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(57) Abrégé/Abstract:
Methods for increasing immunoglobulin A (IgA) levels in a subject having a deficiency thereof are provided herein by administering to the subject an agent that inhibits CXCL13 activity, such as an anti-CXCL13 or an anti-CXCR5 antibody. Further provided are methods for treating an inflammatory disorder in a subject deficient for IgA by administering to the subject an agent that inhibits CXCL13 activity.

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(54) **Title**: METHODS FOR INCREASING IMMUNOGLOBULIN A LEVELS

(57) **Abstract**: Methods for increasing immunoglobulin A (IgA) levels in a subject having a deficiency thereof are provided herein by administering to the subject an agent that inhibits CXCL13 activity, such as an anti-CXCL13 or an anti-CXCR5 antibody. Further provided are methods for treating an inflammatory disorder in a subject deficient for IgA by administering to the subject an agent that inhibits CXCL13 activity.

METHODS FOR INCREASING IMMUNOGLOBULIN A LEVELS

SEQUENCE LISTING

This description contains a sequence listing in electronic form in ASCII text format. A copy of the sequence listing in electronic form is available from the Canadian Intellectual Property Office.

FIELD OF THE INVENTION

The present invention relates generally to increasing immunoglobulin A (IgA) levels in a subject having a deficiency thereof.

BACKGROUND OF THE INVENTION

Immunoglobulins are a group of structurally related proteins composed of heavy and light chains comprised of variable and constant domains. The variable regions of the heavy and light chains determine the molecular specificity of the complete molecule. Immunoglobulins are categorized as IgG, IgM, IgE, IgD, or IgA based on the identity of the constant regions of their heavy chains. Immunoglobulin A (IgA) comprises an alpha (α) constant region in its heavy chains.

IgA is produced by plasma cells located along the mucosal linings of the respiratory, gastrointestinal, and genitourinary tracts. IgA molecules bind to invading pathogens and weaken their ability to penetrate the mucosal layer and to enter the inner tissue and blood stream of the host. See generally J. G. Nedrud et al., "Adjuvants and the Mucosal Immune System", Topics in Vaccine Adjuvant Research, (Spiggs, D. E., Koff, W. C., Eds.) CRC Press, Boca Raton, Fla. (1990). IgA binds to receptors on the cell surface of phagocytic leukocytes and thereby facilitates antibody-dependent cell-mediated killing of invading pathogens. IgA can also bind allergenic substances, thereby preventing the allergens from binding IgE or activating T cells responsible for delayed-type hypersensitivity.

A deficiency of IgA can occur transiently, for example upon exposure to certain drugs or in response to various infections, or permanently, as in patients with congenital IgA deficiency.

It has been found that individuals with low IgA production are more prone to various inflammatory diseases, such as autoimmune diseases and allergies, than those with normal IgA levels. Thus, increasing the levels of either total IgA or antigen-specific IgA may treat or prevent inflammatory diseases.

BRIEF SUMMARY OF THE INVENTION

Methods for increasing immunoglobulin A (IgA) levels in a subject having a deficiency thereof are provided herein by administering an agent that inhibits CXCL13 activity, such as an anti-CXCL13 antibody. Further provided are methods for treating an inflammatory disorder in a subject deficient for IgA by administering to the subject an agent that inhibits CXCL13 activity. The IgA deficiency may be a permanent deficiency that is genetically determined or may be secondary to an infection or exposure to a drug. The administration of the CXCL13 inhibitory agent can prevent the development of an inflammatory disorder, such as an autoimmune disorder, or can treat an active inflammatory disorder.

The following embodiments are encompassed by the present invention.

1. A method for increasing immunoglobulin A (IgA) levels in a subject having a deficiency thereof, said method comprising administering to said subject an effective amount of an agent that inhibits CXCL13 activity.

2. The method of embodiment 1, wherein said IgA deficiency is secondary to an infection or exposure to a drug.

3. The method of embodiment 2, wherein said infection is a mucosal infection.

4. The method of embodiment 2 or 3, wherein said infection is a bacterial infection.

5. The method of embodiment 4, wherein said bacterial infection is a *Heliobacter* infection.

6. The method of embodiment 5, wherein said *Heliobacter* is selected from the group consisting of *Heliobacter pylori*, *Heliobacter heilmannii*, and *Heliobacter suis*.

7. The method of embodiment 6, wherein said *Heliobacter* is *H. suis*.

8. The method of embodiment 1, wherein said IgA deficiency is a primary IgA deficiency.

9. A method for treating an inflammatory disorder in a subject having an immunoglobulin A (IgA) deficiency, comprising administering to said subject an effective amount of an agent that inhibits CXCL13 activity.

10. The method of embodiment 9, wherein said inflammatory disorder is caused by a mucosal infection.

11. The method of embodiment 9 or 10, wherein said inflammatory disorder is caused by a bacterial infection.

12. The method of embodiment 11, wherein said method reduces the burden of said bacterial infection in said subject.

13. The method of embodiment 11 or 12, wherein said bacterial infection is a *Heliobacter* infection.

14. The method of embodiment 13, wherein said *Heliobacter* is selected from the group consisting of *Heliobacter pylori*, *Heliobacter heilmannii*, and *Heliobacter suis*.

15. The method of embodiment 14, wherein said *Heliobacter* is *H. suis*.

16. The method of any one of embodiments 10-15, wherein said mucosal infection is a gastric mucosal infection.

17. The method of any one of embodiments 9-16, wherein said inflammatory disorder is MALT lymphoma.

18. The method of embodiment 17, wherein said MALT lymphoma is a gastric MALT lymphoma.

19. The method of any one of embodiments 9-16, wherein said inflammatory disorder is a gastric or duodenal ulcer.

20. The method of embodiment 9, wherein said inflammatory disorder is an autoimmune disorder.

21. The method of embodiment 20, wherein said autoimmune disorder is selected from the group consisting of rheumatoid arthritis, systemic lupus erythematosus, Graves disease, Type 1 diabetes, myasthenia gravis, and celiac sprue.

22. The method of any one of embodiments 1-21, wherein secretory IgA levels are increased in said subject upon administration of said agent that inhibits CXCL13 activity.

23. The method of embodiment 22, wherein gastric IgA levels are increased in said subject upon administration of said agent that inhibits CXCL13 activity.

24. The method of any one of embodiments 1-23, wherein said method increases IgA antibody responses in a mucosal tissue of said subject.

25. The method of any one of embodiments 1-24, wherein said agent is a binding molecule that specifically binds to CXCR5.

26. The method of any one of embodiments 1-24, wherein said agent is a binding molecule that specifically binds to CXCL13.

27. The method of any one of embodiments 1-26, wherein said binding molecule comprises an antibody or antigen-binding fragment thereof.

28. The method of embodiment 27, wherein said antibody is chimeric, human, or humanized.

29. The method of embodiment 27 or 28, wherein said antibody specifically binds to CXCL13 and comprises a variable heavy (VH) domain having at least 90% sequence identity to the amino acid sequence set forth in SEQ ID NO: 10 or 14.

30. The method of embodiment 29, wherein said antibody that specifically binds to CXCL13 comprises a VH domain having the sequence set forth in SEQ ID NO: 14.

31. The method of any one of embodiments 27-30, wherein said antibody specifically binds to CXCL13 and comprises a variable light (VL) domain having at least 90% sequence identity to the amino acid sequence set forth in SEQ ID NO: 15, 19, or 21.

32. The method of embodiment 31, wherein said antibody that specifically binds to CXCL13 comprises a VL domain having the sequence set forth in SEQ ID NO: 19.

33. The method of embodiment 32, wherein said antibody that specifically binds to CXCL13 comprises a VH domain having the sequence set forth in SEQ ID NO: 14 and a VL domain having the sequence set forth in SEQ ID NO: 19.

34. The method of embodiment 27 or 28, wherein said antibody specifically binds to CXCL13 and comprises a VH domain having at least one of the following complementarily determining regions (CDRs):

a) a CDR1 having at least 90% sequence identity to SEQ ID NO: 11;

b) a CDR2 having at least 90% sequence identity to SEQ ID NO: 12;

and

c) a CDR3 having at least 90% sequence identity to SEQ ID NO: 13.

35. The method of embodiment 34, wherein said antibody that specifically binds to CXCL13 comprises a VH domain comprising a CDR1 having the sequence set forth in SEQ ID NO: 11, a CDR2 having the sequence set forth in SEQ ID NO: 12, and a CDR3 having the sequence set forth in SEQ ID NO: 13.

36. The method of any one of embodiments 27, 28, 34, and 35, wherein said antibody specifically binds to CXCL13 and comprises a VL domain having at least one of the following complementarity determining regions (CDRs):

a) a CDR1 having at least 90% sequence identity to SEQ ID NO: 20;

b) a CDR2 having at least 90% sequence identity to SEQ ID NO: 17; and

c) a CDR3 having at least 90% sequence identity to SEQ ID NO: 18.

37. The method of embodiment 36, wherein said antibody that specifically binds to CXCL13 comprises a VL domain comprising a CDR1 having the sequence set forth in SEQ ID NO: 20, a CDR2 having the sequence set forth in SEQ ID NO: 17, and a CDR3 having the sequence set forth in SEQ ID NO: 18.

38. The method of embodiment 27 or 28, wherein said antibody is selected from the group consisting of MAb 5261, MAb 5378, MAb 5080, MAb 1476, and MAb 3D2.

39. The method of embodiment 38, wherein said antibody is mAb 5378.

40. The method of any one of embodiments 1-24, wherein said agent is a soluble form of CXCR5.

41. The method of any one of embodiments 1-40, wherein said agent inhibits the interaction of CXCL13 with a CXCL13 receptor.

42. The method of embodiment 41, wherein said CXCL13 receptor is CXCR5.

43. The method of any one of embodiments 1-42, wherein said agent inhibits CXCR5 receptor internalization.

44. The method of any one of embodiments 1-43, wherein said agent is administered with a pharmaceutically acceptable carrier.

45. The method of any one of embodiments 1-44, wherein said subject is an animal.

46. The method of embodiment 45, wherein said animal is a mammal.

47. The method of embodiment 46, wherein said mammal is a human.

Various embodiments of the claimed invention relates to an agent that inhibits CXCL13 activity for use in reducing the level of bacteria in a mucosal bacterial infection and increasing secretory immunoglobulin A (IgA) levels in a subject having a deficiency thereof that is secondary to said mucosal bacterial infection, wherein said mucosal bacterial infection is gastric mucosal *Helicobacter* infection and, wherein said agent is an antibody or antigen-binding fragment thereof that specifically binds to CXCL13.

BRIEF DESCRIPTION OF THE DRAWINGS/FIGURES

FIG. 1 shows the level of *H. suis* specific 16S ribosomal RNA in the gastric mucosa of *H. suis* infected mice treated with anti-CXCL13 antibody or isotype control antibody as determined by real-time quantitative PCR.

FIGS. 2A and 2B show the expression of TGF-β (FIG. 2A) and IL-6 (FIG. 2B) mRNA in the stomach of *H. suis* infected mice after isotype control or anti-CXCL13 antibody treatment.

FIGS. 3A and 3B show serum levels of anti- *H. suis* IgG (FIG. 3A) and IgA (FIG. 3B) of *H. suis* infected mice treated with anti-CXCL13 antibody or isotype control antibody.

FIGS. 4A and 4B show levels of anti-*H. suis* IgG (FIG. 4A) and IgA (FIG. 4B) in the gastric juice of *H. suis* infected mice treated with anti-CXCL13 antibody or isotype control antibody.

DETAILED DESCRIPTION OF THE INVENTION

As demonstrated herein, agents that inhibit CXCL13 activity (*e.g.*, an anti-CXCL13 antibody or binding fragment thereof) can reduce bacterial load and increase levels of immunoglobulin A (IgA) specific for the infective agent in mucosal tissue in an animal model for gastric infection (i.e., mice infected with *Helicobacter* bacteria (*see* Nobutani *et al.* (2010)). Administration of an anti-CXCL13 antibody also increased the expression levels of TGF-β and IL-6, which are involved in the upregulation of IgA levels, in the stomachs of uninfected mice. Therefore, agents that inhibit CXCL13 activity are also useful for generally upregulating levels of IgA in IgA deficient subjects.

The term "immunoglobulin A" or "IgA" refers to an immunoglobulin having an alpha (α) constant region in its heavy chains. The terms "immunoglobulin A" and "IgA" encompass monomeric IgA (i.e., a single molecule) and polymeric IgA (composed of more than one molecule), including, but not limited to, dimeric IgA (composed of two molecules) and trimeric IgA (composed of three molecules). IgA monomers are joined together as polymers (e.g., dimers) at the constant regions of their heavy chains by a J chain. The presence of J chains in IgA polymers allows the IgA polymer to attach to secretory component, a protein produced by epithelial cells.

The terms "immunoglobulin A" and "IgA" refer to both subclasses of IgA, IgA1 and IgA2. The light chains of IgA1 are covalently bound to its heavy chains. The light chains of IgA2, however, are bound to each other through disulfide bonds and to its heavy chains by non-covalent interactions. IgA1 predominates in serum, wherein most of it occurs as a monomer. Secretory lymphoid tissues produce more IgA2 than non-secretory lymphoid tissues.

IgA can also be classified based on its location. The terms "immunoglobulin A" and "IgA" refer to both serum IgA (i.e., found in serum) and secretory IgA, which are found in mucosal secretions (e.g., tears, saliva, colostrum, sweat, and secretions from the genitourinary tract, gastrointestinal tract, prostate and respiratory epithelium). Secretory IgA generally occurs as dimers or trimers joined by J chains and comprising secretory component. The secretory component of secretory IgA protects the immunoglobulin from being degraded by proteolytic enzymes, such as those found in the gastrointestinal tract environment. The terms "secretory immunoglobulin A" and "secretory IgA" refer to IgA that is found in mucosal secretions. Thus, the terms "secretory IgA" and "secretory immunoglobulin A" can refer to polymers of IgA, J chains that link the monomers, and the secretory component.

Naïve B cells initially express IgM and/or IgD on their surface, and once activated, the antibodies that are initially produced are primarily of the IgM isotype. If these activated B cells encounter specific signaling molecules, the B cells can undergo a "class switch" to differentiate into a cell that expresses IgG, IgA, or IgE receptors.

During class switching, the constant region of the immunoglobulin heavy chain changes but the variable regions, and therefore antigenic specificity, stay the same.

Multiple studies have indicated that transforming growth factor-beta (TGF-β) induces IgA class switching and interleukin-6 (IL-6) stimulates IgA synthesis (Sonoda *et al.* (1989) *J Exp Med* 170:1415-1420; Beagley *et al.* (1989) *J Exp Med* 169:2133-2148). While not being bound by any theory or mechanism of action, it is believed that agents that inhibit CXCL13 activity increase IgA levels by increasing levels of TGF-β and IL-6.

As demonstrated herein, inhibition of CXCL13 activity leads to increases in the expression levels of TGF-β and IL-6 and levels of IgA and is, therefore, useful for increasing IgA levels in a subject deficient in IgA. As used herein, "IgA deficiency" refers to reduced levels of immunoglobulin A as compared to a control subject. A subject having IgA deficiency can experience reduced levels of serum IgA, reduced levels of secretory IgA, or both, as compared to a suitable control subject. The subject may have reduced levels of secretory IgA in all secretions and at all mucosal surfaces or in only one or more type of mucosal surface and/or secretion. In some embodiments, the subject having an IgA deficiency has reduced levels of gastric IgA as compared to a suitable control.

In some embodiments, the subject having an IgA deficiency has about 95%, about 90%, about 85%, about 80%, about 75%, about 70%, about 65%, about 60%, about 55%, about 50%, about 45%, about 40%, about 35%, about 30%, about 25%, about 20%, about 15%, about 10%, or less of IgA (serum, secretory, or total) than a control subject.

One of ordinary skill in the art would understand how to select a suitable control subject in which to compare a subject believed to have an IgA deficiency. Non-limiting examples of suitable control subjects include subjects that present as healthy individuals, individuals that do not have or are believed not to have an active infection (e.g., mucosal infection) or inflammatory disorder, and a subject that does not have a genetic predisposition or a family history for IgA deficiency.

In those embodiments wherein the subject has a serum IgA deficiency, serum levels of IgA are less than about 0.1g/L, less than about 0.09 g/L, less than about 0.08 g/L, less than about 0.07 g/L, less than about 0.06 g/L, less than about 0.05 g/L, less than about 0.04 g/L, less than about 0.03 g/L, less than about 0.02 g/L, less than about 0.01 g/L, or less.

While the term "IgA deficiency" encompasses all individuals having reduced levels of IgA as compared to a control subject, many individuals having IgA deficiency have otherwise normal levels of IgM and IgG.

IgA deficiency can be primary (inherited) or secondary (acquired). Primary IgA deficiency is genetically determined and primarily congenital, such as most forms of selective IgA deficiency. Selective IgA deficiency has been defined by the Pan-American Group for Immunodeficiency and the European Society for Immunodeficiencies as serum IgA levels of less than 0.07 g/L with normal IgM and IgG levels in individuals greater than or equal to 4 years of age (Notarangelo *et al.* (2009) *J Allergy Clin Immunol* 124:1161-1178).

Certain infections or types of drugs or other agents that suppress the immune system can cause a secondary IgA deficiency, which is generally transient. Exposure to immunosuppressants, D-penicillamine, sulfasalazine, aurothioglucose, fenclofenac, gold, captopril, zonisamide, phenytoin, valproic acid, thyroxine, chloroquine, carabamazepine, hydantoin, levamisole, ibuprofen, salicylic acid, benzene, and cyclosporin A, for example, can result in a transient IgA deficiency, which resolves upon clearance of the drug. Non-limiting examples of infections that can cause secondary IgA deficiency include rubella, cytomegaloviruses, *Toxoplasma gondii*, and Epstein-Barr virus.

In some embodiments, the subject has IgA deficiency secondary to a mucosal infection. In some of these embodiments, the mucosal infection is a bacterial infection. In certain embodiments, the bacterial infection that results in a secondary IgA deficiency is a *Heliobacter* infection, such as *H. pylori*, *H. heilmannii*, or *H. suis*.

In some embodiments of the presently disclosed methods, administration of an agent that inhibits CXCL13 activity to a subject having a deficiency in IgA results in an increase in total IgA (serum and secretory). In other embodiments, the administration of the CXCL13 inhibitory agent results in an increase in secretory IgA. In particular embodiments, the subject that has been administered a CXCL13 inhibitory agent experiences an increase in gastric levels of IgA. In those embodiments wherein the subject is undergoing attack by an infectious agent, the administration of a CXCL13 inhibitory agent can increase levels of IgA specific for the infectious agent, which in some embodiments can lead to increased clearance of the infectious agent.

In certain embodiments, administration of an agent that inhibits CXCL13 activity increases serum, secretory, or total IgA levels by about 1%, about 2%, about 3%, about

4%, about 5%, about 10%, about 15%, about 20%, about 30%, about 40%, about 50%, about 60%, about 70%, about 80%, about 90%, about 100%, or more in the subject.

Given that inhibitors of CXCL13 activity can increase IgA levels, agents that inhibit CXCL13 activity can be used to treat inflammatory disorders in subjects having a deficiency in IgA. Inflammatory diseases are characterized by inflammation and tissue destruction, or a combination thereof. By "anti-inflammatory activity" is intended a reduction or prevention of inflammation. "Inflammatory disease" or “inflammatory disorder” includes any inflammatory immune-mediated process where the initiating event or target of the immune response involves non-self antigen(s), including, for example, alloantigens, xenoantigens, viral antigens, bacterial antigens, self antigens, unknown antigens, or allergens. In some embodiments, the inflammatory disorder is an infectious disease. In one embodiment, the inflammatory disorder is associated with and/or caused by a mucosal infection (e.g., bacterial, viral). In some embodiments, the inflammatory disease is associated with and/or caused by a bacterial infection, *e.g.*, an *E. coli* or a *Helicobacter* infection, *e.g.*, a *H. pylori*, *H. heilmannii*, *H. acinonychis*, *H. anseris*, *H. aurati*, *H. baculiformis*, *H. bilis*, *H. bizzozeronii*, *H. brantae*, *H. candadensis*, *H. canis*, *H. cholecystus*, *H. cinaedi*, *H. cynogastricus*, *H. equorum*, *H. felis*, *H. fenelliae*, *H. ganmani*, *H. hepaticus*, *H. mesocricetorum*, *H. marmotae*, *H. muridarum*, *H. mustelae*, *H. pametensis*, *H. pullorum*, *H. rappini*, *H. rodentium*, *H. salomonis*, *H. suis*, *H. trogontum*, *H. typhlonius, and H. winghamensis* infection. In certain embodiments, the *Helicobacter* infection is a *H. pylori*, a *H. heilmannii*, or a *H. suis* infection.

In a further embodiment, the *Helicobacter*-associated inflammatory disease is MALT lymphoma (e.g., gastric MALT lymphoma), a gastric cancer (*e.g.*, esophageal or stomach cancer), a gastric or duodenal ulcer, gastritis (an inflammation of the stomach lining), or a gastric lesion (*see, e.g.,* Chen *et al.*, *J Clin Pathol 55*(2):133-7 (2002); Genta *et al.*, *Hum Pathol 24*(6):577-83 (1993); Okiyama *et al.*, *Pathol Int 55*(7):398-404 (2005)).

In some embodiments, administration of an agent that inhibits CXCL13 activity results in a reduction in the burden of an infectious agent (e.g., bacteria) in the subject. In some of these embodiments, administration of the anti-CXCL13 agent results in a reduction in the burden of an infectious agent (e.g., bacteria) in the mucosa and in some of these embodiments, levels of the infectious agent (e.g., bacteria) in at least one mucosal secretion is reduced. In some of these embodiments, administration of an anti-CXCL13 agent to a subject having an infection results in a reduction in the levels of an infectious agent (e.g., bacteria) by at least 1%, at least 5%, at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or more in the subject.

In some of those embodiments wherein a CXCL13 inhibitory agent is administered to a subject having an IgA deficiency, the CXCL13 inhibitory agent increases IgA antibody responses in a mucosal tissue of said subject. In these embodiments, the levels of antigen-specific IgA levels (e.g., IgA that specifically recognize an infectious agent) increase, which in some embodiments, results in more efficient clearance of an infectious agent. The term "inflammatory disorder" or "inflammatory disease" includes, but is not limited to, allergic reactions to allergens. Allergic reactions are mediated by immunoglobulin E (IgE). IgA can bind allergenic substances, thereby preventing allergens from binding IgE or activating T cells responsible for delayed-type hypersensitivity. Therefore, the administration of an agent that inhibits CXCL13 activity resulting in an increase in IgA levels can be used to treat or prevent allergic reactions, including, but not limited to, asthma, allergic rhinitis, allergic sinusitis, contact dermatitis, eczema, urticaria, dyspnea, vomiting, bloating, and diarrhea, in response to various allergens, including, but not limited to, certain foods, drugs, insect stings, pollens, latex, and plant toxins.

Further, for purposes of the present invention, the term "inflammatory disease(s)" includes, but is not limited to, "autoimmune disease(s)" also referred to herein as "autoimmune disorder(s)" As used herein, the term "autoimmunity" is generally understood to encompass inflammatory immune-mediated processes involving "self" antigens. In autoimmune diseases, self antigen(s) trigger host immune responses.

In some embodiments, the inflammatory disease is the result of a genetically determined selective IgA-deficiency which may prevent clearing of an infectious agent or precipitate an autoimmune disease, including, but not limited to, rheumatoid arthritis, systemic lupus erythematosus, Graves disease, Type 1 diabetes, myasthenia gravis, Sjogren syndrome, multiple sclerosis, or celiac sprue (Wang *et al.* (2011) *Mol Med* 17(11-12):1383-1396). In some embodiments, the inflammatory disease is a B cell-mediated inflammatory disease. As used herein, the term "B cell-mediated inflammatory disease" is an inflammatory disease as described herein, wherein the pathogenesis, progression, or both the pathogenesis and progression of the disease is primarily dependent upon the activity of B cells. Non-limiting examples of B cell-mediated inflammatory diseases include those that are characterized by the production of autoantibodies.

A "B cell" is a lymphocyte that matures within the bone marrow, and includes a naive B cell, memory B cell, or effector B cell (plasma cells). The B cell herein may be a normal or non-malignant B cell.

A "B-cell surface marker" or "B-cell surface antigen" herein is an antigen expressed on the surface of a B cell that can be targeted with an antagonist that binds thereto. Exemplary B-cell surface markers include, for instance, CD10, CD19, CD20, CD21, CD22, CD23, CD24, CD37, CD40, CD53, CD72, CD73, CD74, CDw75, CDw76, CD77, CDw78, CD79a, CD79b, CD80, CD81, CD82, CD83, CDw84, CD85 and CD86, and CXCR5. The B-cell surface marker of particular interest is preferentially expressed on B cells compared to other non-B-cell tissues of a mammal and may be expressed on both precursor B cells and mature B cells. The preferred B-cell surface markers herein are CD19 and CXCR5.For purposes of the present invention, the term "inflammatory disease(s)" includes, but is not limited to, "autoimmune disease(s)."

According to the presently disclosed methods, an agent that inhibits CXCL13 activity is administered to a subject having an IgA deficiency. In certain embodiments, an agent is administered to a subject in need thereof for the treatment of an inflammatory disorder.

In some embodiments, treatment includes the application or administration of an agent that inhibits CXCL13 activity (*e.g.*, an anti-CXCL13 or anti-CXCR5 binding molecule) to a subject, or application or administration of the agent to an isolated tissue or cell line from a subject, where the subject has an inflammatory disorder, a symptom of an inflammatory disorder, or a predisposition toward an inflammatory disorder. In another embodiment, treatment is also intended to include the application or administration of a pharmaceutical composition comprising the agent that inhibits CXCL13 activity (*e.g.*, an anti-CXCL13 or anti-CXCR5 binding molecule) to a subject, or application or administration of a pharmaceutical composition comprising the agent to an isolated tissue or cell line from a subject, who has an inflammatory disorder, a symptom of an inflammatory disorder, or a predisposition toward an inflammatory disorder.

In accordance with the methods of the present invention, at least one agent that inhibits CXCL13 activity (*e.g.*, anti-CXCL13 or anti-CXCR5 binding molecule) is used to promote a positive therapeutic response with respect to treatment or prevention of an IgA deficiency and/or an inflammatory disorder. By "positive therapeutic response" with respect to an inflammatory disease is intended an improvement in the disease in association with the anti-inflammatory activity, anti-angiogenic activity, anti-apoptotic activity, or the like, of the administered agent, and/or an improvement in the symptoms associated with the disease. That is, an anti-proliferative effect, the prevention of further proliferation of the CXCL13-expressing cell, a reduction in the inflammatory response including but not limited to reduced secretion of inflammatory cytokines, adhesion molecules, proteases, immunoglobulins (in instances where the CXCL13 bearing cell is a B cell), combinations thereof, and the like, increased production of anti-inflammatory proteins, a reduction in the number of autoreactive cells, an increase in immune tolerance, inhibition of autoreactive cell survival, reduction in apoptosis, reduction in endothelial cell migration, increase in spontaneous monocyte migration, reduction in the number of ectopic lymphoid follicles, reduction in the number of B cells present in affected tissues, reduction in the migration of B cells to the affected tissues, reduction in and/or a decrease in one or more symptoms mediated by stimulation of CXCL13-expressing cells can be observed. By "positive therapeutic response" with respect to an infectious disease is intended clearance of the infectious agent, for example, a bacteria and an improvement in the disease symptoms associated with the infection.

Such positive therapeutic responses are not limited to the route of administration and may comprise administration to the donor, the donor tissue (such as for example organ perfusion), the host, any combination thereof, and the like. Clinical response can be assessed using screening techniques such as magnetic resonance imaging (MRI) scan, x-radiographic imaging, computed tomographic (CT) scan, flow cytometry or fluorescence-activated cell sorter (FACS) analysis, histology, gross pathology, and blood chemistry, including but not limited to changes detectable by ELISA, RIA, chromatography, and the like. In addition to these positive therapeutic responses, the subject undergoing therapy with the agent that inhibits CXCL13 activity (*e.g.*, anti-CXCL13 or anti-CXCR5 binding molecule) may experience the beneficial effect of an improvement in the symptoms associated with the inflammatory disorder.

As used herein, the terms "treat" or "treatment" refer to both therapeutic treatment and prophylactic or preventative measures, wherein the object is to prevent or slow down (lessen), reduce the exacerbation of, or prevent the recurrence of an undesired physiological change or disorder, such as the progression of an inflammatory disorder.

Beneficial or desired clinical results include, but are not limited to, alleviation of symptoms, diminishment of extent of disease, stabilized (*i.e.*, not worsening) state of disease, delay or slowing of disease progression, amelioration or palliation of the disease state, and remission (whether partial or total), whether detectable or undetectable. "Treatment" can also mean prolonging survival as compared to expected survival if not receiving treatment. Those in need of treatment include those already with the condition or disorder as well as those prone to have the condition or disorder or those in which the condition or disorder is to be prevented.

By "subject" or "individual" or "animal" or "patient" or "mammal," is meant any subject, particularly a mammalian subject, for whom diagnosis, prognosis, or therapy is desired. Mammalian subjects include humans, domestic animals, farm animals, and zoo, sports, or pet animals such as dogs, cats, guinea pigs, rabbits, rats, mice, horses, cows, and so on.

As used herein, phrases such as "a subject that would benefit from administration of an agent that inhibits CXCL13 activity" and "an animal in need of treatment" includes subjects, such as mammalian subjects, that would benefit from administration of an agent that inhibits CXCL13 activity (*e.g.*, an anti-CXCL13 or anti-CXCR5 antibody) for treatment, *i.e.*, palliation or prevention of an inflammatory disorder. As described in more detail herein, an anti-CXCL13 or anti-CXCR5 antibody can be used in unconjugated form or can be conjugated, *e.g.*, to a drug, prodrug, or an isotope.

The presently disclosed methods utilize an agent that inhibits CXCL13 activity. CXCL13 (otherwise known as homeostatic B Cell-attracting chemokine 1 (BCA-1) or ANGIE, BLC, BLR1L, ANGIE2, or Scyb13) is constitutively expressed in secondary lymphoid organs (*e.g.*, spleen, lymph nodes, and Peyer's patches) by follicular dendritic cells (FDCs) and macrophages. *See* Gunn *et al.*, *Nature 391*:799-803 (1998) and Carlsen *et al.*, *Blood 104*(10):3021-3027 (2004). CXCL13 primarily acts through the G-protein-coupled CXCR5 receptor (Burkitt's lymphoma receptor 1). CXCR5 is expressed, *e.g.*, on mature B lymphocytes, CD4+ follicular helper T cells (Thf cells), a minor subset of CD8+ T cells, and activated tonsillar Treg cells. *See* Legler *et al.*, *J. Exp. Med. 187*:655-660 (1998); Förster *et al.*, *Blood 84*:830-840 (1994); Fazilleau *et al.*, *Immunity 30*:324-335 (2009); Ansel *et al.*, *J. Exp. Med. 190*:1123-1134 (1999); Lim *et al.*, *J. Clin. Invest. 114*(11):1640-1649 (2004); and R. Förster, Chapter in Academic Press Cytokine Reference, Aug. 2000.

As used herein, the terms "CXCL13" and "CXCL13 polypeptide" are used interchangeably. In certain embodiments, CXCL13 may include a full-sized CXCL13 or a fragment thereof, or a CXCL13 variant polypeptide, wherein the fragment of CXCL13 or CXCL13 variant polypeptide retains some or all functional properties of the full-sized CXCL13. The human CXCL13 polynucleotide and polypeptide sequences (SEQ ID NOs: 1 and 2, respectively) have been described, *see*, *e.g.*, Legler, *et. al.*, *J. Exp. Med. 187(4)*:655-660 (1998). The mouse CXCL13 polynucleotide and polypeptide sequences (SEQ ID NOs: 3 and 4, respectively) have been described, *see*, *e.g.*, Gunn, *et. al.*, *Nature 391(6669)*:799-803 (1998). Furthermore, the cynomolgus monkey CXCL13 polypeptide sequence has been described as shown in SEQ ID NO: 5.

As used herein, the terms "CXCR5" and "CXCR5 polypeptide" are used interchangeably. In certain embodiments, CXCR5 may include a full-sized CXCR5 or a fragment thereof, or a CXCR5 variant polypeptide, wherein the fragment of CXCR5 or CXCR5 variant polypeptide retains some or all functional properties of the full-sized CXCR5. The terms "CXCR5" and "CXCR5 polypeptide" also encompass a soluble form of CXCR5. As used herein, the term "soluble form of CXCR5" is a form of CXCR5 that is not bound to a plasma membrane. Full-length CXCR5 is a seven transmembrane receptor. Therefore, non-limiting examples of a soluble form of CXCR5 include fragments of CXCR5 that consist essentially of the extracellular domain (*e.g.*, about the first 60 amino acids). The human CXCR5 polynucleotide and polypeptide sequences are known in the art and provided herein as SEQ ID NOs: 6 and 7, respectively. The murine CXCR5 polynucleotide and polypeptide sequences are known in the art and provided herein as SEQ ID NOs: 8 and 9, respectively.

Agents useful for the inhibition of CXCL13 activity include small molecules, polypeptides, and polynucleotides. In certain embodiments, the agent blocks the binding of CXCL13 to its receptor. In some embodiments, the agent blocks the interaction between CXCL13 and CXCR5. In particular embodiments, the agent is a specific binding molecule that specifically binds CXCL13 or CXCR5. In some of these embodiments, the agent is an anti-CXCL13 or anti-CXCR5 antibody or an antigen-binding fragment thereof. In other embodiments, the agent is a soluble form of CXCR5.

As used herein, the term "polypeptide" is intended to encompass a singular "polypeptide" as well as plural "polypeptides," and refers to a molecule composed of monomers (amino acids) linearly linked by amide bonds (also known as peptide bonds). The term "polypeptide" refers to any chain or chains of two or more amino acids, and does not refer to a specific length of the product. Thus, peptides, dipeptides, tripeptides, oligopeptides, "protein," "amino acid chain," or any other term used to refer to a chain or chains of two or more amino acids, are included within the definition of "polypeptide," and the term "polypeptide" may be used instead of, or interchangeably with any of these terms. The term "polypeptide" is also intended to refer to the products of post-expression modifications of the polypeptide, including without limitation glycosylation, acetylation, phosphorylation, amidation, derivatization by known protecting/blocking groups, proteolytic cleavage, or modification by non-naturally occurring amino acids. A polypeptide may be derived from a natural biological source or produced by recombinant technology, but is not necessarily translated from a designated nucleic acid sequence. It may be generated in any manner, including by chemical synthesis.

A polypeptide useful in the presently disclosed methods may be of a size of about 3 or more, 5 or more, 10 or more, 20 or more, 25 or more, 50 or more, 75 or more, 100 or more, 200 or more, 500 or more, 1,000 or more, or 2,000 or more amino acids. Polypeptides may have a defined three-dimensional structure, although they do not necessarily have such structure. Polypeptides with a defined three-dimensional structure are referred to as folded, and polypeptides that do not possess a defined three-dimensional structure, but rather can adopt a large number of different conformations, are referred to as unfolded. As used herein, the term glycoprotein refers to a protein coupled to at least one carbohydrate moiety that is attached to the protein via an oxygen-containing or a nitrogen-containing side chain of an amino acid residue, *e.g.*, a serine residue or an asparagine residue.

By an "isolated" polypeptide or a fragment, variant, or derivative thereof is intended a polypeptide that is not in its natural milieu. No particular level of purification is required. For example, an isolated polypeptide can be removed from its native or natural environment. Recombinantly produced polypeptides and proteins expressed in host cells are considered isolated for purpose of the invention, as are native or recombinant polypeptides that have been separated, fractionated, or partially or substantially purified by any suitable technique.

Also included as polypeptides useful in the presently disclosed methods are fragments, derivatives, analogs, or variants of polypeptides, and any combination thereof. The terms "fragment," "variant," "derivative," and "analog" when referring to anti-CXCL13 or anti-CXCR5 antibodies or antibody polypeptides include any polypeptides that retain at least some of the antigen-binding properties of the corresponding antibody or antibody polypeptide. Fragments of polypeptides include proteolytic fragments, as well as deletion fragments, in addition to specific antibody fragments discussed elsewhere herein. Variants of anti-CXCL13 or anti-CXCR5 antibodies include fragments as described above, and also polypeptides with altered amino acid sequences due to amino acid substitutions, deletions, or insertions. Variants may occur naturally or be non-naturally occurring. Non-naturally occurring variants may be produced using art-known mutagenesis techniques. Variant polypeptides may comprise conservative or non-conservative amino acid substitutions, deletions, or additions. Variant polypeptides may also be referred to herein as "polypeptide analogs." As used herein a "derivative" of an anti-CXCL13 or anti-CXCR5 antibody or antibody polypeptide refers to a subject polypeptide having one or more residues chemically derivatized by reaction of a functional side group. Also included as "derivatives" are those peptides that contain one or more naturally occurring amino acid derivatives of the twenty standard amino acids. For example, 4-hydroxyproline may be substituted for proline; 5-hydroxylysine may be substituted for lysine; 3-methylhistidine may be substituted for histidine; homoserine may be substituted for serine; and ornithine may be substituted for lysine. Derivatives of anti-CXCL13 and anti-CXCR5 antibodies and antibody polypeptides, may include polypeptides that have been altered so as to exhibit additional features not found on the reference antibody or antibody polypeptide.

In the context of polypeptides, a "linear sequence" or a "sequence" is an order of amino acids in a polypeptide in an amino to carboxyl terminal direction in which residues that neighbor each other in the sequence are contiguous in the primary structure of the polypeptide.

The term "polynucleotide" is intended to encompass a singular nucleic acid as well as plural nucleic acids, and refers to an isolated nucleic acid molecule or construct, *e.g.*, messenger RNA (mRNA) or plasmid DNA (pDNA). A polynucleotide may comprise a conventional phosphodiester bond or a non-conventional bond (*e.g.*, an amide bond, such as found in peptide nucleic acids (PNA)). The term "nucleic acid" refers to any one or more nucleic acid segments, *e.g.*, DNA or RNA fragments, present in a polynucleotide. By "isolated" nucleic acid or polynucleotide is intended a nucleic acid molecule, DNA or RNA, that has been removed from its native environment. For example, a recombinant polynucleotide encoding an anti-CXCL13 or anti-CXCR5 binding molecule, *e.g.*, an antibody or antigen binding fragment thereof, contained in a vector is considered isolated for the purposes of the present invention. Further examples of an isolated polynucleotide include recombinant polynucleotides maintained in heterologous host cells or purified (partially or substantially) polynucleotides in solution. Isolated RNA molecules include *in vivo* or *in vitro* RNA transcripts of polynucleotides of the present invention. Isolated polynucleotides or nucleic acids according to the present invention further include such molecules produced synthetically. In addition, a polynucleotide or a nucleic acid may be or may include a regulatory element such as a promoter, ribosome binding site, or a transcription terminator.

As used herein, a "coding region" is a portion of nucleic acid that consists of codons translated into amino acids. Although a "stop codon" (TAG, TGA, or TAA) is not translated into an amino acid, it may be considered to be part of a coding region, but any flanking sequences, for example promoters, ribosome binding sites, transcriptional terminators, introns, and the like, are not part of a coding region. Two or more coding regions useful in the presently disclosed methods can be present in a single polynucleotide construct, *e.g.*, on a single vector, or in separate polynucleotide constructs, *e.g.*, on separate (different) vectors. Furthermore, any vector may contain a single coding region, or may comprise two or more coding regions, *e.g.*, a single vector may separately encode an immunoglobulin heavy chain variable region and an immunoglobulin light chain variable region. In addition, a vector, polynucleotide, or nucleic acid useful in the presently disclosed methods may encode heterologous coding regions, either fused or unfused to a nucleic acid encoding an anti-CXCL13 or anti-CXCR5 antibody or fragment, variant, or derivative thereof. Heterologous coding regions include without limitation specialized elements or motifs, such as a secretory signal peptide or a heterologous functional domain.

In certain embodiments, the polynucleotide or nucleic acid useful in the presently disclosed methods is DNA. In the case of DNA, a polynucleotide comprising a nucleic acid that encodes a polypeptide normally may include a promoter and/or other transcription or translation control elements operably associated with one or more coding regions. An operable association is when a coding region for a gene product, *e.g.*, a polypeptide, is associated with one or more regulatory sequences in such a way as to place expression of the gene product under the influence or control of the regulatory sequence(s). Two DNA fragments (such as a polypeptide coding region and a promoter associated therewith) are "operably associated" if induction of promoter function results in the transcription of mRNA encoding the desired gene product and if the nature of the linkage between the two DNA fragments does not interfere with the ability of the expression regulatory sequences to direct the expression of the gene product or interfere with the ability of the DNA template to be transcribed. Thus, a promoter region would be operably associated with a nucleic acid encoding a polypeptide if the promoter was capable of effecting transcription of that nucleic acid. The promoter may be a cell-specific promoter that directs substantial transcription of the DNA only in predetermined cells. Other transcription control elements, besides a promoter, for example enhancers, operators, repressors, and transcription termination signals, can be operably associated with the polynucleotide to direct cell-specific transcription. Suitable promoters and other transcription control regions are disclosed herein.

A variety of transcription control regions are known to those skilled in the art. These include, without limitation, transcription control regions that function in vertebrate cells, such as, but not limited to, promoter and enhancer segments from cytomegaloviruses (the immediate early promoter, in conjunction with intron-A), simian virus 40 (the early promoter), and retroviruses (such as Rous sarcoma virus). Other transcription control regions include those derived from vertebrate genes such as actin, heat shock protein, bovine growth hormone and rabbit β-globin, as well as other sequences capable of controlling gene expression in eukaryotic cells. Additional suitable transcription control regions include tissue-specific promoters and enhancers as well as lymphokine-inducible promoters (*e.g.*, promoters inducible by interferons or interleukins).

Similarly, a variety of translation control elements are known to those of ordinary skill in the art. These include, but are not limited to, ribosome binding sites, translation initiation and termination codons, and elements derived from picornaviruses (particularly an internal ribosome entry site, or IRES, also referred to as a CITE sequence).

In other embodiments, a polynucleotide useful in the presently disclosed methods is RNA, for example, in the form of messenger RNA (mRNA).

Polynucleotide and nucleic acid coding regions useful in the presently disclosed methods may be associated with additional coding regions that encode secretory or signal peptides, which direct the secretion of a polypeptide encoded by a polynucleotide of the present invention. According to the signal hypothesis, proteins secreted by mammalian cells have a signal peptide or secretory leader sequence that is cleaved from the mature protein once export of the growing protein chain across the rough endoplasmic reticulum has been initiated. Those of ordinary skill in the art are aware that polypeptides secreted by vertebrate cells generally have a signal peptide fused to the N-terminus of the polypeptide, which is cleaved from the complete or "full length" polypeptide to produce a secreted or "mature" form of the polypeptide. In certain embodiments, the native signal peptide, *e.g.*, an immunoglobulin heavy chain or light chain signal peptide is used, or a functional derivative of that sequence that retains the ability to direct the secretion of the polypeptide that is operably associated with it. Alternatively, a heterologous mammalian signal peptide, or a functional derivative thereof, may be used. For example, the wild-type leader sequence may be substituted with the leader sequence of human tissue plasminogen activator (TPA) or mouse β-glucuronidase.

The term "expression" as used herein refers to a process by which a gene produces a biochemical, for example, a polypeptide. The process includes any manifestation of the functional presence of the gene within the cell including, without limitation, gene knockdown as well as both transient expression and stable expression. It includes without limitation transcription of the gene into messenger RNA (mRNA), and the translation of such mRNA into polypeptide(s). If the final desired product is a biochemical, expression includes the creation of that biochemical and any precursors. Expression of a gene produces a "gene product." As used herein, a gene product can be either a nucleic acid, *e.g.*, a messenger RNA produced by transcription of a gene, or a polypeptide which is translated from a transcript. Gene products described herein further include nucleic acids with post transcriptional modifications, *e.g.*, polyadenylation, or polypeptides with post translational modifications, *e.g.*, methylation, glycosylation, the addition of lipids, association with other protein subunits, proteolytic cleavage, and the like.

A "binding molecule" or "antigen binding molecule" refers in its broadest sense to a molecule that specifically binds an antigenic determinant. In one embodiment, the binding molecule specifically binds to CXCL13 (also called BCA-1). In another embodiment, the binding molecule specifically binds to CXCR5. In another embodiment, a binding molecule useful in the presently disclosed methods is an antibody or an antigen binding fragment thereof, *e.g.*, an anti-CXCL13 or anti-CXCR5 antibody. In another embodiment, a binding molecule comprises at least one heavy or light chain CDR of an antibody molecule. In another embodiment, a binding molecule comprises at least two CDRs from one or more antibody molecules. In another embodiment, a binding molecule comprises at least three CDRs from one or more antibody molecules. In another embodiment, a binding molecule comprises at least four CDRs from one or more antibody molecules. In another embodiment, a binding molecule comprises at least five CDRs from one or more antibody molecules. In another embodiment, a binding molecule comprises at least six CDRs from one or more antibody molecules. In certain embodiments, one or more of the CDRs is from MAb 5261, MAb 5378, MAb 5080, MAb 1476, or 3D2.

In some embodiments, the presently disclosed methods involve certain anti-CXCL13 or anti-CXCR5 antibodies, or antigen-binding fragments, variants, or derivatives thereof. Unless specifically referring to full-sized antibodies such as naturally occurring antibodies, the terms "anti-CXCL13 antibodies" and "anti-CXCR5 antibodies" encompass full-sized antibodies as well as antigen-binding fragments, variants, analogs, or derivatives of such antibodies, *e.g.*, naturally occurring antibody or immunoglobulin molecules or engineered antibody molecules or fragments that bind antigen in a manner similar to antibody molecules.

As used herein, "human" or "fully human" antibodies include antibodies having the amino acid sequence of a human immunoglobulin and include antibodies isolated from human immunoglobulin libraries or from animals transgenic for one or more human immunoglobulins and that do not express endogenous immunoglobulins, as described infra and, for example, in U.S. Pat. No. 5,939,598 by Kucherlapati *et al.* "Human" or "fully human" antibodies also include antibodies comprising at least the variable domain of a heavy chain, or at least the variable domains of a heavy chain and a light chain, where the variable domain(s) have the amino acid sequence of human immunoglobulin variable domain(s).

"Human" or "fully human" antibodies also include "human" or "fully human" antibodies, as described above, that comprise, consist essentially of, or consist of, variants (including derivatives) of known anti-CXCL13 or anti-CXCR5 antibody molecules (*e.g.*, the VH regions and/or VL regions), which antibodies or fragments thereof immunospecifically bind to a CXCL13 or CXCR5 polypeptide or fragment or variant thereof. Standard techniques known to those of skill in the art can be used to introduce mutations in the nucleotide sequence encoding a human anti-CXCL13 or anti-CXCR5 antibody, including, but not limited to, site-directed mutagenesis and PCR-mediated mutagenesis which result in amino acid substitutions. Preferably, the variants (including derivatives) encode less than 50 amino acid substitutions, less than 40 amino acid substitutions, less than 30 amino acid substitutions, less than 25 amino acid substitutions, less than 20 amino acid substitutions, less than 15 amino acid substitutions, less than 10 amino acid substitutions, less than 5 amino acid substitutions, less than 4 amino acid substitutions, less than 3 amino acid substitutions, or less than 2 amino acid substitutions relative to the reference VH region, VHCDR1, VHCDR2, VHCDR3, VL region, VLCDR1, VLCDR2, or VLCDR3.

In certain embodiments, the amino acid substitutions are conservative amino acid substitutions, discussed further below. Alternatively, mutations can be introduced randomly along all or part of the coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for biological activity to identify mutants that retain activity (*e.g.*, the ability to bind a CXCL13 or CXCR5 polypeptide, *e.g.*, human, murine, or both human and murine CXCL13 or CXCR5). Such variants (or derivatives thereof) of "human" or "fully human" antibodies can also be referred to as human or fully human antibodies that are "optimized" or "optimized for antigen binding" and include antibodies that have improved affinity to antigen.

The terms "antibody" and "immunoglobulin" are used interchangeably herein. An antibody or immunoglobulin comprises at least the variable domain of a heavy chain, and normally comprises at least the variable domains of a heavy chain and a light chain. Basic immunoglobulin structures in vertebrate systems are relatively well understood. *See*, *e.g.*, Harlow et al. (1988) Antibodies: A Laboratory Manual (2nd ed.; Cold Spring Harbor Laboratory Press).

As will be discussed in more detail below, the term “immunoglobulin” comprises various broad classes of polypeptides that can be distinguished biochemically. Those skilled in the art will appreciate that heavy chains are classified as gamma, mu, alpha, delta, or epsilon, (γ, μ, α, δ, ε) with some subclasses among them (*e.g.*, γ1-γ4). It is the nature of this chain that determines the "class" of the antibody as IgG, IgM, IgA IgD, or IgE, respectively. The immunoglobulin subclasses (isotypes) *e.g.*, IgG1, IgG2, IgG3, IgG4, IgA1, etc. are well characterized and are known to confer functional specialization. Modified versions of each of these classes and isotypes are readily discernible to the skilled artisan in view of the instant disclosure and, accordingly, are within the scope of the instant invention. The use of all immunoglobulin classes are clearly within the scope of the presently disclosed methods, however, the following discussion will generally be directed to the IgG class of immunoglobulin molecules. With regard to IgG, a standard immunoglobulin molecule comprises two identical light chain polypeptides of a molecular weight of approximately 23,000 Daltons, and two identical heavy chain polypeptides of molecular weight 53,000-70,000. The four chains are typically joined by disulfide bonds in a "Y" configuration wherein the light chains bracket the heavy chains starting at the mouth of the "Y" and continuing through the variable region.

Light chains are classified as either kappa or lambda (κ, λ). Each heavy chain class may be bound with either a kappa or lambda light chain. In general, the light and heavy chains are covalently bonded to each other, and the "tail" portions of the two heavy chains are bonded to each other by covalent disulfide linkages or non-covalent linkages when the immunoglobulins are generated either by hybridomas, B-cells or genetically engineered host cells. In the heavy chain, the amino acid sequences run from an N-terminus at the forked ends of the Y configuration to the C-terminus at the bottom of each chain.

Both the light and heavy chains are divided into regions of structural and functional homology. The terms "constant" and "variable" are used functionally. In this regard, it will be appreciated that the variable domains of both the light (VL or VK) and heavy (VH) chain portions determine antigen recognition and specificity. Conversely, the constant domains of the light chain (CL) and the heavy chain (CH1, CH2 or CH3) confer important biological properties such as secretion, transplacental mobility, Fc receptor binding, complement binding, and the like. By convention, the numbering of the constant region domains increases as they become more distal from the antigen binding site or amino-terminus of the antibody. The N-terminal portion is a variable region and at the C-terminal portion is a constant region; the CH3 and CL domains actually comprise the carboxy-terminus of the heavy and light chain, respectively.

As indicated herein, the variable region allows the antibody to selectively recognize and specifically bind epitopes on antigens. That is, the VL domain and VH domain, or subset of the complementarity determining regions (CDRs) within these variable domains, of an antibody combine to form the variable region that defines a three dimensional antigen binding site. This quaternary antibody structure forms the antigen binding site present at the end of each arm of the Y. More specifically, the antigen binding site is defined by three CDRs on each of the VH and VL chains. In some instances, *e.g.*, certain immunoglobulin molecules derived from camelid species or engineered based on camelid immunoglobulins, a complete immunoglobulin molecule may consist of heavy chains only, with no light chains. *See*, *e.g.*, Hamers-Casterman *et al.*, *Nature 363*:446-448 (1993).

In naturally occurring antibodies, the six "complementarity determining regions" or "CDRs" present in each antigen binding domain are short, non-contiguous sequences of amino acids that are specifically positioned to form the antigen binding domain as the antibody assumes its three dimensional configuration in an aqueous environment. The remainder of the amino acids in the antigen binding domains, referred to as "framework" regions, show less inter-molecular variability. The framework regions largely adopt a β-sheet conformation and the CDRs form loops that connect, and in some cases form part of, the β-sheet structure. Thus, framework regions act to form a scaffold that provides for positioning the CDRs in correct orientation by inter-chain, non-covalent interactions. The antigen binding domain formed by the positioned CDRs defines a surface complementary to the epitope on the immunoreactive antigen. This complementary surface promotes the non-covalent binding of the antibody to its cognate epitope. The amino acids comprising the CDRs and the framework regions, respectively, can be readily identified for any given heavy or light chain variable domain by one of ordinary skill in the art, since they have been precisely defined (see below).

In the case where there are two or more definitions of a term that is used and/or accepted within the art, the definition of the term as used herein is intended to include all such meanings unless explicitly stated to the contrary. A specific example is the use of the term "complementarity determining region" ("CDR") to describe the non-contiguous antigen combining sites found within the variable region of both heavy and light chain polypeptides. This particular region has been described by Kabat et al. (1983) U.S. Dept. of Health and Human Services, "Sequences of Proteins of Immunological Interest" and by Chothia and Lesk, *J. Mol. Biol. 196*:901-917 (1987), where the definitions include overlapping or subsets of amino acid residues when compared against each other. Nevertheless, application of either definition to refer to a CDR of an antibody or variants thereof is intended to be within the scope of the term as defined and used herein. The appropriate amino acid residues that encompass the CDRs as defined by each of the above cited references are set forth below in Table 1 as a comparison. The exact residue numbers that encompass a particular CDR will vary depending on the sequence and size of the CDR. Those skilled in the art can routinely determine which residues comprise a particular CDR given the variable region amino acid sequence of the antibody.

Table 1. CDR Definitions[1]

	Kabat	Chothia
VH CDR1	31-35	26-32
VH CDR2	50-65	52-58
VH CDR3	95-102	95-102
VL CDR1	24-34	26-32
VL CDR2	50-56	50-52
VL CDR3	89-97	91-96

[1]Numbering of all CDR definitions in Table 1 is according to the numbering conventions set forth by Kabat et al. (see below).

Kabat *et al.* also defined a numbering system for variable domain sequences that is applicable to any antibody. One of ordinary skill in the art can unambiguously assign this system of "Kabat numbering" to any variable domain sequence, without reliance on any experimental data beyond the sequence itself. As used herein, "Kabat numbering" refers to the numbering system set forth by Kabat *et al.* (1983) U.S. Dept. of Health and Human Services, "Sequence of Proteins of Immunological Interest." Unless otherwise specified, references to the numbering of specific amino acid residue positions in an anti-CXCL13 antibody or antigen-binding fragment, variant, or derivative thereof of the present invention are according to the Kabat numbering system.

Antibodies or antigen-binding fragments, variants, or derivatives thereof useful in the presently disclosed methods include, but are not limited to, polyclonal, monoclonal, multispecific, human, humanized, primatized, or chimeric antibodies, single-chain antibodies, epitope-binding fragments, *e.g.*, Fab, Fab' and $F(ab')_2$, Fd, Fvs, single-chain Fvs (scFv), disulfide-linked Fvs (sdFv), fragments comprising either a VL or VH domain, fragments produced by a Fab expression library, and anti-idiotypic (anti-Id) antibodies (including, *e.g.*, anti-Id antibodies to anti-CXCL13 or anti-CXCR5 antibodies). ScFv molecules are known in the art and are described, *e.g.*, in U.S. Pat. No. 5,892,019. Immunoglobulin or antibody molecules used in the presently disclosed methods can be of any type (*e.g.*, IgG, IgE, IgM, IgD, IgA, and IgY), class (*e.g.*, IgG1, IgG2, IgG3, IgG4, IgA1, and IgA2, etc.), or subclass of immunoglobulin molecule.

As used herein, the term "heavy chain portion" includes amino acid sequences derived from an immunoglobulin heavy chain. A polypeptide comprising a heavy chain portion comprises at least one of: a CH1 domain, a hinge (*e.g.*, upper, middle, and/or lower hinge region) domain, a CH2 domain, a CH3 domain, or a variant or fragment thereof. For example, a binding polypeptide for use in the presently disclosed methods may comprise a polypeptide chain comprising a CH1 domain; a polypeptide chain comprising a CH1 domain, at least a portion of a hinge domain, and a CH2 domain; a polypeptide chain comprising a CH1 domain and a CH3 domain; a polypeptide chain comprising a CH1 domain, at least a portion of a hinge domain, and a CH3 domain, or a polypeptide chain comprising a CH1 domain, at least a portion of a hinge domain, a CH2 domain, and a CH3 domain. In another embodiment, a polypeptide useful in the presently disclosed methods comprises a polypeptide chain comprising a CH3 domain. Further, a binding polypeptide for use in the presently disclosed methods may lack at least a portion of a CH2 domain (*e.g.*, all or part of a CH2 domain). As set forth above, it will be understood by one of ordinary skill in the art that these domains (*e.g.*, the heavy chain portions) may be modified such that they vary in amino acid sequence from the naturally occurring immunoglobulin molecule.

In certain anti-CXCL13 or anti-CXCR5 antibodies, or antigen-binding fragments, variants, or derivatives thereof disclosed herein, the heavy chain portions of one polypeptide chain of a multimer are identical to those on a second polypeptide chain of the multimer. Alternatively, heavy chain portion-containing monomers useful in the presently disclosed methods are not identical. For example, each monomer may comprise a different target binding site, forming, for example, a bispecific antibody.

The heavy chain portions of a binding molecule for use in the methods disclosed herein may be derived from different immunoglobulin molecules. For example, a heavy chain portion of a polypeptide may comprise a C_{H1} domain derived from an IgG1 molecule and a hinge region derived from an IgG3 molecule. In another example, a heavy chain portion can comprise a hinge region derived, in part, from an IgG1 molecule and, in part, from an IgG3 molecule. In another example, a heavy chain portion can comprise a chimeric hinge derived, in part, from an IgG1 molecule and, in part, from an IgG4 molecule.

As used herein, the term "light chain portion" includes amino acid sequences derived from an immunoglobulin light chain, *e.g.*, a kappa or lambda light chain. Preferably, the light chain portion comprises at least one of a VL or CL domain.

Anti-CXCL13 or anti-CXCR5 antibodies, or antigen-binding fragments, variants, or derivatives thereof useful in the presently disclosed methods may be described or specified in terms of the epitope(s) or portion(s) of an antigen, *e.g.*, a target polypeptide disclosed herein (*e.g.*, CXCL13 or CXCR5) that they recognize or specifically bind. The portion of a target polypeptide that specifically interacts with the antigen binding domain of an antibody is an "epitope," or an "antigenic determinant." A target polypeptide may comprise a single epitope, but typically comprises at least two epitopes, and can include any number of epitopes, depending on the size, conformation, and type of antigen. Furthermore, it should be noted that an "epitope" on a target polypeptide may be or may include non-polypeptide elements, *e.g.*, an epitope may include a carbohydrate side chain.

The minimum size of a peptide or polypeptide epitope for an antibody is thought to be about four to five amino acids. Peptide or polypeptide epitopes preferably contain at least seven, more preferably at least nine and most preferably between at least about 15 to about 30 amino acids. Since a CDR can recognize an antigenic peptide or polypeptide in its tertiary form, the amino acids comprising an epitope need not be contiguous, and in some cases, may not even be on the same peptide chain. A peptide or polypeptide epitope recognized by anti-CXCL13 or anti-CXCR5 antibodies useful in the presently disclosed methods may contain a sequence of at least 4, at least 5, at least 6, at least 7, more preferably at least 8, at least 9, at least 10, at least 15, at least 20, at least 25, or between about 15 to about 30 contiguous or non-contiguous amino acids of CXCL13 or CXCR5.

By "specifically binds," it is generally meant that an antibody binds to an epitope via its antigen binding domain, and that the binding entails some complementarity between the antigen binding domain and the epitope. According to this definition, an antibody is said to "specifically bind" to an epitope when it binds to that epitope, via its antigen binding domain more readily than it would bind to a random, unrelated epitope. The term "specificity" is used herein to qualify the relative affinity by which a certain antibody binds to a certain epitope. For example, antibody "A" may be deemed to have a higher specificity for a given epitope than antibody "B," or antibody "A" may be said to bind to epitope "C" with a higher specificity than it has for related epitope "D."

By "preferentially binds," it is meant that the antibody specifically binds to an epitope more readily than it would bind to a related, similar, homologous, or analogous epitope. Thus, an antibody that "preferentially binds" to a given epitope would more likely bind to that epitope than to a related epitope, even though such an antibody may cross-react with the related epitope.

By way of non-limiting example, an antibody may be considered to bind a first epitope preferentially if it binds said first epitope with a dissociation constant (K_D) that is less than the antibody's K_D for the second epitope. In another non-limiting example, an antibody may be considered to bind a first antigen preferentially if it binds the first epitope with a K_D that is at least one order of magnitude less than the antibody's K_D for the second epitope. In another non-limiting example, an antibody may be considered to bind a first epitope preferentially if it binds the first epitope with a K_D that is at least two orders of magnitude less than the antibody's K_D for the second epitope.

In another non-limiting example, an antibody may be considered to bind a first epitope preferentially if it binds the first epitope with an off rate (k(off)) that is less than the antibody's k(off) for the second epitope. In another non-limiting example, an antibody may be considered to bind a first epitope preferentially if it binds the first epitope with an k(off) that is at least one order of magnitude less than the antibody's k(off) for the second epitope. In another non-limiting example, an antibody may be considered to bind a first epitope preferentially if it binds the first epitope with an k(off) that is at least two orders of magnitude less than the antibody's k(off) for the second epitope. An antibody or antigen-binding fragment, variant, or derivative useful in the methods disclosed herein may be said to bind a target polypeptide disclosed herein (*e.g.*, CXCL13 or CXCR5, *e.g.*, human, murine, or both human and murine CXCL13 or CXCR5) or a fragment or variant thereof with an off rate (k(off)) of less than or equal to 5×10^{-2} sec^{-1}, 10^{-2} sec^{-1}, or 5×10^{-3} sec^{-1}. In certain embodiments, the k(off) is less than or equal to about 3×10^{-2}, *e.g.*, wherein the antibody is 3D2 and the CXCL13 is human or mouse. In another embodiment, the k(off) is less than or equal to about 3×10^{-3}, *e.g.*, wherein the antibody is MAb 5261 and the CXCL13 is human or mouse. In another embodiment, the k(off) is less than or equal to about 4×10^{-3}, *e.g.*, wherein the antibody is MAb 5378 and the CXCL13 is human or mouse. In one embodiment, an antibody useful in the presently disclosed methods may be said to bind a target polypeptide disclosed herein (*e.g.*, CXCL13, *e.g.*, human, murine, or both human and murine CXCL13) or a fragment or variant thereof with an off rate (k(off)) less than or equal to 5×10^{-4} sec^{-1}, 10^{-4} sec^{-1}, 5×10^{-5} sec^{-1}, or 10^{-5} sec^{-1}, 5×10^{-6} sec^{-1}, 10^{-6} sec^{-1}, 5×10^{-7} sec^{-1} or 10^{-7} sec^{-1}.

An antibody or or antigen-binding fragment, variant, or derivative useful in the methods disclosed herein may be said to bind a target polypeptide disclosed herein (*e.g.*, CXCL13 or CXCR5, *e.g.*, human, murine, or both human and murine CXCL13 or CXCR5) or a fragment or variant thereof with an on rate (k(on)) of greater than or equal to 10^3 M^{-1} sec^{-1}, 5×10^3 M^{-1} sec^{-1}, 10^4 M^{-1} sec^{-1}, 5×10^4 M^{-1} sec^{-1}, 10^5 M^{-1} sec^{-1}, 5×10^5 M^{-1} sec^{-1}, 10^6 M^{-1} sec^{-1} or 5×10^6 M^{-1} sec^{-1}. In certain embodiments, the k(on) is greater than or equal to about 5×10^5, *e.g.*, wherein the antibody is 3D2 and the

CXCL13 is human; or the k(on) is greater than or equal to about 1 X 10^5, *e.g.*, wherein the antibody is 3D2 and the CXCL13 is mouse. In another embodiment, the k(on) is greater than or equal to about 1 X 10^6, *e.g.*, wherein the antibody is MAb 5261 and the CXCL13 is human or mouse. In another embodiment, the k(on) is greater than or equal to about 1 X 10^6, *e.g.*, wherein the antibody is MAb 5378 and the CXCL13 is human or mouse. In one embodiment, an antibody useful in the presently disclosed methods may be said to bind a target polypeptide disclosed herein (*e.g.*, CXCL13, *e.g.*, human, murine, or both human and murine CXCL13) or a fragment or variant thereof with an on rate (k(on)) greater than or equal to 10^5 M^{-1} sec^{-1}, 5 X 10^5 M^{-1} sec^{-1}, 10^6 M^{-1} sec^{-1}, or 5 X 10^6 M^{-1} sec^{-1} or 10^7 M^{-1} sec^{-1}.

An antibody is said to competitively inhibit binding of a reference antibody, *e.g.*, an anti-CXCL13 or anti-CXCR5 antibody, to a given epitope if it preferentially binds to that epitope to the extent that it blocks, to some degree, binding of the reference antibody to the epitope. Competitive inhibition may be determined by any method known in the art, for example, competition ELISA assays. An antibody may be said to competitively inhibit binding of the reference antibody to a given epitope by at least 90%, at least 80%, at least 70%, at least 60%, or at least 50%.

As used herein, the term "affinity" refers to a measure of the strength of the binding of an individual epitope with the CDR of an immunoglobulin molecule. See, *e.g.*, Harlow *et al.* (1988) Antibodies: A Laboratory Manual (Cold Spring Harbor Laboratory Press, 2nd ed.) pages 27-28. As used herein, the term "avidity" refers to the overall stability of the complex between a population of immunoglobulins and an antigen, that is, the functional combining strength of an immunoglobulin mixture with the antigen. See, *e.g.*, Harlow at pages 29-34. Avidity is related to both the affinity of individual immunoglobulin molecules in the population with specific epitopes, and also the valencies of the immunoglobulins and the antigen. For example, the interaction between a bivalent monoclonal antibody and an antigen with a highly repeating epitope structure, such as a polymer, would be one of high avidity.

Anti-CXCL13 or anti-CXCR5 antibodies or antigen-binding fragments, variants, or derivatives thereof useful in the presently disclosed methods may also be described or specified in terms of their cross-reactivity. As used herein, the term "cross-reactivity" refers to the ability of an antibody, specific for one antigen, to react with a second antigen; a measure of relatedness between two different antigenic substances. Thus, an antibody is cross reactive if it binds to an epitope other than the one that induced its formation. The cross reactive epitope generally contains many of the same complementary structural features as the inducing epitope, and in some cases, may actually fit better than the original.

For example, certain antibodies have some degree of cross-reactivity, in that they bind related, but non-identical epitopes, *e.g.*, epitopes with at least 95%, at least 90%, at least 85%, at least 80%, at least 75%, at least 70%, at least 65%, at least 60%, at least 55%, and at least 50% identity (as calculated using methods known in the art and described herein) to a reference epitope. An antibody may be said to have little or no cross-reactivity if it does not bind epitopes with less than 95%, less than 90%, less than 85%, less than 80%, less than 75%, less than 70%, less than 65%, less than 60%, less than 55%, and less than 50% identity (as calculated using methods known in the art and described herein) to a reference epitope. An antibody may be deemed "highly specific" for a certain epitope, if it does not bind any other analog, ortholog, or homolog of that epitope.

Anti-CXCL13 or anti-CXCR5 binding molecules, *e.g.*, antibodies or antigen-binding fragments, variants or derivatives thereof, useful in the presently disclosed methods may also be described or specified in terms of their binding affinity to a polypeptide, *e.g.*, CXCL13 or CXCR5, *e.g.*, human, murine, or both human and murine CXCL13 or CXCR5. In certain embodiments, the binding affinities of the antibodies or antigen-binding fragments thereof useful in the presently disclosed methods include those with a dissociation constant or Kd less than or no greater than 5×10^{-2} M, 10^{-2} M, 5×10^{-3} M, 10^{-3} M, 5×10^{-4} M, 10^{-4} M, 5×10^{-5} M, 10^{-5} M, 5×10^{-6} M, 10^{-6} M, 5×10^{-7} M, 10^{-7} M, 5×10^{-8} M, 10^{-8} M, 5×10^{-9} M, 10^{-9} M, 5×10^{-10} M, 10^{-10} M, 5×10^{-11} M, 10^{-11} M, 5×10^{-12} M, 10^{-12} M, 5×10^{-13} M, 10^{-13} M, 5×10^{-14} M, 10^{-14} M, 5×10^{-15} M, or 10^{-15} M. In one embodiment, the anti-CXCL13 or anti-CXCR5 binding molecule, *e.g.*, an antibody or antigen binding fragment thereof, useful in the presently disclosed methods binds human CXCL13 or CXCR5 with a Kd of less than about 5×10^{-9} M to about 5×10^{-10}M, *e.g.*, wherein the antibody is MAb 5261 and the Kd is less than or equal to about 5×10^{-9}M. In another embodiment, the anti-CXCL13 or anti-CXCR5 binding molecule, *e.g.*, an antibody or antigen binding fragment thereof, binds murine CXCL13 or CXCR5 with a Kd of less than about 5×10^{-7} M to about 9×10^{-9}M, *e.g.*, wherein the antibody is MAb 5261 and the Kd is less than or equal to about 8×10^{-9}M.

Anti-CXCL13 or anti-CXCR5 antibodies or antigen-binding fragments, variants or derivatives thereof useful in the presently disclosed methods may be "multispecific," *e.g.*, bispecific, trispecific, or of greater multispecificity, meaning that it recognizes and binds to two or more different epitopes present on one or more different antigens (*e.g.*, proteins) at the same time. Thus, whether an anti-CXCL13 or anti-CXCR5 antibody is "monospecific" or "multispecific," *e.g.*, "bispecific," refers to the number of different epitopes with which a binding polypeptide reacts. Multispecific antibodies may be specific for different epitopes of a target polypeptide described herein or may be specific for a target polypeptide as well as for a heterologous epitope, such as a heterologous polypeptide or solid support material.

As used herein the term "valency" refers to the number of potential binding domains, *e.g.*, antigen binding domains present in a binding polypeptide or CXCL13 or CXCR5 binding molecule, *e.g.*, an antibody or antigen binding fragment thereof. Each binding domain specifically binds one epitope. When a binding polypeptide or CXCL13 or CXCR5 binding molecule comprises more than one binding domain, each binding domain may specifically bind the same epitope, for an antibody with two binding domains, termed "bivalent monospecific," or to different epitopes, for an antibody with two binding domains, termed "bivalent bispecific." An antibody or antigen binding fragment thereof may also be bispecific and bivalent for each specificity (termed "bispecific tetravalent antibodies"). In another embodiment, tetravalent minibodies or domain deleted antibodies can be made.

Bispecific bivalent antibodies, and methods of making them, are described, for instance in U.S. Pat. Nos. 5,731,168; 5,807,706; 5,821,333; and U.S. Patent Appl. Publ. Nos. 2003/020734 and 2002/0155537. Bispecific tetravalent antibodies and methods of making them are described, for instance, in WO 02/096948 and WO 00/44788. See generally, PCT publications WO 93/17715; WO 92/08802; WO 91/00360; WO 92/05793; Tutt *et al., J. Immunol. 147*:60-69 (1991); U.S. Pat. Nos. 4,474,893; 4,714,681; 4,925,648; 5,573,920; 5,601,819; Kostelny *et al., J. Immunol. 148*: 1547-1553 (1992).

As previously indicated, the subunit structures and three dimensional configuration of the constant regions of the various immunoglobulin classes are well known. As used herein, the term “VH domain” includes the amino terminal variable domain of an immunoglobulin heavy chain and the term “CH1 domain” includes the first (most amino terminal) constant region domain of an immunoglobulin heavy chain. The

CH1 domain is adjacent to the VH domain and is amino terminal to the hinge region of an immunoglobulin heavy chain molecule.

As used herein the term “CH2 domain” includes the portion of a heavy chain molecule that extends, *e.g.*, from about residue 244 to residue 360 of an antibody using conventional numbering schemes (residues 244 to 360, Kabat numbering system; and residues 231-340, EU numbering system; see Kabat EA *et al.*). The CH2 domain is unique in that it is not closely paired with another domain. Rather, two N-linked branched carbohydrate chains are interposed between the two CH2 domains of an intact native IgG molecule. It is also well documented that the CH3 domain extends from the CH2 domain to the C-terminal of the IgG molecule and comprises approximately 108 residues.

As used herein, the term "hinge region" includes the portion of a heavy chain molecule that joins the CH1 domain to the CH2 domain. This hinge region comprises approximately 25 residues and is flexible, thus allowing the two N-terminal antigen binding regions to move independently. Hinge regions can be subdivided into three distinct domains: upper, middle, and lower hinge domains (Roux *et al.*, *J. Immunol. 161*:4083 (1998)).

As used herein the term "disulfide bond" includes the covalent bond formed between two sulfur atoms. The amino acid cysteine comprises a thiol group that can form a disulfide bond or bridge with a second thiol group. In most naturally occurring IgG molecules, the CH1 and CL regions are linked by a disulfide bond and the two heavy chains are linked by two disulfide bonds at positions corresponding to 239 and 242 using the Kabat numbering system (position 226 or 229, EU numbering system).

As used herein, the term "chimeric antibody" will be held to mean any antibody wherein the immunoreactive region or site is obtained or derived from a first species and the constant region (which may be intact, partial or modified in accordance with the instant invention) is obtained from a second species. In certain embodiments the target binding region or site will be from a non-human source (*e.g.*, mouse or primate) and the constant region is human (for example, monoclonal antibody (MAb) 1476).

As used herein, the term "engineered antibody" refers to an antibody in which the variable domain in either the heavy or light chain or both is altered by at least partial replacement of one or more CDRs from an antibody of known specificity and, if necessary, by partial framework region replacement and sequence changing. Although the CDRs may be derived from an antibody of the same class or even subclass as the antibody from which the framework regions are derived, it is envisaged that the CDRs will be derived from an antibody of different class and preferably from an antibody from a different species. An engineered antibody in which one or more "donor" CDRs from a non-human antibody of known specificity is grafted into a human heavy or light chain framework region is referred to herein as a "humanized antibody." It may not be necessary to replace all of the CDRs with the complete CDRs from the donor variable domain to transfer the antigen binding capacity of one variable domain to another. Rather, it may only be necessary to transfer those residues that are necessary to maintain the activity of the target binding site. In certain embodiments, the humanized antibody comprises 1, 2, or 3 CDRs from a donor variable heavy domain. In another embodiment, the humanized antibody comprises 1, 2, or 3 CDRs from a donor variable light domain.

It is further recognized that the framework regions within the variable domain in a heavy or light chain, or both, of a humanized antibody may comprise solely residues of human origin, in which case these framework regions of the humanized antibody are referred to as "fully human framework regions." Alternatively, one or more residues of the framework region(s) of the donor variable domain can be engineered within the corresponding position of the human framework region(s) of a variable domain in a heavy or light chain, or both, of a humanized antibody if necessary to maintain proper binding or to enhance binding to the CXCL13 or CXCR5 antigen. A human framework region that has been engineered in this manner would thus comprise a mixture of human and donor framework residues, and is referred to herein as a "partially human framework region."

For example, humanization of an anti-CXCL13 or anti-CXCR5 antibody can be essentially performed following the method of Winter and co-workers (Jones *et al.*, *Nature 321*:522-525 (1986); Riechmann *et al.*, *Nature 332*:323-327 (1988); Verhoeyen *et al.*, *Science 239*:1534-1536 (1988), by substituting rodent or mutant rodent CDRs or CDR sequences for the corresponding sequences of a human anti-CXCL13 antibody. See also U.S. Pat. Nos. 5,225,539; 5,585,089; 5,693,761; 5,693,762; and 5,859,205. The resulting humanized anti-CXCL13 or anti-CXCR5 antibody would comprise at least one rodent or mutant rodent CDR within the fully human framework regions of the variable domain of the heavy and/or light chain of the humanized antibody. In some instances, residues within the framework regions of one or more variable domains of the humanized anti-CXCL13 or anti-CXCR5 antibody are replaced by corresponding non-human (for example, rodent) residues (see, for example, U.S. Pat. Nos. 5,585,089; 5,693,761; 5,693,762; and 6,180,370, in which case the resulting humanized anti-CXCL13 antibody would comprise partially human framework regions within the variable domain of the heavy and/or light chain.

Furthermore, humanized antibodies may comprise residues that are not found in the recipient antibody or in the donor antibody. These modifications are made to further refine antibody performance (*e.g.*, to obtain desired affinity). In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDRs correspond to those of a non-human immunoglobulin and all or substantially all of the framework regions are those of a human immunoglobulin sequence. The humanized antibody optionally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin. For further details see Jones *et al.*, *Nature 331*:522-525 (1986); Riechmann *et al.*, *Nature 332*:323-329 (1988); and Presta, *Curr. Op. Struct. Biol. 2*:593-596 (1992). Accordingly, such "humanized" antibodies may include antibodies wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some or all CDR residues and possibly some framework residues are substituted by residues from analogous sites in rodent antibodies. *See*, for example, U.S. Pat. Nos. 5,225,539; 5,585,089; 5,693,761; 5,693,762; and 5,859,205. See also U.S. Pat. No. 6,180,370, and International Publication No. WO 01/27160, where humanized antibodies and techniques for producing humanized antibodies having improved affinity for a predetermined antigen are disclosed.

Commercial antibodies that bind CXCL13 have been disclosed in the art, *e.g.*, rat anti-mouse MAb 470 (R & D Systems) and mouse anti-human MAb 801 (R & D Systems). In addition, murine anti-CXCL13 antibodies are disclosed in U.S. Patent Application Publication No. 2008 0227704 A1. The monoclonal anti-CXCL13 antibodies MAb 5261, MAb 5378, MAb 5080, MAb 1476, and 3D2 are disclosed in International Application Publication No. WO 2012/031099.

Monoclonal antibody 5261 comprises a variable heavy (VH) domain having the sequence set forth in SEQ ID NO: 14 and a variable light (VL) domain having the sequence set forth in SEQ ID NO: 19. MAb 5261 comprises a human IgGamma1-F allotype constant region within its heavy chain and a human kappa constant region within its light chain. Monoclonal antibody 5378 comprises a variable heavy (VH) domain having the sequence set forth in SEQ ID NO: 14 and a variable light (VL) domain having the sequence set forth in SEQ ID NO: 19. MAb 5378 comprises a murine IgG2a constant region within its heavy chain and a murine kappa constant region within its light chain. MAb 5080 comprises a VH domain having the sequence set forth in SEQ ID NO: 14 and a VL domain having the sequence set forth in SEQ ID NO: 21. MAb 5080 comprises a human IgG1 constant region within its heavy chain and a human kappa constant region within its light chain. Monoclonal antibody 1476 comprises a VH domain having the sequence set forth in SEQ ID NO: 10 and a VL domain having the sequence set forth in SEQ ID NO: 15. MAb 1476 comprises a human IgG1 constant region within its heavy chain and a human kappa constant region within its light chain. Monoclonal antibody 3D2 comprises a VH domain having the sequence set forth in SEQ ID NO: 10 and a VL domain having the sequence set forth in SEQ ID NO: 15. MAb 3D2 comprises a murine IgG1 constant region within its heavy chain and a murine kappa constant region within its light chain.

In some embodiments, the presently disclosed methods utilize the MAb 5261, MAb 5378, MAb 5080, MAb 1476, or 3D2 anti-CXCL13 monoclonal antibodies.

In some embodiments, the antibodies used in the presently disclosed methods comprise anti-CXCL13 antibodies or antigen-binding fragments, variants, or derivatives thereof that bind to CXCL13. In certain embodiments the anti-CXCL13 antibodies bind human, primate, murine, or both human and murine CXCL13. In certain embodiments, the anti-CXCL13 antibodies useful in the presently disclosed methods are humanized. In other embodiments, the anti-CXCL13 antibodies block CXCL13 binding to its receptor, *e.g.*, CXCR5. In certain embodiments, the anti-CXCL13 antibodies useful in the presently disclosed methods are MAb 5261, MAb 5378, MAb 5080, MAb 1476, or 3D2, or antigen-binding fragments, variants, or derivatives thereof. In one embodiment, the presently disclosed methods utilize an isolated binding molecule, *e.g.*, an antibody or antigen binding fragments, variants, and derivatives thereof, which specifically binds to the same CXCL13 or CXCR5 epitope as a reference antibody, *e.g.*, MAb 5261, MAb 5378, MAb 5080, MAb 1476, or 3D2. In another embodiment, the presently disclosed methods involve an isolated binding molecule, *e.g.*, an antibody or antigen binding fragment thereof, which specifically binds to CXCL13, and competitively inhibits a reference antibody, *e.g.*, MAb 5261, MAb 5378, MAb 5080, MAb 1476, or 3D2, from specifically binding to CXCL13, *e.g.*, human, primate, murine, or both human and murine CXCL13.

In certain embodiments, the binding molecule useful in the presently disclosed methods has an amino acid sequence that has at least about 80%, about 85%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about 94%, or about 95% sequence identity of an amino acid sequence for the reference anti-CXCL13 antibody molecule. In a further embodiment, the binding molecule shares at least about 96%, about 97%, about 98%, about 99%, or 100% sequence identity to a reference antibody. In certain embodiments, the reference antibody is MAb 5261, MAb 5378, MAb 5080, MAb 1476, or 3D2.

In another embodiment, the presently disclosed methods utilize an antibody or antigen-binding fragment thereof comprising, consisting essentially of, or consisting of an immunoglobulin heavy chain variable domain (VH domain), where at least one of the CDRs of the VH domain has an amino acid sequence that is at least about 80%, about 85%, about 90%, about 95%, about 96%, about 97%, about 98%, about 99%, or identical to CDR1, CDR2 or CDR3 of SEQ ID NO: 10 or 14.

In another embodiment, the presently disclosed methods utilize an isolated antibody or antigen-binding fragment thereof comprising, consisting essentially of, or consisting of an immunoglobulin heavy chain variable domain (VH domain), where at least one of the CDRs of the VH domain has an amino acid sequence that is at least about 80%, about 85%, about 90%, about 95%, about 96%, about 97%, about 98%, about 99%, or identical to SEQ ID NO: 11, 12, or 13.

In another embodiment, the presently disclosed methods utilize an antibody or antigen-binding fragment thereof comprising, consisting essentially of, or consisting of an immunoglobulin heavy chain variable domain (VH domain), where the VH domain has an amino acid sequence that is at least about 80%, about 85%, about 90%, about 95%, about 96%, about 97%, about 98%, about 99%, or identical to SEQ ID NO: 10 or 14.

In another embodiment, the presently disclosed methods utilize an antibody or antigen-binding fragment thereof comprising, consisting essentially of, or consisting of an immunoglobulin heavy chain variable domain (VH domain), where at least one of the

CDRs of the VH domain has an amino acid sequence identical, except for 1, 2, 3, 4, or 5 conservative amino acid substitutions, to CDR1, CDR2 or CDR3 of SEQ ID NO: 10 or 14

In another embodiment, the presently disclosed methods utilize an antibody or antigen-binding fragment thereof comprising, consisting essentially of, or consisting of an immunoglobulin heavy chain variable domain (VH domain), where at least one of the CDRs of the VH domain has an amino acid sequence identical, except for 1, 2, 3, 4, or 5 conservative amino acid substitutions, to SEQ ID NO: 11, 12, or 13.

In another embodiment, the presently disclosed methods utilize an antibody or antigen-binding fragment thereof comprising, consisting essentially of, or consisting of an immunoglobulin light chain variable domain (VL domain), where at least one of the CDRs of the VL domain has an amino acid sequence that is at least about 80%, about 85%, about 90%, about 95%, about 96%, about 97%, about 98%, about 99%, or identical to CDR1, CDR2 or CDR3 of SEQ ID NO: 15, 19, or 21.

In another embodiment, the presently disclosed methods utilize an antibody or antigen-binding fragment thereof comprising, consisting essentially of, or consisting of an immunoglobulin light chain variable domain (VL domain), where at least one of the CDRs of the VL domain has an amino acid sequence that is at least about 80%, about 85%, about 90%, about 95%, about 96%, about 97%, about 98%, about 99%, or identical to SEQ ID NO: 16, 17, 18, or 20.

In another embodiment, the presently disclosed methods utilize an antibody or antigen-binding fragment thereof comprising, consisting essentially of, or consisting of an immunoglobulin light chain variable domain (VL domain), where the VL domain has an amino acid sequence that is at least about 80%, about 85%, about 90%, about 95%, about 96%, about 97%, about 98%, about 99%, or identical to SEQ ID NO: 15, 19, or 21.

In another embodiment, the presently disclosed methods utilize an antibody or antigen-binding fragment thereof comprising, consisting essentially of, or consisting of an immunoglobulin light chain variable domain (VL domain), where at least one of the CDRs of the VL domain has an amino acid sequence identical, except for 1, 2, 3, 4, or 5 conservative amino acid substitutions, to CDR1, CDR2 or CDR3 of SEQ ID NO: 15, 19, or 21.

In another embodiment, the presently disclosed methods utilize an antibody or antigen-binding fragment thereof comprising, consisting essentially of, or consisting of an immunoglobulin light chain variable domain (VL domain), where at least one of the

CDRs of the VL domain has an amino acid sequence identical, except for 1, 2, 3, 4, or 5 conservative amino acid substitutions, to SEQ ID NO: 16, 17, 18, or 20.

In a further embodiment, the presently disclosed methods utilize an antibody or antigen-binding fragment thereof comprising, consisting essentially of, or consisting of a VL domain that has an amino acid sequence that is at least about 80%, about 85%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or 100% identical to SEQ ID NO: 15, 19, or 21, wherein an anti-CXCL13 antibody comprising the encoded VL domain specifically or preferentially binds to CXCL13.

In certain embodiments, the presently disclosed methods utilize an antibody or antigen-binding fragment thereof comprising, consisting essentially of, or consisting of a VH domain that has the amino acid sequence set forth in SEQ ID NO: 14 and a VL domain that has the amino acid sequence set forth in SEQ ID NO: 19. In some of these embodiments, the antibody comprises a human IgG1 constant region within its heavy chain and a human kappa constant region within its light chain.

In particular embodiments, the presently disclosed methods utilize an antibody or antigen-binding fragment thereof comprising, consisting essentially of, or consisting of a VH domain comprising a CDR1 having the amino acid sequence set forth in SEQ ID NO: 11, a CDR2 having the amino acid sequence set forth in SEQ ID NO: 12, and a CDR3 having the amino acid sequence set forth in SEQ ID NO: 13; and a VL domain comprising a CDR1 having the amino acid sequence set forth in SEQ ID NO: 20, a CDR2 having the amino acid sequence set forth in SEQ ID NO: 17, and a CDR3 having the amino acid sequence set forth in SEQ ID NO: 18. In some of these embodiments, the antibody comprises a human IgG1 constant region within its heavy chain and a human kappa constant region within its light chain.

Suitable biologically active variants of reference anti-CXCL13 or anti-CXCR5 antibodies can be used in the presently disclosed methods. Such variants will retain the desired binding properties of the parent anti-CXCL13 or anti-CXCR5 antibody. Methods for making antibody variants are generally available in the art.

Methods for mutagenesis and nucleotide sequence alterations are well known in the art. *See*, for example, Walker and Gaastra, eds. (1983) Techniques in Molecular Biology (MacMillan Publishing Company, New York); Kunkel, Proc. *Natl. Acad. Sci. USA 82*:488-492 (1985); Kunkel *et al.*, *Methods Enzymol. 154*:367-382 (1987); Sambrook *et al.* (1989) Molecular Cloning: A Laboratory Manual (Cold Spring Harbor, N.Y.); U.S. Pat. No. 4,873,192. Guidance as to appropriate amino acid substitutions that do not affect biological activity of the polypeptide of interest may be found in the model of Dayhoff *et al.* (1978) in Atlas of Protein Sequence and Structure (Natl. Biomed. Res. Found., Washington, D.C.), pp. 345-352. The model of Dayhoff *et al.* uses the Point Accepted Mutation (PAM) amino acid similarity matrix (PAM 250 matrix) to determine suitable conservative amino acid substitutions. Conservative substitutions, such as exchanging one amino acid with another having similar properties, may be preferred. Examples of conservative amino acid substitutions as taught by the PAM 250 matrix of the Dayhoff *et al.* model include, but are not limited to, Gly↔Ala, Val↔Ile↔Leu, Asp↔Glu, Lys↔Arg, Asn↔Gln, and Phe↔Trp↔Tyr.

In constructing variants of an anti-CXCL13 or anti-CXCR5 binding molecule, *e.g.*, an antibody or antigen-binding fragment thereof, or polypeptides of interest, modifications are made such that variants continue to possess the desired properties, *e.g.*, being capable of specifically binding to a CXCL13 or CXCR5, *e.g.*, human, primate, murine, or both human and murine CXCL13 or CXCR5. Obviously, any mutations made in the DNA encoding the variant polypeptide must not place the sequence out of reading frame and preferably will not create complementary regions that could produce secondary mRNA structure. See, *e.g.*, EP Pat. No. EP0075444 B1.

Methods for measuring anti-CXCL13 or anti-CXCR5 binding molecule, e.g., an antibody or antigen-binding fragment thereof, binding specificity include, but are not limited to, standard competitive binding assays, assays for monitoring immunoglobulin secretion by T cells or B cells, T cell proliferation assays, apoptosis assays, ELISA assays, and the like. See, for example, such assays disclosed in WO 93/14125; Shi *et al.*, *Immunity 13*:633-642 (2000); Kumanogoh *et al.*, *J Immunol 169*:1175-1181 (2002); Watanabe *et al.*, *J Immunol 167*:4321-4328 (2001); Wang *et al.*, *Blood 97*:3498-3504 (2001); and Giraudon *et al.*, *J Immunol 172*(2):1246-1255 (2004).

Through its receptor, CXCR5, which is found on a variety of immune cells (*e.g.*, B cells, follicular helper T cells, and recently-activated T cells), CXCL13 induces intracellular changes necessary for maintenance of immune system homeostasis, lymphoid organogenesis, leukocyte trafficking and chemotactic migration as well as development of secondary lymphoid tissue (*e.g.* germinal centers). Therefore, "anti-CXCL13 activity" or "CXCL13 blocking activity" can include activity which modulates

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one or more of the following activities associated with CXCL13: blockade of CXCL13 interaction with its receptor, inhibition of B cell and follicular B-helper T cell migration into inflamed tissues, inhibition of germinal center formation (*e.g.*, in the case of autoimmune diseases), inhibition of secondary or ectopic lymphoid follicles; inhibition of cancer cell proliferation and ability to spread in oncological disorders; or any other activity associated with CXCL13-expressing cells. Anti-CXCL13 activity can also be attributed to a decrease in incidence or severity of diseases associated with CXCL13 expression, including, but not limited to, certain types of autoimmune diseases (*e.g.*, multiple sclerosis, arthritis (*e.g.*, rheumatoid arthritis), chronic gastritis, gastric lymphomas, transplant rejection, Sjogren's Syndrome (SS), systemic lupus erythematosus (SLE), active mixed cryoglobulinemia (MC) vasculitis in Hepatitis C virus infection, juvenile dermatomyositis, and myasthenia gravis) and certain cancers (*e.g.*, Burkitt's lymphoma, non-Hodgkin lymphoma, MALT lymphoma (*e.g.*, gastric MALT lymphoma), carcinoma (*e.g.*, colon, prostate, breast, stomach, esophageal, and pancreatic), and chronic lymphocytic leukemia (CLL)) as well as other inflammatory diseases such as *Helicobacter* infection induced inflammatory diseases, *e.g.*, gastritis, ulcers, and gastric mucosal lesions.

When discussed herein whether any particular polypeptide, including the constant regions, CDRs, VH domains, or VL domains of a reference polypeptide, is at least about 65%, about 70%, about 75%, about 80%, about 85%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or even about 100% identical to another polypeptide, the % identity can be determined using methods and computer programs/software known in the art such as, but not limited to, the BESTFIT program (Wisconsin Sequence Analysis Package, Version 8 for Unix, Genetics Computer Group, University Research Park, 575 Science Drive, Madison, Wis. 53711). BESTFIT uses the local homology algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2:482-489, to find the best segment of homology between two sequences. When using BESTFIT or any other sequence alignment program to determine whether a particular sequence is, for example, 95% identical to a reference sequence according to the present invention, the parameters are set, of course, such that the percentage of identity is calculated over the full length of the reference polypeptide sequence and that gaps in homology of up to 5% of the total number of amino acids in the reference sequence are allowed.

For purposes of the present invention, percent sequence identity may be determined using the Smith-Waterman homology search algorithm using an affine gap search with a gap open penalty of 12 and a gap extension penalty of 2, BLOSUM matrix of 62. The Smith-Waterman homology search algorithm is taught in Smith and Waterman (1981) Adv. Appl. Math. 2:482-489. A variant may, for example, differ from a reference anti-CXCL13 antibody (*e.g.*, MAb 5261, MAb 5378, MAb 5080, MAb 1476, or 3D2) or anti-CXCR5 antibody by as few as 1 to 15 amino acid residues, as few as 1 to 10 amino acid residues, such as 6-10, as few as 5, as few as 4, 3, 2, or even 1 amino acid residue.

The precise chemical structure of a polypeptide capable of specifically binding CXCL13 or CXCR5 and retaining the desired CXCL13 blocking activity depends on a number of factors. As ionizable amino and carboxyl groups are present in the molecule, a particular polypeptide may be obtained as an acidic or basic salt, or in neutral form. All such preparations that retain their biological activity when placed in suitable environmental conditions are included in the definition of anti-CXCL13 or anti-CXCR5 antibodies as used herein. Further, the primary amino acid sequence of the polypeptide may be augmented by derivatization using sugar moieties (glycosylation) or by other supplementary molecules such as lipids, phosphate, acetyl groups and the like. It may also be augmented by conjugation with saccharides. Certain aspects of such augmentation are accomplished through post-translational processing systems of the producing host; other such modifications may be introduced in vitro. In any event, such modifications are included in the definition of an anti-CXCL13 or anti-CXCR5 antibody used herein so long as the desired properties of the anti-CXCL13 or anti-CXCR5 antibody are not destroyed. It is expected that such modifications may quantitatively or qualitatively affect the activity, either by enhancing or diminishing the activity of the polypeptide, in the various assays. Further, individual amino acid residues in the chain may be modified by oxidation, reduction, or other derivatization, and the polypeptide may be cleaved to obtain fragments that retain activity. Such alterations that do not destroy the desired properties (*e.g.*, binding specificity for CXCL13 or CXCR5, binding affinity, and/or CXCL13 blocking activity) do not remove the polypeptide sequence from the definition of anti-CXCL13 or anti-CXCR5 antibodies of interest as used herein.

The art provides substantial guidance regarding the preparation and use of polypeptide variants. In preparing the anti-CXCL13 or anti-CXCR5 binding molecule, *e.g.*, an antibody or antigen-binding fragment thereof, variants, one of skill in the art can readily determine which modifications to the native protein's nucleotide or amino acid sequence will result in a variant that is suitable for use as a therapeutically active component of a pharmaceutical composition used in the methods of the present invention.

The constant region of a reference anti-CXCL13 or anti-CXCR5 antibody may be mutated to alter effector function in a number of ways. For example, see U.S. Pat. No. 6,737,056B1 and U.S. Patent Application Publication No. 2004/0132101A1, which disclose Fc mutations that optimize antibody binding to Fc receptors.

In certain anti-CXCL13 or anti-CXCR5 antibodies, the Fc portion may be mutated to decrease effector function using techniques known in the art. For example, the deletion or inactivation (through point mutations or other means) of a constant region domain may reduce Fc receptor binding of the circulating modified antibody thereby increasing tumor localization. In other cases it may be that constant region modifications consistent with the instant invention moderate complement binding and thus reduce the serum half life and nonspecific association of a conjugated cytotoxin. Yet other modifications of the constant region may be used to modify disulfide linkages or oligosaccharide moieties that allow for enhanced localization due to increased antigen specificity or antibody flexibility. The resulting physiological profile, bioavailability and other biochemical effects of the modifications, such as tumor localization, biodistribution and serum half-life, may easily be measured and quantified using well known immunological techniques without undue experimentation.

In general, CXCR5 binding molecules useful in the presently disclosed methods do not activate the CXCR5 receptor (*i.e.*, are not agonists of the receptor).

A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a side chain with a similar charge. Families of amino acid residues having side chains with similar charges have been defined in the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (e.g., threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Alternatively, mutations can be introduced randomly along all or part of the coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for biological activity to identify mutants that retain activity (*e.g.*, binding specificity for CXCL13 or CXCR5, binding affinity, and/or CXCL13 blocking activity).

For example, it is possible to introduce mutations only in framework regions or only in CDR regions of an antibody molecule. Introduced mutations may be silent or neutral missense mutations, *i.e.*, have no, or little, effect on an antibody's ability to bind antigen. These types of mutations may be useful to optimize codon usage, or improve a hybridoma's antibody production. Alternatively, non-neutral missense mutations may alter an antibody's ability to bind antigen. The location of most silent and neutral missense mutations is likely to be in the framework regions, while the location of most non-neutral missense mutations is likely to be in CDR, though this is not an absolute requirement. One of skill in the art would be able to design and test mutant molecules with desired properties such as no alteration in antigen binding activity or alteration in binding activity (*e.g.*, improvements in antigen binding activity or change in antibody specificity). Following mutagenesis, the encoded protein may routinely be expressed and the functional and/or biological activity of the encoded protein, (*e.g.*, ability to immunospecifically bind at least one epitope of a CXCL13 or CXCR5 polypeptide) can be determined using techniques described herein or by routinely modifying techniques known in the art.

In certain embodiments, the anti-CXCL13 or anti-CXCR5 antibodies useful in the presently disclosed methods comprise at least one optimized complementarity-determining region (CDR) in comparison to a reference anti-CXCL13 or anti-CXCR5 antibody. By "optimized CDR" is intended that the CDR has been modified and optimized sequences selected based on the sustained or improved binding affinity and/or anti-CXCL13 activity that is imparted to an anti-CXCL13 or anti-CXCR5 antibody comprising the optimized CDR.

As discussed in more detail elsewhere herein, anti-CXCL13 or anti-CXCR5 binding molecules, or soluble CXCR5 may further be recombinantly fused to a heterologous polypeptide at the N- or C-terminus or chemically conjugated (including covalent and non-covalent conjugations) to polypeptides or other compositions. For example, anti-CXCL13 or anti-CXCR5 antibodies or soluble CXCR5 may be recombinantly fused or conjugated to molecules useful as labels in detection assays and effector molecules such as heterologous polypeptides, drugs, radionuclides, or toxins.

See, e.g., PCT publications WO 92/08495; WO 91/14438; WO 89/12624; U.S. Pat. No. 5,314,995; and EP 396,387.

As used herein, the terms "linked," "fused," or "fusion" are used interchangeably. These terms refer to the joining together of two more elements or components, by whatever means including chemical conjugation or recombinant means. An "in-frame fusion" refers to the joining of two or more polynucleotide open reading frames (ORFs) to form a continuous longer ORF, in a manner that maintains the correct translational reading frame of the original ORFs. Thus, a recombinant fusion protein is a single protein containing two or more segments that correspond to polypeptides encoded by the original ORFs (which segments are not normally so joined in nature). Although the reading frame is thus made continuous throughout the fused segments, the segments may be physically or spatially separated by, for example, in-frame linker sequence. For example, polynucleotides encoding the CDRs of an immunoglobulin variable region may be fused, in-frame, but be separated by a polynucleotide encoding at least one immunoglobulin framework region or additional CDR regions, as long as the "fused" CDRs are co-translated as part of a continuous polypeptide.

Anti-CXCL13 or anti-CXCR5 antibodies useful in the presently disclosed methods may include derivatives that are modified, *i.e.*, by the covalent attachment of any type of molecule to the antibody such that covalent attachment does not prevent the antibody binding CXCL13 or CXCR5. For example, but not by way of limitation, the antibody derivatives include antibodies that have been modified, *e.g.*, by glycosylation, acetylation, pegylation, phosphorylation, amidation, derivatization by known protecting/blocking groups, proteolytic cleavage, linkage to a cellular ligand or other protein, etc. Any of numerous chemical modifications may be carried out by known techniques, including, but not limited to specific chemical cleavage, acetylation, formylation, etc. Additionally, the derivative may contain one or more non-classical amino acids.

Anti-CXCL13 or anti-CXCR5 binding molecules, *e.g.*, antibodies, or antigen-binding fragments, variants, or derivatives thereof, can be composed of amino acids joined to each other by peptide bonds or modified peptide bonds, *i.e.*, peptide isosteres, and may contain amino acids other than the 20 gene-encoded amino acids. For example, anti-CXCL13 or anti-CXCR5 antibodies may be modified by natural processes, such as posttranslational processing, or by chemical modification techniques that are well known in the art. Such modifications are well described in basic texts and in more detailed monographs, as well as in a voluminous research literature. Modifications can occur anywhere in the anti-CXCL13 or anti-CXCR5 binding molecule, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini, or on moieties such as carbohydrates. It will be appreciated that the same type of modification may be present in the same or varying degrees at several sites in a given anti-CXCL13 or anti-CXCR5 binding molecule. Also, a given anti-CXCL13 or anti-CXCR5 binding molecule may contain many types of modifications. Anti-CXCL13 or anti-CXCR5 binding molecules may be branched, for example, as a result of ubiquitination, and they may be cyclic, with or without branching. Cyclic, branched, and branched cyclic anti-CXCL13 or anti-CXCR5 binding molecules may result from posttranslational natural processes or may be made by synthetic methods. Modifications include acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphotidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cysteine, formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, pegylation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination. (See, for instance, Proteins--Structure and Molecular Properties, T. E. Creighton, W. H. Freeman and Company, NY; 2nd ed. (1993); Johnson, ed. (1983) Posttranslational Covalent Modification of Proteins (Academic Press, NY), pgs. 1-12; Seifter *et al.*, *Meth. Enzymol. 182*:626-646 (1990); Rattan *et al.*, *Ann. NY Acad. Sci. 663*:48-62 (1992)).

The presently disclosed methods encompass the use of fusion proteins comprising an anti-CXCL13 or anti-CXCR5 antibody, or antigen-binding fragment, variant, or derivative thereof, and a heterologous polypeptide. The heterologous polypeptide to which the antibody is fused may be useful for function or is useful to target the anti-CXCL13 or anti-CXCR5 polypeptide expressing cells.

In one embodiment, a fusion protein useful in the presently disclosed methods comprises, consists essentially of, or consists of, a polypeptide having the amino acid sequence of any one or more of the VH domains of an anti-CXCL13 or anti-CXCR5 antibody or the amino acid sequence of any one or more of the VL domains of an anti-

CXCL13 or anti-CXCR5 antibody or fragments or variants thereof, and a heterologous polypeptide sequence.

In another embodiment, a fusion protein for use in the treatment methods disclosed herein comprises, consists essentially of, or consists of a polypeptide having the amino acid sequence of any one, two, three of the CDRs of the VH domain of an anti-CXCL13 or anti-CXCR5 antibody, or fragments, variants, or derivatives thereof, and/or the amino acid sequence of any one, two, three of the CDRs of the VL domain an anti-CXCL13 or anti-CXCR5 antibody, or fragments, variants, or derivatives thereof, and a heterologous polypeptide sequence. In some embodiments, the VH and VL domains of the fusion protein correspond to a single source antibody (or scFv or Fab fragment) that specifically binds at least one epitope of CXCL13 or CXCR5. In some embodiments, two, three, four, five, six, or more of the CDR(s) of the VH domain or VL domain correspond to single source antibody (or scFv or Fab fragment).

Exemplary fusion proteins reported in the literature include fusions of the T cell receptor (Gascoigne *et al.*, *Proc. Natl. Acad. Sci. USA 84*:2936-2940 (1987)); CD4 (Capon *et al.*, *Nature 337*:525-531 (1989); Traunecker *et al.*, *Nature 339*:68-70 (1989); Zettmeissl *et al.*, *DNA Cell Biol. USA 9*:347-353 (1990); and Byrn *et al.*, *Nature 344*:667-670(1990)); L-selectin (homing receptor) (Watson et al., *J. Cell. Biol. 110*:2221-2229 (1990); and Watson *et al.*, *Nature 349*:164-167 (1991)); CD44 (Aruffo *et al.*, *Cell 61*:1303-1313 (1990)); CD28 and B7 (Linsley *et al., J. Exp. Med. 173*:721-730 (1991)); CTLA-4 (Lisley *et al., J. Exp. Med. 174*:561-569 (1991)); CD22 (Stamenkovic *et al., Cell 66*:1133-1144 (1991)); TNF receptor (Ashkenazi *et al., Proc. Natl. Acad. Sci. USA 88*:10535-10539 (1991); Lesslauer *et al., Eur. J. Immunol. 27*:2883-2886 (1991); and Peppel *et al., J. Exp. Med. 174*:1483-1489 (1991)); and IgE receptor a (Ridgway and Gorman, J. Cell. Biol. Vol. 115, Abstract No. 1448 (1991)).

As discussed elsewhere herein, anti-CXCL13 or anti-CXCR5 binding molecules, *e.g.*, antibodies, or antigen-binding fragments, variants, or derivatives thereof, may be fused to heterologous polypeptides to increase the *in vivo* half life of the polypeptides or for use in immunoassays using methods known in the art. For example, in one embodiment, PEG can be conjugated to the anti-CXCL13 or anti-CXCR5 antibodies to increase their half-life *in vivo*. See Leong *et al., Cytokine 16*:106 (2001); Adv. in Drug Deliv. Rev. 54:531 (2002); or Weir *et al., Biochem. Soc. Transactions 30*:512 (2002).

Moreover, anti-CXCL13 or anti-CXCR5 binding molecules, *e.g.*, antibodies, or antigen-binding fragments, variants, or derivatives thereof, can be fused to marker sequences, such as a peptide to facilitate their purification or detection. In certain embodiments, the marker amino acid sequence is a hexa-histidine peptide, such as the tag provided in a pQE vector (QIAGEN™, Inc., 9259 Eton Avenue, Chatsworth, Calif., 91311), among others, many of which are commercially available. As described in Gentz *et al.*, *Proc. Natl. Acad. Sci. USA 86*:821-824 (1989), for instance, hexa-histidine provides for convenient purification of the fusion protein. Other peptide tags useful for purification include, but are not limited to, the "HA" tag, which corresponds to an epitope derived from the influenza hemagglutinin protein (Wilson *et al.*, *Cell 37*:767 (1984)) and the "flag" tag.

Fusion proteins can be prepared using methods that are well known in the art (see for example U.S. Pat. Nos. 5,116,964 and 5,225,538). The precise site at which the fusion is made may be selected empirically to optimize the secretion or binding characteristics of the fusion protein. DNA encoding the fusion protein is then transfected into a host cell for expression.

Anti-CXCL13 and anti-CXCR5 binding molecules, *e.g.*, antibodies , or antigen-binding fragments, variants, or derivatives thereof, may be used in non-conjugated form or may be conjugated to at least one of a variety of molecules, *e.g.*, to improve the therapeutic properties of the molecule, to facilitate target detection, or for imaging or therapy of the patient. Anti-CXCL13 or anti-CXCR5 binding molecules, *e.g.*, antibodies, or antigen-binding fragments, variants, or derivatives thereof, can be labeled or conjugated either before or after purification, or when purification is performed.

In particular, anti-CXCL13 or anti-CXCR5 antibodies, or antigen-binding fragments, variants, or derivatives thereof, may be conjugated to therapeutic agents, prodrugs, peptides, proteins, enzymes, viruses, lipids, biological response modifiers, pharmaceutical agents, or PEG.

Those skilled in the art will appreciate that conjugates may also be assembled using a variety of techniques depending on the selected agent to be conjugated. For example, conjugates with biotin are prepared, *e.g.*, by reacting a binding polypeptide with an activated ester of biotin such as the biotin N-hydroxysuccinimide ester. Similarly, conjugates with a fluorescent marker may be prepared in the presence of a coupling agent, *e.g.*, those listed herein, or by reaction with an isothiocyanate, preferably fluorescein-isothiocyanate. Conjugates of anti-CXCL13 or anti-CXCR5 antibodies, or antigen-binding fragments, variants, or derivatives thereof, are prepared in an analogous manner.

An anti-CXCL13 or anti-CXCR5 binding molecule, *e.g.*, an antibody, or antigen-binding fragment, variant, or derivative thereof, may be conjugated to a therapeutic moiety such as a cytotoxin, a therapeutic agent or a radioactive metal ion. A cytotoxin or cytotoxic agent includes any agent that is detrimental to cells.

Techniques for conjugating various moieties to an antibody, *e.g.*, an anti-CXCL13 or anti-CXCR5 antibody or antigen-binding fragment, variant, or derivative thereof, are well known, *see*, *e.g.*, Amon et al. (1985) "Monoclonal Antibodies for Immunotargeting of Drugs in Cancer Therapy," in Monoclonal Antibodies and Cancer Therapy, ed. Reisfeld et al. (Alan R. Liss, Inc.), pp. 243-56; Hellstrom et al. (1987) "Antibodies for Drug Delivery," in Controlled Drug Delivery, ed. Robinson et al. (2nd ed.; Marcel Dekker, Inc.), pp. 623-53); Thorpe (1985) "Antibody Carriers of Cytotoxic Agents in Cancer Therapy: A Review," in Monoclonal Antibodies '84: Biological and Clinical Applications, ed. Pinchera *et al.*, pp. 475-506; "Analysis, Results, and Future Prospective of the Therapeutic Use of Radiolabeled Antibody in Cancer Therapy," in Monoclonal Antibodies for Cancer Detection and Therapy, ed. Baldwin *et al.*, Academic Press, pp. 303-16 (1985); and Thorpe *et al.*, *Immunol. Rev. 62*:119-58 (1982).

Methods of preparing and administering the agent that inhibits CXCL13 activity (*e.g.*, an anti-CXCL13 or anti-CXCR5 binding molecule) to a subject in need thereof are well known to or are readily determined by those skilled in the art. The route of administration of the agent that inhibits CXCL13 activity (*e.g.*, an anti-CXCL13 or anti-CXCR5 binding molecule) may be, for example, oral, parenteral, by inhalation or topical. The term parenteral as used herein includes, *e.g.*, intravenous, intraarterial, intraperitoneal, intramuscular, subcutaneous, rectal, or vaginal administration. While all these forms of administration are clearly contemplated as being within the scope of the invention, an example of a form for administration would be a solution for injection, in particular for intravenous or intraarterial injection or drip. Usually, a suitable pharmaceutical composition for injection may comprise a buffer (*e.g.* acetate, phosphate or citrate buffer), a surfactant (*e.g.* polysorbate), optionally a stabilizer agent (*e.g.* human albumin), etc. However, in other methods compatible with the teachings herein, agents that inhibit CXCL13 activity (*e.g.*, anti-CXCL13 or anti-CXCR5 binding molecules) can be delivered directly to the site of the adverse cellular population thereby increasing the exposure of the diseased tissue to the therapeutic agent.

As discussed herein, agents that inhibit CXCL13 activity (e.g., anti-CXCL13 or anti-CXCR5 binding molecules) may be administered in a pharmaceutically effective amount for the *in vivo* treatment of inflammatory disorders and for increasing levels of IgA. In this regard, it will be appreciated that the agents that inhibit CXCL13 activity will be formulated so as to facilitate administration and promote stability of the active agent. In certain embodiments, pharmaceutical compositions in accordance with the present invention comprise a pharmaceutically acceptable, non-toxic, sterile carrier such as physiological saline, non-toxic buffers, preservatives and the like. For the purposes of the instant application, a pharmaceutically effective amount of an agent that inhibits CXCL13 activity (*e.g.*, anti-CXCL13 or anti-CXCR5 binding molecule) shall be held to mean an amount sufficient to achieve effective binding to a target and to achieve a benefit, *e.g.*, to ameliorate symptoms of a disease or disorder or to detect a substance or a cell.

The pharmaceutical compositions used in this invention comprise pharmaceutically acceptable carriers, including, *e.g.*, ion exchangers, alumina, aluminum stearate, lecithin, serum proteins, such as human serum albumin, buffer substances such as phosphates, glycine, sorbic acid, potassium sorbate, partial glyceride mixtures of saturated vegetable fatty acids, water, salts or electrolytes, such as protamine sulfate, disodium hydrogen phosphate, potassium hydrogen phosphate, sodium chloride, zinc salts, colloidal silica, magnesium trisilicate, polyvinyl pyrrolidone, cellulose-based substances, polyethylene glycol, sodium carboxymethylcellulose, polyacrylates, waxes, polyethylene-polyoxypropylene-block polymers, polyethylene glycol, and wool fat.

Preparations for parenteral administration include sterile aqueous or non-aqueous solutions, suspensions, and emulsions. Examples of non-aqueous solvents are propylene glycol, polyethylene glycol, vegetable oils such as olive oil, and injectable organic esters such as ethyl oleate. Aqueous carriers include, *e.g.*, water, alcoholic/aqueous solutions, emulsions or suspensions, including saline and buffered media. In the subject invention, pharmaceutically acceptable carriers include, but are not limited to, 0.01-0.1 M, *e.g.*, 0.05 M phosphate buffer or 0.8% saline. Other common parenteral vehicles include sodium phosphate solutions, Ringer's dextrose, dextrose and sodium chloride, lactated Ringer's, or fixed oils. Intravenous vehicles include fluid and nutrient replenishers, electrolyte replenishers, such as those based on Ringer's dextrose, and the like. Preservatives and other additives may also be present such as, for example, antimicrobials, antioxidants, chelating agents, and inert gases and the like.

More particularly, pharmaceutical compositions suitable for injectable use include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersions. In such cases, the composition must be sterile and should be fluid to the extent that easy syringability exists. It should be stable under the conditions of manufacture and storage and will preferably be preserved against the contaminating action of microorganisms, such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (*e.g.*, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. Suitable formulations for use in the therapeutic methods disclosed herein are described in Remington's Pharmaceutical Sciences (Mack Publishing Co.) 16th ed. (1980).

Prevention of the action of microorganisms can be achieved by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, ascorbic acid, thimerosal and the like. In certain cases, it will be preferable to include isotonic agents, for example, sugars, polyalcohols, such as mannitol, sorbitol, or sodium chloride in the composition. Prolonged absorption of the injectable compositions can be brought about by including in the composition an agent which delays absorption, for example, aluminum monostearate and gelatin.

In any case, sterile injectable solutions can be prepared by incorporating an active compound (*e.g.*, an anti-CXCL13 or anti-CXCR5 antibody, or antigen-binding fragment, variant, or derivative thereof, by itself or in combination with other active agents) in the required amount in an appropriate solvent with one or a combination of ingredients enumerated herein, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle, which contains a basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, the preferred methods of preparation are vacuum drying and freeze-drying, which yields a powder of an active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof. The preparations for injections are processed, filled into containers such as ampoules, bags, bottles, syringes or vials, and sealed under aseptic conditions according to methods known in the art. Further, the preparations may be packaged and sold in the form of a kit such as those described in U.S. patent application Ser. No. 09/259,337. Such articles of manufacture will preferably have labels or package inserts indicating that the associated compositions are useful for treating a subject suffering from, or predisposed to a disease or disorder.

Parenteral formulations may be a single bolus dose, an infusion or a loading bolus dose followed with a maintenance dose. These compositions may be administered at specific fixed or variable intervals, *e.g.*, once a day, or on an "as needed" basis.

Certain pharmaceutical compositions used in this invention may be orally administered in an acceptable dosage form including, *e.g.*, capsules, tablets, aqueous suspensions or solutions. Certain pharmaceutical compositions also may be administered by nasal aerosol or inhalation. Such compositions may be prepared as solutions in saline, employing benzyl alcohol or other suitable preservatives, absorption promoters to enhance bioavailability, and/or other conventional solubilizing or dispersing agents.

The amount of an agent that inhibits CXCL13 activity (*e.g.*, anti-CXCL13 or anti-CXCR5 binding molecule) that may be combined with the carrier materials to produce a single dosage form will vary depending upon the host treated and the particular mode of administration. The composition may be administered as a single dose, multiple doses or over an established period of time in an infusion. Dosage regimens also may be adjusted to provide the optimum desired response (*e.g.*, a therapeutic or prophylactic response).

In keeping with the scope of the present disclosure, an agent that inhibits CXCL13 activity (*e.g.*, anti-CXCL13 antibodies, or antigen-binding fragments, variants, or derivatives thereof) may be administered to a human or other animal in accordance with the aforementioned methods of treatment in an amount sufficient to produce a therapeutic effect. The agent that inhibits CXCL13 activity (*e.g.*, anti-CXCL13 or anti-CXCR5 antibodies, or antigen-binding fragments, variants, or derivatives thereof can be administered to such human or other animal in a conventional dosage form prepared by combining the active agent with a conventional pharmaceutically acceptable carrier or diluent according to known techniques. It will be recognized by one of skill in the art that the form and character of the pharmaceutically acceptable carrier or diluent is dictated by the amount of active ingredient with which it is to be combined, the route of administration and other well-known variables. Those skilled in the art will further appreciate that a cocktail comprising one or more species of agents that inhibit CXCL13 activity (*e.g.*, anti-CXCL13 or anti-CXCR5 binding molecules) may prove to be particularly effective.

By "therapeutically effective dose or amount" or "effective amount" is intended an amount of an agent that inhibits CXCL13 activity (*e.g.*, anti-CXCL13 or anti-CXCR5 binding molecule), that when administered brings about a positive therapeutic response with respect to treatment of a patient with a disease to be treated.

Therapeutically effective doses of agents that inhibit CXCL13 activity for treatment of inflammatory disorders and for increasing IgA levels vary depending upon many different factors, including means of administration, target site, physiological state of the patient, whether the patient is human or an animal, other medications administered, and whether treatment is prophylactic or therapeutic. Usually, the patient is a human, but non-human mammals including transgenic mammals can also be treated. Treatment dosages may be titrated using routine methods known to those of skill in the art to optimize safety and efficacy.

The amount of at least one agent that inhibits CXCL13 activity (*e.g.*, anti-CXCL13 or anti-CXCR5 binding molecule) to be administered is readily determined by one of ordinary skill in the art without undue experimentation given the disclosure of the present invention. Factors influencing the mode of administration and the respective amount of at least one agent that inhibits CXCL13 activity (*e.g.*, anti-CXCL13 or anti-CXCR5 binding molecule) include, but are not limited to, the severity of the disease, the history of the disease, and the age, height, weight, health, and physical condition of the individual undergoing therapy. Similarly, the amount of an agent that inhibits CXCL13 activity (*e.g.*, anti-CXCL13 or anti-CXCR5 binding molecule) to be administered will be dependent upon the mode of administration and whether the subject will undergo a single dose or multiple doses of this agent.

In some embodiments, the dosage of an agent that inhibits CXCL13 activity (*e.g.*, anti-CXCL13 or anti-CXCR5 binding molecule) that is administered ranges from about 0.1 mg/kg to about 100 mg/kg, including but not limited to about 0.1 mg/kg, about 0.2 mg/kg, about 0.3 mg/kg, about 0.4 mg/kg, about 0.5 mg/kg, about 0.6 mg/kg, about 0.7 mg/kg, about 0.8 mg/kg, about 0.9 mg/kg, about 1 mg/kg, about 1.5 mg/kg, about 2 mg/kg, about 2.5 mg/kg, about 3 mg/kg, about 3.5 mg/kg, about 4 mg/kg, about 4.5 mg/kg, about 5 mg/kg, about 5.5 mg/kg, about 6 mg/kg, about 6.5 mg/kg, about 7 mg/kg, about 7.5 mg/kg, about 8 mg/kg, about 8.5 mg/kg, about 9 mg/kg, about 9.5 mg/kg, and about 10 mg/kg. In certain embodiments, the dosage that is administered ranges from about 1 mg/kg to about 10 mg/kg. In particular embodiments, about 4 mg/kg to about 5 mg/kg of an agent that inhibits CXCL13 activity (*e.g.*, anti-CXCL13 or anti-CXCR5 binding molecule) is administered to a subject in need thereof. In some of these embodiments, the agent is administered via intraperitoneal injection.

The present invention also provides for the use of an agent that inhibits CXCL13 activity (*e.g.*, anti-CXCL13 or anti-CXCR5 binding molecule) in the manufacture of a medicament for treating an inflammatory disorder and for increasing IgA levels.

The practice of the present invention will employ, unless otherwise indicated, conventional techniques of cell biology, cell culture, molecular biology, transgenic biology, microbiology, recombinant DNA, and immunology, which are within the skill of the art. Such techniques are explained fully in the literature. *See*, for example, Sambrook *et al.*, ed. (1989) Molecular Cloning A Laboratory Manual (2nd ed.; Cold Spring Harbor Laboratory Press); Sambrook *et al.*, ed. (1992) Molecular Cloning: A Laboratory Manual, (Cold Springs Harbor Laboratory, NY); D. N. Glover ed., (1985) DNA Cloning, Volumes I and II; Gait, ed. (1984) Oligonucleotide Synthesis; Mullis et al. U.S. Pat. No. 4,683,195; Hames and Higgins, eds. (1984) Nucleic Acid Hybridization; Hames and Higgins, eds. (1984) Transcription And Translation; Freshney (1987) Culture Of Animal Cells (Alan R. Liss, Inc.); Immobilized Cells And Enzymes (IRL Press) (1986); Perbal (1984) A Practical Guide To Molecular Cloning; the treatise, Methods In Enzymology (Academic Press, Inc., N.Y.); Miller and Calos eds. (1987) Gene Transfer Vectors For Mammalian Cells, (Cold Spring Harbor Laboratory); Wu *et al.*, eds., Methods In Enzymology, Vols. 154 and 155; Mayer and Walker, eds. (1987) Immunochemical Methods In Cell And Molecular Biology (Academic Press, London); Weir and Blackwell, eds., (1986) Handbook Of Experimental Immunology, Volumes I-IV; Manipulating the Mouse Embryo, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., (1986); and in Ausubel et al. (1989) Current Protocols in Molecular Biology (John Wiley and Sons, Baltimore, Md.).

General principles of antibody engineering are set forth in Borrebaeck, ed. (1995) Antibody Engineering (2nd ed.; Oxford Univ. Press). General principles of protein engineering are set forth in Rickwood *et al.*, eds. (1995) Protein Engineering, A Practical Approach (IRL Press at Oxford Univ. Press, Oxford, Eng.). General principles of antibodies and antibody-hapten binding are set forth in: Nisonoff (1984) Molecular Immunology (2nd ed.; Sinauer Associates, Sunderland, Mass.); and Steward (1984) Antibodies, Their Structure and Function (Chapman and Hall, New York, N.Y.). Additionally, standard methods in immunology known in the art and not specifically described are generally followed as in Current Protocols in Immunology, John Wiley &

Sons, New York; Stites *et al.,* eds. (1994) Basic and Clinical Immunology (8th ed; Appleton & Lange, Norwalk, Conn.) and Mishell and Shiigi (eds) (1980) Selected Methods in Cellular Immunology (W.H. Freeman and Co., NY).

Standard reference works setting forth general principles of immunology include Current Protocols in Immunology, John Wiley & Sons, New York; Klein (1982) J., Immunology: The Science of Self-Nonself Discrimination (John Wiley & Sons, NY); Kennett et al., eds. (1980) Monoclonal Antibodies, Hybridoma: A New Dimension in Biological Analyses (Plenum Press, NY); Campbell (1984) "Monoclonal Antibody Technology" in Laboratory Techniques in Biochemistry and Molecular Biology, ed. Burden et al., (Elsevere, Amsterdam); Goldsby et al., eds. (2000) Kuby Immunnology (4th ed.; H. Freemand & Co.); Roitt et al. (2001) Immunology (6th ed.; London: Mosby); Abbas et al. (2005) Cellular and Molecular Immunology (5th ed.; Elsevier Health Sciences Division); Kontermann and Dubel (2001) Antibody Engineering (Springer Verlan); Sambrook and Russell (2001) Molecular Cloning: A Laboratory Manual (Cold Spring Harbor Press); Lewin (2003) Genes VIII (Prentice Hall2003); Harlow and Lane (1988) Antibodies: A Laboratory Manual (Cold Spring Harbor Press); Dieffenbach and Dveksler (2003) PCR Primer (Cold Spring Harbor Press).

It is to be noted that the term "a" or "an" entity refers to one or more of that entity; for example, "an anti-CXCL13 antibody" is understood to represent one or more anti-CXCL13 antibodies. As such, the terms "a" (or "an"), "one or more," and "at least one" can be used interchangeably herein.

All technical and scientific terms used herein have the same meaning. Efforts have been made to ensure accuracy with respect to numbers used (e.g. amounts, temperature, etc.) but some experimental errors and deviations should be accounted for.

Throughout this specification and the claims, the words “comprise,” “comprises,” and “comprising” are used in a non-exclusive sense, except where the context requires otherwise.

As used herein, the term “about,” when referring to a value is meant to encompass variations of, in some embodiments ± 50%, in some embodiments ± 20%, in some embodiments ± 10%, in some embodiments ± 5%, in some embodiments ± 1%, in some embodiments ± 0.5%, and in some embodiments ± 0.1% from the specified amount, as such variations are appropriate to perform the disclosed methods or employ the disclosed compositions.

Where a range of values is provided, it is understood that each intervening value, to the tenth of the unit of the lower limit, unless the context clearly dictates otherwise, between the upper and lower limit of the range and any other stated or intervening value in that stated range, is encompassed within the invention. The upper and lower limits of these small ranges which may independently be included in the smaller ranges is also encompassed within the invention, subject to any specifically excluded limit in the stated range. Where the stated range includes one or both of the limits, ranges excluding either or both of those included limits are also included in the invention.

The following examples are offered by way of illustration and not by way of limitation.

EXPERIMENTAL

Example 1. Evaluation of anti-CXCL13 antibodies in a mouse model for *Helicobacter* infection

Murine Model of *Helicobacter* infection. *Heliobacter* species such as *H. heilmannii* and *H. Pylori* induce gastric MALT lymphoma in patients. A mouse model of *Heliobacter* induced gastric lymphoid follicles was described in Nobutani et al. (2010) *FEMS Immunol Med Microbiol* 60:156-164. The Nobutani et al. mouse model was used herein to test the effect of anti-CXCL13 antibody in reducing infectious burden, by which is meant the titer of bacteria, in that tissue. C57BL/6J mice (n=5) were orally infected with *H. suis*. Starting one week post-infection, the mice received 0.6mg i.p. of either isotype antibody control (MAb 2510) or anti-CXCL13 antibody (MAb 5378) weekly for twelve weeks.

Twelve weeks after *H. suis* infection, the mice were sacrificed. Gastric samples from the mice were evaluated by PCR for expression of *H. suis* specific 16s rRNA genes as a measure of the relative level of infection with *H. suis*. The *H. suis* specific 16s rRNA gene PCR primers are shown below:

F: 5'-TTGGGAGGCTTTGTCTTTCCA-3' (SEQ ID NO: 22)

R: 5'-GATTAGCTCTGCCTCGCGGCT-3' (SEQ ID NO: 23)

PCR amplification reactions involved 1x reaction buffer [20 mM Tris/HCl (pH8.0), 100 mM KCl, 0.1 mM EDTA, 1mM DTT, 0.5% Tween™-20, 0.5% Nonidet™ P40, and 50% glycerol] containing 1 unit of Taq DNA polymerase (TOYOBO™, Osaka, Japan); 10 nmols of each deoxynucleotide triphosphate; 10 pmols of each oligonucleotide primer; and 1 µl of the diluted DNA, which was prepared by 1:10 dilution of the original samples with a DNA concentration of approximately 20-100 ng/μl, in a final volume of 50 μl. Cycling conditions for the 16s rRNA reactions involved 35 cycles of 94 °C for 30 seconds, 56 °C for 30 seconds, and 72 °C for 30 seconds.

Anti-CXCL13 antibody reduces titers of *Helicobacter* infected mice. The relative number of *H. suis* in the gastric mucosa of *H. suis* infected mice treated with anti-CXCL13 antibody or isotype control antibody was determined by real-time quantitative PCR. These results in FIG. 1 show a decrease in titers of *H. suis* in stomachs of infected mice treated with anti-CXCL13 antibody.

Anti-CXCL13 antibody induces TGF-β and IL-6 in Gastric Lymphoid Follicles of *H. suis* infected mice. The mRNA expression levels of TGF-β and IL-6 mRNA in the gastric mucosa of *H. suis* infected mice after treatment with isotype control or anti-CXCL13 antibody (mAb 5378) was determined by reverse transcription PCR. The mucosal and submucosal layers of the stomach were removed from the muscularis and serosa, and then homogenized with 1 ml of TRIZOL Reagent (Invitrogen™). RNA was extracted from the homogenates according to the manufacturer's instructions. RNA was subjected to the reverse transcription reaction using a High Capacity cDNA Reverse Transcription Kit (Applied Biosystems, Foster City, CA) according to the manufacturer's protocol, and quantitative PCR was performed using Power SYBR Green PCR Master Mix (Applied Biosystems) according to the manufacturer's instructions. To allow a relative comparison of RNA expression levels, the data from quantitative PCR were normalized to the amount of β-actin cDNA as an endogenous control. Specific primer pairs (Hokkaido System Science Co. Ltd., Sapporo, Japan) used for quantitative PCR were as follows:

TGF-β sense 5'-TCTTGGTCCAGATCACAACTTCA-3' (SEQ ID NO: 24)

TGF-β antisense 5'-CACTGATACGCCTGAGTGR-3' (SEQ ID NO: 25)

IL-6 sense 5'-GTGAGCGCTGAATCGAAA-3' (SEQ ID NO: 26)

IL-6 antisense 5'-GAGGATACCACTCCCAACAGACC-3' (SEQ ID NO: 27)

β-actin sense 5'-ATCACTGACGCTGATTGCAC-3' (SEQ ID NO: 28)

β-actin antisense 5'-AAGGCCAACCGTGAAAAGAT-3' (SEQ ID NO: 29)

Quantitative real-time PCR involved homogenizing the mucosal and submucosal layers of the stomach with 1 ml of TRIZOL Reagent (Invitrogen) and extracting RNA from the homogenates according to the manufacturer's instructions. RNA was then subjected to the reverse transcription reaction using a High Capacity cDNA Reverse

Transcription Kit (Applied Biosciences, Foster City, CA) according to the manufacturer's instructions, and quantitative real-time PCR was performed using Power SYBR Green PCR Master Mix (Applied Biosciences, Foster City, CA) and ABI Prism 7500 Real Time PCR System (Applied Biosciences, Foster City, CA) according to the manufacturer's instructions. To allow a relative comparison of RNA expression levels, the data from real-time PCR were normalized to the amount of β-actin cDNA as an endogenous control.

FIGS. 2A and 2B show the expression of TGF-β and IL-6 mRNA, respectively, in the stomach of *H. suis* infected mice after isotype control or anti-CXCL13 antibody (MAb 5378) treatment. These results show a significant increase in the expression of both TGF-β and IL-6 mRNA in *H. suis* infected mice treated with an anti-CXCL13 antibody as compared to mice treated with isotype control and uninfected mice. Interestingly, the expression levels of TGF-β and IL-6 in the stomachs of uninfected mice were also significantly induced by treatment with anti-CXCL13 antibodies (MAb 5378) (data not shown).

Because TGF-β and IL-6 can increase expression of IgA, these results suggested that *H. suis* specific IgA may be upregulated by anti-CXCL13 antibody treatment in the *H. suis* infected mouse stomachs. Thus, the treatment of *H. suis* infected mice with anti-CXCL13 antibody might lead to the inhibition of *H. suis* colonization via inducing *H. suis* specific IgA through the activation of TGF-β and IL-6 dependent pathways.

Anti-CXCL13 antibody treatment increases IgA secretion in gastric lymphoid follicles in *Helicobacter* infected mice. The stomachs of mice three months after *H. suis* infection were resected and opened at the greater curvature. Immunofluorescence staining of stomach samples from noninfected wild-type mice, isotype control and anti-CXCL13 antibody (MAb 5378) treated mice for IgA and actin (data not shown) showed an increase in IgA secretion in the gastric lymphoid follicles in *H. suis* infected mice treated with anti-CXCL13 antibody compared to control treatment.

Levels of anti- *H. suis* specific IgG and IgA in the serum and gastric juice of mice after *H. suis* infection. To detect *H. suis* specific IgG in the serum and gastric juice, the gastric juice was centrifuged at 16,000 x g for 5 min at 4°C, and the resultant supernatant was collected. The serum was separated from the blood by centrifugation at 15,000 x g for 10 min at 4°C. Ninety six-well plates were coated overnight at 4°C with 100 μl of a bicarbonate solution (pH 9.6) containing 100 μg/ml *H. pylori* lysate, and blocked by the addition of 1.5% (wt/vol) BSA in PBS for 1 h at 37 °C. The serum and gastric juice, which were diluted at 1:200 and 1:15, respectively, were added to the plates, followed by addition of 100 μl of HRP-conjugated goat anti-mouse IgG antibody (Bio-Rad™ Laboratories, Hercules, CA) diluted at 1:5.000 in PBST containing 0.2% (wt/vol) BSA and anti-mouse IgA. The bound antibody was detected by addition of o-phenylenediamine substrate, and measurement of absorbance at 490 nm was carried out.

Levels of anti-*H. suis* specific IgG and IgA in the serum and gastric juice of *H. suis* infected mice were measured. FIGS. 3A and 4A show that while anti-*H. suis* specific IgG is induced in serum and gastric juice by *H. suis* infection, there were no differences in the levels of anti-*H. suis* specific IgG in the serum or the gastric juice of anti-CXCL13 antibody (MAb 5378) and isotype control antibody treated mice. FIGS. 3B and 4B show that anti-*H. suis* specific IgA is induced in the serum and gastric juice by *H. suis* infection. While there are no significant differences in the levels of anti-*H. suis* specific IgA in the serum of anti-CXCL13 antibody and isotype control antibody treated mice, levels of anti-*H. suis* specific IgA are significantly higher in the gastric juice of the anti-CXCL13 antibody compared to the isotype control antibody treated mice. These results demonstrate that inhibition of CXCL13 produced by inflammatory cells of infected tissue results in an increase in IgA specific for the infectious agent and is associated with enhanced clearance of that bacterial infection.

The foregoing description of the specific embodiments will so fully reveal the general nature of the invention that others can, by applying knowledge within the skill of the art, readily modify and/or adapt for various applications such specific embodiments, without undue experimentation, without departing from the general concept of the present invention. Therefore, such adaptations and modifications are intended to be within the meaning and range of equivalents of the disclosed embodiments, based on the teaching and guidance presented herein. It is to be understood that the phraseology or terminology herein is for the purpose of description and not of limitation, such that the terminology or phraseology of the present specification is to be interpreted by the skilled artisan in light of the teachings and guidance.

Many modifications and other embodiments of the inventions set forth herein will come to mind to one skilled in the art to which these inventions pertain having the benefit of the teachings presented in the foregoing descriptions and the associated drawings. Therefore, it is to be understood that the inventions are not to be limited to the specific embodiments disclosed and that modifications and other embodiments are intended to be included within the scope of the appended claims.

Although specific terms are employed herein, they are used in a generic and descriptive sense only and not for the purpose of limitation.

All publications and patent applications mentioned in the specification are indicative of the level of those skilled in the art to which this invention pertains.

THAT WHICH IS CLAIMED:

1. An agent that inhibits CXCL13 activity for use in reducing the level of bacteria in a mucosal bacterial infection and increasing secretory immunoglobulin A (IgA) levels in a subject having a deficiency thereof that is secondary to said mucosal bacterial infection, wherein said mucosal bacterial infection is gastric mucosal *Helicobacter* infection and, wherein said agent is an antibody or antigen-binding fragment thereof that specifically binds to CXCL13.

2. The agent of claim 1, wherein said *Heliobacter* is selected from the group consisting of *Heliobacter pylori*, *Heliobacter heilmannii*, and *Heliobacter suis*.

3. The agent of claim 1 or 2, wherein said secretory IgA levels that are increased are gastric IgA levels.

4. The agent of claim 1, 2, or 3, wherein said antibody or fragment thereof is chimeric, human, or humanized.

5. The agent of any one of claims 1 to 4, wherein said antibody specifically binds to CXCL13 and comprises:

a VH domain comprising a CDR1 having the sequence set forth in SEQ ID NO: 11, a CDR2 having the sequence set forth in SEQ ID NO: 12, and a CDR3 having the sequence set forth in SEQ ID NO: 13, and a VL domain comprising a CDR1 having the sequence set forth in SEQ ID NO: 20, a CDR2 having the sequence set forth in SEQ ID NO: 17, and a CDR3 having the sequence set forth in SEQ ID NO: 18; or

a VH domain comprising the amino acid sequence set forth in SEQ ID NO: 14 and a VL domain comprising the amino acid sequence set forth in SEQ ID NO: 19.

6. The agent of claim 5, wherein said antibody comprises a VH domain having the sequence set forth in SEQ ID NO: 14 and a VL domain having the sequence set forth in SEQ ID NO: 19.

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7. The agent of any one of claims 1 to 6, wherein said agent inhibits the interaction of CXCL13 with a CXCL13 receptor.

8. The agent of claim 7, wherein said CXCL13 receptor is CXCR5.

9. The agent of any one of claims 1 to 7, wherein said agent inhibits CXCR5 receptor internalization.

10. The agent of any one of claims 1 to 8, wherein said agent is for administration with a pharmaceutically acceptable carrier.

11. The agent of any one of claims 1 to 9, wherein said subject is an animal.

12. The agent of claim 11, wherein said animal is a mammal.

13. The agent of claim 11, wherein said animal is a human.

14. Use of an agent that inhibits CXCL13 for reducing the level of bacteria in a mucosal bacterial infection and increasing secretory immunoglobulin A (IgA) levels in a subject having a deficiency thereof that is secondary to said mucosal bacterial infection, wherein said mucosal bacterial infection is gastric mucosal *Helicobacter* infection, and wherein said agent is an antibody or antigen-binding fragment thereof that specifically binds to CXCL13.

15. Use of an agent that inhibits CXCL13 in preparation of a medicament for reducing the level of bacteria in a mucosal bacterial infection and increasing secretory immunoglobulin A (IgA) levels in a subject having a deficiency thereof that is secondary to said mucosal bacterial infection, wherein said mucosal bacterial infection is gastric mucosal *Helicobacter* infection, and wherein said agent is an antibody or antigen-binding fragment thereof that specifically binds to CXCL13.

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16. The use of claim 14 or 15, wherein said *Heliobacter* is selected from the group consisting of *Heliobacter pylori*, *Heliobacter heilmannii*, and *Heliobacter suis*.

17. The use of claim 14, 15, or 16, wherein said secretory IgA levels that are increased are gastric IgA.

18. The use of any one of claims 14 to 17, wherein said antibody or fragment thereof is chimeric, human, or humanized.

19. The use of any one of claims 14 to 18, wherein said antibody specifically binds to CXCL13 and comprises:

a VH domain comprising a CDR1 having the sequence set forth in SEQ ID NO: 11, a CDR2 having the sequence set forth in SEQ ID NO: 12, and a CDR3 having the sequence set forth in SEQ ID NO: 13, and a VL domain comprising a CDR1comprising a CDR1 having the sequence set forth in SEQ ID NO: 20, a CDR2 having the sequence set forth in SEQ ID NO: 17, and a CDR3 having the sequence set forth in SEQ ID NO: 18; or

a VH domain comprising the amino acid sequence set forth in SEQ ID NO: 14 and a VL domain comprising the amino acid sequence set forth in SEQ ID NO: 19.

20. The use of claim 19, wherein said antibody comprises a VH domain having the sequence set forth in SEQ ID NO: 14 and a VL domain having the sequence set forth in SEQ ID NO: 19.

21. The use of any one of claims 14 to 20, wherein said agent inhibits the interaction of CXCL13 with a CXCL13 receptor.

22. The use of claim 21, wherein said CXCL13 receptor is CXCR5.

23. The use of claim 22, wherein said agent inhibits CXCR5 receptor internalization.

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24. The use of any one of claims 14 to 23, wherein said agent is for administration with a pharmaceutically acceptable carrier.

25. The use of any one of claims 14 to 24, wherein said subject is an animal.

26. The use of claim 25, wherein said animal is a mammal.

27. The use of claim 25, wherein said animal is a human.

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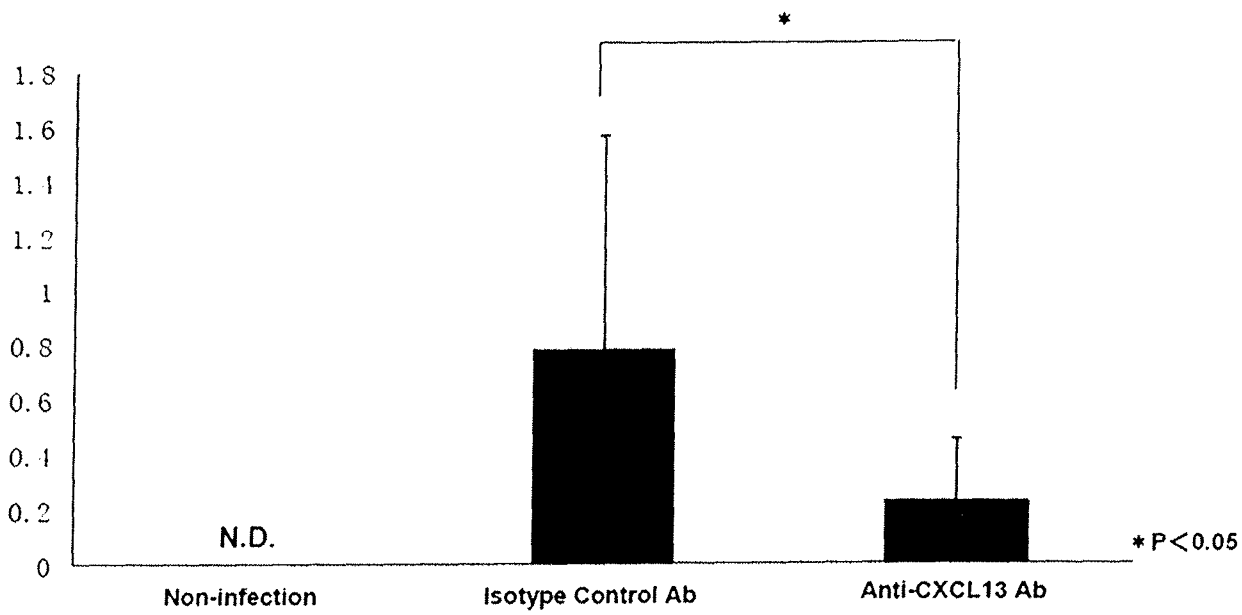
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Anti-CXCL13 Ab

FIG. 1

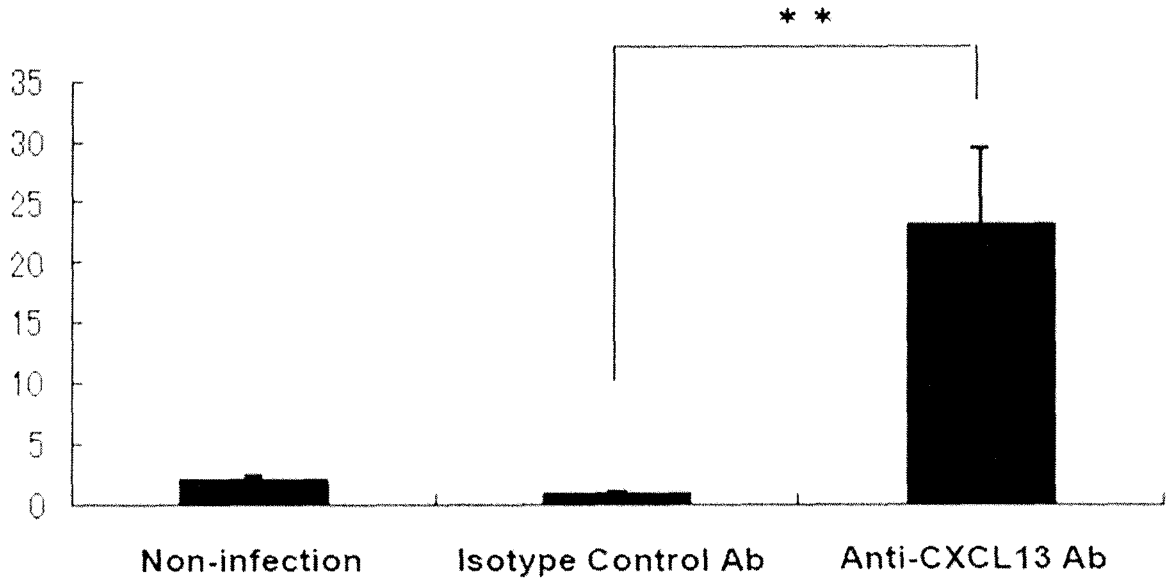
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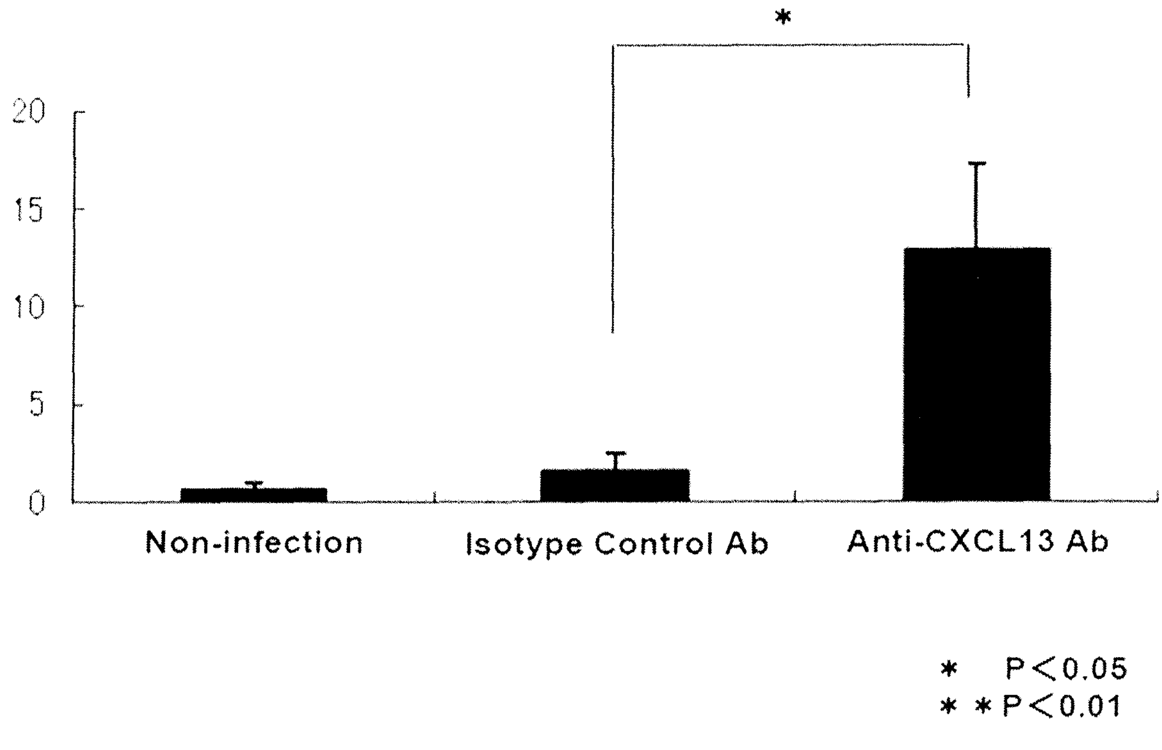
FIG. 2A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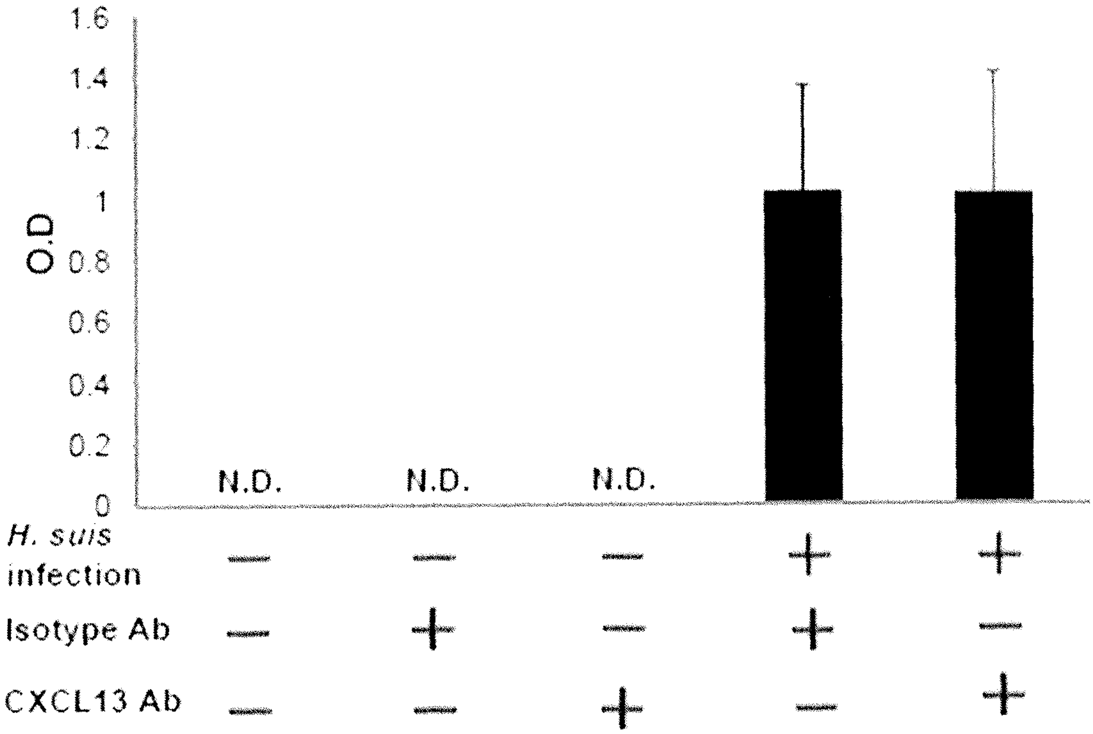
** P<0.01

FIG. 2B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1.2
1
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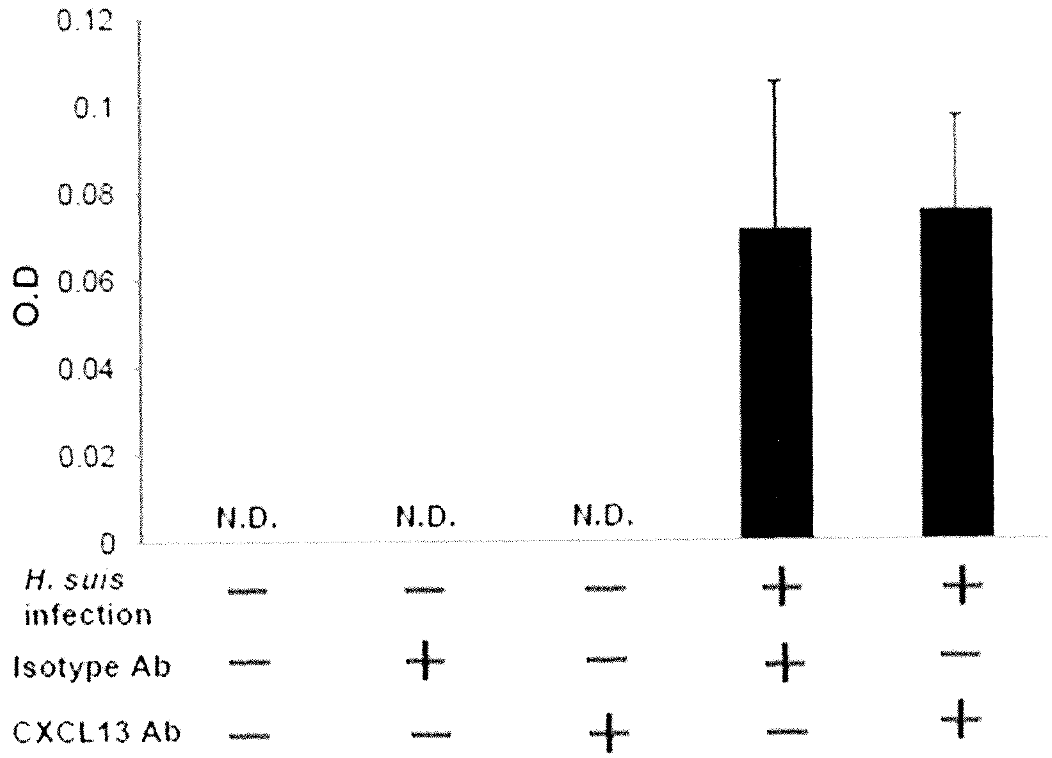
N.D.
N.D.
H. suis infection
Isotype Ab
CXCL13 Ab
—
+

FIG. 3A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0.06
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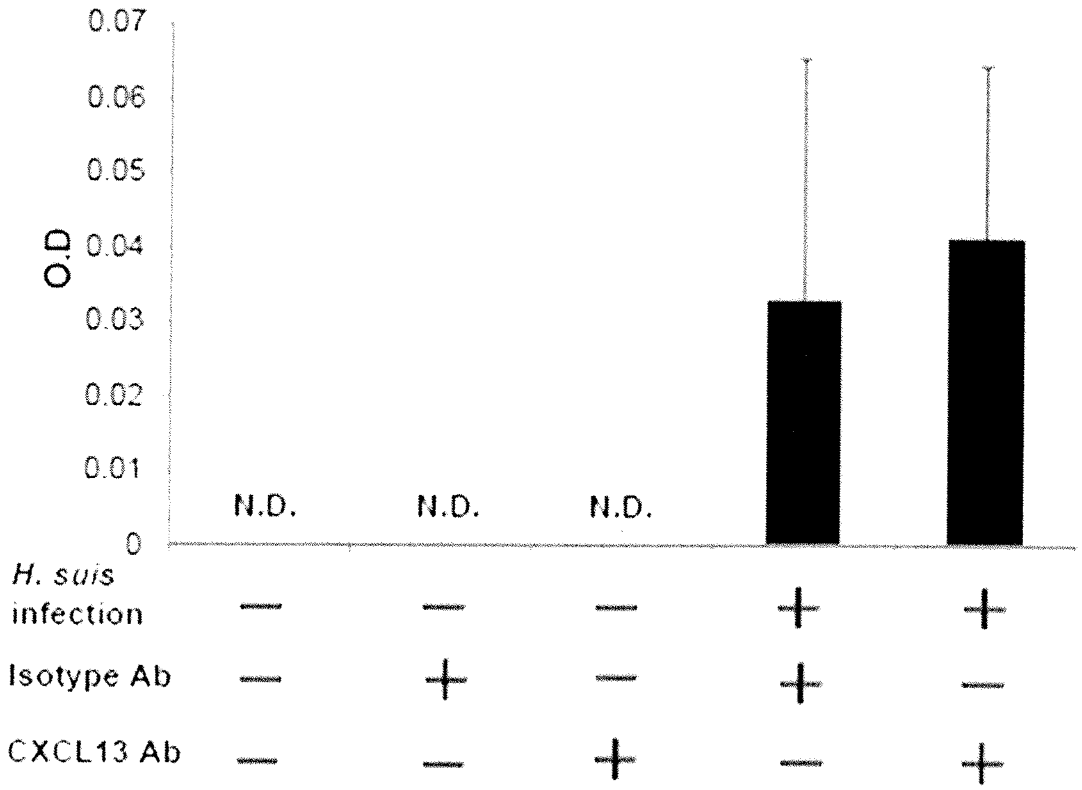
N.D.
N.D.
H. suis infection
Isotype Ab
CXCL13 Ab

FIG. 3B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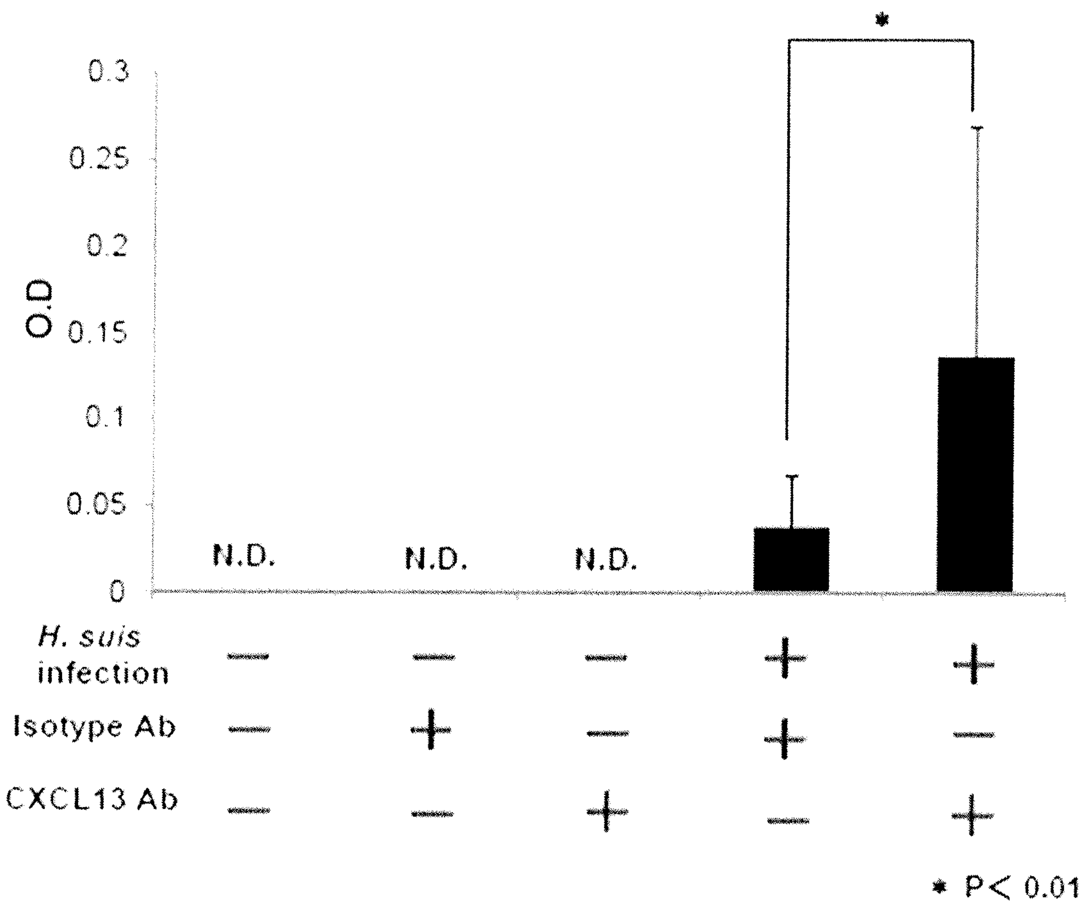
H. suis infection
Isotype Ab
CXCL13 Ab

FIG. 4A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N.D.
H. suis infection
Isotype Ab
CXCL13 Ab
* P< 0.01

FIG. 4B