T K N N L Y L Q M N H L K S E D  3E3 VH protein
61   L D N V K G R F T I S R D N A K N N L Y L Q M S H L K S D D  9G2 VH protein
61   L D N V R G R F T I S R D N A K N N L Y L Q M S H L K S D D  10G8 VH protei

     T A M Y Y C A R D V G L T T F W Y F D V W G T G T T V T V S  Majority
                       100                 110                 120
91   T A M Y Y C A R D V G L T T F W Y F D V W G T G T T V T V S  2B7 VH protein
91   A G M Y Y C A R D V G L T T F W Y F D V W G T G T T V T V S  3E3 VH protein
91   T A M Y Y C A R D V G H T T F W Y F D V W G T G T T V T V S  9G2 VH protein
91   T A M Y Y C A R D V G H T T F W Y F D V W G S G T A V T V S  10G8 VH protei

     S                                                            Majority

121  S                                                            2B7 VH protein
121  S                                                            3E3 VH protein
121  S                                                            9G2 VH protein
121  S                                                            10G8 VH protei
```

Decoration 'Decoration #1': Box residues that differ from the Consensus.

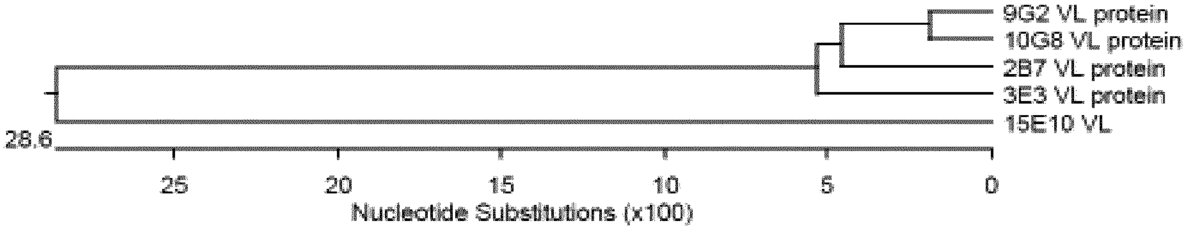
Figure 8

```
     D I V L T Q S P V S L V I S L G Q R A T I S C R A S K S V S  Majority
                       10                  20                  30
1    D I V L T Q S P V S L V I S L G Q R A T I S C R A S K S V S  2B7 VL protein
1    D I V L T Q S P A S L T I S L G Q R A T I S C R A S K S V S  3E3 VL protein
1    D I V L T Q S P V F L V I S L G Q R A T I S C R A S K S V S  9G2 VL protein
1    D I V L T Q S P V F L V V S L G Q R A T I S C R A S K S V S  10G8 VL protei

     A S G Y N F M H W Y Q Q K P G Q P P K V L I K Y A S N L E S  Majority
                       40                  50                  60
31   P S S Y N F M H W Y Q Q R P G Q P P K L L I T Y A S N L E S  2B7 VL protein
31   P S G Y D F M H W Y Q Q K P G Q P P K L L I K Y A S E L E S  3E3 VL protein
31   A S G Y N F M H W Y Q Q K P G Q P P K V L I K Y A S N L E S  9G2 VL protein
31   A A G Y N F M H W Y Q Q K P G Q P P K V L I K Y A S N L E S  10G8 VL protei

     G V P A R F S G S G S G T D F T L N I H P V E E E D A A T Y  Majority
                       70                  80                  90
61   G V P A R F S G S G S G T D F T L N I H P V E E E D A A T Y  2B7 VL protein
61   G V P G R F S G S G S G T D F T L N I H P V E E E D A A T Y  3E3 VL protein
61   G V P A R F S G S G S G T D F T L N I H P V E E E D A A T Y  9G2 VL protein
61   G V P A R F S G S G S G T D F T L N I H P V E E E D A V T Y  10G8 VL protei

     Y C Q H S R E F P F T F G G G T K L E I K                    Majority
                       100                 110
91   Y C Q H S R E F P F T F G G G T R L E I K                    2B7 VL protein
91   F C Q H S R E F P F T F G G G T K L E I K                    3E3 VL protein
91   Y C Q H S R E F P F T F G G G T K L E I K                    9G2 VL protein
91   Y C L H S R E F P F T F G G G T N L E I K                    10G8 VL protei
```

Decoration 'Decoration #1': Box residues that differ from the Consensus.

Figure 9

Phylogenetic tree of VH back ups vs 15E10 VL.meg ClustalW (Slow/Accurate, Gonnet) Page
10 December 2007 17:24



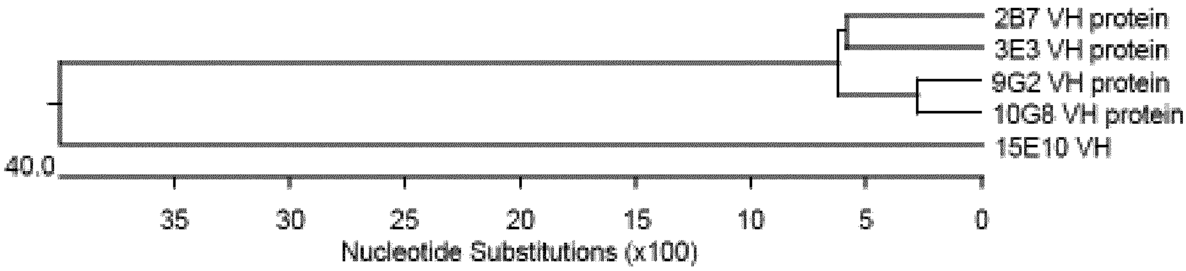
Sequence pair distances of VH back ups vs 15E10 VL.meg ClustalW (Slow/Accurate, Gonnet)
10 December 2007 17:23

Percent Identity (upper right); Divergence (lower left)

	1	2	3	4	5		
1		59.4	58.5	59.4	57.5	1	15E10 VL
2	55.8		91.0	92.8	90.1	2	2B7 VL protein
3	57.7	9.6		91.0	87.4	3	3E3 VL protein
4	55.8	7.6	9.6		96.4	4	9G2 VL protein
5	59.7	10.7	13.8	3.7		5	10G8 VL protein
	1	2	3	4	5		

Figure 10

Phylogenetic tree of VH back ups vs 15E10 VH.meg ClustalW (Slow/Accurate, Gonnet) F
10 December 2007 17:16



Sequence pair distances of VH back ups vs 15E10 VH.meg ClustalW (Slow/Accurate, Gonnet)
10 December 2007 17:16

Percent Identity (upper right); Divergence (lower left)

	1	2	3	4	5		
1		49.2	48.3	50.8	48.3	1	15E10 VH
2	79.9		89.3	94.2	90.1	2	2B7 VH protein
3	82.1	11.6		87.6	83.5	3	3E3 VH protein
4	75.5	6.0	13.6		95.0	4	9G2 VH protein
5	82.1	10.7	18.7	5.1		5	10G8 VH protein
	1	2	3	4	5		

Figure 11: Direct Human OSM Binding ELISA

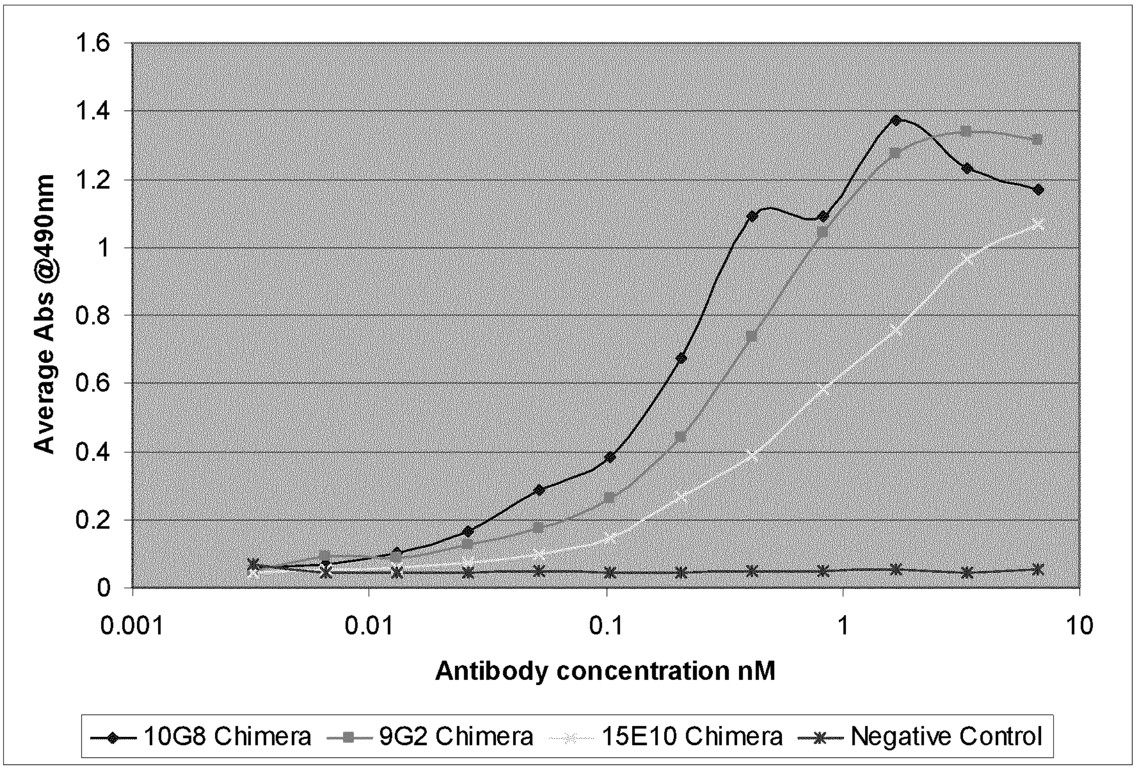


Figure 12: Human gp130 ELISA

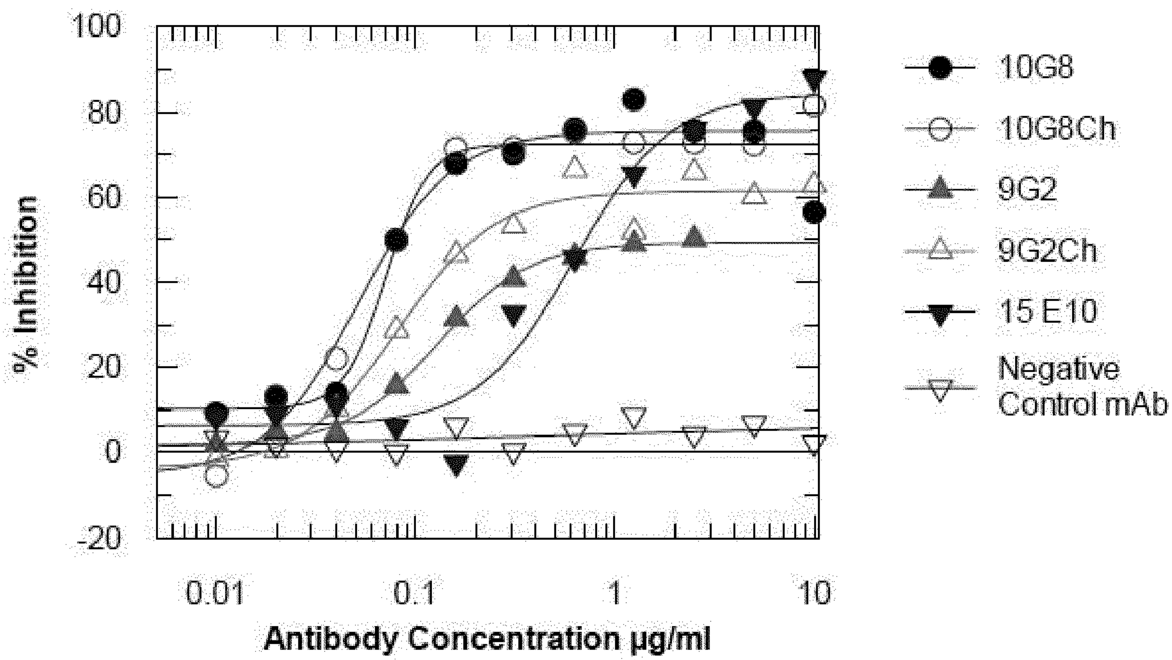


Figure 13: KB Cell Assay

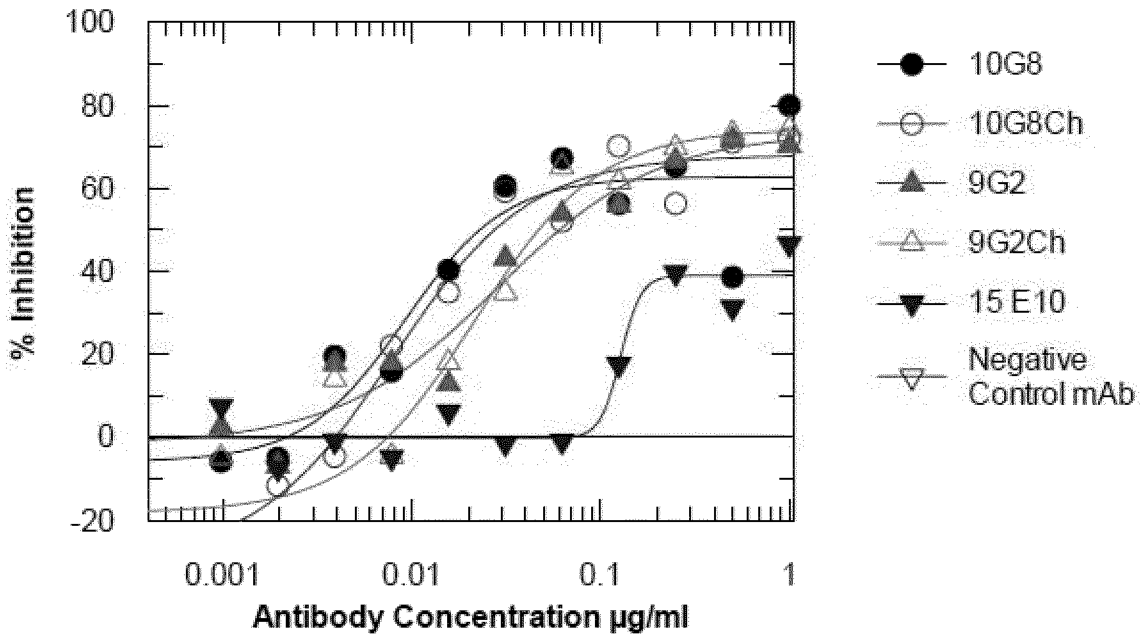


Figure 14: KB Cell Assay

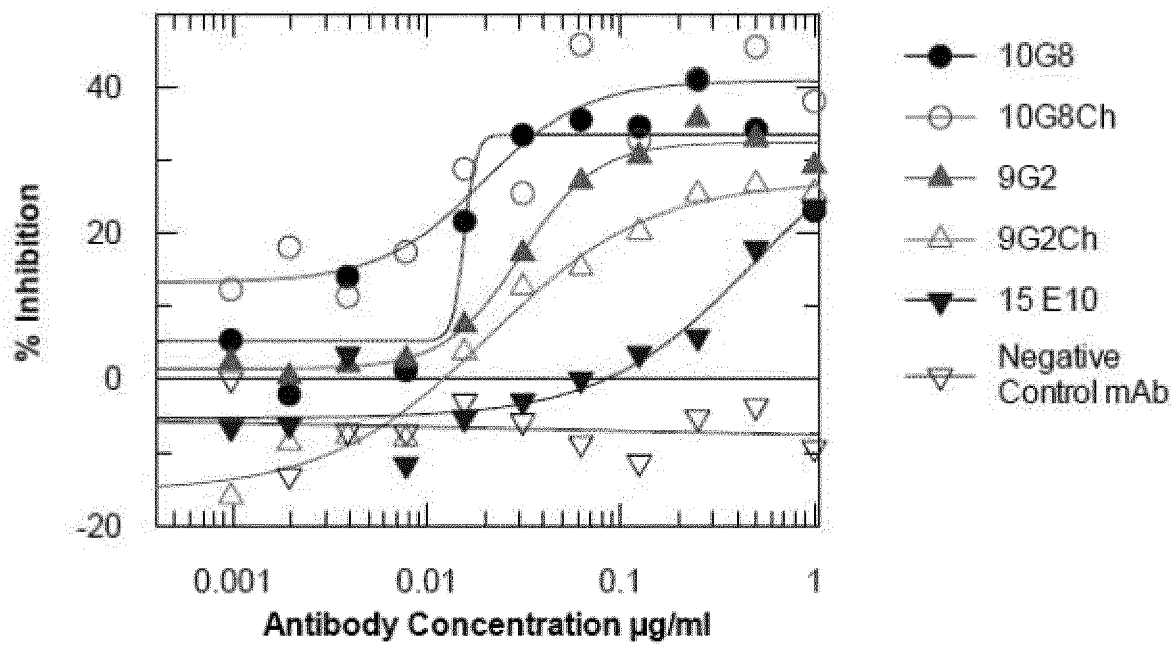


Figure 15: Endogenous OSM Human gp130 Assay

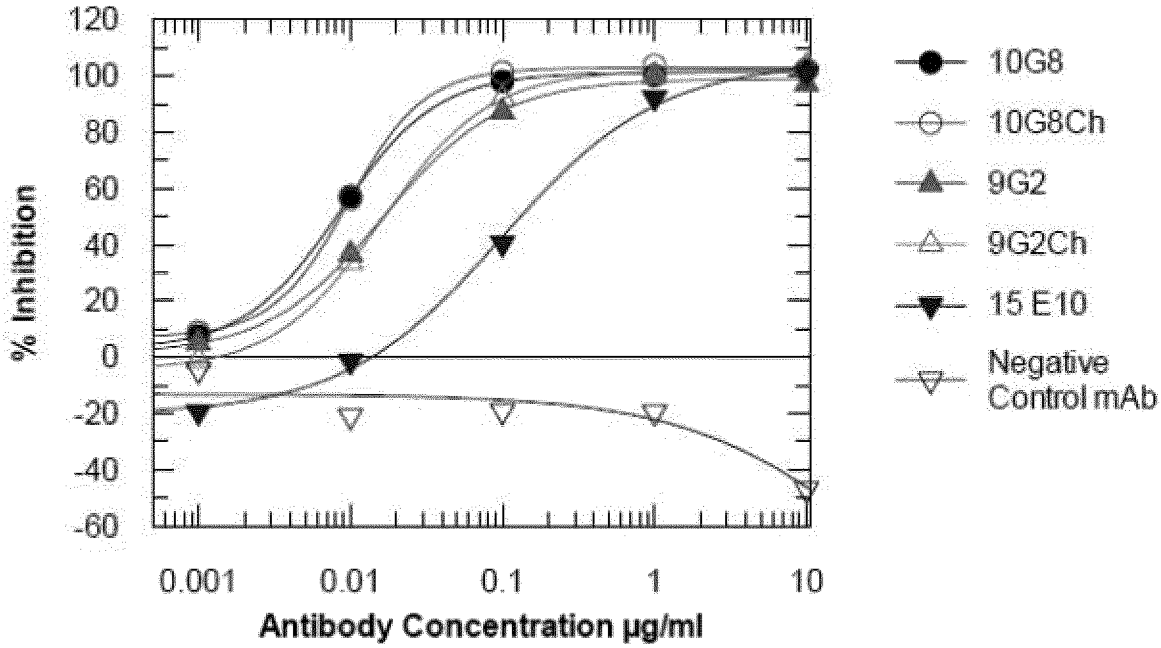


Figure 16: Human LIF KB Cell Assay

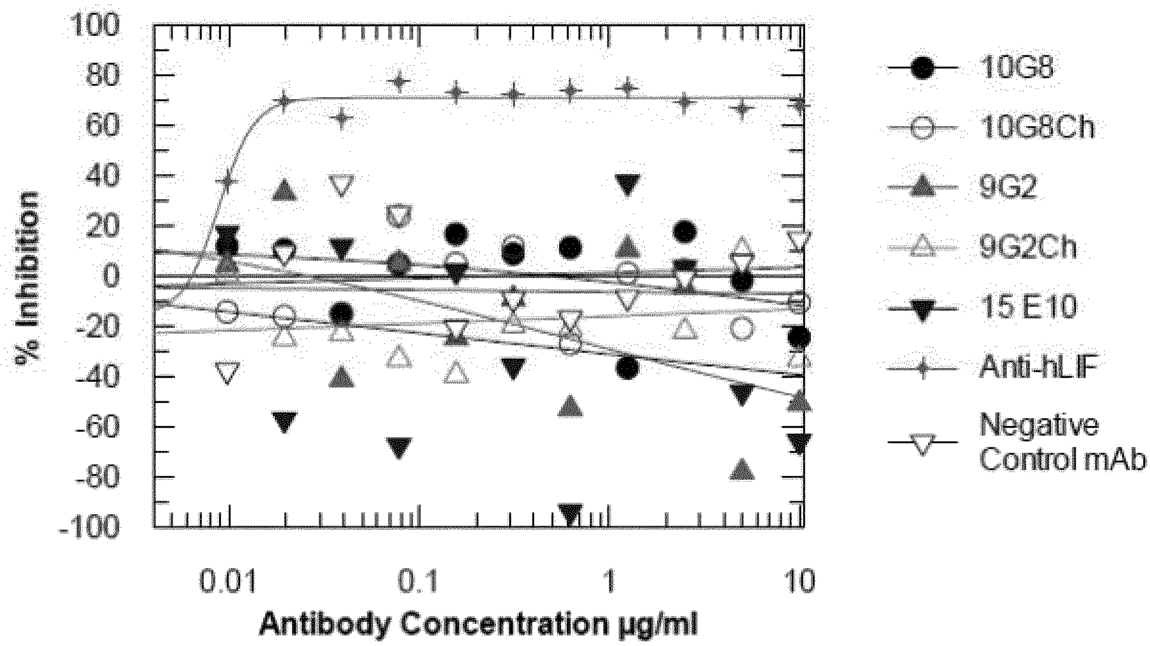


Figure 17: KB Cell Assay

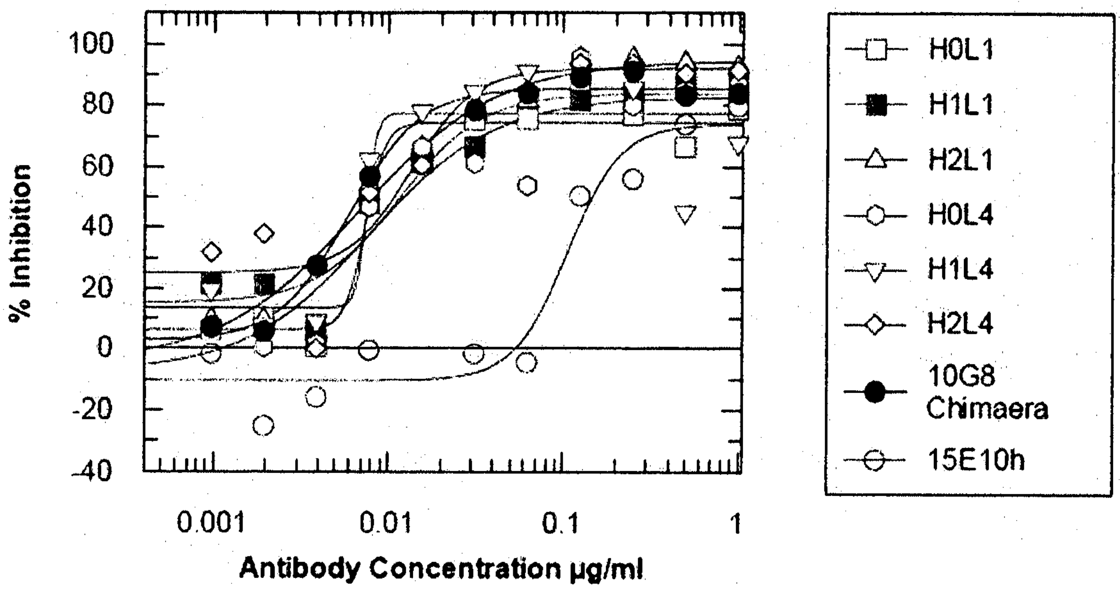


Figure 18: Human gp130 ELISA

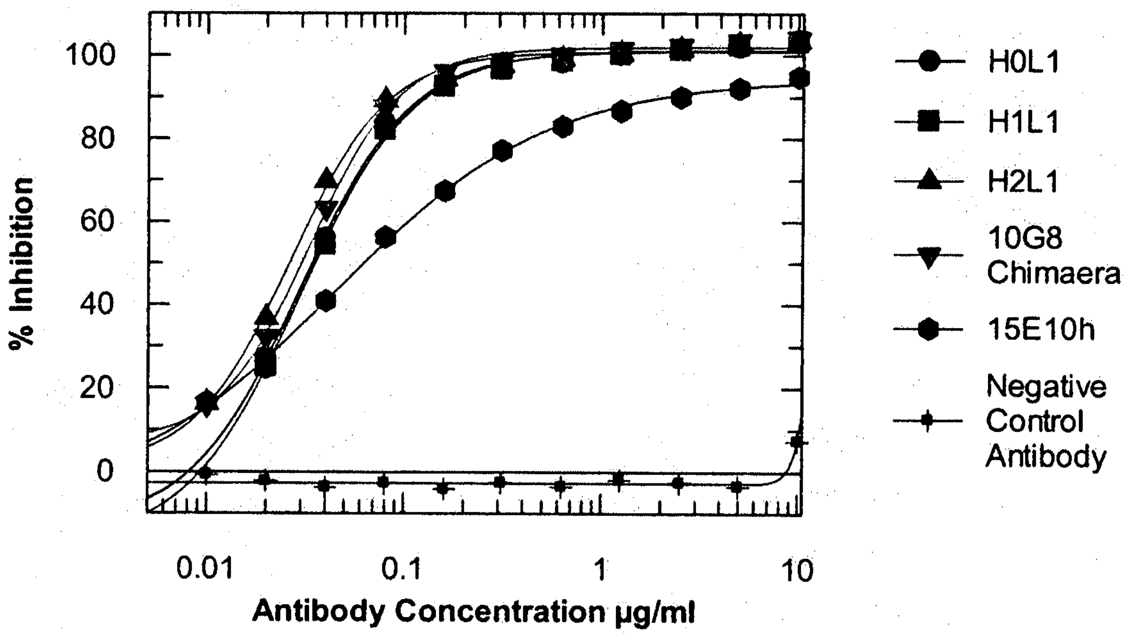


Figure 19: Human OSM-10G8 mAb Binding Complex-

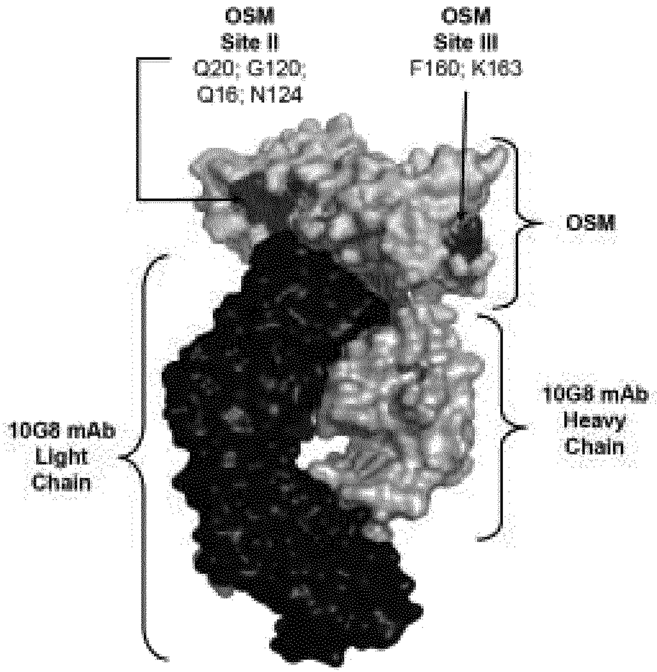


Figure 20: KB Cell Assay-

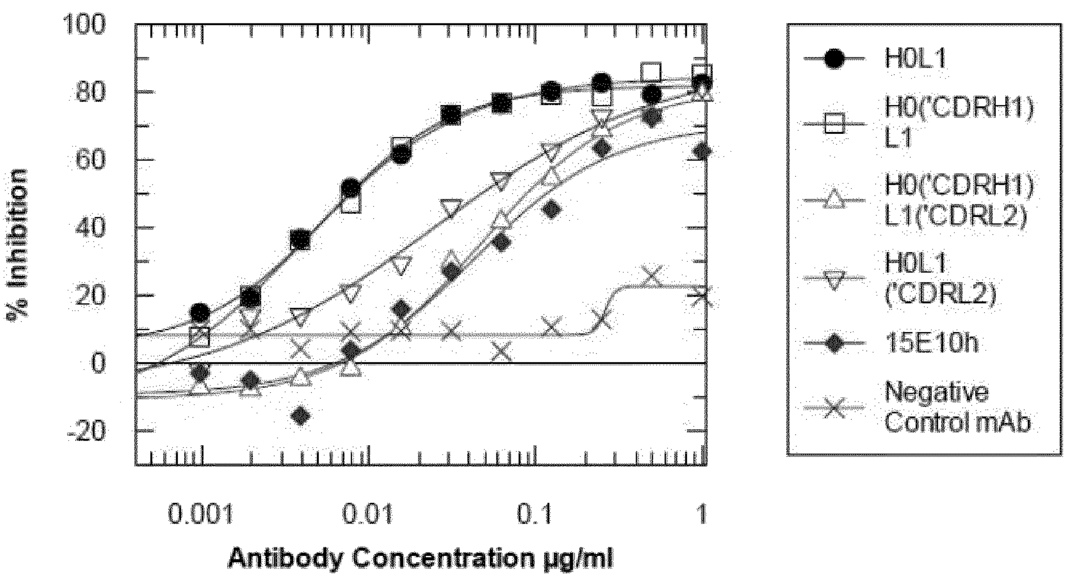


Figure 21: Human gp130 ELISA-

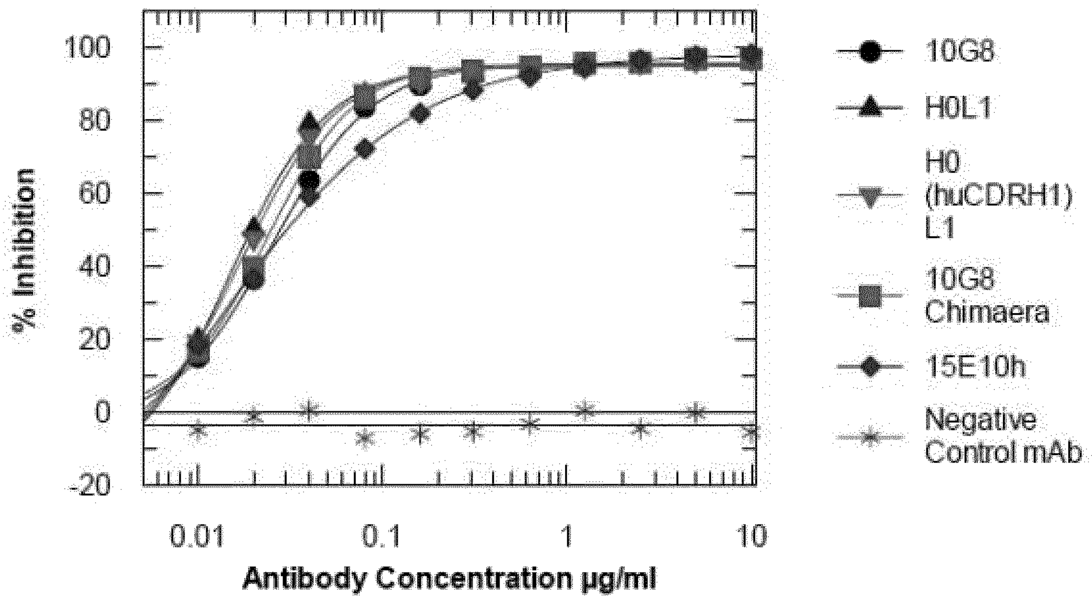


Figure 22: KB Cell Assay-

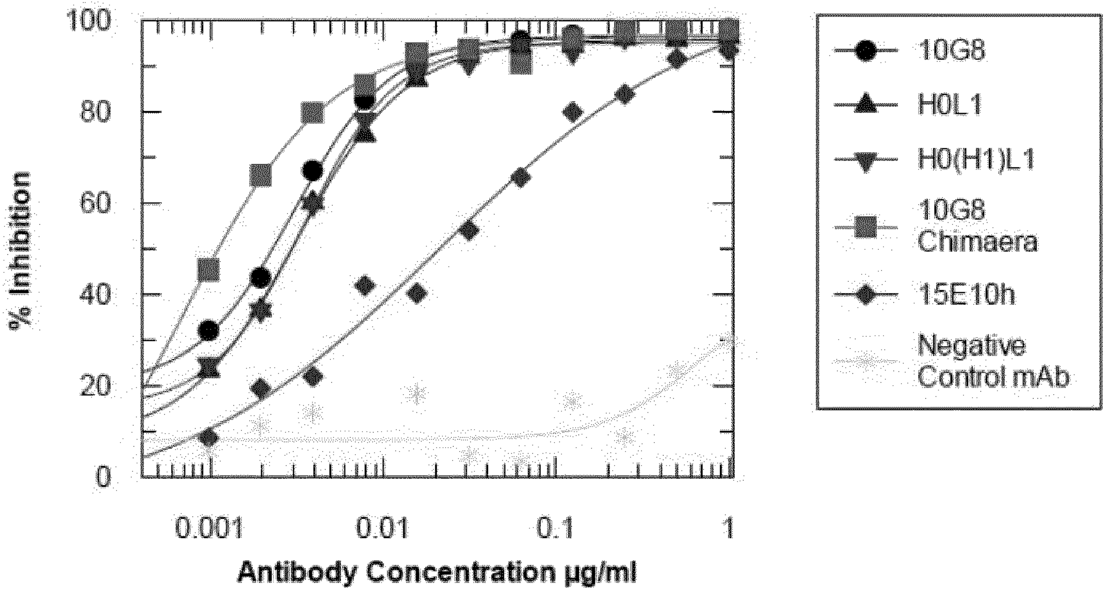


Figure 23: KB Cell Assay-

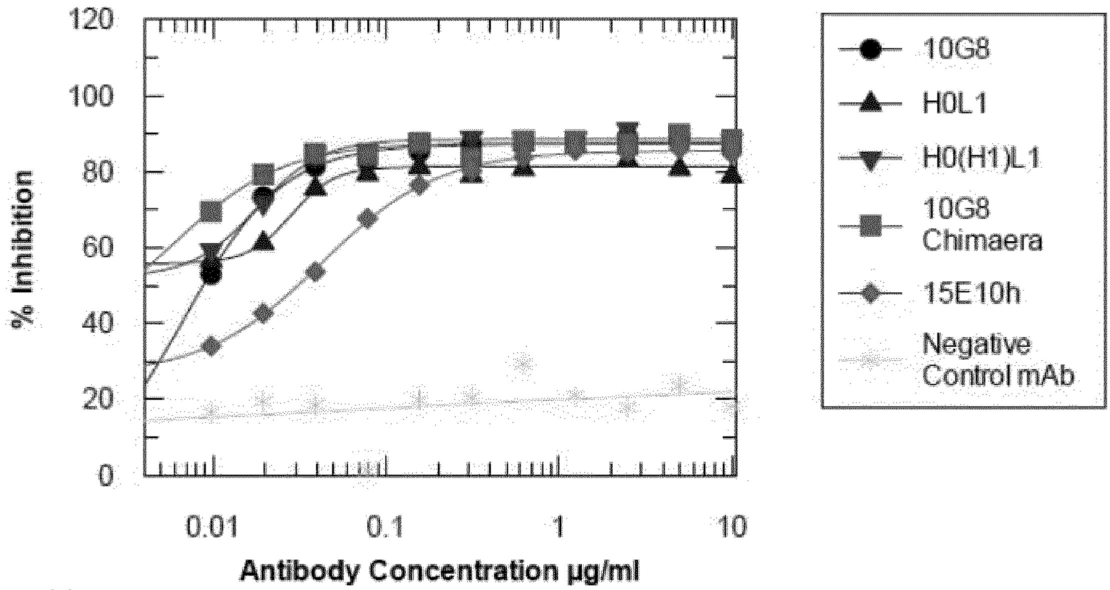


Figure 24:

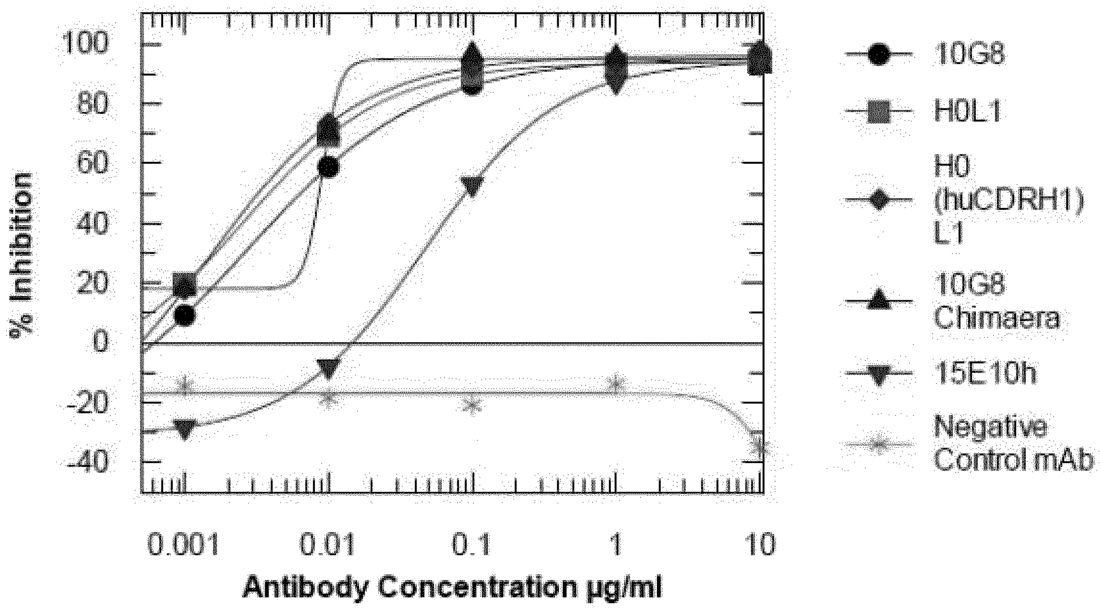


Figure 25:

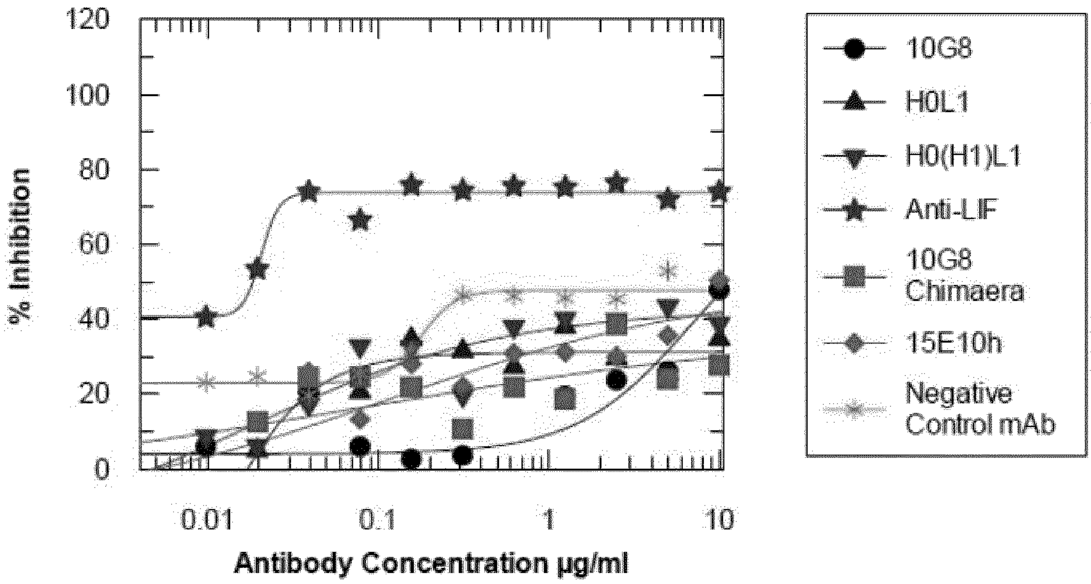


Figure 26: Human Hepatocyte Assay- SAA

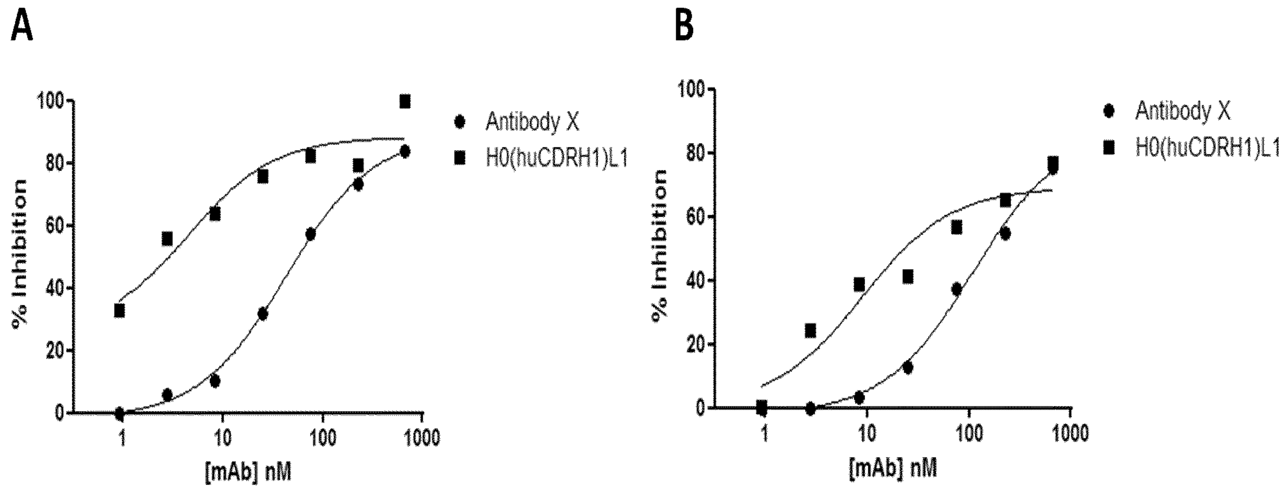


Figure 27: Human Hepatocyte Assay- CRP

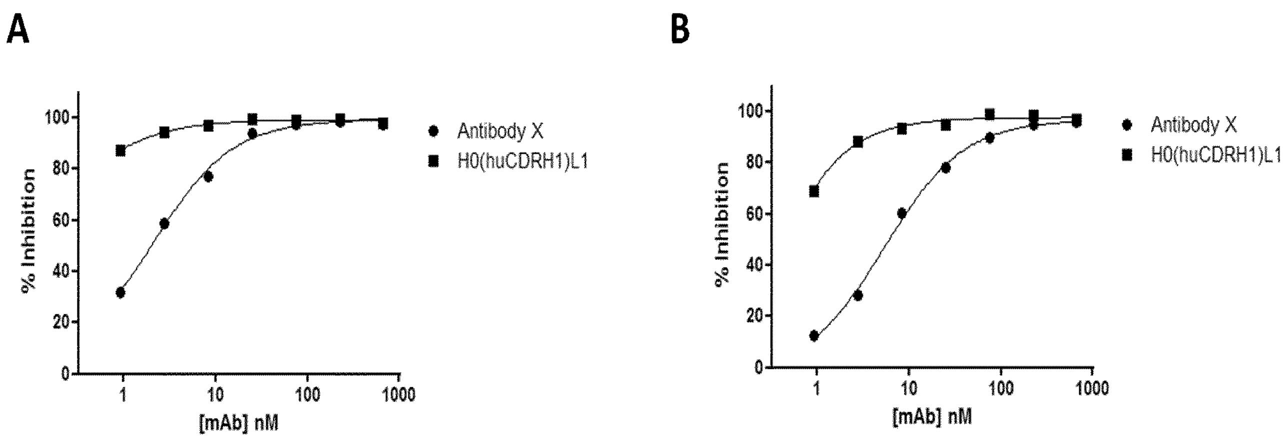


Figure 28: Human Fibroblast-Like Synovioctye Assay- IL-6

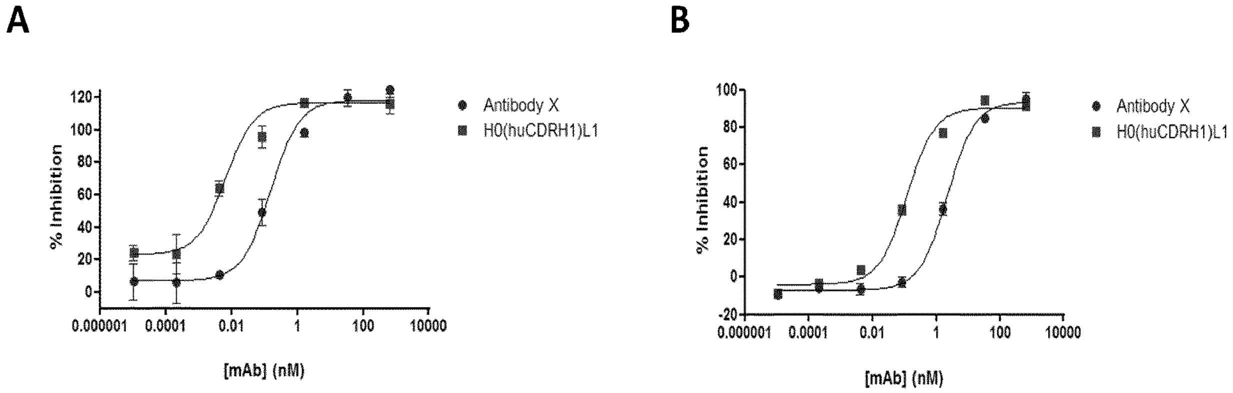


Figure 29: Human Fibroblast-Like Synovioctye Assay- MCP-1

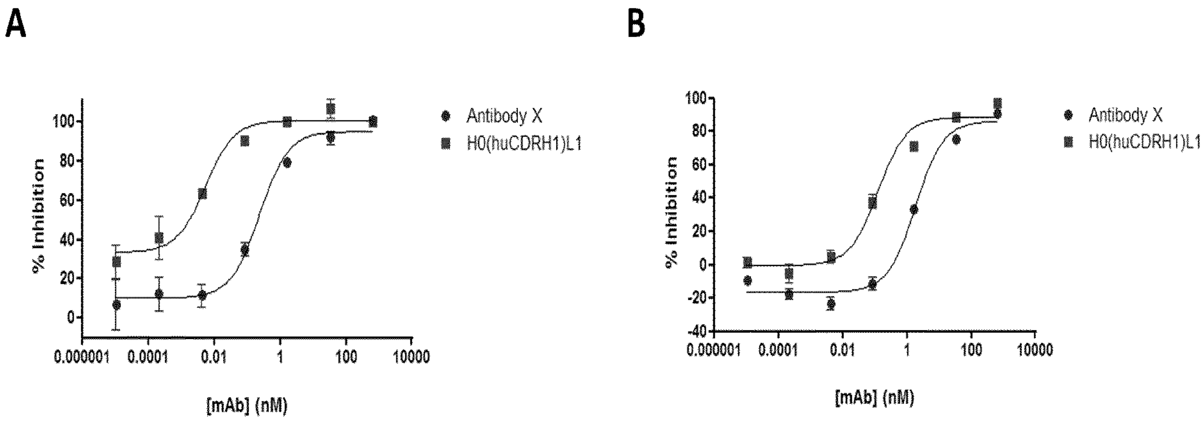


Figure 30: Human Umbilical-Vein Endothelia Cell Assay

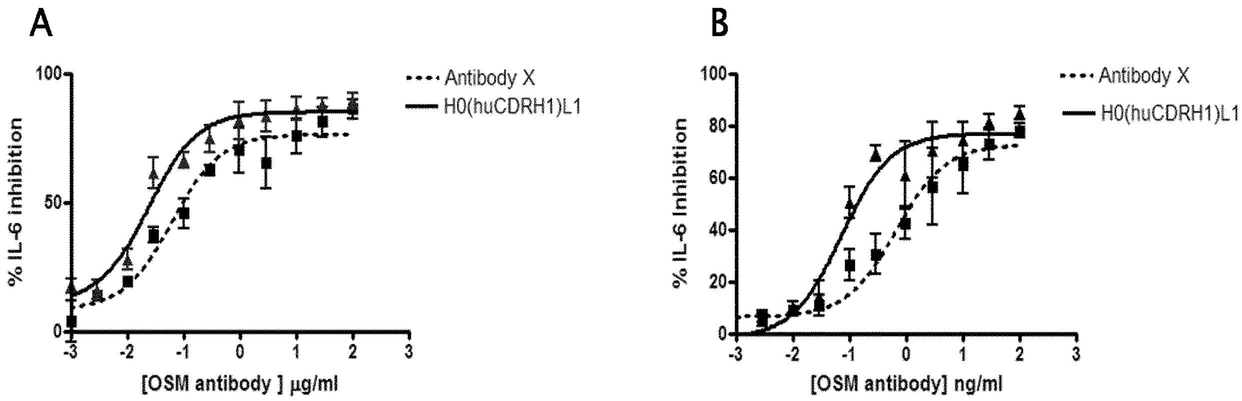


Figure 31: Human Lung Fibroblast Assay- MCP-1

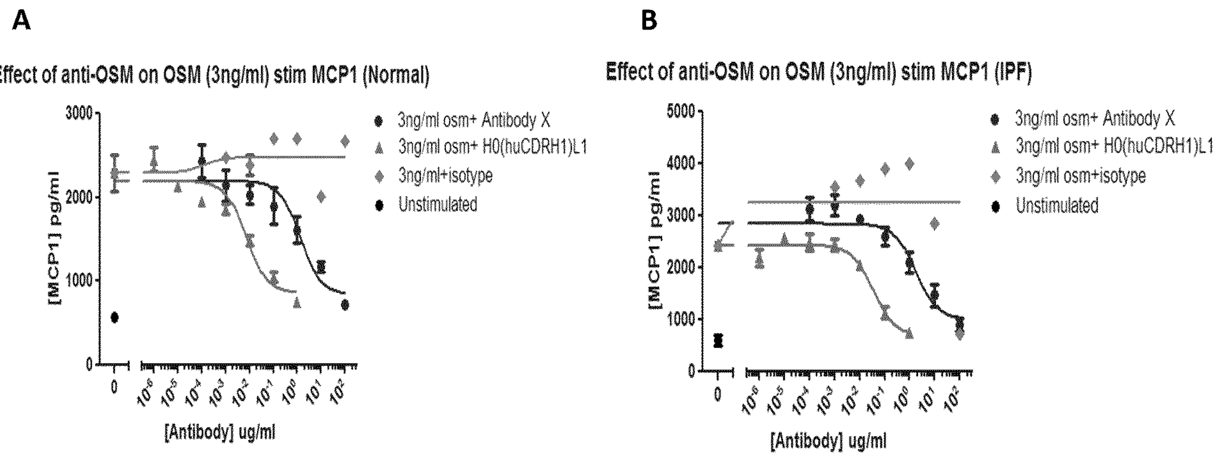


Figure 32: Human Lung Fibroblast Assay- IL-6

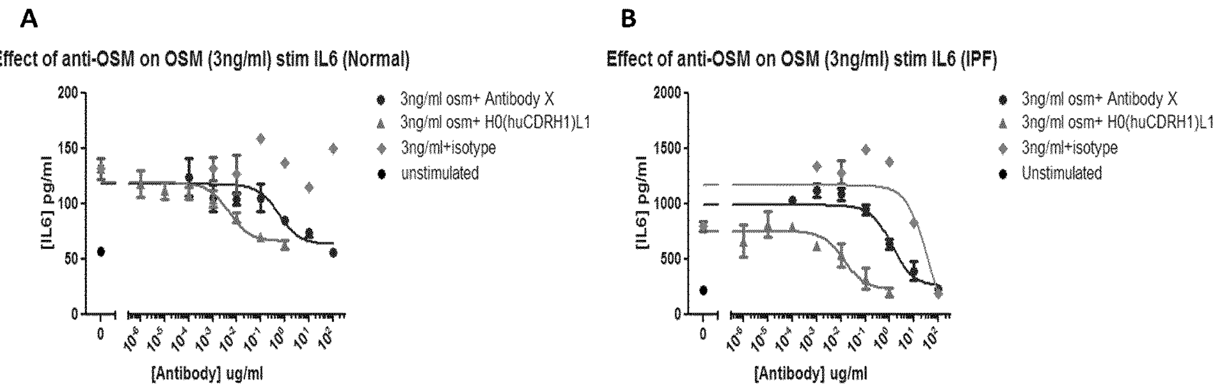


Figure 33.

Pos	95	96	97	98	99	100	100A	100B	100C	100D	101	102
Ala	5.76 E-10	5.72 E-10	4.86 E-10	6.59 E-10	5.41 E-10	8.55 E-09	8.10 E-09	4.81 E-09	3.94 E-10	8.69 E-10	1.55 E-09	3.38 E-10
Cys		6.64 E-10	6.51 E-10	1.50 E-09	7.08 E-10	8.95 E-09	8.92 E-09	8.12 E-09		5.86 E-10		
Asp	**4.42 E-10**			4.94 E-10	4.24 E-09		4,27 E-08	2.32 E-08		6.72 E-10	**3.55 E-10**	
Glu	7.85 E-10		1.10 E-09		1.28 E-09			4.91 E-10	4.82 E-10	6.88 E-10	4.26 E-10	
Phe		6.1 E-10	6.37 E-10	3.25 E-10	2.54 E-07		**4.47 E-10**	3.37 E-09	3.65 E-10	**4.50 E-10**	2.60 E-09	4.25 E-10
Gly	5.17 E-10	4.88 E-10	**3.07 E-10**	1.11 E-09	5.25 E-09	1.81 E-08	6.31 E-08	2.21 E-08	3.88 E-10	6.61 E-10	7.10 E-10	4.06 E-10
His	4.99 E-10	4.80 E-10		**1.74 E-10**	1.56 E-08		3.97 E-08	3.62 E-08	1.20 E-09			
Ile				7.18 E-09	1.69 E-09	1.87 E-08	2.46 E-08	4.55 E-08				
Lys		6.71 E-10		2.45 E-08	4.06 E-09	4.31 E-09		4.71 E-08		8.73 E-10	2.83 E-09	
Leu	5.68 E-10	5.55 E-10	2.19 E-09	7.42 E-10	1.56 E-09	4.20 E-08	3.35 E-09	1.62 E-08	4.24 E-10			4.26 E-10
Met	6.49 E-10		8.09 E-10	6.93 E-09	1.62 E-09		5.19 E-09	4.03 E-08				
Asn					1.33 E-09		6.58 E-09	4.02 E-08				
Pro	4.42 E-10	2.35 E-09	3.15 E-08	9.86 E-10	5.53 E-10	3.65 E-08		1.14 E-08		1.05 E-09	5.01 E-09	4.11 E-10
Gln	5.70 E-10			7.29 E-10			1.46 E-08	3.35 E-09	1.17 E-09		1.10 E-09	3.37 E-10

Arg	6.84 E-09	1.56 E-08	1.85 E-09	3.02 E-09	6.80 E-09			2.13 E-08	1.09 E-09	1.34 E-09	2.18 E-09	5.33 E-10
Ser	7.60 E-10	4.67 E-10	6.32 E-10	1.09 E-09	8.27 E-10	1.65 E-09	1.83 E-08	7.74 E-09	1.20 E-09	6.61 E-10	7.72 E-10	4.44 E-10
Thr	6.32 E-10	4.97 E-10	3.64 E-09	1.66 E-09	**3.99 E-10**	**4.57 E-10**	3.34 E-08	8.57 E-09	1.09 E-09	5.91 E-10	7.07 E-10	
Val	5.70 E-10	**4.88 E-10**	2.01 E-09	1.00 E-09	7.14 E-10	1.45 E-08	9.05 E-09	4.12 E-08	5.60 E-10	6.75 E-10	4.40 E-10	**4.26 E-10**
Trp	1.86 E-08	9.79 E-10	1.67 E-09	3.17 E-10	4.99 E-09		6.90 E-09	**4.95 E-10**	6.87 E-10	7.11 E-10	2.07 E-10	5.33 E-10
Tyr		6.78 E-10		2.07 E-09	4.44 E-10		1.41 E-08	6.76 E-09	**3.64 E-10**	5.09 E-10		

(black box) no binding

BOLD WT residue

(grey box) 3x decrease in binding

(dotted box) Data generated in a separate experiment

Figure 34