ST2L antagonists and methods of use

Cross reference to related applications

This application claims the benefit of United States Application Serial Number 13/798,204, filed 13 March 2013, United Sates Application Serial Number 13/798,226 filed 13 March 2013, United Sates Provisional Application Number 61/640,407, filed 30 April 2012 and United Sates Provisional Application Number 61/640,238, filed 30 April 2012, the entire contents of which are incorporated herein by reference.

Field of the Invention

The present invention relates to ST2L antagonists, polynucleotides encoding the antagonists or fragments thereof, and methods of making and using the foregoing.

Background of the Invention

ST2L (IL-1RL1 or IL-33Rα) is a Toll/IL-1 receptor family member expressed on the cell surface of a wide variety of immune cells including T cell, NK/NKT cells, basophils, eosinophils, mast cells and the newly-described non-B/non-T innate lymphoid type 2 cells, nuocytes, and natural helper cells. ST2L expression is also inducible on dendritic cells (DCs), macrophages, and neutrophils. ST2L is able to downregulate the responsiveness of Toll-like Receptors TLR2, TLR4, and TLR9, but also induce type 2 cytokine release via activation by its ligand IL-33 and association with accessory protein IL-1RAcP. IL-33 has been described as an 'alarmin', as its full-length form resides in the nuclei of epithelial and endothelial cells during homeostasis, but can be cleaved and released during necrosis.

ST2L signaling requires association of the accessory protein IL-1RAcP to preformed ST2L/IL-33 complex. The

accessory protein IL-1RAcP is shared with the IL-1α/β signaling complex. Models of ST2L, IL-33, and IL-1RAcP interactions as well as interactions between IL-1R1 and IL-1RAcP have been proposed (Lingel *et al.*, Cell 17:1398-1410, 2009; Wang *et al.*, Nat Immunol 11:905-11, 2010). Recently, ST2L/IL-33/IL-1RAcP has been shown to form a signaling complex with c-Kit on mast cells, the receptor for stem cell factor (SCF). IL-33 induced cytokine production in primary mast cells in an SCF-dependent manner (Drube *et al.*, Blood 115:3899-906, 2010).

Activation of ST2L leads to excessive type 2 cytokine responses (especially IL-5 and IL-13), mast cell and eosinophil activation, and airway hyper-reactivity, and has also been reported to amplify Th1 and Th17 responses through induction of IFNγ from NKT cells and IL-1β and IL-6 from mast cells. Dysregulation of the ST2L/IL-33 pathway has been implicated in a variety of immune-mediated diseases, including asthma, rheumatoid arthritis, inflammatory bowel disease, atopic dermatitis, allergic rhinitis, nasal polyposis, and systemic sclerosis (reviewed by Palmer and Gabay, Nat Rev Rheumatol 7:321-9, 2011 and Lloyd, Curr Opin Immunol 22:800-6, 2010; Shimizu *et al.*, Hum Molec Gen 14:2919-27, 2005, Kamekura *et al.*, Clin Exp Allergy 42:218-28, 2012; Manetti *et al.*, Ann Rheum Dis 69:598-605, 2010).

Thus, there is a need for ST2L antagonists that are suitable for use in the treatment of ST2L mediated diseases and disorders.

Brief Description of the Drawings

Figure 1 shows inhibition of airway hyper-responsiveness by ST2L Domain I binding mAb CNTO3914 in a model of lung inflammation induced by intranasally administered IL-33 when compared to the isotype control

CNTO5516. Peak airway resistance was measured upon methacholine (MCH) administration at increased doses (mg/ml). **p<0.05 for CNTO3914/IL-33 vs. CNTO5516/IL-33; and ***p<0.001 for CNTO3914/IL-33 vs. PBS with IL-33 treatment group.

Figure 2 shows inhibition of Bronchoalveolar Lavage (BAL) cell recruitment by ST2L Domain I binding mAb CNTO3914 in a model of lung inflammation induced by intranasally administered IL-33 when compared to the isotype control CNTO5516. ***p<0.001.

Figure 3 shows dose-dependent inhibition of release of mouse Mast Cell Protease 1 (MMCP-1) by ST2L Domain I binding mAb CNTO3914 in cell free BAL fluid in a model of lung inflammation induced by intranasally administered IL-33. **p<0.01, ***p<0.001, vs. CNTO5516 (isotype control) with IL-33 treatment.

Figure 4 shows inhibition of IL-33-induced GM-CSF (Figure 4A), IL-5 (Figure 4B), and TNFα (Figure 4C) release by ST2L Domain I binding mAb CNTO3914 by mouse bone marrow-derived mast cells *in vitro*. The CNTO3914 concentrations used are shown as µg/ml and IL-33 concentrations as ng/ml in parenthesis.

Figure 5 shows inhibition of IL-33-induced prostaglandin D2 (PGD_2) release by human cord blood-derived mast cells by ST2L Domain I binding mAb C2494 (STLM62) at indicated IL-33 and C2494 concentrations. MOX-PDG_2: methoxylsamine-PGD_2.

Figure 6 shows inhibition of GM-CSF (Figurue 6A), IL-8 (Figure 6B), IL-5 (Figure 6C), IL-13 (Figure 6D) and IL-10 (Figure 6E) release by indicated concentrations (µg/ml) of ST2L Domain I binding mAbs C2244 and C2494 in human cord blood derived mast cells (hCBMCs) in the presence of 1 ng/ml IL-33 in StemPro-34 medium + 100 ng/ml SCF (stem cell factor).

Figure 7 shows effect on GM-CSF (Figure 7A), IL-8 (Figure 7B), IL-5 (Figure 7C), IL-13 (Figure 7D) and IL-10 (Figure 7E) release by indicated concentrations (µg/ml) of ST2L Domain III binding mAbs C2519 or C2521 in human cord blood-derived mast cell in the presence of 1 ng/ml IL-33 in StemPro-34 medium + 100 ng/ml SCF.

Figure 8 shows effect on A) GM-CSF; B) IL-8; C) IL-5; D) IL-13 and E) IL-10 release by ST2L Domain I binding mAb C2494 and ST2L Domain III binding mAbs ST2M48 (M48), ST2M49 (M49), ST2M50 (M50), and ST2M51 (M51) in human cord blood-derived mast cells (hCBMCs) in the presence of 3 ng/ml IL-33 in RPMI/10%FCS medium + 100ng/ml SCF.

Figure 9 shows average percent (%) inhibition of anti-ST2L antibodies binding Domain I (D1) or Domain III (D3) of ST2L on GM-CSF, IL-5, IL-8, IL-10 and IL-13 release by human cord blood-derived mast cells upon IL-33 and SCF induction as indicated using either 50 µg/ml or 2 µg/ml of each antibody tested. Negative values indicate % activation.

Figure 10 shows heavy chain variable regions (VH) and heavy chain CDR sequences of anti-ST2L antibodies derived from phage display libraries and after subsequent affinity-maturation campaigns.

Figure 11 shows light chain variable regions (VL) and light chain CDR sequences of anti-ST2L antibodies derived from phage display libraries and after subsequent affinity-maturation campaigns.

Figure 12 shows VH and VL regions and sequences of heavy chain CDRs of anti-ST2L antibody STLM208 VH ST2H257 HCDR3 variants.

Figure 13 shows A) VH and B) VL sequences of anti-ST2L antibodies derived from phage display libraries and after subsequent affinity-maturation campaigns.

Figure 14 shows delineation of C2494 VH and VL antigen binding sites transferred to human frameworks (transferred

marked as HFA, "human framework adaptation"). Kabat CDRs are underlined and Chothia HVs indicated in dashed lines above the indicated transferred HFA regions. Numbering of VH and VL residues is according to Chothia. Residues highlighted in grey in VH were not transferred in some HFA variants. C2494 VH: SEQ ID NO: 48; C2494 VH: SEQ ID NO: 52.

Figure 15 shows CDR sequences of human framework adapted (HFA) antibodies derived from C2494.

Figure 16 A) Serum levels of anti-ST2L antibody CNTO3914 **B)** inhibition of bronchoalveolar Lavage (BAL) cell recruitment **C)** inhibition of IL-6 secretion by whole blood cells stimulated with IL-33; **D)** inhibition of MCP1 secretion by whole blood cells stimulated with IL-33 by CNTO3914 24 hours post-dosing in a 6 hour model of lung inflammation induced by intranasally administered IL-33. *p<0.05, **p<0.01, ***p<0.001; NQ = below the limit of detection; @ = one data point is below the limit of detection.

Figure 17. Competition between various anti-ST2L antibodies. **A)** 30 nM labeled C2244 Fab was competed with indicated antibodies for binding to ST2L-ECD coated on microwells. C2244 competed with C2494 but not with C2539. **B)** 10 nM labeled C2494 was competed with indicated antibodies for binding to ST2L-ECD coated on microwells. C2494 competed with STLM208 and STLM213 but not with C2539.

Figure 18 shows a simplified H/D exchange map of the human ST2-ECD (SEQ ID NO: 119) complexed with C2244 Fab. The regions protected by the antibody were displayed in different gray scale as indicated. Segments encompassing residues 18-31 (boxed in dashed line) (corresponding to residues 35-48 of full length ST2L of SEQ ID NO: 1) were protected by the Fab. Region encompassing residues 71-100 (boxed in solid line) (corresponding to residues 88-117 of SEQ ID NO: 1) were heavily glycosylated and not covered by peptides.

Figure 19 shows kinetic and affinity constants for ST2L Domain I binding antibody for ST2L variants as indicated in the figure.

Figure 20 shows inhibition of A) GM-CSF; B) IL-5; C) IL-8; D) IL-13 secretion from primary human lung mast cells by an anti-ST2L antibody STLM208.

Summary of the invention

The invention provides an isolated human or human-adapted antibody antagonist or fragment thereof that specifically binds Domain I (SEQ ID NO: 9) of human ST2L and blocks interleukin-33 (IL-33)/ST2L interaction, comprising: a heavy chain variable region (VH), a light chain variable region (VL), a heavy chain complementarity determining region (HCDR) 1 (HCDR1), 2 (HCDR2), 3 (HCDR3), a light chain complementarity determining region (LCDR) 1 (LCDR1), 2 (LCDR2), and 3 (LCDR3), wherein

a) the HCDR1 comprises the amino acid sequence of SEQ ID NO: 97;

b) the HCDR2 comprises the amino acid sequence of SEQ ID NO: 114;

c) the HCDR3 comprises the amino acid sequence of SEQ ID NO: 84;

d) the LCDR1 comprises the amino acid sequence of SEQ ID NO: 130;

e) the LCDR2 comprises the amino acid sequence of SEQ ID NO: 90; and

f) the LCDR3 comprises the amino acid sequence of SEQ ID NO: 134.

Disclosed are human-adapted antibody antagonists specifically binding human ST2L having certain light

chain and heavy chain variable region sequences, or certain heavy chain and light chain complementarity determining sequences.

Disclosed are human or human-adapted antibody antagonists specifically biding human ST2L at defined epitope regions and/or having certain characteristics as described herein.

The invention also provides an isolated polynucleotide encoding the antibody antagonist or fragment thereof of the invention.

The invention also provides a vector comprising an isolated polynucleotide of the invention.

The invention also provides a host cell comprising a vector of the invention.

The invention also provides a method of producing an antibody of the invention, comprising culturing a host cell of the invention and recovering the antibody from the cell.

The invention also provides a pharmaceutical composition comprising an isolated antibody of the invention and a pharmaceutically accepted carrier.

Disclosed is a method of treating or preventing a ST2L-mediated condition comprising administering a therapeutically effective amount of an isolated antibody to a patient in need thereof for a time sufficient to treat or prevent the ST2L-mediated condition.

Disclosed is a method of inhibiting mast cell response in a patient comprising administering a therapeutically effective amount of an isolated

antibody to a patient in need thereof for a time sufficient to inhibit the mast cell response.

Disclosed is a method of inhibiting interaction of IL-33 and ST2L in a subject, comprising administering to the subject an antibody that specifically binds domain I of ST2L in an amount sufficient to inhibit the interaction of IL-33 and ST2L.

The invention also provides use of the isolated human or human-adapted antibody antagonist or fragment thereof that specifically binds Domain I of human ST2L of the invention in the manufacture of a medicament for the treatment of a ST2L-mediated condition, wherein the ST2L-mediated condition is asthma, airway hyper-reactivity, sarcoidosis, chronic obstructive pulmonary disease (COPD), idiopathic pulmonary fibrosis (IPF), cystic fibrosis, inflammatory bowel disease, (IBD), eosinophilic esophagitis, scleroderma, atopic dermatitis, allergic rhinitis, bullous pemphigoid, chronic urticaria, diabetic nephropathy, rheumatoid arthritis, interstitial cystitis or Graft Versus Host Disease (GVHD), or is is associated with inflammatory cell recruitment in lung, goblet cell hyperplasia, increased mucous secretion or mast cell response.

Detailed Description of the Invention

All publications, including but not limited to patents and patent applications, cited in this specification are herein incorporated by reference as though fully set forth.

It is to be understood that the terminology used herein is for the purpose of describing particular embodiments only and is not intended to be limiting. Unless defined

otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which the invention pertains.

Although any methods and materials similar or equivalent to those described herein can be used in the practice for testing of the present invention, exemplary materials and methods are described herein. In describing and claiming the present invention, the following terminology will be used.

The term "antagonist" as used herein means a molecule that partially or completely inhibits, by any mechanism, ST2L biological activity. Exemplary antagonists are antibodies, fusion proteins, peptides, peptidomimetics, nucleic acids, oligonucleotides and small molecules. Antagonists can be identified using assays for ST2L biological activity described below. ST2L antagonists may inhibit measured ST2L biological activity by 20%, 30%, 40%, 50%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100%.

The term "ST2L" or "huST2L" or "human ST2L" refers to a human ST2L polypeptide having an amino acid sequence shown in GenBank Acc. No. NP_057316. SEQ ID NO: 1 shows the amino acid sequence of the full length human ST2L. "ST2L extracellular domain", "ST2L-ECD" or "huST2L-ECD" as used herein means a polypeptide having amino acids 19-328 of SEQ ID NO: 1. huST2L-ECD has three Ig-like C2-type domains spanning residues 19-122 (Domain I, SEQ ID NO: 9), residues 123-202 (Domain II, SEQ ID NO: 10), and residues 209-324 (Domain III, SEQ ID NO: 11) of SEQ ID NO: 1. "Domain I" or "ST2L Domain I" or "huST2L Domain I" or "D1" refers to the first immunoglobulin-like domain on human ST2L having the sequence shown in SEQ ID NO: 9. "Domain III" or "ST2L Domain III" refers to the third immunoglobulin-like domain on human ST2L having the sequence shown in SEQ ID NO: 11.

The term "IL-33" as used herein includes full length IL-33 (GenBank Acc. No. NP_254274 SEQ ID NO: 3), variants and active forms thereof. IL-33 variants include proteins having amino acid sequences shown in GenBank Acc. No. NP_001186569 and GenBank Acc. No. NP_001186570). IL-33 active forms include a "mature IL-33" having residues 112-270 of SEQ ID NO: 3. Additional active forms include IL-33 fragments having residues 11-270, 115-270, 95-270, 99-270, or 109-270 of SEQ ID NO: 3 (LeFrancais *et al.*, Proc Natl Acad Sci (USA) 109:1673-8, 2012), or any form or combination of forms isolated from cells endogenously expressing IL-33. "IL-33 active form" is a fragment or a variant of IL-33 of SEQ ID NO: 3 that induces ST2L biological activity.

The term "antibodies" as used herein is meant in a broad sense and includes immunoglobulin molecules including polyclonal antibodies, monoclonal antibodies including murine, human, human-adapted, humanized and chimeric monoclonal antibodies, antibody fragments, bispecific or multispecific antibodies formed from at least two intact antibodies or antibody fragments, dimeric, tetrameric or multimeric antibodies, and single chain antibodies.

Immunoglobulins can be assigned to five major classes, namely IgA, IgD, IgE, IgG and IgM, depending on the heavy chain constant domain amino acid sequence. IgA and IgG are further sub-classified as the isotypes IgA_1, IgA_2, IgG_1, IgG_2, IgG_3 and IgG_4. Antibody light chains of any vertebrate species can be assigned to one of two clearly distinct types, namely kappa (κ) and lambda (λ), based on the amino acid sequences of their constant domains.

The term "antibody fragments" refers to a portion of an immunoglobulin molecule that retains the heavy chain and/or the light chain antigen binding site, such as a heavy chain complementarity determining regions (HCDR) 1, 2 and 3, a light chain complementarity determining regions (LCDR) 1, 2

and 3, a heavy chain variable region (VH), or a light chain variable region (VL). Antibody fragments include well known Fab, F(ab')2, Fd and Fv fragments as well as a domain antibodies (dAb) consisting one VH domain. VH and VL domains can be linked together via a synthetic linker to form various types of single chain antibody designs where the VH/VL domains pair intramolecularly, or intermolecularly in those cases when the VH and VL domains are expressed by separate single chain antibody constructs, to form a monovalent antigen binding site, such as single chain Fv (scFv) or diabody; described for example in Int. Pat. Publ. No. WO98/44001, Int. Pat. Publ. No. WO88/01649; Int. Pat. Publ. No. WO94/13804; Int. Pat. Publ. No. WO92/01047

An antibody variable region consists of a "framework" region interrupted by three "antigen binding sites". The antigen binding sites are defined using various terms: (i) Complementarity Determining Regions (CDRs), three in the VH (HCDR1, HCDR2, HCDR3), and three in the VL (LCDR1, LCDR2, LCDR3), are based on sequence variability (Wu and Kabat, J Exp Med 132:211-50, 1970; Kabat *et al.*, Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, Md., 1991). (ii) "Hypervariable regions", "HVR", or "HV", three in the VH (H1, H2, H3) and three in the VL (L1, L2, L3), refer to the regions of an antibody variable domains which are hypervariable in structure as defined by Chothia and Lesk (Chothia and Lesk, Mol Biol 196:901-17, 1987). Other terms include "IMGT-CDRs" (Lefranc *et al.*, Dev Comparat Immunol 27:55-77, 2003) and "Specificity Determining Residue Usage" (SDRU) (Almagro, Mol Recognit 17:132-43, 2004). The International ImMunoGeneTics (IMGT) database (http://www_imgt_org) provides a standardized numbering and definition of antigen-binding sites. The correspondence

between CDRs, HVs and IMGT delineations is described in Lefranc *et al.*, Dev Comparat Immunol 27:55-77, 2003.

"Chothia residues" as used herein are the antibody VL and VH residues numbered according to Al-Lazikani (Al-Lazikani *et al.*, J Mol Biol 273:927-48, 1997).

"Framework" or "framework sequences" are the remaining sequences of a variable region other than those defined to be antigen binding site. Because the antigen binding site can be defined by various terms as described above, the exact amino acid sequence of a framework depends on how the antigen-binding site was defined.

"Human antibody" or "fully human antibody" refers to antibodies containing variable region and constant region sequences derived from human immunoglobulin sequences. Human antibodies of the invention may include substitutions so that they may not be exact copies of expressed human immunoglobulin or germline gene sequences. However, antibodies in which antigen binding sites are derived from a non-human species are not included in the definition of "human antibody".

"Human-adapted" antibodies or "human framework adapted (HFA)" antibodies refers to antibodies adapted according to methods described in U.S. Pat. Publ. No. US2009/0118127 and also refers to antibodies in which antigen-binding site sequences derived from non-human species are grafted onto human frameworks.

"Humanized antibodies" refers to antibodies wherein the antigen binding sites are derived from non-human species and the variable region frameworks are derived from human immunoglobulin sequences. Humanized antibodies may include substitutions in the framework regions so that the framework may not be an exact copy of expressed human immunoglobulin or germline gene sequences.

The term "substantially identical" as used herein means that the two antibody variable region amino acid sequences being compared are identical or have "insubstantial differences". Insubstantial differences are substitutions of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11 amino acids in an antibody or antibody variable region sequence that do not adversely affect antibody properties. Amino acid sequences substantially identical to the variable region sequences disclosed herein are within the scope of the application. In some embodiments, the sequence identity can be about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or higher. Percent identity can be determined for example by pairwise alignment using the default settings of the AlignX module of Vector NTI v.9.0.0 (Invitrogen, Carslbad, CA). The protein sequences of the present invention can be used as a query sequence to perform a search against public or patent databases to, for example, identify related sequences. Exemplary programs used to perform such searches are the XBLAST or BLASTP programs (http_//www_ncbi_nlm/nih_gov), or the GenomeQuest™ (GenomeQuest, Westborough, MA) suite using the default settings.

The term "epitope" as used herein means a portion of an antigen to which an antibody specifically binds. Epitopes usually consist of chemically active (such as polar, non-polar or hydrophobic) surface groupings of moieties such as amino acids or polysaccharide side chains and can have specific three-dimensional structural characteristics, as well as specific charge characteristics. An epitope can be composed of contiguous and/or discontiguous amino acids that form a conformational spatial unit. For a discontiguous epitope, amino acids from differing portions of the linear sequence of the antigen come in close proximity in 3-dimensional space through the folding of the protein

molecule. An exemplary epitope is Domain I of huST2L shown in SEQ ID NO: 9.

The term "paratope" as used herein means a portion of an antibody to which an antigen specifically binds. A paratope can be linear in nature or can be discontinuous, formed by a spatial relationship between non-contiguous amino acids of an antibody rather than a linear series of amino acids. A "light chain paratope" and a "heavy chain paratope" or "light chain paratope amino acid residues" and "heavy chain paratope amino acid residues" refer to antibody light chain and heavy chain residues in contact with an antigen, respectively.

The term "specific binding" or "specifically binds" as used herein refers to antibody binding to a predetermined antigen with greater affinity than for other antigens or proteins. Typically, the antibody binds to a predetermined antigen with a dissociation constant (K_D) of $1x10^{-7}$ M or less, for example $1x10^{-8}$ M or less, $1x10^{-9}$ M or less, $1x10^{-10}$ M or less, $1x10^{-11}$ M or less, or $1x10^{-12}$ M or less, typically with a K_D that is at least ten fold less than its K_D for binding to a non-specific antigen (e.g., BSA, casein, or any other specified polypeptide). The dissociation constant can be measured using standard procedures. Antibodies that specifically bind to a predetermined antigen may, however, have cross-reactivity to other related antigens, for example to the same predetermined antigen from other species (homologs), such as human or monkey, for example *Macaca fascicularis* (cynomolgus).

"Bispecific" as used herein refers to an antibody that binds two distinct antigens or two distinct epitopes within an antigen.

"Monospecific" as used herein refers to an antibody

that binds one antigen or one epitope.

The term "in combination with" as used herein means that the described agents can be administered to an animal together in a mixture, concurrently as single agents or sequentially as single agents in any order.

"Inflammatory condition" as used herein refers to acute or chronic localized or systemic responses to harmful stimuli, such as pathogens, damaged cells, physical injury or irritants, that are mediated in part by the activity of cytokines, chemokines, or inflammatory cells (*e.g.*, neutrophils, monocytes, lymphocytes, macrophages) and is characterized in most instances by pain, redness, swelling, and impairment of tissue function.

The term "ST2L-mediated inflammatory condition" as used herein refers to an inflammatory condition resulting at least partially from inappropriate activation of ST2L signaling pathway. Exemplary ST2L-mediated inflammatory conditions are asthma and allergies.

The term "ST2L-mediated condition" as used herein encompasses all diseases and medical conditions in which ST2L plays a role, whether directly or indirectly, in the disease or medical condition, including the causation, development, progress, persistence or pathology of the disease or condition.

The term "ST2L biological activity" as used herein refers to any activity occurring as a result of ST2L ligand IL-33 binding to ST2L. An exemplary ST2L biological activity results in activation of NF-κB in response to IL-33. NF-κB activation can be assayed using a reporter-gene assay upon induction of ST2L with IL-33 (Fursov *et al.*, Hybridoma 30: 153-62, 2011). Other exemplary ST2L biological activities result in proliferation of Th2 cells, or secretion of pro-inflammatory cytokines and chemokines, for example IL-5, GM-CSF, IL-8, IL-10, or IL-13. The release of cytokines and

chemokines from cells, tissues or in circulation can be measured using well-known immunoassays, such as an ELISA immunoassay.

The term "vector" means a polynucleotide capable of being duplicated within a biological system or that can be moved between such systems. Vector polynucleotides typically contain elements, such as origins of replication, polyadenylation signal or selection markers, that function to facilitate the duplication or maintenance of these polynucleotides in a biological system. Examples of such biological systems may include a cell, virus, animal, plant, and reconstituted biological systems utilizing biological components capable of duplicating a vector. The polynucleotide comprising a vector may be DNA or RNA molecules or a hybrid of these.

The term "expression vector" means a vector that can be utilized in a biological system or in a reconstituted biological system to direct the translation of a polypeptide encoded by a polynucleotide sequence present in the expression vector.

The term "polynucleotide" means a molecule comprising a chain of nucleotides covalently linked by a sugar-phosphate backbone or other equivalent covalent chemistry. Double and single-stranded DNAs and RNAs are typical examples of polynucleotides.

The term "polypeptide" or "protein" means a molecule that comprises at least two amino acid residues linked by a peptide bond to form a polypeptide. Small polypeptides of less than 50 amino acids may be referred to as "peptides".

Conventional one and three-letter amino acid codes are used herein as follows:

Amino acid	Three-letter code	One-letter code
Alanine	ala	A

Arginine	arg	R
Asparagine	asn	N
Aspartate	asp	D
Cysteine	cys	C
Glutamate	glu	E
Glutamine	gln	Q
Glycine	gly	G
Histidine	his	H
Isoleucine	ile	I
Leucine	leu	L
Lysine	lys	K
Methionine	met	M
Phenylalanine	phe	F
Proline	pro	P
Serine	ser	S
Threonine	thr	T
Tryptophan	trp	W
Tyrosine	tyr	Y
Valine	val	V

Compositions of matter

The invention provides antibodies specifically binding ST2L and inhibiting ST2L biological activity, and uses of such antibodies. The inventors have made a surprising finding that antibodies binding to Domain I of human ST2L (SEQ ID NO: 9) block IL-33/ST2L interaction and inhibit a spectrum of ST2L biological activities including IL-33-induced mast cell responses, whereas antibodies binding Domain III of human ST2L (SEQ ID NO: 11) do not block IL-33/ST2L interaction although they are inhibitory in a spectrum of ST2L biological activities. Domain III binding antibodies however have reduced or no inhibitory effect on, or in some cases stimulate IL-33-induced mast cell responses.

In some embodiments described herein, the antibodies that block IL-33/ST2L interaction and inhibit a spectrum of ST2L biological activities including IL-33-induced mast cell responses bind an epitope within human ST2L Domain I, (RCPRQGKPSYTVDW; SEQ ID NO: 210), and optionally ST2L amino acid residues T93 and F94 (residue numbering according to SEQ ID NO: 1).

The term "mast cell response" or "mast cell activity" refers to the IL-33-induced release of cytokines such as GM-CSF, IL-8, IL-5, IL-13, and IL-10, and allergic mediators such as prostaglandin D_2 from mast cells.

The invention provides novel antigen-binding sites binding Domain I of human ST2L as described herein. The structure for carrying an antigen-binding site is typically an antibody VH or VL.

The antibodies of the invention as described herein can be isolated human or human-adapted antibody antagonist or fragment thereof that specifically binds Domain I (SEQ ID NO: 9) of human ST2L. An exemplary antibody binding Domain I of human ST2L (SEQ ID NO: 9) is an antibody STLM15 (C2244) comprising HCDR1, HCDR2 and HCDR3 sequences of SEQ ID NOs: 23, 27 and 31, respectively, and LCDR1, LCDR2 and LCDR3 sequences of SEQ ID NOs: 35, 39 and 43, respectively, or an antibody C2494 (STLM62) comprising HCDR1, HCDR2 and HCDR3 sequences of SEQ ID NOs: 24, 28 and 32, respectively, and LCDR1, LCDR2 and LCDR3 sequences of SEQ ID NOs: 36, 40 and 44, respectively (Table 3). Additional exemplary antibodies binding Domain I of human ST2L are antibodies shown in Table 16 and Figure 13, for example antibodies STLM103, STLM107, STLM108, STLM123, STLM124, STLM208, STLM209, STLM210, STLM211, STLM212, and STLM213. Exemplary human antibody antagonists are shown in Figure 12 and Figure 13. Exemplary human-adapted antagonists are shown in Table 14.

In some embodiments described herein, the isolated human or human-adapted antibody antagonist or fragment thereof that specifically binds Domain I (SEQ ID NO: 9) of human ST2L blocks IL-33/ST2L interaction.

Antibodies can be tested for their ability to block IL-33/ST2L interaction by standard ELISA. For example, plates are coated with extracellular domain of human ST2L (huST2L-ECD) and incubated with an antibody, after which binding of

biotinylated IL-33 onto the plates is measured. Antibodies that "block IL-33/ST2L interaction" or "inhibit IL-33/ST2L interaction" are antibodies that in an ELISA assay using huST2L-ECD coated plates, reduce the signal derived from biotinylated IL-33 bound to the plate by at least 30%, 40%, 50%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100% at 50 µg/ml antibody concentration when compared to binding of IL-33 in the absence of the antibody.

Antibodies can be tested for their inhibition of mast cell responses by assessing their inhibitory activity on for example GM-CSF, IL-5, IL-10 or IL-13 release by human cord blood-derived mast cells or primary human lung mast cells using standard methods and methods exemplified *infra*. Antibodies as described herein that "inhibit mast cell response" or "inhibit mast cell activity" are antibodies that reduce 1-3 ng/ml IL-33-induced GM-CSF, IL-5, IL-13 or IL-10 secretion by at least 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100% at a concentration of 10 µg/ml when compared to mast cells not treated by the antibody. Typically mast cells may be derived from human cord blood or lung parenchyma and small airways $CD34^+$ progenitors by well known methods and as exemplified *infra*. Mast cell culture conditions may affect the measure of % inhibition for an antibody and therefore culture and test conditions may be kept standard using for example StemPro-34 media throughout the 6-10 week long differentiation procedure. At 4 days prior to the cytokine release assay mast cells are stimulated daily with 10 ng/ml IL-4, 10 ng/ml IL-6 and 100 ng/ml SCF. For the cytokine release assay, mast cells can be resuspended in fresh StemPro-34 media or RPMI containing 10% FCS without antibiotics, with 100ng/ml SCF. Suitable plating densities for assays are 65,000 to 75,000 cells/0.16 mls/well. Exemplary antibodies of the invention as described herein

inhibiting mast cell responses are antibodies STLM15, STLM62 and STLM208. Antibody CNTO3914 binds mouse ST2L Domain I without cross-reactivity to human ST2L and inhibits mast cell responses in mouse cells.

Those skilled in the art will appreciate that mast cell responses also include release of IL-1 and IL-32, and chemokines such as CCL1, CCL4, CCL5, CCL18 and CCL23 as well as allergic mediators such as cysteinyl leukotrienes, histamine, as well as a variety of mast cell proteases including tryptase, chymase, carboxypeptidase, and cathepsin G. Antibodies of the invention as described herein can be tested for their ability to inhibit these additional mast cell responses using standard methods. Antibodies of the invention binding Domain I of ST2L and blocking IL-33/ST2L interaction as described herein can be expected to inhibit these additional mast cell responses at least 40%, 50%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or more when tested at a minimum concentration of 10 μg/ml under these conditions.

The antibodies of the invention as described herein bind human ST2L with a dissociation constant (K_D) between about $5x10^{-12}$ M to about $7x10^{-10}$ M, an on rate constant (K_{on}) to human ST2L between about $2x10^{6}$ $M^{-1}s^{-1}$ to about $1x10^{8}$ $M^{-1}s^{-1}$, or an off rate constant (K_{off}) to human ST2L between about $1x10^{-6}$ s^{-1} to about $1x10^{-2}s^{-1}$. For example, the antibodies of the invention as described herein bind human ST2L with a K_D of less than about $7x10^{-10}$ M, less than about $1x10^{-10}$ M, less than about $5x10^{-11}$ M, less than about $1x10^{-11}$ M or less than about $5x10^{-12}$ M.

The antibodies of the invention as described herein may cross-react with *Macaca fascicularis* (cyno)

ST2L (SEQ ID NO: 2) and bind to cyno ST2L with a dissociation constant (K_D) between about $3x10^{-12}$ M to about $2x10^{-9}$ M, an on rate constant (K_{on}) to cyno ST2L between about $4x10^{6}$ $M^{-1}s^{-1}$ to about $1x10^{8}$ $M^{-1}s^{-1}$, or an off rate constant (K_{off}) to cyno ST2L between about $7x10^{-5}s^{-1}$ to about $1x10^{-1}s^{-1}$. For example, the antibodies of the invention as described herein bind cyno ST2L with a K_D of less than about $2x10^{-9}$ M, less than about $1x10^{-9}$ M, less than about $1x10^{-10}$ M, less than about $1x10^{-11}$ M or less than about $3x10^{-12}$ M.

The affinity of an antibody to ST2L can be determined experimentally using any suitable method. Such methods may utilize ProteOn XPR36, Biacore 3000 or KinExA instrumentation, ELISA or competitive binding assays known to those skilled in the art. The measured affinity of a particular antibody/ST2L interaction can vary if measured under different conditions (e.g., osmolarity, pH). Thus, measurements of affinity and other binding parameters (e.g., K_D, K_{on}, K_{off}) are preferably made with standardized conditions and a standardized buffer, such as the buffer described herein. Skilled in the art will appreciate that the internal error for affinity measurements for example using Biacore 3000 or ProteOn (measured as standard deviation, SD) can typically be within 5-33% for measurements within the typical limits of detection. Therefore the term "about" reflects the typical standard deviation in the assay. For example, the typical SD for a K_D of $1x10^{-9}$ M is up to $\pm 0.33x10^{-9}$ M.

The antibodies binding human ST2L with a desired affinity and optionally cross-reacting with cyno ST2L

can be selected from libraries of variants or fragments by panning with human and/or cyno ST2L and optionally by further antibody affinity maturation. Antibodies can be identified based on their inhibition of ST2L biological activity using any suitable method. Such methods may utilize reporter-gene assays or assays measuring cytokine production using well known methods and as described in the application.

Described is an isolated antibody antagonist specifically binding human ST2L comprising:

a heavy chain complementarity determining region (HCDR) 1 (HCDR1)of SEQ ID NO: 160 ($X_1X_2X_3MX_4$); wherein

X_1 is S, F, D, I, G or V;

X_2 is Y or D;

X_3 is A, D or S; and

X_4 is S, F or I;

a HCDR 2 (HCDR2) of SEQ ID NO: 161 ($X_5IX_6GX_7GGX_8TX_9YADSVKG$); wherein

X_5 is A, S, T, Y or D;

X_6 is S, R, E, K, G or A;

X_7 is S, E or N;

X_8 is S, R, E, G, T, D or A; and

X_9 is Y, D, N, A or S; and

a HCDR 3 (HCDR3) of SEQ ID NO: 162 ($X_{10}X_{11}$WSTEGSFFVLDY); wherein

X_{10} is D, A, R, N, Q, P, E, I, H, S, T or Y; and

X_{11} is P, A, H, Y, E, Q, L, S, N, T, V, or I.

Described is an isolated antibody antagonist specifically binding human ST2L comprising:

a light chain complementarity determining region (LCDR) 1 (LCDR1) of SEQ ID NO: 163 ($RASQSVDDX_{12}LA$); wherein

X_{12} is A or D;

a LCDR 2 (LCDR2) of SEQ ID NO: 90 (DASNRAT); and

a LCDR 3 (LCDR3) of SEQ ID NO: 164 ($QQX_{13}X_{14}X_{15}X_{16}X_{17}X_{18}T$); wherein

X_{13} is F or Y;

X_{14} is Y, I or N;

X_{15} is N, G, D or T;

X_{16} is W or A;

X_{17} is P or deleted; and

X_{18} is L or I.

The described antibodies comprising the HCDR1, HCDR2, HCDR3, LCDR1, LCDR2 and LCDR3 sequences of SEQ ID NOs: 160, 161, 162, 163, 90 and 164, respectively, can be made by well known mutagenesis methods using for example HCDR1, HCDR2, HCDR3, LCDR1, LCDR2 and LCDR3 sequences of SEQ ID NOs: 78, 81, 84, 87, 90 and 92, respectively as a template. The heavy chain CDRs and the light chain CDRs of SEQ ID NOs: 160, 161, 162, 163, 90 and 164, respectively, can be grafted to human frameworks, such as frameworks described *infra*. The antibodies can be assayed for binding to ST2L and for their ability to block IL-33/ST2L interaction and for other characteristics such as

affinity to human ST2L and/or cyno ST2L, and inhibition of mast cell responses using methods described herein.

In one embodiment, an isolated antibody antagonist specifically binding human ST2L as described herein comprises:

the HCDR1 of SEQ ID NOs: 78 or 95-108;

the HCDR2 of SEQ ID NOs: 81, 109-118 or 120-129;

the HCDR3 of SEQ ID NOs: 84 or 165-185;

the LCDR1 of SEQ ID NOs: 87 or 130;

the LCDR2 or SEQ ID NO: 90; and

the LCDR3 of SEQ ID NOs: 92 or 131-134.

In another embodiment, an isolated antibody antagonist specifically binding human ST2L comprises HCDR1, HCDR2, HCDR3, LCDR1, LCDR2 and LCDR3 sequences as shown in Figure 10, Figure 11, and Figure 12 and as described herein.

In another embodiment, an isolated antibody antagonist specifically binding human ST2L as described herein comprises:

the HCDR1 of SEQ ID NOs: 23 or 24;

the HCDR2 of SEQ ID NOs: 27 or 28;

the HCDR3 of SEQ ID NOs: 31 or 32;

the LCDR1 of SEQ ID NOs: 35 or 36;

the LCDR2 or SEQ ID NOs: 39 or 40; and

the LCDR3 of SEQ ID NOs: 43 or 44.

In another embodiment, an isolated antibody antagonist specifically binding human ST2L as described herein comprises HCDR1, HCDR2, HCDR3, LCDR1, LCDR2 and LCDR3 sequences:

SEQ ID NOs: 23, 27, 31, 35, 39 and 43, respectively;

SEQ ID NOs: 24, 28, 32, 36, 40 and 44, respectively; (HFA CDRs);
SEQ ID NOs: 24, 28, 146, 36, 40 and 147, respectively; or
SEQ ID NOs: 24, 28, 146, 36, 40 and 44, respectively.

Described is an isolated human or human-adapted antibody antagonist or fragment thereof specifically binding human ST2L as described herein, (SEQ ID NO: 1) comprising a heavy chain variable region (VH) comprising a VH framework derived from human IGHV3-23 (SEQ ID NO: 158), IGHV1-24*01 (SEQ ID NO: 148) or IGHV1-f*01 (SEQ ID NO: 149) framework sequences, and a light chain variable region (VL) comprising a VL framework derived from a human IGKV3-11 (L6) (SEQ ID NO: 159), IGKV3-15*01 (L2) (SEQ ID NO: 150), IGKV1-9*01 (L8) (SEQ ID NO: 151), IGKV1-5*01 (L12) (SEQ ID NO: 152), IGKV1-12*01 (L5) (SEQ ID NO: 153), IGKV1-39*01 (O12) (SEQ ID NO: 154), IGKV1-27*01 (A20) (SEQ ID NO: 155)or IGKV1-33*01 (O18) (SEQ ID NO: 156) framework sequences.

In another embodiment, the isolated antibody specifically binding Domain I of human ST2L as described herein comprises a VH comprising a VH framework derived from human VH 3-23 framework sequences (SEQ ID NO: 158); and a light chain variable region (VL) comprising a VL framework derived from a human Vκ L6 framework sequences (SEQ ID NO: 159). Human framework sequences are well known, and typically include human immunoglobulin germline variable region sequences joined to the joining (J) sequences. The

human VH 3-23 framework amino acid sequence shown in SEQ ID NO: 158 includes human germline VH 3-23 sequence joined to IGHJ4 and the human Vk L6 framework amino acid sequence shown in SEQ ID NO: 159 includes human Vκ L6 germline sequence joined to IGKJ1 as described in Shi *et al.*, J Mol Biol 397:385-96, 2010; Int. Pat. Publ. No. WO2009/085462; and U.S. Pat. Publ. No. US2010/0021477. Exemplary antibodies having a VH sequence derived from human VH 3-23 and a VL sequence derived from human Vκ L6 are those shown in Figure 12 and Figure 13.

Human or human-adapted antibodies comprising heavy or light chain variable regions "derived from" a particular framework or germline sequence refer to antibodies obtained from a system that uses human germline immunoglobulin genes, such as from transgenic mice or from phage display libraries as discussed *infra*. An antibody that is "derived from" a particular framework or germline sequence may contain amino acid differences as compared to the sequence it was derived from, due to, for example, naturally-occurring somatic mutations or intentional substitutions.

In another embodiment, the isolated human or human-adapted antibody antagonist or fragment thereof that specifically binds Domain I (SEQ ID NO: 9) of human ST2L as described herein competes for binding to human ST2L (SEQ ID NO: 1) with an isolated antibody comprising a heavy chain variable region (VH) of SEQ ID NO: 47 and a light chain variable region (VL) of SEQ ID NO: 51 (antibody C2244).

In another embodiment, the isolated antibody of the invention as described herein binds human ST2L at amino acid

residues 35-48 of SEQ ID NO: 1 (RCPRQGKPSYTVDW; SEQ ID NO: 210). The antibody as described herein may further bind human ST2L at amino acid residues T93 and F94 of SEQ ID NO: 1.

Competition between specific binding to human ST2L with antibodies of the invention as described herein comprising certain HCDR1, HCDR2 and HCDR3, and LCDR1, LCDR2 and LCDR3 amino acid sequences or comprising certain VH and VL sequences can be assayed *in vitro* using well known methods. For example, binding of MSD Sulfo-Tag™ NHS-ester-labeled antibody to human ST2L in the presence of an unlabeled antibody can be assessed by ELISA, or Biacore analyses or flow cytometry may be used to demonstrate competition with the antibodies of the current invention. The ability of a test antibody to inhibit the binding of C2244 to human ST2L demonstrates that the test antibody can compete with these antibodies for binding to human ST2L. Such exemplary antibodies are C2494, STLM208 and STLM213 shown in Table 3 and Figure 13.

Antibodies competing with C2244 for binding to Domain I of ST2L as described herein block IL-33/ST2L interaction and inhibit a spectrum of ST2L biological activities, including IL-33-induced mast cell responses. A non-neutralizing (*i.e.* non-inhibiting) epitope is also present on ST2L Domain I, as a second antibody competition group (represented by antibody C2240 which binds Domain I of ST2L, does not compete with C2244, and does not inhibit ST2L signaling).

Antibodies of the invention as described herein binding specific ST2L domains or epitopes can be made by immunizing mice expressing human immunoglobulin loci (Lonberg *et al.*, Nature 368:856-9, 1994; Fishwild *et al.*, Nature Biotechnology 14:845-51, 1996; Mendez *et al.*, Nature Genetics 15:146-56, 1997, US. Pat. Nos. 5,770,429, 7,041,870, and 5,939,598) or Balb/c mice with the peptides encoding the epitopes, for

example a peptide having an amino acid sequence of Domain I of human ST2L: KFSKQSWGLENEALIVRCPRQGKPSYTVDWYYSQTNKSIPTQERNRVFASGQLLKFLPAAV ADSGIYTCIVRSPTFNRTGYANVTIYKKQSDCNVPDYLMYSTV (SEQ ID NO: 9), or a peptide having an amino acid sequence of RCPRQGKPSYTVDW (SEQ ID NO: 210), and using the hybridoma method of Kohler *et al.*, Nature 256:495-97, 1975. The resulting antibodies are tested for their binding to the epitope using standard methods. For example, when the structures of both individual components are known, *in silico* protein-protein docking can be carried out to identify compatible sites of interaction. Hydrogen-deuterium (H/D) exchange can be carried out with the antigen and antibody complex to map regions on the antigen that may be bound by the antibody. Segment and point mutagenesis of the antigen can be used to locate amino acids important for antibody binding. The identified mAbs can further be modified by incorporating altered framework support residues to preserve binding affinity by techniques such as those disclosed in Queen *et al.*, Proc Natl Acad Sci (USA) 86:10029-32, 1989 and Hodgson *et al.*, Bio/Technology 9:421, 1991.

The antibodies of the invention as described herein may be human or human-adapted. The antibodies of the invention as described herein may be of IgA, IgD, IgE, IgG or IgM type.

Antibodies whose antigen-binding site amino acid sequences are substantially identical to those shown in Figure 10, Figure 11, Figure 12, Figure 13, Figure 15, Table 3, Table 9 and Table 12 are encompassed within the scope of the invention. Typically, this involves one or more amino acid substitutions with an amino acid having similar charge or hydrophobic or stereochemical characteristics, and are made to improve antibody properties, for example stability or

affinity. For example, a conservative substitution may involve a substitution of a native amino acid residue with a nonnative residue such that there is little or no effect on the polarity or charge of the amino acid residue at that position. Furthermore, any native residue in the polypeptide may also be substituted with alanine, as has been previously described for alanine scanning mutagenesis (MacLennan *et al.*, Acta Physiol Scand Suppl 643:55-67, 1998; Sasaki *et al.*, Adv Biophys 35:1-24, 1998). Desired amino acid substitutions (whether conservative or non-conservative) can be determined by those skilled in the art at the time such substitutions are desired. For example, amino acid substitutions can be used to identify residues important for the function of the antibodies, such as residues affecting affinity, or residues that impart undesireable properties such as aggregation. Exemplary amino acid substitutions are shown in Figure 12 and Figure 13.

Substitutions in the framework regions, in contrast to antigen binding sites may also be made as long as they do not adversely affect the properties of the antibody. Framework substitutions can be made for example at the Vernier Zone residues (US. Pat. No. 6,649,055) to improve antibody affinity or stability. Substitutions can also be made at those framework positions in the antibody that differ in sequence when compared to the homologous human germline gene sequences to reduce possible immunogenicity. These modifications can be done for example to antibodies derived from *de novo* antibody libraries, such as pIX libraries.

Conservative amino acid substitutions also encompass non-naturally occurring amino acid residues which are typically incorporated by chemical peptide synthesis rather

than by synthesis in biological systems. Amino acid substitutions can be done for example by PCR mutagenesis (US Pat. No. 4,683,195). Libraries of variants can be generated using well known methods, for example using random (NNK) or non-random codons, for example DVK codons, which encode 11 amino acids (ACDEGKNRSYW), and screening the libraries or variants with desired properties.

Although the embodiments illustrated in the Examples comprise pairs of variable regions, pairs of full length antibody chains, or pairs of CDR1, CDR2 and CDR3 regions, one from a heavy chain and one from a light chain, a skilled artisan will recognize that alternative embodiments may comprise single heavy chain variable regions or single light chain variable regions, single full length antibody chains, or CDR1, CDR2 and CDR3 regions from one antibody chain, either heavy or light. The single variable region, full length antibody chain or CDR1, CDR2 and CDR3 region of one chain can be used to screen for corresponding domains in another chain, the two chains capable of forming an antibody that specifically binds ST2L. The screening may be accomplished by phage display screening methods using, e.g., a hierarchical dual combinatorial approach disclosed in PCT Publ. No. WO1992/01047. In this approach, an individual colony containing either a H or L chain clone is used to infect a complete library of clones encoding the other chain (L or H), and the resulting two-chain specific antigen-binding domain is selected in accordance with phage display techniques as described.

The invention provides for isolated VH and VL domains of the antibodies of the invention as described herein and antibodies comprising certain VH and VL domains. VH and VL variable regions for certain antibodies of the invention as described herein are shown in Figure 13 and Table 12.

One embodiment of the invention is an isolated human or human-adapted antibody antagonist or fragment thereof that specifically binds Domain I (SEQ ID NO: 9) of human ST2L comprising the VH at least 90% identical to the VH of SEQ ID NO: 191.

Another embodiment of the invention is an isolated human or human-adapted antibody antagonist or fragment thereof that specifically binds Domain I (SEQ ID NO: 9) of human ST2L comprising the VL at least 94% identical to the VL of SEQ ID NO: 209.

In some embodiments described herein, the invention provides for an antibody comprising the VH of SEQ ID NOs: 143, 144, 145, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204 or 205.

In some embodiments described herein, the invention provides for an antibody comprising the VL of SEQ ID NOs: 135, 136, 137, 138, 139, 140, 141, 142, 206, 207, 208 or 209.

In some embodiments described herein, the invention provides for an antibody comprising

the VH of SEQ ID NOs: 186, 187, 197, 198, 199, 200, 201, 202, 203, 204 or 205 and the VL of SEQ ID NO: 206;

the VH of SEQ ID NOs: 195 or 196 and the VL of SEQ ID NO: 207;

the VH of SEQ ID NOs: 188, 189 or 190 and the VL of SEQ ID NO: 208; or

the VH of SEQ ID NOs: 187, 191, 192, 193 or 194 and the VL of SEQ ID NO: 209.

Another embodiment of the invention an isolated human or human-adapted antibody antagonist or fragment thereof that specifically binds Domain I (SEQ ID NO: 9) of human ST2L comprising:

the HCDR1 of SEQ ID NO: 97;

the HCDR2 of SEQ ID NO: 114;

the HCDR3 of SEQ ID NO: 84;
the LCDR1 of SEQ ID NO: 130;
the LCDR2 of SEQ ID NO: 90;
the LCDR3 of SEQ ID NO: 134; or
the VH of SEQ ID NO: 191 and the VL of SEQ ID NO: 209.

Human mAbs lacking any non-human sequences can be prepared and optimized from phage display libraries by techniques referenced in, *e.g.*, Knappik *et al.*, J Mol Biol 296:57-86, 2000; and Krebs *et al.*, J Immunol Meth 254:67-84 2001. In an exemplary method, the antibodies of the invention are isolated from libraries expressing antibody heavy and light chain variable regions as fusion proteins with bacteriophage pIX coat protein. The antibody libraries are screened for binding to human ST2L-ECD and the obtained positive clones are further characterized, the Fabs isolated from the clone lysates, and expressed as full length IgGs. Exemplary antibody libraries and screening methods are described in Shi *et al.*, J Mol Biol 397:385-96, 2010; Int. Pat. Publ. No. WO2009/085462, and U.S. Ser. No. 12/546850; U.S. Pat. Nos. 5,223,409, 5,969,108, and 5,885,793).

The resulting mAbs can further be modified in their framework regions to change certain framework residues to those present in a matching human germline.

Immune effector properties of the antibodies of the invention may be enhanced or silenced through Fc modifications by techniques known to those skilled in the art. For example, Fc effector functions such as C1q binding, complement dependent cytotoxicity (CDC), antibody-dependent cell-mediated cytotoxicity (ADCC), phagocytosis, down regulation of cell surface receptors (e.g., B cell receptor; BCR), etc. can be provided and/or controlled by modifying residues in the Fc responsible for these activities.

Pharmacokinetic properties could also be enhanced by mutating residues in the Fc domain that extend antibody half-life (Strohl Curr Opin Biotechnol 20:685-91, 2009). Exemplary Fc modifications are IgG4 S228P/L234A/L235A, IgG2 M252Y/S254T/T256E (Dall'Acqua et al., J Biol Chem 281:23514-24, 2006; or IgG2 V234A/G237A/P238S, V234A/G237A/H268Q, H268A/V309L/A330S/P331 or V234A/G237A/P238S/H268A/V309L/A330S/P331S on IgG2 (Intl. Pat. Appl. No. WO2011/066501) (numbering according to the EU numbering).

Additionally, antibodies of the invention as described herein can be post-translationally modified by processes such as glycosylation, isomerization, deglycosylation or non-naturally occurring covalent modification such as the addition of polyethylene glycol moieties (pegylation) and lipidation. Such modifications may occur *in vivo* or *in vitro*. For example, the antibodies of the invention as described herein can be conjugated to polyethylene glycol (PEGylated) to improve their pharmacokinetic profiles. Conjugation can be carried out by techniques known to those skilled in the art. Conjugation of therapeutic antibodies with PEG has been shown to enhance pharmacodynamics while not interfering with function (Knigh *et al.*, Platelets 15:409-18, 2004; Leong *et al.*, Cytokine 16:106-19, 2001; Yang *et al.*, Protein Eng 16:761-70, 2003).

Antibodies or fragments thereof of the invention as described herein modified to improve stability, selectivity, cross-reactivity, affinity, immunogenicity or other desirable biological or biophysical property are within the scope of the invention. Stability of an antibody is influenced by a number of factors, including (1) core packing of individual domains that affects their intrinsic stability, (2) protein/protein

interface interactions that have impact upon the HC and LC pairing, (3) burial of polar and charged residues, (4) H-bonding network for polar and charged residues; and (5) surface charge and polar residue distribution among other intra- and inter-molecular forces (Worn *et al.*, J Mol Biol 305:989-1010, 2001). Potential structure destabilizing residues may be identified based upon the crystal structure of the antibody or by molecular modeling in certain cases, and the effect of the residues on antibody stability can be tested by generating and evaluating variants harboring mutations in the identified residues. One of the ways to increase antibody stability is to raise the thermal transition midpoint (Tm) as measured by differential scanning calorimetry (DSC). In general, the protein Tm is correlated with its stability and inversely correlated with its susceptibility to unfolding and denaturation in solution and the degradation processes that depend on the tendency of the protein to unfold (Remmele *et al.*, Biopharm 13:36-46, 2000). A number of studies have found correlation between the ranking of the physical stability of formulations measured as thermal stability by DSC and physical stability measured by other methods (Gupta *et al.*, AAPS PharmSci 5E8, 2003; Zhang *et al.*, J Pharm Sci 93:3076-89, 2004; Maa *et al.*, Int J Pharm 140:155-68, 1996; Bedu-Addo *et al.*, Pharm Res 21:1353-61, 2004; Remmele *et al.*, Pharm Res 15:200-8, 1997). Formulation studies suggest that a Fab Tm has implication for long-term physical stability of a corresponding mAb. Differences in amino acids in either framework or within the CDRs could have

significant effects on the thermal stability of the Fab domain (Yasui *et al.*, FEBS Lett 353:143-6, 1994).

Antibodies of the invention specifically binding Domain I of human ST2L as described herein can be engineered into bispecific antibodies which are also encompassed within the scope of the invention. The VL and/or the VH regions of the antibodies of the invention can be engineered using published methods into single chain bispecific antibodies as structures such as TandAb® designs (Int. Pat. Publ. No. WO1999/57150; U.S. Pat. Publ. No. US2011/0206672) or into bispecific scFVs as structures such as those disclosed in U.S. Pat. No. US5869620; Int. Pat. Publ. No. WO1995/15388A, 1nt. Pat. Publ. No. WO1997/14719 or Int. Pat. Publ. No WO2011/036460.

The VL and/or the VH regions of the antibodies of the invention as described herein can be engineered into bispecific full length antibodies, where each antibody arm binds a distinct antigen or epitope. Such bispecific antibodies are typically made by modulating the CH3 interactions between the two antibody heavy chains to form bispecific antibodies using technologies such as those described in U.S. Pat. No. US7695936; Int. Pat. Publ. No. WO04/111233; U.S. Pat. Publ. No. US2010/0015133; U.S. Pat. Publ. No. US2007/0287170; Int. Pat. Publ. No. WO2008/119353; U.S. Pat. Publ. No. US2009/0182127; U.S. Pat. Publ. No. US2010/0286374; U.S. Pat. Publ. No. US2011/0123532; Int. Pat. Publ. No. WO2011/131746; Int. Pat. Publ. No. WO2011/143545; or U.S. Pat. Publ. No. US2012/0149876. Additional bispecific structures into which the VL and/or the VH regions of the antibodies of the invention can be incorporated are for example Dual Variable Domain Immunoglobulins (Int. Pat. Publ. No. WO2009/134776), or structures that include various dimerization domains to connect the two antibody arms with different specificity, such as leucine zipper or collagen

dimerization domains (Int. Pat. Publ. No. WO2012/022811, U.S. Pat. No. US5932448; U.S. Pat. No. US6833441).

Another aspect of the invention is an isolated polynucleotide encoding any of the antibody heavy chain variable regions or the antibody light chain variable regions or fragments thereof of the invention or their complement. Certain exemplary polynucleotides are disclosed herein, however, other polynucleotides which, given the degeneracy of the genetic code or codon preferences in a given expression system, encode the antibody antagonists of the invention are also within the scope of the invention. Exemplary polynucleotides of the invention are those shown in SEQ ID NOs: 211, 212, 213 and 214.

Another embodiment of the invention is a vector comprising the polynucleotide of the invention. Such vectors may be plasmid vectors, viral vectors, vectors for baculovirus expression, transposon based vectors or any other vector suitable for introduction of the polynucleotides of the invention into a given organism or genetic background by any means.

Another embodiment of the invention is a host cell comprising the polynucleotide of the invention. Such host cells may be eukaryotic cells, bacterial cells, plant cells or archeal cells. Exemplary eukaryotic cells may be of mammalian, insect, avian or other animal origins. Mammalian eukaryotic cells include immortalized cell lines such as hybridomas or myeloma cell lines such as SP2/0 (American Type Culture Collection (ATCC), Manassas, VA, CRL-1581), NS0 (European Collection of Cell Cultures (ECACC), Salisbury, Wiltshire, UK, ECACC No. 85110503), FO (ATCC CRL-1646) and Ag653 (ATCC CRL-1580) murine cell lines.

An exemplary human myeloma cell line is U266 (ATTC CRL-TIB-196). Other useful cell lines include those derived from Chinese Hamster Ovary (CHO) cells such as CHO-K1SV (Lonza Biologics, Walkersville, MD), CHO-K1 (ATCC CRL-61) or DG44.

Another embodiment of the invention is a method of producing an antibody that specifically binds Domain I of ST2L, comprising culturing a host cell of the invention and recovering the antibody produced by the host cell. Methods of making antibodies and purifying them are well known in the art.

Described is a method of inhibiting interaction of ST2L with IL-33 in a subject comprising administering the subject an antibody specifically binding domain I of ST2L in an amount sufficient to inhibit interaction of ST2L and IL-33.

Methods of Treatment

ST2L antagonists of the invention as described herein, for example ST2L antibody antagonists blocking IL-33/ST2L interaction and binding Domain I of ST2L, antibodies that compete for binding to human ST2L (SEQ ID NO: 1) with an isolated antibody comprising a heavy chain variable region of SEQ ID NO: 47 and a light chain variable region of SEQ ID NO: 51, or antibodies binding human ST2L at amino acid residues 35-48 of SEQ ID NO: 1 (RCPRQGKPSYTVDW; SEQ ID NO: 210) may be utilized to modulate the immune system. Antibodies of the invention as described herein may be more efficient in antagonizing ST2L biological activity when compared to antibodies binding other domains and/or regions on ST2L as the antibodies of the invention are able to more efficiently reduce IL-33-induced mast cell responses. Any antibodies of the invention can be used in the described methods.

Exemplary antibodies that can be used in the described methods are antibodies STLM62, STLM15, STLM103, STLM107, STLM108, STLM123, STLM124, STLM206, STLM207, STLM208, STLM209, STLM210, STLM211, STLM212, STLM213. Without wishing to be bound by any theory, it is suggested that antibody antagonists that bind Domain I and block IL-33/ST2L interaction may inhibit formation of the IL-1RAcP/IL-33/ST2L/cKit complex or downstream signaling on mast cells, whereas Domain III binding antibodies, while being able to inhibit recruitment of IL-1RAcP to the ST2L/IL-33 complex, may be unable to disrupt the formation of the larger IL-1RAcP/IL-33/ST2L/cKit complex specifically found on mast cells. Microarray analysis conducted supports the suggestion as it was demonstrated that anti-ST2L Domain I binding antibodies suppressed the majority of mast cell signaling pathways induced by IL-33, and that anti-ST2L Domain III binding antibodies were only able to inhibit a small subset of these signaling pathways. It is feasible that because IL-33 binds to ST2L prior to the association of the accessory protein IL-1RAcP, blockade of IL-33 binding to ST2L by Domain I-binding antibodies could prevent association of any other accessory protein, including cKit or as-yet unidentified co-receptors. Domain III-binding antibodies, which do not interfere with IL-33 binding to ST2L, could theoretically block IL-1RAcP association but not the association of other co-receptors, including as-yet unidentified co-receptors. Multiple models have been proposed for how IL-1RAcP interacts with the IL-1/IL-1R or ST2L/IL-33 complexes (Lingel *et al.*, Structure 17: 1398-1410, 2009; and reviewed by Thomas *et al.*, Nat Struct & Molec Biol 19: 455-457, 2012). These models indicate that IL-1RAcP could bind to one side of the complex, but which side has not been conclusively shown. Therefore it is feasible that the 'other side'or 'free side' of the complex is available for association with an alternate

co-receptor, that would not be blocked by a Domain III antibody, and off-target effects such as increased recruitment of another co-receptor, resulting in increased signaling, is possible.

In the described methods, any antibody antagonist specifically binding Domain I of human ST2L, antibody antagonist blocking IL-33/ST2L interaction and binding Domain I of human ST2L, antibodies that competes for binding to human ST2L (SEQ ID NO: 1) with an isolated antibody comprising a heavy chain variable region of SEQ ID NO: 47 and a light chain variable region of SEQ ID NO: 51, or antibodies binding human ST2L at amino acid residues 35-48 of SEQ ID NO: 1 (RCPRQGKPSYTVDW; SEQ ID NO: 210) may be used. Additional characteristics of such antibodies include ability of the antibody to block IL-33/ST2L interaction and to inhibit human mast cell responses.

Therefore, antibodies of the invention are suitable for treating a spectrum of ST2L-mediated conditions, ST2L-mediated inflammatory conditions and conditions where inhibition of mast cell responses is desired.

The described methods may be used to treat an animal patient belonging to any classification. Examples of such animals include mammals such as humans, rodents, dogs, cats and farm animals. For example, the antibodies of the invention are useful in the prophylaxis and treatment of ST2L-mediated conditions, such as inflammatory diseases including asthma, airway hyper-reactivity, sarcoidosis, chronic obstructive pulmonary disease (COPD), idiopathic pulmonary fibrosis (IPF), cystic fibrosis, inflammatory bowel disease (IBD), rheumatoid arthritis, eosinophilic esophagitis, scleroderma, atopic dermatitis, allergic rhinitis, bullous pemphigoid, chronic urticaria, diabetic nephropathy, interstitial cystitis or Graft Versus Host Disease (GVHD). The antibodies of the invention are useful

in the prophylaxis and treatment of immune diseases mediated at least in part by mast cells, such as asthma, eczema, itch, allergic rhinitis, allergic conjunctivitis, as well as autoimmune diseases such as rheumatoid arthritis, bullous pemphigoid and multiple sclerosis.

The antibodies of the invention and are also useful in the preparation of a medicament for such treatment, wherein the medicament is prepared for administration in dosages defined herein.

Mast cells play a central role in allergic inflammation and asthma through their release of a variety of mediators (reviewed by Amin, Respir Med 106:9-14, 2012). ST2L is highly expressed on mast cells and its activation leads to expression of many proinflammatory cytokines and other mediators. Inhibition of ST2L activity is proposed to interfere with mast cell mediated inflammatory cell recruitment and to modulate chronic inflammation.

Mast cells are rapid responders to stimulation, including allergen, cold air, pathogen; damage to the epithelium by these stimuli can result in release of IL-33 (reviewed by Zhao and Hu, Cell & Molec Immunol 7: 260-2, 2012). Mast cells release leukotrienes, histamine, prostaglandins, and cytokines to increase vascular permeability and bronchoconstriction, and recruit other immune cells such as neutrophils, eosinophils and T lymphocytes to the site (Henderson *et al.*, JEM 184:1483-94, 1996; White *et al.*, JACI 86:599-605, 1990). Additionally, they enhance immune responses by inducing adhesion molecule upregulation on endothelial cells to increase immune cell trafficking (Meng *et al.*, J Cell Physiol 165:40-53, 1995). Mast cells play an important role in airway remodeling; in asthmatics, an increased number of mast cells is found within the airway smooth muscle (ASM) cell layer, and secrete

mediators to promote ASM proliferation (reviewed by Okayama *et al.*, Curr Opin Immunol 19:687-93, 2007).

Inflammatory pulmonary condition is an example of an inflammatory condition. Exemplary inflammatory pulmonary conditions include infection-induced pulmonary conditions including those associated with viral, bacterial, fungal, parasite or prion infections; allergen-induced pulmonary conditions; pollutant-induced pulmonary conditions such as asbestosis, silicosis, or berylliosis; gastric aspiration-induced pulmonary conditions, immune dysregulation, inflammatory conditions with genetic predisposition such as cystic fibrosis, and physical trauma-induced pulmonary conditions, such as ventilator injury. These inflammatory conditions also include asthma, emphysema, bronchitis, chronic obstructive pulmonary disease (COPD), sarcoidosis, histiocytosis, lymphangiomyomatosis, acute lung injury, acute respiratory distress syndrome, chronic lung disease, bronchopulmonary dysplasia, community-acquired pneumonia, nosocomial pneumonia, ventilator -associated pneumonia, sepsis, viral pneumonia, influenza infection, parainfluenza infection, rotavirus infection, human metapneumovirus infection, respiratory syncitial virus infection and *Aspergillus* or other fungal infections. Exemplary infection-associated inflammatory diseases may include viral or bacterial pneumonia, including severe pneumonia, cystic fibrosis, bronchitis, airway exacerbations and acute respiratory distress syndrome (ARDS). Such infection-associated conditions may involve multiple infections such as a primary viral infection and a secondary bacterial infection. Dysregulated ST2L signaling may play a role in the pathology of pulmonary diseases such as asthma and Chronic Obstructive Pulmonary Disease (COPD) (reviewed in Alcorn *et al.*, Annu Rev Physiol 72:495-516, 2010). Commonly used animal models for asthma and airway inflammation include

the ovalbumin challenge model, methacholine sensitization models and sensitization with *Aspergillus fumigatus* (Hessel *et al.*, Eur J Pharmacol 293:401-12, 1995). Inhibition of cytokine and chemokine production from cultured human bronchial epithelial cells, bronchial fibroblasts or airway smooth muscle cells can also be used as *in vitro* models. The administration of antagonists of the present invention to any of these models can be used to evaluate the use of those antagonists to ameliorate symptoms and alter the course of asthma, airway inflammation, COPD and the like.

Asthma is an inflammatory disease of the lung that is characterized by airway hyperresponsiveness ("AHR"), bronchoconstriction, wheezing, eosinophilic or neutrophilic inflammation, mucus hypersecretion, subepithelial fibrosis, and elevated IgE levels. Patients with asthma experience "exacerbations", a worsening of symptoms, most commonly due to microbial infections of the respiratory tract (*e.g.* rhinovirus, influenza virus, Haemophilus influenza, etc.). Asthmatic attacks can be triggered by environmental factors (*e.g.* ascarids, insects, animals (*e.g.*, cats, dogs, rabbits, mice, rats, hamsters, guinea pigs and birds), fungi, air pollutants (*e.g.*, tobacco smoke), irritant gases, fumes, vapors, aerosols, chemicals, pollen, exercise, or cold air. Apart from asthma, several chronic inflammatory diseases affecting the lung are characterized by neutrophil infiltration to the airways, for example chronic obstructive pulmonary disease (COPD), bacterial pneumonia and cystic fibrosis (Linden *et al.*, Eur Respir J 15:973-7, 2000; Rahman *et al.*, Clin Immunol 115:268-76, 2005), and diseases such as COPD, allergic rhinitis, and cystic fibrosis are characterized by airway hyperresponsiveness (Fahy and O'Byrne, Am J Respir Crit Care Med 163:822-3, 2001). Commonly used animal models for asthma and airway inflammation include the model of methacholine challenge

after ovalbumin sensitization and challenge (Hessel *et al.*, Eur J Pharmacol 293:401-12, 1995). Inhibition of cytokine and chemokine production from cultured human bronchial epithelial cells, bronchial fibroblasts or airway smooth muscle cells can also be used as *in vitro* models. The administration of antibody antagonists of the present invention to any of these models can be used to evaluate the use of those antagonists to ameliorate symptoms and alter the course of asthma, airway inflammation, COPD and the like.

IL-33 signaling through the ST2L receptor on TH2 cells, basophils, mast cells, and the newly described Innate Lymphoid Type 2 Cells results in IL-5 and IL-13 (type 2 cytokine) secretion (ILCs reviewed by Spits *et al.*, Nature Reviews Immunology 13:145-149, 2013). Beneficial effects of therapeutics targeting IL-5 or IL-13 in asthma confirm the relevance of these pathways. IL-5 activates eosinophils, and treatment of a subgroup of severe asthmatics with sputum eosinophilia with a monoclonal antibody that neutralizes IL-5 resulted in fewer exacerbations (Nair et al. N Engl J Med. 2009; 360(10):985-93). IL-13 is reported to contribute to IgE synthesis, mucus secretion and fibrosis. Treatment of severe asthmatics with an anti-IL-13 monoclonal antibody resulted in an improvement in lung function, with a subgroup demonstrating a greater improvement (Corren *et al.*, N. Engl. J. Med., 365:1088-1098, 2011). Other mediators of differential immunological pathways are also involved in asthma pathogenesis, and blocking these mediators, in addition to ST2L, may offer additional therapeutic benefit. Therapies that target multiple type 2 cytokines, or pathways upstream of type 2

cytokine production, could be beneficial in severe disease.

The VH and the VL domains of the ST2L antibodies of the invention may be incorporated into bispecific antibodies and molecules described herein, in which the bispecific antibody specifically binds Domain I of ST2L and a second antigen such as TSLP (thymic stromal lympohpoietin), IL-25, IL-17RB or TSLPR.

IL-25 and TSLP, like IL-33, trigger type 2 cytokine release via distinct signaling complexes: IL-25 (IL-17E) is a member of the IL-17 family and signals through IL-17RA/IL-17RB, and TSLP is a member of the IL-7 family and signals through the TSLPR/IL-7Rα heterodimers (reviewed by Koyasu *et al.*, Immunol 132:475-481, 2011). Animals deficient in IL-33, ST2L, IL-25, IL-17RB, TSLP, or TSLPR demonstrate less severe airway inflammation in at least one of many different types of mouse models of asthma; however lack of protection from airway inflammation may be present in most of these animal models, raising the possibility that exposure of the epithelium to various allergens or pathogens could trigger release of IL-33, IL-25, and TSLP concomitantly. Hammad et al. reported that administration of house dust mite extract to mice resulted in the release of IL-25, TSLP and IL-33 (as well as IL-5 and IL-13 downstream of IL-33) into the airway (Hammad *et al.*, Nat Med 15:210-216, 2009). This suggests that blocking ST2L and TSLP and/or IL-25 may have beneficial effects, particularly in severe airway disease.

In another embodiment of the invention the antibody antagonists specifically binding Domain I of human ST2L can be used to generate bispecific molecules that bind ST2L and TSLP, ST2L and IL-25, ST2L and TSLPR, ST2L and IL-17RA, or ST2L and IL-17RB.

In another embodiment of the invention, the antibody antagonists specifically binding Domain I of human ST2L is a bispecific antibody, wherein the antibody further binds TSLP, IL-25, TSLPR, IL-17RA or IL-17RB.

TSLP, IL-25, TSLPR, IL-17RA and IL-17RB binding antibodies can be generated using methods described herein, such as immunizing mice expressing human immunoglobulin loci (Lonberg *et al.*, Nature 368:856-9, 1994; Fishwild *et al.*, Nature Biotechnology 14:845-51, 1996; Mendez *et al.*, Nature Genetics 15:146-56, 1997, US. Pat. Nos. 5,770,429, 7,041,870, and 5,939,598) or Balb/c mice with the corresponding proteins or extracellular domains of the proteins, or using phage display libraries as described herein. Alternatively, existing antibodies to TSLP, IL-25, TSLPR, IL-17RA and IL-17RB can be used to generate the bispecific molecules. Exemplary IL-25 antibodies that can be used are those described in for example Int. Pat. Publ. No. WO2011/123507.

Arthritis, including osteoarthritis, rheumatoid arthritis, arthritic joints as a result of injury, and the like, are common inflammatory conditions, which would benefit from the therapeutic use of anti-inflammatory proteins, such as the antagonists of the present invention. Activation of ST2L signaling may perpetuate inflammation and further tissue damage in the inflamed joint. Several animal models for rheumatoid arthritis are known. For example, in the collagen-induced arthritis (CIA) model, mice develop chronic inflammatory arthritis that closely resembles human rheumatoid arthritis. ST2L-deficient (ST2KO) mice developed attenuated disease in this model, and pathology in this model was dependent on ST2L expression by mast cells (Xu *et al.*, PNAS 105:10913-8, 2008). In this model, there was reduced infiltration of mononuclear and polymorphonuclear cells and of synovial hyperplasia in the joints of ST2KO mice. The draining LNs of ST2KO mice cultured with collagen (CII)

showed significantly decreased IL-17, IFNγ, and TNFα production. ST2L-deficient mice adoptively transferred with wild-type (WT) bone marrow-derived mast cells (BMMC), before CIA was induced, developed more severe CIA than those engrafted with ST2KO BMMCs. Therefore ST2L signaling by mast cells was critical to the development of arthritis in a mouse model that resembles human rheumatoid arthritis. Administration of the ST2L antibodies of the present invention, which inhibit mast cell responses, to the CIA model mice can be used to evaluate the use of these antagonists to ameliorate symptoms and alter the course of disease.

Exemplary gastrointestinal inflammatory conditions are inflammatory bowel disease (IBD), ulcerative colitis (UC) and Crohn's disease (CD), colitis induced by environmental insults (*e.g.*, gastrointestinal inflammation (*e.g.*, colitis) caused by or associated with (*e.g.*, as a side effect) a therapeutic regimen, such as administration of chemotherapy, radiation therapy, and the like), infections colitis, ischemic colitis, collagenous or lymphocytic colitis, necrotizing enterocolitis, colitis in conditions such as chronic granulomatous disease or celiac disease, food allergies, gastritis, infectious gastritis or enterocolitis (*e.g.*, *Helicobacter pylori*-infected chronic active gastritis) and other forms of gastrointestinal inflammation caused by an infectious agent. Several animal models for gastrointestinal inflammatory conditions exist. Some of the most widely used models are the 2,4,6-trinitrobenesulfonic acid/ethanol (TNBS)-induced colitis model or the oxazalone model, which induce chronic inflammation and

ulceration in the colon (Neurath *et al.*, Intern Rev Immunol 19:51-62, 2000). Another model uses dextran sulfate sodium (DSS), which induces an acute colitis manifested by bloody diarrhea, weight loss, shortening of the colon and mucosal ulceration with neutrophil infiltration. Another model involves the adoptive transfer of naïve $CD45RB^{high}$ CD4 T cells to RAG or SCID mice. In this model, donor naïve T cells attack the recipient gut causing chronic bowel inflammation and symptoms similar to human inflammatory bowel diseases (Read and Powrie, Curr Protoc Immunol Chapter 15 unit 15.13, 2001). The administration of antagonists of the present invention in any of these models can be used to evaluate the potential efficacy of those antagonists to ameliorate symptoms and alter the course of diseases associated with inflammation in the gut, such as inflammatory bowel disease.

Renal fibrosis can develop from either an acute insult such as graft ischemia/reperfusion (Freese *et al.*, Nephrol Dial Transplant 16:2401-6, 2001) or chronic condition such as diabetes (Ritz *et al.*, Nephrol Dial Transplant 11 Suppl 9:38-44, 1996). The pathogenesis is typically characterized by an initial inflammatory response followed by sustained fibrogenesis of the glomerular filtration apparatus and tubular interstitium (Liu, Kidney Int 69:213-7, 2006). Tubulointerstitial fibrosis has been shown to play a critical role in the pathogenesis of renal injury to end-stage renal failure and the proximal tubule cell has been revealed as a central mediator (Phillips and Steadman, Histol Histopathol 17:247-52, 2002; Phillips, Chang Gung Med J 30:2-6, 2007). Fibrogenesis in the tubulointerstitial compartment is mediated in part by activation of resident fibroblasts, which secrete

pro-inflammatory cytokines that stimulate the proximal tubule epithelium to secrete local inflammatory and fibrogenic mediators. Additionally, chemotactic cytokines are secreted by fibroblasts and epithelial cells and provide a directional gradient guiding the infiltration of monocytes/macrophages and T-cells into the tubulointerstitium. The inflammatory infiltrate produces additional fibrogenic and inflammatory cytokines that further activate fibroblast and epithelial cytokine release while also stimulating the epithelium to undergo a phenotypic transition in which the cells deposit excess extracellular matrix components (Simonson, Kidney Int 71:846-54, 2007).

Other exemplary fibrotic conditions may include liver fibrosis (including but not limited to alcohol-induced cirrhosis, viral-induced cirrhosis, autoimmune-induced hepatitis); lung fibrosis (including but not limited to scleroderma, idiopathic pulmonary fibrosis); kidney fibrosis (including but not limited to scleroderma, diabetic nephritis, glomerular nephritis, lupus nephritis); dermal fibrosis (including but not limited to scleroderma, hypertrophic and keloid scarring, burns); myelofibrosis; neurofibromatosis; fibroma; intestinal fibrosis; and fibrotic adhesions resulting from surgical procedures. The fibrosis can be organ specific fibrosis or systemic fibrosis. The organ specific fibrosis can be associated with lung fibrosis, liver fibrosis, kidney fibrosis, heart fibrosis, vascular fibrosis, skin fibrosis, eye fibrosis or bone marrow fibrosis. The lung fibrosis can be associated with idiopathic pulmonary fibrosis, drug induced pulmonary fibrosis, asthma, sarcoidosis or chronic obstructive pulmonary disease. The liver fibrosis can be associated with cirrhosis, schistomasomiasis or cholangitis. The cirrhosis can be selected from alcoholic cirrhosis, post-hepatitis C cirrhosis, primary biliary cirrhosis. The cholangitis can be

sclerosing cholangitis. The kidney fibrosis can be associated with diabetic nephropathy or lupus glomeruloschelerosis. The heart fibrosis can be associated with myocardial infarction. The vascular fibrosis can be associated with postangioplasty arterial restenosis or atherosclerosis. The skin fibrosis can be associated with burn scarring, hypertrophic scarring, keloid, or nephrogenic fibrosing dermatopathy. The eye fibrosis can be associated with retro-orbital fibrosis, postcataract surgery or proliferative vitreoretinopathy. The bone marrow fibrosis can be associated with idiopathic myelofibrosis or drug induced myelofibrosis. The systemic fibrosis can be systemic sclerosis or graft versus host disease.

Other inflammatory conditions and neuropathies, which may be prevented or treated by the described methods are those caused by autoimmune diseases. These conditions and neuropathies include multiple sclerosis, systemic lupus erythematous, and neurodegenerative and central nervous system (CNS) disorders including Alzheimer's disease, Parkinson's disease, Huntington's disease, bipolar disorder and Amyotrophic Lateral Sclerosis (ALS), liver diseases including primary biliary cirrhosis, primary sclerosing cholangitis, non-alcoholic fatty liver disease/steatohepatitis, fibrosis, hepatitis C virus (HCV) and hepatitis B virus (HBV), diabetes and insulin resistance, cardiovascular disorders including atherosclerosis, cerebral hemorrhage, stroke and myocardial infarction, arthritis, rheumatoid arthritis, psoriatic arthritis and juvenile rheumatoid arthritis (JRA), osteoporosis, osteoarthritis, pancreatitis, fibrosis, encephalitis, psoriasis, Giant cell arteritis, ankylosing spondolytis, autoimmune hepatitis, human immunodeficiency virus (HIV), inflammatory skin conditions, transplant, cancer, allergies, endocrine diseases, wound repair, other autoimmune disorders, airway

hyperresponsiveness and cell, virus, or prion-mediated infections or disorders.

Described is a method of treating or preventing a ST2L-mediated condition comprising administering a therapeutically effective amount of an isolated human or human-adapted antibody antagonist that specifically binds Domain I (SEQ ID NO: 9) of human ST2L, blocks IL-33/ST2L interaction, competes for binding to human ST2L (SEQ ID NO: 1) with an isolated antibody comprising a heavy chain variable region (VH) of SEQ ID NO: 47 and a light chain variable region (VL) of SEQ ID NO: 51 and/or binds human ST2L at amino acid residues 35-48 of SEQ ID NO: 1 (RCPRQGKPSYTVDW; SEQ ID NO: 210) to a patient in need thereof for a time sufficient to treat or prevent the ST2L-mediated condition.

Described is a method of inhibiting mast cell response in a patient comprising administering a therapeutically effective amount of an isolated human or human-adapted antibody antagonist that specifically binds Domain I (SEQ ID NO: 9) of human ST2L, blocks IL-33/ST2L interaction, competes for binding to human ST2L (SEQ ID NO: 1) with an isolated antibody comprising a heavy chain variable region (VH) of SEQ ID NO: 47 and a light chain variable region (VL) of SEQ ID NO: 51 and/or binds human ST2L at amino acid residues 35-48 of SEQ ID NO: 1 (RCPRQGKPSYTVDW; SEQ ID NO: 210) to a patient in need thereof for a time sufficient to inhibit the mast cell response.

Described is a method of inhibiting interaction of IL-33 and ST2L in a

subject, comprising administering to the subject an isolated human or human-adapted antibody antagonist that specifically binds Domain I (SEQ ID NO: 9) of human ST2L, blocks IL-33/ST2L interaction, competes for binding to human ST2L (SEQ ID NO: 1) with an isolated antibody comprising a heavy chain variable region (VH) of SEQ ID NO: 47 and a light chain variable region (VL) of SEQ ID NO: 51 and/or binds human ST2L at amino acid residues 35-48 of SEQ ID NO: 1 (RCPRQGKPSYTVDW; SEQ ID NO: 210) in an amount sufficient to inhibit the interaction of IL-33 and ST2L.

In another embodiment, the ST2L-mediated condition is asthma, airway hyper-reactivity, sarcoidosis, chronic obstructive pulmonary disease (COPD), idiopathic pulmonary fibrosis (IPF), cystic fibrosis, inflammatory bowel disease, (IBD), eosinophilic esophagitis, scleroderma, atopic dermatitis, allergic rhinitis, bullous pemphigoid, chronic urticaria, diabetic nephropathy, rheumatoid arthritis, interstitial cystitis or Graft Versus Host Disease (GVHD).

In another embodiment, the ST2L-mediated condition is associated with inflammatory cell recruitment in lung, goblet cell hyperplasia, or increased mucous secretion.

In another embodiment, the ST2L-mediated condition is associated with mast cell response.

In another embodiment, the inhibiting mast cell response comprises inhibiting the level of GM-CSF, IL-5, IL-8, IL-10 or IL-13 released by human cord blood-

derived mast cells by at least 50% with 50 µg/ml antibody.

In another embodiment, the antibody antagonist administered to a patient in need thereof is a bispecific antibody that specifically binds Domain I (SEQ ID NO: 9) of human ST2L, blocks IL-33/ST2L interaction, competes for binding to human ST2L (SEQ ID NO: 1) with an isolated antibody comprising a heavy chain variable region (VH) of SEQ ID NO: 47 and a light chain variable region (VL) of SEQ ID NO: 51 and/or binds human ST2L at amino acid residues 35-48 of SEQ ID NO: 1 (RCPRQGKPSYTVDW; SEQ ID NO: 210), and further binds TSLP, IL-25, TSLPR, IL-17RA or IL-17RB.

Administration/Pharmaceutical Compositions

The "therapeutically effective amount" of the anti-ST2L antibodies effective in the treatment of conditions where modulation of ST2L biological activity is desirable can be determined by standard research techniques. For example, the dosage of the anti-ST2L antibody that will be effective in the treatment of an inflammatory condition such as asthma or rheumatoid arthritis can be determined by administering the anti-ST2L antibody to relevant animal models, such as the models described herein.

In addition, *in vitro* assays can optionally be employed to help identify optimal dosage ranges. Selection of a particular effective dose can be determined (*e.g.*, via clinical trials) by those skilled in the art based upon the consideration of several factors. Such factors include the disease to be treated or prevented, the symptoms involved, the patient's body mass, the patient's immune status and other factors known by the skilled artisan. The precise dose to be employed in the formulation will also depend on the

route of administration, and the severity of disease, and should be decided according to the judgment of the practitioner and each patient's circumstances. Effective doses can be extrapolated from dose-response curves derived from *in vitro* or animal model test systems.

The mode of administration for therapeutic use of the antibody of the invention may be any suitable route that delivers the agent to the host. Pharmaceutical compositions of these antibodies are particularly useful for parenteral administration, e.g., intradermal, intramuscular, intraperitoneal, intravenous, subcutaneous, or intranasal.

The antibody of the invention may be prepared as pharmaceutical compositions containing an effective amount of the agent as an active ingredient in a pharmaceutically acceptable carrier. The term "carrier" refers to a diluent, adjuvant, excipient, or vehicle with which the active compound is administered. Such pharmaceutical vehicles can be liquids, such as water and oils, including those of petroleum, animal, vegetable or synthetic origin, such as peanut oil, soybean oil, mineral oil, sesame oil and the like. For example, 0.4% saline and 0.3% glycine can be used. These solutions are sterile and generally free of particulate matter. They may be sterilized by conventional, well-known sterilization techniques (*e.g.*, filtration). The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, stabilizing, thickening, lubricating and coloring agents, etc. The concentration of the antibody of the invention in such pharmaceutical formulation can vary widely, *i.e.*, from

less than about 0.5%, usually at or at least about 1% to as much as 15 or 20% by weight and will be selected primarily based on required dose, fluid volumes, viscosities, etc., according to the particular mode of administration selected.

Thus, a pharmaceutical composition of the invention for intramuscular injection could be prepared to contain 1 ml sterile buffered water, and between about 1 ng to about 100 mg, *e.g.* about 50 ng to about 30 mg or more preferably, about 5 mg to about 25 mg, of an anti-ST2L antibody of the invention. Similarly, a pharmaceutical composition of the invention for intravenous infusion could be made up to contain about 250 ml of sterile Ringer's solution, and about 1 mg to about 30 mg and preferably 5 mg to about 25 mg of an antagonist of the invention. Actual methods for preparing parenterally administrable compositions are well known and are described in more detail in, for example, "Remington's Pharmaceutical Science", 15th ed., Mack Publishing Company, Easton, PA.

The antibodies of the invention can be lyophilized for storage and reconstituted in a suitable carrier prior to use. This technique has been shown to be effective with conventional immunoglobulins and protein preparations and art-known lyophilization and reconstitution techniques can be employed.

The present invention will now be described with reference to the following specific, non-limiting examples.

MATERIALS AND METHODS (general)

Human and Cynomolgus (*Macaca fascicularis, cyno*) receptor-ligand binding inhibition assay (RLB assay)

96-well plate was coated with 50 µl of 4 µg/ml human ST2L-ECD (amino acids 19-328 of SEQ ID NO: 1) or 2µg/ml cyno ST2L-ECD (amino acids 19-321 of SEQ ID NO: 2) having C-terminal His_6 tag in bicarbonate buffer at 4°C for 16 hrs. All subsequent steps were performed at room temperature. Plate was blocked with 200 µl blocking buffer, and was washed 3 times with 300 µl of wash buffer containing PBS+0.05% Tween. 30 µl of various dilutions of anti-ST2L mAbs were added to the wells and incubated for 1 hour. For human receptor-ligand binding assay 20 µl of biotinylated human IL-33 (residues 112-270 of SEQ ID NO: 3) was added at 100 ng/ml final concentration and incubated for 30 minutes. For cyno receptor-ligand binding assay 20 µl of biotinylated cyno IL-33(residues 112-269 of SEQ ID NO: 4) was added at 200 ng/ml final concentration and incubated for 30 minutes. The plate was washed 3 times with 300 µl of wash buffer. 50 µl of 0.2 µg/ml Streptavidin-HRP (Jackson Immunoresearch) was added and incubated for 30 min. The plate was washed 3 times with 300 µl of wash buffer containing PBS+0.05% Tween. 50 µl of TMB substrate (EMD Biosciences) was added to each well. Reaction was stopped by the addition of 100 µl of 0.2N Sulfuric Acid. OD450 were measured using Envision plate reader (Perkin Elmer).

Generation of chimeric ST2L constructs

Various construct featuring human and mouse ST2L Domain I, II and III swaps were designed and generated using standard molecular biology techniques. The constructs are listed in Table 1. Amino acid numbering corresponds to human ST2L (hST2L)(SEQ ID NO: 1; NP_057316) and mouse ST2L (mST2L)(SEQ ID NO: 5; NP_001020773) proteins.

Table 1.

	Origin of amino acid residues for each Domain in chimeric constructs		
Construct Name	Domain I	Domain II	Domain III
HHM-ST2L	hST2L aa. 19-122	hST2L aa. 123-202	mST2L aa. 209-324
MHM-ST2L	mST2L aa. 28-128	hST2L aa. 123-202	mST2L aa. 209-324
HMH-ST2L	hST2L aa. 19-122	mST2L aa. 129-208	hST2L aa. 203-321
HH-ST2L	hST2L aa.19-122	hST2L aa. 123-205	N/A

hST2L: human ST2L SEQ ID NO: 1

mST2L: mouse ST2L SEQ ID NO: 5

Domain binding determination assay.

Antibody binding to ST2L domain I, II and III was determined using standard capture ELISA assay using electrochemiluminescent detection format (Meso-Scale Discovery (MSD) technology). 10 µg/mL of each antibody was coated onto each well of an MSD HighBind plate (5 µL/well) for 2 hr at room temperature. The plate was blocked with 150 µL of 5% MSD Blocking buffer for 2 hr at room temperature, and washed 3 times with HEPES wash buffer, followed by the addition of 25 µL of sulfo tag labeled huST2L-ECD or mouse ST2L-ECD (amino acids 28-326 of SEQ ID NO: 5) or HHM-ST2L (SEQ ID NO:6) or HMH-ST2L (SEQ ID NO: 8) chimeras or HH-ST2L (residues 19-205 of SEQ ID NO: 1) to the plate in increasing concentrations from 5 nM to 40 nM. The plate was covered with aluminum foil and incubated for 1 hr at room temperature

with gentle shaking. The plate was then washed 3 times with HEPES wash buffer. MSD read buffer (150 µl) was added to each well, and the plate was then read using an MSD Sector Imager 6000.

Those antibodies bound by human ST2L-ECD, HHM-ST2L and HMH-ST2L, but not by mouse ST2L-ECD recognize Domain I of human ST2L-ECD. Antibodies bound by human ST2L-ECD and HMH-ST2L, but not HHM-ST2L and mouse ST2L-ECD, recognize Domain III of human ST2L-ECD. Antibodies bound by human and mouse ST2L-ECD but not HH-ST2L recognize Domain III of human and mouse ST2L-ECD.

Affinity measurements of anti-ST2L mAbs.

Anti-ST2L mAbs, huST2L-ECD and cynoST2L-ECD were expressed using standard methods. Goat anti-human IgG Fcγ fragment-specific Ab (cat# 109-005-098) was obtained from Jackson ImmunoResearch laboratories (West Grove, PA). GLC sensor chips (Bio-Rad cat# 176-5011), CM-5 sensor chips (GE Healthcare cat# BR100014) and reagents for preparation of the capture surface were obtained from Biacore (GE healthcare, Piscataway, NJ) or from Bio-Rad Life Sciences (Bio-Rad, Hercules, CA).

The interactions of anti-ST2L antibodies with His_6-tagged human ST2L-ECD and His_6-tagged cyno ST2L-ECD were studied by ProteOn using a ProteOn XPR36 at 25°C. A biosensor surface was prepared by coupling goat anti-human IgG Fcγ fragment specific antibody (Ab) to the surface of a GLC sensor chip using the manufacturer instructions for amine-coupling chemistry. The coupling buffer was 10 mM sodium acetate, pH 4.5. The goat anti-human IgG Fcγ (about 4500 response units) was immobilized in the horizontal

orientation. The anti-ST2L antibodies were provided purified, or in crude supernatants. In either case these antibodies were diluted in PRB (PBS pH 7.4, supplemented with, 3 mM EDTA, and 0.005% Tween 20) to a concentration of about 0.5 µg/mL. The antibodies were captured (60-130 RU) in the vertical orientation onto the anti-human Fcγ antibody-modified GLC chip. Capture of anti-ST2L mAbs was followed by injection of huST2L ECD in solution (0.024 to 15 nM in 5-fold dilutions) or cynoST2L ECD in solution (0.020 - 5 nM in 4-fold dilutions) in the horizontal orientation. The association was monitored for 4 minutes in all experiments (200 µL injected at 50 µL/min). The dissociation was monitored for 30 minutes. Regeneration of the sensor surface was obtained with three 15 sec pulses of 10 mM glycine pH 1.5. The data were fit using the ProteOn software and using a 1:1 binding model with mass transfer.

Biacore experiments were performed using a Biacore 2000 or a Biacore 3000 optical biosensor (Biacore AB). All experiments were run in BRB (PBS pH 7.4, supplemented with 3 mM EDTA and 0.005% Tween 20) with or without 0.1% BSA at 25°C.

A Biacore biosensor surface was prepared by coupling goat anti-human IgG Fcγ fragment specific Ab to the carboxymethylated dextran surface of a CM-5 chip using manufacturer instructions for amine-coupling chemistry. The coupling buffer was 10 mM sodium acetate, pH 4.5. An average of 6000 response units (RU) of Ab were immobilized in each of four flow cells. The anti-ST2L mAbs were captured (about 33 RU) onto the anti-human Fcγ antibody-modified sensor chip surface. Capture of anti-ST2L mAbs was followed by injection of huST2L ECD in solution (0.2 to 15 nM in 3-fold dilutions) or cynoST2L ECD in solution (0.2 to 15 nM or 0.020 - 5 nM, in 3-fold dilutions). The association was monitored for 4

minutes or 8 minutes (200 µL injected at 50 µl/min or 20 µL/min for C2521 and C2519). The dissociation was monitored for 10 minutes, or up to 2.5 hours. Regeneration of the sensor surface was obtained with injection of 50 mM NaOH and/or injection of 100 mM H_3PO_4.

Data were processed using the Scrubber software, version 1.1g (BioLogic Software). Double reference subtraction of the data was performed by subtracting the curves generated by buffer injection from the reference-subtracted curves for analyte injections to correct for buffer contribution to the signal and instrument noise (Myszka, Journal of Mol Recogn 12:279-84, 1999).

After data processing, the data generated for kinetic and affinity determination were analyzed using the Scrubber software or the BIAevaluation software, version 4.0.1 (Biacore, AB). The kinetic data were analyzed using a simple 1:1 binding model including a term for mass transfer.

Affinity measurement of anti-mouse ST2L mAb (C1999/CNTO3914) to murine ST2L ECD.

Anti-ST2L mAb (C1999/CNTO3914) and murine ST2L extracellular domain (muST2L-ECD) were expressed and purified using standard methods. Anti-murine IgG Fcγ fragment-specific Ab was obtained from Jackson ImmunoResearch laboratories (West Grove, PA). Sensor chips and reagents for preparation of the capture surface were obtained from Biacore (GE healthcare, Piscataway, NJ). The experimental Biacore running buffer (BRB) contained PBS pH 7.4 with 0.005% Tween 20 and 0.1 mg/mL BSA and data were collected at 25°C.

The interaction of anti-ST2L antibody with muST2L-ECD was studied on a Biacore2000 at 25°C. A biosensor surface was prepared by coupling anti-mouse-Fc specific antibody to the surface of a CM4 sensor chip using the manufacturer instructions for amine-coupling chemistry. C1999/CNTO3914

and muST2L-ECD were diluted in BRB. C1999 was captured using the anti-mouse Fcγ antibody (about 85 RU). Capture was followed by injection muST2L ECD (residues 28-326 of SEQ ID NO: 5) in solution (starting at 15 nM, 5 concentrations, in a 3-fold serial dilution). The association was monitored for 8 minutes. The dissociation was monitored for up 6000 seconds. The regenerations were performed using a 1/100 dilution of phosphoric acid. The data were fit using a 1:1 binding model.

Human Basophil cell line assay (basophil cytokine release assay)

KU812 cells (human basophil cell line; ATCC, CRL-2099) were plated in sterile 96-well U-bottom tissue culture plates at 25,000 or 50,000 cells per well in a total 40 µl of RPMI 1640 growth medium (Invitrogen) supplemented with 10% FBS and penicillin/ streptomycin. Anti-human ST2L mAbs and controls were added at various concentrations (50 µl/well) and incubated at 37°C. After 1 hour of incubation, recombinant "mature" IL-33 (amino acids 111-270 of SEQ ID NO: 3) was added at a final concentration of 10 ng/ml in 10 µl of RPMI growth medium. The cells were then incubated at 37°C for 18-24 hours to allow for IL-33-mediated induction of IL-5 and IL-6. Following incubation, the cells were harvested and the cell supernatant was collected for subsequent detection of IL-33-induced IL-5 and IL-6 using either ELISA (R&D systems) or bead-based multiplex analyses (Millipore).

Human Mast cell cytokine release assay and PGD_2 release assay

Mast cells were derived from $CD34^+$ human cord blood cells (Lonza). Frozen vials of >1.0 $x10^6$ $CD34^+$ cord blood cells were rapidly thawed and transferred to a 50

ml conical tube. Drops of warmed or room temp Stem-Pro 34 media + supplements (25mls total; Invitrogen) were slowly added to the cells. The cells were centrifuged at 1,000rpm for 15 minutes and resuspended in media (10mls of StemPro-34, with the following supplements: 30 ng/ml IL-3, 100 ng/ml IL-6, and 100 ng/ml SCF. Cells were plated in 2 wells of a 6-well plate, and cultured for 1 week. On day 4, cells were expanded 1:3 in supplemented Stem Pro-34 media. On day 7, non-adherent cells were removed and plated at $0.5x10^6$/ml in StemPro-34 media containing 10 ng/ml IL-6 and 100 ng/ml SCF. Cells were expanded weekly to maintain cell density at $0.5x10^6$/ml until mast cells were mature at 6-10 weeks (assessed by expression of FcεR1, cKit, and tryptase).

Mature mast cells were cultured at 0.5 x 10^6/ml in StemPro-34 and stimulated daily for 4 days in IL-4 (10ng/ml; Peprotech), IL-6 (10ng/ml; R&D Systems) and SCF (100ng/ml; Invitrogen). Prior to assay, cells were harvested, centrifuged at 1,000 RPM for 10min and resuspended in fresh StemPro-34 media or RPMI containing 10% FCS without antibiotics, with 100ng/ml human recombinant SCF. Cells were plated at a density of 65,000 to 75,000 cells/ 0.16 mls/well in a flat bottom, tissue culture-treated 96-well plate. The anti-ST2L mAbs were added to the plate for a final concentration of 50, 10, 2, 0.4, 0.08, 0.016, 0.0032 µg/ml for 30 minutes prior to the addition of IL-33. Recombinant human "mature" IL-33 (residues 111-270 of SEQ ID NO: 3) was also prepared at 10X (10 or 30 ng/ml) in media + 100ng/ml SCF. 20µl of the 10X IL-33 was

added to the wells, for a final concentration of 1 (Figures 6 and 7A-7E) or 3 ng/ml (Figure 8A-8E), and the plates were incubated overnight at 37°C, 5% CO_2. Culture supernatant was harvested 18-24 hours after stimulation. The plates were centrifuged at 1,000 RPM for 10 minutes. The supernatant was removed and placed into a U bottom 96 well plate and stored at -20°C prior to assaying. Human cytokine kits from Millipore were used to analyze cytokine levels using Luminex™ technology. Levels of PGD2 were measured using the Prostaglandin D2-MOX EIA kit from Cayman Chemical Company, according to manufacturer's instructions. In order to enhance the sensitivity of the ELISA, PGD_2 in the mast cell culture supernatants were converted into non-degradable MOX-PGD_2 (methoxylsamine-PGD_2) by treatment with methoxylsamine hydrochloride (MOX-HCl).

Mouse receptor-ligand binding inhibition assay (mouse RLB assay)

A 96-well clear plate (VWR) was coated with 50 µl of 2 µg/ml goat anti-human IgG, Fcγ fragment-specific (Jackson Immunoresearch) antibody for approximately 16 hours at 4°C. The remaining steps were completed at room temperature. Wells were incubated with blocking buffer, washed and 50 µl of 2 µg/ml mouse ST2L-ECD fused to human Fc was added for 1 hour. The plate was washed and 1 µg/ml of biotinylated mIL-33 with or without anti-mST2L antibodies added. The plate was washed and detection done with streptavidin-HRP (Jackson Immune Research) and signal developed with TMB substrate (RDI Division of Fitzgerald Industries) following manufacturer's instructions.

Mouse and Human reporter gene assays (human or mouse RGA assay)

HEK293 cells were plated at 50,000 cells per well in white clear-bottom tissue culture-treated 96-well plates (NUNC) in DMEM, 10%FBS and incubated in humidified incubator at 37°C, 5% CO_2 for 24 hours. Cells were co-transfected with vectors encoding either human or mouse ST2L-ECD cDNA, NF-κB-Luciferase vector (Stratagene, Agilent Technologies, Santa Clara, CA) using Lipofectamine™ 2000 in Opti-MEM media (Invitrogen) using standard protocols. After 24 hour incubation at 37°C, 5% CO_2, the transfected ells were treated with mouse (R&D Systems, residues 109-266 of SEQ ID NO: 5) or human IL-33 (residues 112-270 or SEQ ID NO: 3) with or without anti-ST2L antibodies for 16 hours at 37°C, 5% CO_2. Luciferase activity was measured using Steady-Glo® reagent (Promega) according to the manufacturer's instructions.

Mouse T-cell proliferation assay

Mouse Th2 cells (D10.G4.1, ATCC) were cultured in complete growth medium: RPMI 1640 medium with 2 mM L-glutamine adjusted to contain 1.5 g/L sodium bicarbonate, 4.5 g/L glucose, 10 mM HEPES, and 1.0 mM sodium pyruvate, and supplemented with: 0.05 mM 2-mercaptoethanol, 10 pg/ml IL-1α, (R&D Systems), 10% fetal bovine serum, 10% rat T-STIM factor with Con A (rat IL-2 culture supplement available from Becton Dickinson). The cells were washed twice with assay media (RPMI, 10%FBS, no IL-1, no T-STIM), resuspended at $1.25x10^5$ cells per ml and plated in 80 µl of medium in white clear bottom tissue culture treated 96-well plates (NUNC, Rochester, NY). Various amounts of mouse IL-33 (residues 109-266 of SEQ ID NO: 5) were added to the cells for the final assay volume of 100 µl. When testing antibody neutralization, control antibodies (spiked in spent hybridoma

medium) or hybridoma supernatants were added to the cells and incubated for 1 hour followed by addition of 20 pg/ml mIL-33. The plates were cultured for 24 hours in humidified incubator at 37C, 5% CO_2. Quantitation of viable cells was achieved with CellTiter-Glo® reagents (Promega, Madison, WI); protocol performed according to the manufacturer's instructions.

Mouse bone marrow derived mast cell assay

Mouse mast cells were derived from bone marrow of Balb/c mice (6 weeks). Cells were plated at 300,000 cells/well in RPMI media (endotoxin free), 10% FBS, 10% WEHI cell line-conditioned medium, 10ng/ml IL-3 (Peprotech), 0.1mM essential amino acids, 1% Penicillin/Streptomycin (Invitrogen). Anti-ST2L mAbs (100, 10, 1, 0.1, or 0.01 µg/ml) were incubated with the cells for 1 hour prior to addition of recombinant mouse "mature" IL-33 (residues 109-266 of SEQ ID NO: 215 (10 ng/ml; R&D Systems). After approximately 24h the supernatants were harvested and frozen until analysis using the Millipore Mouse 22-plex kit for Luminex™, according to manufacturer's instructions.

Cyno endothelial cell assay

Cynomolgus Aortic Endothelial cells cultured in EGM®-2 Endothelial Cell Growth Medium-2 (Lonza) were plated in 96-well tissue culture plates at 10,000 or 20,000 cells per well. 50 µl of anti-ST2L antibodies were added to the cells starting at 100 µg/ml with subsequent 4- or 5-fold dilutions and incubated at 37°C for 1 hour before the addition of recombinant cyno 'mature' IL-33 (SEQ ID NO: 4). Fifty microliters of 20 ng/ml cynomolgus IL-33 was then added to the cells and

incubated at 37°C for 24 hours. To evaluate IL-33-induced cytokine responses the supernatants were harvested and the cytokine levels were assessed by a Non-Human Primate IL-8 kit for Luminex™ (Millipore) according to manufacturer's instructions.

Mouse peritoneal lavage assay

The peritoneums of 6 Balb/c mice was washed with a total of 3 ml PBS to collect peritoneal cells. The majority of these cells were found to be lymphocytes and macrophages, as determined by B220 and F4/80 expression (FACS analysis). Approximately 1% were cKit$^+$ (CD117$^+$) mast cells. Cells were centrifuged and the pellet was resuspended to 1x10^6 cells/ml in Alpha MEM media+ 10% FBS + 100 U/ml Penicillin + 100 µg/ml Streptomycin (Invitrogen). Cells were plated at 200 µl per well in a 96-well plate and rested 2h at 37°C. Anti-ST2L mabs were added to the cells for 30 minutes prior to the addition of 10 ng/ml mouse "mature" IL-33 (R&D Systems; residues 109-266 of SEQ ID NO: 215). Supernatants were collected 24h after IL-33 addition, stored at -20°C until analysis, and analyzed using the Millipore Mouse 22-plex kit for Luminex™ according to manufacturer's instructions.

Example 1. Generation of rat anti-mouse ST2L antibodies

Rats were immunized intraperitoneally with mouse ST2-Fc (R&D Systems (Ser27-Ser342 of SEQ ID NO: 5) and assessed for specific IgG titers. Once sufficient titers were obtained, splenocytes were isolated and fused with FO cells. The resulting hybridomas were plated in 96 well plates or methylcellulose and cultured for 10 days. Antigen specific clones were identified by standard capture ELISA for binding to

mST2-Fc and cross screened against the Fc protein alone. Murine ST2-specific hybridomas were further tested for the inhibition of IL-33 binding to ST2 in an ELISA and for the inhibition of IL-33-induced D10.G4.1 mouse Th2 cell proliferation. Hybridomas exhibiting neutralization in both receptor-ligand binding and cell-based proliferation assays were clonally selected by limiting dilution. Hybridoma V-regions were sequenced and cloned into mouse IgG1 background. ST2L-ECD domain specificity was addressed by standard immunosorbent assay with electrochemiluminescent detection using various human-mouse domain-swap constructs.

Antibody secreted by hybridoma C1999 was cloned into mouse IgG1 background and named CNTO3914. Sequences of CNTO3914 variable regions and CDRs are shown in Table 2. CNTO3914 does not cross-react with human ST2L and binds Domain I of mouse ST2L-ECD.

Table 2.

mAb Name	HCDR1		HCDR2		HCDR3	
	Sequence	SEQ ID NO:	Sequence	SEQ ID NO:	Sequence	SEQ ID NO:
C1999/ CNTO3914	HYGMA	13	SIITDGTSTYYRDSVKG	14	QSDDYFDY	15

mAb Name	LCDR1		LCDR2		LCDR3	
	Sequence	SEQ ID NO:	Sequence	SEQ ID NO:	Sequence	SEQ ID NO:
C1999/ CNTO3914	KSSQSLEYSDGDSYLE	16	GVSNRFS	17	FQATHDPFT	18

mAb Name	VH sequence	SEQ ID NO:
C1999/ CNTO3914	EVQLVESGGGLLQPGRSLKLSCTASGFIFSHYGMAWVRQAPTKGLEWV SSIITDGTSTYYRDSVKGRFTISRDNAKNTQYLQMDSLRSEDTATYYCAR QSDDYFDYWGQGVMVTVSS	19
	VL sequence	SEQ ID NO:
	DVVLTQTPVSLSVTLGDQASISCKSSQSLEYSDGDSYLEWYLQKPGQSP QLLIYGVSNRFSGVPDRFIGSGSGTDFTLKISRVEPEDLGVYYCFQATHDP FTFGSGTKLEIK	20

Example 2. Generation of mouse anti-human ST2L antibodies

Two different immunizations were performed for generation of mouse anti-human ST2 mAbs.

BALB/c were immunized intraperitoneally with soluble ST2-Fc (R&D Systems, SEQ ID NO: 157) and assessed for specific IgG titers. Once sufficient titers were obtained, splenocytes were isolated and fused with FO cells. The resulting hybridomas were plated in 96 well plates and cultured for 10 days. Antigen specific clones were identified by standard capture ELISA for binding to C-terminal His_6-tagged huST2L-ECD and cross-reactivity to His_6-tagged cyno ST2L-ECD. Human ST2L-specific hybridomas cross-reacting with cyno ST2L were further tested for the inhibition of IL-33 binding to huST2L in an ELISA assay and

for the inhibition of NF-κB activation in reporter gene assay. Clones inhibiting in reporter gene assay or in both ELISA and reporter gene assay were selected for further studies.

Antibodies from hybridomas C2494, C2519A and C2521A were selected for further analyses. C2519A and C2521A bind human ST2L at Domain III, and C2494 binds human ST2L at Domain I. Antibody C2494 was cloned into human IgG2 background, and the full length antibody was named STLM62.

Anti-human ST2L mAbs were generated at Genovac Gmbh by proprietary DNA immunization technology using full length ST2L constructs and boosting with the cells transfected to express human ST2L-ECD. Hybridomas were screened for binding to human ST2L-ECD by flow cytometry. Clones that exhibited binding in this assay were confirmed to bind hST2L-ECD and further characterized for binding to cyno ST2L-ECD by standard capture ELISA. Select clones were characterized in receptor-ligand binding inhibition ELISA and reporter gene assay. Clones inhibiting in reporter gene assay or in both ELISA and reporter gene assay were selected for further studies.

Antibody from Genovac hybridoma C2244 was selected for further analyses and cloned into human IgG2 background. The full length antibody was named STLM15. STLM15 binds human ST2L at Domain I.

Sequences of the VH, VL and CDR domains of the mouse anti-human antibodies are shown in Table 3.

Table 3.

mAb Name	HCDR1		HCDR2		HCDR3	
	Sequence	SEQ ID NO:	Sequence	SEQ ID NO:	Sequence	SEQ ID NO:
C2519A	DYNMN	21	NINPYYGSTTYNQKFKG	25	EGDTYLAWFAY	29
C2521A	TYWMN	22	QIFPASGSTYYNEMFKD	26	SENIYYINFQYYFAY	30
C2244/ STLM15	SDYAWN	23	FISYSGDTSFNPSLKS	27	YDGYSFDY	31
C2494/ STLM62	DDYMH	24	RIDPAIGNTEYAPKFQD	28	GDFYAMDY	32

mAb Name	LCDR1		LCDR2		LCDR3	
	Sequence	SEQ ID NO:	Sequence	SEQ ID NO:	Sequence	SEQ ID NO:
C2519A	RSSQSIVYSNGNTYLE	33	KVSNRFS	37	FQGSHVPPT	41
C2521A	RASQNIGTRMH	34	YASESIS	38	QQSNTWPFT	42
C2244/ STLM15	RASKSVSTSGSSYMF	35	LASNLES	39	QHSREIPYT	43
C2494/ STLM62	ITNTDIDDVIH	36	EGNTLRP	40	LQSDNMLT	44

mAb	VH sequence	SEQ ID NO:
C2519A	EFQLQQSGPELVKPGASVKISCKASGYSFTDYNMNWVKQSHGKSLEWI GNINPYYGSTTYNQKFKGKATLTVDKSSNTAYMHLNSLTSEDSAVYYCA REGDTYLAWFAYWGQGTLVTVSA	45
C2521A	QIQLQQSGPELVRPGTSVKISCKASGYTFLTYWMNWVKQRPGQGLEWI GQIFPASGSTYYNEMFKDKATLTVDTSSSTAYMQLSSLTSEDTAVYFCAR SENIYYINFQYYFAYWGQGTTLTVSS	46
C2244/ STLM15	EVQLQESGPGLVKPSQSLSLTCTVTGFSITSDYAWNWIRQFPGSKLEW MGFISYSGDTSFNPSLKSRISVTRDTSKNQFFLQLNSVTTEDTATYYCASY DGYSFDYWGQGTTLTVSS	47
C2494/ STLM62	EVQLQQSVAELVRPGASVKLSCTASAFNIKDDYMHWVKQRPEQGLEW IGRIDPAIGNTEYAPKFQDKATMTADTSSNTAYLQLSSLTSEDTAVYYCA LGDFYAMDYWGQGTSVTVSS	48

mAb	VL sequence	SEQ ID NO:
C2519A	DVLMTQTPLSLPVSLGDQASISCRSSQSIVYSNGNTYLEWYLQKPGQSP KLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVP PTFGGGTKLEIK	49
C2521A	ILLTQSPAILSVSPGERVSFSCRASQNIGTRMHWYQQRTNGSPRLLIKYA SESISGIPSRFSGSGSGTDFTLTISSVESEDIADYYCQQSNTWPFTFGSGTK LEIK	50
C2244/ STLM15	DIVLTQSPASLAISLGQRATISCRASKSVSTSGSSYMFWYQQKPGQPPKL LIYLASNLESGVPARFSGSGSGTDFTLNIHPVEEEDAAAYYCQHSREIPYT FGGGTKLEIK	51
C2494/ STLM62	ETTVTQSPASLSVATGEKVTIRCITNTDIDDVIHWYQQKPGEPPKLLISEG NTLRPGVPSRFSSSGYGTDFVFTIENTLSEDVADYYCLQSDNMLTFGAGT KLELK	52

Example 3. Generation of fully human ST2L antibodies

Human ST2L-binding Fabs were selected from *de novo* pIX phage display libraries as described in Shi *et al.*, J Mol Biol 397:385-96, 2010; Int. Pat. Publ. No. WO2009/085462; U.S. Pat. Publ. No. US2010/0021477). Briefly, the libraries

were generated by diversifying human scaffolds where germline VH genes IGHV1-69*01, IGHV3-23*01, and IGHV5-51*01 were recombined with the human IGHJ-4 minigene *via* the H3 loop, and human germline VLkappa genes O12 (IGKV1-39*01), L6 (IGKV3-11*01), A27 (IGKV3-20*01), and B3 (IGKV4-1*01) were recombined with the IGKJ-1 minigene to assemble complete VH and VL domains. The positions in the heavy and light chain variable regions around H1, H2, L1, L2 and L3 loops corresponding to positions identified to be frequently in contact with protein and peptide antigens were chosen for diversification. Sequence diversity at selected positions was limited to residues occurring at each position in the IGHV or IGLV germline gene families of the respective IGHV or IGLV genes. Diversity at the H3 loop was generated by utilizing short to mid-sized synthetic loops of lengths 7-14 amino acids. The amino acid distribution at H3 was designed to mimic the observed variation of amino acids in human antibodies. Library design is detailed in Shi *et al.*, J Mol Biol 397:385-96, 2010. The scaffolds utilized to generate libraries were named according to their human VH and VL germline gene origin. The three heavy chain libraries were combined with the four germline light chains or germline light chain libraries to generate 24 unique VH:VL combinations for screening. All 24 VH:VL library combinations were utilized in phage panning experiments against huST2L-ECD-Fc.

The libraries were panned using a Fc fusion of the huST2L-ECD (residues 19-328 of SEQ ID NO: 1). Pannings were done in 2 different formats, antigen (Ag) in solution and Ag displayed. For Ag in solution the streptavidin-coated magnetic beads were blocked in PBS with 3% non-fat dry milk. The biotinylated (Bt) antigen huST2L-ECD human Fc fusion (Bt-huST2L-ECD-Fc) with a 10x higher concentration of human Fc protein as competitor was mixed with Fab-pIX phage libraries.

The Fab-pIX phage bound to the Bt-huST2L-ECD-Fc was captured on the blocked streptavidin (SA)-coated magnetic beads. Phage selections were performed for three rounds where the huST2L-ECD-Fc concentrations varied from 100nM, 10nM, 10nM from rounds 1 to 3, respectively. For Ag display the Bt-huST2L-ECD-Fc was coated on SA coated magnetic beads. Fab-pIX phage libraries plus 10x excess of human Fc protein was added simultaneously to the Bt-huST2L-ECD-Fc displayed SA-magnetic beads. Bt-Ag concentrations used were 100nM, 10nM, 10nM for rounds 1 to 3, respectively. Screening was done for both panning formats by ELISA for Fab binding to huST2L-ECD-Fc protein. A total of 79 Fabs with binding to hST2L-Fc were isolated from these selections. Fab HuT2SU-39 was determined by a ranking ELISA to have the best binding activity overall.

An ELISA based IL-33 binding inhibition assay was performed on the 79 Fabs. A total of 32 Fabs showed inhibition of IL-33 binding to huST2L-ECD-Fc. 46 Fabs were chosen for affinity maturation from the pIX *de novo* campaign.

Example 4. Affinity-maturation of fully human ST2L antibodies

Select antibodies were affinity-matured using an "in-line" maturation process described in Shi *et al.*, J Mol Biol 397:385-96, 2010 and WO09085462A1. In this technology, the VH regions of Fab clones obtained in the first selection are combined with libraries of the corresponding VL scaffold. All VH genes from the 46 Fabs identified in Example 3 were cloned into the appropriate VL maturation libraries as pools according to their original VL gene family. The used VL scaffold libraries and their diversification schemes are shown in Table 4. The human VL scaffolds are as follows: IGKV1-39*01 (O12), IGKV3-11 (L6), IGKV3-20 (A27), IGKV4-1*01 (B3) and are described for example in U.S. Pat. Publ. No.

US2012/0108795. For affinity maturation panning, the phage libraries were added to Bt-huST2-ECD-Fc first. After incubation the maturation library phage/Bt-hST2L-ECD-Fc complex was added to the SA-coated magnetic beads. The Bt-huST2-Fc concentrations varied respectively from R1 to R3 at 10nM, 1nM, and 0.1 nM. The final wash of round 3 was performed overnight at room temperature in the presence of 10nM unlabelled huST2L-ECD-Fc to further drive affinity improvement.

Table 4.

		VL library diversification scheme for different scaffolds			
Loop	Position (Kabat)	A27	B3	L6	O12
L1	30	SRNTD	RNDGHSY	SRNAD	SRNAD
	30a	SNR	RNDGHWY	-	
	30e		RNDGHSY	-	
	31	SNRADH	RNDGHWY	NSKD	SNKDG
	32	YFHQSEK	YNWR	YWDFHSAN	YHNDWFSAV
L2	50	ADGS	YWNK	ADKGYFTN	FYTNKADG
L3	91	YSHA	SYWH	RYSGF	SAYHPD
	92	YNDSHIFKG	SYGN	RHNSL	FIYHNDKGRE
	93	SNTDGHR	STER	NDKR	STHNDRG
	94	TYLVFAS	WYSH	WA	TYLVFSRGPI
	96	WYFLIR	YRWH	WYFLIR	LWRFYIN

A total of 161 sequence unique Fabs were obtained from the maturation pannings. Fabs showing highest binding to huST2L-ECD were converted to IgG for further characterization.

MAbs ST2M48, ST2M49, ST2M50 and ST2M51 were selected for further characterization, and their VH, VL and CDR sequences are shown in Table 5. Mabs ST2M48, ST2M49, ST2M50

and ST2M51 bind human ST2L at Domain III, and cross-react with mouse ST2L.

Table 5.

mAb ID	HC ID	HCDR1		HCDR2		HCDR3	
		Sequence	SEQ ID NO:	Sequence	SEQ ID NO:	Sequence	SEQ ID NO:
ST2M48	STLH125	TSYWIG	53	GIIYPGDSYTRYSPSFQG	55	LSGRFDY	57
ST2M49	STLH149	TSYWIG	53	GIIYPGDSYTRYSPSFQG	55	IGGMFDY	58
ST2M50	STLH125	TSYWIG	53	GIIYPGDSYTRYSPSFQG	55	LSGRFDY	57
ST2M51	STLH130	SSYAIS	54	GIIPIFGTANYAQKFQG	56	DTPQLDY	59

mAb ID	LC ID	LCDR1		LCDR2		LCDR3	
		Sequence	SEQ ID NO:	Sequence	SEQ ID NO:	Sequence	SEQ ID NO:
ST2M48	STLL232	RASQSVRDALA	60	FASNRAT	64	QQFNTWPIT	67
ST2M49	STLL216	RASQSVANALA	61	KASNRAT	65	QQYYGWPIT	68
ST2M50	STLL228	RASQSVSNALA	62	FASNRAT	64	QQFFNWPIT	69
ST2M51	TC1L3	RASQSISSYLN	63	YASSLQS	66	QQSYSTPLT	70

mAb Name	VH sequence	SEQ ID NO:
ST2M48	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWM GIIYPGDSYTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARLS GRFDYWGQGTLVTVSS	71
ST2M49	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWM GIIYPGDSYTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARIG GMFDYWGQGTLVTVSS	72
ST2M50	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEW MGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAR YNFFFDYWGQGTLVTVSS	71
ST2M51	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEW MGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAR DTPQLDYWGQGTLVTVSS	73

mAb Name	VL sequence	SEQ ID NO:
ST2M48	EIVLTQSPATLSLSPGERATLSCRASQSVRDALAWYQQKPGQAPRLLIYFA SNRATGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQFNTWPITFGQGT KVEIK	74
ST2M49	EIVLTQSPATLSLSPGERATLSCRASQSVANALAWYQQKPGQAPRLLIYKA SNRATGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQYYGWPITFGQGT KVEIK	75
ST2M50	EIVLTQSPATLSLSPGERATLSCRASQSVDDWLAWYQQKPGQAPRLLIYK ASNRATGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQYNRAPWTFGQ GTKVEIK	76
ST2M51	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYYA SSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPLTFGQGTK VEIK	77

Example 5. Characterization of anti-ST2L antibodies.

Antibodies derived from various campaigns as described above were further characterized for their ability to block IL-33/ST2L interaction, for their inhibition of IL-33-induced signaling as measured by NF-κB reporter gene assay, ability of the antibodies to inhibit mast cell responses, for their affinity against human and cyno ST2L, and cross-reactivity with mouse ST2L. Epitope mapping was done using human/mouse ST2L domain swap chimeric constructs as described in Materials and Methods. Results of the experiments are shown in Tables 6, 7 and 8. In Tables 7 and 8, "+" indicates that the antibody blocks IL-33/ST2L interaction, and "-" indicates it does not block IL-33/ST2L interaction. Experiments with CNTO3914 were done using mouse cells and reagents due to lack of cross-reactivity to human. Human cells and human reagents were used in assays for all other antibodies.

Characterized antibodies were grouped to those that block IL-33/ST2L interaction (mAbs STLM15, STLM62 and CNTO3914) and those that do not block the IL-33/ST2L interaction (mAbs C2519, C2521, ST2M48, ST2M49, ST2M50 and ST2M51). The antibodies blocking IL-33/ST2L interaction bind to ST2L Domain I, whereas the non-blocking antibodies bind to ST2L Domain III. The antibodies tested inhibited ST2L downstream signaling as assessed by the NF-κB reporter gene assay and IL-33-induced cytokine release by the KU812 human basophil cell line, or in case of CNTO3914, assessed by mouse Th2 cell proliferation. Antibodies binding to ST2L Domain I inhibited at higher level human mast cell responses as assessed by cytokine and chemokine secretion when compared to anti-ST2L antibodies binding ST2L Domain III. CNTO3914, which binds mouse ST2L domain I and does not cross-react with human was also able to inhibit IL-33-induced mouse mast cell responses.

Table 6.

mAb	corresponding hybridoma	Affinity to human ST2L			Affinity to cyno ST2L		
		k_{on} ($M^{-1}s^{-1}$)	k_{off} (s^{-1})	K_D (pM)	k_{on} ($M^{-1}s^{-1}$)	k_{off} (s^{-1})	KD (pM)
STLM15	C2244	1.02E+06	4.25E-05	42	4.81E+06	5.30E-05	11
STLM62	C2494	4.26E+06	1.19E-04	28	4.51E+07	5.39E-04	12
na	C2519	4.83E+05	8.70E-05	180	7.14E+04	3.20E-03	44800
na	C2521	6.18E+05	4.90E-05	79	4.47E+05	1.66E-03	3710
ST2M48	na	1.32E+06	7.33E-05	56	1.03E+07	2.65E-03	257
ST2M49	na	1.59E+06	1.61E-04	101	4.66E+07	1.24E-02	266
ST2M50	na	1.15E+06	5.10E-05	45	2.01E+07	2.49E-03	124
ST2M51	na	1.29E+06	4.87E-05	38	4.42E+07	3.36E-03	76

Table 7.

mAb	corresponding hybridoma	RLB*	RGA#	Basophil cytokine release	Mast cell cytokine release	ST2L epitope
STLM15	C2244	+	+	+	+	hD1
STLM62	C2494	+	+	+	+	hD1
	C2519	-	+	+	-	hD3
	C2521	-	+	+	-	hD3
ST2M48	NA	-	+	nt	-	h/mD3
ST2M49	NA	-	+	nt	-	h/mD3
ST2M50	NA	-	+	nt	-	h/mD3
ST2M51	NA	-	+	nt	-	h/mD3

*Receptor-Ligand binding inhibition

#Reporter gene assay

hD1 = human ST2L D1 domain

mD1 = mouse ST2L D1 domain

hD3 - human ST2L D3 domain

h/mD3 = human and mouse ST2L D1 and D3 domains

nt= not tested

Table 8.

mAb	corresponding hybridoma	RLB*	RGA#	T-cell proliferation	Peritoniel cells lavage	Mast cell cytokine release**	ST2L epitope
CNTO3914	C1999	+	+	+	+	+	mD1

*Receptor-Ligand binding inhibition

#Reporter gene assay

**Bone marrow derived

Example 7. ST2L domain I binding antibody CNTO3914 inhibits intranasal IL-33-induced airway hyper-responsiveness (AHR), airway inflammation and mouse mast cell responses.

Four consecutive daily intranasal doses of 2 µg/mouse "mature" IL-33 (R&D Systems) (residues 109-266 of SEQ ID NO:215) were administered to female BALB/c mice. Anti-mouse ST2L antibody CNTO3914 was prophylactically dosed subcutaneously at 20 mg/kg (or 2 mg/kg or 0.2 mg/kg) 24 h prior to the first IL-33 intranasal administration. Control mice received isotype control CNTO5516 or PBS, 24 h prior to the first IL-33 intranasal administration. Airway hyper-responsiveness (AHR) to increasing doses of methacholine was measured using forced maneuvers with Flexivent system (Scireq, Montreal, Quebec, Canada). For measurement of airway hyper-responsiveness (AHR), mice were anesthetized with 100 mg/kg pentobarbital and 13 mg/kg phenytoin and tracheostomized before connecting to FlexiVent. The mice were nebulized with saline for baseline readings and then with two doses (10 and 20 mg/mL) of methacholine. For saline and each dose of methacholine, Resistance (R) values were collected for approximately 2 minutes using the "snapshot" perturbation. The peak resistance was calculated using only

those values with a COD (coefficient of determination) above 0.9.

A separate group of mice was treated and analyzed for cellular response in the lungs. Twenty-four hours following the last mIL-33 isotype or PBS administration, mice were sacrificed by overdose of Sleepaway® I.P. Lungs of the mice were lavaged with 0.7 mls of cold PBS with 0.1% BSA. Resulting bronchioalveolar (BAL) fluids were centrifuged at 1200rpm for 10 minutes and the cell-free supernatants were saved at -80°C until analysis of cytokine/chemokines. The BAL samples were used for total counts using a hemacytometer. For differential BAL counts ~200 cells were counted from cytospin smears after staining with wright giemsa under light microscope.

The cell-free supernatants were collected and stored at -80°C until used for Luminex protein analyses. The lung tissues were removed, and then perfused through the right ventricle using 5mls of cold sterile PBS until adequate perfusion. The lung lobes were then placed in a Fast Prep® tube containing 1ml of PBS + protease inhibitor and frozen and stored at -80°C for cytokine/chemokine profiling. The cytokine/chemokine multiplex assay was performed following the manufacturer's protocol for the Murine Millipore 22-plex. Mouse mast cell protease-1 (mMCP-1) in the BAL fluid was analyzed by ELISA (Moredun Scientific).

Airway hyper-responsiveness

CNTO3914 significantly inhibited airway hyper-responsiveness in the model of lung inflammation induced by intranasally administered IL-33 (Figure 1). CNTO3914 was dosed subcutaneously 24 hr prior to four daily consecutive intranasal administrations of 2 µg/mouse mIL-33. Peak Airway Resistance as determined by Flexivent was significantly decreased with a dose of CNTO3914 at 20mg/kg. Each bar

represents the mean ± SEM of three (CNTO5516, an isotype control antibody) to six mice per group. The results have been repeated in two separate studies. Significance was determined using the Two-Way ANOVA with a Bonferroni post test, CNTO3914/IL-33 **p<0.05 vs. CNTO5516/IL-33; and ***p<0.001, vs. PBS with IL-33 treatment group.

Airway inflammation

CNTO3914 significantly inhibited Bronchoalveolar Lavage (BAL) cell recruitment in the used model (Figure 2). CNTO3914 was dosed subcutaneously 24 hr prior to four daily consecutive intranasal administrations of 2 mg/mouse mIL-33. BAL leukocytes were significantly increased with IL-33 administration and were significantly inhibited by CNTO3914 at 20mg/kg. Each bar represents the mean ± SEM of three (CNTO5516, an isotype control antibody) to six mice per group. The results have been repeated in two separate studies. Significance was determined using the Two-Way ANOVA with a Bonferroni post test, ***p<0.001.

Mast cell responses *in vivo*

Mast cells store proteases including tryptases and chymases in their granules, which are released quickly upon mast cell activation. Mouse Mast Cell Protease 1 (mMCP-1) is a β chymase released by activated mast cells and known to be important for control of parasitic worm infections (Knight *et al.*, J Exp Med 192:1849-56, 2000; Huntley *et al.*, Parasite Immunol 12:85-95, 1990). Measurement of mMCP-1 can be used as a marker of mast cell activation, and has been shown to be induced in a mast cell-dependent model of airway inflammation: house dust mite (Yu and Chen, J Immunol 171:3808-15, 2003). MMCP-1 as determined by ELISA (Moredun Scientific) was significantly increased in BAL fluid from IL-33 administered mice, and was dose-dependently inhibited by

CNTO3914 (Figure 3). Significance was determined using the One-Way ANOVA with a Tukey post test, **p<0.01, ***p<0.001, vs. IL-33 treatment.

Example 8. Anti-ST2L Domain I binding antibodies inhibit mast cell responses *in vitro*

Mast cell responses were assessed by release of chemokines and cytokines by mouse and human mast cells as well as prostaglandin D_2 in human mast cells.

Anti-ST2L Domain I binding antibody CNTO3914 inhibited IL-33-induced cytokine release including GM-CSF (Figure 4A), IL-5 (Figure 4B), and TNFα (Figure 4C) by mouse bone marrow-derived mast cells.

Anti-human ST2L Domain I binding mab C2494 (STLM62) inhibited IL-33-induced PGD_2 release by human cord blood-derived mast cells induced by 3 ng/ml IL-33 at antibody concentrations 2, 10 and 50 µg/ml (Figure 5).

Anti-ST2L Domain I binding antibodies C2494 and C2244 inhibited IL-33-induced GM-CSF, IL-5, IL-8, IL-13 and IL-10 release by human cord blood-derived mast cells at antibody concentrations 50 µg/ml, 10 µg/ml and 2 µg/ml (Figures 6 and 8A-8E). The degree of inhibition was dependent on cytokine/chemokine measured, the antibody and antibody concentration tested, and media used. Calculated average percent (%) inhibition was between 50.6-100% in all assays conducted at antibody concentration 2 µg/ml, and between 62-100% at antibody concentration of 50 µg/ml (Figure 9).

Anti-ST2L Domain III-binding antibodies C2521, C2519, ST2M48, ST2M49, ST2M50, and ST2M51 showed modest or no inhibition on, or stimulated IL-33-induced cytokine release by the mast cells (Figures 7A-7E and 8A-8E) at antibody concentrations 50 µg/ml and 10 µg/ml. The degree of inhibition was dependent on cytokine/chemokine measured, the antibody tested, and media used. Calculated average percent

(%) inhibition was between -594.4 - 31.9% in all assays conducted at antibody concentration 2 µg/ml, and between -481.5 - 36% at antibody concentration of 50 µg/ml (Figure 9). In some assays, antibody ST2M50 inhibited GM-CSF, IL-5, IL-10 and IL-13 secretion at antibody concentration 10 µg/ml (Figures 8A-8E).

Average % inhibition was calculated using the following formula: (1-(concentration of cytokine released in the presence of the mAb)/ (concentration of the same cytokine released in response to IL-33 in the absence of mAb)) x 100. Cytokine concentrations are in pg/ml. In some cases, the % inhibition is a negative value, indicating that the cytokine release in the presence of mAb was actually higher than that released in the absence of mAb. Slight variations in the potency of the mAbs may occur depending on the IL-33 concentrations used to induce cytokine release in the mast cells. Similarly, there may be slight variations in the activity of the mAbs depending on the assay medium used (StemPro-34 vs. RPMI / 10% FCS). All tested ST2L Domain I binding antibodies inhibited all measured cytokine and chemokine releases at least by 50% as measured by average % inhibition at a concentration of 2 µg/ml, 10 µg/ml or 50 µg/ml.

Example 9. **ST2L domain I binding antibodies inhibit intranasal IL-33-induced airway remodeling.**

C57BL/6 mice were dose intranasally with 1 µg/mouse "mature" IL-33 (or PBS) (residues 109-266 of SEQ ID NO: 215) on days D1, D3, D5, D7, and D9 and lungs were analyzed on Day 10 or Day 20. Anti-mouse ST2L antibody CNTO3914 or isotype control (CNTO5516) was dosed subcutaneously at 2 mg/kg 6 h prior to the first IL-33 intranasal administration. Control mice received isotype control CNTO5516 or PBS, 6 h prior to the first IL-33 intranasal administration. Inflated lungs

were fixed in 10% buffered formalin for histology; stains used for analysis included H&E, Masson Trichrome and PAS.

IL-33 treatment induced moderate to marked bronchiolar epithelial hypertrophy and hyperplasia with goblet cell hyperplasia and peribronchiolar infiltrates mixed mainly with eosinophils. Bronchiolar epithelial hypertrophy and hyperplasia were not evident in the animals receiving CNTO3914. The Masson Trichome stains were to determine the amount of collagen present; this staining revealed goblet cell hypertrophy in IL-33 treated animals. In the animals treated with CNTO3914 infiltrates in the alveoli and peribonchiolar regions were absent.

Example 10. Generation of fully human ST2L-antibodies

Additional human ST2L-binding Fabs were selected from *de novo* pIX phage display libraries essentially as described in Example 3 except that the libraries were panned using chimeric HHM-ST2L construct (SEQ ID NO: 6, Table 1) with the biotinylated antigen captured on streptavidin-coated magnetic beads. The phage library was blocked in PBS-T with 3% non-fat dry milk. Competitor protein, MHM-ST2L chimera (SEQ ID NO: 7, Table 1) was added to the blocking solution to drive the phage selection towards Fabs that would bind specifically to the human ST2L Domain I amino acid sequences. Phage selections were performed for three rounds followed by screening by ELISA for Fab binding to hST2L-Fc protein.

Nineteen Fabs with binding to hST2L-Fc were isolated from these selections and were further screened for binding to chimeric ST2L constructs (Table 1) as well as to the mouseST2L and humanST2L proteins to map the domain of specificity, and characterized for their ability to block IL-33/hST2L interaction. Fabs ST2F1, ST2F4 and ST2F6 blocked hIL-33/ST2L interaction and bound Domain I of ST2L and were moved forward into affinity maturation.

Table 9.

Fab ID	VH ID	Framework	HCDR1		HCDR2		HCDR3	
			Sequence	SEQ ID NO:	Sequence	SEQ ID NO:	Sequence	SEQ ID NO:
ST2F6	ST2H41	VH3-23	SYAMS	78	AISGSGGSTYYADSVKG	81	DPWSTEGSFFVLDY	84
ST2F4	ST2H39	VH3-23	SYWMH	79	GISSGGGSTYYADSVKG	82	DGWGTVYFPFDY	85
ST2F1	ST2H35	VH5-51	SYWIG	80	IIYPGDSDTRYSPSFQG	83	DTADFRRWDFDY	86

Fab ID	VL ID	Framework	LCDR1		LCDR2		LCDR3	
			Sequence	SEQ ID NO:	Sequence	SEQ ID NO:	Sequence	SEQ ID NO:
ST2F6	ST2L24	Vk-L6	RASQSVDDALA	87	DASNRAT	90	QQFYNWPLT	92
ST2F4	ST2L23	Vk-L6	RASQSVRDDLA	88	DASNRAT	90	QQYIHAPLT	93
ST2F1	ST2L20	Vk-B3	KSSQSVLYSSNNKNYLA	89	WASTRES	91	QQSNTYPFT	94

Example 11. Affinity-maturation of human ST2L binding Fabs

ST2F1, ST2F4 and ST2F6 were affinity-matured using an "in-line" maturation process described in Shi *et al.*, j Mol Biol 397:385-396, 2010 and Int. Pat. Publ. No. WO2009/085462 and Example 4. Affinity maturation libraries were made for ST2F1, ST2F4 and ST2F6 by diversifying corresponding light chain libraries, B3, L6 and L6, respectively, and combining the libraries with the Fab VH regions. The diversification scheme for light chain residues for the L6 and B3 affinity maturation libraries are shown in Table 10. Position numbering is according to Kabat. For affinity maturation panning, biotinylated huST2-ECD-Fc was captured on streptavidin (SA)-coated magnetic beads at concentrations of 10nM for round 1, 1nM for round 2, and 0.1 nM for round 3. The final wash of round 3 was performed overnight at room temperature in the presence of 10nM unlabelled huST2L-ECD-Fc.

Table 10.

Loop	Position	Scaffold	
		L6	B3
L1	30	SRNAD	RNDGHSY
	30a	-	RNDGHWY
	30e	-	RNDGHSY
	31	NSKD	RNDGHWY
	32	YWDFHSAN	YNWR
L2	50	ADKGYFTN	YWNK
L3	91	RYSGF	SYWH
	92	RHNSL	SYGN
	93	NDKR	STER
	94	WA	WYSH
	96	WYFLIR	YRWH

The ST2F6 light chain maturation library selections yielded improved binders (ST2F14, ST2F17, ST2F31 and ST2F41) (Figure 10 and Figure 11). These were examined as Fabs using ProteOn and demonstrated modest affinity improvements from 2nM to 400pM.

To further improve affinity of ST2F14, ST2F17, ST2F31 and ST2F41, the common heavy chain ST2H41 in ST2F14, ST2F17, ST2F31 and ST2F41 was randomized at HCDR1 and HCDR2 Kabat positions 31, 32, 33, 35, 50, 52, 53, 56 and 58 using a diversification scheme shown in Table 11. The resulting heavy chain library was paired with the four affinity improved light chains ST2L32, ST2L35, ST2L49 and ST2L59, and this library was panned and screened as described for the light chain maturation libraries. Fabs with improved binding relative to ST2F14 were isolated and converted to IgG for further characterization. The resulting antibodies (STLM103, STLM107, STLM108, STLM123, STLM124, STLM206, STLM207, STLM208, STLM209, STLM210, STLM211, STLM212, STLM213, STLM214, STLM215, STLM216, STLM217, STLM218, STLM219,

STLM220, STLM221, STLM222) (Figure 10 and Figure 11) have frameworks derived from VH3-23 or Vκ-L6. All antibodies bind ST2L Domain I and block IL-33/ST2L interaction.

Table 11.

Position	Amino Acids
31	SDNTAY
32	SDAY
33	SDAY
35	SN
50	SDNTAY
52	SANTKDEGR
53	SANEY
56	SANTKDEGR
58	SDNTAY

Additional variants were designed and expressed for STLM208 VH ST2L257 to replace a DP motif at the beginning of HCDR3. The sequences of the variants are shown in Figure 12.

Example 11. Human framework adaptation (HFA) of C2494

The framework adaptation process was done as essentially described in U.S. Pat. Publ. No. US2009/0118127 and Fransson *et al.*, J Mol Biol 398:214-231, 2010. Briefly, the heavy and light chain sequences were compared with the human germline sequences (only the "01" alleles as of Oct 01, 2007) using BLAST search against the IMGT database (Kaas, *et al.*, Nucl. Acids. Res. 32, D208-D210, 2004; Lefranc *et al.*, Nucl. Acid Res., 33, D593-D597, 2005). From this set of human germline genes, redundant genes (100% identical at amino acid level) and those with unpaired cysteine residues were removed. The remaining closest matching human germline genes in both the framework and CDR regions were chosen as the acceptor human frameworks. A total of 9 VL and 7 VH germline human frameworks were selected based upon overall sequence homology and CDR lengths as well as CDR similarity.

FR-4 was selected based on sequence similarity of the IGHJ/IGJK germline genes, JK2 for the VL chains and JH1 for the VH chains (Kaas, *et al.*, Nucl. Acid Res. 32, D208-D210, 2004; Lefranc M.-P *et al.*, Nucl. Acid Res., 33, D593-D597, 2005) with C2494 sequence). Then, the CDRs of C2494 (underlined in Figure 14) were transferred into the selected acceptor human frameworks to generate the HFA variants, except in the region corresponding to the CDR-H1 of V_H. For this region a combination of CDR and HV, or a shorter HCDR2 (referred to as Kabat-7, see U.S. Pat. Publ. No. US2009/0118127) were transferred from the non-human antibody into the human FRs because the HCDR2 residues highlighted in grey in Figure 14 have not been found in contact in antigen-antibody complexes of known structures (Almagro, J Mol Recognit. 17, 132, 2004).

The mature protein sequence of C2494 (VL: SEQ ID NO:52; VH: SEQ ID NO: 48) is shown Figure 14. In the figure, CDR residues (Kabat) are underlined, Chothia HV loops indicated below CDRs, and residues transferred into selected human frameworks indicated under HVs (HFA). HCDR2 residues highlighted in grey were not transferred in all variants.

A 3D homology model for the Fv fragment of C2494 was constructed using the antibody modeling module of MOE (CCG, Montreal). The model was utilized for evaluation of developability liabilities such as exposed methionine and tryptophan residues, potential N-glycosylation and deamidation motifs. In LCDR3, there is a potentially exposed Met (M94) residue, based upon the Fv structural model. To remove it, a variant (STLL280, O12b) with an M94L mutation was generated and characterized. For the heavy chain, the R residue in the CAR motif (Chothia residues 92-94, Figure 14) just before HCDR3 may negatively impact a cluster of negatively charged residues (Chothia residues D31, D32, D96 and D101a, Figure 14), which may be important for binding. A

VH with substitution of arginine for leucine at Chothia residues 94 (CAR →CAL) was generated and characterized.

The mAbs combining designed heavy and light chains, together with the C2494 parents were expressed and assayed for binding to human ST2L. From the generated HFA mAbs, mAbs with VH chains having IGHV1-24*01 (SEQ ID NO: 148) and IGHV1-f*01 (SEQ ID NO: 149) heavy chain frameworks (STLH195 and STLH194) expressed antibodies well and bound ST2L when combined with various HFA light chains having IGKV3-15*01 (L2) (SEQ ID NO: 150), IGKV1-9*01 (L8) (SEQ ID NO: 151), IGKV1-5*01 (L12) (SEQ ID NO: 152), IGKV1-12*01 (L5) (SEQ ID NO: 153), IGKV1-39*01 (O12) (SEQ ID NO: 154), IGKV1-27*01 (A20) (SEQ ID NO: 155)or IGKV1-33*01 (O18) (SEQ ID NO: 156) frameworks (STLL280, STLL278, STLL277, STLL276, STLL275, STLL274, STLL273, STLL272).

Sequences of HFA VH and VL variants are shown in Table 12. Transferred residues are underlined, and additional substitutions described above highlighted in grey. Table 13 shows SEQ ID NOs: as well as unique pDR (plasmid) and CBIS ID for each HFA VH and VL. Heavy and light chain combination for generated mAbs selected for further characterization is shown in Table 14.

Table 15 shows the human frameworks (combined V and J regions) used to transfer C2494 CDRs.

Table 12.

Framework adapted VL chains (coupled to JK2 sequence). CDRs are underlined.

>VL2494 (parent) (SEQ ID NO: 52)
ETTVTQSPASLSVATGEKVTIRCITNTDIDDVIHWYQQKPGEPPKLLISEGNTLRP
GVPSRFSSSGYGTDFVFTIENTLSEDVADYYCLQSDNMLTFGAGTKLELK

>VL2494-IGKV1-33*01 O18 (SEQ ID NO: 135)
DIQMTQSPSSLSASVGDRVTITCITNTDIDDVIHWYQQKPGKAPKLLIYEGNTLRP

GVPSRFSGSGSGTDFTFTISSLQPEDIATYYCLQSDNMLTFGQGTKLEIK

>VL2494-IGKV1-27*01 A20 (SEQ ID NO: 136)
DIQMTQSPSSLSASVGDRVTITCITNTDIDDVIHWYQQKPGKVPKLLIYEGNTLRP
GVPSRFSGSGSGTDFTLTISSLQPEDVATYYCLQSDNMLTFGQGTKLEIK

>VL2494-IGKV1-39*01O12 (SEQ ID NO: 137)
DIQMTQSPSSLSASVGDRVTITCITNTDIDDVIHWYQQKPGKAPKLLIYEGNTLRP
GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCLQSDNMLTFGQGTKLEIK

>VL2494-IGKV1-12*01 L5 (SEQ ID NO: 138)
DIQMTQSPSSVSASVGDRVTITCITNTDIDDVIHWYQQKPGKAPKLLIYEGNTLRP
GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCLQSDNMLTFGQGTKLEIK

>VL2494-IGKV1-5*01 L12 (SEQ ID NO: 139)
DIQMTQSPSTLSASVGDRVTITCITNTDIDDVIHWYQQKPGKAPKLLIYEGNTLRP
GVPSRFSGSGSGTEFTLTISSLQPDDFATYYCLQSDNMLTFGQGTKLEIK

>VL2494-IGKV1-9*01 L8 (SEQ ID NO: 140)
DIQLTQSPSFLSASVGDRVTITCITNTDIDDVIHWYQQKPGKAPKLLIYEGNTLRP
GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQSDNMLTFGQGTKLEIK

>VL2494-IGKV3-15*01 L2 (SEQ ID NO: 141)
EIVMTQSPATLSVSPGERATLSCITNTDIDDVIHWYQQKPGQAPRLLIYEGNTLRP
GIPARFSGSGSGTEFTLTISSLQSEDFAVYYCLQSDNMLTFGQGTKLEIK

>VL2494-IGKV1-39*01 O12b (SEQ ID NO: 142)
DIQMTQSPSSLSASVGDRVTITC ITNTDIDDVIH WYQQKPGKAPKLLIY EGNTLRP
GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC LQSDN▒LT FGQGTKLEIK

Framework adapted VH chains coupled to JH1

>VH2494(parent) (SEQ ID NO: 48)
EVQLQQSVAELVRPGASVKLSCTASAFNIKDDYMHWVKQRPEQGLEWIGRIDPAIGNTEYAPKFQD
KATMTADTSSNTAYLQLSSLTSEDTAVYYCA▒GDFYAMDYWGQGTSVTVSS

>VH2494-IGHV1-f*01 (SEQ ID NO: 143)
EVQLVQSGAEVKKPGATVKISCKVSAFNIKDDYMHWVQQAPGKGLEWMGRIDPAIGNTEYAEKFQG
RVTITADTSTDTAYMELSSLRSEDTAVYYCA▒GDFYAMDYWGQGTLVTVSS

>VH2494-IGHV1-24*01 (SEQ ID NO: 144)
QVQLVQSGAEVKKPGASVKVSCKVSAFNIKDDYMHWVRQAPGKGLEWMGRIDPAIGNTEYAPKFQD
RVTMTEDTSTDTAYMELSSLRSEDTAVYYCA▒GDFYAMDYWGQGTLVTVSS

Table 13.

	HFA-variant	pDR#	CBIS ID	SEQ ID NO:
VH HFA chains	>VH2494-IGHV1-24*01	9870	STLH195	144
	>VH2494-IGHV1-f*01	9871	STLH194	143
VL HFA chains	>VL2494-IGKV1-39*01 O12b	9865	STLL280	142
	>VL2494-IGKV3-15*01 L2	9873	STLL278	141
	>VL2494-IGKV1-9*01 L8	9874	STLL277	140
	>VL2494-IGKV1-5*01 L12	9875	STLL276	139
	>VL2494-IGKV1-12*01 L5	9876	STLL275	138
	>VL2494-IGKV1-39*01 O12	9877	STLL274	137
	>VL2494-IGKV1-27*01 A20	9878	STLL273	136
	>VL2494-IGKV1-33*01 O18	9879	STLL272	135

Table 14.

		VH chains		
		Parent*	>VH2494-IGHV1-24*01	>VH2494-IGHV1-f*01
VL chains	pRD#	pDR4211	pDR9870	pDR9871
Parent*	pDR4212	STLM126	STLM186	STLM196
>VL2494-IGKV1-39*01 O12b	pDR9865	STLM127	STLM187	STLM197
>VL2494-IGKV3-15*01 L2	pDR9873	STLM129	STLM189	STLM199
>VL2494-IGKV1-9*01 L8	pDR9874	STLM130	STLM190	STLM200
>VL2494-IGKV1-5*01 L12	pDR9875	STLM131	STLM191	STLM201
>VL2494-IGKV1-12*01 L5	pDR9876	STLM132	STLM192	STLM202
>VL2494-IGKV1-39*01 O12	pDR9877	STLM133	STLM193	STLM203
>VL2494-IGKV1-27*01 A20	pDR9878	STLM134	STLM194	STLM204
>VL2494-IGKV1-33*01 O18	pDR9879	STLM135	STLM195	STLM205

*Parent = C2494 VH and VL

Table 15.

Frameworks used for Human Framework Adaptation (HFA)		Sequence	SEQ ID NO:
Framework V region origin	Framework J region origin		
IGHV1-24*01	JH1	QVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPE DGETIYAQKFQGRVTMTEDTSTDTAYMELSSLRSEDTAVYYCATWGQGTLVTVSS	148
IGHV1-f*01	JH1	EVQLVQSGAEVKKPGATVKISCKVSGYTFTDYYMHWVQQAPGKGLEWMGLVDPED GETIYAEKFQGRVTITADTSTDTAYMELSSLRSEDTAVYYCATWGQGTLVTVSS	149
IGKV3-15*01 L2	JK2	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGI PARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPTFGQGTKLEIK	150
IGKV1-9*01 L8	JK2	DIQLTQSPSFLSASVGDRVTITCRASQGISSYLAWYQQKPGKAPKLLIYAASTLQSGVP SRFSGSGSGTEFTLTISSLQPEDFATYYCQQLNSYPTFGQGTKLEIK	151
IGKV1-5*01 L12	JK2	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESGV PSRFSGSGSGTEFTLTISSLQPDDFATYYCQQYNSYSTFGQGTKLEIK	152
IGKV1-12*01 L5	JK2	DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASSLQSG VPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQANSFPTFGQGTKLEIK	153
IGKV1-39*01 O12	JK2	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVP SRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPTFGQGTKLEIK	154
IGKV1-27*01 A20	JK2	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAASTLQSGV PSRFSGSGSGTDFTLTISSLQPEDVATYYCQKYNSAPTFGQGTKLEIK	155
IGKV1-33*01 O18	JK2	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGV PSRFSGSGSGTDFTFTISSLQPEDIATYYCQQYDNLPTFGQGTKLEIK	156

Example 12. Design of alanine and human germline mutants for paratope scanning

Site-directed mutagenesis was carried to assess the binding contributions of individual CDR residues as well as some residues having potential effect on other antibody characteristics. Based upon the molecular model of C2494 Fv above a subset of solvent-exposed CDR residues were predicted to be involved in binding antigen. These were mutated to alanine and/or corresponding 'human-like' residue, which is the corresponding residue in the closest matching germline gene. D101aA (Chothia residues), (D104A in SEQ ID NO: 48) substitution in C2494 VH decreased the k_{off} about 4 fold, from $1.43x10^{-4}$ to $3.2x10^{-5}$.

As the D101aA substitution decreased of k_{off} of C2494 Fab in binding to ST2L it was expected that the same mutation may also improve the off-rate in the C2494 HFA variants. Thus, D101aA (Chothia numbering) was

incorporated in the VH of STLH194 (>VH2494-IGHV1-f*01, SEQ ID NO: 143) to generate a VH STLH201 (SEQ ID NO: 145). STLH201 was paired with 7 light chains STLL280, STLL277, STLL276, STLL275, STLL274, STLL273 and STLL272 (Table 13 and Table 14) to generate mAbs STLM226, STLM227, STLM228, STLM229, STLM230, STLM231 and STLM232 which were characterized further. mAbs STLM226, STLM227, STLM228, STLM229, STLM230, STLM231 and STLM232 therefore have identical LCDR1, LCDR2, LCDR3, HCDR1 and HCDR2 sequences when compared to the parent C2494 antibody and a different HCDR3 (SEQ ID NO: 146, GDFYAMAY). In addition, antibody STLM266 VL STLM280 had a unique LCDR3: LQSDNLLT (SEQ ID NO: 147)

STLH201 (SEQ ID NO: 145):

EVQLVQSGAEVKKPGATVKISCKVSAFNIKDDYMHWVQQAPGKGLEWMGRIDPAIGNTEYAEKFQG
RVTITADTSTDTAYMELSSLRSEDTAVYYCA**GDFYAMAY**WGQGTLVTVSS

HCDR3 incorporation D101aA (Chothia numbering)

substitution:

SEQ ID NO: 146: GDFYAMAY

antibody STLM266 VL STLM280 had a unique LCDR3: LQSDNLLT

(SEQ ID NO: 147)

Example 13. Characterization of anti-ST2L antibodies

Antibodies obtained from phage display, hybridoma and human framework adaptation campaigns were characterized in various assays including binding to huST2L-ECD, cynoST2L-ECD, affinity measurements, binding to human/mouse chimeras to determine domain

binding, receptor-ligand inhibition assay, reporter gene assays, and mast cell response assays.

Affinities of the antibodies derived from the phage display campaigns to human and cyno ST2L as well as their binding specificity to human ST2L is shown in Table 16. All antibodies in Table 16 bound Domain I of human ST2L.

Table 16.

	human ST2L affinity			cyno ST2L affinity			ST2L-ECD domain binding
	k_{on} ($M^{-1}s^{-1}$)	k_{off} (s^{-1})	KD (pM)	k_{on} ($M^{-1}s^{-1}$)	k_{off} (s^{-1})	KD (pM)	
STLM103	3.97E+06	1.63E-04	41	6.42E+06	2.02E-04	31	D1
STLM107	2.90E+07	3.41E-04	12	1.00E+08	6.50E-04	7	D1
STLM108	2.29E+06	2.22E-04	97	2.05E+07	5.98E-04	29	D1
STLM123	1.37E+07	2.08E-04	15	1.00E+08	5.19E-04	5	D1
STLM124	1.65E+07	7.56E-04	46	8.71E+07	2.57E-03	30	D1
STLM206	6.39E+06	1.60E-04	25	9.40E+07	5.83E-04	6	D1
STLM207	8.33E+06	3.95E-04	48	1.00E+08	2.07E-03	21	D1
STLM208	5.97E+06	6.76E-05	11	1.39E+07	7.02E-05	5	D1
STLM209	6.59E+06	1.70E-04	26	3.39E+07	3.11E-04	9	D1
STLM210	1.21E+07	2.27E-04	19	5.70E+07	5.28E-04	9	D1
STLM211	1.70E+07	4.83E-04	29	1.00E+08	1.39E-03	14	D1
STLM212	1.24E+07	3.98E-04	32	1.43E+07	3.46E-04	24	D1
STLM213	7.54E+06	1.08E-04	14	1.64E+07	1.24E-04	8	D1
STLM214	9.16E+06	2.99E-04	33	7.20E+06	2.64E-04	37	D1
STLM215	6.91E+06	1.72E-04	25	3.54E+07	3.69E-04	10	D1
STLM216	9.63E+06	1.58E-04	16	7.89E+07	2.64E-04	3	D1
STLM217	7.27E+06	1.26E-04	17	3.81E+07	1.38E-04	4	D1
STLM218	9.89E+06	2.24E-04	23	1.45E+07	2.65E-04	18	D1
STLM219	7.54E+06	2.01E-04	27	1.07E+07	2.30E-04	22	D1
STLM220	5.80E+06	9.53E-05	16	1.60E+07	1.40E-04	9	D1
STLM221	2.73E+06	9.61E-05	35	6.04E+06	1.30E-04	22	D1
STLM222	8.22E+06	3.01E-04	37	1.18E+07	3.45E-04	29	D1
STLM226	2.16E+07	1.93E-03	90	1.00E+08	3.01E-02	301	D1
STLM227	2.66E+07	1.70E-03	64	1.00E+08	2.94E-02	294	D1
STLM228	2.01E+07	1.04E-03	52	1.00E+08	1.55E-02	155	D1
STLM229	1.29E+07	4.45E-04	35	1.00E+08	8.50E-03	85	D1
STLM230	1.11E+07	4.26E-04	38	5.06E+07	7.30E-03	144	D1
STLM231	1.97E+07	9.13E-04	46	8.27E+07	1.43E-02	172	D1
STLM232	1.78E+07	4.49E-04	25	1.00E+08	7.97E-03	80	D1

Affinities of the anti-ST2L antibodies from the HFA campaign in relation to the parent (STLM62, C2494) are shown in Table 17. The affinities were analyzed by ProteOn. The experiments were performed at 25°C using ProteOn's PBS-T-E buffer (PBS, 0.005%P20 and 3 mM EDTA) as running buffer. To

perform the experiments a GLC sensor chip was prepared by covalent immobilization of goat anti-human Fc (~5800 RUs) 122 - 146 response units (RU) of Mab were captured. Mab capture was followed by injection of ST2L-ECD from 0.024-15 nM (5-fold dilutions) for 4 min (200 µL at 50 µL/min). The dissociation was monitored for 30 minutes for all reaction. Regeneration was performed using two 15 sec pulses of 10 mM glycine pH1.5. The data was fitted to a 1:1 with baseline drift model.

Association rates for the samples are fast, the langmuir with mass transfer model was used for curve fitting and estimation of Affinity. All of the samples had faster off rates than the parental clone and control Mab. The difference in off rate was the primary contributor to the lower affinity of the HFA variants when compared to the parent antibody.

Table 17.

	human ST2L affinity			cyno ST2L affinity		
Sample	k_{on} (M-1s-1)	k_{off} (s-1)	K_D (pM)	k_{on} (M-1s-1)	k_{off} (s-1)	K_D (pM)
STLM62 *	1.84E+07	1.59E-04	8.67	3.84E+07	4.57E-04	12.35
STLM187	3.37E+07	1.59E-02	473.00	1.00E+08	1.10E-01	1100.00
STLM190	1.00E+08	5.34E-02	534.00	1.00E+08	1.02E-01	1020.00
STLM191	8.46E+07	2.47E-02	292.00	1.00E+08	6.66E-02	666.00
STLM192	2.11E+07	8.85E-03	420.00	1.00E+08	9.99E-02	999.00
STLM193	4.77E+07	1.27E-02	267.00	1.00E+08	9.32E-02	932.00
STLM194	1.00E+08	7.03E-02	703.00	1.00E+08	1.90E-01	1900.00
STLM195	2.49E+07	6.73E-03	271.00	1.00E+08	7.19E-02	719.00
STLM197	1.83E+07	1.62E-03	88.50	2.97E+07	6.88E-03	232.00
STLM199	2.17E+07	8.97E-04	41.40	7.78E+07	6.57E-03	84.50
STLM200	2.35E+07	1.43E-03	60.80	8.23E+07	1.10E-02	134.00
STLM201	1.76E+07	8.52E-04	48.40	3.55E+07	4.10E-03	116.00
STLM202	2.24E+07	1.19E-03	52.90	7.75E+07	1.04E-02	134.00
STLM203	2.04E+07	9.67E-04	47.30	5.88E+07	6.56E-03	111.00
STLM204	2.97E+07	2.41E-03	81.30	1.00E+08	2.05E-02	205.00
STLM205	1.73E+07	6.95E-04	40.10	4.04E+07	4.04E-03	100.00

*STLM62=C2494, parent antibody

Table 18.

Origin	mAb	RLB IC50, μg/ml	RGA IC50, μg/ml	Cyno endothelial assay	Basophil cytokine release
Phage display	STLM103	0.47	1.92	NT	+
	STLM107	0.44	1.10	NT	++
	STLM108	0.23	2.34	++	++
	STLM116	0.29	6.71	NT	+
	STLM123	0.28	1.25	NT	++
	STLM124	0.35	0.87	++	++
	STLM206	0.40	0.67	++	++
	STLM207	0.36	2.30	NT	++
	STLM208	0.47	0.61	++	++
	STLM209	0.32	0.97	++	++
	STLM210	0.30	2.10	NT	++
	STLM211	0.28	2.52	NT	++
	STLM212	0.33	4.32	NT	+
	STLM213	0.34	0.49	++	++
	STLM214	0.28	2.52	NT	++
	STLM215	0.29	1.30	NT	++
	STLM216	0.30	1.86	NT	++
	STLM217	0.49	1.69	NT	++
	STLM218	0.42	1.33	NT	++
	STLM219	0.29	3.16	NT	++
	STLM220	0.39	0.60	NT	++
	STLM221	0.39	2.79	NT	+
	STLM222	0.25	1.88	NT	++
	STLM226	0.26	0.25	++	++
	STLM227	0.17	0.23	++	++
	STLM228	0.20	0.28	++	++
HFA	STLM229	0.29	0.32	++	++
	STLM230	0.28	0.15	++	++
	STLM231	0.26	1.10	+	+
	STLM232	0.31	0.15	++	++
hybridoma C2494	STLM62*	0.70	0.11	++	++

++ strong inhibition
+ some inhibition
- no inhibition
NT Not tested
* Tested as a hybridoma
RLB = Receptor-Ligand binding inhibition
RGA = Reporter gene assay

Select antibodies were tested for mast cell responses measuring inhibition of 3ng/ml IL-33-induced IL-5, IL-13 and IL-8 release from human cord blood-derived mast cells as described using 100 µg/ml, 10 µg/ml, 1 µg/ml, 0.1 µg/ml or 0.01 µg/ml antibody in RPMI + 10% FCS. In these assay conditions, all antibodies tested inhibited IL-33-induced IL-5, IL-13 and IL-8 cytokine release by about 40%-100% at an antibody concentration 100 µg/ml when compared to a control sample induced with IL-33.

Example 14. Anti-ST2L antibody inhibits downstream signaling pathways in human basophils

Anti-ST2L antibodies were tested for their ability to inhibit p38 MAPK signaling in human basophils.

Whole blood was collected in heparinized tubes and brought to room temperature (RT) prior to initiation of the assay. 1 mL of blood was aliquotted into 50 mL conical tubes and either anti-ST2L antibody (STLB252) or isotype control (CNTO 8937) diluted in PBS was added for a final concentration of 2, 20, or 200 µg/mL. Tubes were swirled gently to mix and placed in incubator at 37°C x 30 minutes, swirling gently after 15 minutes. Blood was then stained with fluorochrome-labeled antibodies against cell surface antigens (CD123-FITC, CRTH2-PCP-CY5.5, and CD45-APC-C7) and tubes were incubated at 37°C for 15 minutes. 1 mL of warmed culture media (RPMI-1640/10% FBS/1% pen-strep) was added to each tube before IL-33 diluted in warmed culture media was added for a final concentration of 10 ng/mL. Samples were incubated at 37°C x 10 minutes prior to the addition of 20 mLs of pre-warmed BD Phosflow Lyse/Fix buffer to each tube, in order to simultaneously lyse the red blood cells and fix the samples. Tubes were mixed well by inverting 10 times and incubated at 37°C x 10 minutes. Samples were washed with 20 mLs sterile RT PBS, resuspended in 2 mLs of 1x RT BD

Perm/Wash Buffer, and incubated at RT x 30 minutes. Samples were washed once with 2 mLs BD Perm/Wash buffer and then resuspended in 400 µL BD Perm/Wash buffer. PE-labelled antibody against intracellular p38-MAPK (vCell Signaling, Cat. 6908S) was added and samples were incubated 30 min at RT, protected from light. Samples were washed once with 5 mLs Perm/Wash buffer before being resuspended in 100 µL FACS buffer and transferred to a 96-well round-bottom plate. Samples were analyzed using a BD LSRII Flow Cytometer utilizing a high-throughput system (HTS) collecting as many events as possible for each sample. Data was analyzed using FloJo software. Basophils were identified as $CD45^{+}CRTH2^{+}CD123^{+}$ and the percent of p38 MAPK positive basophils was assessed for each condition. Pre-incubation of whole blood with anti-ST2L mAB (STLB252) resulted in a dose-dependent inhibition of IL-33 induced p38-MAPK phosphorylation, whereas no effect was seen with isotype control (CNTO 8937). The anti-human ST2L antibody specifically blocked basophil activation by recombinant human IL-33 in the context of whole blood. The results suggest that anti-ST2L antibodies inhibit signaling by endogenous IL-33 *in vivo*.

Table 19.

IL-33 (10 ng/ml)	STLB252 (µg/mL)	Isotype control (µg/mL)	% phosphorylated p38 MAPK
-	0	0	2.2
+	0	0	80.6
+	2	0	44.4
+	20	0	15.7
+	200	0	1.2
+	0	2	76.7
+	0	20	79
+	0	200	77

Example 15. *In vivo* target engagement by anti-ST2L antibody

Intranasal mIL-33 6 hour *in vivo* model of BAL cell recruitment

A single dose of 1.2 µg/mouse mIL-33 (R&D systems #3626-ML/CF) or PBS was administered to male Balb/c mice (6-8 weeks old, Taconic). Rat anti-mouse ST2L antibody CNTO 3914 or at 2, 0.2, 0.06, or 0.02 mg/kg, 24hrs prior to the first mIL-33 intranasal administration. Isotype control (ITC) mAb CNTO 5516 was dosed subcutaneously at 2 mg/kg. Six hours following the mIL-33 (or PBS) administration, mice were sacrificed and blood was collected for serum analysis. Bronchoalveolar lavages (BAL) were performed by injecting two volumes of 0.7 mL of PBS/0.1% BSA into the lungs and retrieving the effluent. The BALs were centrifuged (1200rpm, 10 minutes) and the cell pellet was resuspended in 200µl PBS

for total and differential cell counts using a hemacytometer (on Wright's - Giemsa-stained cytospin preparations).

Measurement of CNTO 3914 in mouse serum

MSD SA-STD plates were blocked with 50 µL per well of assay buffer for 5 minutes. The plates were turned over to remove assay buffer and tapped on paper towels. 50 µl per well of 1.4 µg/mL biotinylated recombinant mouse ST2L/IL1R4/Fc chimera (R&D System) in assay buffer were added and incubated overnight in the refrigerator. 150 µL of assay buffer was added to each well of the pre-coated plates without removing the coating reagent and incubated for 30 minutes. The plates were washed three times with wash buffer on the plate washer. The plates were tapped lightly on paper towels to remove residual wash buffer. 50 µL per well of CNTO 3914 sample was added to each well of the plate. The plate was incubated for one hour with gentle vortexing at ambient temp. The plates were washed three times with wash buffer on the plate washer. 50µL per well of titration of ruthenium-labeled mouse anti-mouse IgG1b (BD Biosciences) was added to each well of the plate. The plate was incubated for one hour with gentle vortexing at ambient temp. The plates were washed three times with wash buffer on the plate washer. 150 µL of read buffer were added to each well of the plate. The plates were immediately read on the MSD sector imager 6000 Reader for luminescence levels.

Whole Blood Assay

Blood was diluted 1:4 in DMEM media + 1% Penicillin+streptomycin solution +/- 10 ng/ml mouse IL-33 in Sarstedt filter tubes. The tubes were incubated at 37°C overnight, then cytokine and chemokine levels were measured on the supernatants using the Millipore Milliplex Mouse

Cytokine/Chemokine Kit according to manufacturer's instructions.

Results

Anti-ST2L antibody was detectable in the serum of mice 24 hours post-dosing with 0.2 or 2 mg/kg CNTO 3914 (Figure 16A).

Intranasal administration of IL-33 induced cell recruitment to the airways at 6h (Figure 16B). Anti-ST2L mAb administration reduced BAL cell recruitment; 0.2 mg/kg was the minimum dose needed to see significant inhibition of BAL cell recruitment (Figure 16B). Statistical significance was calculated using One-way ANOVA.

Whole blood stimulated with mouse IL-33 showed increased levels of cytokine and chemokines, including IL-6 (Figure 16C) and MCP-1 (Figure 16D), after 24h. In mice dosed with 20 mg/kg or 2 mg/kg anti-ST2L mAb CNTO 3914, IL-6 and MCP-1 levels were reduced compared to CNTO5516 (isotypic control anti-mouse IgG1), implying target engagement. The minimum dose that correlated with inhibition in the whole blood assay, 2 mg/kg, also inhibited BAL cell recruitment (Figure 16B).

Collectively this data confirms that the anti-ST2L mAb reaches site of action and the intended pharmacologic effect was accomplished (implies target engagement).

Example 16. Epitopes of anti-ST2L antibodies

Epitope mapping and competition studies were conducted to select anti-ST2L antibodies.

Competition binding assays

Competition binding assays were performed to evaluate different binding epitope groups for anti-ST2L mAbs. 5 µl (10 µg/ml) of ST2L-ECD protein was coated on MSD HighBind plate

(Meso Scale Discovery, Gaithersburg, MD) per well for 2 hr at room temperature. One-hundred and fifty microliters of 5% MSD Blocker A buffer (Meso Scale Discovery, Gaithersburg, MD) was added to each well and incubated for 2 hr at room temperature. Plates were washed three times with 0.1 M HEPES buffer, pH 7.4, followed by the addition of the mixture of the MSD fluorescence dye (sulfo tag, NHS ester) labeled individual anti-ST2L antibody with different competitors. Labeled antibody, 10 or 30 nM, was incubated with increasing concentrations of competitor antibodies, from 1 nM to 2 or 5 µM, and then added to the designated wells in a volume of 25 µL mixture. After 2-hour incubation with gentle shaking at room temperature, plates were washed 3 times with 0.1M HEPES buffer (pH 7.4). MSD Read Buffer T was diluted with distilled water (4-fold) and dispensed at a volume of 150 µL/well and analyzed with a SECTOR Imager 6000.

Following antibodies were used in competition assays: ST2L Domain I binding neutralizing antibodies STLM208, STLM213, C2244 (STLM15) and C2494 (STLM62), ST2L Domain III binding antibody C2539, and a non-neutralizing anti-ST2L antibody C2240 binding Domain I of human ST2L. Figure 17A and 17B shows the competition experiments. Based on the experiment, the epitope bins identified were: BinA: mAbs C2244, C2494, STLM208 or STLM213; BinB: mAb C2240, BinC: C2539. The antibodies blocking IL33/ST2L interaction and inhibiting mast cell responses were found in the same epitope bin and to cross-compete with each other. Summary of the competition data is shown in Table 20.

Table 20.

Competitor	Labeled Antibody			
	C2240	C2539	C2244	C2494
C2240	+	-	-	-
C2539	-	+	-	-
C2244	-	-	+	+
C2494	-	-	+	+
STLM208	-	-	+	+
STLM213	-	-	+	+

Epitope mapping: H/D exchange analysis

For H/D exchange, the procedure used to analyze the antibody perturbation are similar to the one described previously (Hamuro, Y., *et al.*, Journal of Biomolecular Techniques, 14:171-182, 2003; Horn, J. R., *et al.*, Biochemistry, 45: 8488-8498, 2006) with some modification. Recombinant ST2-ECD (expressed from HEK293E with C-terminal His-tag) (residues 18-328 of SEQ ID NO: 157) was incubated in a deuterated water solution for pre-determined times resulting in deuterium incorporation at exchangeable hydrogen atoms. The deuterated ST2-ECD was captured on a column containing immobilized anti-ST2L C2244 Fab molecules and then washed with aqueous buffer. The back-exchanged ST2-ECD protein was eluted from the column and localization of deuterium containing fragments was determined by protease digestion and mass spec analysis.

Figure 18 shows a simplified H/D exchange map of the human ST2-ECD (soluble ST2) complexed with C2244 Fab. Residues 18-31 of ST2-ECD of SEQ ID NO: 119 (amino acid residues RCPRQGKPSYTVDW; SEQ ID NO: 210) were protected by the Fab (corresponding to residues 35-48 of full length ST2L

of SEQ ID NO: 1. The data indicates that C2244 binds to epitope RCPRQGKPSYTVDW; SEQ ID NO: 210), and that antibodies competing with C2244 (C2494, STLM208 or STLM213) are likely to bind the same or overlapping epitope.

Epitope mapping by mutagenesis

Several ST2L mutants were generated having substitutions to corresponding mouse residues at ST2L Domain I. The tested antibodies do not cross-react with mouse ST2L, therefore it is expected that ST2L variants with abolished and/or reduced binding are indicative of epitope residues at the substitution sites on ST2L. Variants were made into construct HH-ST2L having residues 19-205 of full length ST2L of SEQ ID NO: 1 using standard methods. Antibodies were tested for binding to the ST2L variants by ELISA or Proteon.

Surface Plasmon Resonance

Binding studies were performed using the ProteOn XPR36 Protein Interaction Array system (Bio-Rad) (Bravman T, et al. Anal Biochem 358:281-288, 2006). Anti-human/anti-mouse Fc mixture (Jackson ImmunoResearch, Cat#, 109-005-098/115-005-071) was immobilized on the GLC sensor chip by amine-coupling chemistry. Individual anti-ST2L mAb was then captured by flowing (1 μg /mL) antibody solution prepared in PBS containing 0.5% Nonidet P-40 and 0.5% Na-deoxycholate). The signal in the surfaces reached ~250 resonance units (RU, 1 RU = 1 pg protein/mm^2) in the anti-Fc-coated surfaces, confirming that these antibodies specifically capture anti-ST2L mAbs. After 90° rotation of the fluid system, wild type of ST2L-D1D2 or variant proteins (0.5 mg/mL in PBS containing 0.5% Nonidet P-40 and 0.5% Na-deoxycholate) was injected in the parallel flow channels. All of these assays were performed at 25°C. The ST2L-D1D2-dependent signals on the surfaces were obtained by double referencing, subtracting the

response observed on surfaces immobilizing the antibodies alone, and the signal observed injecting the vehicle alone (which allows correction for binding-independent responses). The resulting sensorgrams were fitted by the simplest 1:1 interaction model (ProteOn analysis software), to obtain the corresponding association and dissociation rate constants (k_a and k_d).

Figure 19 shows the ST2L variants that were made and affinity of ST2B206 and ST2B252 anti-ST2L antibodies to the variants. Variant 93NL94 (substitution 93TF94-> 93NL94) reduced binding affinity of both STLM208 and STLB252 by about 5-fold from about $10.8x10^{-12}$ M to about $49.5x10^{-12}$ M. Lack of significant reduction of binding affinity implies that the binding energy for the interaction between antibody and ST2L-D1D2 is a sum of epitope region (RCPRQGKPSYTVDW; SEQ ID NO: 210) identified by H/D exchange analysis and additional contribution from this 93NL94 site. Residue numbering is according to full length human ST2L of SEQ ID NO: 1.

Example 17. ST2L Domain I binding antibodies inhibit primary human lung mast cell responses in vitro

Ability of the ST2L Domain I binding antibodies to inhibit lung mast cell responses were assessed by release of chemokines and cytokines in primary human lung mast cells.

Isolation of primary human lung mast cells

Primary human lung mast cells were isolated from normal non-smoker tissue obtained from the International Institute for the Advancement of Medicine. Cells were dispersed from the lung parenchyma and small airways by mincing, washing, and digesting the parenchyma tissue overnight at 37°C in collagenase and hyaluronidase enzymes. Cells were collected, washed, and subjected to an enrichment procedure using the CD117 MicroBead Kit (human) from MACS Miletnyi Biotec to

positively select the mast cells from the population. Prior to experimentation, mast cells were cultured for 6 weeks in StemPro-34 + 200ng/ml stem cell factor. Two weeks after isolation, cells were phenotypically characterized using flow cytometry to determine the percent mast cell purity. The cells used in subsequent assays were 89% double positive for CD117 (C-kit or stem cell factor receptor) and FcεRI (the high affinity IgE receptor). Furthermore, they were 94.2% positive for ST2L; thereby confirming their mast cell phenotype.

Cytokine release assay from primary human lung mast cells

Primary human lung mast cells that had been cultured in StemPro-34 + 200ng/ml stem cell factor for approximately 6 weeks were collected, and washed by centrifugation in RPMI (10% heat-inactivated FCS). Cells were counted and plated in RPMI / 10% FCS medium at a density of 65,000 cells in a 96 well plate. The Anti-ST2L Domain I binding Mabs were added to the primary lung mast cells, and allowed to bind for 30 minutes at 37°C prior to stimulation with IL-33. Cells were stimulated for 24 hours with 3ng/ml IL-33 in order to initiate accumulation of various mediators into the culture supernatant. Culture supernatant was harvested and stored frozen until assaying in a custom Milliplex 9-plex kit.

Anti-ST2L Domain I binding antibody, STLM208, inhibited IL-33-induced GM-CSF (Figure 20A), IL-5 (Figure 20B), IL-8 (Figure 20C), and IL-13 (Figure 20D) release in primary human lung mast cells at antibody concentrations 100 µg/ml, 10 µg/ml and 1 µg/ml. Similar results were obtained using the cord blood-derived mast cells (data not shown).

CLAIMS

1. An isolated human or human-adapted antibody antagonist or fragment thereof that specifically binds Domain I (SEQ ID NO: 9) of human ST2L and blocks interleukin-33 (IL-33)/ST2L interaction, comprising a heavy chain variable region (VH), a light chain variable region (VL), a heavy chain complementarity determining region (HCDR) 1 (HCDR1), 2 (HCDR2), 3 (HCDR3), a light chain complementarity determining region (LCDR) 1 (LCDR1), 2 (LCDR2), and 3 (LCDR3), wherein
   a) the HCDR1 comprises the amino acid sequence of SEQ ID NO: 97;
   b) the HCDR2 comprises the amino acid sequence of SEQ ID NO: 114;
   c) the HCDR3 comprises the amino acid sequence of SEQ ID NO: 84;
   d) the LCDR1 comprises the amino acid sequence of SEQ ID NO: 130;
   e) the LCDR2 comprises the amino acid sequence of SEQ ID NO: 90; and
   f) the LCDR3 comprises the amino acid sequence of SEQ ID NO: 134.
2. The isolated antibody of claim 1 having a dissociation constant (K_D) to human ST2L between about $5x10^{-12}$ M to about $7x10^{-10}$ M, an on rate constant (K_{on}) to human ST2L between about $2x10^6$ $M^{-1}s^{-1}$ to about $1x10^8$ $M^{-1}s^{-1}$, or an off rate constant (K_{off}) to human ST2L between about $1x10^{-6}$ s^{-1} to about $1x10^{-2}$ s^{-1}.
3. The isolated antibody of claim 2 having a dissociation constant (K_D) to *Macaca fascicularis* (cyno) ST2L (SEQ ID NO: 2) between about $3x10^{-12}$ M to about $2x10^{-9}$ M, an on rate constant (K_{on}) to cyno ST2L between about $4x10^6$ $M^{-1}s^{-1}$ to about

$1x10^{8}$ $M^{-1}s^{-1}$, or an off rate constant (K_{off}) to cyno ST2L between about $7x10^{-5}s^{-1}$ to about $1x10^{-1}s^{-1}$.

4. The isolated antibody of any one of claims 1 to 3, comprising the VH of SEQ ID NO: 191.
5. The isolated antibody of any one of claims 1 to 4, comprising the VL of SEQ ID NO: 209.
6. The isolated antibody of any one of claims 1 to 3, comprising the VH of SEQ ID NO: 191 and the VL of SEQ ID NO: 209.
7. The isolated antibody of any one of claims 1 to 6, wherein the antibody competes for binding to human ST2L (SEQ ID NO: 1) with an isolated antibody comprising a heavy chain variable region (VH) of SEQ ID NO: 47 and a light chain variable region (VL) of SEQ ID NO: 51.
8. The isolated antibody of claim 7, wherein the antibody binds human ST2L at amino acid residues 35-48 of SEQ ID NO: 1 (RCPRQGKPSYTVDW; SEQ ID NO: 210).
9. The isolated antibody of claim 8, wherein the antibody further binds human ST2L at amino acid residues T93 and F94 of SEQ ID NO: 1.
10. The isolated antibody of any one of claims 1 to 3, comprising a heavy chain variable region (VH) comprising a VH framework derived from human IGHV3-23 (SEQ ID NO: 158), IGHV1-24*01 (SEQ ID NO: 148) or IGHV1-f*01 (SEQ ID NO: 149) framework sequences, and a light chain variable region (VL) comprising a VL framework derived from a human IGKV3-11 (L6) (SEQ ID NO: 159), IGKV3-15*01 (L2) (SEQ ID NO: 150), IGKV1-9*01 (L8) (SEQ ID NO: 151), IGKV1-5*01 (L12) (SEQ ID NO: 152), IGKV1-12*01 (L5) (SEQ ID NO: 153), IGKV1-39*01 (O12) (SEQ ID NO: 154), IGKV1-27*01 (A20) (SEQ ID NO: 155)or IGKV1-33*01 (O18) (SEQ ID NO: 156) framework sequences.
11. The isolated antibody of any one of claims 1 to 10 which is of IgG1, IgG2, IgG3, or IgG4 type.

12. The isolated antibody of claim 11having a substitution in an Fc region.

13. The isolated antibody of claim 12, wherein the substitution comprises a substitution M252Y/S254T/T256E, V234A/G237A/P238S/H28A/V309L/A330S/P331S or P238S/L234A/L235A, wherein residue numbering is according to the EU numbering.

14. The isolated antibody of claim 10 comprising the VH at least 90% identical to the VH of SEQ ID NO: 191 and the VL at least 94% identical to the VL of SEQ ID NO: 209.

15. The isolated antibody of claim 14 comprising the VH of SEQ ID NOs: 143, 144, 145, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204 or 205 and the VL of SEQ ID NOs: 135, 136, 137, 138, 139, 140, 141, 142, 206, 207, 208 or 209.

16. The isolated antibody of claim 15, comprising the VH and the VL of:

a) SEQ ID NO: 186 and SEQ ID NO: 206, respectively;

b) SEQ ID NO: 187 and SEQ ID NO: 206, respectively;

c) SEQ ID NO: 197 and SEQ ID NO: 206, respectively;

d) SEQ ID NO: 198 and SEQ ID NO: 206, respectively;

e) SEQ ID NO: 199 and SEQ ID NO: 206, respectively;

f) SEQ ID NO: 200 and SEQ ID NO: 206, respectively;

g) SEQ ID NO: 201 and SEQ ID NO: 206, respectively;

h) SEQ ID NO: 202 and SEQ ID NO: 206, respectively;

i) SEQ ID NO: 203 and SEQ ID NO: 206, respectively;

j) SEQ ID NO: 204 and SEQ ID NO: 206, respectively;

k) SEQ ID NO: 205 and SEQ ID NO: 206, respectively;

l) SEQ ID NO: 195 and SEQ ID NO: 207, respectively;

m) SEQ ID NO: 196 and SEQ ID NO: 207, respectively;

n) SEQ ID NO: 188 and SEQ ID NO: 208, respectively;

o) SEQ ID NO: 189 and SEQ ID NO: 208, respectively;

p) SEQ ID NO: 190 and SEQ ID NO: 208, respectively;

q) SEQ ID NO: 187 and SEQ ID NO: 209, respectively;

r) SEQ ID NO: 191 and SEQ ID NO: 209, respectively;

s) SEQ ID NO: 192 and SEQ ID NO: 209, respectively;

t) SEQ ID NO: 193 and SEQ ID NO: 209, respectively; or

u) SEQ ID NO: 194 and SEQ ID NO: 209, respectively.

17. An isolated polynucleotide encoding the antibody antagonist or fragment thereof of any one of the preceding claims.

18. A vector comprising an isolated polynucleotide of claim 17.

19. A host cell comprising a vector of claim 18.

20. A method of producing an antibody of any one of claims 1 to 16, comprising culturing a host cell of claim 19 and recovering the antibody from the cell.

21. A pharmaceutical composition comprising an isolated antibody of any one of claims 1 to 16 and a pharmaceutically accepted carrier.

22. The use of the isolated human or human-adapted antibody antagonist or fragment thereof that specifically binds Domain I of human ST2L of any one of claims 1-16 in the manufacture of a medicament for the treatment of a ST2L-mediated condition , wherein the ST2L-mediated condition is asthma, airway hyper-reactivity, sarcoidosis, chronic obstructive pulmonary disease (COPD), idiopathic pulmonary fibrosis (IPF), cystic fibrosis, inflammatory bowel disease, (IBD), eosinophilic esophagitis, scleroderma, atopic dermatitis, allergic rhinitis, bullous pemphigoid, chronic urticaria, diabetic nephropathy, rheumatoid arthritis, interstitial cystitis or Graft Versus Host Disease (GVHD), or is is associated with inflammatory cell recruitment in lung, goblet cell hyperplasia, increased mucous secretion or mast cell response.