ONCOSTATIN M RECEPTOR ANTIGEN BINDING PROTEINS

CROSS-REFERENCE TO RELATED APPLICATIONS

[001] This application claims the benefit of priority to U.S. Provisional Appl. No. 61/829,082, filed May 30, 2013, the content of which is incorporated by reference in its entirety herein.

BACKGROUND OF THE INVENTION

[002] Oncostatin M (OSM) and Interleukin-31 (IL-31) are members of the IL-6 superfamily and share a receptor subunit, oncostatin M receptor-β (OSMR) (Dillon et al., Nat. Immunol. 5(7): 752-60, 2004). All of the members of this family, except IL-31, share the common chain of glycoprotein 130 (gp130) in their multimeric receptor complexes. OSM signals through a heterodimeric receptor complex containing OSMR and gp130, while IL-31 utilizes a gp130-like receptor, IL-31R, in combination with OSMR (Dillon et al., *supra*; Dreuw et al., J. Biol. Chem. 279(34): 36113-20, 2004). In general, OSMR and gp130 are expressed fairly ubiquitously across tissues and cell types, and can be induced under a variety of stimulation conditions. IL-31R expression appears to be relatively more restricted and tightly regulated. In human and mice alike, IL-31R mRNA expression is detectable at low levels in tissues such as trachea, skeletal muscle, thymus and bone marrow (Dillon et al., *supra*). Although the level of expression is starkly different, both IL-31R and OSMR are co-expressed on a multitude of tissues, including skin and intestinal epithelial cells, suggesting those tissues should respond to IL-31 (Dillon et al., *supra*; Dambacher et al., Gut 56(9): 1257-65, 2007). While OSMR is expressed constitutively in the lung on epithelial cells, IL-31R expression is at negligible to low levels in the lung tissue, but upregulated upon various methods of airway challenge (Dillon et al., *supra*; Jawa et al., J. Interferon Cytokine Res. 28(4): 207-19, 2008).

[003] Secreted primarily by T lymphocytes, macrophages, and neutrophils, OSM and IL-31 are both upregulated in a variety of disease states that involve inflammation. OSM has been implicated in diverse biological roles including bone formation, cartilage degradation, cholesterol uptake, pain and inflammation (Cawston et al., Arthritis Rheum. 41(10):1760-71, 1998; Hasegawa et al., Rheumatology (Oxford) 38(7): 612-7, 1999; Levy et al., J. Hepatol. 32(2): 218-26, 2000; Manicourt et al., Arthritis. Rheum. 43(2): 281-8, 2000; de Hooge et al., Am J. Pathol. 160(5):1733-43, 2002; Luzina et al., Arthritis Rheum 48(8): 2262-74, 2003; Morikawa et al., J. Neurosci. 24(8): 1941-7, 2004; Kong et al., J. Lipid Res. 46(6): 1163-71,

2005). OSM has been demonstrated to be a potent modulator of extracellular matrix (ECM) in a variety of contexts, suggesting that OSM is able to mediate seemingly opposite pathological consequences, including fibrosis (an excess of ECM) and cartilage degradation (a breakdown of ECM). Depending on tissue type and environmental milieu, both of these effects have been observed when OSM has been overexpressed or exogenously administered into lungs or joints of mice, respectively (Richards et al., Biochem. Soc. Trans. 30(2): 107-11, 2002; Hui et al., Arthritis Rheum. 48(12): 3404-18, 2003; Rowan et al., Am. J. Pathol. 162(6): 1975-84, 2003). In addition, OSM has previously been shown to be upregulated in human pathologies where these types of consequences exist (Cawston et al., *supra*; Hasegawa et al., *supra*; Levy et al., *supra*; Manicourt et al., *supra*; Luzina et al., *supra*). Predominantly, a locally-acting cytokine, OSM is upregulated in the synovial fluid from joints of patients with rheumatoid arthritis (RA) (Cawston et al., *supra*; Manicourt et al., *supra*), in the broncheoalevolar lavage (BAL) fluid of patients with scleroderma-associated interstitial lung disease (Luzina et al., *supra*), idiopathic pulmonary fibrosis (IPF), and in the livers of patients with cirrhosis (Levy et al., *supra*). The proposed impact on ECM by OSM can be attributed in part to the ability of OSM to shift the balance between matrix metalloproteinases (MMPs) and tissue inhibitors of MMPs (TIMPs). TIMPs bind to MMPs in a 1:1 ratio with a high affinity that results in a loss of MMP proteolytic activity. TIMP-1 and TIMP-3 have been previously shown to be differentially regulated by OSM, resulting in an increase in TIMP-1 and a decrease in TIMP-3 (Gatsios et al., Eur. J. Biochem. 241(1): 56-63, 1996). In addition to regulating the digestion of extracellular matrix components, MMPs are also implicated in the cleaving and subsequent activation of a number of proteins, including TGF-β, a potent pro-fibrotic cytokine (Leask et al., FASEB J. 18(7): 816-27, 2004). OSM has also been reported to be capable of directly inducing the transcription of type I collagen *in vitro* (Hasegawa et al., J. Rheumatol. 25(2): 308-13, 1998).

[004] Expression of both OSM and IL-31 has been found in the skin of patients with psoriasis and atopic dermatitis, and mutations in OSMR and IL-31R have been linked to systemic cutaneous amyloidosis. System-wide transgenic overexpression of IL-31 induced a pruritic inflammatory response in the skin of mice. Both OSM and IL-31 both signal through OSMR on neurons where they have been suggested to promote nociceptive and pruritic responses.

[005] Collectively, these links to human diseases and the ability of OSM and IL-31 to promote a diverse array of pathologies, including at least inflammation, extracellular matrix remodeling, pain, and pruritis, suggest blockade of OSMR is a useful target for therapeutic intervention in many diseases and disorders associated with OSMR.

SUMMARY OF THE INVENTION

[006] The invention provides anti-OSMR antigen binding proteins, e.g., antibodies and functional fragments thereof, having properties amenable to commercial production and therapeutic use in humans. The anti-OSMR antigen binding proteins are useful in methods of treating diseases and disorders associated with OSMR and, particularly, those associated with the binding of OSM or IL-31 to OSMR. Provided herein are OSMR-binding antibodies that bind OSMR with high affinity and effectively block OSM and/or IL-31 binding to OSMR, thereby reducing OSMR-mediated signaling in the cell.

[007] In a first aspect, the OSMR antigen binding protein comprises a) a light chain variable domain having at least 90% identity, at least 95% identity, or is identical to the amino acid sequence set forth in SEQ ID NO:27, SEQ ID NO:28, or SEQ ID NO:29; b) a heavy chain variable domain having at least 90% identity, at least 95% identity, or is identical to the amino acid sequence set forth in SEQ ID NO:9, SEQ ID NO:10, or SEQ ID NO:11; or c) the light chain variable domain of a) and the heavy chain variable domain of b).

[008] Preferred antigen binding proteins of the first aspect include those comprising a light chain variable domain having at least 90%, at least 95%, or is identical to the amino acid sequence set forth in SEQ ID NO:27 and a heavy chain variable domain having at least 90%, at least 95%, or is identical to the amino acid sequence set forth in SEQ ID NO:9; those comprising a light chain variable domain having at least 90%, at least 95%, or is identical to the amino acid sequence set forth in SEQ ID NO:28 and a heavy chain variable domain having at least 90%, at least 95%, or is identical to the amino acid sequence set forth in SEQ ID NO:10; and those comprising a light chain variable domain having at least 90%, at least 95%, or is identical to the amino acid sequence set forth in SEQ ID NO:29 and a heavy chain variable domain having at least 90%, at least 95%, or is identical to the amino acid sequence set forth in SEQ ID NO:11.

OSMR antigen binding proteins comprising a heavy chain variable domain having the above-defined sequence relatedness to SEQ ID NO:9 can optionally contain an amino acid other than asparagine (for example, aspartic acid) at the position corresponding to position 73 in SEQ ID NO:9. In such embodiments, the heavy chain variable domain optionally comprises the amino acid sequence set forth in SEQ ID NO:53.

OSMR antigen binding proteins comprising a heavy chain variable domain having the above-defined sequence relatedness to SEQ ID NO:10 can optionally contain an amino acid other than

asparagine (for example, aspartic acid) at the position corresponding to position 73 in SEQ ID NO:10. In such embodiments, the heavy chain variable domain optionally comprises the amino acid sequence set forth in SEQ ID NO:54.

[009] In a second aspect, the OSMR antigen binding protein comprises a) a light chain variable domain having no more than ten or no more than five amino acid additions, deletions or substitutions from the amino acid sequence set forth in SEQ ID NO:27, SEQ ID NO:28, or SEQ ID NO:29; b) a heavy chain variable domain having no more than ten or no more than five amino acid additions, deletions or substitutions from the amino acid sequence set forth in SEQ ID NO:9, SEQ ID NO:10, or SEQ ID NO:11; or c) the light chain variable domain of a) and the heavy chain variable domain of b).

[0010] Preferred antigen binding proteins of the second aspect include those comprising a light chain variable domain having no more than ten or no more than five amino acid additions, deletions or substitutions from the amino acid sequence set forth in SEQ ID NO:27 and a heavy chain variable domain having no more than ten or no more than five amino acid additions, deletions or substitutions from the amino acid sequence set forth in SEQ ID NO:9; those comprising a light chain variable domain having no more than ten or no more than five amino acid additions, deletions or substitutions from the amino acid sequence set forth in SEQ ID NO:28 and a heavy chain variable domain having no more than ten or no more than five amino acid additions, deletions or substitutions from the amino acid sequence set forth in SEQ ID NO:10; and those comprising a light chain variable domain having no more than ten or no more than five amino acid additions, deletions or substitutions from the amino acid sequence set forth in SEQ ID NO:29 and a heavy chain variable domain having no more than ten or no more than five amino acid additions, deletions or substitutions from the amino acid sequence set forth in SEQ ID NO:11.

OSMR antigen binding proteins comprising a heavy chain variable domain having the above-defined sequence relatedness to SEQ ID NO:9 can optionally contain an amino acid other than asparagine (for example, aspartic acid) at the position corresponding to position 73 in SEQ ID NO:9. In such embodiments, the heavy chain variable domain optionally comprises the amino acid sequence set forth in SEQ ID NO:53.

OSMR antigen binding proteins comprising a heavy chain variable domain having the above-defined sequence relatedness to SEQ ID NO:10 can optionally contain an amino acid other than asparagine (for example, aspartic acid) at the position corresponding to position 73 in SEQ ID

NO:10. In such embodiments, the heavy chain variable domain optionally comprises the amino acid sequence set forth in SEQ ID NO:54.

[0011] In a third aspect, the OSMR antigen binding protein contains a light chain variable domain comprising a) an LCDR1 having no more than three amino acid additions, deletions, or substitutions from the LCDR1 sequence set forth in SEQ ID NO:30; an LCDR2 having no more than three amino acid additions, deletions, or substitutions from the LCDR2 sequence set forth in SEQ ID NO:33; and an LCDR3 having no more than three amino acid additions, deletions, or substitutions from the LCDR3 sequence set forth in SEQ ID NO:36; b) an LCDR1 having no more than three amino acid additions, deletions, or substitutions from the LCDR1 sequence set forth in SEQ ID NO:31; an LCDR2 having no more than three amino acid additions, deletions, or substitutions from the LCDR2 sequence set forth in SEQ ID NO:34; and an LCDR3 having no more than three amino acid additions, deletions, or substitutions from the LCDR3 sequence set forth in SEQ ID NO:37; or c) an LCDR1 having no more than three amino acid additions, deletions, or substitutions from the LCDR1 sequence set forth in SEQ ID NO:32; an LCDR2 having no more than three amino acid additions, deletions, or substitutions from the LCDR2 sequence set forth in SEQ ID NO:35; and an LCDR3 having no more than three amino acid additions, deletions, or substitutions from the LCDR3 sequence set forth in SEQ ID NO:38; and a heavy chain variable domain comprising d) an HCDR1 having no more than three amino acid additions, deletions, or substitutions from the HCDR1 sequence set forth in SEQ ID NO:12; an HCDR2 having no more than three amino acid additions, deletions, or substitutions from the HCDR2 sequence set forth in SEQ ID NO:15; and an HCDR3 having no more than three amino acid additions, deletions, or substitutions from the HCDR3 sequence set forth in SEQ ID NO:18; e) an HCDR1 having no more than three amino acid additions, deletions, or substitutions from the HCDR1 sequence set forth in SEQ ID NO:13; an HCDR2 having no more than three amino acid additions, deletions, or substitutions from the HCDR2 sequence set forth in SEQ ID NO:16; and an HCDR3 having no more than three amino acid additions, deletions, or substitutions from the HCDR3 sequence set forth in SEQ ID NO:19; or f) an HCDR1 having no more than three amino acid additions, deletions, or substitutions from the HCDR1 sequence set forth in SEQ ID NO:14; an HCDR2 having no more than three amino acid additions, deletions, or substitutions from the HCDR2 sequence set forth in SEQ ID NO:17; and an HCDR3 having no more than three amino acid additions, deletions, or substitutions from the HCDR3 sequence set forth in SEQ ID NO:20.

[0012] Preferred OSMR antigen binding proteins of third aspect include those comprising the light chain variable domain of a) and the heavy chain variable domain of d); those comprising the light chain variable domain of b) and the heavy chain variable domain of e); and those comprising the light chain variable domain of c) and the heavy chain variable domain of f).

OSMR antigen binding proteins comprising the light chain variable domain of a) and the heavy chain variable domain of d) can optionally contain a heavy chain variable domain that comprises an amino acid other than asparagine (for example, aspartic acid) at the position corresponding to position 73 in SEQ ID NO:9. In such embodiments, the heavy chain variable domain optionally comprises the amino acid sequence set forth in SEQ ID NO:53.

OSMR antigen binding proteins comprising the light chain variable domain of b) and the heavy chain variable domain of e) can optionally contain a heavy chain variable domain that comprises an amino acid other than asparagine (for example, aspartic acid) at the position corresponding to position 73 in SEQ ID NO:10. In such embodiments, the heavy chain variable domain optionally comprises the amino acid sequence set forth in SEQ ID NO:54.

[0013] In a fourth aspect of the invention, the OSMR antigen binding protein of the first, second, or third aspect binds to human OSMR with an affinity of less than or equal to 1×10^{-10} M.

[0014] In a fifth aspect of the invention, the OSMR antigen binding protein of the first, second, third, or fourth aspect inhibits binding of human OSM to human OSMR and/or human IL-31 to human OSMR.

[0015] In a sixth aspect of the invention, the OSMR antigen binding protein of the first, second, third, fourth, or fifth aspect reduces human OSM-mediated and/or human IL-31-mediated OSMR signaling in human OSMR-expressing cells.

[0016] In a seventh aspect of the invention, the OSMR antigen binding protein of the sixth aspect reduces cynomolgus monkey OSM-mediated and/or IL-31-mediated OSMR signaling in cynomolgus monkey OSMR-expressing cells.

[0017] In an eighth aspect of the invention, the OSMR antigen binding protein of the first, second, third, fourth, fifth, sixth or seventh aspect is an antibody, such as a human antibody. Preferred antibodies include those antibodies that comprise a light chain having the amino acid sequence set forth in SEQ ID NO:24 and a heavy chain having the amino acid sequence set forth in SEQ ID NO:6; those that comprise a light chain having the amino acid sequence set forth in SEQ ID:25 and a heavy chain having the amino acid sequence set forth in SEQ ID

NO:7; and those that comprise a light chain having the amino acid sequence set forth in SEQ ID:26 and a heavy chain having the amino acid sequence set forth in SEQ ID NO:8.

Additional antibodies include those antibodies that comprise a light chain having the amino acid sequence set forth in SEQ ID NO:24 and a heavy chain having the amino acid sequence set forth in SEQ ID NO:50; those that comprise a light chain having the amino acid sequence set forth in SEQ ID:25 and a heavy chain having the amino acid sequence set forth in SEQ ID NO:51; and those that comprise a light chain having the amino acid sequence set forth in SEQ ID:26 and a heavy chain having the amino acid sequence set forth in SEQ ID NO:52.

[0018] In a ninth aspect, the invention provides nucleic acids or isolated nucleic acids encoding one or more polypeptide components of a OSMR antigen binding protein, e.g., an antibody light chain or antibody heavy chain. In preferred embodiments the nucleic acid encodes a polypeptide comprising:

[0019] a) a light chain variable domain having at least 95% identity to the amino acid sequence set forth in SEQ ID NO:27, SEQ ID NO:28, or SEQ ID NO:29;

[0020] b) a heavy chain variable domain having at least 95% identity to the amino acid sequence set forth in SEQ ID NO:9, SEQ ID NO:10, or SEQ ID NO:11;

[0021] c) a light chain variable domain having no more than five amino acid additions, deletions or substitutions from the amino acid sequence set forth in SEQ ID NO:27, SEQ ID NO:28, or SEQ ID NO:29;

[0022] d) a heavy chain variable domain having no more than five amino acid additions, deletions or substitutions from the amino acid sequence set forth in SEQ ID NO:9, SEQ ID NO:10, or SEQ ID NO:11;

[0023] e) a light chain variable domain comprising:

[0024] i) an LCDR1 having no more than three amino acid additions, deletions, or substitutions from the LCDR1 sequence set forth in SEQ ID NO:30; an LCDR2 having no more than three amino acid additions, deletions, or substitutions from the LCDR2 sequence set forth in SEQ ID NO:33; and an LCDR3 having no more than three amino acid additions, deletions, or substitutions from the LCDR3 sequence set forth in SEQ ID NO:36;

[0025] ii) an LCDR1 having no more than three amino acid additions, deletions, or substitutions from the LCDR1 sequence set forth in SEQ ID NO:31; an LCDR2 having no more than three amino acid additions, deletions, or substitutions from the LCDR2 sequence set

forth in SEQ ID NO:34; and an LCDR3 having no more than three amino acid additions, deletions, or substitutions from the LCDR3 sequence set forth in SEQ ID NO:37; or

[0026] iii) an LCDR1 having no more than three amino acid additions, deletions, or substitutions from the LCDR1 sequence set forth in SEQ ID NO:32; an LCDR2 having no more than three amino acid additions, deletions, or substitutions from the LCDR2 sequence set forth in SEQ ID NO:35; and an LCDR3 having no more than three amino acid additions, deletions, or substitutions from the LCDR3 sequence set forth in SEQ ID NO:38; or

[0027] f) a heavy chain variable domain comprising:

[0028] i) an HCDR1 having no more than three amino acid additions, deletions, or substitutions from the HCDR1 sequence set forth in SEQ ID NO:12; an HCDR2 having no more than three amino acid additions, deletions, or substitutions from the HCDR2 sequence set forth in SEQ ID NO:15; and an HCDR3 having no more than three amino acid additions, deletions, or substitutions from the HCDR3 sequence set forth in SEQ ID NO:18;

[0029] ii) an HCDR1 having no more than three amino acid additions, deletions, or substitutions from the HCDR1 sequence set forth in SEQ ID NO:13; an HCDR2 having no more than three amino acid additions, deletions, or substitutions from the HCDR2 sequence set forth in SEQ ID NO:16; and an HCDR3 having no more than three amino acid additions, deletions, or substitutions from the HCDR3 sequence set forth in SEQ ID NO:19; or

[0030] iii) an HCDR1 having no more than three amino acid additions, deletions, or substitutions from the HCDR1 sequence set forth in SEQ ID NO:14; an HCDR2 having no more than three amino acid additions, deletions, or substitutions from the HCDR2 sequence set forth in SEQ ID NO:17; and an HCDR3 having no more than three amino acid additions, deletions, or substitutions from the HCDR3 sequence set forth in SEQ ID NO:20.

In certain embodiments, the nucleic acid or isolated nucleic acid encodes a polypeptide that comprises the amino acid sequence set forth in SEQ ID NO:53 or SEQ ID NO:54.

In certain embodiments, the nucleic acid or isolated nucleic acid encodes a polypeptide that comprises the amino acid sequence set forth in SEQ ID NO:50, SEQ ID NO:51, or SEQ ID NO:52.

[0031] In certain embodiments of the ninth aspect, the nucleic acid or isolated nucleic acid encodes an antibody light chain and is at least 80%, at least 90%, at least 95%, or is 100% identical to the nucleotide sequence set forth in SEQ ID NO:21, SEQ ID NO:22, or SEQ ID

NO:23. In other embodiments of the ninth aspect, the nucleic acid or isolated nucleic acid encodes an antibody heavy chain and is at least 80%, at least 90%, at least 95%, or is 100% identical to the nucleotide sequence set forth in SEQ ID NO:3, SEQ ID NO:4, or SEQ ID NO:5.

In certain embodiments, the heavy chain is encoded by a nucleic acid comprising a nucleotide sequence set forth in SEQ ID NO:47, SEQ ID NO:48, or SEQ ID NO:49.

[0032] In a tenth aspect, the invention provides an expression vector comprising one or more nucleic acids or isolated nucleic acids of the eighth aspect. In certain embodiments, the expression vector encodes an antibody light chain, an antibody heavy chain, or both an antibody light chain and a heavy chain.

[0033] In an eleventh aspect, the invention provides a recombinant host cell comprising one or more nucleic acids or isolated nucleic acids of the ninth aspect operably linked to a promoter, including recombinant host cells comprising one or more expression vectors of the tenth aspect of the invention. In preferred embodiments, the recombinant host cell secretes an antibody that binds OSMR. Preferred host cells are mammalian host cells, including CHO cell lines.

[0034] In a twelfth aspect, the invention provides methods of treating an autoimmune disorder, an inflammatory disorder, or a disorder associated with extracellular matrix deposition or remodeling, said method comprising administering a therapeutically effective amount of an OSMR antigen binding protein of any one of the first, second, third, fourth, fifth, sixth, sixth, seventh, or eighth aspects to a patient in need thereof. In preferred embodiments, the OSMR antigen binding protein is an antibody comprising a light chain variable domain amino acid sequence as set forth in SEQ ID NO:27 and a heavy chain variable domain amino acid sequence as set forth in SEQ ID NO:9 (e.g., Ab1), an antibody comprising a light chain variable domain amino acid sequence as set forth in SEQ ID NO:28 and a heavy chain variable domain amino acid sequence as set forth in SEQ ID NO:10 (e.g., Ab2), or an antibody comprising a light chain variable domain amino acid sequence as set forth in SEQ ID NO:29 and a heavy chain variable domain amino acid sequence as set forth in SEQ ID NO:11 (e.g., Ab3). In some embodiments, the OSMR antigen binding protein is an antibody comprising a light chain variable domain amino acid sequence as set forth in SEQ ID NO:27 and a heavy chain variable domain amino acid sequence as set forth in SEQ ID NO:53, or an antibody comprising a light chain variable domain amino acid sequence as set forth in SEQ ID NO:28 and a heavy chain variable domain amino acid sequence as set forth in SEQ ID NO:54. In

preferred embodiments, the OSMR antigen binding protein inhibits binding of OSM to OSMR or IL-31 to OSMR. In particularly preferred embodiments, the autoimmune disorder, inflammatory disorder, or disorder associated with extracellular matrix deposition or remodeling is fibrosis, cartilage degradation, arthritis, rheumatoid arthritis, scleroderma, scleroderma-associated interstitial lung disease, idiopathic pulmonary fibrosis, cirrhosis, psoriasis, atopic dermatitis, systemic cutaneous amyloidosis, primary cutaneous amyloidosis, inflammation, pruritic inflammation, prurigo nodularis, and pain.

[0035] In a thirteenth aspect, the invention provides a method of making an OSMR antigen binding protein of any one of the first, second, third, fourth, fifth, sixth, sixth, seventh, or eighth aspects by culturing a recombinant host cell of the eleventh aspect and isolating the OSMR antigen binding protein from said culture.

[0036] In a fourteenth aspect, the invention provides OSMR antigen binding proteins of any one of the first, second, third, fourth, fifth, sixth, sixth, seventh, or eighth aspects that cross-compete with an antibody selected from the group consisting of:

[0037] a) an antibody comprising a light chain comprising the amino acid sequence set forth in SEQ ID:24 and a heavy chain comprising the amino acid sequence set forth in SEQ ID NO:6;

[0038] b) an antibody comprising a light chain comprising the amino acid sequence set forth in SEQ ID:25 and a heavy chain comprising the amino acid sequence set forth in SEQ ID NO:7; and

[0039] c) an antibody comprising a light chain comprising the amino acid sequence set forth in SEQ ID:26 and a heavy chain comprising the amino acid sequence set forth in SEQ ID NO:8.

DETAILED DESCRIPTION

[0040] The section headings used herein are for organizational purposes only and are not to be construed as limiting the subject matter described. All references cited within the body of this specification are expressly incorporated by reference in their entirety.

[0041] Standard techniques may be used for recombinant DNA, oligonucleotide synthesis, tissue culture and transformation, protein purification, etc. Enzymatic reactions and purification techniques may be performed according to the manufacturer's specifications or as commonly accomplished in the art or as described herein. The following procedures and techniques may be generally performed according to conventional methods well known in the art and as described in various general and more specific references that are cited and discussed

throughout the specification. *See, e.g.*, Sambrook *et al.*, 2001, *Molecular Cloning: A Laboratory Manuel*, 3rd ed., Cold Spring Harbor Laboratory Press, cold Spring Harbor, N.Y., which is incorporated herein by reference for any purpose. Unless specific definitions are provided, the nomenclature used in connection with, and the laboratory procedures and techniques of, analytic chemistry, organic chemistry, and medicinal and pharmaceutical chemistry described herein are those well known and commonly used in the art. Standard techniques may be used for chemical synthesis, chemical analyses, pharmaceutical preparation, formulation, and delivery and treatment of patients.

OSMR

[0042] The antigen binding proteins described herein bind to OSMR. OSM and IL-31 signal through OSMR. OSMR is a member of the type I cytokine receptor family. OSMR heterodimerizes with glycoprotein 130 (also known as gp130, interleukin 6 signal transducer (IL6ST), IL6-beta, or CD130) to form the type II OSMR. OSMR also heterodimerizes with IL-31 receptor A (IL31RA) to form the IL-31 receptor and, thus, transduces OSM- and IL-31-induced signaling events. In exemplary embodiments, an OSMR antigen binding protein binds OSMR and prevents OSM- and/or IL-31-mediated signaling in cells expressing OSMR.

[0043] Human OSMR sequences are known in the art. In various aspects, human OSMR protein sequences are provided in GenBank Accession Nos. AAI25210, AAI25211, NP_003990, and EAW55976. An exemplary human OSMR amino acid sequence (SEQ ID NO: 1) is provided in Table 1. The protein is made up of several domains: Amino acids 1-27 correspond to the signal sequence which may be cleaved during processing of the protein in mammalian cells; amino acids 28-740 correspond to the extracellular domain; and amino acids 741-761 correspond to the transmembrane domain. In preferred embodiments, the antigen binding proteins described herein bind to the extracellular domain of OSMR and prevent the interaction of OSM and/or IL-31 with OSMR.

[0044] Human OSM sequences are known in the art. In various aspects, human OSM protein sequences are provided in GenBank Accession Nos. CAG30420, CAG46504, NP_065391, P13725, AAC05173, EAW59864, and AAH11589. An exemplary human OSM amino acid sequence (SEQ ID NO: 39) is provided in Table 1. Amino acids 1-25 correspond to the signal sequence; amino acids 26-220 correspond to the mature protein; and amino acids 221-252 correspond to the propeptide sequence.

[0045] Human IL-31 sequences are known in the art. In various aspects, human IL-31 protein sequences are provided in GenBank Accession Nos. NP_001014358, AAS86448, AAI32999, AAI33001, Q6EBC2, and EAW98310. An exemplary human IL-31 amino acid sequence (SEQ ID NO: 41) is provided in Table 1. Amino acids 1-23 correspond to the putative signal sequence.

[0046] Human IL31RA sequences are known in the art. In various aspects, human IL31RA protein sequences are provided in GenBank Accession Nos. AAS86447, NP_001229567, and CBL94051. An exemplary human IL31RA (v4, isoform 3) amino acid sequence (SEQ ID NO: 43) is provided in Table 1. Amino acids 1-32 correspond to the signal sequence; and amino acids 533-553 correspond to the transmembrane sequence.

[0047] Human gp130 sequences are known in the art. In various aspects, human gp130 protein sequences are provided in GenBank Accession Nos. AAI17403, AAI17405, EAW54936, NP_002175, ABK41905, and AAA59155. An exemplary human gp130 amino acid sequence (SEQ ID NO: 45) is provided in Table 1. The protein is made up of several domains: Amino acids 1-22 correspond to the signal sequence; amino acids 23-619 correspond to the extracellular domain; amino acids 620-641 correspond to the transmembrane domain; and amino acids 642-918 correspond to the cytoplasmic domain.

Table 1

Human OSMR amino acid sequence (SEQ ID NO:1)

MALFAVFQTTFFLTLLSLRTYQSEVLAERLPLTPVSLKVSTNSTRQSLHLQWTVHNLPY
HQELKMVFQIQISRIETSNVIWVGNYSTTVKWNQVLHWSWESELPLECATHFVRIKSL
VDDAKFPEPNFWSNWSSWEEVSVQDSTGQDILFVFPKDKLVEEGTNVTICYVSRNIQN
NVSCYLEGKQIHGEQLDPHVTAFNLNSVPFIRNKGTNIYCEASQGNVSEGMKGIVLFVS
KVLEEPKDFSCETEDFKTLHCTWDPGTDTALGWSKQPSQSYTLFESFSGEKKLCTHKN
WCNWQITQDSQETYNFTLIAENYLRKRSVNILFNLTHRVYLMNPFSVNFENVNATNAI
MTWKVHSIRNNFTYLCQIELHGEGKMMQYNVSIKVNGEYFLSELEPATEYMARVRCA
DASHFWKWSEWSGQNFTTLEAAPSEAPDVWRIVSLEPGNHTVTLFWKPLSKLHANGK
ILFYNVVVENLDKPSSSELHSIPAPANSTKLILDRCSYQICVIANNSVGASPASVIVISADP
ENKEVEEERIAGTEGGFSLSWKPQPGDVIGYVVDWCDHTQDVLGDFQWKNVGPNTTS
TVISTDAFRPGVRYDFRIYGLSTKRIACLLEKKTGYSQELAPSDNPHVLVDTLTSHSFTL
SWKDYSTESQPGFIQGYHVYLKSKARQCHPRFEKAVLSDGSECCKYKIDNPEEKALIV
DNLKPESFYEFFITPFTSAGEGPSATFTKVTTPDEHSSMLIHILLPMVFCVLLIMVMCYL
KSQWIKETCYPDIPDPYKSSILSLIKFKENPHLIIMNVSDCIPDAIEVVSKPEGTKIQFLGT
RKSLTETELTKPNYLYLLPTEKNHSGPGPCICFENLTYNQAASDSGSCGHVPVSPKAPS
MLGLMTSPENVLKALEKNYMNSLGEIPAGETSLNYVSQLASPMFGDKDSLPTNPVEAP
HCSEYKMQMAVSLRLALPPPTENSSLSSITLLDPGEHYC

Human OSM amino acid sequence (SEQ ID NO:39) MGVLLTQRTLLSLVLALLFPSMASMAAIGSCSKEYRVLLGQLQKQTDLMQDTSRLLDP YIRIQGLDVPKLREHCRERPGAFPSEETLRGLGRRGFLQTLNATLGCVLHRLADLEQRL PKAQDLERSGLNIEDLEKLQMARPNILGLRNNIYCMAQLLDNSDTAEPTKAGRGASQP PTPTPASDAFQRKLEGCRFLHGYHRFMHSVGRVFSKWGESPNRSRRHSPHQALRKGV RRTRPSRKGKRLMTRGQLPR
Human IL-31 amino acid sequence (SEQ ID NO:41) MASHSGPSTSVLFLFCCLGGWLASHTLPVRLLRPSDDVQKIVEELQSLSKMLLKDVEEE KGVLVSQNYTLPCLSPDAQPPNNIHSPAIRAYLKTIRQLDNKSVIDEIIEHLDKLIFQDAP ETNISVPTDTHECKRFILTISQQFSECMDLALKSLTSGAQQATT

Human IL31RA amino acid sequence (SEQ ID NO:43)

MKLSPQPSCVNLGMMWTWALWMLPSLCKFSLAALPAKPENISCVYYYRKNLTCTWS
PGKETSYTQYTVKRTYAFGEKHDNCTTNSSTSENRASCSFFLPRITIPDNYTIEVEAENG
DGVIKSHMTYWRLENIAKTEPPKIFRVKPVLGIKRMIQIEWIKPELAPVSSDLKYTLRFR
TVNSTSWMEVNFAKNRKDKNQTYNLTGLQPFTEYVIALRCAVKESKFWSDWSQEKM
GMTEEEAPCGLELWRVLKPAEADGRRPVRLLWKKARGAPVLEKTLGYNIWYYPESNT
NLTETMNTTNQQLELHLGGESFWVSMISYNSLGKSPVATLRIPAIQEKSFQCIEVMQAC
VAEDQLVVKWQSSALDVNTWMIEWFPDVDSEPTTLSWESVSQATNWTIQQDKLKPF
WCYNISVYPMLHDKVGEPYSIQAYAKEGVPSEGPETKVENIGVKTVTITWKEIPKSERK
GIICNYTIFYQAEGGKGFSKTVNSSILQYGLESLKRKTSYIVQVMASTSAGGTNGTSINF
KTLSFSVFEHILITSLIGGGLLILIILTVAYGLKKPNKLTHLCWPTVPNPAESSIATWHGDD
FKDKLNLKESDDSVNTEDRILKPCSTPSDKLVIDKLVVNFGNVLQEIFTDEARTGQENN
LGGEKNGTRILSSCPTSI

Human gp130 amino acid sequence (SEQ ID NO:45)

MLTLQTWLVQALFIFLTTESTGELLDPCGYISPESPVVQLHSNFTAVCVLKEKCMDYFH
VNANYIVWKTNHFTIPKEQYTIINRTASSVTFTDIASLNIQLTCNILTFGQLEQNVYGITII
SGLPPEKPKNLSCIVNEGKKMRCEWDGGRETHLETNFTLKSEWATHKFADCKAKRDT
PTSCTVDYSTVYFVNIEVWVEAENALGKVTSDHINFDPVYKVKPNPPHNLSVINSEELS
SILKLTWTNPSIKSVIILKYNIQYRTKDASTWSQIPPEDTASTRSSFTVQDLKPFTEYVFRI
RCMKEDGKGYWSDWSEEASGITYEDRPSKAPSFWYKIDPSHTQGYRTVQLVWKTLPP
FEANGKILDYEVTLTRWKSHLQNYTVNATKLTVNLTNDRYLATLTVRNLVGKSDAAV
LTIPACDFQATHPVMDLKAFPKDNMLWVEWTTPRESVKKYILEWCVLSDKAPCITDW
QQEDGTVHRTYLRGNLAESKCYLITVTPVYADGPGSPESIKAYLKQAPPSKGPTVRTK
KVGKNEAVLEWDQLPVDVQNGFIRNYTIFYRTIIGNETAVNVDSSHTEYTLSSLTSDTL
YMVRMAAYTDEGGKDGPEFTFTTPKFAQGEIEAIVVPVCLAFLLTTLLGVLFCFNKRD
LIKKHIWPNVPDPSKSHIAQWSPHTPPRHNFNSKDQMYSDGNFTDVSVVEIVANDKKPF
PEDLKSLDLFKKEKINTEGHSSGIGGSSCMSSSRPSISSSDENESSQNTSSTVQYSTVVHS
GYRHQVPSVQVFSRSESTQPLLDSEERPEDLQLVDHVDGGDGILPRQQYFKQNCSQHE
SSPDISHFERSKQVSSVNEEDFVRLKQQISDHISQSCGSGQMKMFQEVSAADAFGPGTE
GQVERFETVGMEAATDEGMPKSYLPQTVRQGGYMPQ

[0048] In particular embodiments of the present invention, antigen binding proteins described herein bind both human and cynomolgus monkey OSMR with high affinity, including those that bind with high affinity and block interaction of cynomolgus monkey OSM and/or IL-31 to cynomolgus monkey OSMR. These characteristics allow informative toxicology studies in non-human primates.

[0049] A Rhesus macaque (*Macaca mulatta*) OSMR protein sequence is known in the art and is provided in GenBank Accession No. XP_001083745. An exemplary cynomolgus monkey (*Macaca fascicularis*) OSMR amino acid sequence (SEQ ID NO:2) is provided in Table 2. The

protein is made up of several domains: Amino acids 1-27 correspond to the signal sequence which may be cleaved during processing of the protein in mammalian cells; amino acids 28-737 correspond to the extracellular domain; and amino acids 738-757 correspond to the transmembrane domain. In preferred embodiments, the antigen binding proteins described herein bind to the extracellular domain of OSMR and prevent the interaction of OSM and/or IL-31 with OSMR.

[0050] A Rhesus macaque (*Macaca mulatta*) OSM protein sequence is known in the art and is provided in GenBank Accession No. NP_001181403. An exemplary cynomolgus monkey (*Macaca fascicularis*) OSM amino acid sequence (SEQ ID NO:40) is provided in Table 2. Amino acids 1-196 correspond to the mature cynomolgus OSM.

[0051] A Rhesus macaque (*Macaca mulatta*) IL-31 protein sequence is known in the art and is provided in GenBank Accession No. XP_001096743. An exemplary cynomolgus monkey (*Macaca fascicularis*) IL-31 amino acid sequence (SEQ ID NO:42) is provided in Table 2. This sequence represents the mature cynomolgus monkey IL-31.

[0052] An exemplary cynomolgus monkey (*Macaca fascicularis*) IL31RA amino acid sequence (SEQ ID NO: 44) is provided in Table 2. Amino acids 1-19 correspond to the signal sequence; and amino acids 520-540 correspond to the transmembrane domain.

[0053] A Rhesus macaque (*Macaca mulatta*) gp130 protein sequence is known in the art and is provided in GenBank Accession No. NP_001252920. An exemplary cynomolgus monkey (*Macaca fascicularis*) gp130 amino acid sequence (SEQ ID NO: 46) is provided in Table 2. The protein is made up of several domains: Amino acids 1-22 correspond to the signal sequence; amino acids 23-619 correspond to the extracellular domain; amino acids 620-641 correspond to the transmembrane domain; and amino acids 642-918 correspond to the cytoplasmic domain.

Table 2

Cynomolgus monkey OSMR amino acid sequence (SEQ ID NO:2) MALFVVFQTTFFLILLSLRTYQSEVLAERLPLTPVSLKVSTNSIHQSLHLQWTVHNLPY HQELKMVFQIQISRIETSNVVWVGNYSTPVKWNQVLHWSWESELPLECATHFVRIKSV IDDASFPEPNFWSNWSSWEEVSVQDYLGRGTLFVFPKDKLVEEGSNVTICYVSRNIQN NVSCYLEGKQIHGEQLDPHVTAFNLNSVPFIRNRGTNIYCEASQGNVSKGIEGIVLFVSK VLEEPKDFSCESQDFKTLHCTWDPGTDTALGWSKQPSQSYTLFESFSGEKKLCTHKNW CNWQITQDSQEMYNFTLIAENYLRKRSVNILFNLTHRVYLMNPFSVNFENVNATNAIM TWKVHSMRNNFTYLCQIELHGEGKMMQYDVSINVNGEYFLSELEPATEYMARVRCA DASHFWKWTEWSGQNFTTLEAAPSEAPDVWRSVNSEPGNHTVTLFWKPLSKLHANG KILFYNVVVENLDKPSRSELRSIPAPANSTKLILDRCSYQICVTANNSVGASPASIIVISA DPENKEVEEERIAGTEGGFSLSWKPQPGDVIGYVVDWCDHPQDVLQWKNVGPNTTST VISTDAFRPGVRYDFRIYGLSTKRIACLLEKKTGYSQELAPSDNPHVLVDMLTSHSFTLS WKDYSTESQPGFIQGYHVYLKSKARQCHPRFQKAVLSDGSECCRYKIDNPEEKALIVD NLKPESFYEFFVTPFTSAGEGPNATFTKVTTPDEHSSMLIRILLPMVFCVLLIMIVCYLKS QWIKETCYPDIPDPYKSSILSLIKFKENPHLTIMNVSDCIPDAIEVVSKPEGTKIQLLGTR KSLTETELTKPNYLYLLPTEKNHSGPGPCICFENFTYNQAASDAGSCGHVPVPPKAPPS MLGLMTSPENVLKALEKNYMNSLGEVPAGETSLNYVSQLASPMSGDKDSLPTNPVEP PHCSEYKMQMAVPLRLALPPPTENSSLSSITLLDPGEHYR
Cynomolgus monkey OSM amino acid sequence (SEQ ID NO:40) AAMGSCSKEYRMLLGQLQKQTDLMQDTSRLLDPYIRIQGLDIPKLREHCRESPGAFPSE ETLRGLGRRGFLQTLNATLGRILHRLADLEQHLPKAQDLERSGLNIEDLEKLQMARPN VLGLRNNVYCMAQLLDNSDMTEPTKAGRGTPQPPTPTPTSDVFQRKLEGCSFLRGYH RFMHSVGRVFSKWGESPNRSRR
Cynomolgus monkey IL-31 amino acid sequence (SEQ ID NO:42) TLPVHFLQPSDIQKIVEELQSLSKMLLKDVKEDKGVLVSQNYTLPCLTPDAQPPNIIHSP AIRAYLKTIRQLDNKSVIDEIIEHLDKLIFQDAPETNISVPTDTHECKRFILTISQQFSECM DLALKSLTSGAQQATT
Cynomolgus monkey IL31RA amino acid sequence (SEQ ID NO:44) MMWTWALWMFPLLCKFGLAALPAKPENISCVYYYRKNLTCTWSPGKETSYTQYTAK RTYAFGKKHDNCTTSSSTSENRASCSFFLPRITIPDNYTIEVEAENGDGVIKSDMTCWRL EDIAKTEPPEIFSVKPVLGIKRMIRIEWIKPELAPVSSDLKYALRFRTVNSTSWMEVNFA KNRKDTNQTYNLMGLQAFTEYVVALRCAVKESKFWSDWSQEKMGMTEEEAPCGLEL WRVLKPTEVDGRRPVRLLWKKARGAPVLEKTLGYNIWYFPENNTNLTETVNTTNQQL ELHLGGESYWVSMISYNSLGKSPVTTLRIPAIQEKSFRCIEVMQACLAEDQLVVKWQSS ALDVNTWMIEWFPDMDSEHPTLSWESVSQATNWTIQQDKLKPFWCYNISVYPMLHD KVGEPYSIQAYAKEGIPSKGPETKVENIGVKTVTITWKEIPKSERKGIICNYTIFYQAEGG TGFSKTVNSSILQYGLESLKRKTSYTVRVMASTSAGGINGTSINFKTLSFSVFEILITSLI GGGLLILIILTVAYGLKKPNKLTHLCWPSVPNPAESSIATWRGDDFKDKLNLKESDDSV NTEDRILKPCSTPSDKLVIDKSVVNFGNVLQEMFTDEARTGQENNLGGEKNENRILSSC PTSI

Cynomolgus monkey gp130 amino acid sequence (SEQ ID NO:46)

MLTLQTWVVQALFIFLTTESIGELLDPCGYISPESPVVQLHSNFTAVCVLKEKCMDYFH
VNANYIVWKTNHFTIPKEQYTIINRTASSVTFTDISSLNIQLTCNILTFGQLEQNVYGITI
SGLPPEKPKNLSCIVNEGKKMRCEWNRGRETHLETNFTLKSEWATHKFADCKAKRDT
PTSCTVDYSTVYFVNIEVWVEAENALGKVTSDHINFDPVYKVKPNPPHNLSVINSEELS
SILKLTWTNPSIKSVIRLKYNIQYRTKDASTWSQIPPEDTASTRSSFTVQDLKPFTEYVFR
ICCMKEDGKGYWSDWSEEANGITYEDRPSKAPSFWYKIDPSHAQGYRTVQLMWKTLP
PFEANGKILDYEVTLTRWKSHLQNYTVNDTKLTVNLTNDRYVATLTARNLVGKSDAA
VLTIPACDFQATHPVMDLKAFPKDNMLWVEWTTPRESVKKYILEWCVLSDKAPCIAD
WQQEDGTVHRTHLRGNLAESKCYLITVTPVYADGPGSPESIKAYLKQAPPSKGPTVRT
KKVGKNEAVLEWDQLPVDVQNGFIRNYTIFYRTIIGNETAVNVDSSHTEYTLSSLTSDT
LYMVRMAAYTDEGGKDGPEFTFTTPKFAQGEIEAIVVPVCLAFLLTTLLGVLFCFNKR
DLIKKHIWPNVPDPSKSHIAQWSPHTPPRHNFSSKDQMYSDGNFTDVSVVEIEANDKKP
FPEDLKSLDLFKKEKINTEGHSSGIGGSSCMSSSRPSISSSDENESSQNTSSTVQYSTVVH
SGYRHQVPSVQVFSRSESTQPLLDSEERPEDLQLVDHVDGSDDILPRQQYFKQNCSQHE
SSPDISHFERSKQVSSVNEEDFVRLKQQISDHISQSCGSGEMKMFQEVSAADPFGPGTE
GQVERFETIGMEAAIDEGMPKSYLPQTVRQGGYMPQ

OSMR Antigen Binding Proteins

[0054] The present invention provides antigen binding proteins that specifically bind OSMR. Embodiments of antigen binding proteins comprise peptides and/or polypeptides that specifically bind OSMR. Such peptides or polypeptides may optionally include one or more port-translational modifications. Embodiments of antigen binding proteins include antibodies and fragments thereof, as variously defined herein, that specifically bind OSMR. These include antibodies that specifically bind human OSMR, including those that inhibit OSM and/or IL-31 from binding and/or activating OSMR.

[0055] The antigen binding proteins of the invention specifically bind to OSMR. "Specifically binds" as used herein means that the antigen binding protein preferentially binds OSMR over other proteins. In some embodiments "specifically binds" means the OSMR antigen binding protein has a higher affinity for OSMR than for other proteins. OSMR antigen binding proteins that specifically bind OSMR may have a binding affinity for human OSMR of less than or equal to 1×10^{-7} M, less than or equal to 2×10^{-7} M, less than or equal to 3×10^{-7} M, less than or equal to 4×10^{-7} M, less than or equal to 5×10^{-7} M, less than or equal to 6×10^{-7} M, less than or equal to 7×10^{-7} M, less than or equal to 8×10^{-7} M, less than or equal to 9×10^{-7} M, less than or equal to 1×10^{-8} M, less than or equal to 2×10^{-8} M, less than or equal to 3×10^{-8} M, less than or equal to 4×10^{-8} M, less than or equal to 5×10^{-8} M, less than or equal to 6×10^{-8} M, less than or equal to 7×10^{-8} M, less than or equal to 8×10^{-8} M, less than or equal to 9×10^{-8} M, less than or equal to 1×10^{-9} M, less than or equal to 2×10^{-9} M, less than or equal to 3

x 10^{-9} M, less than or equal to 4 x 10^{-9} M, less than or equal to 5 x 10^{-9} M, less than or equal to 6 x 10^{-9} M, less than or equal to 7 x 10^{-9} M, less than or equal to 8 x 10^{-9} M, less than or equal to 9 x 10^{-9} M, less than or equal to 1 x 10^{-10} M, less than or equal to 2 x 10^{-10} M, less than or equal to 3 x 10^{-10} M, less than or equal to 4 x 10^{-10} M, less than or equal to 5 x 10^{-10} M, less than or equal to 6 x 10^{-10} M, less than or equal to 7 x 10^{-10} M, less than or equal to 8 x 10^{-10} M, less than or equal to 9 x 10^{-10} M, less than or equal to 1 x 10^{-11} M, less than or equal to 2 x 10^{-11} M, less than or equal to 3 x 10^{-11} M, less than or equal to 4 x 10^{-11} M, less than or equal to 5 x 10^{-11} M, less than or equal to 6 x 10^{-11} M, less than or equal to 7 x 10^{-11} M, less than or equal to 8 x 10^{-11} M, less than or equal to 9 x 10^{-11} M, less than or equal to 1 x 10^{-12} M, less than or equal to 2 x 10^{-12} M, less than or equal to 3 x 10^{-12} M, less than or equal to 4 x 10^{-12} M, less than or equal to 5 x 10^{-12} M, less than or equal to 6 x 10^{-12} M, less than or equal to 7 x 10^{-12} M, less than or equal to 8 x 10^{-12} M, or less than or equal to 9 x 10^{-12} M.

[0056] Methods of measuring the binding affinity of an antigen binding protein are well known in the art. Methods in common use for affinity determination include Surface Plasmon Resonance (SPR) (Morton and Myszka "Kinetic analysis of macromolecular interactions using surface plasmon resonance biosensors" *Methods in Enzymology* (1998) 295, 268-294), Bio-Layer Interferometry, (Abdiche *et al* "Determining Kinetics and Affinities of Protein Interactions Using a Parallel Real-time Label-free Biosensor, the Octet" *Analytical Biochemistry* (2008) 377, 209-217), Kinetic Exclusion Assay (KinExA) (Darling and Brault "Kinetic exclusion assay technology: characterization of molecular interactions" *Assay and Drug Dev Tech (2004)* 2, 647-657), isothermal calorimetry (Pierce et al "Isothermal Titration Calorimetry of Protein-Protein Interactions" *Methods (*1999) 19, 213-221) and analytical ultracentrifugation (Lebowitz *et al* "Modern analytical ultracentrifugation in protein science: A tutorial review" *Protein Science* (2002), 11:2067–2079). Example 5 provides exemplary methods of affinity determination.

[0057] It is understood that when reference is made to the various embodiments of the OSMR-binding antibodies herein, that it also encompasses OSMR-binding fragments thereof. An OSMR-binding fragment comprises any of the antibody fragments or domains described herein that retains the ability to specifically bind to OSMR. The OSMR-binding fragment may be in any of the scaffolds described herein.

[0058] In certain therapeutic embodiments, an OSMR antigen binding protein inhibits binding of OSM and/or IL-31 to OSMR and/or inhibits one or more biological activities associated with the binding of OSM and/or IL-31 to OSMR, e.g., OSM- and/or IL-31-mediated signaling. Such

antigen binding proteins are said to be "neutralizing." In certain embodiments, the neutralizing OSMR antigen binding protein specifically binds OSMR and inhibits binding of OSM and/or IL-31 to OSMR from anywhere between 10% to 100%, such as by at least about 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99% or more. For example, OSMR antigen binding proteins may be tested for neutralizing ability by determining the ability of the antigen binding protein to block binding of OSM and/or IL-31 to OSMR, see, e.g., the human OSMR and cynomolgus OSMR blocking assays of Examples 2 and 3, respectively. Alternatively, OSMR antigen binding proteins may be tested for neutralizing ability in an assay that measures the effect of the presence of the OSMR antigen binding protein in an assay measuring OSM- and/or IL-31-mediated biological function. For example, the ability of OSM to induce a biological response, such as stimulation of plasminogen activator activity in cultured bovine aortic endothelial cells, regulation of IL-6 expression in human endothelial cells, and stimulation of LDL uptake and up-regulation of cell surface LDL receptors in HepG2 cells. Alternatively, the ability of IL-31 to induce inflammation in the skin.

[0059] Embodiments of antigen binding proteins comprise a scaffold structure, as variously defined herein, with one or more complementarity determining regions (CDRs). Embodiments further include antigen binding proteins comprising a scaffold structure with one or more antibody variable domains, either heavy or light. Embodiments include antibodies that comprise a light chain variable domain selected from the group consisting of Ab1 Light Chain Variable Domain (LCv), Ab2 LCv, and Ab3 LCv (SEQ ID NOS:27-29, respectively) and/or a heavy chain variable domain selected from the group consisting of Ab1 Heavy Chain Variable Domain (HCv), Ab2 HCv, and Ab3 HCv (SEQ ID NOS:9-11, respectively), and fragments, derivatives, muteins, and variants thereof.

An exemplary heavy chain variable domain variant of SEQ ID NO:9 contains an amino acid other than asparagine (for example, aspartic acid) at the position corresponding to position 73 in SEQ ID NO:9. The amino acid sequence set forth in SEQ ID NO:53 is an example of a heavy chain variable domain variant of SEQ ID NO:9.

An exemplary heavy chain variable domain variant of SEQ ID NO:10 contains an amino acid other than asparagine (for example, aspartic acid) at the position corresponding to position 73

in SEQ ID NO:10. The amino acid sequence set forth in SEQ ID NO:54 is an example of a heavy chain variable domain variant of SEQ ID NO:10.

[0060] An exemplary light chain comprising Ab1 LCv is a light chain comprising the amino acid sequence set forth in SEQ ID NO:24.

[0061] An exemplary light chain comprising Ab2 LCv is a light chain comprising the amino acid sequence set forth in SEQ ID NO:25.

[0062] An exemplary light chain comprising Ab3 LCv is a light chain comprising the amino acid sequence set forth in SEQ ID NO:26.

[0063] An exemplary heavy chain comprising Ab1 HCv is a heavy chain comprising the amino acid sequence set forth in SEQ ID NO:6.

An exemplary heavy chain comprising a variant of Ab1 HCv is a heavy chain comprising the amino acid sequence set forth in SEQ ID NO:50.

[0064] An exemplary heavy chain comprising Ab2 HCv is a heavy chain comprising the amino acid sequence set forth in SEQ ID NO:7.

An exemplary heavy chain comprising a variant of Ab2 HCv is a heavy chain comprising the amino acid sequence set forth in SEQ ID NO:51.

[0065] An exemplary heavy chain comprising Ab3 HCv is a heavy chain comprising the amino acid sequence set forth in SEQ ID NO:8.

An exemplary heavy chain comprising a variant of Ab3 HCv is a heavy chain comprising the amino acid sequence set forth in SEQ ID NO:52.

[0066] Additional examples of scaffolds that are envisioned include, but are not limited to,: fibronectin, neocarzinostatin CBM4-2, lipocalins, T-cell receptor, protein -A domain (protein Z), Im9, TPR proteins, zinc finger domains, pVIII, avian pancreatic polypeptide, GCN4, WW domain Src homology domain 3, PDZ domains, TEM-1 beta-lactamase, thioredoxin, staphylococcal nuclease, PHD-finger domains, CL-2, BPTI, APPI, HPSTI, ecotin, LACI-D1, LDTI, MTI-II, scorpion toxins, insect defensin-A peptide, EETI-II, Min-23, CBD, PBP, cytochrome b-562, Ldl receptor domains, gamma-crystallin, ubiquitin, transferrin, and or C-type lectin-like domains. Non-antibody scaffolds and their use as therapeutics are reviewed in Gebauer and Skerra, *Curr. Opin. Chem. Biol.*, 13:245-255 (2009) and Binz et al., Nat. Biotech., 23(10):1257-68 (2005), which are incorporated herein by reference in its entirety.

[0067] Aspects of the invention include antibodies comprising the following variable domains: Ab1 LCv/Ab1 HCv (SEQ ID NO:27/SEQ ID NO:9), Ab2 LCv/Ab2 HCv (SEQ ID NO:28/SEQ ID NO:10), Ab3 LCv/Ab3 HCv (SEQ ID NO:29/SEQ ID NO:11), and combinations thereof, as well as fragments, derivatives, muteins and variants thereof.

Also included are antibodies comprising the following variable domains: SEQ ID NO:27/SEQ ID NO:53; and SEQ ID NO:28/SEQ ID NO:54.

[0068] Exemplary antibodies of the invention include Ab1 (SEQ ID NO:24/SEQ ID NO:6), Ab2 (SEQ ID NO:25/SEQ ID NO:7), and Ab3 (SEQ ID NO:26/SEQ ID NO:8).

Additional exemplary antibodies include: SEQ ID NO:24/SEQ ID NO:50; SEQ ID NO:25/SEQ ID NO:51; and SEQ ID NO:26/SEQ ID NO:52.

[0069] Typically, each variable domain of an antibody light or heavy chain comprises three CDRs. The heavy chain variable domain comprises a heavy chain CDR1 (HCDR1), a heavy chain CDR2 (HCDR2), and a heavy chain CDR3 (HCDR3). The light chain variable domain comprises a light chain CDR1 (LCDR1), a light chain CDR2 (LCDR2), and a light chain CDR3 (LCDR3). In certain embodiments, an antigen binding protein comprises one or more CDRs contained within the preferred variable domains described herein.

[0070] Examples of such CDRs include, but are not limited to:

[0071] the CDRs of Ab1 LCv: LCDR1 (SEQ ID NO:30), LCDR2 (SEQ ID NO:33), and LCDR3 (SEQ ID NO:36);

[0072] the CDRs of Ab2 LCv: LCDR1 (SEQ ID NO:31), LCDR2 (SEQ ID NO:34), and LCDR3 (SEQ ID NO:37);

[0073] the CDRs of Ab3 LCv: LCDR1 (SEQ ID NO:32), LCDR2 (SEQ ID NO:35), and LCDR3 (SEQ ID NO:38);

[0074] the CDRs of Ab1 HCv: HCDR1 (SEQ ID NO:12), HCDR2 (SEQ ID NO:15), and HCDR3 (SEQ ID NO:18);

[0075] the CDRs of Ab2 HCv: HCDR1 (SEQ ID NO:13), HCDR2 (SEQ ID NO:16), and HCDR3 (SEQ ID NO:19); and

[0076] the CDRs of Ab3 HCv: HCDR1 (SEQ ID NO:14), HCDR2 (SEQ ID NO:17), and HCDR3 (SEQ ID NO:20).

[0077] In some embodiments, the antigen binding protein comprises: A) a polypeptide, e.g., a light chain, that comprises an LCDR1 having an amino acid sequence selected from the group consisting of SEQ ID NOS:30, 31, and 32; an LCDR2 having an amino acid sequence selected from the group consisting of SEQ ID NOS:33, 34, and 35; and/or an LCDR3 having an amino acid sequence selected from the group consisting of SEQ ID NOS:36, 37, and 38; and/or B) a polypeptide, e.g., a heavy chain, that comprises an HCDR1 having an amino acid sequence selected from the group consisting of SEQ ID NOS:12, 13, and 14; an HCDR2 having an amino acid sequence selected from the group consisting of SEQ ID NOS:15, 16, and 17; and/or an HCDR3 having an amino acid sequence selected from the group consisting of SEQ ID NOS:18, 19, and 20.

[0078] In further embodiments, the antigen binding protein comprise A) a light chain amino acid sequence that comprises a LCDR1, LCDR2, and LCDR3 of any of Ab1 LCv, Ab2 LCv, and Ab3 LCv and B) a heavy chain amino acid sequence that comprises a HCDR1, HCDR2, and HCDR3 of any of Ab1 HCv, Ab2 HCv, and Ab3 HCv.

[0079] In certain embodiments, the CDRs include no more than one, no more than two, no more than three, no more than four, no more than five, or no more than six amino acid additions, deletions, or substitutions from an exemplary CDR set forth herein.

[0080] Aspects of the invention include antibodies comprising a light chain variable domain selected from the group consisting of SEQ ID NOS:27, 28, and 29. Aspects of the invention include antibodies comprising a heavy chain variable domain selected from the group consisting of SEQ ID NOS:9, 10, and 11. Further aspects of the invention include antibodies comprising A) a light chain variable domain selected from the group consisting of SEQ ID NOS:27, 28, and 29, and B) a heavy chain variable domain selected from the group consisting of SEQ ID NOS:9, 10, and 11.

[0081] Antibodies of the invention can comprise any constant region known in the art. The light chain constant region can be, for example, a kappa- or lambda-type light chain constant region, e.g., a human kappa- or lambda-type light chain constant region. The heavy chain constant region can be, for example, an alpha-, delta-, epsilon-, gamma-, or mu-type heavy chain constant region, e.g., a human alpha-, delta-, epsilon-, gamma-, or mu-type heavy chain constant region. In one embodiment the light or heavy chain constant region is a fragment, derivative, variant, or mutein of a naturally occurring constant region.

[0082] Aspects of the invention include antibodies comprising a light chain variable region selected from the group consisting of SEQ ID NOS:27, 28, and 29 having no more than one, no more than two, no more than three, no more than four, no more than five, no more than six, no more than seven, no more than eight, no more than nine, or no more than ten amino acid additions, deletions, or substitutions. Aspects of the invention include antibodies comprising a heavy chain variable region selected from the group consisting of SEQ ID NOS:9, 10, and 11 having no more than one, no more than two, no more than three, no more than four, no more than five, no more than six, no more than seven, no more than eight, no more than nine, or no more than ten amino acid additions, deletions, or substitutions. Further aspects of the invention include antibodies comprising A) comprising a light chain variable region selected from the group consisting of SEQ ID NOS:27, 28, and 29 having no more than one, no more than two, no more than three, no more than four, no more than five, no more than six, no more than seven, no more than eight, no more than nine, or no more than ten amino acid additions, deletions, or substitutions, and B) a heavy chain variable region selected from the group consisting of SEQ ID NOS:9, 10, and 11 having no more than one, no more than two, no more than three, no more than four, no more than five, no more than six, no more than seven, no more than eight, no more than nine, or no more than ten amino acid additions, deletions, or substitutions.

[0083] In one variation, the antigen binding protein comprises an amino acid sequence that is at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to a light chain variable region amino acid sequence selected from the group consisting of SEQ ID NOS:27, 28, and 29. In another variation, the antigen binding protein comprises an amino acid sequence that is at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to a heavy chain variable region amino acid sequence selected from the group consisting of SEQ ID NOS:9, 10, and 11. In yet a further embodiment, the antigen binding protein comprises A) an amino acid sequence that is at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to a light chain variable region amino

acid sequence selected from the group consisting of SEQ ID NOS:27, 28, and 29, and B) an amino acid sequence that is at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to a heavy chain variable region amino acid sequence selected from the group consisting of SEQ ID NOS:9, 10, and 11.

OSMR antigen binding proteins comprising a heavy chain variable domain having the above-defined sequence relatedness to SEQ ID NO:9 can optionally contain an amino acid other than asparagine (for example, aspartic acid) at the position corresponding to position 73 in SEQ ID NO:9. In such embodiments, the heavy chain variable domain optionally comprises the amino acid sequence set forth in SEQ ID NO:53.

OSMR antigen binding proteins comprising a heavy chain variable domain having the above-defined sequence relatedness to SEQ ID NO:10 can optionally contain an amino acid other than asparagine (for example, aspartic acid) at the position corresponding to position 73 in SEQ ID NO:10. In such embodiments, the heavy chain variable domain optionally comprises the amino acid sequence set forth in SEQ ID NO:54.

[0084] In certain embodiments, the antigen binding protein comprises a light chain and/or heavy chain CDR3. In some embodiments, the antigen binding protein comprises an amino acid sequence selected from the group of sequences set forth in SEQ ID NOS:36, 37, 38, 18, 19, and 20. In certain embodiments, the amino acid sequence includes no more than one, no more than two, no more than three, no more than four, no more than five, or no more than six amino acid additions, deletions, or substitutions from the exemplary sequence set forth in SEQ ID NOS:36, 37, 38, 18, 19, and 20. Thus, embodiments of the invention include antigen binding protein comprising an amino acid sequence that is at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to an amino acid sequence selected from the group of sequences set forth in SEQ ID NOS:36, 37, 38, 18, 19, and 20.

[0085] In certain embodiments, the antigen binding protein comprises a light chain and/or heavy chain CDR2. In some embodiments, the antigen binding protein comprises an amino acid sequence selected from the group of sequences set forth in SEQ ID NOS:33, 34, 35, 15, 16, and 17. In certain embodiments, the amino acid sequence includes no more than one, no

more than two, no more than three, no more than four, no more than five, or no more than six amino acid additions, deletions, or substitutions from the exemplary sequence set forth in SEQ ID NOS:33, 34, 35, 15, 16, and 17. Thus, embodiments of the invention include antigen binding protein comprising an amino acid sequence that is at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to an amino acid sequence selected from the group of sequences set forth in SEQ ID NOS:33, 34, 35, 15, 16, and 17.

[0086] In certain embodiments, the antigen binding protein comprises a light chain and/or heavy chain CDR1. In some embodiments, the antigen binding protein comprises an amino acid sequence selected from the group of sequences set forth in SEQ ID NOS:30, 31, 32, 12, 13, and 14. In certain embodiments, the amino acid sequence includes no more than one, no more than two, no more than three, no more than four, no more than five, or no more than six amino acid additions, deletions, or substitutions from the exemplary sequence set forth in SEQ ID NOS:30, 31, 32, 12, 13, and 14. Thus, embodiments of the invention include antigen binding protein comprising an amino acid sequence that is at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to an amino acid sequence selected from the group of sequences set forth in SEQ ID NOS:30, 31, 32, 12, 13, and 14.

[0087] The antigen binding proteins of the invention comprise the scaffolds of traditional antibodies, including human and monoclonal antibodies, bispecific antibodies, diabodies, minibodies, domain antibodies, synthetic antibodies (sometimes referred to herein as "antibody mimetics"), chimeric antibodies, antibody fusions (sometimes referred to as "antibody conjugates"), and fragments of each, respectively. The above described CDRs, including various combinations of the CDRs, may be grafted into any of the following scaffolds.

[0088] As used herein, the term "antibody" refers to the various forms of monomeric or multimeric proteins comprising one or more polypeptide chains that specifically binds to an antigen, as variously described herein. In certain embodiments, antibodies are produced by recombinant DNA techniques. In additional embodiments, antibodies are produced by enzymatic or chemical cleavage of naturally occurring antibodies. In another aspect, the antibody is selected from the group consisting of: a) a human antibody; b) a humanized antibody; c) a chimeric antibody; d) a monoclonal antibody; e) a polyclonal antibody; f) a

recombinant antibody; g) an antigen-binding fragment; h) a single chain antibody; i) a diabody; j) a triabody, k) a tetrabody, l) a Fab fragment; m) a $F(ab')_2$ fragment, n) an IgA antibody, o) an IgD antibody, p) an IgE antibody, q) an IgG1 antibody, r) an IgG2 antibody, s) an IgG3 antibody, t) an IgG4 antibody, and u) an IgM antibody.

[0089] A variable region or domain comprises at least three heavy or light chain CDRs embedded within a framework region (designated framework regions FR1, FR2, FR3, and FR4). Kabat *et al.*, 1991, *Sequences of Proteins of Immunological Interest*, Public Health Service N.I.H., Bethesda, MD. Traditional antibody structural units typically comprise a tetramer. Each tetramer is typically composed of two identical pairs of polypeptide chains, each pair having one "light" and one "heavy" chain. The amino-terminal portion of each chain includes a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The carboxy-terminal portion of each chain defines a constant region primarily responsible for effector function. Human light chains are classified as kappa or lambda light chains. Heavy chains are classified as mu, delta, gamma, alpha, or epsilon, and define the antibody's isotype as IgM, IgD, IgG, IgA, and IgE, respectively. IgG has several subclasses, including, but not limited to IgG1, IgG2, IgG3, and IgG4. IgM has subclasses, including, but not limited to IgM1 and IgM2. Embodiments of the invention include all such classes and subclasses of antibodies that incorporate a variable domain or CDR of the antigen binding proteins, as described herein.

[0090] Some naturally occurring antibodies, such as those found in camels and llamas, are dimers consisting of two heavy chains and include no light chains. The invention encompasses dimeric antibodies of two heavy chains, or fragments thereof, that can bind to OSMR.

[0091] The variable regions of the heavy and light chains typically exhibit the same general structure of relatively conserved framework regions (FR) joined by three hypervariable regions, i.e., the complementarity determining regions or CDRs. The CDRs are primarily responsible for antigen recognition and binding. The CDRs from the two chains of each pair are aligned by the framework regions, enabling binding to a specific epitope. From N-terminal to C-terminal, both light and heavy chains comprise the domains FR1, CDR1, FR2, CDR2, FR3, CDR3, and FR4. The assignment of amino acids to each domain is in accordance with the definitions of Kabat.

[0092] CDRs constitute the major surface contact points for antigen binding. The CDR3 or the light chain and, particularly, CDR3 of the heavy chain may constitute the most important

determinants in antigen binding within the light and heavy chain variable regions. In some antibodies, the heavy chain CDR3 appears to constitute the major area of contact between the antigen and the antibody. In vitro selection schemes in which CDR3 alone is varied can be used to vary the binding properties of an antibody or determine which residues contribute to the binding of an antigen.

[0093] Naturally occurring antibodies typically include a signal sequence, which directs the antibody into the cellular pathway for protein secretion and which is typically not present in the mature antibody. A polynucleotide encoding an antibody of the invention may encode a naturally occurring a signal sequence or a heterologous signal sequence as described below.

[0094] In one embodiment, the antigen binding protein is an antibody comprising from one to six of the exemplary CDRs described herein. The antibodies of the invention may be of any type including IgM, IgG (including IgG1, IgG2, IgG3, IgG4), IgD, IgA, or IgE antibody. In a specific embodiment the antigen binding protein is an IgG type antibody, e.g., a IgG1 antibody.

[0095] In some embodiments, for example when the antigen binding protein is an antibody with complete heavy and light chains, the CDRs are all from the same species, e.g., human. Alternatively, for example in embodiments wherein the antigen binding protein contains less than six CDRs from the sequences outlined above, additional CDRs may be either from other species or may be different human CDRs than those depicted in the exemplary sequences. For example, HCDR3 and LCDR3 regions from the appropriate sequences identified herein may be used with HCDR1, HCDR2, LCDR1, and LCDR2 being optionally selected from alternate species or different human antibody sequences, or combinations thereof. For example, the CDRs of the invention can replace the CDR regions of commercially relevant chimeric or humanized antibodies.

[0096] Specific embodiments utilize scaffold components of the antigen binding proteins that are human components. In some embodiments, however, the scaffold components can be a mixture from different species. As such, if the antigen binding protein is an antibody, such antibody may be a chimeric antibody and/or humanized antibody. In general, both "chimeric antibodies" and humanized antibodies" refer to antibodies that combine regions from more than one species. For example, "chimeric antibodies" traditionally comprise variable region(s) from a mouse (or rat, in some cases) and the constant region(s) from a human.

[0097] "Humanized antibodies" generally refer to non-human antibodies that have had the variable domain framework regions swapped for sequences found in human antibodies.

Generally, in a humanized antibody, the entire antibody, except one or more CDRs, is encoded by a polynucleotide of human origin or is identical to such an antibody except within one or more CDRs. The CDRs, some or all of which are encoded by nucleic acids originating in a non-human organism, are grafted into the beta-sheet framework of a human antibody variable region to create an antibody, the specificity of which is determined by the engrafted CDRs. The creation of such antibodies is described in, *e.g.*, WO 92/11018, Jones 1986, *Nature* 321:522-525, Verhoeyen *et al.*, 1988, *Science* 239:1534-1536. Humanized antibodies can also be generated using mice with a genetically engineered immune system (Roque et al., 2004, Biotechnol. Prog. 20:639-654). In the exemplary embodiments described herein, the identified CDRs are human, and thus both humanized and chimeric antibodies in this context include some non-human CDRs; for example, humanized antibodies may be generated that comprise the HCDR3 and LCDR3 regions, with one or more of the other CDR regions being of a different species origin.

[0098] In one embodiment, the OSMR antigen binding protein is a multispecific antibody, and notably a bispecfic antibody, also sometimes referred to as "diabodies." These are antibodies that bind to two or more different antigens or different epitopes on a single antigen. In certain embodiments, a bispecific antibody binds OSMR and an antigen on a human effector cell (e.g., T cell). Such antibodies are useful in targeting an effector cell response against OSMR expressing cells, such as an OSMR-expressing tumor cell. In preferred embodiments, the human effector cell antigen is CD3. U.S. Pat. No. 7,235,641. Methods of making bispecific antibodies are known in the art. One such method involves engineering the Fc portion of the heavy chains such as to create "knobs" and "holes" which facilitate heterodimer formation of the heavy chains when co-expressed in a cell. U.S. 7,695,963. Another method also involves engineering the Fc portion of the heavy chain but uses electrostatic steering to encourage heterodimer formation while discouraging homodimer formation of the heavy chains when co-expressed in a cell. WO 09/089,004, which is incorporated herein by reference in its entirety.

[0099] In one embodiment, the OSMR antigen binding protein is a minibody. Minibodies are minimized antibody-like proteins comprising a scFv joined to a CH3 domain (Hu *et al.*, 1996, *Cancer Res.* 56:3055-3061).

[00100] In one embodiment, the OSMR antigen binding protein is a domain antibody; *see*, for example U.S. Patent No. 6,248,516. Domain antibodies (dAbs) are functional binding domains of antibodies, corresponding to the variable regions of either the heavy (VH) or light (VL) chains of human antibodies. dABs have a molecular weight of approximately 13 kDa, or

less than one-tenth the size of a full antibody. dABs are well expressed in a variety of hosts including bacterial, yeast, and mammalian cell systems. In addition, dAbs are highly stable and retain activity even after being subjected to harsh conditions, such as freeze-drying or heat denaturation. *See*, for example, US Patent 6,291,158; 6,582,915; 6,593,081; 6,172,197; US Serial No. 2004/0110941; European Patent 0368684; US Patent 6,696,245, WO04/058821, WO04/003019 and WO03/002609.

[00101] In one embodiment, the OSMR antigen binding protein is an antibody fragment, that is a fragment of any of the antibodies outlined herein that retain binding specificity to OSMR. In various embodiments, the antibody binding proteins comprise, but are not limited to, a F(ab), F(ab'), F(ab')2, Fv, or a single chain Fv fragments. At a minimum, an antibody, as meant herein, comprises a polypeptide that can bind specifically to OSMR comprising all or part of a light or heavy chain variable region, such as one or more CDRs.

[00102] Further examples of OSMR-binding antibody fragments include, but are not limited to, (i) the Fab fragment consisting of VL, VH, CL and CH1 domains, (ii) the Fd fragment consisting of the VH and CH1 domains, (iii) the Fv fragment consisting of the VL and VH domains of a single antibody; (iv) the dAb fragment (Ward *et al.*, 1989, *Nature* 341:544-546) which consists of a single variable, (v) isolated CDR regions, (vi) $F(ab')_2$ fragments, a bivalent fragment comprising two linked Fab fragments (vii) single chain Fv molecules (scFv), wherein a VH domain and a VL domain are linked by a peptide linker which allows the two domains to associate to form an antigen binding site (Bird *et al.*, 1988, *Science* 242:423-426, Huston *et al.*, 1988, *Proc. Natl. Acad. Sci. U.S.A.* 85:5879-5883), (viii) bispecific single chain Fv dimers (PCT/US92/09965) and (ix) "diabodies" or "triabodies", multivalent or multispecific fragments constructed by gene fusion (Tomlinson *et. al.*, 2000, *Methods Enzymol.* 326:461-479; WO94/13804; Holliger *et al.*, 1993, *Proc. Natl. Acad. Sci. U.S.A.* 90:6444-6448). The antibody fragments may be modified. For example, the molecules may be stabilized by the incorporation of disulphide bridges linking the VH and VL domains (Reiter *et al.*, 1996, *Nature Biotech.* 14:1239-1245). Aspects of the invention include embodiments wherein the non-CDR components of these fragments are human sequences.

[00103] In one embodiment, the OSMR antigen binding protein is a fully human antibody. In this embodiment, as outlined above, specific structures comprise complete heavy and light chains depicted comprising the CDR regions. Additional embodiments utilize one or more of the CDRs of the invention, with the other CDRs, framework regions, J and D regions, constant regions, etc., coming from other human antibodies. For example, the CDRs of the

invention can replace the CDRs of any number of human antibodies, particularly commercially relevant antibodies

[00104] Single chain antibodies may be formed by linking heavy and light chain variable domain (Fv region) fragments via an amino acid bridge (short peptide linker), resulting in a single polypeptide chain. Such single-chain Fvs (scFvs) have been prepared by fusing DNA encoding a peptide linker between DNAs encoding the two variable domain polypeptides (V_L and V_H). The resulting polypeptides can fold back on themselves to form antigen-binding monomers, or they can form multimers (*e.g.*, dimers, trimers, or tetramers), depending on the length of a flexible linker between the two variable domains (Kortt *et al.*, 1997, Prot. Eng. 10:423; Kortt *et al.*, 2001, Biomol. Eng. 18:95-108). By combining different V_L and V_H-comprising polypeptides, one can form multimeric scFvs that bind to different epitopes (Kriangkum *et al.*, 2001, Biomol. Eng. 18:31-40). Techniques developed for the production of single chain antibodies include those described in U.S. Patent No. 4,946,778; Bird, 1988, Science 242:423; Huston *et al.*, 1988, Proc. Natl. Acad. Sci. USA 85:5879; Ward *et al.*, 1989, Nature 334:544, de Graaf *et al.*, 2002, Methods Mol Biol. 178:379-87. Single chain antibodies derived from antibodies provided herein (including but not limited to scFvs comprising the variable domain combinations of Ab1 LCv/Ab1 HCv (SEQ ID NO:27/SEQ ID NO:9), Ab2 LCv/Ab2 HCv (SEQ ID NO:28/SEQ ID NO:10), and Ab3 LCv/Ab3 HCv (SEQ ID NO:29/SEQ ID NO:11), and combinations thereof are encompassed by the present invention. Exemplary single chain antibodies include the following variable domain combinations: SEQ ID NO:27/SEQ ID NO:53; and SEQ ID NO:28/SEQ ID NO:54.

[00105] In one embodiment, the OSMR antigen binding protein is an antibody fusion protein (sometimes referred to herein as an "antibody conjugate"). The conjugate partner can be proteinaceous or non-proteinaceous; the latter generally being generated using functional groups on the antigen binding protein and on the conjugate partner. In certain embodiments, the antibody is conjugated to a non-proteinaceous chemical (drug) to form an antibody drug conjugate.

[00106] In one embodiment, the OSMR antigen binding protein is an antibody analog, sometimes referred to as "synthetic antibodies." For example, a variety of work utilizes either alternative protein scaffolds or artificial scaffolds with grafted CDRs. Such scaffolds include, but are not limited to, mutations introduced to stabilize the three-dimensional structure of the binding protein as well as wholly synthetic scaffolds consisting for example of biocompatible polymers. *See*, for example, Komdorfer *et al.*, 2003, *Proteins: Structure, Function, and*

Bioinformatics, Volume 53, Issue 1:121-129. Roque *et al.*, 2004, *Biotechnol. Prog.* 20:639-654. In addition, peptide antibody mimetics ("PAMs") can be used, as well as work based on antibody mimetics utilizing fibronection components as a scaffold.

[00107] By "protein," as used herein, is meant at least two covalently attached amino acids, which includes proteins, polypeptides, oligopeptides and peptides. In some embodiments, the two or more covalently attached amino acids are attached by a peptide bond. The protein may be made up of naturally occurring amino acids and peptide bonds, for example when the protein is made recombinantly using expression systems and host cells, as outlined below. Alternatively, the protein may include synthetic amino acids (*e.g.*, homophenylalanine, citrulline, ornithine, and norleucine), or peptidomimetic structures, *i.e.*, "peptide or protein analogs", such as peptoids (*see*, Simon *et al.*, 1992, *Proc. Natl. Acad. Sci. U.S.A.* 89:9367, incorporated by reference herein), which can be resistant to proteases or other physiological and/or storage conditions. Such synthetic amino acids may be incorporated in particular when the antigen binding protein is synthesized *in vitro* by conventional methods well known in the art. In addition, any combination of peptidomimetic, synthetic and naturally occurring residues/structures can be used. "Amino acid" also includes imino acid residues such as proline and hydroxyproline. The amino acid "R group" or "side chain" may be in either the (L)- or the (S)-configuration. In a specific embodiment, the amino acids are in the (L)- or (S)-configuration.

[00108] In certain aspects, the invention provides recombinant antigen binding proteins that bind OSMR and, in some embodiments, a recombinant human OSMR or portion thereof. In this context, a "recombinant protein" is a protein made using recombinant techniques using any techniques and methods known in the art, *i.e.*, through the expression of a recombinant nucleic acid as described herein. Methods and techniques for the production of recombinant proteins are well known in the art. Embodiments of the invention include recombinant antigen binding proteins that bind wild-type OSMR and variants thereof.

[00109] "Consisting essentially of" means that the amino acid sequence can vary by about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15% relative to the recited SEQ ID NO: sequence and still retain biological activity, as described herein.

[00110] In some embodiments, the antigen binding proteins of the invention are isolated proteins or substantially pure proteins. An "isolated" protein is unaccompanied by at least some of the material with which it is normally associated in its natural state, for example

constituting at least about 5%, or at least about 50% by weight of the total protein in a given sample. It is understood that the isolated protein may constitute from 5 to 99.9% by weight of the total protein content depending on the circumstances. For example, the protein may be made at a significantly higher concentration through the use of an inducible promoter or high expression promoter, such that the protein is made at increased concentration levels. The definition includes the production of an antigen binding protein in a wide variety of organisms and/or host cells that are known in the art.

[00111] For amino acid sequences, sequence identity and/or similarity is determined by using standard techniques known in the art, including, but not limited to, the local sequence identity algorithm of Smith and Waterman, 1981, *Adv. Appl. Math.* 2:482, the sequence identity alignment algorithm of Needleman and Wunsch, 1970, *J. Mol. Biol.* 48:443, the search for similarity method of Pearson and Lipman, 1988, *Proc. Nat. Acad. Sci. U.S.A.* 85:2444, computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Drive, Madison, Wis.), the Best Fit sequence program described by Devereux *et al.*, 1984, *Nucl. Acid Res.* 12:387-395, preferably using the default settings, or by inspection. Preferably, percent identity is calculated by FastDB based upon the following parameters: mismatch penalty of 1; gap penalty of 1; gap size penalty of 0.33; and joining penalty of 30, "Current Methods in Sequence Comparison and Analysis," Macromolecule Sequencing and Synthesis, Selected Methods and Applications, pp 127-149 (1988), Alan R. Liss, Inc.

[00112] An example of a useful algorithm is PILEUP. PILEUP creates a multiple sequence alignment from a group of related sequences using progressive, pairwise alignments. It can also plot a tree showing the clustering relationships used to create the alignment. PILEUP uses a simplification of the progressive alignment method of Feng & Doolittle, 1987, *J. Mol. Evol.* 35:351-360; the method is similar to that described by Higgins and Sharp, 1989, *CABIOS* 5:151-153. Useful PILEUP parameters including a default gap weight of 3.00, a default gap length weight of 0.10, and weighted end gaps.

[00113] Another example of a useful algorithm is the BLAST algorithm, described in: Altschul *et al.*, 1990, *J. Mol. Biol.* 215:403-410; Altschul *et al.*, 1997, *Nucleic Acids Res.* 25:3389-3402; and Karin *et al.*, 1993, *Proc. Natl. Acad. Sci. U.S.A.* 90:5873-5787. A particularly useful BLAST program is the WU-BLAST-2 program which was obtained from Altschul *et al.*, 1996, *Methods in Enzymology* 266:460-480. WU-BLAST-2 uses several search parameters, most of which are set to the default values. The adjustable parameters are set with

the following values: overlap span=1, overlap fraction=0.125, word threshold (T)=11. The HSP S and HSP S2 parameters are dynamic values and are established by the program itself depending upon the composition of the particular sequence and composition of the particular database against which the sequence of interest is being searched; however, the values may be adjusted to increase sensitivity.

[00114] An additional useful algorithm is gapped BLAST as reported by Altschul *et al.*, 1993, *Nucl. Acids Res.* 25:3389-3402. Gapped BLAST uses BLOSUM-62 substitution scores; threshold T parameter set to 9; the two-hit method to trigger ungapped extensions, charges gap lengths of k a cost of 10+k; X_u set to 16, and X_g set to 40 for database search stage and to 67 for the output stage of the algorithms. Gapped alignments are triggered by a score corresponding to about 22 bits.

[00115] Generally, the amino acid homology, similarity, or identity between individual variant CDRs are at least 80% to the sequences depicted herein, and more typically with preferably increasing homologies or identities of at least 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, and almost 100%. In a similar manner, "percent (%) nucleic acid sequence identity" with respect to the nucleic acid sequence of the binding proteins identified herein is defined as the percentage of nucleotide residues in a candidate sequence that are identical with the nucleotide residues in the coding sequence of the antigen binding protein. A specific method utilizes the BLASTN module of WU-BLAST-2 set to the default parameters, with overlap span and overlap fraction set to 1 and 0.125, respectively.

[00116] Generally, the nucleic acid sequence homology, similarity, or identity between the nucleotide sequences encoding individual variant CDRs and the nucleotide sequences depicted herein are at least 80%, and more typically with preferably increasing homologies or identities of at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99%, and almost 100%.

[00117] Thus, a "variant CDR" is one with the specified homology, similarity, or identity to the parent CDR of the invention, and shares biological function, including, but not limited to, at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% of the specificity and/or activity of the parent CDR.

[00118] While the site or region for introducing an amino acid sequence variation is predetermined, the mutation *per se* need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted

at the target codon or region and the expressed antigen binding protein CDR variants screened for the optimal combination of desired activity. Techniques for making substitution mutations at predetermined sites in DNA having a known sequence are well known, for example, M13 primer mutagenesis and PCR mutagenesis. Screening of the mutants is done using assays of antigen binding protein activities, such as OSMR binding.

[00119] Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about one (1) to about twenty (20) amino acid residues, although considerably larger insertions may be tolerated. Deletions range from about one (1) to about twenty (20) amino acid residues, although in some cases deletions may be much larger.

[00120] Substitutions, deletions, insertions or any combination thereof may be used to arrive at a final derivative or variant. Generally these changes are done on a few amino acids to minimize the alteration of the molecule, particularly the immunogenicity and specificity of the antigen binding protein. However, larger changes may be tolerated in certain circumstances. Conservative substitutions are generally made in accordance with the following chart depicted as Table 3.

Table 3

Original Residue	Exemplary Substitutions
Ala	Ser
Arg	Lys
Asn	Gln, His
Asp	Glu
Cys	Ser
Gln	Asn
Glu	Asp
Gly	Pro
His	Asn, Gln
Ile	Leu, Val
Leu	Ile, Val
Lys	Arg, Gln, Glu
Met	Leu, Ile
Phe	Met, Leu, Tyr
Ser	Thr
Thr	Ser
Trp	Tyr
Tyr	Trp, Phe
Val	Ile, Leu

[00121] Substantial changes in function or immunological identity are made by selecting substitutions that are less conservative than those shown in TABLE 3. For example,

substitutions may be made which more significantly affect: the structure of the polypeptide backbone in the area of the alteration, for example the alpha-helical or beta-sheet structure; the charge or hydrophobicity of the molecule at the target site; or the bulk of the side chain. The substitutions which in general are expected to produce the greatest changes in the polypeptide's properties are those in which (a) a hydrophilic residue, *e.g.*, seryl or threonyl, is substituted for (or by) a hydrophobic residue, *e.g.*, leucyl, isoleucyl, phenylalanyl, valyl or alanyl; (b) a cysteine or proline is substituted for (or by) any other residue; (c) a residue having an electropositive side chain, *e.g.*, lysyl, arginyl, or histidyl, is substituted for (or by) an electronegative residue, *e.g.*, glutamyl or aspartyl; or (d) a residue having a bulky side chain, *e.g.*, phenylalanine, is substituted for (or by) one not having a side chain, e.g., glycine.

[00122] The variants typically exhibit the same qualitative biological activity and will elicit the same immune response as the naturally-occurring analogue, although variants also are selected to modify the characteristics of the antigen binding protein proteins as needed. Alternatively, the variant may be designed such that the biological activity of the antigen binding protein is altered. For example, glycosylation sites may be altered or removed as discussed herein.

[00123] Other derivatives of OSMR antibodies within the scope of this invention include covalent or aggregative conjugates of OSMR antibodies, or fragments thereof, with other proteins or polypeptides, such as by expression of recombinant fusion proteins comprising heterologous polypeptides fused to the N-terminus or C-terminus of a OSMR antibody polypeptide. For example, the conjugated peptide may be a heterologous signal (or leader) polypeptide, *e.g.*, the yeast alpha-factor leader, or a peptide such as an epitope tag. OSMR antibody-containing fusion proteins can comprise peptides added to facilitate purification or identification of the OSMR antibody (*e.g.*, poly-His). An OSMR antibody polypeptide also can be linked to the FLAG peptide as described in Hopp *et al.*, *Bio/Technology* 6:1204, 1988, and U.S. Patent 5,011,912. The FLAG peptide is highly antigenic and provides an epitope reversibly bound by a specific monoclonal antibody (mAb), enabling rapid assay and facile purification of expressed recombinant protein. Reagents useful for preparing fusion proteins in which the FLAG peptide is fused to a given polypeptide are commercially available (Sigma, St. Louis, MO).

[00124] In one embodiment, an oligomer is prepared using polypeptides derived from immunoglobulins. Preparation of fusion proteins comprising certain heterologous polypeptides fused to various portions of antibody-derived polypeptides (including the Fc domain) has been

described, *e.g.*, by Ashkenazi *et al.*, 1991, PNAS USA 88:10535; Byrn *et al.*, 1990, Nature 344:677; and Hollenbaugh *et al.*, 1992 "Construction of Immunoglobulin Fusion Proteins", in *Current Protocols in Immunology*, Suppl. 4, pages 10.19.1 - 10.19.11.

[00125] One embodiment of the present invention is directed to a dimer comprising two fusion proteins created by fusing an OSMR binding fragment of an OSMR antibody to the Fc region of an antibody. The dimer can be made by, for example, inserting a gene fusion encoding the fusion protein into an appropriate expression vector, expressing the gene fusion in host cells transformed with the recombinant expression vector, and allowing the expressed fusion protein to assemble much like antibody molecules, whereupon interchain disulfide bonds form between the Fc moieties to yield the dimer.

[00126] The term "Fc polypeptide" as used herein includes native and mutein forms of polypeptides derived from the Fc region of an antibody. Truncated forms of such polypeptides containing the hinge region that promotes dimerization also are included. Fusion proteins comprising Fc moieties (and oligomers formed therefrom) offer the advantage of facile purification by affinity chromatography over Protein A or Protein G columns.

[00127] One suitable Fc polypeptide, described in PCT application WO 93/10151 (hereby incorporated by reference), is a single chain polypeptide extending from the N-terminal hinge region to the native C-terminus of the Fc region of a human IgG antibody. Another useful Fc polypeptide is the Fc mutein described in U.S. Patent 5,457,035 and in Baum *et al.*, 1994, *EMBO J.* 13:3992-4001. The amino acid sequence of this mutein is identical to that of the native Fc sequence presented in WO 93/10151, except that amino acid 19 has been changed from Leu to Ala, amino acid 20 has been changed from Leu to Glu, and amino acid 22 has been changed from Gly to Ala. The mutein exhibits reduced affinity for Fc receptors.

[00128] In other embodiments, the variable portion of the heavy and/or light chains of a OSMR antibody may be substituted for the variable portion of an antibody heavy and/or light chain.

[00129] Another method for preparing oligomeric OSMR antibody derivatives involves use of a leucine zipper. Leucine zipper domains are peptides that promote oligomerization of the proteins in which they are found. Leucine zippers were originally identified in several DNA-binding proteins (Landschulz *et al.*, *Science* 240:1759-64, 1988), and have since been found in a variety of different proteins. Among the known leucine zippers are naturally occurring peptides and derivatives thereof that dimerize or trimerize. Examples of leucine

zipper domains suitable for producing soluble oligomeric proteins are described in PCT application WO 94/10308, and the leucine zipper derived from lung surfactant protein D (SPD) described in Hoppe *et al.*, 1994, *FEBS Letters* 344:191, hereby incorporated by reference. The use of a modified leucine zipper that allows for stable trimerization of a heterologous protein fused thereto is described in Fanslow *et al.*, 1994, *Semin. Immunol.* 6:267-78. In one approach, recombinant fusion proteins comprising OSMR antibody fragment or derivative fused to a leucine zipper peptide are expressed in suitable host cells, and the soluble oligomeric OSMR antibody fragments or derivatives that form are recovered from the culture supernatant.

[00130] Covalent modifications of antigen binding proteins are included within the scope of this invention, and are generally, but not always, done post-translationally. For example, several types of covalent modifications of the antigen binding protein are introduced into the molecule by reacting specific amino acid residues of the antigen binding protein with an organic derivatizing agent that is capable of reacting with selected side chains or the N- or C-terminal residues.

[00131] Cysteinyl residues most commonly are reacted with α-haloacetates (and corresponding amines), such as chloroacetic acid or chloroacetamide, to give carboxymethyl or carboxyamidomethyl derivatives. Cysteinyl residues also are derivatized by reaction with bromotrifluoroacetone, α-bromo-β-(5-imidozoyl)propionic acid, chloroacetyl phosphate, N-alkylmaleimides, 3-nitro-2-pyridyl disulfide, methyl 2-pyridyl disulfide, p-chloromercuribenzoate, 2-chloromercuri-4-nitrophenol, or chloro-7-nitrobenzo-2-oxa-1,3-diazole.

[00132] Histidyl residues are derivatized by reaction with diethylpyrocarbonate at pH 5.5-7.0 because this agent is relatively specific for the histidyl side chain. Para-bromophenacyl bromide also is useful; the reaction is preferably performed in 0.1M sodium cacodylate at pH 6.0.

[00133] Lysinyl and amino terminal residues are reacted with succinic or other carboxylic acid anhydrides. Derivatization with these agents has the effect of reversing the charge of the lysinyl residues. Other suitable reagents for derivatizing alpha-amino-containing residues include imidoesters such as methyl picolinimidate; pyridoxal phosphate; pyridoxal; chloroborohydride; trinitrobenzenesulfonic acid; O-methylisourea; 2,4-pentanedione; and transaminase-catalyzed reaction with glyoxylate.

[00134] Arginyl residues are modified by reaction with one or several conventional reagents, among them phenylglyoxal, 2,3-butanedione, 1,2-cyclohexanedione, and ninhydrin. Derivatization of arginine residues requires that the reaction be performed in alkaline conditions because of the high pK_a of the guanidine functional group. Furthermore, these reagents may react with the groups of lysine as well as the arginine epsilon-amino group.

[00135] The specific modification of tyrosyl residues may be made, with particular interest in introducing spectral labels into tyrosyl residues by reaction with aromatic diazonium compounds or tetranitromethane. Most commonly, N-acetylimidizole and tetranitromethane are used to form O-acetyl tyrosyl species and 3-nitro derivatives, respectively. Tyrosyl residues are iodinated using ^{125}I or ^{131}I to prepare labeled proteins for use in radioimmunoassay, the chloramine T method described above being suitable.

[00136] Carboxyl side groups (aspartyl or glutamyl) are selectively modified by reaction with carbodiimides (R'—N=C=N--R'), where R and R' are optionally different alkyl groups, such as 1-cyclohexyl-3-(2-morpholinyl-4-ethyl) carbodiimide or 1-ethyl-3-(4-azonia-4,4-dimethylpentyl) carbodiimide. Furthermore, aspartyl and glutamyl residues are converted to asparaginyl and glutaminyl residues by reaction with ammonium ions.

[00137] Derivatization with bifunctional agents is useful for crosslinking antigen binding proteins to a water-insoluble support matrix or surface for use in a variety of methods. Commonly used crosslinking agents include, *e.g.*, 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), and bifunctional maleimides such as bis-N-maleimido-1,8-octane. Derivatizing agents such as methyl-3-[(p-azidophenyl)dithio]propioimidate yield photoactivatable intermediates that are capable of forming crosslinks in the presence of light. Alternatively, reactive water-insoluble matrices such as cyanogen bromide-activated carbohydrates and the reactive substrates described in U.S. Pat. Nos. 3,969,287; 3,691,016; 4,195,128; 4,247,642; 4,229,537; and 4,330,440 are employed for protein immobilization.

[00138] Glutaminyl and asparaginyl residues are frequently deamidated to the corresponding glutamyl and aspartyl residues, respectively. Alternatively, these residues are deamidated under mildly acidic conditions. Either form of these residues falls within the scope of this invention.

[00139] Other modifications include hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, methylation of the α-amino groups of lysine, arginine, and histidine side chains (T. E. Creighton, Proteins: Structure and Molecular Properties, W. H. Freeman & Co., San Francisco, 1983, pp. 79-86), acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

[00140] Another type of covalent modification of the antigen binding protein included within the scope of this invention comprises altering the glycosylation pattern of the protein. As is known in the art, glycosylation patterns can depend on both the sequence of the protein (e.g., the presence or absence of particular glycosylation amino acid residues, discussed below), or the host cell or organism in which the protein is produced. Particular expression systems are discussed below.

[00141] Glycosylation of polypeptides is typically either N-linked or O-linked. N-linked refers to the attachment of the carbohydrate moiety to the side chain of an asparagine residue. The tri-peptide sequences asparagine-X-serine and asparagine-X-threonine, where X is any amino acid except proline, are the recognition sequences for enzymatic attachment of the carbohydrate moiety to the asparagine side chain. Thus, the presence of either of these tri-peptide sequences in a polypeptide creates a potential glycosylation site. O-linked glycosylation refers to the attachment of one of the sugars N-acetylgalactosamine, galactose, or xylose, to a hydroxyamino acid, most commonly serine or threonine, although 5-hydroxyproline or 5-hydroxylysine may also be used.

[00142] Addition of glycosylation sites to the antigen binding protein is conveniently accomplished by altering the amino acid sequence such that it contains one or more of the above-described tri-peptide sequences (for N-linked glycosylation sites). The alteration may also be made by the addition of, or substitution by, one or more serine or threonine residues to the starting sequence (for O-linked glycosylation sites). For ease, the antigen binding protein amino acid sequence is preferably altered through changes at the DNA level, particularly by mutating the DNA encoding the target polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

[00143] Another means of increasing the number of carbohydrate moieties on the antigen binding protein is by chemical or enzymatic coupling of glycosides to the protein. These procedures are advantageous in that they do not require production of the protein in a host cell that has glycosylation capabilities for N- and O-linked glycosylation. Depending on the

coupling mode used, the sugar(s) may be attached to (a) arginine and histidine, (b) free carboxyl groups, (c) free sulfhydryl groups such as those of cysteine, (d) free hydroxyl groups such as those of serine, threonine, or hydroxyproline, (e) aromatic residues such as those of phenylalanine, tyrosine, or tryptophan, or (f) the amide group of glutamine. These methods are described in WO 87/05330 published Sep. 11, 1987, and in Aplin and Wriston, 1981, *CRC Crit. Rev. Biochem.*, pp. 259-306.

[00144] Removal of carbohydrate moieties present on the starting antigen binding protein may be accomplished chemically or enzymatically. Chemical deglycosylation requires exposure of the protein to the compound trifluoromethanesulfonic acid, or an equivalent compound. This treatment results in the cleavage of most or all sugars except the linking sugar (N-acetylglucosamine or N-acetylgalactosamine), while leaving the polypeptide intact. Chemical deglycosylation is described by Hakimuddin *et al.*, 1987, *Arch. Biochem. Biophys.* 259:52 and by Edge *et al.*, 1981, *Anal. Biochem.* 118:131. Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo- and exo-glycosidases as described by Thotakura *et al.*, 1987, *Meth. Enzymol.* 138:350. Glycosylation at potential glycosylation sites may be prevented by the use of the compound tunicamycin as described by Duskin *et al.*, 1982, *J. Biol. Chem.* 257:3105. Tunicamycin blocks the formation of protein-N-glycoside linkages.

[00145] Another type of covalent modification of the antigen binding protein comprises linking the antigen binding protein to various nonproteinaceous polymers, including, but not limited to, various polyols such as polyethylene glycol, polypropylene glycol or polyoxyalkylenes, in the manner set forth in U.S. Pat. Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337. In addition, as is known in the art, amino acid substitutions may be made in various positions within the antigen binding protein to facilitate the addition of polymers such as PEG.

[00146] In some embodiments, the covalent modification of the antigen binding proteins of the invention comprises the addition of one or more labels.

[00147] The term "labeling group" means any detectable label. Examples of suitable labeling groups include, but are not limited to, the following: radioisotopes or radionuclides (*e.g.*, ^{3}H, ^{14}C, ^{15}N, ^{35}S, ^{90}Y, ^{99}Tc, ^{111}In, ^{125}I, ^{131}I), fluorescent groups (*e.g.*, FITC, rhodamine, lanthanide phosphors), enzymatic groups (*e.g.*, horseradish peroxidase, β-galactosidase, luciferase, alkaline phosphatase), chemiluminescent groups, biotinyl groups, or predetermined

polypeptide epitopes recognized by a secondary reporter (*e.g.*, leucine zipper pair sequences, binding sites for secondary antibodies, metal binding domains, epitope tags). In some embodiments, the labeling group is coupled to the antigen binding protein *via* spacer arms of various lengths to reduce potential steric hindrance. Various methods for labeling proteins are known in the art and may be used in performing the present invention.

[00148] In general, labels fall into a variety of classes, depending on the assay in which they are to be detected: a) isotopic labels, which may be radioactive or heavy isotopes; b) magnetic labels (*e.g.*, magnetic particles); c) redox active moieties; d) optical dyes; enzymatic groups (*e.g.* horseradish peroxidase, β-galactosidase, luciferase, alkaline phosphatase); e) biotinylated groups; and f) predetermined polypeptide epitopes recognized by a secondary reporter (*e.g.*, leucine zipper pair sequences, binding sites for secondary antibodies, metal binding domains, epitope tags, etc.). In some embodiments, the labeling group is coupled to the antigen binding protein *via* spacer arms of various lengths to reduce potential steric hindrance. Various methods for labeling proteins are known in the art and may be used in performing the present invention.

[00149] Specific labels include optical dyes, including, but not limited to, chromophores, phosphors and fluorophores, with the latter being specific in many instances. Fluorophores can be either "small molecule" fluores, or proteinaceous fluores.

[00150] By "fluorescent label" is meant any molecule that may be detected *via* its inherent fluorescent properties. Suitable fluorescent labels include, but are not limited to, fluorescein, rhodamine, tetramethylrhodamine, eosin, erythrosin, coumarin, methyl-coumarins, pyrene, Malacite green, stilbene, Lucifer Yellow, Cascade BlueJ, Texas Red, IAEDANS, EDANS, BODIPY FL, LC Red 640, Cy 5, Cy 5.5, LC Red 705, Oregon green, the Alexa-Fluor dyes (Alexa Fluor 350, Alexa Fluor 430, Alexa Fluor 488, Alexa Fluor 546, Alexa Fluor 568, Alexa Fluor 594, Alexa Fluor 633, Alexa Fluor 660, Alexa Fluor 680), Cascade Blue, Cascade Yellow and R-phycoerythrin (PE) (Molecular Probes, Eugene, OR), FITC, Rhodamine, and Texas Red (Pierce, Rockford, IL), Cy5, Cy5.5, Cy7 (Amersham Life Science, Pittsburgh, PA). Suitable optical dyes, including fluorophores, are described in Molecular Probes Handbook by Richard P. Haugland, hereby expressly incorporated by reference.

[00151] Suitable proteinaceous fluorescent labels also include, but are not limited to, green fluorescent protein, including a Renilla, Ptilosarcus, or Aequorea species of GFP (Chalfie *et al.*, 1994, *Science* 263:802-805), EGFP (Clontech Laboratories, Inc., Genbank Accession

Number U55762), blue fluorescent protein (BFP, Quantum Biotechnologies, Inc. 1801 de Maisonneuve Blvd. West, 8th Floor, Montreal, Quebec, Canada H3H 1J9; Stauber, 1998, *Biotechniques* 24:462-471; Heim *et al.*, 1996, *Curr. Biol.* 6:178-182), enhanced yellow fluorescent protein (EYFP, Clontech Laboratories, Inc.), luciferase (Ichiki *et al.*, 1993, *J. Immunol.* 150:5408-5417), β galactosidase (Nolan *et al.*, 1988, *Proc. Natl. Acad. Sci. U.S.A.* 85:2603-2607) and Renilla (WO92/15673, WO95/07463, WO98/14605, WO98/26277, WO99/49019, U.S. Patent Nos. 5292658, 5418155, 5683888, 5741668, 5777079, 5804387, 5874304, 5876995, 5925558). All of the above-cited references are expressly incorporated herein by reference.

[00152] The exemplary antigen binding proteins described herein have properties based on the distinct epitope on OSMR bound by the antigen binding protein. The term "epitope" means the amino acids of a target molecule that are contacted by an antigen binding protein, e.g., an antibody, when the antigen binding protein is bound to the target molecule. An epitope can be contiguous or non-contiguous (e.g., (i) in a single-chain polypeptide, amino acid residues that are not contiguous to one another in the polypeptide sequence but that within the context of the target molecule are bound by the antigen binding protein, or (ii) in a multimeric receptor comprising two or more individual components, e.g., OSMR and gp130 or OSMR and IL-31 receptor A, amino acid residues are present on one or more of the individual components but are still bound by the antigen binding protein. Epitope determinants can include chemically active surface groupings of molecules such as amino acids, sugar side chains, phosphoryl or sulfonyl groups, and can have specific three dimensional structural characteristics, and/or specific charge characteristics. Generally, antigen binding proteins specific for a particular target molecule will preferentially recognize an epitope on the target molecule in a complex mixture of proteins and/or macromolecules.

[00153] Methods of characterizing the epitope bound by an antigen binding protein are well known in the art, including, but not limited to, binning (cross-competition) (Miller *et al* "Epitope binning of murine monoclonal antibodies by a multiplexed pairing assay" *J Immunol Methods* (2011) 365, 118-25), peptide mapping (e.g., PEPSPOT™) (Albert *et al* "The B-cell Epitope of the Monoclonal Anti-Factor VIII Antibody ESH8 Characterized by Peptide Array Analysis" 2008 *Thromb. Haemost.* 99, 634-7), mutagenesis methods such as chimeras (Song *et al* "Epitope Mapping of Ibalizumab, a Humanized Anti-CD4 Monoclonal Antibody with Anti-HIV-1 Activity in Infected Patients" *J. Virol.* (2010) 84, 6935-6942) , alanine scanning (Cunningham and Wells "High-resolution epitope mapping of HGH-receptor interactions by

alanine-scanning mutagenesis" *Science* (1989) 244, 1081–1085), arginine scanning (Lim *et al* "A diversity of antibody epitopes can induce signaling through the erythropoietin receptor" *Biochemistry* (2010) 49, 3797–3804), HD exchange methods (Coates *et al* "Epitope mapping by amide hydrogen/deuterium exchange coupled with immobilization of antibody, on-line proteolysis, liquid chromatography and mass spectrometry" *Rapid Commun. Mass Spectrom.* (2009) 23 639– 647), NMR cross saturation methods (Morgan *et al* "Precise epitope mapping of malaria parasite inhibitory antibodies by TROSY NMR cross-saturation" *Biochemistry* (2005) 44, 518-23), and crystallography (Gerhardt *et al* "Structure of IL-17A in complex with a potent, fully human neutralizing antibody" *J. Mol. Biol* (2009) 394, 905-21). The methods vary in the level of detail they provide as to the amino acids comprising the epitope. Example 4 provides an exemplary method of epitope binning.

[00154] Antigen binding proteins of the present invention include those that have an overlapping epitope with an exemplary antigen binding protein described herein, e.g., Ab1, Ab2, or Ab3. In certain embodiments, the antigen binding protein has an identical epitope as to the exemplary antigen binding proteins. In other embodiments, the antigen binding protein binds only a subset of the same amino acids as the exemplary antigen binding protein.

[00155] In certain embodiments, the OSMR antigen binding protein has an identical or overlapping epitope as Ab1, Ab2, or Ab3, and comprises a) a light chain variable domain having at least 90% identity, at least 95% identity, or is identical to the amino acid sequence set forth in SEQ ID NO:27, SEQ ID NO:28, or SEQ ID NO:29; b) a heavy chain variable domain having at least 90% identity, at least 95% identity, or is identical to the amino acid sequence set forth in SEQ ID NO:9, SEQ ID NO:10, or SEQ ID NO:11; or c) the light chain variable domain of a) and the heavy chain variable domain of b).

[00156] In certain embodiments, the OSMR antigen binding protein has an identical or overlapping epitope as Ab1, Ab2, or Ab3, and comprises a light chain variable domain having at least 90%, at least 95%, or is identical to the amino acid sequence set forth in SEQ ID NO:27 and a heavy chain variable domain having at least 90%, at least 95%, or is identical to the amino acid sequence set forth in SEQ ID NO:9; those comprising a light chain variable domain having at least 90%, at least 95%, or is identical to the amino acid sequence set forth in SEQ ID NO:28 and a heavy chain variable domain having at least 90%, at least 95%, or is identical to the amino acid sequence set forth in SEQ ID NO:10; and those comprising a light chain variable domain having at least 90%, at least 95%, or is identical to the amino acid sequence set

forth in SEQ ID NO:29 and a heavy chain variable domain having at least 90%, at least 95%, or is identical to the amino acid sequence set forth in SEQ ID NO:11.

[00157] In certain embodiments, the OSMR antigen binding protein has an identical or overlapping epitope as Ab1, Ab2, or Ab3, and comprises a) a light chain variable domain having no more than ten or no more than five amino acid additions, deletions or substitutions from the amino acid sequence set forth in SEQ ID NO:27, SEQ ID NO:28, or SEQ ID NO:29; b) a heavy chain variable domain having no more than ten or no more than five amino acid additions, deletions or substitutions from the amino acid sequence set forth in SEQ ID NO:9, SEQ ID NO:10, or SEQ ID NO:11; or c) the light chain variable domain of a) and the heavy chain variable domain of b).

[00158] In certain embodiments, the OSMR antigen binding protein has an identical or overlapping epitope as Ab1, Ab2, or Ab3, and comprises a light chain variable domain having no more than ten or no more than five amino acid additions, deletions or substitutions from the amino acid sequence set forth in SEQ ID NO:27 and a heavy chain variable domain having no more than ten or no more than five amino acid additions, deletions or substitutions from the amino acid sequence set forth in SEQ ID NO:9; those comprising a light chain variable domain having no more than ten or no more than five amino acid additions, deletions or substitutions from the amino acid sequence set forth in SEQ ID NO:28 and a heavy chain variable domain having no more than ten or no more than five amino acid additions, deletions or substitutions from the amino acid sequence set forth in SEQ ID NO:10; and those comprising a light chain variable domain having no more than ten or no more than five amino acid additions, deletions or substitutions from the amino acid sequence set forth in SEQ ID NO:29 and a heavy chain variable domain having no more than ten or no more than five amino acid additions, deletions or substitutions from the amino acid sequence set forth in SEQ ID NO:11.

An exemplary heavy chain variable domain variant of SEQ ID NO:9 contains an amino acid other than asparagine (for example, aspartic acid) at the position corresponding to position 73 in SEQ ID NO:9. The amino acid sequence set forth in SEQ ID NO:53 is an example of a heavy chain variable domain variant of SEQ ID NO:9.

An exemplary heavy chain variable domain variant of SEQ ID NO:10 contains an amino acid other than asparagine (for example, aspartic acid) at the position corresponding to position 73 in SEQ ID NO:10. The amino acid sequence set forth in SEQ ID NO:54 is an example of a heavy chain variable domain variant of SEQ ID NO:10.

[00159] In certain embodiments, the OSMR antigen binding protein has an identical or overlapping epitope as Ab1, Ab2, or Ab3, and comprises a light chain variable domain comprising a) an LCDR1 having no more than three amino acid additions, deletions, or substitutions from the LCDR1 sequence set forth in SEQ ID NO:30; an LCDR2 having no more than three amino acid additions, deletions, or substitutions from the LCDR2 sequence set forth in SEQ ID NO:33; and an LCDR3 having no more than three amino acid additions, deletions, or substitutions from the LCDR3 sequence set forth in SEQ ID NO:36; b) an LCDR1 having no more than three amino acid additions, deletions, or substitutions from the LCDR1 sequence set forth in SEQ ID NO:31; an LCDR2 having no more than three amino acid additions, deletions, or substitutions from the LCDR2 sequence set forth in SEQ ID NO:34; and an LCDR3 having no more than three amino acid additions, deletions, or substitutions from the LCDR3 sequence set forth in SEQ ID NO:37; or c) an LCDR1 having no more than three amino acid additions, deletions, or substitutions from the LCDR1 sequence set forth in SEQ ID NO:32; an LCDR2 having no more than three amino acid additions, deletions, or substitutions from the LCDR2 sequence set forth in SEQ ID NO:35; and an LCDR3 having no more than three amino acid additions, deletions, or substitutions from the LCDR3 sequence set forth in SEQ ID NO:38; and a heavy chain variable domain comprising d) an HCDR1 having no more than three amino acid additions, deletions, or substitutions from the HCDR1 sequence set forth in SEQ ID NO:12; an HCDR2 having no more than three amino acid additions, deletions, or substitutions from the HCDR2 sequence set forth in SEQ ID NO:15; and an HCDR3 having no more than three amino acid additions, deletions, or substitutions from the HCDR3 sequence set forth in SEQ ID NO:18; e) an HCDR1 having no more than three amino acid additions, deletions, or substitutions from the HCDR1 sequence set forth in SEQ ID NO:13; an HCDR2 having no more than three amino acid additions, deletions, or substitutions from the HCDR2 sequence set forth in SEQ ID NO:16; and an HCDR3 having no more than three amino acid additions, deletions, or substitutions from the HCDR3 sequence set forth in SEQ ID NO:19; or f) an HCDR1 having no more than three amino acid additions, deletions, or substitutions from the HCDR1 sequence set forth in SEQ ID NO:14; an HCDR2 having no more than three amino acid additions, deletions, or substitutions from the HCDR2 sequence set forth in SEQ ID NO:17; and an HCDR3 having no more than three amino acid additions, deletions, or substitutions from the HCDR3 sequence set forth in SEQ ID NO:20.

[00160] Preferred OSMR antigen binding proteins described immediately above include those comprising the light chain variable domain of a) and the heavy chain variable domain of

d); those comprising the light chain variable domain of b) and the heavy chain variable domain of e); and those comprising the light chain variable domain of c) and the heavy chain variable domain of f).

OSMR antigen binding proteins comprising the light chain variable domain of a) and the heavy chain variable domain of d) can optionally contain a heavy chain variable domain that comprises an amino acid other than asparagine (for example, aspartic acid) at the position corresponding to position 73 in SEQ ID NO:9. In such embodiments, the heavy chain variable domain optionally comprises the amino acid sequence set forth in SEQ ID NO:53.

OSMR antigen binding proteins comprising the light chain variable domain of b) and the heavy chain variable domain of e) can optionally contain a heavy chain variable domain that comprises an amino acid other than asparagine (for example, aspartic acid) at the position corresponding to position 73 in SEQ ID NO:10. In such embodiments, the heavy chain variable domain optionally comprises the amino acid sequence set forth in SEQ ID NO:54.

[00161] Antigen binding proteins that have an identical epitope or overlapping epitope will often cross-compete for binding to the antigen. Thus, in certain embodiments, an antigen binding protein of the invention cross-competes with Ab1, Ab2, or Ab3. To "cross-compete" or "cross-competition" means the antigen binding proteins compete for the same epitope or binding site on a target. Such competition can be determined by an assay in which the reference antigen binding protein (e.g., antibody or antigen-binding portion thereof) prevents or inhibits specific binding of a test antigen binding protein, and vice versa. Numerous types of competitive binding assays can be used to determine if a test molecule competes with a reference molecule for binding. Examples of assays that can be employed include solid phase direct or indirect radioimmunoassay (RIA), solid phase direct or indirect enzyme immunoassay (EIA), sandwich competition assay (see, e.g., Stahli et al. (1983) *Methods in Enzymology* 9:242-253), solid phase direct biotin-avidin EIA (see, e.g., Kirkland et al., (1986) *J. Immunol.* 137:3614-9), solid phase direct labeled assay, solid phase direct labeled sandwich assay, Luminex (Jia *et al.* "A novel method of Multiplexed Competitive Antibody Binning for the characterization of monoclonal antibodies" *J. Immunological Methods* (2004) 288, 91–98) and surface plasmon resonance (Song *et al.* "Epitope Mapping of Ibalizumab, a Humanized Anti-CD4 Monoclonal Antibody with Anti-HIV-1 Activity in Infected Patients" *J. Virol.* (2010) 84, 6935-42). An exemplary method of determining cross-competition is described in Example 5. Usually, when a competing antigen binding protein is present in excess, it will inhibit binding of a reference antigen binding protein to a common antigen by at least 50%, 55%, 60%, 65%,

70%, or 75%. In some instances, binding is inhibited by at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or more.

Polynucleotides Encoding OSMR Antigen Binding Proteins

[00162] Encompassed within the invention are nucleic acids or isolated nucleic acids encoding OSMR antigen binding proteins, including antibodies, as defined herein. Preferred nucleic acids include those that encode the exemplary light and heavy chains described herein.

[00163] An exemplary nucleic acid encoding Ab1 LC is a nucleic acid comprising the sequence set forth in SEQ ID NO:21.

[00164] An exemplary nucleic acid encoding Ab2 LC is a nucleic acid comprising the sequence set forth in SEQ ID NO:22.

[00165] An exemplary nucleic acid encoding Ab3 LC is a nucleic acid comprising the sequence set forth in SEQ ID NO:23.

[00166] An exemplary nucleic acid encoding Ab1 HC is a nucleic acid comprising the sequence set forth in SEQ ID NO:3.

[00167] An exemplary nucleic acid encoding Ab2 HC is a nucleic acid comprising the sequence set forth in SEQ ID NO:4.

[00168] An exemplary nucleic acid encoding Ab3 HC is a nucleic acid comprising the sequence set forth in SEQ ID NO:5.

An exemplary nucleic acid encoding a variant Ab1 HC is a nucleic acid comprising the sequence set forth in SEQ ID NO:47.

An exemplary nucleic acid encoding a variant Ab2 HC is a nucleic acid comprising the sequence set forth in SEQ ID NO:48.

An exemplary nucleic acid encoding a variant Ab3 HC is a nucleic acid comprising the sequence set forth in SEQ ID NO:49.

[00169] Aspects of the invention include polynucleotide variants (*e.g.*, due to degeneracy) that encode the amino acid sequences described herein.

[00170] Aspects of the invention include a variety of embodiments including, but not limited to, the following exemplary embodiments.

[00171] An isolated nucleic acid comprising a polynucleotide, wherein said polynucleotide encodes one or more polypeptides comprising an amino acid sequence selected from the group consisting of:

[00172] A. 1. a light chain variable domain sequence that is at least 90% identical to a light chain variable domain sequence set forth in SEQ ID NOS:27-29;

[00173] 2. a heavy chain variable domain sequence that is at least 90% identical to a heavy chain variable domain sequence set forth in SEQ ID NOS:9-11;

[00174] 3. a light chain variable domain of (1) and a heavy chain variable domain of (2); and

[00175] B. a light chain variable domain comprising a CDR1, CDR2, CDR3 and/or a heavy chain variable domain comprising a CDR1, CDR2, CDR3 that are the same or differ by no more than a total of three amino acid additions, substitutions, and/or deletions in each CDR from the following sequences:

[00176] 1. a light chain CDR1 (SEQ ID NO:30), CDR2 (SEQ ID NO:33), CDR3 (SEQ ID NO:36) or a heavy chain CDR1 (SEQ ID NO:12), CDR2 (SEQ ID NO:15), CDR3 (SEQ ID NO:18) of Ab1;

[00177] 2. a light chain CDR1 (SEQ ID NO:31), CDR2 (SEQ ID NO:34), CDR3 (SEQ ID NO:37) or a heavy chain CDR1 (SEQ ID NO:13), CDR2 (SEQ ID NO:16), CDR3 (SEQ ID NO:19) of Ab2; and

[00178] 3. a light chain CDR1 (SEQ ID NO:32), CDR2 (SEQ ID NO:35), CDR3 (SEQ ID NO:38) or a heavy chain CDR1 (SEQ ID NO:14), CDR2 (SEQ ID NO:17), CDR3 (SEQ ID NO:20) of Ab3.

In some embodiments, the nucleic acid encodes a polypeptide that comprises the amino acid sequence set forth in SEQ ID NO:53 or SEQ ID NO:54.

In some embodiments, the nucleic acid encodes a polypeptide that comprises the amino acid sequence set forth in SEQ ID NO:50, SEQ ID NO:51, or SEQ ID NO:52.

[00179] In preferred embodiments, the polypeptide encoded by the nucleic acid or isolated nucleic acid is a component of an antigen binding protein that binds OSMR.

[00180] Nucleotide sequences corresponding to the amino acid sequences described herein, to be used as probes or primers for the isolation of nucleic acids or as query sequences

for database searches, can be obtained by "back-translation" from the amino acid sequences, or by identification of regions of amino acid identity with polypeptides for which the coding DNA sequence has been identified. The well-known polymerase chain reaction (PCR) procedure can be employed to isolate and amplify a DNA sequence encoding an OSMR antigen binding proteins or a desired combination of OSMR antigen binding protein polypeptide fragments. Oligonucleotides that define the desired termini of the combination of DNA fragments are employed as 5' and 3' primers. The oligonucleotides can additionally contain recognition sites for restriction endonucleases, to facilitate insertion of the amplified combination of DNA fragments into an expression vector. PCR techniques are described in Saiki et al., *Science* 239:487 (1988); *Recombinant DNA Methodology*, Wu et al., eds., Academic Press, Inc., San Diego (1989), pp. 189-196; and *PCR Protocols: A Guide to Methods and Applications*, Innis *et. al.*, eds., Academic Press, Inc. (1990).

[00181] Nucleic acid molecules of the invention include DNA and RNA in both single-stranded and double-stranded form, as well as the corresponding complementary sequences. DNA includes, for example, cDNA, genomic DNA, chemically synthesized DNA, DNA amplified by PCR, and combinations thereof. The nucleic acid molecules of the invention include full-length genes or cDNA molecules as well as a combination of fragments thereof. The nucleic acids of the invention are preferentially derived from human sources, but the invention includes those derived from non-human species, as well.

[00182] In some embodiments, nucleic acids of the invention are isolated nucleic acids. An "isolated nucleic acid" is a nucleic acid that has been separated from adjacent genetic sequences present in the genome of the organism from which the nucleic acid was isolated, in the case of nucleic acids isolated from naturally-occurring sources. In the case of nucleic acids synthesized enzymatically from a template or chemically, such as PCR products, cDNA molecules, or oligonucleotides for example, it is understood that the nucleic acids resulting from such processes are isolated nucleic acids. An isolated nucleic acid molecule refers to a nucleic acid molecule in the form of a separate fragment or as a component of a larger nucleic acid construct. In one preferred embodiment, the nucleic acids are substantially free from contaminating endogenous material. The nucleic acid molecule has preferably been derived from DNA or RNA isolated at least once in substantially pure form and in a quantity or concentration enabling identification, manipulation, and recovery of its component nucleotide sequences by standard biochemical methods (such as those outlined in Sambrook et al., *Molecular Cloning: A Laboratory Manual*, 2nd ed., Cold Spring Harbor Laboratory, Cold

Spring Harbor, NY (1989)). Such sequences are preferably provided and/or constructed in the form of an open reading frame uninterrupted by internal non-translated sequences, or introns, that are typically present in eukaryotic genes. Sequences of non-translated DNA can be present 5' or 3' from an open reading frame, where the same do not interfere with manipulation or expression of the coding region.

[00183] The present invention also includes nucleic acids or isolated nucleic acids that hybridize under moderately stringent conditions, and more preferably highly stringent conditions, to nucleic acids encoding OSMR antigen binding proteins as described herein. The basic parameters affecting the choice of hybridization conditions and guidance for devising suitable conditions are set forth by Sambrook,, Fritsch, and Maniatis (1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., chapters 9 and 11; and Current Protocols in Molecular Biology, 1995, Ausubel et al., eds., John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4), and can be readily determined by those having ordinary skill in the art based on, for example, the length and/or base composition of the DNA. One way of achieving moderately stringent conditions involves the use of a prewashing solution containing 5 x SSC, 0.5% SDS, 1.0 mM EDTA (pH 8.0), hybridization buffer of about 50% formamide, 6 x SSC, and a hybridization temperature of about 55 degrees C (or other similar hybridization solutions, such as one containing about 50% formamide, with a hybridization temperature of about 42 degrees C), and washing conditions of about 60 degrees C, in 0.5 x SSC, 0.1% SDS. Generally, highly stringent conditions are defined as hybridization conditions as above, but with washing at approximately 68 degrees C, 0.2 x SSC, 0.1% SDS. SSPE (1xSSPE is 0.15M NaCl, 10 mM NaH.sub.2 PO.sub.4, and 1.25 mM EDTA, pH 7.4) can be substituted for SSC (1xSSC is 0.15M NaCl and 15 mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete. It should be understood that the wash temperature and wash salt concentration can be adjusted as necessary to achieve a desired degree of stringency by applying the basic principles that govern hybridization reactions and duplex stability, as known to those skilled in the art and described further below (see, e.g., Sambrook et al., 1989). When hybridizing a nucleic acid to a target nucleic acid of unknown sequence, the hybrid length is assumed to be that of the hybridizing nucleic acid. When nucleic acids of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the nucleic acids and identifying the region or regions of optimal sequence complementarity. The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length should be 5 to 10.degrees C less than the melting

temperature (Tm) of the hybrid, where Tm is determined according to the following equations. For hybrids less than 18 base pairs in length, Tm (degrees C) = 2(# of A + T bases) + 4(# of #G + C bases). For hybrids above 18 base pairs in length, Tm (degrees C) = 81.5 + 16.6($\log_{10}$ [Na^+]) + 0.41(% G + C) - (600/N), where N is the number of bases in the hybrid, and [Na^+] is the concentration of sodium ions in the hybridization buffer ([Na^+] for 1xSSC = 0.165M). Preferably, each such hybridizing nucleic acid has a length that is at least 15 nucleotides (or more preferably at least 18 nucleotides, or at least 20 nucleotides, or at least 25 nucleotides, or at least 30 nucleotides, or at least 40 nucleotides, or most preferably at least 50 nucleotides), or at least 25% (more preferably at least 50%, or at least 60%, or at least 70%, and most preferably at least 80%) of the length of the nucleic acid of the present invention to which it hybridizes, and has at least 60% sequence identity (more preferably at least 70%, at least 75%, at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99%, and most preferably at least 99.5%) with the nucleic acid of the present invention to which it hybridizes, where sequence identity is determined by comparing the sequences of the hybridizing nucleic acids when aligned so as to maximize overlap and identity while minimizing sequence gaps as described in more detail above.

[00184] The variants according to the invention are ordinarily prepared by site specific mutagenesis of nucleotides in the DNA encoding the antigen binding protein, using cassette or PCR mutagenesis or other techniques well known in the art, to produce DNA encoding the variant, and thereafter expressing the recombinant DNA in cell culture as outlined herein. However, antigen binding protein fragments comprising variant CDRs having up to about 100-150 residues may be prepared by *in vitro* synthesis using established techniques. The variants typically exhibit the same qualitative biological activity as the naturally occurring analogue, *e.g.*, binding to OSMR, although variants can also be selected which have modified characteristics as will be more fully outlined below.

[00185] As will be appreciated by those in the art, due to the degeneracy of the genetic code, an extremely large number of nucleic acids may be made, all of which encode the CDRs (and heavy and light chains or other components of the antigen binding protein) of the present invention. Thus, having identified a particular amino acid sequence, those skilled in the art could make any number of different nucleic acids, by simply modifying the sequence of one or more codons in a way which does not change the amino acid sequence of the encoded protein.

[00186] The present invention also provides expression systems and constructs in the form of plasmids, expression vectors, transcription or expression cassettes which comprise at least one polynucleotide as above. In addition, the invention provides host cells comprising such expression systems or constructs.

[00187] Typically, expression vectors used in any of the host cells will contain sequences for plasmid maintenance and for cloning and expression of exogenous nucleotide sequences. Such sequences, collectively referred to as "flanking sequences" in certain embodiments will typically include one or more of the following nucleotide sequences: a promoter, one or more enhancer sequences, an origin of replication, a transcriptional termination sequence, a complete intron sequence containing a donor and acceptor splice site, a sequence encoding a leader sequence for polypeptide secretion, a ribosome binding site, a polyadenylation sequence, a polylinker region for inserting the nucleic acid encoding the polypeptide to be expressed, and a selectable marker element. Each of these sequences is discussed below.

[00188] Optionally, the vector may contain a "tag"-encoding sequence, *i.e.*, an oligonucleotide molecule located at the 5' or 3' end of the OSMR antigen binding protein coding sequence; the oligonucleotide sequence encodes polyHis (such as hexaHis), or another "tag" such as FLAG, HA (hemaghutinin influenza virus), or *myc*, for which commercially available antibodies exist. This tag is typically fused to the polypeptide upon expression of the polypeptide, and can serve as a means for affinity purification or detection of the OSMR antigen binding protein from the host cell. Affinity purification can be accomplished, for example, by column chromatography using antibodies against the tag as an affinity matrix. Optionally, the tag can subsequently be removed from the purified OSMR antigen binding protein by various means such as using certain peptidases for cleavage.

[00189] Flanking sequences may be homologous (*i.e.*, from the same species and/or strain as the host cell), heterologous (*i.e.*, from a species other than the host cell species or strain), hybrid (*i.e.*, a combination of flanking sequences from more than one source), synthetic or native. As such, the source of a flanking sequence may be any prokaryotic or eukaryotic organism, any vertebrate or invertebrate organism, or any plant, provided that the flanking sequence is functional in, and can be activated by, the host cell machinery.

[00190] Flanking sequences useful in the vectors of this invention may be obtained by any of several methods well known in the art. Typically, flanking sequences useful herein will have been previously identified by mapping and/or by restriction endonuclease digestion and

can thus be isolated from the proper tissue source using the appropriate restriction endonucleases. In some cases, the full nucleotide sequence of a flanking sequence may be known. Here, the flanking sequence may be synthesized using the methods described herein for nucleic acid synthesis or cloning.

[00191] Whether all or only a portion of the flanking sequence is known, it may be obtained using polymerase chain reaction (PCR) and/or by screening a genomic library with a suitable probe such as an oligonucleotide and/or flanking sequence fragment from the same or another species. Where the flanking sequence is not known, a fragment of DNA containing a flanking sequence may be isolated from a larger piece of DNA that may contain, for example, a coding sequence or even another gene or genes. Isolation may be accomplished by restriction endonuclease digestion to produce the proper DNA fragment followed by isolation using agarose gel purification, Qiagen® column chromatography (Chatsworth, CA), or other methods known to the skilled artisan. The selection of suitable enzymes to accomplish this purpose will be readily apparent to one of ordinary skill in the art.

[00192] An origin of replication is typically a part of those prokaryotic expression vectors purchased commercially, and the origin aids in the amplification of the vector in a host cell. If the vector of choice does not contain an origin of replication site, one may be chemically synthesized based on a known sequence, and ligated into the vector. For example, the origin of replication from the plasmid pBR322 (New England Biolabs, Beverly, MA) is suitable for most gram-negative bacteria, and various viral origins (*e.g.*, SV40, polyoma, adenovirus, vesicular stomatitus virus (VSV), or papillomaviruses such as HPV or BPV) are useful for cloning vectors in mammalian cells. Generally, the origin of replication component is not needed for mammalian expression vectors (for example, the SV40 origin is often used only because it also contains the virus early promoter).

[00193] A transcription termination sequence is typically located 3' to the end of a polypeptide coding region and serves to terminate transcription. Usually, a transcription termination sequence in prokaryotic cells is a G-C rich fragment followed by a poly-T sequence. While the sequence is easily cloned from a library or even purchased commercially as part of a vector, it can also be readily synthesized using methods for nucleic acid synthesis such as those described herein.

[00194] A selectable marker gene encodes a protein necessary for the survival and growth of a host cell grown in a selective culture medium. Typical selection marker genes

encode proteins that (a) confer resistance to antibiotics or other toxins, *e.g.*, ampicillin, tetracycline, or kanamycin for prokaryotic host cells; (b) complement auxotrophic deficiencies of the cell; or (c) supply critical nutrients not available from complex or defined media. Specific selectable markers are the kanamycin resistance gene, the ampicillin resistance gene, and the tetracycline resistance gene. Advantageously, a neomycin resistance gene may also be used for selection in both prokaryotic and eukaryotic host cells.

[00195] Other selectable genes may be used to amplify the gene that will be expressed. Amplification is the process wherein genes that are required for production of a protein critical for growth or cell survival are reiterated in tandem within the chromosomes of successive generations of recombinant cells. Examples of suitable selectable markers for mammalian cells include dihydrofolate reductase (DHFR) and promoterless thymidine kinase genes. Mammalian cell transformants are placed under selection pressure wherein only the transformants are uniquely adapted to survive by virtue of the selectable gene present in the vector. Selection pressure is imposed by culturing the transformed cells under conditions in which the concentration of selection agent in the medium is successively increased, thereby leading to the amplification of both the selectable gene and the DNA that encodes another gene, such as an antigen binding protein antibody that binds to OSMR polypeptide. As a result, increased quantities of a polypeptide such as an OSMR antigen binding protein are synthesized from the amplified DNA.

[00196] A ribosome-binding site is usually necessary for translation initiation of mRNA and is characterized by a Shine-Dalgarno sequence (prokaryotes) or a Kozak sequence (eukaryotes). The element is typically located 3' to the promoter and 5' to the coding sequence of the polypeptide to be expressed. In certain embodiments, one or more coding regions may be operably linked to an internal ribosome binding site (IRES), allowing translation of two open reading frames from a single RNA transcript.

[00197] In some cases, such as where glycosylation is desired in a eukaryotic host cell expression system, one may manipulate the various pre- or prosequences to improve glycosylation or yield. For example, one may alter the peptidase cleavage site of a particular signal peptide, or add prosequences, which also may affect glycosylation. The final protein product may have, in the -1 position (relative to the first amino acid of the mature protein) one or more additional amino acids incident to expression, which may not have been totally removed. For example, the final protein product may have one or two amino acid residues found in the peptidase cleavage site, attached to the amino-terminus. Alternatively, use of

some enzyme cleavage sites may result in a slightly truncated form of the desired polypeptide, if the enzyme cuts at such area within the mature polypeptide.

[00198] Expression and cloning vectors of the invention will typically contain a promoter that is recognized by the host organism and operably linked to the molecule encoding the OSMR antigen binding protein. Promoters are untranscribed sequences located upstream (*i.e.*, 5') to the start codon of a structural gene (generally within about 100 to 1000 bp) that control transcription of the structural gene. Promoters are conventionally grouped into one of two classes: inducible promoters and constitutive promoters. Inducible promoters initiate increased levels of transcription from DNA under their control in response to some change in culture conditions, such as the presence or absence of a nutrient or a change in temperature. Constitutive promoters, on the other hand, uniformly transcribe gene to which they are operably linked, that is, with little or no control over gene expression. A large number of promoters, recognized by a variety of potential host cells, are well known. A suitable promoter is operably linked to the DNA encoding heavy chain or light chain comprising an OSMR antigen binding protein of the invention by removing the promoter from the source DNA by restriction enzyme digestion and inserting the desired promoter sequence into the vector.

[00199] Suitable promoters for use with yeast hosts are also well known in the art. Yeast enhancers are advantageously used with yeast promoters. Suitable promoters for use with mammalian host cells are well known and include, but are not limited to, those obtained from the genomes of viruses such as polyoma virus, fowlpox virus, adenovirus (such as Adenovirus 2), bovine papilloma virus, avian sarcoma virus, cytomegalovirus, retroviruses, hepatitis-B virus and most preferably Simian Virus 40 (SV40). Other suitable mammalian promoters include heterologous mammalian promoters, for example, heat-shock promoters and the actin promoter.

[00200] Additional promoters which may be of interest include, but are not limited to: SV40 early promoter (Benoist et al., 1981, *Nature* 290:304-310); CMV promoter (Thornsen *et al.*, 1984, *Proc. Natl. Acad. U.S.A.* 81:659-663); the promoter contained in the 3' long terminal repeat of Rous sarcoma virus (Yamamoto *et al.*, 1980, *Cell* 22:787-797); herpes thymidine kinase promoter (Wagner *et al.*, 1981, *Proc. Natl. Acad. Sci. U.S.A.* 78:1444-1445); promoter and regulatory sequences from the metallothionine gene Prinster *et al.*, 1982, *Nature* 296:39-42); and prokaryotic promoters such as the beta-lactamase promoter (Villa-Kamaroff *et al.*, 1978, *Proc. Natl. Acad. Sci. U.S.A.* 75:3727-3731); or the tac promoter (DeBoer *et al.*, 1983, *Proc. Natl. Acad. Sci. U.S.A.* 80:21-25). Also of interest are the following animal

transcriptional control regions, which exhibit tissue specificity and have been utilized in transgenic animals: the elastase I gene control region that is active in pancreatic acinar cells (Swift *et al.*, 1984, *Cell* 38:639-646; Ornitz *et al.*, 1986, *Cold Spring Harbor Symp. Quant. Biol.* 50:399-409; MacDonald, 1987, *Hepatology* 7:425-515); the insulin gene control region that is active in pancreatic beta cells (Hanahan, 1985, *Nature* 315:115-122); the immunoglobulin gene control region that is active in lymphoid cells (Grosschedl *et al.*, 1984, *Cell* 38:647-658; Adames *et al.*, 1985, *Nature* 318:533-538; Alexander *et al.*, 1987, *Mol. Cell. Biol.* 7:1436-1444); the mouse mammary tumor virus control region that is active in testicular, breast, lymphoid and mast cells (Leder *et al.*, 1986, *Cell* 45:485-495); the albumin gene control region that is active in liver (Pinkert *et al.*, 1987, *Genes and Devel.* 1 :268-276); the alpha-feto-protein gene control region that is active in liver (Krumlauf *et al.*, 1985, *Mol. Cell. Biol.* 5:1639-1648; Hammer *et al.*, 1987, *Science* 253:53-58); the alpha 1-antitrypsin gene control region that is active in liver (Kelsey *et al.*, 1987, *Genes and Devel.* 1:161-171); the beta-globin gene control region that is active in myeloid cells (Mogram *et al.*, 1985, *Nature* 315:338-340; Kollias *et al.*, 1986, *Cell* 46:89-94); the myelin basic protein gene control region that is active in oligodendrocyte cells in the brain (Readhead *et al.*, 1987, *Cell* 48:703-712); the myosin light chain-2 gene control region that is active in skeletal muscle (Sani, 1985, *Nature* 314:283-286); and the gonadotropic releasing hormone gene control region that is active in the hypothalamus (Mason *et al.*, 1986, *Science* 234:1372-1378).

[00201] An enhancer sequence may be inserted into the vector to increase transcription of DNA encoding light chain or heavy chain comprising an OSMR antigen binding protein of the invention by higher eukaryotes. Enhancers are cis-acting elements of DNA, usually about 10-300 bp in length, that act on the promoter to increase transcription. Enhancers are relatively orientation and position independent, having been found at positions both 5' and 3' to the transcription unit. Several enhancer sequences available from mammalian genes are known (e.g., globin, elastase, albumin, alpha-feto-protein and insulin). Typically, however, an enhancer from a virus is used. The SV40 enhancer, the cytomegalovirus early promoter enhancer, the polyoma enhancer, and adenovirus enhancers known in the art are exemplary enhancing elements for the activation of eukaryotic promoters. While an enhancer may be positioned in the vector either 5' or 3' to a coding sequence, it is typically located at a site 5' from the promoter. A sequence encoding an appropriate native or heterologous signal sequence (leader sequence or signal peptide) can be incorporated into an expression vector, to promote extracellular secretion of the antibody. The choice of signal peptide or leader depends on the

type of host cells in which the antibody is to be produced, and a heterologous signal sequence can replace the native signal sequence. Examples of signal peptides that are functional in mammalian host cells include the following: the signal sequence for interleukin-7 (IL-7) described in US Patent No. 4,965,195; the signal sequence for interleukin-2 receptor described in Cosman *et al.*, 1984, *Nature* 312:768; the interleukin-4 receptor signal peptide described in EP Patent No. 0367 566; the type I interleukin-1 receptor signal peptide described in U.S. Patent No. 4,968,607; the type II interleukin-1 receptor signal peptide described in EP Patent No. 0 460 846.

[00202] The vector may contain one or more elements that facilitate expression when the vector is integrated into the host cell genome. Examples include an EASE element (Aldrich et al. 2003 *Biotechnol Prog.* 19:1433-38) and a matrix attachment region (MAR). MARs mediate structural organization of the chromatin and may insulate the integrated vactor from "position" effect. Thus, MARs are particularly useful when the vector is used to create stable transfectants. A number of natural and synthetic MAR-containing nucleic acids are known in the art, *e.g.*, U.S. Pat. Nos. 6,239,328; 7,326,567; 6,177,612; 6,388,066; 6,245,974; 7,259,010; 6,037,525; 7,422,874; 7,129,062.

[00203] Expression vectors of the invention may be constructed from a starting vector such as a commercially available vector. Such vectors may or may not contain all of the desired flanking sequences. Where one or more of the flanking sequences described herein are not already present in the vector, they may be individually obtained and ligated into the vector. Methods used for obtaining each of the flanking sequences are well known to one skilled in the art.

[00204] After the vector has been constructed and a nucleic acid molecule encoding light chain, a heavy chain, or a light chain and a heavy chain comprising an OSMR antigen binding sequence has been inserted into the proper site of the vector, the completed vector may be inserted into a suitable host cell for amplification and/or polypeptide expression. The transformation of an expression vector for an OSMR antigen binding protein into a selected host cell may be accomplished by well known methods including transfection, infection, calcium phosphate co-precipitation, electroporation, microinjection, lipofection, DEAE-dextran mediated transfection, or other known techniques. The method selected will in part be a function of the type of host cell to be used. These methods and other suitable methods are well known to the skilled artisan, and are set forth, for example, in Sambrook *et al.*, 2001, *supra*.

[00205] A host cell, when cultured under appropriate conditions, synthesizes an OSMR antigen binding protein that can subsequently be collected from the culture medium (if the host cell secretes it into the medium) or directly from the host cell producing it (if it is not secreted). The selection of an appropriate host cell will depend upon various factors, such as desired expression levels, polypeptide modifications that are desirable or necessary for activity (such as glycosylation or phosphorylation) and ease of folding into a biologically active molecule. A host cell may be eukaryotic or prokaryotic.

[00206] Mammalian cell lines available as hosts for expression are well known in the art and include, but are not limited to, immortalized cell lines available from the American Type Culture Collection (ATCC) and any cell lines used in an expression system known in the art can be used to make the recombinant polypeptides of the invention. In general, host cells are transformed with a recombinant expression vector that comprises DNA encoding a desired anti-OSMR antibody polypeptide. Among the host cells that may be employed are prokaryotes, yeast or higher eukaryotic cells. Prokaryotes include gram negative or gram positive organisms, for example *E. coli* or bacilli. Higher eukaryotic cells include insect cells and established cell lines of mammalian origin. Examples of suitable mammalian host cell lines include the COS-7 line of monkey kidney cells (ATCC CRL 1651) (Gluzman *et al.*, 1981, Cell 23:175), L cells, 293 cells, C127 cells, 3T3 cells (ATCC CCL 163), Chinese hamster ovary (CHO) cells, or their derivatives such as Veggie CHO and related cell lines which grow in serum-free media (Rasmussen *et al.*, 1998, *Cytotechnology* 28: 31), HeLa cells, BHK (ATCC CRL 10) cell lines, and the CV1/EBNA cell line derived from the African green monkey kidney cell line CV1 (ATCC CCL 70) as described by McMahan *et al.*, 1991, EMBO J. 10: 2821, human embryonic kidney cells such as 293, 293 EBNA or MSR 293, human epidermal A431 cells, human Colo205 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HL-60, U937, HaK or Jurkat cells. Optionally, mammalian cell lines such as HepG2/3B, KB, NIH 3T3 or S49, for example, can be used for expression of the polypeptide when it is desirable to use the polypeptide in various signal transduction or reporter assays. Alternatively, it is possible to produce the polypeptide in lower eukaryotes such as yeast or in prokaryotes such as bacteria. Suitable yeasts include Saccharomyces cerevisiae, Schizosaccharomyces pombe, Kluyveromyces strains, Candida, or any yeast strain capable of expressing heterologous polypeptides. Suitable bacterial strains include Escherichia coli, Bacillus subtilis, Salmonella typhimurium, or any bacterial strain capable of expressing heterologous polypeptides. If the

polypeptide is made in yeast or bacteria, it may be desirable to modify the polypeptide produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional polypeptide. Such covalent attachments can be accomplished using known chemical or enzymatic methods. The polypeptide can also be produced by operably linking the nucleic acid or isolated nucleic acid of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, e.g., Invitrogen, San Diego, CA, U.S.A. (the MaxBac® kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), and Luckow and Summers, *Bio/Technology* 6:47 (1988). Cell-free translation systems could also be employed to produce polypeptides using RNAs derived from nucleic acid constructs disclosed herein. Appropriate cloning and expression vectors for use with bacterial, fungal, yeast, and mammalian cellular hosts are described by Pouwels *et al.* (*Cloning Vectors: A Laboratory Manual*, Elsevier, New York, 1985). A host cell that comprises a nucleic acid or an isolated nucleic acid of the invention, preferably operably linked to at least one expression control sequence, is a "recombinant host cell".

[00207] In certain embodiments, cell lines may be selected through determining which cell lines have high expression levels and constitutively produce antigen binding proteins with OSMR binding properties. In another embodiment, a cell line from the B cell lineage that does not make its own antibody but has a capacity to make and secrete a heterologous antibody can be selected.

Cell-Depleting OSMR Antigen Binding Proteins

[00208] In preferred embodiments, the OSMR antigen binding protein binds OSMR and inhibits OSM and/or IL-31 binding, thereby reducing OSM- and/or IL-31-mediated signaling in OSMR-expressing cells. In certain embodiments, however, the OSMR antigen binding protein binds OSMR and targets an OSMR-expressing cell for depletion. In various aspects, the OSMR antigen binding protein inhibits OSM and/or IL-31 binding and targets the OSMR cell for depletion.

[00209] Cell-depleting OSMR antigen binding proteins are particularly useful for treating diseases or disorders associated with over expression of OSMR, e.g., an autoimmune disease, inflammatory disease, a disease or disorder associated with extracellular matrix

deposition or remodeling, or an OSMR-expressing tumor. Methods of targeting cells with antigen binding proteins, e.g. antibodies, are well known in the art. Exemplary embodiments are discussed below.

Antibody Drug Conjugates

[00210] Embodiments of the invention include antibody drug conjugates (ADCs). Generally the ADC comprises an antibody conjugated to a chemotherapeutic agent, e.g., a cytotoxic agent, a cytostatic agent, a toxin, or a radioactive agent. A linker molecule can be used to conjugate the drug to the antibody. A wide variety of linkers and drugs useful in ADC technology are known in the art and may be used in embodiments of the present invention. (See US20090028856; US2009/0274713; US2007/0031402; WO2005/084390; WO2009/099728; US5208020; US5416064; US5475092; 5585499; 6436931; 6372738; and 6340701, all incorporated herein by reference).

Linkers

[00211] In certain embodiments, the ADC comprises a linker made up of one or more linker components. Exemplary linker components include 6-maleimidocaproyl, maleimidopropanoyl, valine-citrulline, alanine-phenylalanine, p-aminobenzyloxycarbonyl, and those resulting from conjugation with linker reagents, including, but not limited to, N-succinimidyl 4-(2-pyridylthio) pentanoate ("SPP"), N-succinimidyl 4-(N-maleimidomethyl) cyclohexane-1 carboxylate ("SMCC," also referred to herein also as "MCC"), and N-succinimidyl (4-iodo-acetyl) aminobenzoate ("SIAB").

[00212] Linkers may be a "cleavable" linker or a "non-cleavable" linker (Ducry and Stump, *Bioconjugate Chem*, 2010, *21*, 5-13; incorporated herein by reference in its entirety) Cleavable linkers are designed to release the drug when subjected to certain environment factors, e.g., when internalized into the target cell. Cleavable linkers include acid labile linkers, protease sensitive linkers, photolabile linkers, dimethyl linker or disulfide-containing linkers. Non-cleavable linkers tend to remain covalently associated with at least one amino acid of the antibody and the drug upon internalization by and degradation within the target cell. An exemplary non-cleavable linker is MCC.

Drugs

[00213] In certain embodiments, the antibody is conjugated to a chemotherapeutic agent. Examples of chemotherapeutic agents include alkylating agents, such as thiotepa and cyclophosphamide (CYTOXAN™); alkyl sulfonates such as busulfan, improsulfan and

piposulfan; aziridines, such as benzodopa, carboquone, meturedopa, and uredopa; ethylenimines and methylamelamines including altretamine, triethylenemelamine, trietylenephosphoramide, triethylenethiophosphaoramide and trimethylolomelamine; acetogenins (especially bullatacin and bullatacinone); a camptothecin (including the synthetic analogue topotecan); bryostatin; callystatin; CC-1065 (including its adozelesin, carzelesin and bizelesin synthetic analogues); cryptophycins (particularly cryptophycin 1 and cryptophycin 8); dolastatin; duocarmycin (including the synthetic analogues, KW-2189 and CBI-TMI); eleutherobin; pancratistatin; a sarcodictyin; spongistatin; nitrogen mustards such as chlorambucil, chlornaphazine, cholophosphamide, estramustine, ifosfamide, mechlorethamine, mechlorethamine oxide hydrochloride, melphalan, novembichin, phenesterine, prednimustine, trofosfamide, uracil mustard; nitrosureas such as carmustine, chlorozotocin, fotemustine, lomustine, nimustine, ranimustine; antibiotics, such as the enediyne antibiotics (e.g. calicheamicin, especially calicheamicin .gamma1 and calicheamicin theta I, see, e.g., Angew Chem. Intl. Ed. Engl. 33:183-186 (1994); dynemicin, including dynemicin A; an esperamicin; as well as neocarzinostatin chromophore and related chromoprotein enediyne antibiotic chromomophores), aclacinomysins, actinomycin, authramycin, azaserine, bleomycins, cactinomycin, carabicin, caminomycin, carzinophilin; chromomycins, dactinomycin, daunorubicin, detorubicin, 6-diazo-5-oxo-L-norleucine, doxorubicin (including morpholino-doxorubicin, cyanomorpholino-doxorubicin, 2-pyrrolino-doxorubicin and deoxydoxorubicin), epirubicin, esorubicin, idarubicin, marcellomycin, nitomycins, mycophenolic acid, nogalamycin, olivomycins, peplomycin, potfiromycin, puromycin, quelamycin, rodorubicin, streptonigrin, streptozocin, tubercidin, ubenimex, zinostatin, zorubicin; anti-metabolites, such as methotrexate and 5-fluorouracil (5-FU); folic acid analogues, such as denopterin, methotrexate, pteropterin, trimetrexate; purine analogs, such as fludarabine, 6-mercaptopurine, thiamiprine, thioguanine; pyrimidine analogs such as, ancitabine, azacitidine, 6-azauridine, carmofur, cytarabine, dideoxyuridine, doxifluridine, enocitabine, floxuridine, 5-FU; androgens, such as calusterone, dromostanolone propionate, epitiostanol, mepitiostane, testolactone; anti-adrenals, such as aminoglutethimide, mitotane, trilostane; folic acid replenisher, such as frolinic acid; aceglatone; aldophosphamide glycoside; aminolevulinic acid; amsacrine; bestrabucil; bisantrene; edatraxate; defofamine; demecolcine; diaziquone; elfomithine; elliptinium acetate; an epothilone; etoglucid; gallium nitrate; hydroxyurea; lentinan; lonidamine; maytansinoids, such as maytansine and ansamitocins; mitoguazone; mitoxantrone; mopidamol; nitracrine; pentostatin; phenamet; pirarubicin; podophyllinic acid; 2-ethylhydrazide; procarbazine; PSK®; razoxane; rhizoxin; sizofuran; spirogermanium; tenuazonic acid; triaziquone; 2,2',2''-

trichlorotriethylamine; trichothecenes (especially T-2 toxin, verracurin A, roridin A and anguidine); urethan; vindesine; dacarbazine; mannomustine; mitobronitol; mitolactol; pipobroman; gacytosine; arabinoside ("Ara-C"); cyclophosphamide; thiotepa; taxoids, e.g. paclitaxel (TAXOL™, Bristol-Myers Squibb Oncology, Princeton, NJ) and doxetaxel (TAXOTERE®, Rhone-Poulenc Rorer, Antony, France); chlorambucil; gemcitabine; 6-thioguanine; mercaptopurine; methotrexate; platinum analogs such as cisplatin and carboplatin; vinblastine; platinum; etoposide (VP-16); ifosfamide; mitomycin C; mitoxantrone; vincristine; vinorelbine; navelbine; novantrone; teniposide; daunomycin; aminopterin; xeloda; ibandronate; CPT-11; topoisomerase inhibitor RFS 2000; difluoromethylomithine (DMFO); retinoic acid; capecitabine; and pharmaceutically acceptable salts, acids or derivatives of any of the above. Also included in this definition are anti-hormonal agents that act to regulate or inhibit hormone action on tumors, such as anti-estrogens including for example tamoxifen, raloxifene, aromatase inhibiting 4(5)-imidazoles, 4-hydroxytamoxifen, trioxifene, keoxifene, LY117018, onapristone, and toremifene (Fareston); and anti-androgens, such as flutamide, nilutamide, bicalutamide, leuprolide, and goserelin; siRNA and pharmaceutically acceptable salts, acids or derivatives of any of the above. Other chemotherapeutic agents that can be used with the present invention are disclosed in US Publication No. 20080171040 or US Publication No. 20080305044, each of which is incorporated herein in its entirety by reference.

[00214] It is contemplated that an antibody may be conjugated to two or more different chemotherapeutic agents or a pharmaceutical composition may comprise a mixture of antibodies wherein the antibody component is identical except for being conjugated to a different chemotherapeutic agent. Such embodiments may be useful for targeting multiple biological pathways with a target cell.

[00215] In preferred embodiments, the ADC comprises an antibody conjugated to one or more maytansinoid molecules, which are mitotic inhibitors that act by inhibiting tubulin polymerization. Maytansinoids, including various modifications, are described in US Pat. Nos. 3896111; 4151042; 4137230; 4248870; 4256746; 4260608; 4265814; 4294757; 4307016; 4308268; 4309428; 4313946; 4315929; 4317821; 4322348; 4331598; 4361650; 4364866; 4424219; 4450254; 4362663; 4371533; and WO 2009/099728. Maytansinoid drug moieties may be isolated from natural sources, produced using recombinant technology, or prepared synthetically. Exemplary maytansinoids include C-19-dechloro (US Pat No. 4256746), C-20-hydroxy (or C-20-demethyl) +/- C-19-dechloro (US Pat. Nos. 4307016 and 4361650), C-20-demethoxy (or C-20-acyloxy (-OCOR), +/- dechrolo (US Pat. No. 4294757), C-9-SH (US Pat.

No. 4,424,219), C-14-alkoxymethyl (demethoxy/CH2OR) (U.S. Pat. No. 4,331,598), C-14-hydroxymethyl or acyloxymethyl (CH2OH or CH2OAc) (U.S. Pat. No. 4,450,254), C-15-hydroxy/acyloxy (U.S. Pat. No. 4,364,866), C-15-methoxy (U.S. Pat. Nos. 4,313,946 and 4,315,929), C-18-N-demethyl (U.S. Pat. Nos. 4,362,663 and 4,322,348), and 4,5-deoxy (U.S. Pat. No. 4,371,533).

[00216] Various positions on maytansinoid compounds may be used as the linkage position, depending upon the type of link desired. For example, for forming an ester linkage, the C-3 position having a hydroxyl group, the C-14 position modified with hydrozymethyl, the C-15 position modified with a hydroxyl a group, and the C-20 position having a hydroxyl group are all suitable (US Pat. Nos. 5208020, RE39151, and 6913748; US Patent Appl. Pub. Nos. 20060167245 and 20070037972, and WO 2009099728).

[00217] Preferred maytansinoids include those known in the art as DM1, DM3, and DM4 (US Pat. Appl. Pub. Nos. 2009030924 and 20050276812, incorporated herein by reference).

[00218] ADCs containing maytansinoids, methods of making such ADCs, and their therapeutic use are disclosed in US Patent Nos. 5208020 and 5416064, US Pat. Appl. Pub. No. 20050276812, and WO 2009099728 (all incorporated by reference herein). Linkers that are useful for making maytansinoid ADCs are know in the art (US Pat. No. 5208020 and US Pat. Appl. Pub. Nos. 2005016993 and 20090274713; all incorporated herein by reference). Maytansinoid ADCs comprising an SMCC linker may be prepared as disclosed in US Pat. Publ. No. 2005/0276812.

Effector Function-Enhanced Antibodies

[00219] One of the functions of the Fc portion of an antibody is to communicate to the immune system when the antibody binds its target. This is considered "effector function." Communication leads to antibody-dependent cellular cytotoxicity (ADCC), antibody-dependent cellular phagocytosis (ADCP), and/or complement dependent cytotoxicity (CDC). ADCC and ADCP are mediated through the binding of the Fc to Fc receptors on the surface of cells of the immune system. CDC is mediated through the binding of the Fc with proteins of the complement system, e.g., C1q.

[00220] The IgG subclasses vary in their ability to mediate effector functions. For example, IgG1 is much superior to IgG2 and IgG4 at mediating ADCC and CDC. Thus, in

embodiments wherein a cell expressing OSMR is targeted for destruction, an anti-OSMR IgG1 antibody would be preferred.

[00221] The effector function of an antibody can be increased, or decreased, by introducing one or more mutations into the Fc. Embodiments of the invention include antigen binding proteins, e.g., antibodies, having an Fc engineered to increase effector function (U.S. 7,317,091 and Strohl, *Curr. Opin. Biotech.*, 20:685-691, 2009; both incorporated herein by reference in its entirety). . Exemplary IgG1 Fc molecules having increased effector function include (based on the Kabat numbering scheme) those have the following substitutions:

[00222] S239D/I332E

[00223] S239D/A330S/I332E

[00224] S239D/A330L/I332E

[00225] S298A/D333A/K334A

[00226] P247I/A339D

[00227] P247I/A339Q

[00228] D280H/K290S

[00229] D280H/K290S/S298D

[00230] D280H/K290S/S298V

[00231] F243L/R292P/Y300L

[00232] F243L/R292P/Y300L/P396L

[00233] F243L/R292P/Y300L/V305I/P396L

[00234] G236A/S239D/I332E

[00235] K326A/E333A

[00236] K326W/E333S

[00237] K290E/S298G/T299A

[00238] K290N/S298G/T299A

[00239] K290E/S298G/T299A/K326E

[00240] K290N/S298G/T299A/K326E

[00241] Further embodiments of the invention include antigen binding proteins, e.g., antibodies, having an Fc engineered to decrease effector function. Exemplary Fc molecules having decreased effector function include (based on the Kabat numbering scheme) those have the following substitutions:

[00242] N297A (IgG1)

[00243] L234A/L235A (IgG1)

[00244] V234A/G237A (IgG2)

[00245] L235A/G237A/E318A (IgG4)

[00246] H268Q/V309L/A330S/A331S (IgG2)

[00247] C220S/C226S/C229S/P238S (IgG1)

[00248] C226S/C229S/E233P/L234V/L235A (IgG1)

[00249] L234F/L235E/P331S (IgG1)

[00250] S267E/L328F (IgG1)

[00251] Another method of increasing effector function of IgG Fc-containing proteins is by reducing the fucosylation of the Fc. Removal of the core fucose from the biantennary complex-type oligosachharides attached to the Fc greatly increased ADCC effector function without altering antigen binding or CDC effector function. Several ways are known for reducing or abolishing fucosylation of Fc-containing molecules, e.g., antibodies. These include recombinant expression in certain mammalian cell lines including a FUT8 knockout cell line, variant CHO line Lec13, rat hybridoma cell line YB2/0, a cell line comprising a small interfering RNA specifically against the FUT8 gene, and a cell line coexpressing β-1,4-*N*-acetylglucosaminyltransferase III and Golgi α-mannosidase II. Alternatively, the Fc-containing molecule may be expressed in a non-mammalian cell such as a plant cell, yeast, or prokaryotic cell, e.g., E. coli. Thus, in certain embodiments of the invention, a composition comprises an antibody, e.g., Ab1, Ab2, or Ab3 having reduced fucosylation or lacking fucosylation altogether.

Pharmaceutical Compositions

[00252] In some embodiments, the invention provides a pharmaceutical composition comprising a therapeutically effective amount of one or a plurality of the antigen binding proteins of the invention together with a pharmaceutically effective diluents, carrier,

solubilizer, emulsifier, preservative, and/or adjuvant. In certain embodiments, the antigen binding protein is an antibody. Pharmaceutical compositions of the invention include, but are not limited to, liquid, frozen, and lyophilized compositions.

[00253] Preferably, formulation materials are nontoxic to recipients at the dosages and concentrations employed. In specific embodiments, pharmaceutical compositions comprising a therapeutically effective amount of an OSMR antigen binding protein, e.g., an OSMR-binding antibody, are provided.

[00254] In certain embodiments, the pharmaceutical composition may contain formulation materials for modifying, maintaining or preserving, for example, the pH, osmolarity, viscosity, clarity, color, isotonicity, odor, sterility, stability, rate of dissolution or release, adsorption or penetration of the composition. In such embodiments, suitable formulation materials include, but are not limited to, amino acids (such as glycine, glutamine, asparagine, arginine, proline, or lysine); antimicrobials; antioxidants (such as ascorbic acid, sodium sulfite or sodium hydrogen-sulfite); buffers (such as borate, bicarbonate, Tris-HCl, citrates, phosphates or other organic acids); bulking agents (such as mannitol or glycine); chelating agents (such as ethylenediamine tetraacetic acid (EDTA)); complexing agents (such as caffeine, polyvinylpyrrolidone, beta-cyclodextrin or hydroxypropyl-beta-cyclodextrin); fillers; monosaccharides; disaccharides; and other carbohydrates (such as glucose, mannose or dextrins); proteins (such as serum albumin, gelatin or immunoglobulins); coloring, flavoring and diluting agents; emulsifying agents; hydrophilic polymers (such as polyvinylpyrrolidone); low molecular weight polypeptides; salt-forming counterions (such as sodium); preservatives (such as benzalkonium chloride, benzoic acid, salicylic acid, thimerosal, phenethyl alcohol, methylparaben, propylparaben, chlorhexidine, sorbic acid or hydrogen peroxide); solvents (such as glycerin, propylene glycol or polyethylene glycol); sugar alcohols (such as mannitol or sorbitol); suspending agents; surfactants or wetting agents (such as pluronics, PEG, sorbitan esters, polysorbates such as polysorbate 20, polysorbate, triton, tromethamine, lecithin, cholesterol, tyloxapal); stability enhancing agents (such as sucrose or sorbitol); tonicity enhancing agents (such as alkali metal halides, preferably sodium or potassium chloride, mannitol sorbitol); delivery vehicles; diluents; excipients and/or pharmaceutical adjuvants. See, REMINGTON'S PHARMACEUTICAL SCIENCES, 18" Edition, (A. R. Genrmo, ed.), 1990, Mack Publishing Company.

[00255] In certain embodiments, the optimal pharmaceutical composition will be determined by one skilled in the art depending upon, for example, the intended route of

administration, delivery format and desired dosage. See, for example, REMINGTON'S PHARMACEUTICAL SCIENCES, *supra*. In certain embodiments, such compositions may influence the physical state, stability, rate of in vivo release and rate of in vivo clearance of the antigen binding proteins of the invention. In certain embodiments, the primary vehicle or carrier in a pharmaceutical composition may be either aqueous or non-aqueous in nature. For example, a suitable vehicle or carrier may be water for injection, physiological saline solution or artificial cerebrospinal fluid, possibly supplemented with other materials common in compositions for parenteral administration. Neutral buffered saline or saline mixed with serum albumin are further exemplary vehicles. In specific embodiments, pharmaceutical compositions comprise Tris buffer of about pH 7.0-8.5, or acetate buffer of about pH 4.0-5.5, and may further include sorbitol or a suitable substitute therefor. In certain embodiments of the invention, OSMR antigen binding protein compositions may be prepared for storage by mixing the selected composition having the desired degree of purity with optional formulation agents (REMINGTON'S PHARMACEUTICAL SCIENCES, *supra*) in the form of a lyophilized cake or an aqueous solution. Further, in certain embodiments, the OSMR antigen binding protein product may be formulated as a lyophilizate using appropriate excipients such as sucrose.

[00256] The pharmaceutical compositions of the invention can be selected for parenteral delivery. Alternatively, the compositions may be selected for inhalation or for delivery through the digestive tract, such as orally. Preparation of such pharmaceutically acceptable compositions is within the skill of the art. The formulation components are present preferably in concentrations that are acceptable to the site of administration. In certain embodiments, buffers are used to maintain the composition at physiological pH or at a slightly lower pH, typically within a pH range of from about 5 to about 8.

[00257] When parenteral administration is contemplated, the therapeutic compositions for use in this invention may be provided in the form of a pyrogen-free, parenterally acceptable aqueous solution comprising the desired OSMR antigen binding protein in a pharmaceutically acceptable vehicle. A particularly suitable vehicle for parenteral injection is sterile distilled water in which the OSMR antigen binding protein is formulated as a sterile, isotonic solution, properly preserved. In certain embodiments, the preparation can involve the formulation of the desired molecule with an agent, such as injectable microspheres, bio-erodible particles, polymeric compounds (such as polylactic acid or polyglycolic acid), beads or liposomes, that may provide controlled or sustained release of the product which can be delivered via depot injection. In certain embodiments, hyaluronic acid may also be used, having the effect of

promoting sustained duration in the circulation. In certain embodiments, implantable drug delivery devices may be used to introduce the desired antigen binding protein.

[00258] Pharmaceutical compositions of the invention can be formulated for inhalation. In these embodiments, OSMR antigen binding proteins are advantageously formulated as a dry, inhalable powder. In specific embodiments, OSMR antigen binding protein inhalation solutions may also be formulated with a propellant for aerosol delivery. In certain embodiments, solutions may be nebulized. Pulmonary administration and formulation methods therefore are further described in International Patent Application No. PCT/US94/001875, which is incorporated by reference and describes pulmonary delivery of chemically modified proteins.

[00259] It is also contemplated that formulations can be administered orally. OSMR antigen binding proteins that are administered in this fashion can be formulated with or without carriers customarily used in the compounding of solid dosage forms such as tablets and capsules. In certain embodiments, a capsule may be designed to release the active portion of the formulation at the point in the gastrointestinal tract when bioavailability is maximized and pre-systemic degradation is minimized. Additional agents can be included to facilitate absorption of the OSMR antigen binding protein. Diluents, flavorings, low melting point waxes, vegetable oils, lubricants, suspending agents, tablet disintegrating agents, and binders may also be employed.

[00260] Additional pharmaceutical compositions will be evident to those skilled in the art, including formulations involving OSMR antigen binding proteins in sustained- or controlled-delivery formulations. Techniques for formulating a variety of other sustained- or controlled-delivery means, such as liposome carriers, bio-erodible microparticles or porous beads and depot injections, are also known to those skilled in the art. See, for example, International Patent Application No. PCT/US93/00829, which is incorporated by reference and describes controlled release of porous polymeric microparticles for delivery of pharmaceutical compositions. Sustained-release preparations may include semipermeable polymer matrices in the form of shaped articles, e.g., films, or microcapsules. Sustained release matrices may include polyesters, hydrogels, polylactides (as disclosed in U.S. Pat. No. 3,773,919 and European Patent Application Publication No. EP 058481, each of which is incorporated by reference), copolymers of L-glutamic acid and gamma ethyl-L-glutamate (Sidman et al., 1983, Biopolymers 2:547-556), poly (2-hydroxyethyl-methacrylate) (Langer et al., 1981, J. Biomed. Mater. Res. 15:167-277 and Langer, 1982, Chem. Tech. 12:98-105), ethylene vinyl acetate

(Langer et al., 1981, *supra*) or poly-D(-)-3-hydroxybutyric acid (European Patent Application Publication No. EP 133,988). Sustained release compositions may also include liposomes that can be prepared by any of several methods known in the art. See, e.g., Eppstein et al., 1985, Proc. Natl. Acad. Sci. U.S.A. 82:3688-3692; European Patent Application Publication Nos. EP 036,676; EP 088,046 and EP 143,949, incorporated by reference.

[00261] Pharmaceutical compositions used for *in vivo* administration are typically provided as sterile preparations. Sterilization can be accomplished by filtration through sterile filtration membranes. When the composition is lyophilized, sterilization using this method may be conducted either prior to or following lyophilization and reconstitution. Compositions for parenteral administration can be stored in lyophilized form or in a solution. Parenteral compositions generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

[00262] Aspects of the invention includes self-buffering OSMR antigen binding protein formulations, which can be used as pharmaceutical compositions, as described in international patent application WO 06138181A2 (PCT/US2006/022599), which is incorporated by reference in its entirety herein.

[00263] As discussed above, certain embodiments provide OSMR antigen binding proteins protein compositions, particularly pharmaceutical OSMR antigen binding protein compositions that comprise, in addition to the OSMR antigen binding protein, one or more excipients such as those illustratively described in this section and elsewhere herein. Excipients can be used in the invention in this regard for a wide variety of purposes, such as adjusting physical, chemical, or biological properties of formulations, such as adjustment of viscosity, and or processes of the invention to improve effectiveness and or to stabilize such formulations and processes against degradation and spoilage due to, for instance, stresses that occur during manufacturing, shipping, storage, pre-use preparation, administration, and thereafter.

[00264] A variety of expositions are available on protein stabilization and formulation materials and methods useful in this regard, such as Arakawa et al., "Solvent interactions in pharmaceutical formulations," Pharm Res. 8(3): 285-91 (1991); Kendrick et al., "Physical stabilization of proteins in aqueous solution," in: RATIONAL DESIGN OF STABLE PROTEIN FORMULATIONS: THEORY AND PRACTICE, Carpenter and Manning, eds. Pharmaceutical Biotechnology. 13: 61-84 (2002), and Randolph et al., "Surfactant-protein

interactions," Pharm Biotechnol. 13: 159-75 (2002), each of which is herein incorporated by reference in its entirety, particularly in parts pertinent to excipients and processes of the same for self-buffering protein formulations in accordance with the current invention, especially as to protein pharmaceutical products and processes for veterinary and/or human medical uses.

[00265] Salts may be used in accordance with certain embodiments of the invention to, for example, adjust the ionic strength and/or the isotonicity of a formulation and/or to improve the solubility and/or physical stability of a protein or other ingredient of a composition in accordance with the invention.

[00266] As is well known, ions can stabilize the native state of proteins by binding to charged residues on the protein's surface and by shielding charged and polar groups in the protein and reducing the strength of their electrostatic interactions, attractive, and repulsive interactions. Ions also can stabilize the denatured state of a protein by binding to, in particular, the denatured peptide linkages (--CONH) of the protein. Furthermore, ionic interaction with charged and polar groups in a protein also can reduce intermolecular electrostatic interactions and, thereby, prevent or reduce protein aggregation and insolubility.

[00267] Ionic species differ significantly in their effects on proteins. A number of categorical rankings of ions and their effects on proteins have been developed that can be used in formulating pharmaceutical compositions in accordance with the invention. One example is the Hofmeister series, which ranks ionic and polar non-ionic solutes by their effect on the conformational stability of proteins in solution. Stabilizing solutes are referred to as "kosmotropic." Destabilizing solutes are referred to as "chaotropic." Kosmotropes commonly are used at high concentrations (e.g., >1 molar ammonium sulfate) to precipitate proteins from solution ("salting-out"). Chaotropes commonly are used to denture and/or to solubilize proteins ("salting-in"). The relative effectiveness of ions to "salt-in" and "salt-out" defines their position in the Hofmeister series.

[00268] Free amino acids can be used in OSMR antigen binding protein formulations in accordance with various embodiments of the invention as bulking agents, stabilizers, and antioxidants, as well as other standard uses. Lysine, proline, serine, and alanine can be used for stabilizing proteins in a formulation. Glycine is useful in lyophilization to ensure correct cake structure and properties. Arginine may be useful to inhibit protein aggregation, in both liquid and lyophilized formulations. Methionine is useful as an antioxidant.

[00269] Polyols include sugars, e.g., mannitol, sucrose, and sorbitol and polyhydric alcohols such as, for instance, glycerol and propylene glycol, and, for purposes of discussion herein, polyethylene glycol (PEG) and related substances. Polyols are kosmotropic. They are useful stabilizing agents in both liquid and lyophilized formulations to protect proteins from physical and chemical degradation processes. Polyols also are useful for adjusting the tonicity of formulations.

[00270] Among polyols useful in select embodiments of the invention is mannitol, commonly used to ensure structural stability of the cake in lyophilized formulations. It ensures structural stability to the cake. It is generally used with a lyoprotectant, e.g., sucrose. Sorbitol and sucrose are among preferred agents for adjusting tonicity and as stabilizers to protect against freeze-thaw stresses during transport or the preparation of bulks during the manufacturing process. Reducing sugars (which contain free aldehyde or ketone groups), such as glucose and lactose, can glycate surface lysine and arginine residues. Therefore, they generally are not among preferred polyols for use in accordance with the invention. In addition, sugars that form such reactive species, such as sucrose, which is hydrolyzed to fructose and glucose under acidic conditions, and consequently engenders glycation, also is not among preferred polyols of the invention in this regard. PEG is useful to stabilize proteins and as a cryoprotectant and can be used in the invention in this regard.

[00271] Embodiments of the OSMR antigen binding protein formulations further comprise surfactants. Protein molecules may be susceptible to adsorption on surfaces and to denaturation and consequent aggregation at air-liquid, solid-liquid, and liquid-liquid interfaces. These effects generally scale inversely with protein concentration. These deleterious interactions generally scale inversely with protein concentration and typically are exacerbated by physical agitation, such as that generated during the shipping and handling of a product.

[00272] Surfactants routinely are used to prevent, minimize, or reduce surface adsorption. Useful surfactants in the invention in this regard include polysorbate 20, polysorbate 80, other fatty acid esters of sorbitan polyethoxylates, and poloxamer 188.

[00273] Surfactants also are commonly used to control protein conformational stability. The use of surfactants in this regard is protein-specific since, any given surfactant typically will stabilize some proteins and destabilize others.

[00274] Polysorbates are susceptible to oxidative degradation and often, as supplied, contain sufficient quantities of peroxides to cause oxidation of protein residue side-chains,

especially methionine. Consequently, polysorbates should be used carefully, and when used, should be employed at their lowest effective concentration. In this regard, polysorbates exemplify the general rule that excipients should be used in their lowest effective concentrations.

[00275] Embodiments of OSMR antigen binding protein formulations further comprise one or more antioxidants. To some extent deleterious oxidation of proteins can be prevented in pharmaceutical formulations by maintaining proper levels of ambient oxygen and temperature and by avoiding exposure to light. Antioxidant excipients can be used as well to prevent oxidative degradation of proteins. Among useful antioxidants in this regard are reducing agents, oxygen/free-radical scavengers, and chelating agents. Antioxidants for use in therapeutic protein formulations in accordance with the invention preferably are water-soluble and maintain their activity throughout the shelf life of a product. EDTA is a preferred antioxidant in accordance with the invention in this regard.

[00276] Antioxidants can damage proteins. For instance, reducing agents, such as glutathione in particular, can disrupt intramolecular disulfide linkages. Thus, antioxidants for use in the invention are selected to, among other things, eliminate or sufficiently reduce the possibility of themselves damaging proteins in the formulation.

[00277] Formulations in accordance with the invention may include metal ions that are protein co-factors and that are necessary to form protein coordination complexes, such as zinc necessary to form certain insulin suspensions. Metal ions also can inhibit some processes that degrade proteins. However, metal ions also catalyze physical and chemical processes that degrade proteins.

[00278] Magnesium ions (10-120 mM) can be used to inhibit isomerization of aspartic acid to isoaspartic acid. Ca^{+2} ions (up to 100 mM) can increase the stability of human deoxyribonuclease. Mg^{+2}, Mn^{+2}, and Zn^{+2}, however, can destabilize rhDNase. Similarly, Ca^{+2} and Sr^{+2} can stabilize Factor VIII, it can be destabilized by Mg^{+2}, Mn^{+2} and Zn^{+2}, Cu^{+2} and Fe^{+2}, and its aggregation can be increased by Al^{+3} ions.

[00279] Embodiments of the OSMR antigen binding protein formulations further comprise one or more preservatives. Preservatives are necessary when developing multi-dose parenteral formulations that involve more than one extraction from the same container. Their primary function is to inhibit microbial growth and ensure product sterility throughout the shelf-life or term of use of the drug product. Commonly used preservatives include benzyl

alcohol, phenol and m-cresol. Although preservatives have a long history of use with small-molecule parenterals, the development of protein formulations that includes preservatives can be challenging. Preservatives almost always have a destabilizing effect (aggregation) on proteins, and this has become a major factor in limiting their use in multi-dose protein formulations. To date, most protein drugs have been formulated for single-use only. However, when multi-dose formulations are possible, they have the added advantage of enabling patient convenience, and increased marketability. A good example is that of human growth hormone (hGH) where the development of preserved formulations has led to commercialization of more convenient, multi-use injection pen presentations. At least four such pen devices containing preserved formulations of hGH are currently available on the market. Norditropin (liquid, Novo Nordisk), Nutropin AQ (liquid, Genentech) & Genotropin (lyophilized--dual chamber cartridge, Pharmacia & Upjohn) contain phenol while Somatrope (Eli Lilly) is formulated with m-cresol.

[00280] Several aspects need to be considered during the formulation and development of preserved dosage forms. The effective preservative concentration in the drug product must be optimized. This requires testing a given preservative in the dosage form with concentration ranges that confer anti-microbial effectiveness without compromising protein stability.

[00281] As might be expected, development of liquid formulations containing preservatives are more challenging than lyophilized formulations. Freeze-dried products can be lyophilized without the preservative and reconstituted with a preservative containing diluent at the time of use. This shortens the time for which a preservative is in contact with the protein, significantly minimizing the associated stability risks. With liquid formulations, preservative effectiveness and stability should be maintained over the entire product shelf-life (.about.18 to 24 months). An important point to note is that preservative effectiveness should be demonstrated in the final formulation containing the active drug and all excipient components.

[00282] OSMR antigen binding protein formulations generally will be designed for specific routes and methods of administration, for specific administration dosages and frequencies of administration, for specific treatments of specific diseases, with ranges of bio-availability and persistence, among other things. Formulations thus may be designed in accordance with the invention for delivery by any suitable route, including but not limited to orally, aurally, opthalmically, rectally, and vaginally, and by parenteral routes, including intravenous and intra-arterial injection, intramuscular injection, and subcutaneous injection.

[00283] Once the pharmaceutical composition has been formulated, it may be stored in sterile vials as a solution, suspension, gel, emulsion, solid, crystal, or as a dehydrated or lyophilized powder. Such formulations may be stored either in a ready-to-use form or in a form (e.g., lyophilized) that is reconstituted prior to administration. The invention also provides kits for producing a single-dose administration unit. The kits of the invention may each contain both a first container having a dried protein and a second container having an aqueous formulation. In certain embodiments of this invention, kits containing single and multi-chambered pre-filled syringes (e.g., liquid syringes and lyosyringes) are provided.

[00284] The therapeutically effective amount of an OSMR antigen binding protein-containing pharmaceutical composition to be employed will depend, for example, upon the therapeutic context and objectives. One skilled in the art will appreciate that the appropriate dosage levels for treatment will vary depending, in part, upon the molecule delivered, the indication for which the OSMR antigen binding protein is being used, the route of administration, and the size (body weight, body surface or organ size) and/or condition (the age and general health) of the patient. In certain embodiments, the clinician may titer the dosage and modify the route of administration to obtain the optimal therapeutic effect. A typical dosage may range from about 0.1 μg/kg to up to about 30 mg/kg or more, depending on the factors mentioned above. In specific embodiments, the dosage may range from 1.0 μg/kg up to about 20 mg/kg, optionally from 10 μg/kg up to about 10 mg/kg or from 100 μg/kg up to about 5 mg/kg.

[00285] A therapeutic effective amount of an OSMR antigen binding protein preferably results in a decrease in severity of disease symptoms, in an increase in frequency or duration of disease symptom-free periods, or in a prevention of impairment or disability due to the disease affliction.

[00286] Pharmaceutical compositions may be administered using a medical device. Examples of medical devices for administering pharmaceutical compositions are described in U.S. Patent Nos. 4,475,196; 4,439,196; 4,447,224; 4,447, 233; 4,486,194; 4,487,603; 4,596,556; 4,790,824; 4,941,880; 5,064,413; 5,312,335; 5,312,335; 5,383,851; and 5,399,163, all incorporated by reference herein.

Methods of Diagnosing or Treating a OSMR-Associated Disease or Disorder

[00287] The OSMR antigen binding proteins of the invention are particularly useful for detecting OSMR in a biological sample. In certain embodiments, a biological sample obtained

from a patient is contacted with a OSMR antigen binding protein. Binding of the OSMR antigen binding protein to OSMR is then detected to determine the presence or relative amount of OSMR in the sample. Such methods may be useful in diagnosing or determining patients that are amenable to treatment with an OSMR antigen binding protein.

[00288] In certain embodiments, an OSMR antigen binding protein of the invention is used to diagnose, detect, or treat an autoimmune disorder, inflammatory disorder, or disorder associated with extracellular matrix deposition or remodeling.

[00289] In treating these disorders, the OSMR antigen binding protein may target OSMR-expressing cells of the immune system for destruction and/or may block the interaction of OSMR with OSM and/or IL-31.

[00290] Diseases or disorders that are associated with OSMR-mediated signaling are particularly amenable to treatment with one or more OSMR antigen binding proteins disclosed herein. Such disorders include, but are not limited to, inflammation, pain, pruritis, prurigo nodularis, dermatitis, asthma, autoimmune disease, paraneoplastic autroimmune diseases, cartilage inflammation, fibrosis (including, but not limited to, pulmonary fibrosis and skin fibrosis), fibrotic disease, chronic obstructive pulmonary disease (COPD), interstitial pneumonitis, abnormal collagen deposition, systemic cutaneous amyloidosis, primary cutaneous amyloidosis, Behcet's disease, nasal polyposis, liver cirrhosis, cartilage degradation, bone degradation, arthritis, rheumatoid arthritis, juvenile arthritis, juvenile rheumatoid arthritis, pauciarticular juvenile rheumatoid arthritis, polyarticular juvenile rheumatoid arthritis, systemic onset juvenile rheumatoid arthritis, juvenile ankylosing spondylitis, juvenile enteropathic arthritis, juvenile reactive arthritis, juvenile Reter's Syndrome, SEA Syndrome (Seronegativity, Enthesopathy, Arthropathy Syndrome), juvenile dermatomyositis, juvenile psoriatic arthritis, juvenile scleroderma, juvenile systemic lupus erythematosus, juvenile vasculitis, pauciarticular rheumatoid arthritis, polyarticular rheumatoid arthritis, systemic onset rheumatoid arthritis, ankylosing spondylitis, enteropathic arthritis, reactive arthritis, Reter's Syndrome, SEA Syndrome (Seronegativity, Enthesopathy, Arthropathy Syndrome), dermatomyositis, psoriatic arthritis, scleroderma, scleroderma-associated interstitial lung disease, vasculitis, myolitis, polymyolitis, dermatomyolitis, polyarteritis nodossa, Wegener's granulomatosis, arteritis, ploymyalgia rheumatica, sarcoidosis, scleroderma, sclerosis, primary biliary sclerosis, sclerosing cholangitis, Sjogren's syndrome, psoriasis, plaque psoriasis, guttate psoriasis, inverse psoriasis, pustular psoriasis, erythrodermic psoriasis, dermatitis, atopic dermatitis, atherosclerosis, lupus, Still's disease, Systemic Lupus Erythematosus (SLE), myasthenia gravis,

inflammatory bowel disease (IBD), Crohn's disease, ulcerative colitis, celiac disease, multiple sclerosis (MS), asthma, COPD, rhinosinusitis, rhinosinusitis with polyps, eosinophilic esophogitis, eosinophilic bronchitis, bronchitis, Guillain-Barre disease, Type I diabetes mellitus, thyroiditis (e.g., Graves' disease), Addison's disease, Reynaud's phenomenon, autoimmune hepatitis, GVHD, transplantation rejection, kidney damage, cardiovascular disease, infection, sepsis, HIV infection, trauma, kidney allograft nephropathy, IgA nephropathy, diabetic nephropathy, diabetic retinopathy, macular degeneration, biliary atresia, congestive heart failure, atherosclerosis, restenosis, radiation-induced fibrosis, chemotherapy-induced fibrosis, burns, surgical trauma, glomerulosclerosis, and the like.

[00291] In preferred embodiments, the autoimmune disorder, inflammatory disorder, or disorder associated with extracellular matrix deposition or remodeling is fibrosis, cartilage degradation, arthritis, rheumatoid arthritis, scleroderma, scleroderma-associated interstitial lung disease, idiopathic pulmonary fibrosis, cirrhosis, psoriasis, atopic dermatitis, systemic cutaneous amyloidosis, primary cutaneous amyloidosis, inflammation, pruritic inflammation, prurigo nodularis, and pain.

[00292] In certain embodiments, an OSMR antigen binding protein of the invention is used to diagnose, detect, or treat a cancer or tumorigenic disorder. In treating a cancer or tumorigenic disorder, the OSMR antigen binding protein may target OSMR-expressing cells for destruction and/or may block the interaction of OSM and/or IL-31 with OSMR, thereby reducing OSMR mediated signaling. It is contemplated that the OSMR antigen binding proteins that block OSM- and/or IL-31-mediated signaling would be useful in promoting improved survival in cancer patients. Cancer or tumorigenic disorders that may be diagnosed, detected or treated with an OSMR antigen binding protein include, but are not limited to, solid tumors generally, lung cancer, ovarian cancer, breast cancer, prostate cancer, endometrial cancer, renal cancer, esophageal cancer, pancreatic cancer, squamous cell carcinoma, uveal melanoma, cervical cancer, colorectal cancer, bladder, brain, pancreatic, head, neck, liver, leukemia, lymphoma and Hodgkin's disease, multiple myeloma, melanoma, gastric cancer, astrocytic cancer, stomach, and pulmonary adenocarcinoma.

[00293] The antigen binding proteins may be used to inhibit tumor growth, progression, and/or metastasis. Such inhibition can be monitored using various methods. For instance, inhibition can result in reduced tumor size and/or a decrease in metabolic activity within a tumor. Both of these parameters can be measured by MRI or PET scans, for example. Inhibition can also be monitored by biopsy to ascertain the level of necrosis, tumor cell death,

and the level of vascularity within the tumor. The extent of metastasis can be monitored using known methods.

[00294] The use of any and all examples, or exemplary language (e.g., "such as") provided herein, is intended merely to better illuminate embodiments of the invention and does not pose a limitation on the scope of the invention unless otherwise claimed. No language in the specification should be construed as indicating any non-claimed element as essential to the practice of the invention.

EXAMPLES

[00295] The following examples, both actual and prophetic, are provided for the purpose of illustrating specific embodiments or features of the present invention and are not intended to limit its scope.

EXAMPLE 1: Production of Anti-OSMR Antibodies Using the XENOMOUSE® Platform

[00296] Fully human antibodies directed against human OSMR were generated using XENOMOUSE® technology (as described in United States Patent Nos. 6,114,598; 6,162,963; 6,833,268; 7,049,426; 7,064,244, which are incorporated herein by reference in their entirety; and in Green *et al.*, *Nature Genetics* 7:13-21, 1994; Mendez *et al.*, *Nature Genetics* 15:146-56; 1997; Green *et al.*, *J. Ex. Med.* 188:483-95, 1998; and Kellermann et al., *Current Opinion in Biotechnology*, 13:593–7, 2002).

[00297] To produce antibodies to OSMR, two different strains of XENOMOUSE® animals, i.e., XMG2-KL and XMG4-KL mice, were immunized with human OSMR-Fc soluble proteins (prepared by Amgen, Seattle, WA). A suitable amount of immunogen (i.e., ten µg/mouse of soluble human OSMR-Fc protein) was used for initial immunization of XENOMOUSE® animals according to the methods disclosed in U.S. Patent Application Serial No. 08/759,620, filed December 3, 1996 and International Patent Application Nos. WO 98/24893, published June 11, 1998 and WO 00/76310, published December 21, 2000, the disclosures of which are hereby incorporated by reference. Following the initial immunization, subsequent boost immunizations of immunogen (five µg/mouse of soluble human OSMR-Fc protein) were administered on a schedule and for the duration necessary to induce a suitable titer of anti-OSMR antibody in the mice.

[00298] Sera were collected at approximately four weeks after the first injection and specific titers were determined by ELISA. The protocol used to titer the XENOMOUSE®

animals was as follows: Costar 3368 medium binding plates were coated with neutravadin @ 8μg/mL (50 μL/well) and incubated at 4°C in 1XPBS/0.05% azide overnight. Plates were washed using TiterTek 3-cycle wash with RO water. Plates were blocked using 250 μL of 1XPBS/1%milk and incubated for at least 30 minutes at RT. Block was washed off using TiterTek 3-cycle wash with RO water. One then captured biotinylated huOSMR-FNFH (prepared by Amgen, Seattle, WA) at 2 μg/mL in 1XPBS/1%milk/10mM Ca2+ (assay diluent) 50 μl/well and incubated for 1hr at RT. One then washed using TiterTek 3-cycle wash with RO water. For the primary antibody, sera was titrated 1:3 in duplicate from 1:100. This was done in assay diluent 50 μL/well and incubated for 1hr at RT. One then washed using TiterTek 3-cycle wash with RO water. The secondary antibody was goat anti Human IgG Fc HRP @ 400 ng/mL in assay diluent at 50 μL/well. This was incubated for 1hr at RT. This was then washed using TiterTek 3-cycle wash with RO water and patted dry on paper towels. For the substrate, one-step TMB solution (Neogen, Lexington, Kentucky) was used (50 μL/well) and the substrate was allowed to develop for 30 min at RT.

[00299] Animals exhibiting suitable titers were identified. Five XMG2KL animals were identified with a specific IgG immune response to OSMR. Spleens and draining lymph nodes were harvested from these animals and pooled together for hybridoma generation. Five XMG4KL animals with specific immune responses were similarly harvested and advanced as a separate fusion screening campaign. Enriched B cells from immune animals were fused to non-secretory myeloma P3 x 63Ag8.653 cells ((American Type Culture Collection CRL-1580; Kearney et al, *J. Immunol.* 123: 1548-50, 1979) to generate hybridomas using standard techniques (Kohler et al., *Nature* 256, 495-7, 1975).

[00300] Hybridomas were then plated at high density (multiple different hybridoma clones per well) onto 96-well tissue culture plates and grown for four weeks. Hybridoma line supernatants were screened for binding to full length human and cynomolgus OSMR expressed on transiently transfected 293T cells by Fluorometric Microvolume Assay Technology (FMAT) (Applied Biosystems, Foster City, CA). Briefly, in 384-well FMAT plates, 40 μl mixture of 3,000 OSMR 293T transfected cells and 15,000 parental 293T cells were combined with 15 μL of hybridoma supernatant and 10 μL of anti-human light chain (hukappa/hulambda) Alexa647 (Invitrogen, Carlsbad, CA) labeled secondary antibody (1.0 μg /mL final concentration). Plates were then incubated for three hours at room temperature and fluorescence was read using the FMAT reader. These screens identified 885 hybridoma lines which bind to both human and cynomologous OSMR.

EXAMPLE 2: Human OSMR-Blocking Assays

[00301] The ability of OSMR antibodies to block signaling through human OSMR was determined using two assays with either human oncostatin M (OSM) or human interleukin 31 (IL-31) as the ligand. In combination, the assays were used to determine if the antibodies could inhibit signaling of OSMR triggered through the binding of OSM and/or IL-31.

[00302] In the first screen, antibodies were evaluated for their ability to block the signaling of OSM through OSMR. Stimulation of primary normal human lung fibroblasts with OSM induces phosphorylation of STAT3 and its subsequent translocation to the nucleus. Cells were seeded at 3000 cells per well in Costar 384-well plates and allowed to adhere overnight. Cells were pre-treated with antibody supernatants for twenty minutes, and then stimulated with 80 pM human OSM for 30 minutes. Cells were then washed 3X in PBS, fixed with a 3.5% formaldehyde solution, washed (3X in PBST) and permeabilized with a 0.5% Triton X-100 solution. Cells were then stained with an anti-phosphoSTAT3 antibody for an hour, washed and stained with an AlexaFluor conjugated antibody (all contained within the HitKit from Cellomics). Plates were covered and read on the ArrayScan instrument using the Cellomics proprietary algorithm to generate a Nuclear Intensity value and a Cytoplasmic Intensity value. Results were reported as the difference between these two values, and were further normalized to control data containing maximally stimulated cells and media-treated cells (POC).

[00303] In the second assay, antibodies were evaluated for their ability to inhibit a proliferative signal of IL-31 through OSMR in a stable cell line that overexpressed human IL-31RA4 and OSMR. BaF3 cells were stably transfected with two plasmids: pcDNA3.1 + huOSMRb (NeoR) and pcDNA3.1 + huIL31RA4 (ZeoR). In the absence of murine Il-3, this cell line is only able to proliferate in response to human IL-31 and, therefore, could be used to specifically evaluate the blocking ability of anti-OSMR antibodies. BaF3 cells were plated in 96-well plates at a density of 20,000 cells per well. Antibodies and ligand (huIL-31, Peprotech) were added to the wells to a final volume of 100 µL, and plates were incubated for 72 hours in 5% CO2, 37C humidified chamber. Following incubation, 20 µL of Alamar Blue was added to each well and plates were returned to the incubator. Plates were read on a Molecular Devices Vmax Plate reader (570-600 nm) at various timepoints post-addition of Alamar Blue.

[00304] The results of the two assays are presented in Table 4 below. Over 3000 hybridoma supernatants were screened for blocking ability in these two assays; the top 200

blockers were further tested in a 4-point titration, with 14 being chosen for production of recombinant protein and further testing. The IC50 for three exemplary antibodies (antibodies 1-3) is shown for both assays. Some antibodies inhibited OSM-induced STAT3 translocation more completely than they inhibited IL-31-induced proliferation, and *vice versa*. All three antibodies, however, were potent inhibitors of OSM- and IL-31 mediated signaling.

Table 4

IC50	Ab1	Ab2	Ab3
OSM	157 pM	252 pM	1.35 nM
IL-31	35.2 pM	27.6 pM	780 pM

EXAMPLE 3: Cynomolgus OSMR Blocking Assays

[00305] The ability of OSMR antibodies to block signaling through cynomolgus OSMR was explored using two assays with either human OSM or human IL-31 as the ligand.

[00306] In the first screen, antibodies were evaluated for their ability to block the signaling of OSM through cynomolgus OSMR by using a primary kidney epithelial cell line. Stimulation of these cells with cynomolgus (cyno) OSM induces phosphorylation of STAT3 and its subsequent translocation to the nucleus. Cells were seeded at 3000 cells per well in Costar 384-well plates and allowed to adhere overnight. Cells were pre-treated with antibody supernatants for twenty minutes, and then stimulated with 80 pM cyno OSM for 30 minutes. Cells were then washed 3X in PBS, fixed with a 3.5% formaldehyde solution, washed (3X in PBST) and permeabilized with a 0.5% Triton X-100 solution. Cells were then stained with an anti-phosphoSTAT3 antibody for an hour, washed and stained with an AlexaFluor conjugated antibody (all contained within the HitKit from Cellomics). Plates were covered and read on the ArrayScan instrument using the Cellomics proprietary algorithm to generate a Nuclear Intensity value and a Cytoplasmic Intensity value. Results were reported as the difference between these two values, and were further normalized to control data containing maximally stimulated cells and media-treated cells (POC).

[00307] In the second assay, antibodies were evaluated for their ability to inhibit a proliferative signal of IL-31 through cynomolgus OSMR in a stable cell line that overexpressed

cyno IL-31RA and OSMR. Similarly to Example 2, BaF3 cells were plated in 96-well plates at a density of 20,000 cells per well. Antibodies and ligand (cynomolgus IL-31, in-house, i.e., Amgen, Seattle, WA) were added to the wells to a final volume of 100 µL, and plates were incubated for 72 hours in 5% CO2, 37C humidified chamber. Following incubation, 20 µL of Alamar Blue was added to each well and plates were returned to the incubator. Plates were read on Molecular Devices Vmax Plate reader (570-600 nm) at various timepoints post-addition of Alamar Blue.

[00308] The results of the two assays are presented in Table 5 below with the IC50 for each antibody shown for both assays. The results confirm that each of antibodies 1, 2, and 3 are potent inhibitors of OSM- and IL-31 mediated signaling.

Table 5

IC50	**Ab1**	**Ab2**	**Ab3**
OSM	1.26 nM	518 pM	1.24 nM
IL-31	225 pM	29.3 pM	6.87 nM

EXAMPLE 4: Epitope Binning of Anti-OSMR Antibodies

[00309] Antibody competition studies were performed to characterize the epitopes of the anti-OSMR xenomouse antibodies. Antibodies that compete with each other can be thought of as binding the same site on the target. In these experiments, OSMR or irrelevant antibodies were captured onto streptavidin-coated Luminex beads pre-bound to a capture antibody (biotinylated monovalent mouse anti-human IgG Fc antibody). OSMR antigen or buffer (no antigen) was added to wells, and a probe antibody was added to each well and detected with a PE-labeled monovalent mouse anti-human IgG Fc antibody. Mean fluorescence intensity of each well was measured. For a full reference, *see* Jia et al., *J. Immunol. Methods* 288: 91-8, 2004. Detection of fluorescence in a given well indicated that the probe antibody was able to bind to OSMR, even in the presence of the other OSMR antibody, demonstrating that they are binding to separate epitopes. A minimum of three bins were found as shown in Table 6 below.

Table 6

Bin 1	Ab4
Bin 2	Ab1, Ab2, Ab3, Ab5, Ab6, Ab7, Ab8, Ab9, Ab10, Ab11, Ab12, and Ab13
Bin 3	Ab14

EXAMPLE 5: Affinity Determination of Anti-OSMR Antibodies

[00310] The affinities of anti-OSMR antibodies were determined. Kinetic rate constant determinations were performed to investigate the interaction of antibodies 1-3 (Abs 1-3) to human OSMR.

[00311] Biosensor analysis was conducted at 25°C in a HBS-EP+ (1X) buffer system (10 mM HEPES pH 7.4, 150 mM NaCl, 3.0 mM EDTA, 0.05% Surfactant P20) using a Biacore 3000 optical biosensor equipped with a CM5 sensor chip. All reagents were kept at 8°C prior to injection. Goat anti-human IgG (Jackson ImmunoResearch, #109-005-098) was immobilized (~3000 RU) to the sensor chip via standard amine coupling to Flow Cells 1 and 2 and then blocked with ethanolamine. hOSMR.FH was prepared in running buffer at 150 nM and diluted 3-fold to 0.617 nM. Antibodies 1-3 were diluted (0.25 to 0.5 µg/mL) in running buffer. The antibodies were injected (15 µL) over Flow Cell 2 at a flow rate of 10 µL/min. About 50 RU of antibody was captured. The surface was allowed to stabilize (90 s) and then each concentration (150, 50.0, 16.7, 5.56, 1.85 and 0.617) of hOSMR was passed over Flow Cells 1 and 2 at a flow rate of 50 µL/min to observe the association (5 min) and dissociation (5 min). Samples were run in duplicate and in random order.

[00312] Buffer analyte blanks (0 nM hOSMR) were injected before, in-between, and after sample injections. Antibodies were injected (15 µL) over Flow Cell 2 at a flow rate of 10 µL/min. About 50 RU of antibody was captured. The surface was allowed to stabilize (90 s) and then each concentration (150 nM) of hOSMR was passed over Flow Cells 1 and 2 at a flow rate of 50 µL/min to observe the association (5 min) and dissociation (1 -2 hr). The samples were run in triplicate.

[00313] Buffer analyte blanks (0 nM hOSMR) were injected before and after the sample injections. The surface was regenerated at a flow rate of 50 µL/min with two injections of 10 mM glycine (pH 1.5, 50 µL). This was followed by a buffer blank injection (15 s).

[00314] Data was analyzed with Scrubber 2.0 software as follows. Data from Flow Cell 2 was subtracted from the data from Flow Cell 1 (blank reference). The reference subtracted data (2-1) was then subtracted (double referenced) from the nearest 0 nM concentration data. The double referenced long dissociation data was fit to a 1:1 binding model to determine the dissociation rate constant (kd). This dissociation rate constant was used as a fixed parameter to fit the double referenced short dissociation data to a 1:1 binding model in order to determine the association rate constant (ka) and the equilibrium dissociation constant (Kd).

[00315] The reagents were well-behaved under the experimental conditions and the data (see Table 7 below) fit fairly well to a 1:1 binding model.

Table 7

Antibody	Antigen	k_a (1/Ms)	k_d (1/s)	K_d (pM)
Ab1	huOSMR	4.47×10^5	9.95×10^{-5}	221
Ab2	huOSMR	5.50×10^5	1.81×10^{-5}	32.7
Ab3	huOSMR	9.47×10^4	1.02×10^{-4}	1080

EXAMPLE 6: Anti-OSMR Antibodies

[00316] Fully human antibodies directed against human OSMR were generated using XENOMOUSE® technology described above in Example 1. Each of antibodies 1, 2, and 3 were demonstrated to be potent inhibitors of OSM- and/or IL-31-mediated signaling. Sequences of antibodies 1, 2, and 3 (i.e., Ab1, Ab2, and Ab3) were determined and are set forth in Table 8 below.

Table 8

Description	SEQ ID NO	Sequence
Ab1 – Heavy Chain nucleotide	3	caggtgcagctggtgcagtctggggctgaggtgaagaagcctggggc ctcagtgaaggtctcctgcaaggcttctggatacaccttcaccagtt atgatatcaactgggtgcgacaggccactggacaggggcttgagtgg atgggatggatgaaccctaatagtggtaacacagactatgcacagaa gttccagggcagagtcaccatgaccaggaacatttccataagcacgg cctacattgagctgagcagcctgagatctgaggacacggccgtttat tactgtgcgagagatatggtggctgcgaatacggattactacttcta

		ctacggtatggacgtctggggccaagggaccacggtcaccgtctcct cagctagcaccaagggcccatcggtcttccccctggcgccctgctcc aggagcacctccgagagcacagcggccctgggctgcctggtcaagga ctacttccccgaaccggtgacggtgtcgtggaactcaggcgctctga ccagcggcgtgcacaccttcccagctgtcctacagtcctcaggactc tactccctcagcagcgtggtgaccgtgccctccagcaacttcggcac ccagacctacacctgcaacgtagatcacaagcccagcaacaccaagg tggacaagacagttgagcgcaaatgttgtgtcgagtgcccaccgtgc ccagcaccacctgtggcaggaccgtcagtcttcctcttcccccaaa acccaaggacaccctcatgatctcccggaccctgaggtcacgtgcg tggtggtggacgtgagccacgaagaccccgaggtccagttcaactgg tacgtggacggcgtggaggtgcataatgccaagacaaagccacggga ggagcagttcaacagcacgttccgtgtggtcagcgtcctcaccgttg tgcaccaggactggctgaacggcaaggagtacaagtgcaaggtctcc aacaaaggcctcccagccccatcgagaaaaccatctccaaaaccaa agggcagccccgagaaccacaggtgtacaccctgccccatcccggg aggagatgaccaagaaccaggtcagcctgacctgcctggtcaaaggc ttctaccccagcgacatcgccgtggagtgggagagcaatgggcagcc ggagaacaactacaagaccacacctcccatgctggactccgacggct ccttcttcctctacagcaagctcaccgtggacaagagcaggtggcag caggggaacgtcttctcatgctccgtgatgcatgaggctctgcacaa ccactacacgcagaagagcctctccctgtctccgggtaaa
Ab2 – Heavy Chain nucleotide	4	caggtgcagctggtgcagtctggggctgaggtgaagaagcctggggc ctcagtgaaggtctcctgcaaggcttctggatacaccttcaccagtt atgaaatcaactgggtgcgacaggccactggacaagggcttgagtgg atgggatggatgaaccctaacagtggttacacaggctatgcacagaa gtttccagggcagagtcaccatgaccaggaacacctccataagcacag cctacatggaaatgagcagcctgagatctgaggacacggccgtgtat tactgtgcgagagatatagtggctgcgaatacggattactacttcta ttatggtatggacgtctggggccaagggaccacggtcaccgtctcct cagctagcaccaagggcccatcggtcttccccctggcgccctgctcc aggagcacctccgagagcacagcggccctgggctgcctggtcaagga ctacttccccgaaccggtgacggtgtcgtggaactcaggcgctctga ccagcggcgtgcacaccttcccagctgtcctacagtcctcaggactc tactccctcagcagcgtggtgaccgtgccctccagcaacttcggcac ccagacctacacctgcaacgtagatcacaagcccagcaacaccaagg tggacaagacagttgagcgcaaatgttgtgtcgagtgcccaccgtgc ccagcaccacctgtggcaggaccgtcagtcttcctcttcccccaaa acccaaggacaccctcatgatctcccggaccctgaggtcacgtgcg tggtggtggacgtgagccacgaagaccccgaggtccagttcaactgg tacgtggacggcgtggaggtgcataatgccaagacaaagccacggga ggagcagttcaacagcacgttccgtgtggtcagcgtcctcaccgttg tgcaccaggactggctgaacggcaaggagtacaagtgcaaggtctcc aacaaaggcctcccagccccatcgagaaaaccatctccaaaaccaa agggcagccccgagaaccacaggtgtacaccctgccccatcccggg aggagatgaccaagaaccaggtcagcctgacctgcctggtcaaaggc ttctaccccagcgacatcgccgtggagtgggagagcaatgggcagcc ggagaacaactacaagaccacacctcccatgctggactccgacggct ccttcttcctctacagcaagctcaccgtggacaagagcaggtggcag caggggaacgtcttctcatgctccgtgatgcatgaggctctgcacaa ccactacacgcagaagagcctctccctgtctccgggtaaa
Ab3 – Heavy Chain nucleotide	5	caggttcatctggtgcagtctggagctgaggtgaagaagcctggggc ctcagtgaaggtctcctgcaaggcttctggttacacctttaccagct atggtatcagctgggtgcgacaggcccctggacaagggcttgagtgg atgggatggctcagcacttacagtggtaacacaaactatgcacagaa gctccagggcagagtcaccatgaccacagacacatccacgagcacag

		cctacatggagctgaggagcctgagatctgacgacacggccgtgtat tactgtgcgagagggaacttctactactacggtatggacgtctgggg ccagggaccacggtcaccgtctcctcagctagcaccaagggcccat cggtcttccccctggcgccctgctccaggagcacctccgagagcaca gcggccctgggctgcctggtcaaggactacttccccgaaccggtgac ggtgtcgtggaactcaggcgctctgaccagcggcgtgcacaccttcc cagctgtcctacagtcctcaggactctactccctcagcagcgtggtg accgtgccctccagcaacttcggcacccagacctacacctgcaacgt agatcacaagcccagcaacaccaaggtggacaagacagttgagcgca aatgttgtgtcgagtgcccaccgtgcccagcaccacctgtggcagga ccgtcagtcttcctcttccccccaaaacccaaggacaccctcatgat ctcccggacccctgaggtcacgtgcgtggtggtggacgtgagccacg aagaccccgaggtccagttcaactggtacgtggacggcgtggaggtg cataatgccaagacaaagccacgggaggagcagttcaacagcacgtt ccgtgtggtcagcgtcctcaccgttgtgcaccaggactggctgaacg gcaaggagtacaagtgcaaggtctccaacaaaggcctcccagccccc atcgagaaaaccatctccaaaaccaaagggcagccccgagaaccaca ggtgtacaccctgcccccatcccgggaggagatgaccaagaaccagg tcagcctgacctgcctggtcaaaggcttctaccccagcgacatcgcc gtggagtgggagagcaatgggcagccggagaacaactacaagaccac acctcccatgctggactccgacggctccttcttcctctacagcaagc tcaccgtggacaagagcaggtggcagcaggggaacgtcttctcatgc tccgtgatgcatgaggctctgcacaaccactacacgcagaagagcct ctccctgtctccgggtaaa
Ab1 – Heavy Chain protein	6	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEW MGWMNPNSGNTDYAQKFQGRVTMTRNISISTAYIELSSLRSEDTAVY YCARDMVAANTDYYFYYGMDVWGQGTTVTVSSASTKGPSVFPLAPCS RSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPC PAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNW YVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVS NKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPGK
Ab2 – Heavy Chain protein	7	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYEINWVRQATGQGLEW MGWMNPNSGYTGYAQKFQGRVTMTRNTSISTAYMEMSSLRSEDTAVY YCARDIVAANTDYYFYYGMDVWGQGTTVTVSSASTKGPSVFPLAPCS RSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPC PAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNW YVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVS NKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQRSLSLSPGK
Ab3 – Heavy Chain protein	8	QVHLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEW MGWLSTYSGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVY YCARGNFYYYGMDVWGQGTTVTVSSASTKGPSVFPLAPCSRSTSEST AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVV TVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAG PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEV HNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAP IEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK
Ab1 – Heavy Chain Variable	9	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEW

Region		MGWMNPNSGNTDYAQKFQGRVTMTRNISISTAYIELSSLRSEDTAVY YCARDMVAANTDYYFYYGMDVWGQGTTVTVSS
Ab2 – Heavy Chain Variable Region	10	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYEINWVRQATGQGLEW MGWMNPNSGYTGYAQKFQGRVTMTRNTSISTAYMEMSSLRSEDTAVY YCARDIVAANTDYYFYYGMDVWGQGTTVTVSS
Ab3 – Heavy Chain Variable Region	11	QVHLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEW MGWLSTYSGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVY YCARGNFYYYGMDVWGQGTTVTVSS
Ab1 – Heavy Chain CDR1	12	SYDIN
Ab2 – Heavy Chain CDR1	13	SYEIN
Ab3 – Heavy Chain CDR1	14	SYGIS
Ab1 – Heavy Chain CDR2	15	WMNPNSGNTDYAQKFQG
Ab2 – Heavy Chain CDR2	16	WMGWMNPNSGYTGYAQKFQG
Ab3 – Heavy Chain CDR2	17	WLSTYSGNTNYAQKLQG
Ab1 – Heavy Chain CDR3	18	DMVAANTDYYFYYGMDV
Ab2 – Heavy Chain CDR3	19	DIVAANTDYYFYYGMDV
Ab3 – Heavy Chain CDR3	20	GNFYYYGMDV
Ab1 – Light Chain nucleotide	21	cagtctgtgctgactcagccaccctcagcatctgggacccccgggca gagggtcaccatctcttgttctggaagcagctccaacgtcggaagta atactgtaagctggtaccaacagctcccaggaacggcccccaaactc ctcatctatactaataatcggcggccctccgggtccctgaccgatt ctctggctccaagtctggcacctcagcctccctggccatcagtgggc tccagtctgaggatgaggctgattatttctgtgcagcgttagatgac agtctgaatggtgtggtattcggcggagggaccaaactgaccgtcct aggccaacccgaaagcggcgccctcggtcactctgttcccgccctcct ctgaggagcttcaagccaacaaggccacactggtgtgtctcataagt gacttctacccgggagccgtgacagtggcctggaaggcagatagcag ccccgtcaaggcgggagtggagaccaccacaccctccaaacaaagca acaacaagtacgcggccagcagctatctgagcctgacgcctgagcag tggaagtcccacagaagctacagctgccaggtcacgcatgaagggag caccgtggagaagacagtggcccctacagaatgttca
Ab2 – Light Chain nucleotide	22	cagtctgtgctgactcagccaccctcagcgtctgggacccccgggca gagggtcaccatctcttgttctggaagcaactccaacatcggaagta atacbgtcaactggtaccaccagctcccaggaacggcccccaaactc ctcatctataatattaataagcggccctcaggggtccctgaccgatt ctctggctccaagtctggctcctcagcctccctggccatcagtgggc tccagtctgaggatgaggctgattattactgttcaacatgggatgac agcctggatggtgtggtattcggcggagggaccaagctgaccgtcct aggccaacccgaaagcggcgccctcggtcactctgttcccgccctcct ctgaggagcttcaagccaacaaggccacactggtgtgtctcataagt gacttctacccgggagccgtgacagtggcctggaaggcagatagcag ccccgtcaaggcgggagtggagaccaccacaccctccaaacaaagca acaacaagtacgcggccagcagctatctgagcctgacgcctgagcag tggaagtcccacagaagctacagctgccaggtcacgcatgaagggag caccgtggagaagacagtggcccctacagaatgttca
Ab3 – Light Chain nucleotide	23	gaaattgtgttgacgcagtctccaggcaccctgtctttgtctccagg ggaaagagccaccctctcctgcagggccagtcagagtgttagcagca

		gctacttagcctggtaccagcagaaacctggccaggctcccaggctc ctcatctttggtgcttccagcagggccactggcatcccagacaggtt cagtggcagtgggtctgggacagacttcactctcaccatcagcagac tggagcctgaagattttgcagtgtattactgtcagcagtatggtagc tcgcctccgatcaccttcggccaagggacacgactggagattaaacg tacggtggctgcaccatctgtcttcatcttcccgccatctgatgagc agttgaaatctggaactgcctctgttgtgtgcctgctgaataacttc tatcccagagaggccaaagtacagtggaaggtggataacgccctcca atcgggtaactcccaggagagtgtcacagagcaggacagcaaggaca gcacctacagcctcagcagcaccctgacgctgagcaaagcagactac gagaaacacaaagtctacgcctgcgaagtcacccatcagggcctgag ctcgcccgtcacaaagagcttcaacaggggagagtgt
Ab1 – Light Chain protein	24	QSVLTQPPSASGTPGQRVTISCSGSSSNVGSNTVSWYQQLPGTAPKL LIYTNNRRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYFCAALDD SLNGVVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLIS DFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQ WKSHRSYSCQVTHEGSTVEKTVAPTECS
Ab2 – Light Chain protein	25	QSVLTQPPSASGTPGQRVTISCSGSNSNIGSNTVNWYHQLPGTAPKL LIYNINKRPSGVPDRFSGSKSGSSASLAISGLQSEDEADYYCSTWDD SLDGVVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLIS DFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQ WKSHRSYSCQVTHEGSTVEKTVAPTECS
Ab3 – Light Chain protein	26	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIFGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPPITFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNF YPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADY EKHKVYACEVTHQGLSSPVTKSFNRGEC
Ab1 – Light Chain Variable	27	QSVLTQPPSASGTPGQRVTISCSGSSSNVGSNTVSWYQQLPGTAPKL LIYTNNRRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYFCAALDD SLNGVVFGGGTKLTVLG
Ab2 – Light Chain Variable	28	QSVLTQPPSASGTPGQRVTISCSGSNSNIGSNTVNWYHQLPGTAPKL LIYNINKRPSGVPDRFSGSKSGSSASLAISGLQSEDEADYYCSTWDD SLDGVVFGGGTKLTVLG
Ab3 – Light Chain Variable	29	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIFGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPPITFGQGTRLEIKR
Ab1 – Light Chain CDR1	30	SGSSSNVGSNTVS
Ab2 – Light Chain CDR1	31	SGSNSNIGSNTVN
Ab3 – Light Chain CDR1	32	RASQSVSSSYLA
Ab1 – Light Chain CDR2	33	TNNRRPS
Ab2 – Light Chain CDR2	34	NINKRPS
Ab3– Light Chain CDR2	35	GASSRAT
Ab1 – Light Chain CDR3	36	AALDDSLNGVV
Ab2 – Light Chain CDR3	37	STWDDSLDGVV
Ab3 – Light Chain CDR3	38	QQYGSSPPTT

EXAMPLE 7: Modified Anti-OSMR Antibodies

[00317] Modified versions of Ab1, Ab2, and Ab3 were generated. For all three modified forms of the antibodies, the lysine at the C terminus of the heavy chain was removed. For Ab1 and Ab2, the glycosylation site at position 73 was removed by substituting the asparagine at position 73 with an aspartic acid. These variants are referred to as Ab1-N73D and Ab2-N73D. The sequences of the modified antibodies are set forth in Table 9 below (the modified nucleotides and amino acids are underlined).

Table 9

Description	SEQ ID NO	Sequence
Ab1 version 2 – Heavy Chain nucleotide (N73D / C-terminal lysine deleted)	47	caggtgcagctggtgcagtctggggctgaggtgaagaagcctggggc ctcagtgaaggtctcctgcaaggcttctggatacaccttcaccagtt atgatatcaactgggtgcgacaggccactggacaggggcttgagtgg atgggatggatgaaccctaatagtggtaacacagactatgcacagaa gttccagggcagagtcaccatgaccagg**g**acatttccataagcacgg cctacattgagctgagcagcctgagatctgaggacacggccgtttat tactgtgcgag**g**agatatggtggctgcgaatacggattactacttcta ctacggtatggacgtctggggccaagggaccacggtcaccgtctcct cagctagcaccaagggcccatcggtcttccccctggcgccctgctcc aggagcacctccgagagcacagcggccctgggctgcctggtcaagga ctacttccccgaaccggtgacggtgtcgtggaactcaggcgctctga ccagcggcgtgcacaccttcccagctgtcctacagtcctcaggactc tactccctcagcagcgtggtgaccgtgccctccagcaacttcggcac ccagacctacacctgcaacgtagatcacaagcccagcaacaccaagg tggacaagacagttgagcgcaaatgttgtgtcgagtgcccaccgtgc ccagcaccacctgtggcaggaccgtcagtcttcctcttcccccaaa acccaaggacaccctcatgatctcccggaccctgaggtcacgtgcg tggtggtggacgtgagccacgaagaccccgaggtccagttcaactgg tacgtggacggcgtggaggtgcataatgccaagacaaagccacggga ggagcagttcaacagcacgttccgtgtggtcagcgtcctcaccgttg tgcaccaggactggctgaacggcaaggagtacaagtgcaaggtctcc aacaaaggcctcccagccccatcgagaaaaccatctccaaaaccaa agggcagccccgagaaccacaggtgtacaccctgcccccatcccggg aggagatgaccaagaaccaggtcagcctgacctgcctggtcaaaggc ttctaccccagcgacatcgccgtggagtgggagagcaatgggcagcc ggagaacaactacaagaccacacctcccatgctggactccgacggct ccttcttcctctacagcaagctcaccgtggacaagagcaggtggcag caggggaacgtcttctcatgctccgtgatgcatgaggctctgcacaa ccactacacgcagaagagcctctccctgtctccgggt
Ab2 version 2 – Heavy Chain nucleotide (N73D / C-terminal lysine deleted)	48	caggtgcagctggtgcagtctggggctgaggtgaagaagcctggggc ctcagtgaaggtctcctgcaaggcttctggatacaccttcaccagtt atgaaatcaactgggtgcgacaggccactggacaagggcttgagtgg atgggatggatgaaccctaacagtggttacacaggctatgcacagaa gttccagggcagagtcaccatgaccagg**g**acacctccataagcacag cctacatggaaatgagcagcctgagatctgaggacacggccgtgtat tactgtgcgagagatatagtggctgcgaatacggattactacttcta ttatggtatggacgtctggggccaagggaccacggtcaccgtctcct

		cagctagcaccaagggcccatcggtcttcccctggcgccctgctcc aggagcacctccgagagcacagcggccctgggctgcctggtcaagga ctacttccccgaaccggtgacggtgtcgtggaactcaggcgctctga ccagcggcgtgcacaccttcccagctgtcctacagtcctcaggactc tactccctcagcagcgtggtgaccgtgccctccagcaacttcggcac ccagacctacacctgcaacgtagatcacaagcccagcaacaccaagg tggacaagacagttgagcgcaaatgttgtgtcgagtgcccaccgtgc ccagcaccacctgtggcaggaccgtcagtcttcctcttcccccaaa acccaaggacaccctcatgatctcccggacccctgaggtcacgtgcg tggtggtggacgtgagccacgaagaccccgaggtccagttcaactgg tacgtggacggcgtggaggtgcataatgccaagacaaagccacggga ggagcagttcaacagcacgttccgtgtggtcagcgtcctcaccgttg tgcaccaggactggctgaacggcaaggagtacaagtgcaaggtctcc aacaaaggcctcccagccccatcgagaaaaccatctccaaaaccaa agggcagccccgagaaccacaggtgtacaccctgccccatcccggg aggagatgaccaagaaccaggtcagcctgacctgcctggtcaaaggc ttctaccccagcgacatcgccgtggagtgggagagcaatgggcagcc ggagaacaactacaagaccacacctcccatgctggactccgacggct ccttcttcctctacagcaagctcaccgtggacaagagcaggtggcag caggggaacgtcttctcatgctccgtgatgcatgaggctctgcacaa ccactacacgcagaagagcctctccctgtctccgggt
Ab3 – Heavy Chain nucleotide (C-terminal lysine deleted)	49	caggttcatctggtgcagtctggagctgaggtgaagaagcctggggc ctcagtgaaggtctcctgcaaggcttctggttacacctttaccagct atggtatcagctgggtgcgacaggcccctggacaagggcttgagtgg atgggatggctcagcacttacagtggtaacacaaactatgcacagaa gctccagggcagagtcaccatgaccacagacacatccacgagcacag cctacatggagctgaggagcctgagatctgacgacacggccgtgtat tactgtgcgagagggaacttctactactacggtatggacgtctgggg ccagggaccacggtcaccgtctcctcagctagcaccaagggcccat cggtcttccccctggcgccctgctccaggagcacctccgagagcaca gcggccctgggctgcctggtcaaggactacttccccgaaccggtgac ggtgtcgtggaactcaggcgctctgaccagcggcgtgcacaccttcc cagctgtcctacagtcctcaggactctactccctcagcagcgtggtg accgtgccctccagcaacttcggcacccagacctacacctgcaacgt agatcacaagcccagcaacaccaaggtggacaagacagttgagcgca aatgttgtgtcgagtgcccaccgtgcccagcaccacctgtggcagga ccgtcagtcttcctcttccccccaaaacccaaggacaccctcatgat ctcccggacccctgaggtcacgtgcgtggtggtggacgtgagccacg aagaccccgaggtccagttcaactggtacgtggacggcgtggaggtg cataatgccaagacaaagccacgggaggagcagttcaacagcacgtt ccgtgtggtcagcgtcctcaccgttgtgcaccaggactggctgaacg gcaaggagtacaagtgcaaggtctccaacaaaggcctcccagccccc atcgagaaaaccatctccaaaaccaaagggcagccccgagaaccaca ggtgtacaccctgccccatcccgggaggagatgaccaagaaccagg tcagcctgacctgcctggtcaaaggcttctaccccagcgacatcgcc gtggagtgggagagcaatgggcagccggagaacaactacaagaccac acctcccatgctggactccgacggctccttcttcctctacagcaagc tcaccgtggacaagagcaggtggcagcaggggaacgtcttctcatgc tccgtgatgcatgaggctctgcacaaccactacacgcagaagagcct ctccctgtctccgggt
Ab1 version 2 – Heavy Chain protein (N73D / C-terminal lysine deleted)	50	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEW MGWMNPNSGNTDYAQKFQGRVTMTRDISISTAYIELSSLRSEDTAVY YCARDMVAANTDYYFYYGMDVWGQGTTVTVSSASTKGPSVFPLAPCS RSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPC PAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNW

		YVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVS NKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPG
Ab2 version 2 – Heavy Chain protein (N73D / C-terminal lysine deleted)	51	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYEINWVRQATGQGLEW MGWMNPNSGYTGYAQKFQGRVTMTPDTSISTAYMEMSSLRSEDTAVY YCARDIVAANTDYYFYYGMDVWGQGTTVTVSSASTKGPSVFPLAPCS RSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPC PAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNW YVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVS NKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPG
Ab3 version 2 – Heavy Chain protein (C-terminal lysine deleted)	52	QVHLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEW MGWLSTYSGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVY YCARGNFYYYGMDVWGQGTTVTVSSASTKGPSVFPLAPCSRSTSEST AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVV TVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAG PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEV HNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAP IEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPG
Ab1 version 2 – Heavy Chain Variable Region (N73D / C-terminal lysine deleted)	53	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEW MGWMNPNSGNTDYAQKFQGRVTMTRDTSISTAYIELSSLRSEDTAVY YCARDMVAANTDYYFYYGMDVWGQGTTVTVSS
Ab2 version 2 – Heavy Chain Variable Region (N73D / C-terminal lysine deleted)	54	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYEINWVRQATGQGLEW MGWMNPNSGYTGYAQKFQGRVTMTPDTSISTAYMEMSSLRSEDTAVY YCARDIVAANTDYYFYYGMDVWGQGTTVTVSS

[00318] ELISA experiments were performed under various formats (Capture ELISA for avidity-less format; Sandwich ELISA for solution phase format; and Direct ELISA for solid state avidity format) using antibodies containing the variable regions of Ab1 or Ab2 (or the N73D variant of Ab1 or Ab2) with different Fc regions.

[00319] Ab1 and Ab2 each contain CH1, CH2, CH3 domains of human IgG2 origin. As used herein, the terms "Ab1" and "Ab1 IgG2 WT" refer to the same antibody. Similarly, the terms "Ab2" and "Ab2 IgG2 WT" refer to the same antibody.

[00320] Antibodies identified as "IgG4P agly / IgG1" contain the variable regions of Ab1 or Ab2 (or the N73D variant of Ab1 or Ab2) fused to the CH1 domian from human IgG4, the hinge from human IgG4 with a Ser to Pro mutation (at position 228) to reduce shuffling, the CH2 domian from human IgG4 with an Asn to Gln mutation (at position 297) to eliminate the

N-linked glycosylation site, and the CH3 domain from human IgG1. The "IgG4P agly / IgG1" framework is described in US published patent application number US 2012/0100140.

[00321] The ELISA results indicated that removal of glycosylation sites via the N73D substitution did not affect the binding of the modified antibodies to OSMR. See Table 10.

Table 10

Antibody	**Capture (EC50) nM**	**Sandwich (EC50) nM**	**Direct (EC50) nM**
Ab1 IgG2 WT	10.2	0.581	0.184
Ab1 N73D IgG2	4.85	0.359	0.0728
Ab1 N73D IgG4P agly / IgG1	2.86	0.05	0.0626
Ab2 IgG2 WT	3.63	0.366	0.182
Ab2 N73D IgG2	5.49	0.343	0.179
Ab2 N73D IgG4P agly / IgG1	1.61	0.064	0.0558

[00322] Binding studies were performed using the BIAcore method. Antibodies containing the variable regions of Ab1 or Ab2 (or the N73D variant of Ab1 or Ab2) with different Fc regions were immobilized on a CM4 chip (GE lifesciences) as per manufacturer's protocols. Soluble OSMR was used as the analyte. Removing the glycosylation site on Ab1 and Ab2 via the N73D substitution improved the binding affinities. For Ab1, the substitution improved Kon rate, whereas for Ab2 it improved Koff rate. See Table 11.

Table 11

Antibody	**Kon (M-1s-1)**	**Koff (1/s)**	**KD (M)**

Ab1 IgG2 WT	1.64E+05	1.50E-04	0.913E-9
Ab1 N73D IgG2	2.49E+05	1.68E-04	0.675E-9
Ab2 IgG2 WT	1.88E+05	1.89E-04	1.01E-09
Ab2 N73D IgG2	1.73E+05	4.99E-05	0.289E-9

[00323] The stability of Fab fragments was determined by assessing the thermal unfolding of antibodies. High melting temperature of Fab fragments correlates directly to increased stability. Removal of glycosylation sites on Ab2 via the N73D substitution did not affect the thermal stability of Fab fragments and showed minor effects on Ab1, as assessed by differential scanning fluorimery experiments. See Table 12.

Table 12

Antibody	**Fab Tm (Celsius)**	**Standard Error (Celsius)**
Ab1 IgG2 WT	73.24	0.0097
Ab1 N73D IgG2	71.21	0.005
Ab1 N73D IgG4P agly / IgG1	74.23	0.014
Ab2 IgG2 WT	76.71	0.0096
Ab2 N73D IgG2	76.54	0.14
Ab2 N73D IgG4P agly / IgG1	76.69	0.018

[00324] The ability of modified anti-OSMR antibodies to block signaling through human OSMR was assessed. The modified antibodies were evaluated for their ability to inhibit proliferation of a BaF_hu-IL31R/OSMR/gp130 cell line in the presence of IL31, OSM, or IL31

and OSM. The results are presented in Tables 13 and 14 below, with the IC50 for each antibody shown. The results confirm that the modified versions of Ab1 and Ab2 are potent inhibitors of OSM- and IL-31-mediated signaling.

Table 13

Antibody	IL31 (IC50)	OSM (IC50)	IL31/OSM (IC50)
Ab2	0.3828	0.3528	~1.9
Ab1 IgG2 WT	0.6691	0.5298	4.004
Ab1 N73D IgG2	0.7565	0.5226	3.702
Ab1 N73D IgG4P agly / IgG1	0.4672	0.5657	3.080

Table 14

Antibody	IL31 (IC50)	OSM (IC50)	IL31/OSM (IC50)
Ab2	0.4426	0.4019	1.8
Ab2 IgG2 WT	0.3671	0.4758	2.049
Ab2 N73D IgG2	0.2191	0.1859	1.474
Ab2 N73D IgG4P agly / IgG1	0.2838	0.2401	1.276

[00325] The disclosure has been described in terms of particular embodiments found or proposed to comprise specific modes for the practice of the disclosure. Various modifications and variations of the described invention will be apparent to those skilled in the art without departing from the scope and spirit of the invention. Although the invention has been described in connection with specific embodiments, it should be understood that the invention as claimed should not be unduly limited to such specific embodiments. Indeed, various modifications of the described modes for carrying out the invention that are obvious to those skilled in the relevant fields are intended to be within the scope of the following claims.

Claims

1. An anti-oncostatin M receptor (OSMR) antibody, comprising:

a light chain variable domain comprising a light chain complementary-determining region 1 (LCDR1) defined by SEQ ID NO:31, a light chain complementary-determining region 2 (LCDR2) defined by SEQ ID NO:34, and a light chain complementary-determining region 3 (LCDR3) defined by SEQ ID NO:37; and

a heavy chain variable domain comprising a heavy chain complementary-determining region 1 (HCDR1) defined by SEQ ID NO:13, a heavy chain complementary-determining region 2 (HCDR2) defined by SEQ ID NO:16, and a heavy chain complementary-determining region 3 (HCDR3) defined by SEQ ID NO:19.

2. The anti-OSMR antibody of claim 1, wherein the light chain variable domain has the amino acid sequence set forth in SEQ ID NO:28.

3. The anti-OSMR antibody of claim 1, wherein the heavy chain variable domain has the amino acid sequence set forth in SEQ ID NO:54.

4. The anti-OSMR antibody of claim 1, wherein:
the light chain variable domain has the amino acid sequence set forth in SEQ ID NO:28; and the heavy chain variable domain has the amino acid sequence set forth in SEQ ID NO:54.

5. The anti-OSMR antibody of claim 1, wherein the light chain of the antibody comprises the amino acid sequence set forth in SEQ ID NO:25.

6. The anti-OSMR antibody of claim 1, wherein the antibody is a monoclonal antibody.

7. The anti-OSMR antibody of claim 6, wherein the antibody is a human antibody.

8. The anti-OSMR antibody of claim 1, wherein the antibody inhibits binding of human oncostatin M (OSM) or human interleukin 31 to human OSMR.

9. The anti-OSMR antibody of claim 1, wherein the antibody reduces human OSM-mediated or human interleukin 31-mediated OSMR signaling in human OSMR-expressing cells.

10. The anti-OSMR antibody of claim 4, wherein the antibody is a monoclonal antibody.

11. The anti-OSMR antibody of claim 10, wherein the antibody is a human antibody.

12. The anti-OSMR antibody of claim 4, wherein the light chain of the antibody comprises the amino acid sequence set forth in SEQ ID NO:25.

13. The anti-OSMR antibody of claim 4, wherein the antibody inhibits binding of human OSM or human interleukin 31 to human OSMR.

14. The anti-OSMR antibody of claim 4, wherein the antibody reduces human OSM-mediated or human interleukin 31-mediated OSMR signaling in human OSMR-expressing cells.

15. A pharmaceutical composition comprising the anti-OSMR antibody of claim 1.

16. A pharmaceutical composition comprising the anti-OSMR antibody of claim 4.