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(54) Title: BISPECIFIC ANTIBODIES AND METHODS OF USING THE SAME

(57) Abstract: The present invention relates to antagonizing the activity of IL-17A, IL-17F and IL-23 using bispecific antibodies that comprise a binding entity that is cross-reactive for IL-17A and IL-17F and a binding entity that binds IL-23p19. The present invention relates to novel bispecific antibody formats and methods of using the same.

BISPECIFIC ANTIBODIES AND METHODS OF USING THE SAME

BACKGROUND OF THE INVENTION

[0001] Cytokines are soluble, small proteins that mediate a variety of biological effects, including the induction of immune cell proliferation, development, differentiation, and/or migration, as well as the regulation of the growth and differentiation of many cell types (see, for example, Arai et al., *Annu. Rev. Biochem.* 59:783 (1990); Mosmann, *Curr. Opin. Immunol.* 3:311 (1991); Paul et al., *Cell*, 76:241 (1994)). Cytokine-induced immune functions can also include an inflammatory response, characterized by a systemic or local accumulation of immune cells. Although they do have host-protective effects, these immune responses can produce pathological consequences when the response involves excessive and/or chronic inflammation, as in autoimmune disorders (such as multiple sclerosis) and cancer/neoplastic diseases (Oppenheim et al., eds., *Cytokine Reference*, Academic Press, San Diego, CA (2001); von Andrian et al., *New Engl. J. Med.*, 343:1020 (2000); Davidson et al., *New Engl. J. Med.*, 345:340 (2001); Lu et al., *Mol. Cancer Res.*, 4:221 (2006); Dalgleish et al., *Cancer Treat Res.*, 130:1 (2006)).

[0002] IL-17A, IL-17F and IL-23 are cytokines involved in inflammation. IL-17A induces the production of inflammatory cytokines such as IL-1β, TNF-α, IL-6, and IL-23 by synovial fibroblasts, monocytes, and macrophages, all of which promote inflammation and Th17 development. IL-17A also induces an array of chemokines, including CXCL-1, CXCL-2, CXCL-5, CXCL-8, CCL-2, and CCL-20, leading to recruitment of T cells, B cells, monocytes, and neutrophils. Lundy, S.K., *Arthritis Res. Ther.*, 9:202 (2007). IL-17F shares the greatest homology (55%) with IL-17A and is also a proinflammatory cytokine. Both IL-17A and IL-17F are produced by Th17 cells, whereas the other IL-17 family members, IL-17B, IL-17C, and IL-17D, are produced by non-T cell sources. IL-17A and IL-17F can exist as IL-17A homodimers and IL-17F homodimers or as IL-17A/F heterodimers. Liang, S.C. et al., *J. Immunol.*, 179:7791-7799 (2007). IL-17A is increased in rheumatoid arthritis sera and synovial fluid, and is present in the T-cell rich areas of the synovium. Shahrara, S., *Arthritis Res. Ther.*, 10:R93 (2005). IL-17A can also orchestrate bone and cartilage damage. An effective

blockade of IL-17 will need to neutralize IL-17A homodimers, IL-17F homodimers and IL-17A/F heterodimers.

[0003] IL-23 is a type-1 heterodimer, comprising a 19 kilodalton (kD) fourfold helical core α subunit (IL-23p19), disulfide linked to an additional 40kD distinct β subunit (IL-12p40). IL-23 is a key cytokine in bridging the innate and adaptive arms of the immune response; it is produced early in response to an antigen challenge, and is essential for driving early local immune responses. Furthermore, IL-23 plays a central role in the activation of NK cells, the enhancement of T cell proliferation and the regulation of antibody production. IL-23 also regulates pro-inflammatory cytokines (*e.g.*, IFN-γ), which are important in cell-mediated immunity against intracellular pathogens. Recent reports have indicated that in humans increased amounts of IL-23 have been associated with several autoimmune diseases including rheumatoid arthritis (RA), Lyme arthritis, inflammatory bowel disease (IBD), Crohn's disease (CD), psoriasis and multiple sclerosis (MS). IL-23p19 knock-out mice were resistant to autoimmune encephalomyelitis (EAE), collagen-induced arthritis (CIA) and central nervous system autoimmune induction. IL-23 is not essential for the development of human Th17 cells, but appears to be required for their survival and/or expansion. Paradowska-Gorycka, A., *Scandinavian Journal of Immunology*, 71:134-145 (2010). Genetic studies revealed an association between IL-23 receptor genes and susceptibility to several autoimmune diseases including CD, RA and Graves' ophthalmopathy. The IL-23-Th17 axis is crucial to autoimmune disease development. Leng et al., *Archives of Medical Research*, 41:221-225 (2010).

[0004] The demonstrated activities of IL-17A, IL-17F and IL-23p19 in mediating and promoting several autoimmune diseases illustrate the clinical potential of, and need for, molecules which can antagonize these targets. The present invention, as set forth herein, meets these and other needs.

BRIEF DESCRIPTION OF THE DRAWINGS

[0005] Fig. 1 is a schematic illustration of a whole antibody and its modular components.

[0006] Fig. 2 depicts a model of a bispecific antibody designated biAbFabL which contains a whole antibody with a C-terminal Fab unit of the second arm of the bispecific antibody attached via a linker, and which utilizes a common light chain.

[0007] Fig. 3 depicts a model of a bispecific antibody designated taFab which contains a whole antibody with an N-terminal Fab unit of the second arm of the bispecific antibody attached via a linker. As with the heavy chain portion, there are two light chains for each arm of the bispecific attached via a linker.

[0008] Fig. 4 depicts a model of a bispecific antibody designated Heterodimeric Fc, that resembles a traditional antibody, however, contains two different heavy chains which associate through an electrostatic complementarity association in the C_{H3} region. The Heterodimeric Fc utilizes a common light chain.

[0009] Fig. 5 depicts a model of a bispecific antibody designated VCVFc which contains a whole antibody with a Fv unit of the second arm of the bispecific antibody inserted between the Fab region and the hinge via linkers.

[0010] Fig. 6 depicts a model of a bispecific antibody designated VCDFc which contains a whole antibody with a single domain antibody for the second arm of the bispecific antibody inserted between the Fab region and the hinge via linkers.

[0011] Fig. 7 illustrates the ELISA results showing strong antibody binding to IL-23p19 and lack of cross reactivity to IL-12.

[0012] Fig. 8 illustrates the potent neutralization of IL-23 signaling as observed in the kit225 assay.

[0013] Fig. 9 shows the Biacore results of 7B7, STELARA® (ustekinumab, an anti-IL-23p40 antibody) and human IL-23 receptor ability to bind the various IL-23p19 alanine shaved mutants, wild-type and purified wild-type L-23p19 (positive control) and a negative control. 7B7 mAb binding is shown in the left column, STELARA® is shown in the center column and hIL-23R-Fc binding is shown in the right column. The four mutants shown with the star were chosen for scale-up to confirm these results.

[0014] Fig. 10 shows a Biacore kinetic analysis of IL-23p19 antibody binding to the IL-23 alanine mutants.

[0015] Fig. 11 schematically illustrates the process used to identify and select the 7B7 antibody (anti-IL-23p19).

[0016] Fig. 12 schematically illustrates the clinical disease scores over time in the marmoset EAE model.

[0017] Fig. 13 schematically illustrates the MRI lesion score in the marmoset EAE model.

[0018] Fig. 14 schematically illustrates the MRI optic nerve score in the marmoset EAE model.

[0019] Fig. 15 shows the overlay of all four structures of the Fab with IL-17A or IL-17F, aligned by the interleukin.

[0020] Fig. 16 graphically shows the cell functional activity of the IL-17A mutants.

[0021] Fig. 17 graphically shows the cell functional activity of the IL-17F mutants.

[0022] Fig. 18 is a schematic overly of the 9nM IL-17A mutants binding BiAb3 demonstrating the accelerated off-rate of mutants containing Y108A mutation and combinations thereof.

[0023] Fig. 19 shows the computational energetic analysis of IL-17A mutants binding to BiAb3.

DETAILED DESCRIPTION OF THE INVENTION

[0024] The present invention provides, in one embodiment, bispecific antibodies comprising an IL-17A/F binding entity that binds to IL-17A and IL-17F and an IL-23 binding entity that binds to IL-23 via p19. The invention also includes isolated nucleic acids encoding the heavy chains and light chains of the bispecific antibodies of the invention, as well as vectors comprising the nucleic acids, host cells comprising the vectors, and methods of making and using the bispecific antibodies.

[0025] In other embodiments, the present invention provides compositions comprising the bispecific antibodies and kits comprising the bispecific antibodies, as well as articles of manufacture comprising the bispecific antibodies.

[0026] The bispecific antibodies of the present invention are useful for the inhibition of proinflammatory cytokines, *e.g.*, IL-17A, IL-17F and IL-23p19. The antibodies can be used to reduce, limit, neutralize, or block the proinflammatory effects of the IL-17A homodimer, the IL-17F homodimer, or the IL-17A/F heterodimer.

Likewise, the antibodies can be used to reduce, limit, neutralize, or block the pro-cancerous effects of the IL-17A homodimer, the IL-17F homodimer, or the IL-17A/F heterodimer. In such cases, the anti-IL-23p19 portion of the antibody is used to reduce, limit, neutralize, or block production of new T cells that would produce IL-17A and/or IL-17F, including homodimers and heterodimers. The bispecific antibodies described herein can be used to treat inflammatory disorders and autoimmune diseases, such as multiple sclerosis (e.g., relapsing-remitting multiple sclerosis, secondary-progressive multiple sclerosis, primary-progressive multiple sclerosis and progressive-relapsing multiple sclerosis), inflammatory bowel disease, psoriasis, systemic sclerosis, systemic lupus erythematosus, antineutrophil cytoplasmic antibodies (ANCA)-associated vasculitis (AAV) and giant cell arteritis. The bispecific antibodies described herein can also be used to treat cancer, including angiogenesis. For instance, the bispecific antibodies as described herein can be used to treat multiple-myeloma-induced lytic bone disease (Sotomayor, E.M., *Blood*, 116(18):3380-3382 (2010)).

[0027] In the description that follows, a number of terms are used extensively. The following definitions are provided to facilitate understanding of the invention.

[0028] Unless otherwise specified, "a", "an", "the", and "at least one" are used interchangeably and mean one or more than one.

[0029] "Antibodies" (Abs) and "immunoglobulins" (Igs) are glycoproteins having the same structural characteristics. While antibodies exhibit binding specificity to a specific antigen, immunoglobulins include both antibodies and other antibody-like molecules that lack antigen specificity. Polypeptides of the latter kind are, for example, produced at low levels by the lymph system and at increased levels by myelomas. Thus, as used herein, the term "antibody" or "antibody peptide(s)" refers to an intact antibody, or an antigen-binding fragment thereof that competes with the intact antibody for specific binding and includes chimeric, humanized, fully human, and bispecific antibodies. In certain embodiments, antigen-binding fragments are produced, for example, by recombinant DNA techniques. In additional embodiments, antigen-binding fragments are produced by enzymatic or chemical cleavage of intact antibodies. Antigen-binding fragments include, but are not limited to, Fab, Fab′, $F(ab)^2$, $F(ab')^2$, Fv, and single-chain antibodies.

[0030] The term "isolated antibody" as used herein refers to an antibody that has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials which would interfere with diagnostic or therapeutic uses for the antibody, and may include enzymes, hormones, and other proteinaceous or nonproteinaceous solutes. In preferred embodiments, the antibody will be purified (1) to greater than 95% by weight of antibody as determined by the Lowry method, and most preferably more than 99% by weight, (2) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (3) to homogeneity by SDS-PAGE under reducing or nonreducing conditions using Coomassie blue or, preferably, silver stain. Isolated antibody includes the antibody in situ within recombinant cells since at least one component of the antibody's natural environment will not be present. Ordinarily, however, isolated antibody will be prepared by at least one purification step.

[0031] The term "agonist" refers to any compound including a protein, polypeptide, peptide, antibody, antibody fragment, large molecule, or small molecule (less than 10 kD), that increases the activity, activation or function of another molecule.

[0032] The term "antagonist" refers to any compound including a protein, polypeptide, peptide, antibody, antibody fragment, large molecule, or small molecule (less than 10 kD), that decreases the activity, activation or function of another molecule.

[0033] The term "bind(ing) of a polypeptide " includes, but is not limited to, the binding of a ligand polypeptide of the present invention to a receptor; the binding of a receptor polypeptide of the present invention to a ligand; the binding of an antibody of the present invention to an antigen or epitope; the binding of an antigen or epitope of the present invention to an antibody; the binding of an antibody of the present invention to an anti-idiotypic antibody; the binding of an anti-idiotypic antibody of the present invention to a ligand; the binding of an anti-idiotypic antibody of the present invention to a receptor; the binding of an anti-anti-idiotypic antibody of the present invention to a ligand, receptor or antibody, etc.

[0034] A "bispecific" or "bifunctional" antibody is a hybrid antibody having two different heavy/light chain pairs and two different binding sites. Bispecific antibodies may be produced by a variety of methods including, but not limited to, fusion

of hybridomas or linking of Fab′ fragments. See, *e.g.*, Songsivilai et al., *Clin. Exp. Immunol.*, 79:315-321 (1990); Kostelny et al., *J. Immunol.*, 148:1547-1553 (1992).

[0035] As used herein, the term "epitope" refers to the portion of an antigen to which an antibody specifically binds. Thus, the term "epitope" includes any protein determinant capable of specific binding to an immunoglobulin or T-cell receptor. Epitopic determinants usually consist of chemically active surface groupings of molecules such as amino acids or sugar side chains and usually have specific three dimensional structural characteristics, as well as specific charge characteristics. More specifically, the term "IL-17 epitope", "IL-23 epitope" and/or "IL-23/p19 epitope" as used herein refers to a portion of the corresponding polypeptide having antigenic or immunogenic activity in an animal, preferably in a mammal, and most preferably in a mouse or a human. An epitope having immunogenic activity is a portion of, for example, an IL-17A or IL-17F or IL-23/p19 polypeptide that elicits an antibody response in an animal. An epitope having antigenic activity is a portion of, for example, an IL-17A or IL-17F or IL-23/p19 polypeptide to which an antibody immunospecifically binds as determined by any method well known in the art, for example, by immunoassays, protease digest, crystallography or H/D-Exchange. Antigenic epitopes need not necessarily be immunogenic. Such epitopes can be linear in nature or can be a discontinuous epitope. Thus, as used herein, the term "conformational epitope" refers to a discontinuous epitope formed by a spatial relationship between amino acids of an antigen other than an unbroken series of amino acids.

[0036] As used herein, the term "immunoglobulin" refers to a protein consisting of one or more polypeptides substantially encoded by immunoglobulin genes. One form of immunoglobulin constitutes the basic structural unit of an antibody. This form is a tetramer and consists of two identical pairs of immunoglobulin chains, each pair having one light and one heavy chain. In each pair, the light and heavy chain variable regions are together responsible for binding to an antigen, and the constant regions are responsible for the antibody effector functions.

[0037] Full-length immunoglobulin "light chains" (about 25 Kd or about 214 amino acids) are encoded by a variable region gene at the NH2-terminus (about 110 amino acids) and a kappa or lambda constant region gene at the COOH--terminus. Full-length immunoglobulin "heavy chains" (about 50 Kd or about 446 amino acids), are

similarly encoded by a variable region gene (about 116 amino acids) and one of the other aforementioned constant region genes (about 330 amino acids). Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, and define the antibody's isotype as IgG (such as IgG1, IgG2, IgG3 and IgG4), IgM, IgA, IgD and IgE, respectively. Within light and heavy chains, the variable and constant regions are joined by a "J" region of about 12 or more amino acids, with the heavy chain also including a "D" region of about 10 more amino acids. (See generally, *Fundamental Immunology* (Paul, W., ed., 2nd Edition, Raven Press, NY (1989)), Chapter 7 (incorporated by reference in its entirety for all purposes).

[0038] An immunoglobulin light or heavy chain variable region consists of a "framework" region interrupted by three hypervariable regions. Thus, the term "hypervariable region" refers to the amino acid residues of an antibody which are responsible for antigen binding. The hypervariable region comprises amino acid residues from a "Complementarity Determining Region" or "CDR" (Kabat et al., *Sequences of Proteins of Immunological Interest*, 5th Edition, Public Health Service, National Institutes of Health, Bethesda, MD (1991)) and/or those residues from a "hypervariable loop" (Chothia et al., *J. Mol. Biol.* 196: 901-917 (1987)) (both of which are incorporated herein by reference). "Framework Region" or "FR" residues are those variable domain residues other than the hypervariable region residues as herein defined. The sequences of the framework regions of different light or heavy chains are relatively conserved within a species. Thus, a "human framework region" is a framework region that is substantially identical (about 85% or more, usually 90-95% or more) to the framework region of a naturally occurring human immunoglobulin. The framework region of an antibody, that is the combined framework regions of the constituent light and heavy chains, serves to position and align the CDR's. The CDR's are primarily responsible for binding to an epitope of an antigen. Accordingly, the term "humanized" immunoglobulin refers to an immunoglobulin comprising a human framework region and one or more CDR's from a non-human (usually a mouse or rat) immunoglobulin. The non-human immunoglobulin providing the CDR's is called the "donor" and the human immunoglobulin providing the framework is called the "acceptor". Constant regions need not be present, but if they are, they must be substantially identical to human immunoglobulin constant regions, *i.e.*, at least about 85-90%, preferably about 95% or more identical. Hence, all parts of a

humanized immunoglobulin, except possibly the CDR's, are substantially identical to corresponding parts of natural human immunoglobulin sequences. Further, one or more residues in the human framework region may be back mutated to the parental sequence to retain optimal antigen-binding affinity and specificity. In this way, certain framework residues from the non-human parent antibody are retained in the humanized antibody in order to retain the binding properties of the parent antibody while minimizing its immunogenicity. The term "human framework region" as used herein includes regions with such back mutations. A "humanized antibody" is an antibody comprising a humanized light chain and a humanized heavy chain immunoglobulin. For example, a humanized antibody would not encompass a typical chimeric antibody as defined above, *e.g.*, because the entire variable region of a chimeric antibody is non-human.

[0039] The term "humanized" immunoglobulin refers to an immunoglobulin comprising a human framework region and one or more CDR's from a non-human, *e.g.*, mouse, rat or rabbit, immunoglobulin. The non-human immunoglobulin providing the CDR's is called the "donor" and the human immunoglobulin providing the framework is called the "acceptor". Constant regions need not be present, but if they are, they must be substantially identical to human immunoglobulin constant regions, *i.e.*, at least about 85-90%, preferably about 95% or more identical. Hence, all parts of a humanized immunoglobulin, except possibly the CDR's and possibly a few back-mutated amino acid residues in the framework region (*e.g.*, 1-15 residues), are substantially identical to corresponding parts of natural human immunoglobulin sequences. A "humanized antibody" is an antibody comprising a humanized light chain and a humanized heavy chain immunoglobulin. For example, a humanized antibody would not encompass a typical chimeric antibody as defined above, *e.g.*, because the entire variable region of a chimeric antibody is non-human.

[0040] As used herein, the term "human antibody" includes an antibody that has an amino acid sequence of a human immunoglobulin and includes antibodies isolated from human immunoglobulin libraries or from animals transgenic for one or more human immunoglobulin and that do not express endogenous immunoglobulins, as described, for example, by Kucherlapati et al. in U.S. Patent No. 5,939,598.

[0041] The term "genetically altered antibodies" means antibodies wherein the amino acid sequence has been varied from that of a native antibody. Because of the

relevance of recombinant DNA techniques in the generation of antibodies, one need not be confined to the sequences of amino acids found in natural antibodies; antibodies can be redesigned to obtain desired characteristics. The possible variations are many and range from the changing of just one or a few amino acids to the complete redesign of, for example, the variable and/or constant region. Changes in the constant region will, in general, be made in order to improve or alter characteristics, such as complement fixation, interaction with membranes and other effector functions. Changes in the variable region will be made in order to improve the antigen binding characteristics.

[0042] A "Fab fragment" is comprised of one light chain and the C_{H1} and variable regions of one heavy chain. The heavy chain of a Fab molecule cannot form a disulfide bond with another heavy chain molecule.

[0043] A "Fab′ fragment" contains one light chain and one heavy chain that contains more of the constant region, between the C_{H1} and C_{H2} domains, such that an interchain disulfide bond can be formed between two heavy chains to form a $F(ab')_2$ molecule.

[0044] A "$F(ab')_2$ fragment" contains two light chains and two heavy chains containing a portion of the constant region between the C_{H1} and C_{H2} domains, such that an interchain disulfide bond is formed between two heavy chains.

[0045] A "Fv fragment" contains the variable regions from both heavy and light chains but lacks the constant regions.

[0046] A "single domain antibody" is an antibody fragment consisting of a single domain Fv unit, *e.g.*, V_H or V_L. Like a whole antibody, it is able to bind selectively to a specific antigen. With a molecular weight of only 12–15 kDa, single-domain antibodies are much smaller than common antibodies (150–160 kDa) which are composed of two heavy protein chains and two light chains, and even smaller than Fab fragments (~50 kDa, one light chain and half a heavy chain) and single-chain variable fragments (~25 kDa, two variable domains, one from a light and one from a heavy chain). The first single-domain antibodies were engineered from heavy-chain antibodies found in camelids. Although most research into single-domain antibodies is currently based on heavy chain variable domains, light chain variable domains and nanobodies derived from light chains have also been shown to bind specifically to target epitopes.

[0047] The term "monoclonal antibody" or "mAb" or "MAb" or "Mab" or "mab" as used herein is not limited to antibodies produced through hybridoma technology. The term "monoclonal antibody" or "mAb" or "MAb" or "Mab" or "mab" refer to an antibody that is derived from a single clone, including any eukaryotic, prokaryotic, or phage clone, and not the method by which it is produced.

[0048] As used herein, "nucleic acid" or "nucleic acid molecule" refers to polynucleotides, such as deoxyribonucleic acid (DNA) or ribonucleic acid (RNA), oligonucleotides, fragments generated by the polymerase chain reaction (PCR), and fragments generated by any of ligation, scission, endonuclease action, and exonuclease action. Nucleic acid molecules can be composed of monomers that are naturally-occurring nucleotides (such as DNA and RNA), or analogs of naturally-occurring nucleotides (*e.g.,* α-enantiomeric forms of naturally-occurring nucleotides), or a combination of both. Modified nucleotides can have alterations in sugar moieties and/or in pyrimidine or purine base moieties. Sugar modifications include, for example, replacement of one or more hydroxyl groups with halogens, alkyl groups, amines, and azido groups, or sugars can be functionalized as ethers or esters. Moreover, the entire sugar moiety can be replaced with sterically and electronically similar structures, such as aza-sugars and carbocyclic sugar analogs. Examples of modifications in a base moiety include alkylated purines and pyrimidines, acylated purines or pyrimidines, or other well-known heterocyclic substitutes. Nucleic acid monomers can be linked by phosphodiester bonds or analogs of such linkages. Analogs of phosphodiester linkages include phosphorothioate, phosphorodithioate, phosphoroselenoate, phosphorodiselenoate, phosphoroanilothioate, phosphoranilidate, phosphoramidate, and the like. The term "nucleic acid molecule" also includes so-called "peptide nucleic acids", which comprise naturally-occurring or modified nucleic acid bases attached to a polyamide backbone. Nucleic acids can be either single stranded or double stranded.

[0049] The term "complement of a nucleic acid molecule" refers to a nucleic acid molecule having a complementary nucleotide sequence and reverse orientation as compared to a reference nucleotide sequence.

[0050] The term "degenerate nucleotide sequence" denotes a sequence of nucleotides that includes one or more degenerate codons as compared to a reference nucleic acid molecule that encodes a polypeptide. Degenerate codons contain different

triplets of nucleotides, but encode the same amino acid residue (*i.e.,* GAU and GAC triplets each encode Asp).

[0051] An "isolated nucleic acid molecule" is a nucleic acid molecule that is not integrated in the genomic DNA of an organism. For example, a DNA molecule that encodes a growth factor that has been separated from the genomic DNA of a cell is an isolated DNA molecule. Another example of an isolated nucleic acid molecule is a chemically-synthesized nucleic acid molecule that is not integrated in the genome of an organism. A nucleic acid molecule that has been isolated from a particular species is smaller than the complete DNA molecule of a chromosome from that species.

[0052] A "nucleic acid molecule construct" is a nucleic acid molecule, either single- or double-stranded, that has been modified through human intervention to contain segments of nucleic acid combined and juxtaposed in an arrangement not existing in nature.

[0053] "Complementary DNA (cDNA)" is a single-stranded DNA molecule that is formed from an mRNA template by the enzyme reverse transcriptase. Typically, a primer complementary to portions of mRNA is employed for the initiation of reverse transcription. Those skilled in the art also use the term "cDNA" to refer to a double-stranded DNA molecule consisting of such a single-stranded DNA molecule and its complementary DNA strand. The term "cDNA" also refers to a clone of a cDNA molecule synthesized from an RNA template.

[0054] A "promoter" is a nucleotide sequence that directs the transcription of a structural gene. Typically, a promoter is located in the 5′ non-coding region of a gene, proximal to the transcriptional start site of a structural gene. Sequence elements within promoters that function in the initiation of transcription are often characterized by consensus nucleotide sequences. These promoter elements include RNA polymerase binding sites, TATA sequences, CAAT sequences, differentiation-specific elements (DSEs; McGehee et al., *Mol. Endocrinol.*, 7:551 (1993)), cyclic AMP response elements (CREs), serum response elements (SREs; Treisman, *Seminars in Cancer Biol.*, 1:47 (1990)), glucocorticoid response elements (GREs), and binding sites for other transcription factors, such as CRE/ATF (O'Reilly et al., *J. Biol. Chem.*, 267:19938 (1992)), AP2 (Ye et al., *J. Biol. Chem.*, 269:25728 (1994)), SP1, cAMP response element binding protein (CREB; Loeken, *Gene Expr.*, 3:253 (1993)) and octamer factors (see, in

general, Watson et al., eds., *Molecular Biology of the Gene*, 4th Edition, The Benjamin/Cummings Publishing Company, Inc. (1987), and Lemaigre et al., *Biochem. J.*, 303:1 (1994)). If a promoter is an inducible promoter, then the rate of transcription increases in response to an inducing agent. In contrast, the rate of transcription is not regulated by an inducing agent if the promoter is a constitutive promoter. Repressible promoters are also known.

[0055] A "regulatory element" is a nucleotide sequence that modulates the activity of a core promoter. For example, a regulatory element may contain a nucleotide sequence that binds with cellular factors enabling transcription exclusively or preferentially in particular cells, tissues, or organelles. These types of regulatory elements are normally associated with genes that are expressed in a "cell-specific", "tissue-specific", or "organelle-specific" manner.

[0056] An "enhancer" is a type of regulatory element that can increase the efficiency of transcription, regardless of the distance or orientation of the enhancer relative to the start site of transcription.

[0057] "Heterologous DNA" refers to a DNA molecule, or a population of DNA molecules, that does not exist naturally within a given host cell. DNA molecules heterologous to a particular host cell may contain DNA derived from the host cell species (*i.e.,* endogenous DNA) so long as that host DNA is combined with non-host DNA (*i.e.,* exogenous DNA). For example, a DNA molecule containing a non-host DNA segment encoding a polypeptide operably linked to a host DNA segment comprising a transcription promoter is considered to be a heterologous DNA molecule. Conversely, a heterologous DNA molecule can comprise an endogenous gene operably linked with an exogenous promoter. As another illustration, a DNA molecule comprising a gene derived from a wild-type cell is considered to be heterologous DNA if that DNA molecule is introduced into a mutant cell that lacks the wild-type gene.

[0058] An "expression vector" is a nucleic acid molecule encoding a gene that is expressed in a host cell. Typically, an expression vector comprises a transcription promoter, a gene, and a transcription terminator. Gene expression is usually placed under the control of a promoter, and such a gene is said to be "operably linked to" the promoter. Similarly, a regulatory element and a core promoter are operably linked if the regulatory element modulates the activity of the core promoter.

[0059] A "recombinant host" is a cell that contains a heterologous nucleic acid molecule, such as a cloning vector or expression vector. In the present context, an example of a recombinant host is a cell that produces an antagonist of the present invention from an expression vector. In contrast, such an antagonist can be produced by a cell that is a "natural source" of said antagonist, and that lacks an expression vector.

[0060] The terms "amino-terminal" and "carboxyl-terminal" are used herein to denote positions within polypeptides. Where the context allows, these terms are used with reference to a particular sequence or portion of a polypeptide to denote proximity or relative position. For example, a certain sequence positioned carboxyl-terminal to a reference sequence within a polypeptide is located proximal to the carboxyl terminus of the reference sequence, but is not necessarily at the carboxyl terminus of the complete polypeptide.

[0061] A "fusion protein" is a hybrid protein expressed by a nucleic acid molecule comprising nucleotide sequences of at least two genes. For example, a fusion protein can comprise at least part of a IL-17RA polypeptide fused with a polypeptide that binds an affinity matrix. Such a fusion protein provides a means to isolate large quantities of IL-17A using affinity chromatography.

[0062] The term "receptor" denotes a cell-associated protein that binds to a bioactive molecule termed a "ligand." This interaction mediates the effect of the ligand on the cell. Receptors can be membrane bound, cytosolic or nuclear; monomeric (*e.g.,* thyroid stimulating hormone receptor, beta-adrenergic receptor) or multimeric (*e.g.,* PDGF receptor, growth hormone receptor, IL-3 receptor, GM-CSF receptor, G-CSF receptor, erythropoietin receptor and IL-6 receptor). Membrane-bound receptors are characterized by a multi-domain structure comprising an extracellular ligand-binding domain and an intracellular effector domain that is typically involved in signal transduction. In certain membrane-bound receptors, the extracellular ligand-binding domain and the intracellular effector domain are located in separate polypeptides that comprise the complete functional receptor.

[0063] In general, the binding of ligand to receptor results in a conformational change in the receptor that causes an interaction between the effector domain and other molecule(s) in the cell, which in turn leads to an alteration in the metabolism of the cell. Metabolic events that are often linked to receptor-ligand interactions include gene

transcription, phosphorylation, dephosphorylation, increases in cyclic AMP production, mobilization of cellular calcium, mobilization of membrane lipids, cell adhesion, hydrolysis of inositol lipids and hydrolysis of phospholipids.

[0064] The term "expression" refers to the biosynthesis of a gene product. For example, in the case of a structural gene, expression involves transcription of the structural gene into mRNA and the translation of mRNA into one or more polypeptides.

[0065] The term "complement/anti-complement pair" denotes non-identical moieties that form a non-covalently associated, stable pair under appropriate conditions. For instance, biotin and avidin (or streptavidin) are prototypical members of a complement/anti-complement pair. Other exemplary complement/anti-complement pairs include receptor/ligand pairs, antibody/antigen (or hapten or epitope) pairs, sense/antisense polynucleotide pairs, and the like. Where subsequent dissociation of the complement/anti-complement pair is desirable, the complement/anti-complement pair preferably has a binding affinity of less than 10^9 M^{-1}.

[0066] As used herein, a "therapeutic agent" is a molecule or atom which is conjugated to an antibody moiety to produce a conjugate which is useful for therapy. Examples of therapeutic agents include drugs, toxins, immunomodulators, chelators, boron compounds, photoactive agents or dyes, and radioisotopes.

[0067] A "detectable label" is a molecule or atom which can be conjugated to an antibody moiety to produce a molecule useful for diagnosis. Examples of detectable labels include chelators, photoactive agents, radioisotopes, fluorescent agents, paramagnetic ions, or other marker moieties.

[0068] The term "affinity tag" is used herein to denote a polypeptide segment that can be attached to a second polypeptide to provide for purification or detection of the second polypeptide or provide sites for attachment of the second polypeptide to a substrate. In principal, any peptide or protein for which an antibody or other specific binding agent is available can be used as an affinity tag. Affinity tags include a poly-histidine tract, protein A (Nilsson et al., *EMBO J.,* 4:1075 (1985); Nilsson et al., *Methods Enzymol.,* 198:3 (1991)), glutathione S transferase (Smith et al., *Gene,* 67:31 (1988)), Glu-Glu affinity tag (Grussenmeyer et al., *Proc. Natl. Acad. Sci. USA,* 82:7952 (1985)), substance P, FLAG® peptide (Hopp et al., *Biotechnology,* 6:1204 (1988)), streptavidin binding peptide, or other antigenic epitope or binding domain. See, in general, Ford et

al., *Protein Expression and Purification*, 2:95 (1991). DNA molecules encoding affinity tags are available from commercial suppliers (*e.g.,* Pharmacia Biotech, Piscataway, NJ).

[0069] An "IL-17A binding entity" is a binding entity, such as an antibody, that specifically binds to IL-17A in its homodimeric form (IL-17A/IL-17A) and in its heterodimeric form (IL-17A/IL-17F).

[0070] An "IL-17F binding entity" is a binding entity, such as an antibody, that specifically binds to IL-17F in its homodimeric form (IL-17F/IL-17F) and in its heterodimeric form (IL-17A/IL-17F).

[0071] An "IL-17A/F binding entity" is a binding entity, such as an antibody, that specifically binds to IL-17A and IL-17F by recognizing and binding to the same or similar epitope, *e.g.*, continuous or discontinuous epitope, shared by IL-17A and IL-17F. The IL-17A/F binding entity binds to the IL-17A homodimer, IL-17F homodimer and IL-17A/IL-17F heterodimer.

[0072] One problem is that IL-17A, IL-17F and IL-23p19 are overexpressed in and implicated in the cause and/or sustainability of several inflammatory and/or autoimmune disorders. One solution several embodiments of the present invention provide is to inhibit or reduce the ability of these cytokines to cell-signal by administering a bispecific antibody which binds to each cytokine and inhibits or reduces each cytokine, e.g., homodimeric or heterodimeric form, from signaling through their cognate receptor.

[0073] Another problem is that in creating a bispecific IL-17A/F and IL-23p19 bispecific antibody, e.g, biAb3, difficulties were encountered to generate a bispecific antibody which had high affinity to IL-17A and was an effective neutralizer, e.g., IC50, of IL-17A. The mouse parent antibody (e.g, chimeric 339.15, 339.15.3.5, 339.15.5.3 or 339.15.3.6) as shown in Table 1 had an IL-17A/F IC50 of 0.30nM and an IL-17F IC50 of 0.26nM, but only had an IL-17A IC50 of 11nM. The antibodies ability to inhibit or neutralize IL-17A from signaling needed to be enhanced. As shown in Table 3, mouse parent chimeric 339.15 and humanized parent 339.134 had a similar binding affinity towards IL-17A. Furthermore, as shown in Table 8, humanized parent 339.134 ability to inhibit IL-17A (IC50 of 1.3nM) was still significantly reduced as compared to its ability to inhibit IL-17A/F (IC50 of 0.27nM) and IL-17F (IC50 of 0.24nM). This problem was surprisingly overcome by utilizing the light chain of the IL-23p19 antibody of biAb3 (SEQ ID NO:17). When the IL-23p19 light chain was paired with the

humanized heavy chain of 339.134, the resulting monoclonal antibody significantly increased its ability to inhibit IL-17A from signaling (see Table 9) and significantly increased its affinity for IL-17A (see Table 10). The critical residue in the now shared IL-23p19 / IL-17A/F light chain of, for example, biAb3, that may have provided this enhanced affinity and neutralization ability may be Y108 or Tyr108 of SEQ ID NO:2 as evidence by the X-ray crystallography and alanine mutant studies of Example 9.

[0074] In one embodiment, the present invention provides bispecific antibodies, antibodies and antigen-binding fragments thereof. The bispecific antibodies of the invention comprise an IL-17A binding entity that binds to IL-17A and an IL-23 binding entity that binds to IL-23 via p19. In another aspect, the bispecific antibodies of the invention comprise an IL-17F binding entity that binds to IL-17F and a IL-23 binding entity that binds to IL-23 via p19. In another aspect, the bispecific antibodies of the invention comprise an IL-17A/F binding entity that binds to IL-17A and IL-17F and a IL-23 binding entity that binds to IL-23 via p19. The binding entity that binds to IL-23 via p19 is referred to hereinafter as a binding entity that binds to IL-23 or an "IL-23 binding entity". The polynucleotide sequence of the human IL-17A is shown in SEQ ID NO:1 and the corresponding polypeptide sequence is shown in SEQ ID NO:2. The signal sequence of the IL-17A polypeptide is amino acid residues 1-23 of SEQ ID NO:2. Thus, amino acid residues 24-155 of SEQ ID NO:2 constitute the mature IL-17A polypeptide. Antibodies (and antigen-binding fragments thereof) and bispecific antibodies disclosed herein that bind to IL-17A bind to the mature IL-17A polypeptide (amino acid residues 24-155 of SEQ ID NO:2). The polynucleotide sequence of the human IL-17F is shown in SEQ ID NO:3 and the corresponding polypeptide sequence is shown in SEQ ID NO:4. The signal sequence of the IL-17F polypeptide is amino acid residues 1-30 of SEQ ID NO:4. Thus, amino acid residues 31-163 of SEQ ID NO:4 constitute the mature IL-17F polypeptide. Antibodies (and antigen-binding fragments thereof) and bispecific antibodies disclosed herein that bind to IL-17F bind to the mature IL-17F polypeptide (amino acid residues 31-163 of SEQ ID NO:4). The polynucleotide sequence of the human p19 subunit of IL-23 is shown in SEQ ID NO:5 and the corresponding polypeptide sequence is shown in SEQ ID NO:6. The signal sequence of the IL-23p19 polypeptide is amino acid residues 1-19 of SEQ ID NO:6. Thus, amino acid residues 20-189 of SEQ ID NO:6 constitute the mature IL-23p19 polypeptide. Antibodies (and

antigen-binding fragments thereof) and bispecific antibodies disclosed herein that bind to IL-23p19 bind to the mature IL-23p19 polypeptide (amino acid residues 20-189 of SEQ ID NO:6).

[0075] In one aspect of the invention, the IL-17A/F binding entity comprises an antibody, *i.e.*, two pairs of immunoglobulin chains, each pair having one light and one heavy chain, and the IL-23 binding entity comprises two Fab fragments each comprising a light chain and the C_{H1} and variable regions of a heavy chain, and the Fab fragments of the IL-23 binding entity are linked to the C-termini of the heavy chains (Fc) of the IL-17A/F binding entity. This bispecific antibody format is referred to herein as biAbFabL (see Fig. 2). In another embodiment, each of the light chain and the C_{H1} and variable regions of the heavy chain comprising the Fab fragments of the IL-23 binding entity are linked to the N-termini of the light chains and heavy chains, respectively, of the IL-17A/F binding entity. This bispecific antibody format is referred to herein as taFab (see Fig. 3).

[0076] In another aspect of the invention, the IL-23 binding entity comprises an antibody, *i.e.*, two pairs of immunoglobulin chains, each pair having one light and one heavy chain, and the IL-17A/F binding entity comprises two Fab fragments each comprising a light chain and the C_{H1} and variable regions of a heavy chain, and the Fab fragments of the IL-17A/F binding entity are linked to the C-termini of the heavy chains (Fc) of the IL-23 binding entity. This bispecific antibody format is referred to herein as biAbFabL (See Fig. 2). In another embodiment, each of the light chain and the C_{H1} and variable regions of the heavy chain comprising the Fab fragments of the IL-17A/F binding entity are linked to the N-termini of the light chain and heavy chain, respectively, of the IL-23 binding entity. This bispecific antibody format is referred to herein as taFab (see Fig. 3).

[0077] In another aspect of the invention, the IL-23 binding entity comprises a light chain and an IL-23 heavy chain and the IL-17A/F binding entity comprises a light chain and an IL-17A/F heavy chain. This bispecific antibody resembles a traditional antibody except that it comprises two different heavy chains that associate through an electrostatic complementarity association in the C_{H3} regions. It utilizes a common light chain. This bispecific antibody format is referred to herein as Heterodimeric Fc (see Fig. 4).

[0078] In another embodiment, the present invention provides bispecific antibodies comprising a first binding entity comprising an antibody, *i.e.*, two pairs of immunoglobulin chains, each pair having one light chain and one heavy chain, and a second binding entity comprising an Fv unit, *i.e.*, the variable domains from a heavy and a light chain, and in which the second binding entity comprising the Fv unit is positioned between the Fab region and the hinge of the first binding entity as shown in Fig. 5. The Fv unit is linked to the Fab region of the first binding entity by linker molecules. More specifically, the Fv unit comprises a variable light domain which is linked to the light chain constant region of the Fab fragment, and a variable heavy domain which is linked to the C_{H1} region of the Fab fragment. This bispecific antibody format is referred to herein as VCVFc. The first binding entity and second binding entity of a VCVFc do not have to share a common light chain, while the first binding entity and second binding entity of a biAbFabL do have to share a common light chain. In one aspect of this embodiment of the invention, the first binding entity specifically binds a lymphocyte antigen, cytokine, cytokine receptor, growth factor, growth factor receptor, interleukin (*e.g.*, IL-17A, IL-17F, IL-17A/F and IL-23) or interleukin receptor and the second binding entity specifically binds a lymphocyte antigen, cytokine, cytokine receptor, growth factor, growth factor receptor, interleukin (*e.g.*, IL-17A, IL-17F, IL-17A/F and IL-23) or interleukin receptor. In another aspect of this embodiment of the invention, the first binding entity is an IL-17A/F binding entity and the second binding entity is an IL-23 binding entity. In another aspect of this embodiment of the invention, the first binding entity is an IL-23 binding entity and the second binding entity is an IL-17A/F binding entity.

[0079] In another embodiment, the present invention provides bispecific antibodies comprising a first binding entity comprising an antibody, *i.e.*, two pairs of immunoglobulin chains, each pair having one light chain and one heavy chain, and a second binding entity comprising a single domain antibody. This bispecific antibody format is referred to herein as VCDFc. An illustration of a VCDFc bispecific antibody is shown in Fig. 6. The second binding entity comprising the single domain antibody is positioned between the Fab region, more specifically the C_{H1} region of the Fab fragment, and the hinge of the first binding entity. The single domain antibody is linked to the C_{H1} region of the Fab of the first binding entity by linker molecules (for example, but not

limited to, 10mer G_4S, which is represented by the equation $(G_4S)_2$, or SSASTKGPS (SEQ ID NO:86)). In one aspect of this embodiment of the invention, the first binding entity specifically binds a lymphocyte antigen, cytokine, cytokine receptor, growth factor, growth factor receptor, interleukin (*e.g.*, IL-17A, IL-17F, IL-17A/F and IL-23) or interleukin receptor and the second binding entity specifically binds a lymphocyte antigen, cytokine, cytokine receptor, growth factor, growth factor receptor, interleukin (*e.g.*, IL-17A, IL-17F, IL-17A/F and IL-23) or interleukin receptor. In one aspect of this embodiment of the invention, the first binding entity is an IL-23 binding entity and the second binding entity is an IL-17A/F binding entity. In another aspect of this embodiment of the invention, the first binding entity is an IL-17A/F binding entity and the second binding entity is an IL-23 binding entity.

[0080] The amino acid sequences of the binding entities are preferably based upon the sequences of human and/or humanized monoclonal antibodies against a lymphocyte antigen, cytokine, cytokine receptor, growth factor, growth factor receptor, interleukin (*e.g.*, IL-17A, IL-17F, IL-17A/F and IL-23) or interleukin receptor.

[0081] In one embodiment of the foregoing aspects of the invention, the light chains of the IL-17A/F binding entity and the IL-23 binding entity of the bispecific antibody each comprise a variable domain comprising a CDR1 having the amino acid sequence of SEQ ID NO:22, a CDR2 having the amino acid sequence of SEQ ID NO:23, and a CDR3 having the sequence of SEQ ID NO:24. In another embodiment, the light chains of the IL-17A/F binding entity and the IL-23 binding entity each comprise a variable domain comprising the amino acid sequence of SEQ ID NO:9. In another embodiment, the light chains of the IL-17A/F binding entity and the IL-23 binding entity each comprise a constant domain comprising the amino acid sequence of SEQ ID NO:10. In another embodiment, the light chains of the IL-17A/F binding entity and the IL-23 binding entity each comprise a variable domain comprising the amino acid sequence of SEQ ID NO:9 and a constant domain comprising the amino acid sequence of SEQ ID NO:10.

[0082] In another embodiment of the foregoing aspects of the invention, the heavy chain of the IL-17A/F binding entity of the bispecific antibody comprises a variable domain comprising a CDR1 having the amino acid sequence of SEQ ID NO:25, a CDR2 having the amino acid sequence of SEQ ID NO:26, and a CDR3 having the

amino acid sequence of SEQ ID NO:27. In another embodiment, the heavy chain of the IL-17A/F binding entity comprises a variable domain comprising the amino acid sequence of SEQ ID NO:13. In another embodiment, when the IL-17A/F binding entity comprises an antibody, the heavy chain constant domain comprises the amino acid sequence of SEQ ID NO:8, SEQ ID NO:11, SEQ ID NO:127 or SEQ ID NO:128. In another embodiment, when the IL-17A/F binding entity comprises a Fab fragment, the C_{H1} region of the heavy chain comprises the amino acid sequence of SEQ ID NO:14 or SEQ ID NO:15.

[0083] In another embodiment of the foregoing aspects of the invention, the IL-17A/F binding entity of the bispecific antibody comprises a heavy chain variable domain having at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% sequence identity with the amino acid sequence of SEQ ID NO:13. Optionally, all of the substitutions, additions or deletions are within the framework region of the heavy chain variable domain. Optionally, the IL-17A/F binding entity of the bispecific antibody comprises a heavy chain variable domain having at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% sequence identity with the amino acid sequence of SEQ ID NO:13, wherein the variable domain comprises a CDR1 having the amino acid sequence of SEQ ID NO:25, a CDR2 having the amino acid sequence of SEQ ID NO:26, and a CDR3 having the amino acid sequence of SEQ ID NO:27. Optionally, the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO:13. Optionally, the three IL-17A/F heavy chain variable domain CDRs include a CDR1 region comprising an amino acid sequence having at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% sequence identity with the amino acid sequence of SEQ ID NO:25; a CDR2 region comprising an amino acid sequence having at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% sequence identity with the amino acid sequence of SEQ ID NO:26; and a CDR3 region comprising an amino acid sequence having at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% sequence identity with the amino acid sequence of SEQ ID NO:27. Optionally, the IL-17A/F heavy chain variable domain CDR1 has the amino

acid sequence of SEQ ID NO:25; the heavy chain variable domain CDR2 has the amino acid sequence of SEQ ID NO:26; and the heavy chain variable domain CDR3 has the amino acid sequence of SEQ ID NO:27. The IL-17A/F and/or IL-23p19 binding entity comprises a light chain variable domain having at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% sequence identity with the amino acid sequence of SEQ ID NO:9. Optionally, all of the substitutions, additions or deletions are within the framework region of the light chain variable domain. Optionally, the IL-17A/F and/or IL-23p19 binding entity of the bispecific antibody comprises a light chain variable domain having at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% sequence identity with the amino acid sequence of SEQ ID NO:9, wherein the variable domain comprises a CDR1 having the amino acid sequence of SEQ ID NO:22, a CDR2 having the amino acid sequence of SEQ ID NO:23, and a CDR3 having the amino acid sequence of SEQ ID NO:24. Optionally, the light chain variable domain comprises the amino acid sequence of SEQ ID NO:9. Optionally, the three IL-17A/F and/or IL-23p19 light chain variable domain CDRs include a CDR1 region comprising an amino acid sequence having at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% sequence identity with the amino acid sequence of SEQ ID NO:22; a CDR2 region comprising an amino acid sequence having at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% sequence identity with the amino acid sequence of SEQ ID NO:23; and a CDR3 region comprising an amino acid sequence having at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% sequence identity with the amino acid sequence of SEQ ID NO:24. Optionally, the IL-17A/F and/or IL-23p19 light chain variable domain CDR1 has the amino acid sequence of SEQ ID NO:22; the IL-17A/F and/or IL-23p19 light chain variable domain CDR2 has the amino acid sequence of SEQ ID NO:23; and the IL-17A/F and/or IL-23p19 light chain variable domain CDR3 has the amino acid sequence of SEQ ID NO:24. The IL-23p19 binding entity comprises a heavy chain variable domain having at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% sequence identity with the amino acid sequence of SEQ

ID NO:7. Optionally, all of the substitutions, additions or deletions are within the framework region of the IL-23p19 heavy chain variable domain. Optionally, the IL-23p19 binding entity of the bispecific antibody comprises a heavy chain variable domain having at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% sequence identity with the amino acid sequence of SEQ ID NO:7, wherein the variable domain comprises a CDR1 having the amino acid sequence of SEQ ID NO:19, a CDR2 having the amino acid sequence of SEQ ID NO:20, and a CDR3 having the amino acid sequence of SEQ ID NO:21. Optionally, the IL-23p19 heavy chain variable domain comprises the amino acid sequence of SEQ ID NO:7. Optionally, the three IL-23p19 heavy chain variable domain CDRs include a CDR1 region comprising an amino acid sequence having at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% sequence identity with the amino acid sequence of SEQ ID NO:19; a CDR2 region comprising an amino acid sequence having at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% sequence identity with the amino acid sequence of SEQ ID NO:20; and a CDR3 region comprising an amino acid sequence having at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% sequence identity with the amino acid sequence of SEQ ID NO:21. Optionally, the IL-23p19 heavy chain variable domain CDR1 has the amino acid sequence of SEQ ID NO:19; the heavy chain variable domain CDR2 has the amino acid sequence of SEQ ID NO:20; and the heavy chain variable domain CDR3 has the amino acid sequence of SEQ ID NO:21.

[0084] In another embodiment of the foregoing aspects of the invention, the heavy chain of the IL-23 binding entity of the bispecific antibody comprises a variable domain comprising a CDR1 having the amino acid sequence of SEQ ID NO:19, a CDR2 having the amino acid sequence of SEQ ID NO:20, and a CDR3 having the amino acid sequence of SEQ ID NO:21. In another embodiment, the heavy chain of the IL-23 binding entity comprises a variable domain comprising the amino acid sequence of SEQ ID NO:7. In another embodiment, when the IL-23 binding entity comprises an antibody, the heavy chain constant domain comprises the amino acid sequence of SEQ ID NO:8, SEQ ID NO:11, SEQ ID NO:127 or SEQ ID NO:128. In some embodiments, the C-

terminal lysine of SEQ ID NO:8 has been cleaved, and so the heavy chain constant domain comprises the amino acid sequence of residues 1-326 of SEQ ID NO:8. In another embodiment, when the IL-23 binding entity comprises a Fab fragment, the C_{H1} region of the heavy chain comprises the amino acid sequence of SEQ ID NO:14 or SEQ ID NO:15.

[0085] In another embodiment of the foregoing aspects of the invention, when the IL-23 binding entity or IL-17A/F binding entity of the bispecific antibody is an Fv unit, the variable domain of the light chain comprises a CDR1 having the amino acid sequence of SEQ ID NO:22, a CDR2 having the amino acid sequence of SEQ ID NO:23, and a CDR3 having the sequence of SEQ ID NO:24. In another embodiment, the light chains of the IL-17A/F binding entity and the IL-23 binding entity each comprise a variable domain comprising the amino acid sequence of SEQ ID NO:9.

[0086] In another embodiment of the foregoing aspects of the invention, when the IL-17A/F binding entity of the bispecific antibody is an Fv unit, the variable domain of the heavy chain comprises a CDR1 having the amino acid sequence of SEQ ID NO:25, a CDR2 having the amino acid sequence of SEQ ID NO:26, and a CDR3 having the amino acid sequence of SEQ ID NO:27. In another embodiment, the heavy chain of the IL-17A/F binding entity comprises a variable domain comprising the amino acid sequence of SEQ ID NO:13.

[0087] In another embodiment of the foregoing aspects of the invention, when the IL-23 binding entity of the bispecific antibody is an Fv unit, the variable domain of the heavy chain comprises a CDR1 having the amino acid sequence of SEQ ID NO:19, a CDR2 having the amino acid sequence of SEQ ID NO:20, and a CDR3 having the amino acid sequence of SEQ ID NO:21. In another embodiment, the heavy chain of the IL-23 binding entity comprises a variable domain comprising the amino acid sequence of SEQ ID NO:7.

[0088] In another embodiment of the foregoing aspects of the invention, the Fab fragments of the IL-23 binding entity of the bispecific antibody are linked to the C-termini of the heavy chains (Fc) of the IL-17A/F binding entity, or the Fab fragments of the IL-17A/F binding entity are linked, for example, to the C-termini of the heavy chains (Fc) of the IL-23 binding entity by a linker molecule (see, for example, Fig. 2). In another embodiment, each of the light chain and the C_{H1} and variable regions of the

heavy chain comprising the Fab fragments of the IL-23 binding entity are linked to the N-termini of the light chain and heavy chain, respectively, of the IL-17A/F binding entity, or each of the light chain and the C_{H1} and variable regions of the heavy chain comprising the Fab fragments of the IL-17A/F binding entity are linked to the N-termini of the light chain and heavy chain, respectively, of the IL-23 binding entity by a linker molecule (see, for example, Fig. 3). In another embodiment of the VCVFc bispecific antibody, each of the light chain variable region and the heavy chain variable region of the Fv unit comprising the second binding entity are linked to each of the light chain constant region and the C_{H1} region, respectively, of the Fab fragment of the first binding entity by a linker molecule (see Fig. 5). Suitable linker molecules are known in the art and include, for example, short polypeptides. A suitable linker may include a short polypeptide, which contains glycine, which confers flexibility, and serine or threonine, which confer solubility. A suitable linker may comprise Gly_4Ser_1 units. For example, the linker may be $(Gly_4Ser_1)_x$, wherein x is 1, 2, or 3. Optionally, the linker polypeptide has the amino acid sequence of SEQ ID NO:12. In another embodiment of the VCVFc bispecific antibodies, the linker for the light chain has the amino acid sequence of SEQ ID NO:85 and the linker for the heavy chain has the amino acid sequence of SEQ ID NO:86.

[0089] In another embodiment of the foregoing aspects of the invention, the bispecific antibody comprises a pair of heavy chains each comprising the amino acid sequence of SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:74, or SEQ ID NO:84 and a pair of light chains each comprising the amino acid sequence of SEQ ID NO:17. In a preferred embodiment, the bispecific antibody comprises a pair of heavy chains comprising the amino acid sequence of SEQ ID NO:74 and a pair of light chains each comprising the amino acid sequence of SEQ ID NO:17.

[0090] In another embodiment of the foregoing aspects of the invention, an IL-17A/F antibody (or an antigen-binding fragment thereof) or the IL-17A/F binding entity of the bispecific antibody, such as a biAbFabL (see Fig. 2), a taFab (see Fig. 3), a heterodimeric Fc (see Fig. 4), a VCVFc (see Fig. 5) or a VCDFc (see Fig. 6) binds (a) an IL-17A homodimer with a binding affinity (K_{D1}) of at least 1×10^{-9} M, at least 5×10^{-9} M, at least 1×10^{-10} M, at least 5×10^{-10} M, at least 8×10^{-10} M or at least at least 1×10^{-11} M; (b) an IL-17F homodimer with a binding affinity (K_{D1}) of at least 1×10^{-9} M, at least 5×10^{-9} M, at least 1×10^{-10} M, at least 2×10^{-10} M, at least 3×10^{-10} M, at least 4×10^{-10} M,

at least 5 x 10^{-10} M or at least 1 x 10^{-11} M; and/or (c) an IL-17A/F heterodimer with a binding affinity (K_{D1}) of at least 1 x 10^{-8} M, at least 5 x 10^{-8} M, at least 1 x 10^{-9} M, at least 2 x 10^{-9} M, at least 3 x 10^{-9} M, at least 4 x 10^{-9} M, at least 5 x 10^{-9} M, at least 6 x 10^{-9} M, at least 7 x 10^{-9} M, at least 9 x 10^{-9} M, at least 1 x 10^{-10} M or at least 5 x 10^{-10} M, wherein the binding affinity is measured by surface plasmon resonance, such as Biacore.

[0091] In another embodiment of the foregoing aspects of the invention, an IL-23p19 antibody (or an antigen-binding fragment thereof) or the IL-23p19 binding entity of the bispecific antibody, such as a biAbFabL (see Fig. 2), a taFab (see Fig. 3), a heterodimeric Fc (see Fig. 4), a VCVFc (see Fig. 5) or a VCDFc (see Fig. 6) binds IL-23p19 with a binding affinity (K_{D1}) of at least 1 x 10^{-9} M, at least 5 x 10^{-9} M, at least 1 x 10^{-10} M, at least 2 x 10^{-10} M, at least 3 x 10^{-10} M, at least 4 x 10^{-10} M, at least 5 x 10^{-10}, at least 6 x 10^{-10}, at least 7 x 10^{-10}, at least 8 x 10^{-10} or at least 9 x 10^{-10}, at least 1 x 10^{-11}, wherein the binding affinity is measured by surface plasmon resonance, such as Biacore.

[0092] In another embodiment of the foregoing aspects of the invention, the IL-17A/F binding entity of the bispecific antibody, such as a biAbFabL (see Fig. 2), a taFab (see Fig. 3), a heterodimeric Fc (see Fig. 4), a VCVFc (see Fig. 5) or a VCDFc (see Fig. 6) binds (a) an IL-17A homodimer with a binding affinity (K_{D1}) of at least 1 x 10^{-9} M, at least 5 x 10^{-9} M, at least 1 x 10^{-10} M, at least 5 x 10^{-10} M, at least 8 x 10^{-10} M or at least at least 1 x 10^{-11} M; (b) an IL-17F homodimer with a binding affinity (K_{D1}) of at least 1 x 10^{-9} M, at least 5 x 10^{-9} M, at least 1 x 10^{-10} M, at least 2 x 10^{-10} M, at least 3 x 10^{-10} M, at least 4 x 10^{-10} M, at least 5 x 10^{-10} M or at least 1 x 10^{-11} M; and/or (c) an IL-17A/F heterodimer with a binding affinity (K_{D1}) of at least 1 x 10^{-8} M, at least 5 x 10^{-8} M, at least 1 x 10^{-9} M, at least 2 x 10^{-9} M, at least 3 x 10^{-9} M, at least 4 x 10^{-9} M, at least 5 x 10^{-9} M, at least 6 x 10^{-9} M, at least 7 x 10^{-9} M, at least 9 x 10^{-9} M, at least 1 x 10^{-10} M or at least 5 x 10^{-10} M; and the IL-23p19 binding entity of the bispecific antibody binds IL-23p19 with a binding affinity (K_{D1}) of at least 1 x 10^{-9} M, at least 5 x 10^{-9} M, at least 1 x 10^{-10} M, at least 2 x 10^{-10} M, at least 3 x 10^{-10} M, at least 4 x 10^{-10} M, at least 5 x 10^{-10}, at least 6 x 10^{-10}, at least 7 x 10^{-10}, at least 8 x 10^{-10} or at least 9 x 10^{-10}, at least 1 x 10^{-11}, wherein the binding affinity is measured by surface plasmon resonance, such as Biacore.

[0093] In another embodiment of the foregoing aspects of the invention, an IL-17A/F antibody (or an antigen-binding fragment thereof) or the IL-17A/F binding entity of the bispecific antibody neutralizes or inhibits (a) IL-17A induction of G-CSF in

primary human small airway epithelial cells (SAEC) with an IC_{50} of 0.5 pm or less; (b) IL-17F induction G-CSF in primary human small airway epithelial cells (SAEC) with an IC_{50} of 2.0 nM or less, 1.5 nM or less, 1.4 nM or less, 1.3 nM or less, 1.2 nM or less, 1.1 nM or less, or 1.0 nM or less; and/or (c) IL-17A/F induction G-CSF in primary human small airway epithelial cells (SAEC) with an IC_{50} of 1.3 nM or less, 1.2 nM or less, 1.1 nM or less, 1.0 nM or less, 0.9 nM or less, 0.8 nM or less, 0.7 nM or less, 0.6 nM or less, or 0.5 nM or less.

[0094] In another embodiment of the foregoing aspects of the invention, an IL-17A/F antibody (or an antigen-binding fragment thereof) or the IL-17A/F binding entity of the bispecific antibody neutralizes or inhibits (a) IL-17A induction of IL-6 in human primary fibroblast cells (HFFF) with an IC_{50} of 0.5 nM or less, 0.4 nM or less, 0.3 nM or less, 0.2 nM or less, 0.1 nM or less, 0.09 nM or less, 0.08 nM or less, 0.07 nM or less, 0.06 nM or less, 0.05 nM or less, 0.04 nM or less, 0.03 nM or less, 0.02 nM or less, or 0.01 nM or less; (b) IL-17F induction of IL-6 in human primary fibroblast cells (HFFF) with an IC_{50} of 30 nM or less, 28 nM or less, 26 nM or less, 25 nM or less, 22 nM or less, 20 nM or less, 19 nM or less, 18 nM or less, 17 nM or less, 16 nM or less, 15 nM or less, 14 nM or less, 13 nM or less, 12 nM or less, 11 nM or less, or 10 nM or less; and/or (c) IL-17A/F induction of IL-6 in human primary fibroblast cells (HFFF) with an IC_{50} of 30 nM or less, 28 nM or less, 26 nM or less, 22 nM or less, 20 nM or less, 18 nM or less, 17 nM or less, 16 nM or less, 15 nM or less, 14 nM or less, 13 nM or less, 12 nM or less, 11 nM or less, 10 nM or less, 9.5 nM or less, 9.4 nM or less, 9.3 nM or less, 9.2 nM or less, 9.1 nM or less, or 9.0 nM or less.

[0095] In another embodiment of the foregoing aspects of the invention, an IL-23p19 antibody (or an antigen-binding fragment thereof) or the IL-23p19 binding entity of the bispecific antibody neutralizes or inhibits (a) IL-23 induced IL-17A and IL-17F production in murine splenocytes with an IC_{50} of 0.5 nM or less, 0.4 nM or less, 0.3 nM or less, 0.2 nM or less, 0.1 nM or less, 0.09 nM or less, 0.08 nM or less, 0.07 nM or less, or 0.06 nM or less.

[0096] In another embodiment of the foregoing aspects of the invention, an IL-23p19 antibody (or an antigen-binding fragment thereof) or the IL-23p19 binding entity of the bispecific antibody neutralizes or inhibits IL-23 induced STAT3 phosphorylation in activated primary human T cells with an IC_{50} of 0.1 nM or less, 0.2

nM or less, 0.3 nM or less, 0.4 nM or less, 0.5 nM or less, 0.8 nM or less, 0.9 nM or less, 0.01 nM or less, 0.02 nM or less, 0.03 nM or less, 0.04 nM or less, or 0.05 nM or less.

[0097] In another embodiment of the foregoing aspects of the invention, the IL-17A/F binding entity of the bispecific antibody, such as a biAbFabL (see Fig. 2), a taFab (see Fig. 3), a heterodimeric Fc (see Fig. 4), a VCVFc (see Fig. 5) or a VCDFc (see Fig. 6) binds (a) an IL-17A homodimer with a binding affinity (K_{D1}) of at least 1 x 10^{-9} M, at least 5 x 10^{-9} M, at least 1 x 10^{-10} M, at least 5 x 10^{-10} M, at least 8 x 10^{-10} M or at least at least 1 x 10^{-11} M; (b) an IL-17F homodimer with a binding affinity (K_{D1}) of at least 1 x 10^{-9} M, at least 5 x 10^{-9} M, at least 1 x 10^{-10} M, at least 2 x 10^{-10} M, at least 3 x 10^{-10} M, at least 4 x 10^{-10} M, at least 5 x 10^{-10} M or at least 1 x 10^{-11} M; and/or (c) an IL-17A/F heterodimer with a binding affinity (K_{D1}) of at least 1 x 10^{-8} M, at least 5 x 10^{-8} M, at least 1 x 10^{-9} M, at least 2 x 10^{-9} M, at least 3 x 10^{-9} M, at least 4 x 10^{-9} M, at least 5 x 10^{-9} M, at least 6 x 10^{-9} M, at least 7 x 10^{-9} M, at least 9 x 10^{-9} M, at least 1 x 10^{-10} M or at least 5 x 10^{-10} M. Optionally, the IL-23p19 binding entity of the bispecific antibody binds IL-23p19 with a binding affinity (K_{D1}) of at least 1 x 10^{-9} M, at least 5 x 10^{-9} M, at least 1 x 10^{-10} M, at least 2 x 10^{-10} M, at least 3 x 10^{-10} M, at least 4 x 10^{-10} M, at least 5 x 10^{-10}, at least 6 x 10^{-10}, at least 7 x 10^{-10}, at least 8 x 10^{-10} or at least 9 x 10^{-10}, at least 1 x 10^{-11}, wherein the binding affinity is measured by surface plasmon resonance, such as Biacore. Optionally, the IL-17A/F binding entity of the bispecific antibody neutralizes or inhibits (a) IL-17A induction of G-CSF in primary human small airway epithelial cells (SAEC) with an IC_{50} of 0.5 pm or less; (b) IL-17F induction G-CSF in primary human small airway epithelial cells (SAEC) with an IC_{50} of 2.0 nM or less, 1.5 nM or less, 1.4 nM or less, 1.3 nM or less, 1.2 nM or less, 1.1 nM or less, or 1.0 nM or less; and/or (c) IL-17A/F induction G-CSF in primary human small airway epithelial cells (SAEC) with an IC_{50} of 1.3 nM or less, 1.2 nM or less, 1.1 nM or less, 1.0 nM or less, 0.9 nM or less, 0.8 nM or less, 0.7 nM or less, 0.6 nM or less, or 0.5 nM or less. Optionally, the IL-17A/F binding entity of the bispecific antibody neutralizes or inhibits (a) IL-17A induction of IL-6 in human primary fibroblast cells (HFFF) with an IC_{50} of 0.5 nM or less, 0.4 nM or less, 0.3 nM or less, 0.2 nM or less, 0.1 nM or less, 0.09 nM or less, 0.08 nM or less, 0.07 nM or less, 0.06 nM or less, 0.05 nM or less, 0.04 nM or less, 0.03 nM or less, 0.02 nM or less, or 0.01 nM or less; (b) IL-17F induction of IL-6 in human primary fibroblast cells (HFFF) with an IC_{50} of 30 nM or less, 28 nM or less, 26 nM or

less, 25 nM or less, 22 nM or less, 20 nM or less, 19 nM or less, 18 nM or less, 17 nM or less, 16 nM or less, 15 nM or less, 14 nM or less, 13 nM or less, 12 nM or less, 11 nM or less, or 10 nM or less; and/or (c) IL-17A/F induction of IL-6 in human primary fibroblast cells (HFFF) with an IC_{50} of 30 nM or less, 28 nM or less, 26 nM or less, 22 nM or less, 20 nM or less, 18 nM or less, 17 nM or less, 16 nM or less, 15 nM or less, 14 nM or less, 13 nM or less, 12 nM or less, 11 nM or less, 10 nM or less, 9.5 nM or less, 9.4 nM or less, 9.3 nM or less, 9.2 nM or less, 9.1 nM or less, or 9.0 nM or less. Optionally, the IL-23p19 binding entity of the bispecific antibody neutralizes or inhibits IL-23 induced STAT3 phosphorylation in activated primary human T cells with an IC_{50} of 0.1 nM or less, 0.2 nM or less, 0.3 nM or less, 0.4 nM or less, 0.5 nM or less, 0.8 nM or less, 0.9 nM or less, 0.01 nM or less, 0.02 nM or less, 0.03 nM or less, 0.04 nM or less, or 0.05 nM or less.

[0098] In another embodiment of the foregoing aspects of the invention, the bispecific antibody comprises a pair of heavy chains comprising the amino acid sequence of SEQ ID NO:28 and a pair of light chains comprising the amino acid sequence of SEQ ID NO:17 is referred to herein as "biAb1", “bAb1” or “23/17bAb1”. A bispecific antibody comprising a pair of heavy chains each comprising the amino acid sequence of SEQ ID NO:18 and a pair of light chains each comprising the amino acid sequence of SEQ ID NO:17 is referred to herein as "biAb2", “bAb2” or “23/17bAb2”. A bispecific antibody comprising a pair of heavy chains each comprising the amino acid sequence of SEQ ID NO:74 and a pair of light chains each comprising the amino acid sequence of SEQ ID NO:17 is referred to herein as "biAb3", “bAb3” or “23/17bAb3”. A bispecific antibody comprising a pair of heavy chains comprising the amino acid sequence of SEQ ID NO:29 and a pair of light chains each comprising the amino acid sequence of SEQ ID NO:17 is referred to herein as "biAb4", “bAb4” or “23/17bAb4”.

[0099] In another embodiment of the foregoing aspects of the invention, the bispecific antibody comprises a pair of heavy chains each comprising the amino acid sequence of SEQ ID NO:77 and a pair of light chains each comprising the amino acid sequence of SEQ ID NO:79 and is referred to herein as "taFab1".

[00100] In another embodiment of the foregoing aspects of the invention, the bispecific antibody comprises an IL-23 heavy chain comprising the amino acid sequence of SEQ ID NO:63, an IL-17A/F heavy chain comprising the amino acid sequence of SEQ

ID NO:65, and a pair of light chains each comprising the sequence of SEQ ID NO:17, and is referred to herein as "hetero1". In another embodiment, the bispecific antibody comprises an IL-23 heavy chain comprising the amino acid sequence of SEQ ID NO:61, an IL-17A/F heavy chain comprising the amino acid sequence of SEQ ID NO:81, and a pair of light chains each comprising the sequence of SEQ ID NO:17, and is referred to herein as "hetero2".

[00101] In another embodiment of the foregoing aspects of the invention, the bispecific antibody in the VCVFc format, see Fig. 5, has a pair of heavy chains each comprising the amino acid sequence of SEQ ID NO:88 and a pair of light chains each comprising the amino acid sequence of SEQ ID NO:90, or a pair of heavy chains each comprising the amino acid sequence of SEQ ID NO:92 and a pair of light chains each comprising the amino acid sequence of SEQ ID NO:94, or a pair of heavy chains each comprising the amino acid sequence of SEQ ID NO:96 and a pair of light chains each comprising the amino acid sequence of SEQ ID NO:90, or a pair of heavy chains each comprising the amino acid sequence of SEQ ID NO:98 and a pair of light chains each comprising the amino acid sequence of SEQ ID NO:94, or a pair of heavy chains each comprising the amino acid sequence of SEQ ID NO:100 and a pair of light chains each comprising the amino acid sequence of SEQ ID NO:102, or a pair of heavy chains each comprising the amino acid sequence of SEQ ID NO:104 and a pair of light chains each comprising the amino acid sequence of SEQ ID NO:106, or a pair of heavy chains each comprising the amino acid sequence of SEQ ID NO:112 and a pair of light chains each comprising the amino acid sequence of SEQ ID NO:114, or a pair of heavy chains each comprising the amino acid sequence of SEQ ID NO:116 and a pair of light chains each comprising the amino acid sequence of SEQ ID NO:118.

[00102] In another embodiment of the foregoing aspects of the invention, an isolated monoclonal antibody or antigen-binding fragment thereof that specifically binds to IL-17A (SEQ ID NO:2) and IL-17F (SEQ ID NO:4) comprising a heavy chain variable domain and a light chain variable domain, wherein the heavy chain variable domain comprises the amino acid residues of SEQ ID NO:13 and a light chain variable domain comprises the amino acid residues of SEQ ID NO:9. Optionally, the monoclonal antibody comprises a human constant region, *e.g.*, IgG1, IgG2, IgG3 or IgG4. The IgG4 human constant region may have a Serine to Proline mutation at position 241 according

to Kabat. Optionally, the heavy chain comprises the amino acid residues of SEQ ID NOs:16, 18, 28, 29 or 74. Optionally, the light chain comprises the amino acid residues of SEQ ID NO:17. Optionally, the heavy chain comprises the amino acid residues of SEQ ID NOs:16, 18, 28, 29 or 74, and the light chain comprises the amino acid residues of SEQ ID NO:17. Optionally, a bispecific antibody comprises the monoclonal antibody.

[00103] Heavy chain and light chain constant regions include, IgG1.1 (SEQ ID NO:11, which may be encoded by SEQ ID NO:82), IgG1.1f without a C-terminal Lysine (SEQ ID NO:127), IgG1.1f with a C-terminal Lysine (SEQ ID NO:128), human kappa constant region (SEQ ID NO:10, which may be encoded by SEQ ID NO:83), or IgG4.1 (SEQ ID NO:8). The IgG4 heavy chain constant domain may include a variant of wild-type IgG4 that has a mutation in the hinge region, S228P (EU index numbering system) or S241P (Kabat numbering system). Changing the serine at 241 (Kabat) to proline (found at that position in IgG1 and IgG2) in a mouse/human chimeric heavy chain leads to the production of a homogeneous antibody and abolishes the heterogeneity. Further, the variant IgG4 has significantly extended serum half-life and shows an improved tissue distribution compared to the original chimeric IgG4. Angal et al., Molecular Immunology, 30(1):105-108 (1993); Schuurman et al., Molecular Immunology, 38:1-8 (2001); Lewis et al., Molecular Immunology, 46:3488-3494 (2009).

[00104] In another embodiment of the foregoing aspects of the invention, an isolated monoclonal antibody or antigen-binding fragment thereof that specifically binds to IL-23p19 (SEQ ID NO:6) comprising a heavy chain variable domain and a light chain variable domain, wherein the heavy chain variable domain comprises the amino acid residues of SEQ ID NO:7, and wherein the light chain variable domain comprises the amino acid residues of SEQ ID NO:9. Optionally, the monoclonal antibody comprises a human constant region, *e.g.*, IgG1, IgG2, IgG3 or IgG4. Optionally, the IgG4 human constant region has a Serine to Proline mutation at position 241 according to Kabat. Optionally, the heavy chain comprises the amino acid residues of SEQ ID NOs:16, 18, 28, 29 or 74. Optionally, the light chain comprises the amino acid residues of SEQ ID NO:17. Optionally, the heavy chain comprises the amino acid residues of SEQ ID NOs:16, 18, 28, 29 or 74, and the light chain comprises the amino acid residues of SEQ ID NO:17. Optionally, a bispecific antibody comprises the monoclonal antibody.

[00105] In another embodiment of the foregoing aspects of the invention, the antibody, bispecific antibody, or antigen-binding fragment thereof, specifically binds IL-23p19, wherein the antibody or antigen-binding fragment binds a discontinuous epitope on IL-23p19 comprising a first epitope and a second epitope, wherein the first epitope consists of at least one amino acid of amino acid residues 33-59 of SEQ ID NO:6 and the second epitope consists of at least one amino acid of amino acid residues 89-125 of SEQ ID NO:6. Optionally, the antibody, bispecific antibody, or antigen-binding fragment thereof binds to at least amino acid residue 54 of SEQ ID NO:6 of the first epitope. Optionally, the antibody, bispecific antibody, or antigen-binding fragment thereof binds to at least amino acid residue 55 of SEQ ID NO:6 of the first epitope. Optionally, the antibody, bispecific antibody, or antigen-binding fragment thereof binds to at least amino acid residues 54 and 55 of SEQ ID NO:6 of the first epitope. Optionally, the antibody, bispecific antibody, or antigen-binding fragment thereof binds to at least amino acid residue 116 of SEQ ID NO:6 of the second epitope. Optionally, the antibody, bispecific antibody, or antigen-binding fragment thereof binds to at least amino acid residues 54 and 55 of SEQ ID NO:6 of the first epitope, and to least amino acid residue 116 of SEQ ID NO:6 of the second epitope.

[00106] In another embodiment of the foregoing aspects of the invention, the antibody, bispecific antibody, or antigen-binding fragment thereof specifically binds IL-23p19, wherein the antibody or antigen-binding fragment binds a discontinuous epitope on IL-23p19 comprising a first epitope and a second epitope, wherein the antibody or antigen-binding fragment binds to at least amino acid residues 54 and 55 of SEQ ID NO:6 of the first epitope, and to least amino acid residue 116 of SEQ ID NO:6 of the second epitope.

[00107] In another embodiment of the foregoing aspects of the invention, an IL-17A/F binding entity specifically binds IL-17A (IL-17A/IL-17A homodimer and IL-17A/IL-17F heterodimer) at an epitope comprising at least amino acid residue 108 (Tyr) of SEQ ID NO:2, wherein the IL-17A/F binding entity is a monoclonal antibody or antigen-binding fragment thereof. Optionally, the epitope on IL-17A is determined by alanine mutagenesis and/or X-ray crystallography. The epitope on which the IL-17A/F binding entity binds IL-17A may be a continuous or a discontinuous epitope.

[00108] In another embodiment of the foregoing aspects of the invention, the IL-17A/F cross-reactive monoclonal antibody or an tigen-binding fragment thereof binds IL-17A at an epitope comprising at least amino acid residue 108 (Tyr) of SEQ ID NO:2. Optionally, the epitope on IL-17A is determined by alanine mutagenesis and/or X-ray crystallography. The epitope on which the IL-17A/F cross-reactive monoclonal antibody or an tigen-binding fragment thereof binds IL-17A may be a continuous or a discontinuous epitope.

[00109] The bispecific antibodies of the invention may be used alone or as immunoconjugates with a cytotoxic agent. In some embodiments, the agent is a chemotherapeutic agent. In some embodiments, the agent is a radioisotope, including, but not limited to Lead-212, Bismuth-212, Astatine-211, Iodine-131, Scandium-47, Rhenium-186, Rhenium-188, Yttrium-90, Iodine-123, Iodine-125, Bromine-77, Indium-111, and fissionable nuclides such as Boron-10 or an Actinide. In other embodiments, the agent is a toxin or cytotoxic drug, including but not limited to ricin, abrin, modified *Pseudomonas* enterotoxin A, *Pseudomonas* exotoxin, calicheamicin, adriamycin, 5-fluorouracil, diphtheria toxin, and the like. Methods of conjugation of antibodies to such agents are known in the literature, and include direct and indirect conjugation.

[00110] Suitable detectable molecules may be directly or indirectly attached to the antibodies of the present invention. Suitable detectable molecules include radionuclides, enzymes, substrates, cofactors, inhibitors, fluorescent markers, chemiluminescent markers, magnetic particles and the like. For indirect attachment of a detectable or cytotoxic molecule, the detectable or cytotoxic molecule can be conjugated with a member of a complementary/ anticomplementary pair, where the other member is bound to the binding polypeptide or antibody portion. For these purposes, biotin/streptavidin is an exemplary complementary/ anticomplementary pair.

[00111] The bispecific antibodies, antibodies and antigen-binding fragments of the invention also include derivatives that are modified, *e.g.*, by the covalent attachment of any type of molecule to the antibody such that covalent attachment does not prevent the antibody from binding to its epitope. Examples of suitable derivatives include, but are not limited to fucosylated antibodies, glycosylated antibodies, acetylated antibodies, pegylated antibodies, phosphorylated antibodies, and amidated antibodies. The antibodies and derivatives thereof of the invention may themselves by derivatized by

known protecting/blocking groups, proteolytic cleavage, linkage to a cellular ligand or other proteins, and the like. In some embodiments of the invention, at least one heavy chain of the antibody is fucosylated. In some embodiments, the fucosylation is N-linked. In some preferred embodiments, at least one heavy chain of the antibody comprises a fucosylated, N-linked oligosaccharide.

[00112] The bispecific antibodies, antibodies and antigen-binding fragments of the invention include variants having single or multiple amino acid substitutions, deletions, additions, or replacements that retain the biological properties (*e.g.*, block the binding of IL-17A or IL-17F and/or IL-23 to their respective receptors, inhibit the biological activity of IL-17A or IL-17F and IL-23) of the antibodies of the invention. The skilled person can produce variants having single or multiple amino acid substitutions, deletions, additions or replacements. These variants may include, inter alia: (a) variants in which one or more amino acid residues are substituted with conservative or nonconservative amino acids, (b) variants in which one or more amino acids are added to or deleted from the polypeptide, (c) variants in which one or more amino acids include a substituent group, and (d) variants in which the polypeptide is fused with another peptide or polypeptide such as a fusion partner, a protein tag or other chemical moiety, that may confer useful properties to the polypeptide, such as, for example, an epitope for an antibody, a polyhistidine sequence, a biotin moiety and the like. Antibodies of the invention may include variants in which amino acid residues from one species are substituted for the corresponding residue in another species, either at the conserved or nonconserved positions. In another embodiment, amino acid residues at nonconserved positions are substituted with conservative or nonconservative residues. The techniques for obtaining these variants, including genetic (suppressions, deletions, mutations, etc.), chemical, and enzymatic techniques, are known to the person having ordinary skill in the art.

[00113] The invention also includes isolated nucleic acids encoding the bispecific antibodies of the invention, which includes, for instance, the light chain, light chain variable region, light chain constant region, heavy chain, heavy chain variable region, heavy chain constant region, linkers, and any and all components and combinations thereof of the bispecific antibodies disclosed herein. Nucleic acids of the invention include nucleic acids having at least 80%, more preferably at least about 90%,

more preferably at least about 95%, and most preferably at least about 98% homology to nucleic acids of the invention. The terms "percent similarity", "percent identity" and "percent homology" when referring to a particular sequence are used as set forth in the University of Wisconsin GCG® software program. Nucleic acids of the invention also include complementary nucleic acids. In some instances, the sequences will be fully complementary (no mismatches) when aligned. In other instances, there may be up to about a 20% mismatch in the sequences. In some embodiments of the invention are provided nucleic acids encoding both a heavy chain and a light chain of an antibody of the invention.

[00114] Nucleic acids of the invention can be cloned into a vector, such as a plasmid, cosmid, bacmid, phage, artificial chromosome (BAC, YAC) or virus, into which another genetic sequence or element (either DNA or RNA) may be inserted so as to bring about the replication of the attached sequence or element. In some embodiments, the expression vector contains a constitutively active promoter segment (such as but not limited to CMV, SV40, Elongation Factor or LTR sequences) or an inducible promoter sequence such as the steroid inducible pIND vector (Invitrogen), where the expression of the nucleic acid can be regulated. Expression vectors of the invention may further comprise regulatory sequences, for example, an internal ribosomal entry site. The expression vector can be introduced into a cell by transfection, for example.

[00115] Thus in another embodiment, the present invention provides an expression vector comprising the following operably linked elements; a transcription promoter; a nucleic acid molecule encoding the heavy chain of a bispecific antibody of the invention; and a transcription terminator. In another embodiment, the present invention provides an expression vector comprising the following operably linked elements; a transcription promoter; a nucleic acid molecule encoding the light chain of a bispecific antibody of the invention; and a transcription terminator. Recombinant host cells comprising such vectors and expressing the heavy and light chains are also provided.

[00116] In another embodiment, the present invention provides an expression vector comprising the following operably linked elements; a transcription promoter; a first nucleic acid molecule encoding the heavy chain of a bispecific antibody, antibody or antigen-binding fragment of the invention; a second nucleic acid molecule encoding the

light chain of a bispecific antibody, antibody or antigen-binding fragment of the invention; and a transcription terminator. In another embodiment, the present invention provides an expression vector comprising the following operably linked elements; a first transcription promoter; a first nucleic acid molecule encoding the heavy chain of a bispecific antibody, antibody or antigen-binding fragment of the invention; a first transcription terminator; a second transcription promoter a second nucleic acid molecule encoding the light chain of a bispecific antibody, antibody or antigen-binding fragment of the invention; and a second transcription terminator. Recombinant host cells comprising such vectors and expressing the heavy and light chains are also provided.

[00117] Antibody-producing cells containing a nucleic acid encoding the heavy chain and a nucleic acid encoding the light chain of the bispecific antibodies, antibodies or antigen-binding fragments of the invention can be used to produce the bispecific antibodies, antibodies or antigen-binding fragments in accordance with techniques known in the art. The present invention, in one embodiment, provides a method of producing a bispecific antibody, antibody or antigen-binding fragment of the invention comprising culturing a recombinant host cell expressing the heavy and light chains and isolating the bispecific antibody, antibody or antigen-binding fragment produced by the cell.

[00118] The recombinant host cell may be a prokaryotic cell, for example a *E. coli* cell, or a eukaryotic cell, for example a mammalian cell or a yeast cell. Yeast cells include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, and *Pichia pastoris* cells. Mammalian cells include VERO, HeLa, Chinese hamster Ovary (CHO), W138, baby hamster kidney (BHK), COS-7, MDCK, human embryonic kidney line 293, normal dog kidney cell lines, normal cat kidney cell lines, monkey kidney cells, African green monkey kidney cells, COS cells, and non-tumorigenic mouse myoblast G8 cells, fibroblast cell lines, myeloma cell lines, mouse NIH/3T3 cells, LMTK31 cells, mouse sertoli cells, human cervical carcinoma cells, buffalo rat liver cells, human lung cells, human liver cells, mouse mammary tumor cells, TRI cells, MRC 5 cells, and FS4 cells. Antibody-producing cells of the invention also include any insect expression cell line known, such as for example, Spodoptera frugiperda cells. In a preferred embodiment, the cells are mammalian cells. In another preferred embodiment, the mammalian cells are CHO cells.

[00119] The antibody-producing cells preferably are substantially free of IL-17A, IL-17F and IL-23 binding competitors. In preferred embodiments, the antibody-producing cells comprise less than about 10%, preferably less than about 5%, more preferably less than about 1%, more preferably less than about 0.5%, more preferably less than about 0.1%, and most preferably 0% by weight IL-17A, IL-17F, or IL-23 binding competitors. In some embodiments, the antibodies produced by the antibody-producing cells are substantially free of IL-17A, IL-17F, and IL-23 competitors. In preferred embodiments, antibodies produced by the antibody-producing cells comprise less than about 10%, preferably less than about 5%, more preferably less than about 1%, more preferably less than about 0.5%, more preferably less than about 0.1%, and most preferably 0% by weight both IL-17 and IL-23 binding competitors.

[00120] Methods of antibody purification are known in the art. In some embodiments of the invention, methods for antibody purification include filtration, affinity column chromatography, cation exchange chromatography, anion exchange chromatography, and concentration. The filtration step preferably comprises ultrafiltration, and more preferably ultrafiltration and diafiltration. Filtration is preferably performed at least about 5-50 times, more preferably 10 to 30 times, and most preferably 14 to 27 times. Affinity column chromatography, may be performed using, for example, PROSEP® Affinity Chromatography (Millipore, Billerica, Mass.). In a preferred embodiment, the affinity chromatography step comprises PROSEP®-vA column chromatography. Eluate may be washed in a solvent detergent. Cation exchange chromatography may include, for example, SP-Sepharose Cation Exchange Chromatography. Anion exchange chromatography may include, for example but not limited to, Q-Sepharose Fast Flow Anion Exchange. The anion exchange step is preferably non-binding, thereby allowing removal of contaminants including DNA and BSA. The antibody product is preferably nanofiltered, for example, using a Pall DV 20 Nanofilter. The antibody product may be concentrated, for example, using ultrafiltration and diafiltration. The method may further comprise a step of size exclusion chromatography to remove aggregates.

[00121] The bispecific antibodies, antibodies or antigen-binding fragments may also be produced by other methods known in the art, for example by chemical coupling of antibodies and antibody fragments.

[00122] The bispecific antibodies, antibodies or antigen-binding fragments of the present invention are useful, for example, for the inhibition of proinflammatory cytokines, such as IL-17A, IL-17F and IL-23/p19. The antibodies can be used to reduce, limit, neutralize, or block the proinflammatory effects of the IL-17A homodimer, the IL-17F homodimer, and/or the IL-17A/F heterodimer. Likewise, the antibodies can be used to reduce, limit, neutralize, or block the pro-cancerous effects of the IL-17A homodimer, the IL-17F homodimer, or the IL-17A/F heterodimer. In such cases, the anti-IL-23p19 portion of the antibody is used to reduce, limit, neutralize, or block production of new T cells that would produce IL-17A and/or IL-17F, including homodimers and heterodimers. The bispecific antibodies, antibodies or antigen-binding fragments described herein can be used to treat inflammatory disorders and autoimmune diseases, such as multiple sclerosis (e.g., relapsing-remitting multiple sclerosis, secondary-progressive multiple sclerosis, primary-progressive multiple sclerosis and progressive-relapsing multiple sclerosis), cystic fibrosis, inflammatory bowel disease, psoriasis, systemic sclerosis, systemic lupus erythematosus, lupus nephritis, IgA nephropathy, diabetic kidney disease, minimal change disease (lipoid nephrosis), focal segmental glomerulosclerosis (FSGS), nephrogenic systemic fibrosis (NSF), nephrogenic fibrosing dermopathy, fibrosing cholestatic hepatitis, eosinophilic fasciitis (Shulman's syndrome), scleromyxedema (popular mucinosis), scleroderma, lichen sclerosusetatrophicus, POEMs syndrome (Crow-Fukase syndrome, Takatsuki disease or PEP syndrome), nephrotic syndrome, graft-versus-host-disease (GVHD), graft-versus-host-disease (GVHD) (from a transplant, such as blood, bone marrow, kidney, pancreas, liver, orthotopic liver, lung, heart, intestine, small intestine, large intestine, thymus, allogeneic stem cell, reduced-intensity allogeneic, bone, tendon, cornea, skin, heart valves, veins, arteries, blood vessels, stomach and testis), antineutrophil cytoplasmic antibodies (ANCA)-associated vasculitis (AAV), giant cell arteritis and multiple-myeloma-induced lytic bone disease. The bispecific antibodies, antibodies or antigen-binding fragments described herein can also be used to treat cancer, including angiogenesis.

[00123] The bispecific antibodies, antibodies or antigen-binding fragments of the present invention inhibit the activity of IL-17A and/or IL-17F and IL-23 (via the p19 subunit), and thus, inhibit the production, maintenance, and activity of new and existing IL-17A and IL-17F and IL-17-producing T cells (Th17). The invention further concerns

the use of the bispecific antibodies, antibodies or antigen-binding fragments of the present invention in the treatment of inflammatory diseases characterized by the presence of elevated levels of IL-17A, IL-17F, and/or IL-23, and in the treatment of cancers characterized by the presence of elevated levels of IL- 17A, IL-17F, and/or IL-23.

[00124] The bispecific antibodies, antibodies or antigen-binding fragments of the present invention may block, inhibit, reduce, antagonize or neutralize the activity of IL-17A, IL-17F, (including both homodimers and the heterodimer), and IL-23/p19 thus are advantageous over therapies that target only one or two of these three cytokines.

[00125] The antibodies, *e.g.*, bispecific antibodies, of the invention are thus useful to:

(1) Block, inhibit, reduce, antagonize or neutralize signaling via IL-17A or IL-17F and IL-23 in the treatment of cancer, acute inflammation, and chronic inflammatory diseases such as inflammatory bowel disease (IBD), Crohn's disease, ulcerative colitis, irritable bowel syndrome (IBS), cystic fibrosis, chronic colitis, Sjögren's syndrome, splenomegaly, inflammation in chronic kidney disease (CKD), psoriasis, psoriatic arthritis, rheumatoid arthritis, and other diseases associated with the induction of acute-phase response.

(2) Block, inhibit, reduce, antagonize or neutralize signaling via IL-17A or IL-17F or IL-23 in the treatment of autoimmune diseases such as insulin-dependent diabetes mellitus (IDDM), multiple sclerosis (MS) (e.g., relapsing-remitting multiple sclerosis, secondary-progressive multiple sclerosis, primary-progressive multiple sclerosis and progressive-relapsing multiple sclerosis), systemic Lupus erythematosus (SLE), myasthenia gravis, rheumatoid arthritis, Sjögren's syndrome, IBS and IBD to prevent or inhibit signaling in immune cells (*e.g.*, lymphocytes, monocytes, leukocytes) via their receptors (*e.g.*, IL-23Rα, IL-12Rβ1, IL-17RA and IL-17RC). Blocking, inhibiting, reducing, or antagonizing signaling via IL-23Rα, IL-12Rβ1, IL-17RA and IL-17RC, using the antibodies of the present invention, also benefits diseases of the pancreas, kidney, pituitary and neuronal cells and may be used to treat IDDM, non-insulin dependent diabetes mellitus (NIDDM), pancreatitis, and pancreatic carcinoma.

[00126] For example, the bispecific antibodies, antibodies or antigen-binding fragments of the present invention are useful in therapeutic treatment of inflammatory diseases, particularly as antagonists to IL-17A, IL-17F, and IL-23/p19, in the treatment of

inflammatory diseases such as multiple sclerosis (MS) (e.g., relapsing-remitting multiple sclerosis, secondary-progressive multiple sclerosis, primary-progressive multiple sclerosis and progressive-relapsing multiple sclerosis), inflammatory bowel disease (IBD), and cancer. These antagonists are capable of binding, blocking, inhibiting, reducing, antagonizing or neutralizing IL-17A, IL-17F, their homodimers and heterodimers, and IL-23 (via p19) (either individually or together) in the treatment of atopic and contact dermatitis, systemic sclerosis, systemic lupus erythematosus (SLE), antineutrophil cytoplasmic antibodies (ANCA)-associated vasculitis (AAV), giant cell arteritis, multiple sclerosis (MS) (e.g., relapsing-remitting multiple sclerosis, secondary-progressive multiple sclerosis, primary-progressive multiple sclerosis and progressive-relapsing multiple sclerosis), colitis, endotoxemia, arthritis, rheumatoid arthritis (RA), Sjögren's syndrome, psoriatic arthritis, adult respiratory disease (ARD), septic shock, multiple organ failure, inflammatory lung injury such as idiopathic pulmonary fibrosis, asthma, chronic obstructive pulmonary disease (COPD), airway hyper-responsiveness, chronic bronchitis, allergic asthma, psoriasis, eczema, IBS and inflammatory bowel disease (IBD) such as ulcerative colitis and Crohn's disease, *Helicobacter pylori* infection, lupus nephritis, IgA nephropathy, diabetic kidney disease, minimal change disease (lipoid nephrosis), focal segmental glomerulosclerosis (FSGS), nephrogenic systemic fibrosis (NSF), nephrogenic fibrosing dermopathy, fibrosing cholestatic hepatitis, eosinophilic fasciitis (Shulman's syndrome), scleromyxedema (popular mucinosis), scleroderma, lichen sclerosusetatrophicus, POEMs syndrome (Crow-Fukase syndrome, Takatsuki disease or PEP syndrome), nephrotic syndrome, transplant rejection, graft-versus-host-disease (GVHD), graft-versus-host-disease (GVHD) (from a transplant, such as blood, bone marrow, kidney, pancreas, liver, orthotopic liver, lung, heart, intestine, small intestine, large intestine, thymus, allogeneic stem cell, reduced-intensity allogeneic, bone, tendon, cornea, skin, heart valves, veins, arteries, blood vessels, stomach and testis), intraabdominal adhesions and/or abscesses as results of peritoneal inflammation (*e.g.*, from infection, injury, etc.), nephrotic syndrome, cystic fibrosis (Tan, H.-L. et al., *American Journal of Respiratory and Critical Care Medicine*, 184(2):252-258 (2011)), lytic bone disease (*e.g.*, multiple-myeloma-induced lytic bone disease) (Sotomayor, E.M., *Blood*, 116(18):3380-3382 (2010)), organ allograft rejection, streptococcal cell wall (SCW)-induced arthritis, osteoarthritis, gingivitis/periodontitis,

herpetic stromal keratitis, restenosis, Kawasaki disease, age-related macular degeneration (AMD; *e.g.*, wet form of AMD and dry form of AMD) (Wei, L. et al., *Cell Reports*, *2*:1151-1158 (Nov. 29, 2012), immune mediated renal diseases, liver fibrosis (Meng, F. et al., *Gastroenterology*, 143:765-776 (2012), pulmonary fibrosis (Meng, F. et al., *Gastroenterology*, 143:765-776 (2012), hepatobiliary diseases, myocarditis (Ding, H.-S., *Mol. Biol. Rep.*, 39(7):7473-7478 (Feb. 14, 2012); Valente, A.J. et al., *Cellular Signalling*, 24:560-568 (2012)), cardiac fibrosis (Valente, A.J. et al., *Cellular Signalling*, 24:560-568 (2012)), adverse myocardial remodeling (Valente, A.J. et al., *Cellular Signalling*, 24:560-568 (2012)), atherosclerosis (Ding, H.-S., *Mol. Biol. Rep.*, 39(7):7473-7478 (Feb. 14, 2012), cardiac ischemia/reperfusion injury (Ding, H.-S., *Mol. Biol. Rep.*, 39(7):7473-7478 (Feb. 14, 2012), heart failure (Ding, H.-S., *Mol. Biol. Rep.*, 39(7):7473-7478 (Feb. 14, 2012) and cancers/neoplastic diseases that are characterized by IL-17 and/or IL-23 expression, including but not limited to prostate, renal, colon, ovarian and cervical cancer, and leukemias (Tartour et al., *Cancer Res.*, 59:3698 (1999); Kato et al., *Biochem. Biophys. Res. Commun.*, 282:735 (2001); Steiner et al., *Prostate*, 56:171 (2003); Langowksi et al., *Nature*, May 10 [Epub ahead of print], (2006)).

[00127] For example, the bispecific antibodies, antibodies or antigen-binding fragments of the present invention are useful, *e.g.*, antagonists to IL-17A, IL-17F, and IL-23/p19, in therapeutic treatment of inflammatory diseases, particularly in the treatment of Acquired Immunodeficiency Syndrome (AIDS, which is a viral disease with an autoimmune component), alopecia areata, ankylosing spondylitis, antiphospholipid syndrome, autoimmune Addison's disease, autoimmune hemolytic anemia, autoimmune hepatitis, autoimmune inner ear disease (AIED), autoimmune lymphoproliferative syndrome (ALPS), autoimmune thrombocytopenic purpura (ATP), Behcet's disease, cardiomyopathy, celiac sprue-dermatitis hepetiformis; chronic fatigue immune dysfunction syndrome (CFIDS), chronic inflammatory demyelinating polyneuropathy (CIPD), cicatricial pemphigold, cold agglutinin disease, crest syndrome, Degos' disease, dermatomyositis-juvenile, discoid lupus (*e.g.*, childhood discoid lupus erythematosus, generalized discoid lupus erythematosus and localized discoid lupus erythematosus), chilblain lupus erythematosus, lupus erythematosus-lichen planus overlap syndrome, lupus erythematosus panniculitis, tumid lupus erythematosus, verrucous lupus erythematosus cutaneous, systemic lupus erythematosus, subacute cutaneous lupus

erythematosus, acute cutaneous lupus erythematosus, essential mixed cryoglobulinemia, fibromyalgia-fibromyositis, Graves' disease, Guillain-Barre syndrome, Hashimoto's thyroiditis, idiopathic pulmonary fibrosis, idiopathic thrombocytopenia purpura (ITP), IgA nephropathy, insulin-dependent diabetes mellitus, juvenile chronic arthritis (Still's disease), juvenile rheumatoid arthritis, rheumatoid arthritis (RA), Meniere's disease, mixed connective tissue disease, multiple sclerosis (MS) (e.g., relapsing-remitting multiple sclerosis, secondary-progressive multiple sclerosis, primary-progressive multiple sclerosis and progressive-relapsing multiple sclerosis), myasthenia gravis, pernacious anemia, polyarteritis nodosa, polychondritis, polyglandular syndromes, polymyalgia rheumatica, polymyositis and dermatomyositis, primary agammaglobulinemia, primary biliary cirrhosis, eczema, psoriasis, psoriatic arthritis, Raynaud's phenomena, Reiter's syndrome, adult respiratory disease (ARD), rheumatic fever, arthritis, sarcoidosis, scleroderma (*e.g.*, progressive systemic sclerosis (PSS), also known as systemic sclerosis (SS)), Sjögren's syndrome, stiff-man syndrome, systemic lupus erythematosus (SLE), antineutrophil cytoplasmic antibodies (ANCA)-associated vasculitis (AAV), giant cell arteritis, Takayasu arteritis, temporal arteritis/giant cell arteritis, endotoxia, sepsis or septic shock, toxic shock syndrome, multiple organ failure, inflammatory lung injury such as idiopathic pulmonary fibrosis, colitis, inflammatory bowel disease (IBD) such as ulcerative colitis and Crohn's disease, irritable bowel syndrome (IBS), uveitis, vitiligo, Wegener's granulomatosis, Alzheimer's disease, atopic allergy, allergy, asthma, bronchial asthma, chronic obstructive pulmonary disease (COPD), airway hyper-responsiveness, allergic asthma, glomerulonephritis, hemolytic anemias, *Helicobacter pylori* infection, intraabdominal adhesions and/or abscesses as results of peritoneal inflammation (*e.g.*, from infection, injury, etc.), nephrotic syndrome, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome, organ allograft rejection, lupus nephritis, IgA nephropathy, diabetic kidney disease, minimal change disease (lipoid nephrosis), focal segmental glomerulosclerosis (FSGS), nephrogenic systemic fibrosis (NSF), nephrogenic fibrosing dermopathy, fibrosing cholestatic hepatitis, eosinophilic fasciitis (Shulman's syndrome), scleromyxedema (popular mucinosis), scleroderma, lichen sclerosusetatrophicus, POEMs syndrome (Crow-Fukase syndrome, Takatsuki disease or PEP syndrome), nephrotic syndrome, graft-versus-host-disease (GVHD), graft-versus-host-disease (GVHD) (from a transplant, such as blood, bone marrow, kidney, pancreas,

liver, orthotopic liver, lung, heart, intestine, small intestine, large intestine, thymus, allogeneic stem cell, reduced-intensity allogeneic, bone, tendon, cornea, skin, heart valves, veins, arteries, blood vessels, stomach and testis), lytic bone disease (*e.g.*, multiple myeloma-induced lytice bone disease), cystic fibrosis, age-related mascular degeneration (AMD; *e.g.*, wet AMD and dry AMD), liver fibrosis, pulmonary fibrosis, atherosclerosis, cardiac ischemia/reperfusion injury, heart failure, myocarditis, cardiac fibrosis, adverse myocardial remodeling, diabetic retinopathy and ventilator induced lung injury.

[00128] Accordingly, in one embodiment, the present invention provides a method of inhibiting one or more of proinflammatory cytokines, *e.g.*, IL-17A, IL-17F and IL-23, in a mammal in need of such treatment comprising administering a therapeutically effective amount of a bispecific antibody, antibody or antigen-binding fragment to a mammal in need of such treatment. In a preferred embodiment, the mammal is a human. The method may be used to treat a disorder characterized by elevated expression of IL-17A, IL-17F, or IL-23. The bispecific antibody, antibody or antigen-binding fragment maybe administered with another pharmaceutical agent, either in the same formulation or separately.

[00129] In another embodiment, the present invention provides a method of treating an immune related disorder in a mammal in need thereof, comprising administering to the mammal a therapeutically effective amount of an IL-17A/F polypeptide, an agonist thereof, or an antagonist (such as an IL-17A/F binding entity which includes an IL-17A/F cross-reactive antibody) thereto. In a preferred aspect, the immune related disorder is selected form the group consisting of: systemic lupus erythematosis (SLE), rheumatoid arthritis (RA), osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, Sjögren's syndrome, systemic vasculitis, sarcoidosis, autoimmune hemolytic anemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central and peripheral nervous systems such as multiple sclerosis (MS) (e.g., relapsing-remitting multiple sclerosis, secondary-progressive multiple sclerosis, primary-progressive multiple sclerosis and progressive-relapsing multiple sclerosis), idiopathic demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic inflammatory demyelinating polyneuropathy, hepatobiliary diseases such as

infectious, autoimmune chronic active hepatitis, primary biliary cirrhosis, granulomatous hepatitis, and sclerosing cholangitis, inflammatory bowel disease (IBD), Crohn's disease, ulcerative colitis, gluten-sensitive enteropathy, and Whipple's disease, autoimmune or immune-mediated skin diseases including bullous skin diseases, erythema multiforme and contact dermatitis, antineutrophil cytoplasmic antibodies (ANCA)-associated vasculitis (AAV), giant cell arteritis, psoriasis, psoriatic arthritis, allergic diseases such as asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity and urticaria, immunologic diseases of the lung such as eosinophilic pneumonia, idiopathic pulmonary fibrosis and hypersensitivity pneumonitis, lupus nephritis, IgA nephropathy, diabetic kidney disease, minimal change disease (lipoid nephrosis), focal segmental glomerulosclerosis (FSGS), nephrogenic systemic fibrosis (NSF), nephrogenic fibrosing dermopathy, fibrosing cholestatic hepatitis, eosinophilic fasciitis (Shulman's syndrome), scleromyxedema (popular mucinosis), scleroderma, lichen sclerosusetatrophicus, POEMs syndrome (Crow-Fukase syndrome, Takatsuki disease or PEP syndrome), nephrotic syndrome, graft-versus-host-disease (GVHD), graft-versus-host-disease (GVHD) (from a transplant, such as blood, bone marrow, kidney, pancreas, liver, orthotopic liver, lung, heart, intestine, small intestine, large intestine, thymus, allogeneic stem cell, reduced-intensity allogeneic, bone, tendon, cornea, skin, heart valves, veins, arteries, blood vessels, stomach and testis), lytic bone disease (*e.g.*, multiple myeloma-induced lytice bone disease), cystic fibrosis, age-related mascular degeneration (AMD; *e.g.*, wet AMD and dry AMD), liver fibrosis, pulmonary fibrosis, atherosclerosis, cardiac ischemia/reperfusion injury, heart failure, myocarditis, cardiac fibrosis, adverse myocardial remodeling, transplantation associated diseases including graft rejection and graft-versus-host-disease.

[00130] In another embodiment, the present invention provides a method for inhibiting inflammation in a mammal in need of such treatment comprising administering a therapeutically effective amount of a bispecific antibody, antibody or antigen-binding fragment of the invention to a mammal in need of such treatment. In a preferred embodiment, the mammal is a human. The inflammation may be associated with a disease selected from the group consisting of multiple sclerosis (MS) (e.g., relapsing-remitting multiple sclerosis, secondary-progressive multiple sclerosis, primary-progressive multiple sclerosis and progressive-relapsing multiple sclerosis), chronic

inflammation, Sjögren's syndrome, autoimmune diabetes, rheumatoid arthritis (RA) and other arthritic conditions, asthma, systemic sclerosis, atopic dermatitis, antineutrophil cytoplasmic antibodies (ANCA)-associated vasculitis (AAV), giant cell arteritis, systemic lupus erythematosus (SLE), Degos' disease, dermatomyositis-juvenile, discoid lupus (*e.g.*, childhood discoid lupus erythematosus, generalized discoid lupus erythematosus and localized discoid lupus erythematosus), chilblain lupus erythematosus, lupus erythematosus-lichen planus overlap syndrome, lupus erythematosus panniculitis, tumid lupus erythematosus, verrucous lupus erythematosus cutaneous, systemic lupus erythematosus, subacute cutaneous lupus erythematosus, acute cutaneous lupus erythematosus, essential mixed cryoglobulinemia, fibromyalgia-fibromyositis, Graves' disease, lytic bone disease (*e.g.*, multiple myeloma-induced lytice bone disease), cystic fibrosis, age-related mascular degeneration (AMD; *e.g.*, wet AMD and dry AMD), liver fibrosis, pulmonary fibrosis, atherosclerosis, cardiac ischemia/reperfusion injury, heart failure, myocarditis, cardiac fibrosis, adverse myocardial remodeling, Guillain-Barre syndrome, Hashimoto's thyroiditis, psoriasis, psoritic arthritis, Crohn's Disease, ulcerative colitis, irritable bowel syndrome (IBS), inflammatory bowel disease (IBD), lupus nephritis, IgA nephropathy, diabetic kidney disease, minimal change disease (lipoid nephrosis), focal segmental glomerulosclerosis (FSGS), nephrogenic systemic fibrosis (NSF), nephrogenic fibrosing dermopathy, fibrosing cholestatic hepatitis, eosinophilic fasciitis (Shulman's syndrome), scleromyxedema (popular mucinosis), scleroderma, lichen sclerosusetatrophicus, POEMs syndrome (Crow-Fukase syndrome, Takatsuki disease or PEP syndrome), nephrotic syndrome, graft-versus-host-disease (GVHD), graft-versus-host-disease (GVHD) (from a transplant, such as blood, bone marrow, kidney, pancreas, liver, orthotopic liver, lung, heart, intestine, small intestine, large intestine, thymus, allogeneic stem cell, reduced-intensity allogeneic, bone, tendon, cornea, skin, heart valves, veins, arteries, blood vessels, stomach and testis). The bispecific antibody, antibody or antigen-binding fragment made be administered with another pharmaceutical agent, for example an anti-inflammatory agent, either in the same formulation or separately.

[00131] In another embodiment, the present invention provides a composition comprising an antibody, *e.g.*, a bispecific antibody, as described herein and a pharmaceutically acceptable carrier. A pharmaceutical composition comprising an

antibody, *e.g.*, a bispecific antibody, of the invention can be formulated according to known methods to prepare pharmaceutically useful compositions, whereby the therapeutic proteins are combined in a mixture with a pharmaceutically acceptable carrier. A composition is said to be a "pharmaceutically acceptable carrier" if its administration can be tolerated by a recipient patient. Sterile phosphate-buffered saline is one example of a pharmaceutically acceptable carrier. Other suitable carriers are well-known to those in the art. See, for example, Gennaro, ed., *Remington's Pharmaceutical Sciences*, 19th Edition, Mack Publishing Company (1995).

[00132] For pharmaceutical use, an antibody, *e.g.*, a bispecific antibody, of the present invention are formulated for parenteral, particularly intravenous or subcutaneous, delivery according to conventional methods. Intravenous administration may be by bolus injection, controlled release, *e.g.*, using mini-pumps or other appropriate technology, or by infusion over a typical period of one to several hours. In general, pharmaceutical formulations will include an antibody, *e.g.*, a bispecific antibody, of the invention in combination with a pharmaceutically acceptable carrier, such as saline, buffered saline, 5% dextrose in water or the like. Formulations may further include one or more excipients, preservatives, solubilizers, buffering agents, albumin to prevent protein loss on vial surfaces, etc. When utilizing such a combination therapy, the antibodies, which include bispecific antibodies, may be combined in a single formulation or may be administered in separate formulations. Methods of formulation are well known in the art and are disclosed, for example, in Gennaro, ed., *Remington's Pharmaceutical Sciences*, Mack Publishing Co., Easton PA (1990), which is incorporated herein by reference. Therapeutic doses will generally be in the range of 0.1 to 100 mg/kg of patient weight per day, preferably 0.5-20 mg/kg per day, with the exact dose determined by the clinician according to accepted standards, taking into account the nature and severity of the condition to be treated, patient traits, etc. Determination of dose is within the level of ordinary skill in the art. More commonly, the antibodies will be administered over one week or less, often over a period of one to three days. Generally, the dosage of administered antibodies will vary depending upon such factors as the patient's age, weight, height, sex, general medical condition and previous medical history. Typically, it is desirable to provide the recipient with a dosage of antibodies which is in the range of

from about 1 pg/kg to 10 mg/kg (amount of agent/body weight of patient), although a lower or higher dosage also may be administered as circumstances dictate.

[00133] Administration of an antibody, *e.g.*, bispecific antibody, of the invention to a subject can be intravenous, intraarterial, intraperitoneal, intramuscular, subcutaneous, intrapleural, intrathecal, by perfusion through a regional catheter, or by direct intralesional injection. When administering therapeutic antibodies by injection, the administration may be by continuous infusion or by single or multiple boluses.

[00134] Additional routes of administration include oral, mucosal-membrane, pulmonary, and transcutaneous. Oral delivery is suitable for polyester microspheres, zein microspheres, proteinoid microspheres, polycyanoacrylate microspheres, and lipid-based systems (see, for example, DiBase et al., "Oral Delivery of Microencapsulated Proteins", in Sanders et al., eds., *Protein Delivery: Physical Systems*, pp. 255-288, Plenum Press (1997)). The feasibility of an intranasal delivery is exemplified by such a mode of insulin administration (see, for example, Hinchcliffe et al., *Adv. Drug Deliv. Rev.,* 35:199 (1999)). Dry or liquid particles comprising antibodies of the invention can be prepared and inhaled with the aid of dry-powder dispersers, liquid aerosol generators, or nebulizers (*e.g.,* Pettit et al., *TIBTECH,* 16:343 (1998); Patton et al., *Adv. Drug Deliv. Rev.,* 35:235 (1999)). This approach is illustrated by the AERX® diabetes management system, which is a hand-held electronic inhaler that delivers aerosolized insulin into the lungs. Studies have shown that proteins as large as 48,000 kDa have been delivered across skin at therapeutic concentrations with the aid of low-frequency ultrasound, which illustrates the feasibility of trascutaneous administration (Mitragotri et al., *Science,* 269:850 (1995)). Transdermal delivery using electroporation provides another means to administer a molecule having IL-17 and IL-23/p19 binding activity (Potts et al., *Pharm. Biotechnol.,* 10:213 (1997)).

[00135] For purposes of therapy, compositions comprising an antibody, *e.g.*, a bispecific antibody, of the invention and a pharmaceutically acceptable carrier are administered to a patient in a therapeutically effective amount. A combination of an antibody, *e.g.*, a bispecific antibody, of the present invention and a pharmaceutically acceptable carrier is said to be administered in a "therapeutically effective amount" if the amount administered is physiologically significant. An agent is physiologically significant if its presence results in a detectable change in the physiology of a recipient

patient. For example, an agent used to treat inflammation is physiologically significant if its presence alleviates the inflammatory response. Effective treatment may be assessed in a variety of ways. In one embodiment, effective treatment is determined by reduced inflammation. In other embodiments, effective treatment is marked by inhibition of inflammation. In still other embodiments, effective therapy is measured by increased well-being of the patient including such signs as weight gain, regained strength, decreased pain, thriving, and subjective indications from the patient of better health.

[00136] A pharmaceutical composition comprising an antibody, *e.g.*, a bispecific antibody, of the invention can be furnished in liquid form, in an aerosol, or in solid form. Liquid forms, are illustrated by injectable solutions and oral suspensions. Exemplary solid forms include capsules, tablets, and controlled-release forms. The latter form is illustrated by miniosmotic pumps and implants (Bremer et al., *Pharm. Biotechnol.,* 10:239 (1997); Ranade, "Implants in Drug Delivery", in Ranade et al., eds., *Drug Delivery Systems*, pp. 95-123, CRC Press (1995); Bremer et al., "Protein Delivery with Infusion Pumps", in Sanders et al., eds., *Protein Delivery: Physical Systems*, pp. 239-254, Plenum Press (1997); Yewey et al., "Delivery of Proteins from a Controlled Release Injectable Implant", in Sanders et al., eds., *Protein Delivery: Physical Systems*, pp. 93-117, Plenum Press (1997).

[00137] Liposomes provide one means to deliver therapeutic polypeptides to a subject intravenously, intraperitoneally, intrathecally, intramuscularly, subcutaneously, or via oral administration, inhalation, or intranasal administration. Liposomes are microscopic vesicles that consist of one or more lipid bilayers surrounding aqueous compartments (see, generally, Bakker-Woudenberg et al., *Eur. J. Clin. Microbiol. Infect. Dis.,* 12(Suppl. 1):S61 (1993), Kim, *Drugs,* 46:618 (1993), and Ranade, "Site-Specific Drug Delivery Using Liposomes as Carriers", in Ranade et al., eds., *Drug Delivery Systems*, pp. 3-24, CRC Press (1995)). Liposomes are similar in composition to cellular membranes and as a result, liposomes can be administered safely and are biodegradable. Depending on the method of preparation, liposomes may be unilamellar or multilamellar, and liposomes can vary in size with diameters ranging from 0.02 μm to greater than 10 μm. A variety of agents can be encapsulated in liposomes: hydrophobic agents partition in the bilayers and hydrophilic agents partition within the inner aqueous space(s) (see, for example, Machy et al., *Liposomes in Cell Biology and Pharmacology,* John Libbey

(1987), and Ostro et al., *American J. Hosp. Pharm.,* 46:1576 (1989)). Moreover, it is possible to control the therapeutic availability of the encapsulated agent by varying liposome size, the number of bilayers, lipid composition, as well as the charge and surface characteristics of the liposomes.

[00138] Liposomes can absorb to virtually any type of cell and then slowly release the encapsulated agent. Alternatively, an absorbed liposome may be endocytosed by cells that are phagocytic. Endocytosis is followed by intralysosomal degradation of liposomal lipids and release of the encapsulated agents (Scherphof et al., *Ann. N.Y. Acad. Sci.,* 446:368 (1985)). After intravenous administration, small liposomes (0.1 to 1.0 μm) are typically taken up by cells of the reticuloendothelial system, located principally in the liver and spleen, whereas liposomes larger than 3.0 μm are deposited in the lung. This preferential uptake of smaller liposomes by the cells of the reticuloendothelial system has been used to deliver chemotherapeutic agents to macrophages and to tumors of the liver.

[00139] The reticuloendothelial system can be circumvented by several methods including saturation with large doses of liposome particles, or selective macrophage inactivation by pharmacological means (Claassen et al., *Biochim. Biophys. Acta,* 802:428 (1984)). In addition, incorporation of glycolipid- or polyethelene glycol-derivatized phospholipids into liposome membranes has been shown to result in a significantly reduced uptake by the reticuloendothelial system (Allen et al., *Biochim. Biophys. Acta,* 1068:133 (1991); Allen et al., *Biochim. Biophys. Acta,* 1150:9 (1993)).

[00140] Liposomes can also be prepared to target particular cells or organs by varying phospholipid composition or by inserting receptors or ligands into the liposomes. For example, liposomes, prepared with a high content of a nonionic surfactant, have been used to target the liver (Hayakawa et al., Japanese Patent No. 04-244,018; Kato et al., *Biol. Pharm. Bull.,* 16:960 (1993)). These formulations were prepared by mixing soybean phospatidylcholine, α-tocopherol, and ethoxylated hydrogenated castor oil (HCO-60) in methanol, concentrating the mixture under vacuum, and then reconstituting the mixture with water. A liposomal formulation of dipalmitoylphosphatidylcholine (DPPC) with a soybean-derived sterylglucoside mixture (SG) and cholesterol (Ch) has also been shown to target the liver (Shimizu et al., *Biol. Pharm. Bull.,* 20:881 (1997)).

[00141] Alternatively, various targeting ligands can be bound to the surface of the liposome, such as antibodies, antibody fragments, carbohydrates, vitamins, and

transport proteins. For example, liposomes can be modified with branched type galactosyllipid derivatives to target asialoglycoprotein (galactose) receptors, which are exclusively expressed on the surface of liver cells (Kato et al., *Crit. Rev. Ther. Drug Carrier Syst.,* 14:287 (1997); Murahashi et al., *Biol. Pharm. Bull.,* 20:259 (1997)). Similarly, Wu et al., *Hepatology,* 27:772 (1998), have shown that labeling liposomes with asialofetuin led to a shortened liposome plasma half-life and greatly enhanced uptake of asialofetuin-labeled liposome by hepatocytes. On the other hand, hepatic accumulation of liposomes comprising branched type galactosyllipid derivatives can be inhibited by preinjection of asialofetuin (Murahashi et al., *Biol. Pharm. Bull.,* 20:259 (1997)). Polyaconitylated human serum albumin liposomes provide another approach for targeting liposomes to liver cells (Kamps et al., *Proc. Nat'l Acad. Sci. USA,* 94:11681 (1997)). Moreover, Geho et al. U.S. Patent No. 4,603,044, describe a hepatocyte-directed liposome vesicle delivery system, which has specificity for hepatobiliary receptors associated with the specialized metabolic cells of the liver.

[00142] In a more general approach to tissue targeting, target cells are prelabeled with biotinylated antibodies specific for a ligand expressed by the target cell (Harasym et al., *Adv. Drug Deliv. Rev.,* 32:99 (1998)). After plasma elimination of free antibody, streptavidin-conjugated liposomes are administered. In another approach, targeting antibodies are directly attached to liposomes (Harasym et al., *Adv. Drug Deliv. Rev.,* 32:99 (1998)).

[00143] Antibodies can be encapsulated within liposomes using standard techniques of protein microencapsulation (see, for example, Anderson et al., *Infect. Immun.,* 31:1099 (1981), Anderson et al., *Cancer Res.,* 50:1853 (1990), and Cohen et al., *Biochim. Biophys. Acta,* 1063:95 (1991), Alving et al. "Preparation and Use of Liposomes in Immunological Studies", in Gregoriadis, ed., *Liposome Technology,* 2nd Edition, Vol. III, p. 317, CRC Press (1993), Wassef et al., *Meth. Enzymol.,* 149:124 (1987)). As noted above, therapeutically useful liposomes may contain a variety of components. For example, liposomes may comprise lipid derivatives of poly(ethylene glycol) (Allen et al., *Biochim. Biophys. Acta,* 1150:9 (1993)).

[00144] Degradable polymer microspheres have been designed to maintain high systemic levels of therapeutic proteins. Microspheres are prepared from degradable polymers such as poly(lactide-co-glycolide) (PLG), polyanhydrides, poly (ortho esters),

nonbiodegradable ethylvinyl acetate polymers, in which proteins are entrapped in the polymer (Gombotz et al., *Bioconjugate Chem.*, 6:332 (1995); Ranade, "Role of Polymers in Drug Delivery", in Ranade et al., eds., *Drug Delivery Systems*, pp. 51-93, CRC Press (1995); Roskos et al., "Degradable Controlled Release Systems Useful for Protein Delivery", in Sanders et al., eds., *Protein Delivery: Physical Systems*, pp. 45-92, Plenum Press (1997); Bartus et al., *Science,* 281:1161 (1998); Putney et al., *Nature Biotechnology,* 16:153 (1998); Putney, *Curr. Opin. Chem. Biol.,* 2:548 (1998)). Polyethylene glycol (PEG)-coated nanospheres can also provide carriers for intravenous administration of therapeutic proteins (see, for example, Gref et al., *Pharm. Biotechnol.,* 10:167 (1996).

[00145] The formulation can also contain more than one active compound as necessary for the particular indication being treated, preferably those with complementary activities that do not adversely affect each other. Alternatively, or in addition, the composition can comprise an agent that enhances its function, such as, for example, a cytotoxic agent, cytokine, chemotherapeutic agent, or growth-inhibitory agent. Such molecules are suitably present in combination in amounts that are effective for the purpose intended.

[00146] In one embodiment, an antibody, *e.g.*, a bispecific antibody, of the invention is administered in combination therapy, *i.e.*, combined with other agents, *e.g.*, therapeutic agents, that are useful for treating pathological conditions or disorders, such as autoimmune disorders and inflammatory diseases. The term "in combination" in this context means that the agents are given substantially contemporaneously, either simultaneously or sequentially. If given sequentially, at the onset of administration of the second compound, the first of the two compounds is preferably still detectable at effective concentrations at the site of treatment.

[00147] For example, the combination therapy can include one or more an antibodies, *e.g.*, bispecific antibodies, of the invention coformulated with, and/or coadministered with, one or more additional therapeutic agents, *e.g.*, one or more cytokine and growth factor inhibitors, immunosuppressants, anti-inflammatory agents, metabolic inhibitors, enzyme inhibitors, and/or cytotoxic or cytostatic agents, as described in more detail below. Furthermore, one or more antibodies, *e.g.*, bispecific antibodies, described herein may be used in combination with two or more of the

therapeutic agents described herein. Such combination therapies may advantageously utilize lower dosages of the administered therapeutic agents, thus avoiding possible toxicities or complications associated with the various monotherapies.

[00148] Preferred therapeutic agents used in combination with an antibody, *e.g.*, bispecific antibody, of the invention are those agents that interfere at different stages in an inflammatory response. In one embodiment, one or more antibodies, *e.g.*, bispecific antibodies, described herein may be coformulated with, and/or coadministered with, one or more additional agents such as other cytokine or growth factor antagonists (*e.g.*, soluble receptors, peptide inhibitors, small molecules, ligand fusions); or antibodies or antigen binding fragments thereof that bind to other targets (*e.g.*, antibodies that bind to other cytokines or growth factors, their receptors, or other cell surface molecules); and anti-inflammatory cytokines or agonists thereof. Nonlimiting examples of the agents that can be used in combination with the antibodies described herein, include, but are not limited to, antagonists of one or more interleukins (ILs) or their receptors, *e.g.*, antagonists of IL-1, IL-2, IL-6, IL-7, IL-8, IL-12, IL-13, IL-15, IL-16, IL-18, IL-20, IL-21, IL-22 and IL-31; antagonists of cytokines or growth factors or their receptors, such as tumor necrosis factor (TNF), LT, EMAP-II, GM-CSF, FGF and PDGF. Antibodies of the invention can also be combined with inhibitors of, *e.g.*, antibodies to, cell surface molecules such as CD2, CD3, CD4, CD8, CD20 (*e.g.*, the CD20 inhibitor rituximab (RITUXAN®)), CD25, CD28, CD30, CD40, CD45, CD69, CD80 (B7.1), CD86 (B7.2), CD90, or their ligands, including CD154 (gp39 or CD40L), or LFA-1/ICAM-1 and VLA-4/VCAM-1 (Yusuf-Makagiansar et al., *Med. Res. Rev.*, 22:146-167 (2002)). Preferred antagonists that can be used in combination with one or more antibodies, *e.g.*, bispecific antibodies, described herein include antagonists of IL-1, IL-6, IL-12, TNF-alpha, IL-15, IL-18, IL-20, IL-22 and IL-31.

[00149] Examples of those agents include IL-12 antagonists, such as chimeric, humanized, human or *in vitro*-generated antibodies (or antigen binding fragments thereof) that bind to IL-12 (preferably human IL-12), *e.g.*, the antibody disclosed in WO 00/56772; IL-12 receptor inhibitors, *e.g.*, antibodies to human IL-12 receptor; and soluble fragments of the IL-12 receptor, *e.g.*, human IL-12 receptor. Examples of IL-15 antagonists include antibodies (or antigen binding fragments thereof) against IL-15 or its receptor, *e.g.*, chimeric, humanized, human or *in vitro*-generated antibodies to human IL-

15 or its receptor, soluble fragments of the IL-15 receptor, and IL-15-binding proteins. Examples of IL-18 antagonists include antibodies, *e.g.*, chimeric, humanized, human or *in vitro*-generated antibodies (or antigen binding fragments thereof), to human IL-18, soluble fragments of the IL-18 receptor, and IL-18 binding proteins (IL-18BP). Examples of IL-1 antagonists include Interleukin-1-converting enzyme (ICE) inhibitors, such as Vx740, IL-1 antagonists, *e.g.*, IL-1 RA (anikinra, KINERET®, Amgen), sIL1RII (Immunex), and anti-IL-1 receptor antibodies (or antigen binding fragments thereof).

[00150] Examples of TNF antagonists include chimeric, humanized, human or *in vitro*-generated antibodies (or antigen binding fragments thereof) to TNF (*e.g.*, human TNF-alpha), such as (HUMIRA®, D2E7, human TNF-alpha antibody), CDP-571/CDP-870/BAY-10-3356 (humanized anti-TNF-alpha antibody; Celltech/Pharmacia), cA2 (chimeric anti-TNF-alpha antibody; REMICADE®, Centocor); anti-TNF antibody fragments (*e.g.*, CPD870); soluble fragments of the TNF receptors, *e.g.*, p55 or p75 human TNF receptors or derivatives thereof, *e.g.*, 75 kdTNFR-IgG (75 kD TNF receptor-IgG fusion protein, ENBREL®; Immunex), p55 kdTNFR-IgG (55 kD TNF receptor-IgG fusion protein (Lenercept)); enzyme antagonists, *e.g.*, TNF-alpha converting enzyme (TACE) inhibitors (*e.g.*, an alpha-sulfonyl hydroxamic acid derivative, and N-hydroxyformamide TACE inhibitor GW 3333, -005, or -022); and TNF-bp/s-TNFR (soluble TNF binding protein). Preferred TNF antagonists are soluble fragments of the TNF receptors, *e.g.*, p55 or p75 human TNF receptors or derivatives thereof, *e.g.*, 75 kdTNFR-IgG, and TNF-alpha converting enzyme (TACE) inhibitors.

[00151] In other embodiments, one or more antibodies, *e.g.*, bispecific antibodies, described herein may be administered in combination with one or more of the following: IL-13 antagonists, *e.g.*, soluble IL-13 receptors (sIL-13) and/or antibodies against IL-13; IL-2 antagonists, *e.g.*, DAB 486-IL-2 and/or DAB 389-IL-2 (IL-2 fusion proteins, Seragen), and/or antibodies to IL-2R, *e.g.*, anti-Tac (humanized anti-IL-2R, Protein Design Labs). Yet another combination includes one or more antibodies, *e.g.*, bispecific antibodies, of the invention, antagonistic small molecules, and/or inhibitory antibodies in combination with nondepleting anti-CD4 inhibitors (DEC-CE9.1/SB 210396; nondepleting primatized anti-CD4 antibody; IDEC/SmithKline). Yet other preferred combinations include antagonists of the costimulatory pathway CD80 (B7.1) or CD86 (B7.2), including antibodies, soluble receptors or antagonistic ligands; as well as p-

selectin glycoprotein ligand (PSGL), anti-inflammatory cytokines, *e.g.*, IL-4 (DNAX/Schering); IL-10 (SCH 52000; recombinant IL-10 DNAX/Schering); IL-13 and TGF-beta, and agonists thereof (*e.g.*, agonist antibodies).

[00152] In other embodiments, one or more antibodies, *e.g.*, bispecific antibodies, of the invention can be coformulated with, and/or coadministered with, one or more anti-inflammatory drugs, immunosuppressants, or metabolic or enzymatic inhibitors. Nonlimiting examples of the drugs or inhibitors that can be used in combination with the antibodies described herein, include, but are not limited to, one or more of: nonsteroidal anti-inflammatory drug(s) (NSAIDs), *e.g.*, ibuprofen, tenidap, naproxen, meloxicam, piroxicam, diclofenac, and indomethacin; sulfasalazine; corticosteroids such. as prednisolone; cytokine suppressive anti-inflammatory drug(s) (CSAIDs); inhibitors of nucleotide biosynthesis, *e.g.*, inhibitors of purine biosynthesis, folate antagonists (*e.g.*, methotrexate (N-[4-[[(2,4-diamino-6-pteridinyl)methyl]methylamino] benzoyl]-L-glutamic acid); and inhibitors of pyrimidine biosynthesis, *e.g.*, dihydroorotate dehydrogenase (DHODH) inhibitors. Preferred therapeutic agents for use in combination with one or more antibodies, *e.g.*, bispecific antibodies, of the invention include NSAIDs, CSAIDs, (DHODH) inhibitors (*e.g.*, leflunomide), and folate antagonists (*e.g.*, methotrexate).

[00153] Examples of additional inhibitors include one or more of: corticosteroids (oral, inhaled and local injection); immunosuppresants, *e.g.*, cyclosporin, tacrolimus (FK-506); and mTOR inhibitors, *e.g.*, sirolimus (rapamycin – RAPAMUNE® or rapamycin derivatives, *e.g.*, soluble rapamycin derivatives (*e.g.*, ester rapamycin derivatives, *e.g.*, CCI-779); agents which interfere with signaling by proinflammatory cytokines such as TNF-alpha or IL-1 (*e.g.*, IRAK, NIK, IKK, p38 or MAP kinase inhibitors); COX2 inhibitors, *e.g.*, celecoxib, rofecoxib, and variants thereof; phosphodiesterase inhibitors, *e.g.*, R973401 (phosphodiesterase Type IV inhibitor); phospholipase inhibitors, *e.g.*, inhibitors of cytosolic phospholipase 2 (cPLA2) (*e.g.*, trifluoromethyl ketone analogs); inhibitors of vascular endothelial cell growth factor or growth factor receptor, *e.g.*, VEGF inhibitor and/or VEGF-R inhibitor; and inhibitors of angiogenesis. Preferred therapeutic agents for use in combination with the antibodies of the invention are immunosuppresants, *e.g.*, cyclosporin, tacrolimus (FK-506); mTOR inhibitors, *e.g.*, sirolimus (rapamycin) or rapamycin derivatives, *e.g.*, soluble rapamycin

derivatives (*e.g.*, ester rapamycin derivatives, *e.g.*, CCI-779); COX2 inhibitors, *e.g.*, celecoxib and variants thereof; and phospholipase inhibitors, *e.g.*, inhibitors of cytosolic phospholipase 2 (cPLA2), *e.g.*, trifluoromethyl ketone analogs.

[00154] Additional examples of therapeutic agents that can be combined with an antibody, *e.g.*, bispecific antibody, of the invention include one or more of: 6-mercaptopurines (6-MP); azathioprine sulphasalazine; mesalazine; olsalazine; chloroquine/hydroxychloroquine (PLAQUENIL®); pencillamine; aurothiornalate (intramuscular and oral); azathioprine; coichicine; beta-2 adrenoreceptor agonists (salbutamol, terbutaline, salmeteral); xanthines (theophylline, aminophylline); cromoglycate; nedocromil; ketotifen; ipratropium and oxitropium; mycophenolate mofetil; adenosine agonists; antithrombotic agents; complement inhibitors; and adrenergic agents.

[00155] Nonlimiting examples of agents for treating or preventing arthritic disorders (*e.g.*, rheumatoid arthritis, inflammatory arthritis, rheumatoid arthritis, juvenile rheumatoid arthritis, osteoarthritis and psoriatic arthritis), with which an antibody, *e.g.*, bispecific antibody, of the invention may be combined include one or more of the following: IL-12 antagonists as described herein; NSAIDs; CSAIDs; TNFs, *e.g.*, TNF-alpha, antagonists as described herein; nondepleting anti-CD4 antibodies as described herein; IL-2 antagonists as described herein; anti-inflammatory cytokines, *e.g.*, IL-4, IL-10, IL-13 and TGF-alpha, or agonists thereof; IL-1 or IL-1 receptor antagonists as described herein; phosphodiesterase inhibitors as described herein; Cox-2 inhibitors as described herein; iloprost: methotrexate; thalidomide and thalidomide-related drugs (*e.g.*, Celgen); leflunomide; inhibitor of plasminogen activation, *e.g.*, tranexamic acid; cytokine inhibitor, *e.g.*, T-614; prostaglandin E1; azathioprine; an inhibitor of interleukin-1 converting enzyme (ICE); zap-70 and/or 1ck inhibitor (inhibitor of the tyrosine kinase zap-70 or 1ck); an inhibitor of vascular endothelial cell growth factor or vascular endothelial cell growth factor receptor as described herein; an inhibitor of angiogenesis as described herein; corticosteroid anti-inflammatory drugs (*e.g.*, SB203580); TNF-convertase inhibitors; IL-11; IL-13; IL-17 inhibitors; gold; penicillamine; chloroquine; hydroxychloroquine; chlorambucil; cyclophosphamide; cyclosporine; total lymphoid irradiation; antithymocyte globulin; CD5-toxins; orally administered peptides and collagen; lobenzarit disodium; cytokine regulating agents (CRAs) HP228 and HP466

(Houghten Pharmaceuticals, Inc.); ICAM-1 antisense phosphorothioate oligodeoxynucleotides (ISIS 2302; Isis Pharmaceuticals, Inc.); soluble complement receptor 1 (TP 10; T Cell Sciences, Inc.); prednisone; orgotein; glycosaminoglycan polysulphate; minocycline (MINOCIN®); anti-IL2R antibodies; marine and botanical lipids (fish and plant seed fatty acids); auranofin; phenylbutazone; meclofenamic acid; flufenamic acid; intravenous immune globulin; zileuton; mycophenolic acid (RS-61443); tacrolimus (FK-506); sirolimus (rapamycin); amiprilose (therafectin); cladribine (2-chlorodeoxyadenosine); and azaribine. Preferred combinations include one or more antibodies, *e.g.*, bispecific antibodies, of the invention in combination with methotrexate or leflunomide, and in moderate or severe rheumatoid arthritis cases, cyclosporine.

[00156] Preferred examples of inhibitors to use in combination with one or more antibodies, *e.g.*, bispecific antibodies, of the invention to treat arthritic disorders include TNF antagonists (*e.g.*, chimeric, humanized, human or *in vitro*-generated antibodies, or antigen binding fragments thereof, that bind to TNF; soluble fragments of a TNF receptor, *e.g.*, p55 or p75 human TNF receptor or derivatives thereof, *e.g.*, 75 kdTNFR-IgG (75 kD TNF receptor-IgG fusion protein, ENBREL®), p55 kD TNF receptor-IgG fusion protein; TNF enzyme antagonists, *e.g.*, TNF-alpha converting enzyme (TACE) inhibitors); antagonists of IL-12, IL-15, IL-18, IL-22; T cell and B cell-depleting agents (*e.g.*, anti-CD4 or anti-CD22 antibodies); small molecule inhibitors, *e.g.*, methotrexate and leflunomide; sirolimus (rapamycin) and analogs thereof, *e.g.*, CCI-779; cox-2 and cPLA2 inhibitors; NSAIDs; p38 inhibitors, TPL-2, Mk-2 and NFκB inhibitors; RAGE or soluble RAGE; P-selectin or PSGL-1 inhibitors (*e.g.*, small molecule inhibitors, antibodies thereto, *e.g.*, antibodies to P-selectin); estrogen receptor beta (ERB) agonists or ERB-NFκB antagonists. Most preferred additional therapeutic agents that can be coadministered and/or coformulated with one or more antibodies, *e.g.*, bispecific antibodies, of the invention include one or more of: a soluble fragment of a TNF receptor, *e.g.*, p55 or p75 human TNF receptor or derivatives thereof, *e.g.*, 75 kdTNFR-IgG (75 kD TNF receptor-IgG fusion protein, ENBREL®); methotrexate, leflunomide, or a sirolimus (rapamycin) or an analog thereof, *e.g.*, CCI-779.

[00157] Nonlimiting examples of agents for treating or preventing multiple sclerosis (e.g., relapsing-remitting multiple sclerosis, secondary-progressive multiple sclerosis, primary-progressive multiple sclerosis and progressive-relapsing multiple

sclerosis) with one or more antibodies, *e.g.*, bispecific antibodies, of the invention can be combined include the following: interferons, *e.g.*, interferon-alpha1a (*e.g.*, AVONEX®, Biogen) and interferon-1b (BETASERON®, Chiron/Berlex); Copolymer 1 (Cop-1; COPAXONE®, Teva Pharmaceutical Industries, Inc.); dimethyl fumarate (*e.g.*, BG-12; Biogen); hyperbaric oxygen; intravenous immunoglobulin; cladribine; TNF antagonists as described herein; corticosteroids; prednisolone; methylprednisolone; azathioprine; cyclophosphamide; cyclosporine; cyclosporine A, methotrexate; 4-aminopyridine; and tizanidine. Additional antagonists that can be used in combination with antibodies of the invention include antibodies to or antagonists of other human cytokines or growth factors, for example, TNF, LT, IL-1, IL-2, IL-6, EL-7, IL-8, IL-12 IL-15, IL-16, IL-18, EMAP-11, GM-CSF, FGF, and PDGF. Antibodies as described herein can be combined with antibodies to cell surface molecules such as CD2, CD3, CD4, CD8, CD25, CD28, CD30, CD40, CD45, CD69, CD80, CD86, CD90 or their ligands. One or more antibodies, *e.g.*, bispecific antibodies, of the invention may also be combined with agents, such as methotrexate, cyclosporine, FK506, rapamycin, mycophenolate mofetil, leflunomide, NSAIDs, for example, ibuprofen, corticosteroids such as prednisolone, phosphodiesterase inhibitors, adenosine agonists, antithrombotic agents, complement inhibitors, adrenergic agents, agents which interfere with signaling by proinflammatory cytokines as described herein, IL-1b converting enzyme inhibitors (*e.g.*, Vx740), anti-P7s, PSGL, TACE inhibitors, T-cell signaling inhibitors such as kinase inhibitors, metalloproteinase inhibitors, sulfasalazine, azathloprine, 6-mercaptopurines, angiotensin converting enzyme inhibitors, soluble cytokine receptors and derivatives thereof, as described herein, and anti-inflammatory cytokines (*e.g.*, IL-4, IL-10, IL-13 and TGF).

[00158] Preferred examples of therapeutic agents for multiple sclerosis (e.g., relapsing-remitting multiple sclerosis, secondary-progressive multiple sclerosis, primary-progressive multiple sclerosis and progressive-relapsing multiple sclerosis) with which the antibodies of the invention can be combined include dimethyl fumarate (*e.g.*, BG-12; Biogen), interferon-beta, for example, IFN-beta-1a and IFN-beta-1b; COPAXONE®, corticosteroids, IL-1 inhibitors, TNF inhibitors, antibodies to CD40 ligand and CD80, IL-12 antagonists.

[00159] Nonlimiting examples of agents for treating or preventing inflammatory bowel disease (*e.g.*, Crohn's disease, ulcerative colitis) with which an

antibody, *e.g.*, bispecific antibody, of the invention can be combined include the following: budenoside; epidermal growth factor; corticosteroids; cyclosporine; sulfasalazine; aminosalicylates; 6-mercaptopurine; azathioprine; metronidazole; lipoxygenase inhibitors; mesalamine; olsalazine; balsalazide; antioxidants; thromboxane inhibitors; IL-1 receptor antagonists; anti-IL-1 monoclonal antibodies; anti-IL-6 monoclonal antibodies (*e.g.*, anti-IL-6 receptor antibodies and anti-IL-6 antibodies); growth factors; elastase inhibitors; pyridinyl-imidazole compounds; TNF antagonists as described herein; IL-4, IL-10, IL-13 and/or TGF.beta. cytokines or agonists thereof (*e.g.*, agonist antibodies); IL-11; glucuronide- or dextran-conjugated prodrugs of prednisolone, dexamethasone or budesonide; ICAM-1 antisense phosphorothioate oligodeoxynucleotides (ISIS 2302; Isis Pharmaceuticals, Inc.); soluble complement receptor 1 (TP10; T Cell Sciences, Inc.); slow-release mesalazine; methotrexate; antagonists of platelet activating factor (PAF); ciprofloxacin; and lignocaine.

[00160] Nonlimiting examples of agents for treating or preventing psoriasis with which an antibody, *e.g.*, bispecific antibody, of the invention can be combined include the following: corticosteroids; vitamin D_3 and analogs thereof; retinoiods (*e.g.*, soriatane); methotrexate; cyclosporine, 6-thioguanine; Accutane; hydrea; hydroxyurea; sulfasalazine; mycophenolate mofetil; azathioprine; tacrolimus; fumaric acid esters; biologics such as AMEVIVE®, ENBREL®, HUMIRA®, Raptiva and REMICADE®, Ustekinmab, and XP-828L; phototherapy; and photochemotherapy (*e.g.*, psoralen and ultraviolet phototherapy combined).

[00161] Nonlimiting examples of agents for treating or preventing inflammatory airway/respiratory disease (*e.g.*, chronic obstructive pulmonary disorder, asthma) with which an antibody, *e.g.*, bispecific antibody, of the invention can be combined include the following: beta2-adrenoceptor agonists (*e.g.*, salbutamol (albuterol USAN), levalbuterol, terbutaline, bitolterol); long-acting beta2-adrenoceptor agonists (*e.g.*, salmeterol, formoterol, bambuterol); adrenergic agonists (*e.g.*, inhaled epinephrine and ephedrine tablets); anticholinergic medications (*e.g.*, ipratropium bromide); combinations of inhaled steroids and long-acting bronchodilators (*e.g.*, fluticasone/salmeterol (ADVAIR® in the United States, and Seretide in the United Kingdom)) or. budesonide/formoterol (SYMBICORT®)); inhaled glucocorticoids (*e.g.*, ciclesonide, beclomethasone, budesonide, flunisolide, fluticasone, mometasone,

triamcinolone); leukotriene modifiers (*e.g.*, montelukast, zafirlukast, pranlukast, and zileuton); mast cell stabilizers (*e.g.*, cromoglicate (cromolyn), and nedocromil); antimuscarinics/anticholinergics (*e.g.*, ipratropium, oxitropium, tiotropium); methylxanthines (*e.g.*, theophylline, aminophylline); antihistamines; IgE blockers (*e.g.*, Omalizumab); M.sub.3 muscarinic antagonists (anticholinergics) (*e.g.*, ipratropium, tiotropium); cromones (*e.g.*, chromoglicate, nedocromil); zanthines (*e.g.*, theophylline); and TNF antagonists (*e.g.*, infliximab, adalimumab and etanercept).

[00162] In one embodiment, an antibody, *e.g.*, bispecific antibody, of the invention can be used in combination with one or more antibodies directed at other targets involved in regulating immune responses, *e.g.*, transplant rejection.

[00163] Nonlimiting examples of agents for treating or preventing immune responses with which an antibody, *e.g.*, bispecific antibody, of the invention can be combined include the following: antibodies against other cell surface molecules, including but not limited to CD25 (interleukin-2 receptor-a), CD11a (LFA-1), CD54 (ICAM-1), CD4, CD45, CD28/CTLA4 (CD80 (B7.1), *e.g.*, CTLA4 Ig -abatacept (ORENCIA®)), ICOSL, ICOS and/or CD86 (B7.2). In yet another embodiment, an antibody of the invention is used in combination with one or more general immunosuppressive agents, such as cyclosporin A or FK506.

[00164] In other embodiments, antibodies are used as vaccine adjuvants against autoimmune disorders, inflammatory diseases, etc. The combination of adjuvants for treatment of these types of disorders are suitable for use in combination with a wide variety of antigens from targeted self-antigens, *i.e.*, autoantigens, involved in autoimmunity, *e.g.*, myelin basic protein; inflammatory self-antigens, *e.g.*, amyloid peptide protein, or transplant antigens, *e.g.*, alloantigens. The antigen may comprise peptides or polypeptides derived from proteins, as well as fragments of any of the following: saccharides, proteins, polynucleotides or oligonucleotides, autoantigens, amyloid peptide protein, transplant antigens, allergens, or other macromolecular components. In some instances, more than one antigen is included in the antigenic composition.

[00165] For example, desirable vaccines for moderating responses to allergens in a vertebrate host, which contain the adjuvant combinations of this invention, include those containing an allergen or fragment thereof. Examples of such allergens are

described in U.S. Patent No. 5,830,877 and PCT Publication No. WO 99/51259, which are hereby incorporated by reference in their entireties, and include pollen, insect venoms, animal dander, fungal spores and drugs (such as penicillin). The vaccines interfere with the production of IgE antibodies, a known cause of allergic reactions. In another example, desirable vaccines for preventing or treating disease characterized by amyloid deposition in a vertebrate host, which contain the adjuvant combinations of this invention, include those containing portions of amyloid peptide protein (APP). This disease is referred to variously as Alzheimer's disease, amyloidosis or amyloidogenic disease. Thus, the vaccines of this invention include the adjuvant combinations of this invention plus Aβ peptide, as well as fragments of Aβ peptide and antibodies to Aβ peptide or fragments thereof.

[00166] In another embodiment, pharmaceutical compositions may be supplied as a kit comprising a container that comprises an antibody, bispecific antibody or antigen-binding fragment of the invention. Antibodies, *e.g.*, bispecific antibodies, of the invention can be provided in the form of an injectable solution for single or multiple doses, or as a sterile powder that will be reconstituted before injection. Alternatively, such a kit can include a dry-powder disperser, liquid aerosol generator, or nebulizer for administration of the antibody, *e.g.*, bispecific antibody. Such a kit may further comprise written information on indications and usage of the pharmaceutical composition. Moreover, such information may include a statement that the antibody composition is contraindicated in patients with known hypersensitivity to IL-17 and IL-23.

[00167] In a further embodiment, the invention provides an article of manufacture, comprising: (a) a composition of matter comprising an antibody, bispecific antibody or antigen-binding fragment as described herein; (b) a container containing said composition; and (c) a label affixed to said container, or a package insert included in said container referring to the use of said antibody in the treatment of an immune related disease.

[00168] In another aspect, the composition comprises a further active ingredient, which may, for example, be a further antibody or an anti-inflammatory, cytotoxic or chemotherapeutic agent. Preferably, the composition is sterile.

[00169] The antibodies, bispecific antibodies and antigen-binding fragments as described herein are also useful to prepare medicines and medicaments for the treatment

of immune-related and inflammatory diseases, including for example, multiple sclerosis (MS) (e.g., relapsing-remitting multiple sclerosis, secondary-progressive multiple sclerosis, primary-progressive multiple sclerosis and progressive-relapsing multiple sclerosis), irritable bowel syndrome (IBS), inflammatory bowel disease (IBD) such as ulcerative colitis and Crohn's disease, atopic dermatitis, contact dermatitis, systemic sclerosis, systemic lupus erythematosus (SLE), antineutrophil cytoplasmic antibodies (ANCA)-associated vasculitis (AAV), giant cell arteritis, multiple sclerosis (MS), colitis, endotoxemia, arthritis, rheumatoid arthritis (RA), osteoarthritis, Sjögren's syndrome, psoriasis, psoriatic arthritis, adult respiratory disease (ARD), septic shock, multiple organ failure, inflammatory lung injury such as idiopathic pulmonary fibrosis, asthma, chronic obstructive pulmonary disease (COPD), airway hyper-responsiveness, chronic bronchitis, allergic asthma, eczema, *Helicobacter pylori* infection, intraabdominal adhesions and/or abscesses as results of peritoneal inflammation (*e.g.*, from infection, injury, etc.), nephrotic syndrome, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome, organ allograft rejection, graft vs. host disease (GVHD), lupus nephritis, IgA nephropathy, diabetic kidney disease, minimal change disease (lipoid nephrosis), focal segmental glomerulosclerosis (FSGS), nephrogenic systemic fibrosis (NSF), nephrogenic fibrosing dermopathy, fibrosing cholestatic hepatitis, eosinophilic fasciitis (Shulman's syndrome), scleromyxedema (popular mucinosis), scleroderma, lichen sclerosusetatrophicus, POEMs syndrome (Crow-Fukase syndrome, Takatsuki disease or PEP syndrome), nephrotic syndrome, graft-versus-host-disease (GVHD), graft-versus-host-disease (GVHD) (from a transplant, such as blood, bone marrow, kidney, pancreas, liver, orthotopic liver, lung, heart, intestine, small intestine, large intestine, thymus, allogeneic stem cell, reduced-intensity allogeneic, bone, tendon, cornea, skin, heart valves, veins, arteries, blood vessels, stomach and testis), lytic bone disease (*e.g.*, multiple myeloma-induced lytice bone disease), cystic fibrosis, age-related mascular degeneration (AMD; *e.g.*, wet AMD and dry AMD), liver fibrosis, pulmonary fibrosis, atherosclerosis, cardiac ischemia/reperfusion injury, heart failure, myocarditis, cardiac fibrosis, adverse myocardial remodeling, transplant rejection, streptococcal cell wall (SCW)-induced arthritis, gingivitis/periodontitis, herpetic stromal keratitis, gluten-sensitive enteropathy restenosis, Kawasaki disease, and immune mediated renal diseases. In a specific aspect, such medicines and medicaments comprise a therapeutically effective

amount of a bispecific antibody, antibody or antigen-binding fragment of the invention with a pharmaceutically acceptable carrier. In an embodiment, the admixture is sterile.

[00170] The complete disclosure of all patents, patent applications, and publications, and electronically available material (*e.g.*, GENBANK® amino acid and nucleotide sequence submissions) cited herein are incorporated by reference. The foregoing detailed description and examples have been given for clarity of understanding only. No unnecessary limitations are to be understood therefrom. The invention is not limited to the exact details shown and described, for variations obvious to one skilled in the art will be included within the invention defined by the claims.

[00171] The invention is further illustrated by the following non-limiting examples.

Example 1

Humanization of a Murine Anti-Human IL-17A/F Dual Specific Antibody

Selection of Hybridoma Clones and Variable Region Identification

[00172] Recombinant human proteins IL-17A, IL-17A/F, and IL-17F were produced using an HEK293 transient expression system at ZymoGenetics Inc., a Bristol-Myers Squibb Company (Seattle, WA, USA). BALB/c mice (Charles River Laboratories, Wilmington, MA) were immunized and boosted with recombinant human IL-17F conjugated to BSA followed by immunizations with recombinant human IL-17A conjugated to BSA. The mice with sera containing the highest anti-IL-17F and anti-IL-17A antibody binding activity were given a final pre-fusion boost of IL-17F. Four days later, the splenocytes and lymph node cells were fused with Ag8.653 myeloma cells to generate antibody producing hybridomas. Hybridoma culture supernatants were screened for IL-17F and IL-17A binding by plate based ELISA and IL-17F and IL-17A neutralization in the IL-17A/F cell-based assay. Hybridoma cells corresponding to the supernatant sample that bound and neutralized both IL-17F and IL-17A were cloned in order to isolate a monoclonal hybridoma, 339.15.3.5 (designated as 339.15) producing the neutralizing monoclonal antibody of interest. Hybridoma 339.15 was isotyped using the ISOSTRIP® Mouse Monoclonal Antibody Isotyping Kit (Roche, Indianapolis, IN, USA)

and RNA was isolated using the QIAGEN® RNeasy kit (Qiagen, Valencia, CA, USA). Variable regions were cloned using the SMART RACE cDNA Amplification Kit (Clontech, Mountain View, CA, USA), utilizing 5′ RACE technology and gene specific 3′ primers designed to mouse constant region sequences. Heavy and light variable region sequences were cloned using the TOPO® TA Cloning Kit for Sequencing (Invitrogen, Carlsbad, CA, USA). Gene sequences were verified by comparing the sequence to the N-terminal amino acid sequencing performed on antibody purified from hybridoma 339.15.

[00173] Variable region sequences were cloned from 339.15.3.5, 339.15.5.3 and 339.15.3.6 and were shown to contain the exact same variable region sequences. The sequence from 339.15.3.5 was used for subsequent humanization, and the 339.15.3.6 hybridoma clone was deposited on November 7, 2006, with the American Type Tissue Culture Collection (ATCC, 10801 University Blvd, Manassas, VA 20110-2209) patent depository as original deposits under the Budapest Treaty and was given ATCC® Patent Deposit Designation PTA-7988. Hybridoma clone 339.15.3.6 (ATCC® Patent Deposit Designation PTA-7988) and 339.15.5.3 (ATCC Patent Deposit Designation PTA-7987) are also disclosed, for example, in U.S. Patent Nos. 7,790,163, 7,910,703 and 8,333,968.

Molecular Modeling of Chimeric and Humanized Anti-Human IL-17A/F Variable Region Sequences

[00174] All variable region models were constructed and viewed using the MOE Software Suite, Version 2008 (Chemical Computing Group, Montreal, Canada).

Anti-Human IL-17A/F Humanized Antibody Design

[00175] Murine complementarity determining regions (CDR) were grafted onto human germline framework sequences. The sequences were compared to germline amino acid sequences in V-Base (MRC, Center for Protein Engineering, UK). One germline gene was chosen for the variable heavy region, VH1-03. Several germline genes were chosen for the variable light region; VKVI A26, VKI A20, VKVI A14, VKIII L6, and VKI L14. The VKVI germline gene family showed the highest homology to the murine sequence, however, being an under represented germline family in the human antibody repertoire, other germline families with high homology were also considered. Murine

Kabat defined CDR regions were grafted on human Kabat defined framework regions for both the heavy and light chains.

Construction, Expression, and Purification of Humanized Anti-IL-17A/F Antibodies

[00176] Humanized variable region sequences were ordered from GeneART, Inc. (GeneART, Inc. Burlingame, CA, USA). Humanized and murine variable region sequences were fused to human kappa constant region (SEQ ID NO:10) or IgG1.1 (SEQ ID NO:11), an effector minus variant of wild-type IgG1 that has mutations resulting in the reduction of Fc γ receptor I binding and ability to fix complement (Gross et al., *Immunity*, 15:289-302 (2001)), utilizing overlap PCR (Horton et al., *Gene*, 77:61-68 (1989)) and/or restriction enzyme cloning into pTT5, an HEK293-6E transient expression vector (NCR Biotechnology Research Institute, Ottawa, ON, CAN). All constructs were expressed using the mod2610 (ATGCGGCGGAGAGGCTGGTCCTGGATCTTCCTGTTTCTGCTGAGCGGAACAG CCGGCGTGCTGAGC, SEQ ID NO:30) signal sequence, although any nucleic acid sequence that encodes the amino acid sequence MRRRGWSWIFLFLLSGTAGVLS (SEQ ID NO:31) may be used. The HEK293-6E suspension cells were transfected with expression constructs using polyethylenimine reagent and cultivated in F17 medium (Invitrogen, Grand Island, NY, USA) with the addition of 5 mM L-glutamine and 25 μg/mL G418. After 24 hours, 1/40th volume of 20% Tryptone NI (Organotechnie SAS, La Courneuve, FR) was added. At approximately 120 hours post transfection, conditioned media was harvested and passed through a 0.2 μm filter. Protein was purified from the filtered conditioned media using a combination of Mab Select SuRe Affinity Chromatography (GE Healthcare, Piscataway, NJ, USA) and SUPERDEX® 200 Size Exclusion Chromatography (GE Healthcare, Piscataway, NJ, USA). Content was estimated by absorbance at UV-A280nm and quality evaluated by analytical size exclusion high performance liquid chromatography, SDS PAGE, and western blot.

Anti-Human IL-17A/F Humanization Panel Bioassay Activity; NIH/3T3/KZ170 NF-κB Luciferase Reporter Assay to Measure Human IL-17A, IL-17A/F, and IL-17F Activity by NF-κB Induction

[00177] A murine fibroblast cell line (NIH/3T3, ATCC® #CRL-1658) was stably transfected with an NF-κB luciferase reporter designated KZ170 and cloned out. NIH/3T3/KZ170 clone 1 cells were seeded at 10,000 cells/well in plating media (DMEM plus 3% FBS, 1mM sodium pyruvate, 2mM L-glutamine (HyClone Laboratories, South Logan, UT)) in 96-well, white opaque, solid bottom luciferase plates (Corning Incorporated, Corning, NY) and incubated overnight at 37 °C, 5% CO_2. The following day serial dilutions of recombinant human IL-17A, IL-17A/F, or IL-17F (ZymoGenetics, A Bristol-Myers Squibb Company, Seattle, WA, USA) were made up in assay media (DMEM plus 0.5% BSA, 1mM sodium pyruvate, 2mM L-glutamine, 10mM HEPES (HyClone Laboratories, South Logan, UT)) and added to the plates containing the cells and incubated together at 37 °C, 5% CO_2 for 4 hours. Additionally the assay was used to measure neutralization of human IL-17A, IL-17A/F and IL-17F activity. A half maximal concentration (EC_{50}, effective concentration at 50 percent) of human IL-17A, IL-17A/F or IL-17F was combined with serial dilutions of anti-human IL-17A/F antibodies described herein in assay media and added to the plates containing the cells and incubated together at 37 °C, 5% CO_2 for 4 hours. Following incubation the media was removed and cells lysed before being read on the Berthold Centro XS^3 Luminometer (Berthold Technologies, Wildbad, Germany) using flash substrate (Promega Corporation, Madison, WI) according to manufacturer's instructions. Increases in mean fluorescence intensity (via activation of the NF-κB luciferase reporter) were indicative of a human IL-17A, IL-17A/F, IL-17F receptor-ligand interaction. Decreases in mean fluorescence intensity were indicative of neutralization of the human IL-17A, IL-17A/F, IL-17F receptor-ligand interaction. IC_{50} (inhibitory concentration at 50 percent) values were calculated using GraphPad Prism 4 software (GraphPad Software, Inc., San Diego CA) for each anti-human IL-17A/F antibody.

Anti-Human IL-17A/F Humanization CDR Grafted and Chimeric Panel Bioassay Activity; NIH/3T3/KZ170 NF-κB Luciferase Reporter Assay Results

[00178] IL-17A, IL-17A/F and IL-17F induce activation of the NF-κB luciferase reporter in a dose dependent manner with an EC_{50} concentration determined to be 0.15nM for IL-17A, 0.50 nM for IL-17A/F and 0.50 nM for IL-17F. Tables 1 and 2 present example IC_{50} data for the anti-IL-17A/F antibodies described herein.

Table 1

Name	**VH** MVC# SEQ ID NO:	**VL** MVC# SEQ ID NO:	**IL-17A** **IC_{50} nM**	**IL-17A/F** **IC_{50} nM**	**IL-17F** **IC_{50} nM**
Chimeric 339.15	**Ms VH VR370** MVC823 SEQ ID NO:32	**Ms VL VR371** MVC824 SEQ ID NO:34	11	0.30	0.26
339-07	**VR370e3 VH1-03** MVC840 SEQ ID NO:36	**Ms VL** MVC824 SEQ ID NO:34	>600	31	5.5
339-08	**Ms VH VR370** MVC823 SEQ ID NO:32	**VR371e3 VKVI A26** MVC841 SEQ ID NO:38	1.5	0.96	0.81
339-02	**Ms VH VR370** MVC823 SEQ ID NO:32	**VR371e2 VKI A20** MVC717 SEQ ID NO:40	1.1	0.80	0.79
339-01	**Ms VH VR370** MVC823 SEQ ID NO:32	**VR371e1 VKVI A14** MVC716 SEQ ID NO:42	9.6	0.26	0.20
339-09	**Ms VH VR370** MVC823 SEQ ID NO:32	**VR371e4 VKIII L6** MVC842 SEQ ID NO:44	7.2	0.20	0.21
339-32	**Ms VH VR370** MVC823 SEQ ID NO:32	**VR371e10 VKI L14** MVC856 SEQ ID NO:46	7.0	1.5	0.35

Name	**VH** MVC# SEQ ID NO:	**VL** MVC# SEQ ID NO:	**IL-17A** **IC_{50} nM**	**IL-17A/F** **IC_{50} nM**	**IL-17F** **IC_{50} nM**
339-33	**VR370e3 VH1-03** MVC840 SEQ ID NO:36	**VR371e3 VKVI A26** MVC841 SEQ ID NO:38	>600	9.7	1.7
339-126	**VR370e3 VH1-03** MVC840 SEQ ID NO:36	**VR371e2 VKI A20** MVC717 SEQ ID NO:40	>600	24	1.6

Anti-Human IL-17A/F Humanization CDR Grafted with Framework Back Mutation Panel Bioassay Activity Table: NIH/3T3/KZ170 NF-κB Luciferase Reporter Assay Results

Table 2

Name	**VH** MVC# SEQ ID NO:	**VL** MVC# SEQ ID NO:	**IL-17A** **IC_{50} nM**	**IL-17A/F** **IC_{50} nM**	**IL-17F** **IC_{50} nM**
339-35	**VR370e4 NKSH** MVC850 SEQ ID NO:48	**VR371e3 VKVI A26** MVC841 SEQ ID NO:38	>600	2.4	0.64
339-71	**VR370e41 KALV** MVC869 SEQ ID NO:50	**VR371e3 VKVI A26** MVC841 SEQ ID NO:38	16	0.37	0.20
339-37	**VR370e6 SF** MVC852 SEQ ID NO:52	**VR371e3 VKVI A26** MVC841 SEQ ID NO:38	>600	20	3.5

Name	VH MVC# SEQ ID NO:	VL MVC# SEQ ID NO:	IL-17A IC_{50} nM	IL-17A/F IC_{50} nM	IL-17F IC_{50} nM
339-38	**VR370e7 NKSH KALV** MVC853 SEQ ID NO:54	**VR371e3 VKVI A26** MVC841 SEQ ID NO:38	8.2	0.27	0.27
339-39	**VR370e8 NKSH KALV SF** MVC854 SEQ ID NO:56	**VR371e3 VKVI A26** MVC841 SEQ ID NO:38	7.6	0.23	0.25
339-127	**VR370e4 NKSH** MVC850 SEQ ID NO:48	**VR371e2 VKI A20** MVC717 SEQ ID NO:40	190	3.4	0.50
339-128	**VR370e41 KALV** MVC869 SEQ ID NO:50	**VR371e2 VKI A20** MVC717 SEQ ID NO:40	5.1	0.41	0.25
339-105	**VR370e6 SF** MVC852 SEQ ID NO:52	**VR371e2 VKI A20** MVC717 SEQ ID NO:40	>600	23	2.6
339-125	**VR370e7 NKSH KALV** MVC853 SEQ ID NO:54	**VR371e2 VKI A20** MVC717 SEQ ID NO:40	1.5	0.81	0.83
339-104	**VR370e8 NKSH KALV SF** MVC854 SEQ ID NO:56	**VR371e2 VKI A20** MVC717 SEQ ID NO:40	1.5	0.83	0.83
339-134	**VR370e96 NK KALV** MVC978 SEQ ID NO:58	**VR371e2 VKI A20** MVC717 SEQ ID NO:40	1.4	0.26	0.24

Anti-Human IL-17A/F Humanization Panel Biacore Activity; Measurement of Binding Affinities to Human IL-17A, IL-17A/F, and IL-17F Via Surface Plasmon Resonance (Biacore)

[00179] Humanized anti-human IL-17A/F monoclonal antibodies were evaluated for their binding affinity to human IL-17A, human IL-17A/F, and human IL-17F using surface plasmon resonance.

[00180] Kinetic rate constants and equilibrium dissociation constants were measured for the interaction of the humanized anti-human IL-17A/F antibodies with human IL-17A, IL-17A/F, and IL-17F via surface plasmon resonance. The association rate constant (k_a ($M^{-1}s^{-1}$)) is a value that reflects the rate of the antigen-antibody complex formation. The dissociation rate constant (k_d (s^{-1})) is a value that reflects the stability of this complex. By dividing the dissociation rate constant by the association rate constant (k_d/k_a) the equilibrium dissociation constant (K_D (M)) is obtained. This value describes the binding affinity of the interaction. Antibodies with similar K_D can have widely variable association and dissociation rate constants. Consequently, measuring both the k_a and k_d of antibodies helps to more uniquely describe the affinity of the antibody-antigen interaction.

[00181] Binding kinetics and affinity studies were performed on a BIACORE® T100 system (GE Healthcare, Piscataway, NJ). Methods for the BIACORE® T100 were programmed using BIACORE® T100 Control Software, v 2.0. For these experiments, the humanized anti-human IL-17A/F antibodies were captured onto a CM4 sensor chip via either goat anti-human IgG Fc-gamma antibody (Jackson ImmunoResearch, West Grove, PA) or goat anti-mouse IgG Fc-gamma antibody (Jackson ImmunoResearch). Binding experiments with the IL-17 molecules were performed at 25 °C in a buffer of 10 mM HEPES, 150 mM NaCl, 3 mM EDTA, 0.05% Surfactant P20 (GE Healthcare), 1 mg/mL bovine serum albumin, pH 7.4.

[00182] The capture antibody, goat anti-human IgG Fc-gamma, was diluted to concentration of 20 μg/mL in 10 mM sodium acetate pH 5.0, and then covalently immobilized to all four flow cells of a CM4 sensor chip using amine coupling chemistry (EDC:NHS). After immobilization of the antibody, the remaining active sites on the flow cell were blocked with 1 M ethanolamine. A capture antibody density of approximately

5000 RU was obtained. The humanized anti-human IL-17A/F antibodies were captured onto flow cell 2, 3, or 4 of the CM4 chip at a density ranging from 60-150 RU. Capture of the test antibodies to the immobilized surface was performed at a flow rate of 10 μL/min. The BIACORE® instrument measures the mass of protein bound to the sensor chip surface, and thus, capture of the test antibody was verified for each cycle. Serial dilutions of human IL-17A, IL-17A/F, or IL-17F (ZymoGenetics, A Bristol-Myers, Squibb Company, Seattle, WA, USA) were prepared from 100 nM – 0.032 nM (1:5 serial dilutions). The serial dilutions were injected over the surface and allowed to specifically bind to the test antibody captured on the sensor chip. Duplicate injections of each antigen concentration were performed with an association time of 7 minutes and dissociation time of 15 minutes. Kinetic binding studies were performed with a flow rate of 50 μL/min. In between cycles, the flow cell was washed with 20 mM hydrochloric acid to regenerate the surface. This wash step removed both the captured test antibody and any bound antigen from the immobilized antibody surface. The test antibody was subsequently captured again in the next cycle.

[00183] Data was compiled using the BIACORE® T100 Evaluation software (version 2.0). Data was processed by subtracting reference flow cell and blank injections. Baseline stability was assessed to ensure that the regeneration step provided a consistent binding surface throughout the sequence of injections. Duplicate injection curves were checked for reproducibility. Based on the binding of the bivalent IL-17 molecules to a bivalent antibody, the bivalent analyte binding interaction model was determined to be appropriate for interactions with the IL-17 molecules. The bivalent analyte model is previously described in West, A.P. et al., *Biochemistry*, 39:9698-9708 (2000); and West, A.P. et al., *J. Mol. Biol.*, 313:385-397 (2001). An affinity constant (K_{D1}) under the bivalent analyte model may be calculated from the ratio of rate constants (k_{d1}/k_{a1}) as determined by surface plasmon resonance. The reference subtracted binding curves were globally fit to the appropriate binding model with a multiple Rmax and with the RI set to zero. The data fit well to the binding models with good agreement between the experimental and theoretical binding curves. The chi^2 and standard errors associated the fits were low. There was no trending in the residuals.

Anti-Human IL-17A/F Humanization Panel Biacore Activity

[00184] The results of the binding experiments with human IL-17A, IL-17A/F, and IL-17F are in Tables 3, 4, and 5 respectively.

Anti-Human IL-17A/F Humanized Antibodies Binding Affinity for IL-17A

Table 3

Name	**k_{a1} ($M^{-1}s^{-1}$)**	**k_{d1} (s^{-1})**	**K_{D1} (M)**
Mouse 339.15	4.E+06	7.E-03	2.E-09
339-02 SEQ ID NO:32 SEQ ID NO:40	2.E+06	6.E-03	3.E-09
Chimeric 339.15 SEQ ID NO:32 SEQ ID NO:34	3.E+06	1.E-02	4.E-09
339-38 SEQ ID NO:54 SEQ ID NO:38	4.E+06	5.E-03	1.E-9
339-125 SEQ ID NO:54 SEQ ID NO:40	2.E+06	3.E-03	1.E-9
339-134 SEQ ID NO:58 SEQ ID NO:40	2.E+06	3.E-03	1.E-9

Anti-IL-17A/F Humanized Antibodies Binding Affinity for IL-17A/F

Table 4

Name	**k_{a1} ($M^{-1}s^{-1}$)**	**k_{d1} (s^{-1})**	**K_{D1} (M)**
Mouse 339.15	1.E+06	2.E-04	2.E-10

Name	k_{a1} ($M^{-1}s^{-1}$)	k_{d1} (s^{-1})	K_{D1} (M)
339-02 SEQ ID NO:32 SEQ ID NO:40	Not Determined		
Chimeric 339.15 SEQ ID NO:32 SEQ ID NO:33	Not Determined		
339-38 SEQ ID NO:54 SEQ ID NO:40	1.E+06	4.E-04	4.E-10
339-125 SEQ ID NO:54 SEQ ID NO:40	2.E+06	6.E-04	3.E-10
339-134 SEQ ID NO:58 SEQ ID NO:40	2.E+06	5.E-04	2.E-10

Anti-IL-17A/F Humanized Antibodies Binding Affinity for IL-17F

Table 5

Name	k_{a1} ($M^{-1}s^{-1}$)	k_{d1} (s^{-1})	K_{D1} (M)
Mouse 339.15	2.E+06	1.E-04	5.E-11
339-02 SEQ ID NO:32 SEQ ID NO:40	1.E+06	5.E-04	4E-10
Chimeric 339.15 SEQ ID NO:32 SEQ ID NO:34	1.E+06	5.E-04	4E-10

339-38 SEQ ID NO:54 SEQ ID NO:40	2.E+06	6.E-04	3.E-10
339-125 SEQ ID NO:54 SEQ ID NO:40	2.E+06	2.E-04	1.E-10
339-134 SEQ ID NO:58 SEQ ID NO:40	2.E+06	2.E-04	1.E-10

Example 2

7B7 Antibody Selection and Hybridoma Generation

Epitope binning approach by surface plasmon resonance technology (using Biacore) to group antibodies based on their binding and blocking properties as shown in Fig. 11.

[00185] Antibodies were grouped and selected based on their ability to:

1. Specifically bind p19 subdomain only of IL-23;
2. Specifically block only IL-23 receptor (IL-23R) and not block IL-12 receptor (IL-12R); and
3. Not compete with any antibody that could bind specifically to p40 subdomain of IL-23.

[00186] Materials such as antibodies with previously known selectivity for p19 or p40 subdomains of IL-23 and IL-23R or IL-12R were all chosen to be coated on a BIACORE® CM5 chip. The coating density varied between 500 to 8000 Resonance Units (RUs). Antibodies that were to be binned were titrated serially (1:2 or 1:3) to 8 concentrations, from starting concentrations that ranged from 10 to 100 μg/mL in a 96-well ELISA plate. To each of the well, 10nM of IL-23 antigen was added. The antibodies on plate were allowed to form a complex with antigen and reach equilibrium overnight at 4 °C. The complexes were injected over the CM5 chip at a flow rate of 20 μL/min for two minutes. The signal, as binding resonance units (RUs) at end of two

minutes was noted. The antibody-antigen complex was able complete or not compete with the material that was coated on the chip. If the antibody in complex with antigen was able to compete with the material on chip, with increasing concentration of the antibody, the binding RU decreased and if it did not compete, the binding RU increased. Based on this observation, all anti-IL23 antibodies were binned according to their binding selectivities and competing abilities.

Transgenic HCo12 J/K HUMAB® mice from the Medarex colonies in Milpitas, CA were immunized with recombinant human IL-23-his in RIBI adjuvant.

[00187] Sera from immunized mice were tested for expression of IL-23 specific antibodies by a modified indirect dual ELISA. Briefly, microtiter plates (COSTAR®, 96-well flat bottom, #9018) were coated with mouse anti-his protein at 2.5 µg/ml in PBS, 50 µl/well, incubated at 4 °C overnight, and then blocked with 1% BSA in PBS. HuIL-23 at 2.5µg/ml or HuIL-12 was added to plates for capture at 50 µl/well and incubated at room temperature for one hour. Plates were washed with PBS Tween, and dilutions of sera were added and incubated for 1 hour. The plates were washed with PBS-Tween and incubated with goat-anti-human gamma heavy chain conjugated with HRP (Jackson ImmunoResearch Cat. 109-036-098) for 1 hour. After 3x washing, the plates were developed with ABTS (Moss, CAT #ABTS-1000) substrate and OD's analyzed at 415nm. Data were analyzed and expressed as serum titer which is defined as the highest dilution of serum which results in an antigen positive signal of at least twice background. Mouse 215094 was selected for hybridoma generation based upon relatively high titers on IL-23 with lower cross reactivity to IL-12 when compared to other mice in the cohort (see Table 6).

Table 6. Serum Titers

Mouse ID	Genotype	Hu IL23-his	Hu IL12-his
215088	HCo12:01[J/K]	>109, 350	>109, 350
215090	HCo12:01[J/K]	>109, 350	>109, 350
215092	HCo12:01[J/K]	>109, 350	>109, 350
215094	HCo12:01[J/K]	>109, 350	12, 150
215096	HCo12:01[J/K]	>109, 350	36, 450

Mouse ID	Genotype	Hu IL23-his	Hu IL12-his
215098	HCo12:01[J/K]	36, 450	1, 350
215089	HCo12:01[J/K]	>109, 350	1, 350
215091	HCo12:01[J/K]	>109, 350	>109, 350
215093	HCo12:01[J/K]	>109, 350	4,050
215095	HCo12:01[J/K]	>109, 350	>109, 350
215097	HCo12:01[J/K]	>109, 350	>109, 350
215099	HCo12:01[J/K]	12150	12, 150

[00188] The genotype of Mouse 215094 is provided below in Table 7.

Table 7. Mouse 215094 Genotype

Mouse ID	Sex	Date of birth	Genotype
215094	M	10/11/2009	HCo12(15087)+^;JHD++;JKD++;KCo5(9272)+^;

[00189] The spleen from mouse 215094 was used to generate hybridomas with mouse myeloma cells (ATCC CRL-1580) by electric field based electrofusion using a CytoPulse large chamber cell fusion electroporation device in a procedure designated fusion 2378.

[00190] Conditioned media from the resulting hybridomas were initially screened for expression of human IgG γ/κ in a standard automated assay followed by ELISA for IL-23 binding with a counter screen ELISA on IL-12 to identify specific clones as previously described. Hybridoma selection criteria for testing were samples with OD's greater than 1.5 on huIL23 plates and less than 0.15 on huIL12.

[00191] Fusion 2378 generated total of 827 human IgG positive hybridomas of which, 128 were IL-23 specific. Hybridoma 7B7 was selected for further testing based on its strong binding to IL-23 and lack of cross reactivity to IL-12, when compared to anti-p19 and anti-p40 positive control antibodies; an example of hybridomas, including 7B7 selected by ELISA is given in Fig. 7. The isotype of subclone 7B7.D4 was confirmed as human IgG1, kappa by ELISA.

[00192] Hybridoma conditioned medium from all IL-23p-19 specific MAbs were screened for IL-23 neutralizing activity in a cell-based assay. Kit225, a human T-

cell line established from a patient with T-cell chronic lymphocytic leukemia, have been shown to respond to IL-23 with dose dependant STAT3 phosphorylation (pSTAT3). Human IL-23 at EC_{50} with and without the addition of hybridoma conditioned medium or a control neutralizing anti-p19 antibody was used to stimulate cells for 15 minutes. Cells were lysed and inhibition of IL-23 dependant STAT3 phosphorylation was assessed by ELISA (Cell Signaling Technology, PATHSCAN® Cat #7300) where reduced O.D. indicates reduced levels of pSTAT3. Hybridoma 7B7 was selected for sub-cloning and further characterization based upon the potent neutralization of IL-23 signaling observed in the Kit225 assay and as shown in Fig. 8.

[00193] Using assays similar to those described above, selective binding of IL-23 and neutralization of IL-23 signaling was demonstrated for the 7B7 subclone 1413.2378.7B7.D4.H2 which was subsequently submitted for sequencing (IL-23p19 7B7 heavy chain variable domain is shown in SEQ ID NO:7, and the light chain variable domain is shown in SEQ ID NO:9).

Example 3

Generation of Anti-Human IL-23/IL-17A/F Bispecific Antibodies

Construction and Expression of Mammalian Anti-Human IL-23/IL-17A/F Bispecific Molecules

[00194] Partial or whole genes were synthesized at GeneART, Inc. (GeneART, Inc. Burlingame, CA, USA) or GenScript (GenScript, Piscataway, NJ, USA) and inserted into pTT5, an HEK293-6E transient expression vector (NCR Biotechnology Research Institute, Ottawa, ON, Canada) via restriction enzyme cloning. MVC1059 (SEQ ID NO:62), and MVC1061 (SEQ ID NO:60) were ordered as complete constructs from GenScript (GenScript, Piscataway, NJ, USA). All constructs were expressed using the mod2610 (SEQ ID NO:30) signal sequence. The biAbFabL is a bispecific antibody which contains a whole antibody with a C-terminal Fab unit of the second arm of the bispecific attached via a linker (*e.g.*, 10mer G_4S) and utilizes a common light chain (see Fig. 2). The taFab is a bispecific antibody which contains a whole antibody with an N-terminal Fab unit of the second arm of the bispecific attached via a linker, such as $(Gly_4Ser_1)_x$, wherein x is 1, 2 or 3, and the linker of SEQ ID NO:12. As with the heavy

chain portion, there are two light chains for each arm of the bispecific attached via a linker, such as $(Gly_4Ser_1)_x$, wherein x is 1, 2 or 3, and the linker of SEQ ID NO:12 (see Fig. 3). The Heterodimeric Fc is a bispecific antibody that resembles a traditional antibody, however, contains two different heavy chains which associate through an electrostatic complementarity association in the C_{H3} region. The Heterodimeric Fc utilizes a common light chain (see Fig. 4). Heavy chain and light chain constant regions include, IgG1.1 (SEQ ID NO:11, which may be encoded by SEQ ID NO:82), IgG1.1f without a C-terminal Lysine (SEQ ID NO:127), IgG1.1f with a C-terminal Lysine (SEQ ID NO:128), human kappa constant region (SEQ ID NO:10, which may be encoded by SEQ ID NO:83), or IgG4.1 (SEQ ID NO:8). The IgG4 heavy chain constant domain may be a variant of wild-type IgG4 that has a mutation in the hinge region, S228P (EU index numbering system) or S241P (Kabat numbering system). Changing the serine at 241 (Kabat) to proline (found at that position in IgG1 and IgG2) in a mouse/human chimeric heavy chain leads to the production of a homogeneous antibody and abolishes the heterogeneity. Further, the variant IgG4 has significantly extended serum half-life and shows an improved tissue distribution compared to the original chimeric IgG4. Angal et al., *Molecular Immunology*, 30(1):105-108 (1993); Schuurman et al., *Molecular Immunology*, 38:1-8 (2001); Lewis et al., *Molecular Immunology*, 46:3488-3494 (2009).

[00195] Transformation of electrocompetent *E. coli* host cells (DH10B) was performed using 1 µl of the yeast DNA preparation and 20 µl of *E. coli* cells. The cells were electropulsed at 2.0 kV, 25 µF, and 400 ohms. Following electroporation, 600 µl SOC (2% BACTO® Tryptone (Difco, Detroit, MI), 0.5% yeast extract (Difco), 10 mM NaCl, 2.5 mM KCl, 10 mM $MgCl_2$, 10 mM $MgSO_4$, 20 mM glucose) was added and the cells were plated in 50 µl and 550 µl aliquots on two LB AMP plates (LB broth (Lennox), 1.8% BACTO® Agar (Difco), 100 mg/L Ampicillin).

[00196] Five colonies from each construct were subjected to sequence analysis. One clone containing the correct sequence was selected. DNA sequencing was performed using ABI PRISM® BigDye Terminator v3.1 Cycle Sequencing Kit (Applied Biosystems, Foster City, CA). Sequencing reactions were purified using Edge BioSystems Preforma Centriflex Gel Filtration Cartridges (Gaithersburg, MD) and run on an Applied Biosystems 3730 DNA Analyzer (Applied Biosystems, Foster City, CA). Resultant sequence data was assembled and edited using SEQUENCHER® v4.6 software

(GeneCodes Corporation, Ann Arbor, MI.). One clone containing the correct sequence was selected and large-scale plasmid DNA was isolated using a commercially available kit (QIAGEN® Plasmid Mega Kit, Qiagen, Valencia, CA) according to manufacturer's instructions.

[00197] The HEK293-6E suspension cells were transfected with expression constructs using polyethylenimine reagent and cultivated in F17 medium (Invitrogen, Grand Island, NY, USA) with the addition of 5 mM L-glutamine and 25 μg/mL G418. After 24 hours, 1/40th volume of 20% Tryptone NI (Organotechnie SAS, La Courneuve, FR) was added. At approximately 120 hours post transfection, conditioned media was harvested and passed through a 0.2 μm filter. Protein was purified from the filtered conditioned media using a combination of Mab Select SuRe Affinity Chromatography (GE Healthcare, Piscataway, NJ, USA) and SUPERDEX® 200 Size Exclusion Chromatography (GE Healthcare, Piscataway, NJ, USA). Content was estimated by absorbance at UV-A280nm and quality evaluated by analytical size exclusion high performance liquid chromatography, SDS PAGE, and western blot.

Anti-Human IL-23/IL-17A/F Bispecific Antibody Composition

[00198] A whole antibody and its modular components is depicted in Fig. 1. The biAbFabL format is depicted in Fig. 2. The taFab format is depicted in Fig. 3. The heterodimeric Fc format is depicted in Fig. 4. The VCVFc format is depicted in Fig. 5. The VCDFc format is depicted in Fig. 6.

Anti-Human IL-23/IL-17A/F Bispecific Antibodies Bioassay Activity; NIH/3T3/KZ170 NF-κB Luciferase Reporter Assay to Measure Human IL-17A, IL-17A/F, and IL-17F Activity by NF-κB Induction

[00199] The material and methods for this assay are described in Example 1 hereinabove.

Anti-Human IL-23/IL-17A/F Bispecific Antibodies Bioassay Activity; Baf3/huIL-23Rα/huIL-12Rβ1 Transfectants Phospho-STAT3 Assay to Measure Human IL-23 Activity by Phospho-STAT3 Induction

[00200] A murine bone marrow derived cell line (Baf3) was stably transfected with human IL-23Rα and human IL-12Rβ1 and cloned. Baf3/huIL-23Rα/huIL-12Rβ1 clone 6 cells were washed three times with assay media (RPMI 1640 plus 10% fetal bovine serum, 2mM L-Glutamine, 1mM Sodium Pyruvate (HyClone Laboratories, South Logan, UT), and 2μM β-Mercaptoethanol (Sigma-Aldrich, St. Louis, MO)) before being plated out at 50,000 cells/well in 96-well, round-bottom tissue culture plates. Serial dilutions of recombinant human IL-23 (ZymoGenetics, A Bristol-Myers Squibb Company, Seattle WA, USA) were made up in assay media and added to the plates containing the cells and incubated together at 37 °C, 5% CO_2 for 15 minutes. Additionally the assay was also used to measure neutralization of IL-23 activity. A half maximal concentration (EC_{50}, effective concentration at 50 percent) of IL-23 was combined with serial dilutions of anti-human IL-23/IL-17A/F antibodies described herein and incubated together at 37 °C, 5% CO_2 for 15 minutes in assay media prior to addition to cells. Following pre-incubation, treatments were added to the plates containing the cells and incubated together at 37 °C, 5% CO_2 for 15 minutes. Following incubation, cells were washed with ice-cold wash buffer and put on ice to stop the reaction according to manufacturer's instructions (BIO-PLEX® Cell Lysis Kit, Bio-Rad Laboratories, Hercules, CA). Cells were then spun down at 2000 rpm at 4 °C for 5 minutes prior to dumping the media. Fifty μL/well lysis buffer was added to each well; lysates were pipetted up and down five times while on ice, then agitated on a plate shaker for 20 minutes at 300 rpm and 4 °C. Plates were centrifuged at 3200 rpm at 4 °C for 20 minutes. Supernatants were collected and transferred to a new micro titer plate for storage at -80 °C.

[00201] Capture beads (BIO-PLEX® Phospho-STAT3 Assay, Bio-Rad Laboratories) were combined with 50 μL of 1:1 diluted lysates and added to a 96-well filter plate according to manufacturer's instructions (BIO-PLEX® Phosphoprotein Detection Kit, Bio-Rad Laboratories). The aluminum foil-covered plate was incubated overnight at room temperature, with shaking at 300 rpm. The plate was transferred to a microtiter vacuum apparatus and washed three times with wash buffer. After addition of 25 μL/well detection antibody, the foil-covered plate was incubated at room temperature for 30 minutes with shaking at 300 rpm. The plate was filtered and washed three times with wash buffer. Streptavidin-PE (50 μL/well) was added, and the foil-covered plate

was incubated at room temperature for 15 minutes with shaking at 300 rpm. The plate was filtered and washed three times with bead resuspension buffer. After the final wash, beads were resuspended in 125 µL/well of bead suspension buffer, shaken for 30 seconds, and read on an array reader (BIO-PLEX® 100, Bio-Rad Laboratories) according to the manufacturer's instructions. Data was analyzed using analytical software (BIO-PLEX® Manager 4.1, Bio-Rad Laboratories). Increases in the level of the phosphorylated STAT3 transcription factor present in the lysates were indicative of an IL-23 receptor-ligand interaction. Decreases in the level of the phosphorylated STAT3 transcription factor present in the lysates were indicative of neutralization of the IL-23 receptor-ligand interaction. IC_{50} (inhibitory concentration at 50 percent) values were calculated using GraphPad Prism 4 software (GraphPad Software, Inc., San Diego CA) for each anti-human IL-23/IL-17A/F antibody.

Anti-Human IL-23/IL-17A/F Bispecific Antibody Bioassay Activity; NIH/3T3/KZ170 NF-κB Luciferase Reporter Assay and Baf3/huIL-23Rα/huIL-12Rβ1 Transfectants Phospho-STAT3 Assay Results

[00202] Human IL-17A, IL-17A/F and IL-17F induce activation of the NF-κB luciferase reporter in a dose dependent manner with an EC_{50} concentration determined to be 0.33nM for IL-17A, 1nM for IL-17A/F and 1nM for IL-17F and IL-23 induces STAT3 phosphorylation in a dose dependent manner with an EC_{50} concentration determined to be 0.02nM. The IC_{50} data for the anti-human IL-23/IL-17A/F bispecific antibodies is shown below in Table 8.

Anti-Human IL-23/17A/F Bispecific Antibody Table

Table 8

Name	**Heavy Chain** MVC# SEQ ID NO:	**Light Chain** MVC# SEQ ID NO:	**IL-17A IC_{50} nM**	**IL-17A/F IC_{50} nM**	**IL-17F IC_{50} nM**	**IL-23 IC_{50} nM**

Name	**Heavy Chain** MVC# SEQ ID NO:	**Light Chain** MVC# SEQ ID NO:	**IL-17A IC_{50} nM**	**IL-17A/F IC_{50} nM**	**IL-17F IC_{50} nM**	**IL-23 IC_{50} nM**
339-134 mAb IgG1.1	MVC978 SEQ ID NO:64	MVC717 SEQ ID NO:66	1.3	0.27	0.24	Not Done
IL23.6 (7B7) mAb IgG1.1	MVC1003 SEQ ID NO:68	MVC1002 SEQ ID NO:17*	Not Done	Not Done	Not Done	0.014
23/17bAb1 IgG1.1	MVC1006 SEQ ID NO:28*	MVC1002 SEQ ID NO:17*	0.064	0.76	0.96	0.015
23/17bAb2 IgG1.1	MVC1007 SEQ ID NO:18*	MVC1002 SEQ ID NO:17*	0.052	0.43	0.44	0.041
23/17bAb3 IgG4.1	MVC1036 SEQ ID NO:74	MVC1002 SEQ ID NO:17*	0.022	0.20	0.23	0.012
23/17bAb4 IgG4.1	MVC1037 SEQ ID NO:29*	MVC1002 SEQ ID NO:17*	0.035	0.18	0.87	0.048
23/17taFab1 IgG1.1	MVC1008 SEQ ID NO:76	MVC 1009 SEQ ID NO:78	1.5	3.9	2.3	0.018

Name	**Heavy Chain** MVC# SEQ ID NO:	**Light Chain** MVC# SEQ ID NO:	**IL-17A IC_{50} nM**	**IL-17A/F IC_{50} nM**	**IL-17F IC_{50} nM**	**IL-23 IC_{50} nM**
23/17hetero1 IgG1.1	MVC1059 SEQ ID NO:62 MVC1060 SEQ ID NO:64	MVC1002 SEQ ID NO:17*	0.34	0.78	0.33	0.060
23/17hetero2 IgG1.1	MVC1061 SEQ ID NO:60 MVC1062 SEQ ID NO:80	MVC1002 SEQ ID NO:17*	0.71	2.33	0.96	0.055

*The amino acid sequence of SEQ ID NO:17 may be encoded by the sequence of SEQ ID NO:70; the amino acid sequence of SEQ ID NO:28 may be encoded by the sequence of SEQ ID NO:71; the amino acid sequence of SEQ ID NO:18 may be encoded by the sequence of SEQ ID NO:72; the amino acid sequence of SEQ ID NO:29 may be encoded by the sequence of SEQ ID NO:75.

Anti-Human IL-23/IL-17A/F Bispecific Antibodies Bioassay Activity; Primary Human SAEC Assay to Measure Human IL-17A, IL-17AF, and IL-17F Activity by G-CSF Induction

[00203] Primary human small airway epithelial cells (SAEC) were seeded at 8,000 cells/well in Small Airway Epithelial Growth Medium (SAGM) (cells and media: Lonza, Walkersville, MD) in 96-well flat bottom tissue culture plates (Corning Incorporated, Corning, NY) and incubated overnight at 37 °C, 5% CO_2. The following

day serial dilutions of human IL-17A, IL-17A/F, or IL-17F (ZymoGenetics, A Bristol-Myers Squibb Company, Seattle, WA, USA) were made up in SAGM media and added to the plates containing the cells and incubated together at 37 °C, 5% CO_2 for 24 hours. Additionally the assay was used to measure neutralization of IL-17A, IL-17A/F and IL-17F activity. A half maximal concentration (EC_{50}, effective concentration at 50 percent) of IL-17A, IL-17A/F or IL-17F was combined with serial dilutions of anti-human IL-23/IL-17A/F bispecific antibodies described herein in SAGM media and added to the plates containing the cells and incubated together at 37 °C, 5% CO_2 for 24 hours. After incubation the supernatants were spun down, collected and frozen at -80 °C until ready to process. Human G-CSF protein levels in the supernatants were measured using a commercial bead based human G-CSF cytokine ELISA according to manufactures instructions (Procarta/Affymetrix, Santa Clara, CA). Increases in human G-CSF levels in the supernatant were indicative of a human IL-17A, IL-17A/F, IL-17F receptor-ligand interaction. Decreases in human G-CSF levels in the supernatant were indicative of neutralization of the human IL-17A, IL-17A/F, IL-17F receptor-ligand interaction. IC_{50} (inhibitory concentration at 50 percent) values were calculated using GraphPad Prism 4 software (GraphPad Software, Inc., San Diego CA) for each anti-human IL-23/IL-17A/F bispecific antibody.

Anti-Human IL-23/IL-17A/F Bispecific Antibodies Bioassay Activity; Primary Human SAEC Assay Results

[00204] Human IL-17A, IL-17A/F and IL-17F induce human G-CSF production in a dose dependent manner with an EC_{50} concentration determined to be 0.03nM for IL-17A, 3nM for IL-17A/F and 3nM for IL-17F. Bispecific antibodies tested include 23/17bAb1 (SEQ ID NO:28 and SEQ ID NO:17), 23/17bAb2 (SEQ ID NO:18 and SEQ ID NO:17), 23/17bAb3 (SEQ ID NO:74 and SEQ ID NO:17), 23/17bAb4 (SEQ ID NO:29 and SEQ ID NO:17). The humanized anti-human IL-17A/F antibody 339-134 mAb (SEQ ID NO:65 and SEQ ID NO:67) was also tested. The IC_{50} data for the anti-human IL-23/IL-17A/F bispecific antibodies is shown below in Table 9. This data indicates that the anti-IL-23/IL-17A/F bispecific antibodies inhibit human IL-17A, IL-17A/F, IL-17F mediated IL-6 production were equally potent.

Anti-Human IL-23/IL-17A/F Bispecific Antibodies Bioassay Activity; Primary Human Fibroblast Assay to Measure Human IL-17A, IL-17A/F, and IL-17F Activity by IL-6 Induction

[00205] A primary human fibroblast cell line (HFFF2, Cat #86031405, Health Protection Agency Culture Collections, Porton Down Salisbury, UK) was seeded at 5,000 cells/well in assay media (DMEM plus 10% FBS and 2mM L-glutamine (HyClone Laboratories, South Logan, UT)) in 96-well flat bottom plates (Corning Incorporated, Corning, NY) and incubated overnight at 37 °C, 5% CO_2. The following day serial dilutions of recombinant human IL-17A, IL-17AF, or IL-17F (ZymoGenetics, A Bristol-Myers Squibb Company, Seattle, WA 98117) were made up in assay media and added to the plates containing the cells and incubated together at 37 °C, 5% CO_2 for 24 hours. Additionally the assay was used to measure neutralization of human IL-17A, IL-17A/F and IL-17F activity. A half maximal concentration (EC_{50}, effective concentration at 50 percent) of human IL-17A, IL-17A/F or IL-17F was combined with serial dilutions of anti-human IL-23/IL-17A/F antibodies described herein in assay media and added to the plates containing the cells and incubated together at 37 °C, 5% CO_2 for 24 hours. After incubation the supernatants were spun down, collected and frozen at -80 °C until ready to process. Human IL-6 protein levels in the supernatants were measured using a commercial bead based human IL-6 cytokine ELISA according to manufactures instructions (Bio-Rad Laboratories, Hercules, CA). Increases in human IL-6 levels in the supernatant were indicative of a human IL-17A, IL-17A/F, IL-17F receptor-ligand interaction. Decreases in human IL-6 levels in the supernatant were indicative of neutralization of the human IL-17A, IL-17A/F, IL-17F receptor-ligand interaction. IC_{50} (inhibitory concentration at 50 percent) values were calculated using GraphPad Prism 4 software (GraphPad Software, Inc., San Diego CA) for each anti-human IL-23/IL-17A/F bispecific antibody.

Anti-Human IL-23/IL-17A/F Bispecific Antibodies Bioassay Activity; Primary Human Fibroblast Assay Results

[00206] Human IL-17A, IL-17A/F and IL-17F induce human IL-6 production in a dose dependent manner with an EC_{50} concentration determined to be 0.08nM for IL-17A, 25nM for IL-17AF and 25nM for IL-17F. Bispecific antibodies tested include

23/17bAb1 (SEQ ID NO:28 and SEQ ID NO:17), 23/17bAb2 (SEQ ID NO:18 and SEQ ID NO:17), 23/17bAb3 (SEQ ID NO:74 and SEQ ID NO:17), 23/17bAb4 (SEQ ID NO:29 and SEQ ID NO:17). Humanized anti-human IL-17A/F antibody 339-134 mAb (SEQ ID NO:64 and SEQ ID NO:66) was also tested. The IC_{50} data for the anti-human IL-23/IL-17A/F bispecific antibodies is shown below in Table 9. These data indicate that the anti-human IL-23/IL-17A/F bispecific antibodies inhibit human IL-17A, IL-17A/F, IL-17F mediated IL-6 production were equally potent.

Anti-Human IL-23/IL-17A/F Bispecific Antibodies Bioassay Activity; Murine Splenocyte Assay to Measure Human IL-23 Activity by Murine IL-17A and IL-17F Induction

[00207] A single cell suspension of murine splenocytes was prepared from whole spleens harvested from BALB/c mice. After red blood cell lysis with ACK buffer (0.010 M $KHCO_3$, 0.0001 M EDTA, 0.150 M NH_4Cl, pH 7.2) splenocytes were washed and resuspended in assay media (RPMI 1640 plus 10% FBS, non-essential amino acids, 1mM Sodium Pyruvate, 2mM L-glutamine, 10mM HEPES, 100 units/mL Pen/Strep (HyClone Laboratories, South Logan, UT), 50μM 2-mercaptoethanol (Sigma-Aldrich, St. Louis, MO), and 50 ng/ml human IL-2 (R&D Systems, Minneapolis, MN)). Splenocytes were seeded at 500,000 cells per well in 96-well round bottom plates. Serial dilutions of recombinant human IL-23 (BDC 50220AN087 heterodimer material) were made up in assay media and added to the plates containing the cells and incubated together at 37 °C, 5% CO_2 for 24 hours. Additionally the assay was also used to measure neutralization of human IL-23 activity. A half maximal concentration (EC_{50}, effective concentration at 50 percent) of human IL-23 was combined with serial dilutions of anti-human IL-23/IL-17A/F bispecific antibodies described herein and incubated together at 37 °C, 5% CO_2 for 15 minutes in assay media prior to addition to cells. Following pre-incubation, treatments were added to the plates containing the cells and incubated together at 37 °C, 5% CO_2 for 24 hours. After incubation the supernatants were spun down, collected and frozen at -80 °C until ready to process. The protein levels of murine IL-17A and IL-17F in the supernatants were measured using commercial plate based murine IL-17A and IL-17F ELISA's according to manufacturer's instructions (eBiosciences, San Diego, CA). Increases in murine IL-17A and IL-17F levels in the supernatant were indicative of an IL-23 receptor-ligand interaction. Decreases in murine

IL-17A and IL-17F levels in the supernatant were indicative of neutralization of the IL-23 receptor-ligand interaction. IC_{50} (inhibitory concentration at 50 percent) values were calculated using GraphPad Prism 4 software (GraphPad Software, Inc., San Diego CA) for each anti-human IL-23/IL-17A/F bispecific antibody.

Anti-Human IL-23/IL-17A/F Bispecific Antibodies Bioassay Activity; Murine Splenocyte Assay Results

[00208] Human IL-23 induced murine IL-17A and IL-17F in a dose dependent manner with an EC_{50} concentration determined to be 0.01nM. Bispecific antibodies tested include 23/17bAb1 (SEQ ID NO:28 and SEQ ID NO:17), 23/17bAb2 (SEQ ID NO:18 and SEQ ID NO:17), 23/17bAb3 (SEQ ID NO:74 and SEQ ID NO:17), 23/17bAb4 (SEQ ID NO:29 and SEQ ID NO:17). The anti-human IL-23.6 (7B7) mAb (SEQ ID NO:68 and SEQ ID NO:17) was also tested. The IC_{50} data for the anti-human IL-23/IL-17A/F bispecific antibodies is shown below in Table 9. This data indicates that the anti-human IL-23/IL-17A/F bispecific antibodies inhibit human IL-23 induced murine IL-17A and IL-17F production.

Anti-Human IL-23/IL-17A/F Bispecific Antibodies Bioassay Activity; Primary Human T Cell Phospho-STAT3 Assay to Measure Human IL-23 Activity by Phospho-STAT3 Induction

[00209] *Leukopheresis PBMC:* Normal human donors (ZymoGenetics' normal donor pool) were selected at random and were voluntarily apheresed at the FHCRC (Seattle, WA). The leukopheresis PBMC were delivered to ZymoGenetics in a sterile blood-collection bag. The cells were poured into a sterile 500 mL plastic bottle, diluted to 400 mL with room temperature PBS plus 1 mM EDTA (HyClone Laboratories, South Logan, UT) and transferred to 250 mL conical tubes. The 250 mL tubes were centrifuged at 1500 rpm for 10 minutes to pellet the cells. The cell supernatant was then removed and discarded. The cell pellets were then combined and suspended in 400 mL PBS plus 1 mM EDTA. The cell suspension (25 mL/tube) was overlaid onto FICOLL® (20 mL/tube) in 50 mL conical tubes (total of 16 tubes). The tubes were centrifuged at 2000 rpm for 20 minutes at room temperature. The interface layer ("buffy coat") containing the white blood cells and residual platelets was collected, pooled and washed repeatedly

with PBS plus 1 mM EDTA until the majority of the platelets had been removed. The white blood cells were then suspended in 100 mL of ice-cold Cryopreservation medium (70% RPMI 1640, 20% FCS, 10% DMSO (HyClone Laboratories)) and distributed into sterile cryovials (1 mL cells/vial). The cryovials placed in a -80 °C freezer for 24 hours before transfer to a liquid-nitrogen freezer. The white blood-cell yield from a typical apheresis is 0.5 – 1.0 x 10^{10} cells. Apheresis cells processed in this manner contain T cells, B cells, NK cells, monocytes and dendritic cells.

[00210] *Preparation of Activated T Cells:* T cells must be activated in order to express the IL-12 receptor and be able to respond to IL-12 and IL-23. Cryopreserved leukopheresis PBMC were thawed, transferred to a sterile 50 mL conical tube, and washed with 50 mL of warm assay media (RPMI 1640 plus 10% FBS (HyClone Laboratories)) and incubated in a 37 °C water bath for 1 hour to allow the cells to recover. The cells were then centrifuged and the cell-supernatant discarded. The cell pellet was resuspended in assay media and distributed into sterile 162 cm^2 tissue culture flasks at 2 x 10^7 cells per flask in 90 mL assay media containing 5 μg/mL PHA-M (Roche, Basel, Switzerland). The cells were then cultured at 37 °C in a humidified incubator for a total of 5 days. The cells were "rested" by harvesting on the afternoon of day 4, replacing the culture medium with fresh assay media without PHA and returning to the incubator for the remainder of the 5 day culture period.

[00211] *Phospho-STAT3 Assay:* Activated human T cells were harvested on day 5 of culture and resuspended in fresh assay media and were plated out at 2 x 10^5 cells/well in U-bottom 96-well plates. Serial dilutions of recombinant human IL-23 (BDC 50220AN087 heterodimer material) were made up in assay media and added to the plates containing the cells and incubated together at 37 °C, 5% CO_2 for 15 minutes. Additionally the assay was also used to measure neutralization of IL-23 activity. A half maximal concentration (EC_{50}, effective concentration at 50 percent) of IL-23 was combined with serial dilutions of anti-human IL-23/IL-17AF antibodies described herein and incubated together at 37 °C, 5% CO_2 for 15 minutes in assay media prior to addition to cells. Following pre-incubation, treatments were added to the plates containing the cells and incubated together at 37 °C, 5% CO_2 for 15 minutes. Following incubation, cells were washed with ice-cold wash buffer and put on ice to stop the reaction according to manufacturer's instructions (BIO-PLEX® Cell Lysis Kit, Bio-Rad Laboratories,

Hercules, CA). Cells were then spun down at 2000 rpm at 4 °C for 5 minutes prior to dumping the media. Fifty μL/well lysis buffer was added to each well; lysates were pipetted up and down five times while on ice, then agitated on a plate shaker for 20 minutes at 300 rpm and 4 °C. Plates were centrifuged at 3200 rpm at 4 °C for 20 minutes. Supernatants were collected and transferred to a new micro titer plate for storage at -80 °C.

[00212] Capture beads (BIO-PLEX® Phospho-STAT3 Assay, Bio-Rad Laboratories) were combined with 50 μL of 1:1 diluted lysates and added to a 96-well filter plate according to manufacturer's instructions (BIO-PLEX® Phosphoprotein Detection Kit, Bio-Rad Laboratories). The aluminum foil-covered plate was incubated overnight at room temperature, with shaking at 300 rpm. The plate was transferred to a microtiter vacuum apparatus and washed three times with wash buffer. After addition of 25 μL/well detection antibody, the foil-covered plate was incubated at room temperature for 30 minutes with shaking at 300 rpm. The plate was filtered and washed three times with wash buffer. Streptavidin-PE (50 μL/well) was added, and the foil-covered plate was incubated at room temperature for 15 minutes with shaking at 300 rpm. The plate was filtered and washed three times with bead resuspension buffer. After the final wash, beads were resuspended in 125 μL/well of bead suspension buffer, shaken for 30 seconds, and read on an array reader (BIO-PLEX® 100, Bio-Rad Laboratories) according to the manufacturer's instructions. Data was analyzed using analytical software (BIO-PLEX® Manager 4.1, Bio-Rad Laboratories). Increases in the level of the phosphorylated STAT3 transcription factor present in the lysates were indicative of an IL-23 receptor-ligand interaction. Decreases in the level of the phosphorylated STAT3 transcription factor present in the lysates were indicative of neutralization of the IL-23 receptor-ligand interaction. IC_{50} (inhibitory concentration at 50 percent) values were calculated using GraphPad Prism 4 software (GraphPad Software, Inc., San Diego CA) for each anti-human IL-23/IL-17A/F bispecific antibody.

Anti-Human IL-23/IL-17A/F Bispecific Antibodies Bioassay Activity; Primary Human T Cell Phospho-STAT3 Assay Results

[00213] Human IL-23 induces STAT3 phosphorylation in a dose dependent manner with an EC_{50} concentration determined to be 0.02nM. Bispecific antibodies

tested include 23/17bAb1 (SEQ ID NO:28 and SEQ ID NO:17), 23/17bAb2 (SEQ ID NO:18 and SEQ ID NO:17), 23/17bAb3 (SEQ ID NO:74 and SEQ ID NO:17), 23/17bAb4 (SEQ ID NO:29 and SEQ ID NO:17). The anti-human IL-23.6 (7B7) mAb (SEQ ID NO:68 and SEQ ID NO:17) was also tested. The IC_{50} data for the anti-human IL-23/IL-17A/F antibodies is shown below in Table 9.

Anti-Human IL-23/IL-17A/F Bispecific Antibody Bioassay Activity; Primary Human SAEC Assay, Primary Human Fibroblast Assay, Murine Splenocyte Assay and Primary Human T Cell Phospho-STAT3 Assay Results

Table 9

Profile		**23/17bAb1 IgG1.1** SEQ ID NO:28 SEQ ID NO:17	**23/17bAb2 IgG1.1** SEQ ID NO:18 SEQ ID NO:17	**23/17bAb3 IgG4.1** SEQ ID NO:74 SEQ ID NO:17	**23/17bAb4 IgG4.1** SEQ ID NO:29 SEQ ID NO:17	**339-134 mAbIgG1.1** SEQ ID NO:64 SEQ ID NO:66	**IL23.6(7B7) mAbIgG1.1** SEQ ID NO:68 SEQ ID NO:17
Cellular Potency Hu. primary epithelial cells (SAEC) IC_{50}	IL-17A EC_{50} = 0.03 nM	< 0.5 pM	< 0.5 pM	< 0.5 pM	≤ 0.5 pM	0.5 nM	Not Done
	IL-17AF EC_{50} = 3 nM	1.4 nM	1.3 nM	0.5 nM	1.4 nM	1.3 nM	Not Done
	IL-17F EC_{50} = 3 nM	0.8 nM	1.6 nM	1.0 nM	1.3 nM	1.1 nM	Not Done
Cellular Potency Hu. primary fibroblast cells (HFFF) IC_{50}	IL-17A EC_{50} = 0.08 nM	0.07 nM	0.07 nM	0.03 nM	0.1 nM	0.9 nM	Not Done
	IL-17AF EC_{50} = 25 nM	17 nM	12 nM	9.4 nM	9.1 nM	13 nM	Not Done
	IL-17F EC_{50} = 25 nM	19 nM	15 nM	10 nM	12 nM	15 nM	Not Done

Profile		**23/17bAb1 IgG1.1** SEQ ID NO:28 SEQ ID NO:17	**23/17bAb2 IgG1.1** SEQ ID NO:18 SEQ ID NO:17	**23/17bAb3 IgG4.1** SEQ ID NO:74 SEQ ID NO:17	**23/17bAb4 IgG4.1** SEQ ID NO:29 SEQ ID NO:17	**339-134 mAbIgG1.1** SEQ ID NO:64 SEQ ID NO:66	**IL23.6(7B7) mAbIgG1.1** SEQ ID NO:68 SEQ ID NO:17
Cellular potency Murine splenocyte assay IC_{50}	IL-23 EC_{50} = 0.01 nM	0.1 nM	0.06 nM	0.1 nM	0.08 nM	Not Done	0.09 nM
Cellular potency Primary T cell assay IC_{50}	IL-23 EC_{50} = 0.02 nM	0.04 nM	0.05nM	0.04 nM	0.1 nM	Not Done	0.04 nM

[00214] Anti-Human IL-23/IL-17A/F Bispecific Antibodies Co-Binding Activity; Primary Human Fibroblast Assay to measure the inhibition of human IL-17A, IL-7A/F, or IL-F while simultaneously bound to human IL-23. The Primary Human T Cell Phospho-STAT3 Assay to measure the inhibition of human IL-23 while simultaneously bound to human IL-17A, IL-7A/F, or IL-17F.

[00215] The primary human fibroblast assay was run in the presence of excess amounts of IL-23 at 30 nM. The primary human T cell phospho-STAT3 assay was run in the presence of excess amounts of IL-17A, IL-17A/F, IL-17F at 30 nM.

Anti-Human IL-23/IL-17A/F Bispecific Antibodies Bioassay Co-Binding Results

[00216] Bispecific antibodies tested include 23/17bAb1 (SEQ ID NO:28 and SEQ ID NO:17), 23/17bAb2 (SEQ ID NO:18 and SEQ ID NO:17), 23/17bAb3 (SEQ ID NO:74 and SEQ ID NO:17), 23/17bAb4 (SEQ ID NO:29 and SEQ ID NO:17), and 23/17taFab1 (SEQ ID NO:76 and SEQ ID NO:78). The anti-human IL-23/IL-17A/F bispecific antibodies when examined in the presence of human IL-23 did not interfere with human IL-17A, IL-17A/F, IL-17F inhibition. The anti-human IL-23/IL-17A/F bispecific antibodies when examined in the presence of human IL-17A, IL-17A/F, IL-17F did not interfere with human IL-23 inhibition.

Measurement of Binding Affinities of Anti-Human IL-23/IL-17A/F Bispecific Antibodies to Human IL-17A, IL-17A/F, IL-17F, and Human IL-23 Via Surface Plasmon Resonance (Biacore)

[00217] Anti-human IL-23/IL-17A/F bispecific antibodies were evaluated for their binding affinity to human IL-17A, human IL-17A/F, human IL-17F, and human IL-23 using surface plasmon resonance.

[00218] Kinetic rate constants and equilibrium dissociation constants were measured for the interaction of the anti-human IL-23/IL-17A/F bispecific antibodies with human IL-17A, IL-17A/F, IL-17F, and human IL-23 via surface plasmon resonance. The association rate constant (k_a ($M^{-1}s^{-1}$)) is a value that reflects the rate of the antigen-antibody complex formation. The dissociation rate constant (k_d (s^{-1})) is a value that reflects the stability of this complex. By dividing the dissociation rate constant by the association rate constant (k_d/k_a) the equilibrium dissociation constant (K_D (M)) is obtained. This value describes the binding affinity of the interaction. Antibodies with similar K_D can have widely variable association and dissociation rate constants. Consequently, measuring both the k_a and

k_d of antibodies helps to more uniquely describe the affinity of the antibody-antigen interaction.

[00219] Binding kinetics and affinity studies were performed on a BIACORE® T100 system (GE Healthcare, Piscataway, NJ). Methods for the BIACORE® T100 were programmed using BIACORE® T100 Control Software, v 2.0. For these experiments, the monoclonal and bispecific antibodies were captured onto a CM4 sensor chip via goat anti-human IgG Fc-gamma antibody (Jackson ImmunoResearch, West Grove, PA). Binding experiments with the human IL-17 molecules were performed at 25 °C in a buffer of 10 mM HEPES, 150 mM NaCl, 3 mM EDTA, 0.05% Surfactant P20 (GE Healthcare), 1 mg/mL bovine serum albumin, pH 7.4. Binding experiments with the IL-23/IL-12B heterodimer were performed at 25 °C in a buffer of 10 mM HEPES, 500 mM NaCl, 3 mM EDTA, 0.05% Surfactant P20 (Biacore), 1 mg/mL bovine serum albumin, pH 7.4.

[00220] The capture antibody, goat anti-human IgG Fc-gamma, was diluted to concentration of 20 μg/mL in 10 mM sodium acetate pH 5.0, and then covalently immobilized to all four flow cells of a CM4 sensor chip using amine coupling chemistry (EDC:NHS). After immobilization of the antibody, the remaining active sites on the flow cell were blocked with 1 M ethanolamine. A capture antibody density of approximately 5000 RU was obtained. The anti-human IL-23/IL-17A/F antibodies were captured onto flow cell 2, 3, or 4 of the CM4 chip at a density ranging from 60-150 RU. Capture of the test antibodies to the immobilized surface was performed at a flow rate of 10 μL/min. The BIACORE® instrument measures the mass of protein bound to the sensor chip surface, and thus, capture of the test antibody was verified for each cycle. Serial dilutions of human recombinant IL-17A, IL-17A/F, or IL-17F (ZymoGenetics, A Bristol-Myers Squibb Company, Seattle, WA, USA) were prepared from 100 nM – 0.032 nM (1:5 serial dilutions), while serial dilutions of human recombinant IL-23 (ZymoGenetics, A Bristol-Myers Squibb Company, Seattle, WA, USA) were prepared from 200 nM – 0.064 nM (1:5 serial dilutions). The serial dilutions were injected over the surface and allowed to specifically bind to the test antibody captured on the sensor chip. Duplicate injections of each antigen concentration were performed with an association time of 7 minutes and dissociation time of 15 minutes. Kinetic binding studies were performed with a flow rate of 50 μL/min. In between cycles, the flow cell was washed with 20 mM hydrochloric acid to regenerate the surface. This wash step removed both the captured test antibody and any bound antigen from the immobilized antibody surface. The test antibody was subsequently captured again in the next cycle.

[00221] Data was compiled using the BIACORE® T100 Evaluation software (version 2.0). Data was processed by subtracting reference flow cell and blank injections. Baseline stability was assessed to ensure that the regeneration step provided a consistent binding surface throughout the sequence of injections. Duplicate injection curves were checked for reproducibility. Based on the binding of the bivalent IL-17 molecules to a bivalent antibody, the bivalent analyte binding interaction model was determined to be appropriate for interactions with the IL-17 molecules. Based on the binding of the IL-23/IL-12B heterodimer to a bivalent antibody, the 1:1 binding interaction model was determined to be appropriate for interactions with the IL-23 molecule. The reference subtracted binding curves were globally fit to the appropriate binding model with a multiple Rmax and with the RI set to zero. The data fit well to the binding models with good agreement between the experimental and theoretical binding curves. The chi^2 and standard errors associated the fits were low. There was no trending in the residuals.

Anti-Human IL-23/IL-17A/F Bispecific Antibodies Biacore Activity

[00222] The results of the binding experiments with human IL-17A, IL-17A/F, and IL-17F are shown in Tables 10, 11, and 12, respectively. The results of the binding experiments with the human IL-23/IL-12B heterodimer are shown in Table 13.

Anti-Human IL-23/IL-17A/F Bispecific Antibodies Binding Affinity for IL-17A

Table 10

Bispecific Antibody	**k_{a1} ($M^{-1}s^{-1}$)**	**k_{d1} (s^{-1})**	**K_{D1} (M)**
23/17bAb1 IgG1.1 SEQ ID NO:28 SEQ ID NO:17	2.E+05	6.E-05	3.E-10
23/17bAb2 IgG1.1 SEQ ID NO:18 SEQ ID NO:17	5.E+05	4.E-04	8.E-10

Bispecific Antibody	k_{a1} ($M^{-1}s^{-1}$)	k_{d1} (s^{-1})	K_{D1} (M)
23/17bAb3 IgG4.1 SEQ ID NO:74 SEQ ID NO:17	4.E+05	5.E-05	1.E-10
23/17bAb4 IgG4.1 SEQ ID NO:29 SEQ ID NO:17	5.E+05	3.E-04	6.E-10
23/17taFab1 IgG1.1 SEQ ID NO:76 SEQ ID NO:78	3.E+05	2.E-03	7.E-9

Anti-Human IL-23/IL-17A/F Bispecific Antibodies Binding Affinity for IL-17A/F

Table 11

Bispecific Antibody	k_{a1} ($M^{-1}s^{-1}$)	k_{d1} (s^{-1})	K_{D1} (M)
23/17bAb1 IgG1.1 SEQ ID NO:28 SEQ ID NO:17	2.E+05	9.E-05	4.E-10
23/17bAb2 IgG1.1 SEQ ID NO:18 SEQ ID NO:17	4.E+05	7.E-04	2.E-9
23/17bAb3 IgG4.1 SEQ ID NO:74 SEQ ID NO:17	2.E+05	2.E-04	1.E-9

Bispecific Antibody	k_{a1} ($M^{-1}s^{-1}$)	k_{d1} (s^{-1})	K_{D1} (M)
23/17bAb4 **IgG4.1** SEQ ID NO:29 SEQ ID NO:17	3.E+05	1.E-03	3.E-9
23/17taFab1 **IgG1.1** SEQ ID NO:76 SEQ ID NO:78	1.E+05	5.E-04	5.E-9

Anti-Human IL-23/IL-17A/F Bispecific Antibodies Binding Affinity for IL-17F

Table 12

Bispecific Antibody	k_{a1} ($M^{-1}s^{-1}$)	k_{d1} (s^{-1})	K_{D1} (M)
23/17bAb1 **IgG1.1** SEQ ID NO:28 SEQ ID NO:17	8.E+05	3.E-04	4.E-10
23/17bAb2 **IgG1.1** SEQ ID NO:18 SEQ ID NO:17	3.E+06	7.E-04	2.E-10
23/17bAb3 **IgG4.1** SEQ ID NO:74 SEQ ID NO:17	6.E+05	2.E-04	3.E-10
23/17bAb4 **IgG4.1** SEQ ID NO:29 SEQ ID NO:17	2.E+06	7.E-04	4.E-10

Bispecific Antibody	k_{a1} ($M^{-1}s^{-1}$)	k_{d1} (s^{-1})	K_{D1} (M)
23/17taFab1 IgG1.1 SEQ ID NO:76 SEQ ID NO:78	3.E+05	7.E-04	2.E-9

Anti-Human IL-23/IL-17A/F Bispecific Antibodies Binding Affinity for IL23/IL-12B

Table 13

Antibody or Bispecific Antibody	k_{a1} ($M^{-1}s^{-1}$)	k_{d1} (s^{-1})	K_{D1} (M)
7B7Mab SEQ ID NO:68 SEQ ID NO: 17	3.E+05	2.E-04	7.E-10
23/17bAb1 IgG1.1 SEQ ID NO:28 SEQ ID NO:17	4.E+05	2.E-04	5.E-10
23/17bAb2 IgG1.1 SEQ ID NO:18 SEQ ID NO:17	2.E+05	8.E-05	4.E-10
23/17bAb3 IgG4.1 SEQ ID NO:74 SEQ ID NO: 17	4.E+05	2.E-04	5.E-10
23/17bAb4 IgG4.1 SEQ ID NO:29 SEQ ID NO:17	7.E+04	7.E-05	1.E-9

Antibody or Bispecific Antibody	k_{a1} ($M^{-1}s^{-1}$)	k_{d1} (s^{-1})	K_{D1} (M)
23/17taFab1 IgG1.1 SEQ ID NO:76 SEQ ID NO:78	3.E+05	2.E-04	7.E-10

Simultaneous Co-binding of IL-17A/F and IL-23 to the Anti-Human IL-23/IL-17A/F Bispecific Antibodies Via Surface Plasmon Resonance (Biacore)

[00223] Anti-Human IL-23/IL-17A/F bispecific antibodies were evaluated via surface plasmon resonance for ability to simultaneously co-bind both IL-23 and IL-17A/F.

[00224] For co-binding experiments in the first orientation, the human IL-17 molecules were covalently immobilized to flow cells 2-4 of a CM5 sensor chip using amine coupling chemistry (EDC:NHS). After immobilization, the remaining active sites on the flow cells were blocked with 1 M ethanolamine. Human IL-17A, IL-17A/F, and IL-17F (ZymoGenetics, A Bristol-Myers Squibb Company, Seattle, WA, USA) were immobilized onto flow cells 2, 3, or 4 respectively. The immobilization levels of these molecules ranged from 4500 – 5200 RU. Flow cell 1 was used as the reference surface. The bispecific antibodies were subsequently diluted to either 25 or 50 μg/mL, flowed over the surface, and captured onto flow cells 2-4 of the sensor chip. Following capture of the bispecific antibody, the IL-23/IL-12B heterodimer (ZymoGenetics, A Bristol-Myers Squibb Company, Seattle, WA, USA) was diluted to 500 nM and flowed over the surface to demonstrate co-binding. Binding studies were performed with a flow rate of 10 μL/min, an association time of 10 minutes, and a dissociation time of 5 minutes.

[00225] For co-binding experiments in the second orientation, a mouse anti-human IL-12 (p40/p70) monoclonal antibody (BD Pharmingen, San Jose, CA) was covalently immobilized onto flow cells 1-4 of a CM5 sensor chip using amine coupling chemistry (EDC:NHS). After immobilization, the remaining active sites on the flow cells were blocked with 1 M ethanolamine. The human IL-23/IL-12B heterodimer (ZymoGenetics, A Bristol-Myers Squibb Company, Seattle, WA, USA) was diluted to 500 nM and captured onto flow cells 1-4 via the IL-12B subunit. The capture level of the IL-23/IL-12B was approximately 4000 RU. The bispecific antibodies were subsequently diluted to either 25 or 50 μg/mL, flowed over the surface, and captured via the human IL-23 subunit onto flow cells 2-4 of the

sensor chip. Flow cell 1 was used as the reference surface. Following capture of the bispecific antibody, human IL-17A, IL-17A/F, and IL-17F (ZymoGenetics, A Bristol-Myers Squibb Company, Seattle, WA, USA) were diluted to 500 nM and flowed over the surface to demonstrate co-binding. Binding studies were performed with a flow rate of 10 μL/min, an association time of 10 minutes, and a dissociation time of 5 minutes.

[00226] All binding experiments were performed at 25 °C in a buffer of 10 mM HEPES, 500 mM NaCl, 3 mM EDTA, 0.05% Surfactant P20 (GE Healthcare), 1 mg/mL bovine serum albumin, pH 7.4. Between cycles, the flow cell was washed with 20 mM hydrochloric acid to regenerate the surface. This wash step removed both the captured test antibody and any bound antigen from the chip surface. Data was compiled using BIACORE® T100 Evaluation software (version 2.0). Data was processed by subtracting reference flow cell and blank injections. Baseline stability was assessed to ensure that the regeneration step provided a consistent binding surface throughout the sequence of injections.

Simultaneous Co-binding of IL-17A/F and IL-23 to the Anti-Human IL-23/IL-17A/F Bispecific Antibodies Via Surface Plasmon Resonance (Biacore) Results

[00227] Bispecific antibodies tested include 23/17bAb1 (SEQ ID NO:28 and SEQ ID NO:17), 23/17bAb2 (SEQ ID NO:18 and SEQ ID NO:17), 23/17bAb3 (SEQ ID NO:74 and SEQ ID NO:17), 23/17bAb4 (SEQ ID NO:29 and SEQ ID NO:17), and 23/17taFab1 (SEQ ID NO:76 and SEQ ID NO:78). All bispecific antibodies were able to simultaneously co-bind both human IL-23 and human IL-17A/F, demonstrating that both arms of the bispecific antibodies were functional.

Demonstration of IL-17A/F Specific Binding of the Anti-Human IL-23/IL-17A/F Bispecific Antibodies Via Surface Plasmon Resonance (Biacore)

[00228] Anti-Human IL-23/IL-17A/F bispecific antibodies were evaluated via surface plasmon resonance for lack of cross reactivity to human IL-17B, human IL-17C, human IL-17D, and human IL-17E (ZymoGenetics, A Bristol-Myers Squibb Company, Seattle, WA, USA).

[00229] Binding studies were performed on a BIACORE® T100 (GE Healthcare, Piscataway, NJ). Methods were programmed using BIACORE® T100 Control Software, v 2.0. Goat anti-human IgG Fc-gamma specific antibody (Jackson ImmunoResearch, West Grove, PA) was covalently immobilized to flow cells 1-3 of a CM4 sensor chip using amine coupling chemistry (EDC:NHS). The purified bispecific antibodies were subsequently

captured onto either flow cell 2 or flow cell 3 of the sensor chip at a density of approximately 150 RU. Flow cell 1 was used as the reference surface.

[00230] Human IL-17B, IL-17C, IL-17D, and IL-17E (ZymoGenetics, A Bristol-Myers Squibb Company, Seattle, WA, USA) were injected over the captured antibody surface (flow cell 2) and the reference flow cell (flow cell 1) at concentrations of 500, 100, 20, and 4 nM. As a positive control for this set of experiments, human IL-23 (ZymoGenetics, A Bristol-Myers Squibb Company, Seattle, WA, USA) was injected at concentrations of 100, 20, 4 and 0.8 nM. Binding studies were performed with a flow rate of 50 μL/min, an association time of 5 minutes, and a dissociation time of 5 minutes. All binding experiments were performed at 25 °C in a buffer of 10 mM HEPES, 500 mM NaCl, 3 mM EDTA, 0.05% Surfactant P20 (GE Healthcare), 1 mg/mL bovine serum albumin, pH 7.4. Between cycles, the flow cell was washed with 20 mM hydrochloric acid to regenerate the surface. This wash step removed both the captured test antibody and any bound antigen from the chip surface. Data was compiled using BIACORE® T100 Evaluation software (version 2.0). Data was processed by subtracting reference flow cell and blank injections. Baseline stability was assessed to ensure that the regeneration step provided a consistent binding surface throughout the sequence of injections.

Demonstration of IL-17A/F Specific Binding of the Anti-Human IL-23/IL-17A/F Bispecific Antibodies Via Surface Plasmon Resonance (Biacore) Results

[00231] No binding of human IL-17B, IL-17C, IL-17D, or IL17E to the bispecific antibodies was observed. Bispecific antibodies tested include 23/17bAb1 (SEQ ID NO:28 and SEQ ID NO:17), 23/17bAb2 (SEQ ID NO:18 and SEQ ID NO:17), 23/17bAb3 (SEQ ID NO:74 and SEQ ID NO:17), 23/17bAb4 (SEQ ID NO:29 and SEQ ID NO:17). In contrast, the IL-23 positive control demonstrated a dose dependent binding that was consistent with the previous studies.

Example 4

Anti-Human IL-23/17A/F bAbs Prevent Human IL-17A, F and AF-Mediated Increases in Serum Concentrations of Murine KC (CXCL1) in Mice

[00232] IL-17A, F and AF are able to induce the production of a number of downstream factors that in turn play a role in host defense, but also contribute to disease pathology, especially when produced at abnormally high levels or under chronic conditions.

One of these downstream mediators is CXCL1 (also known as GRO-α in human, or KC in mice), a chemokine that has important neutrophil chemoattractant activity and plays a role in inflammation. The ability of anti-human IL23/17A/F bispecific antibodies (bAbs) to reduce IL-17A, F and AF-mediated increases in GRO-α in mice was evaluated in order to show that the bAbs would be efficacious against IL-17-induced activities in an *in vivo* setting and thus that the bAbs would be useful in treating human diseases in which IL-17A, F or AF play a role. However, because these bAbs do not cross react with mouse IL-17A, F or AF, it was necessary to deliver human (h) IL-17A, F or AF to mice to induce the production of GRO-α (or in the case of mice, induce the production of KC, which is the murine analogue of GRO-α) which could then be neutralized in the presence of the anti-human IL23/17A/F bAbs.

[00233] For these experiments, female BALB/c mice (age 7 – 9 wk) were used. At time 18 hours, the mice received an intra-peritoneal (i.p.) injection of either the vehicle (PBS) or a dose of one of the anti-human IL-23/17A/F bAbs as shown in Table 14 and 15, in the left-hand column. At time 0, they received a subcutaneous (s.c.) injection of one of the following recombinant human proteins: 0.175 mg/kg hIL-17A, 0.9 mg/kg hIL-17F or 0.5 mg/kg hIL-17AF. Control mice received a s.c. injection of the vehicle (PBS) instead of one of the hIL-17 proteins. Two hours later, the mice were bled via the retro-orbital sinus under isoflurane gas anesthesia, serum was collected following centrifugation of the blood, and the serum was then stored at 80 °C until analyzed for serum KC concentrations using a commercial ELISA as per the manufacturer's instructions (Quantikine Mouse CXCL1/KC Immunoassay, R&D Systems, Inc., Minneapolis, MN).

[00234] As shown in Table 14 and 15, mice treated with the bAbs showed a dose-dependent increase in the inhibition of hIL-17A, F or AF-induced serum KC (CXCL1) concentrations indicating that the bAbs were efficacious in reducing the activities mediated by these IL-17 ligands. CXCL1 is just one example of a biological readout in response to IL-17A, F or AF; there are numerous other important downstream readouts that also play a role in diseases in which IL-17A, F or AF play a role that could be used as endpoint measurement.

Table 14. Percent Inhibition of Human IL-17A or F-mediated Increases in Serum Concentrations of Murine KC by i.p. bAbs, Relative to the Concentrations of Vehicle-Treated Mice (n = 3-4 per Group)

	% Inhibition of IL-17A-Mediated Serum KC Levels	% Inhibition of IL-17F-Mediated Serum KC Levels
Vehicle (PBS)	0	0
1 mg/kg bAb1	81	76
5 mg/kg bAb1	90	88
12 mg/kg bAb1	100	97
1 mg/kg bAb2	91	68
5 mg/kg bAb2	93	83
12 mg/kg bAb2	84	90
1 mg/kg bAb3	78	95
5 mg/kg bAb3	94	89
12 mg/kg bAb3	93	90
1 mg/kg bAb4	94	51
5 mg/kg bAb4	87	89
12 mg/kg bAb4	94	92

Table 15. Percent Inhibition of Human IL-17AF-mediated Increases in Serum Concentrations of Murine KC (pg/mL) by i.p. bAbs, Relative to the Concentrations of Vehicle-Treated Mice (n = 4 per Group)

	% Inhibition of IL-17AF-Mediated Serum KC Levels
Vehicle (PBS)	0
0.3 mg/kg bAb1	55
10 mg/kg bAb1	100
0.3 mg/kg bAb2	40
10 mg/kg bAb2	90
0.3 mg/kg bAb3	70
10 mg/kg bAb3	96
0.3 mg/kg bAb4	10
10 mg/kg bAb4	72

Example 5

Anti-Human IL-23/17A/F bAbs Prevent Human IL-23-Mediated Increases in Serum Concentrations of Mouse IL-17AF and F in Mice

[00235] IL-23 is able to induce the differentiation of Th17 cells which in turn, can lead to the production of IL-17A, IL-17F and IL-17AF. These cytokines are implicated in a number of diseases and therapeutics that can inhibit IL-23 and IL-17A, F and AF would be efficacious in the treatment of these diseases. The ability of anti-human IL23/17A/F bispecific antibodies (bAbs) to reduce IL-23-mediated increases in IL-17A, F and AF in mice was evaluated in order to show that the bAbs would be efficacious against IL-23-induced activities in an *in vivo* setting, and thus that the bAbs would be useful in treating human diseases in which IL-23 and Th17 cells play a role. However, because these bAbs do not cross react with mouse IL-23 it was necessary to deliver human (h) IL-23 to mice to induce the production of mouse IL-17 F and AF which could then be neutralized in the presence of the anti-human IL23/17A/F bAbs. Concentrations of mouse IL-17A were too low to accurately measure in the mouse serum but the trends were expected to be similar as compared to the trends observed for serum IL-17F and AF.

[00236] For these experiments, female C57BL/6 mice (age 7 – 9 wk) were used. At 10:30 am on day 1, they each received 5 micrograms of mouse (m) IL-2 via an intra-peritoneal (i.p.) injection. At 8:30 am on day 2, the mice received an i.p. injection of either the vehicle (PBS) or a dose of one of the anti-human IL-23/17A/F bAbs as shown in Table 16, in the left-hand column. At 11 am on day 2 the mice each received 5 micrograms of mIL-2 and 10 micrograms of hIL-23, and at 5:20 pm on day 2, the mice received 10 micrograms each of mIL-2 and hIL-23 via i.p. injections. At 9:30 am on day 3, each of the mice received another 5 micrograms of mIL-2 and 10 micrograms of hIL-23 by i.p. injection. At 4:30 pm on day 3, the mice were bled via the retro-orbital sinus under isoflurane gas anesthesia, serum was collected following centrifugation of the blood, and the serum stored at -80 °C until analyzed for serum concentrations of mouse IL-17F and AF using ELISAs and luminex assays that specifically measured these components.

[00237] As shown in Table 16, mice treated with the bAbs showed a dose-dependent increase in the inhibition of hIL-23 induced serum concentrations of mouse 17F or AF indicating that the bAbs were efficacious in reducing the activities mediated by hIL-23.

Table 16. Percent Inhibition of Human IL-23 Mediated Increases in Serum Concentrations of Mouse IL-17F or AF by i.p. bAbs, Relative to the Concentrations of Vehicle-Treated Mice (n = 3 per Group)

	% Inhibition of IL-23-Mediated Serum mIL-17F Levels	% Inhibition of IL-23-Mediated Serum mIL-17AF Levels
Vehicle (PBS)	0	0
1 mg/kg bAb1	49	22
5 mg/kg bAb1	99	94
12 mg/kg bAb1	96	94
1 mg/kg bAb2	21	17
5 mg/kg bAb2	82	71
12 mg/kg bAb2	67	97
1 mg/kg bAb3	0	45
5 mg/kg bAb3	38	91
12 mg/kg bAb3	65	95
1 mg/kg bAb4	0	62
5 mg/kg bAb4	27	74
12 mg/kg bAb4	49	97

Example 6

VCVFc Bispecific Antibodies

Construction and Expression of Mammalian VCVFc Bispecific Molecules

[00238] Whole genes were synthesized at GenScript (GenScript, Piscataway, NJ, USA) and inserted into pTT5, an HEK293-6E transient expression vector (NCR Biotechnology Research Institute, Ottawa, ON, CAN) via restriction enzyme cloning. Most constructs were expressed using the mod2610 (SEQ ID NO:30) signal sequence. The VCVFc is a bispecific antibody which contains a whole antibody with a Fv unit of the second arm of the bispecific inserted between the Fab region and the hinge via a linker (for example, but not limited to, 10mer G_4S for either chain, or RTVAAPS (SEQ ID NO:85) for the light

chain and SSASTKGPS (SEQ ID NO:86) for the heavy chain). An illustration of a VCVFc bispecific antibody is shown in Fig. 5.

[00239] The HEK293-6E suspension cells were transfected with expression constructs using polyethylenimine reagent and cultivated in F17 medium (Invitrogen, Grand Island, NY, USA) with the addition of 5 mM L-glutamine and 25 μg/mL G418. After 24 hours, 1/40th volume of 20% Tryptone NI (Organotechnie SAS, La Courneuve, FR) was added. At approximately 120 hours post transfection, conditioned media was harvested and passed through a 0.2 μm filter. Protein was purified from the filtered conditioned media using a combination of Mab Select SuRe Affinity Chromatography (GE Healthcare, Piscataway, NJ, USA) and SUPERDEX® 200 Size Exclusion Chromatography (GE Healthcare, Piscataway, NJ, USA). Content was estimated by absorbance at UV-A280nm and quality evaluated by analytical size exclusion high performance liquid chromatography, SDS PAGE, and western blot.

IL-23/IL-17A/F VCVFc Bispecific Antibodies Bioassay Activity; NIH/3T3/KZ170 NF-κB Luciferase Reporter Assay to Measure Human IL-17A, IL-17A/F, and IL-17F Activity by NF-κB Induction

[00240] The bioassay was performed as described in Example 1 hereinabove.

IL-23/IL-17A/F VCVFc Bispecific Antibodies Bioassay Activity; Baf3/huIL-23Rα/huIL-12Rβ1 Transfectants Phospho-STAT3 Assay to Measure Human IL-23Activity by Phospho-STAT3 Induction

[00241] The bioassay was performed as described in Example 3 hereinabove.

PDGF-C/PDGF-D VCVFc Bispecific Antibodies Bioassay Activity; Normal Human Lung Fibroblasts (NHLF) Proliferation Assay to Measure Human PDGF-C and PDGF-D Mitogenic Activity

[00242] A primary normal human lung fibroblast cell line (NHLF, CC-2512, Lonza, Walkersville, MD) was seeded at 1,000 cells/well in growth media (FGM-2 BulletKit, Lonza, Walkersville, MD) and incubated overnight at 37 °C, 5% CO_2. The following day media was removed and serial dilutions of recombinant human PDGF-C and PDGF-D (ZymoGenetics) were made up in assay media (FBM plus 0.1% BSA, Lonza, Walkersville, MD) and added to the plates containing the cells and incubated together at 37 °C, 5% CO_2 for 48 hours. Additionally the assay was used to measure neutralization PDGF-C and PDGF-D

activity. A sub maximal concentration of PDGF-C or PDGF-D was combined with serial dilutions of anti-human PDGF-C/D or anti-human PDGFRα/β VCVFc antibodies described herein in assay media and added to the plates containing the cells and incubated together at 37 °C, 5% CO_2 for 48 hours. Cells were pulsed with 1μCi/well of Thymidine [Methyl-^{3}H] (PerkinElmer, Waltham, MA) and incubated at 37 °C, 5% CO_2 for an additional 24 hours. Following incubation mitogenic activity was assessed by measuring the amount of ^{3}H-Thymidine incorporation. Media was removed and cells trypsinized for 10 minutes at 37 °C before being harvested on FilterMate harvester (Packard Instrument Co., Meriden, CT) and read on TOPCOUNT® microplate scintillation counter (Packard Instrument Co., Meriden, CT) according to manufactures instructions. Increases in ^{3}H-Thymidine incorporation were indicative of a PDGF-C or PDGF-D receptor-ligand interaction. Decreases in ^{3}H-Thymidine incorporation were indicative of neutralization of the PDGF-C or PDGF-D receptor-ligand interaction. IC_{50} (inhibitory concentration at 50 percent) values were calculated using GraphPad Prism 4 software (GraphPad Software, Inc., San Diego CA) for each PDGF-C/PDGF-D or PDGFRα/PDGFRβ VCVFc bispecific antibody.

IL-23/IL-17A/F VCVFc Bispecific Antibody Bioassay Activity; NIH/3T3/KZ170 NF-κB Luciferase Reporter Assay and Baf3/huIL-23Rα/huIL-12Rβ1 Transfectants Phospho-STAT3 Assay Results

[00243] Human IL-17A, IL-17A/F and IL-17F induce activation of the NF-κB luciferase reporter in a dose dependent manner with an EC_{50} concentration determined to be 0.15nM for IL-17A, 0.5nM for IL-17A/F and 0.5nM for IL-17F and IL-23 induces STAT3 phosphorylation in a dose dependent manner with an EC_{50} concentration determined to be 0.02nM. The IC_{50} data for the anti-human IL-23/IL-17A/F VCVFc bispecific antibodies are shown below in Tables 17, 18 and 19.

IL-23/17A/F VCVFc Bispecific Antibody Table

Table 17

Name	**Heavy Chain** MVC# SEQ ID NO:	**Light Chain** MVC# SEQ ID NO:	**IL-17A** **IC_{50} nM**	**IL-17A/F** **IC_{50} nM**	**IL-17F** **IC_{50} nM**	**IL-23** **IC_{50} nM**
339-134 mAb IgG1.1	MVC978 SEQ ID	MVC717 SEQ ID	3	0.9	0.4	Not Done

Name	**Heavy Chain** MVC# SEQ ID NO:	**Light Chain** MVC# SEQ ID NO:	**IL-17A** **IC_{50} nM**	**IL-17A/F** **IC_{50} nM**	**IL-17F** **IC_{50} nM**	**IL-23** **IC_{50} nM**
	NO:64	NO:66				
IL23.6 (7B7) mAb IgG1.1	MVC1003 SEQ ID NO:68	MVC1002 SEQ ID NO:17	Not Done	Not Done	Not Done	0.2
23/17VCV1 IgG1.1	MVC1020 SEQ ID NO:87	MVC1021 SEQ ID NO:89	20	3	3	0.008
23/17VCV2 IgG1.1	MVC1022 SEQ ID NO:91	MVC1023 SEQ ID NO:93	0.4	0.4	0.9	0.3

Table 18

Name	**Heavy Chain** MVC# SEQ ID NO:	**Light Chain** MVC# SEQ ID NO:	**IL-17A** **IC_{50} nM**	**IL-17A/F** **IC_{50} nM**	**IL-17F** **IC_{50} nM**	**IL-23** **IC_{50} nM**
339-134 mAb IgG1.1	MVC978 SEQ ID NO:64	MVC717 SEQ ID NO:66	1.2	0.23	0.28	Not Done
IL23.6 (7B7) mAb IgG1.1	MVC1003 SEQ ID NO:68	MVC1002 SEQ ID NO:17	Not Done	Not Done	Not Done	0.0030
23/17VCV3 IgG4.1	MVC1119 SEQ ID NO:95	MVC1021 SEQ ID NO:89	16	9.7	6.0	0.011
23/17VCV4 IgG4.1	MVC1120 SEQ ID NO:97	MVC1023 SEQ ID NO:93	0.20	0.34	0.20	0.47

Name	**Heavy Chain** MVC# SEQ ID NO:	**Light Chain** MVC# SEQ ID NO:	**IL-17A** **IC_{50} nM**	**IL-17A/F** **IC_{50} nM**	**IL-17F** **IC_{50} nM**	**IL-23** **IC_{50} nM**
23/17VCV5 IgG1.1	MVC1122 SEQ ID NO:99	MVC1121 SEQ ID NO:101	15	8.7	7.0	0.0038
23/17VCV6 IgG1.1	MVC1124 SEQ ID NO:103	MVC1123 SEQ ID NO:105	0.38	0.35	0.29	0.043

Table 19

Name	**Heavy Chain** MVC# SEQ ID NO:	**Light Chain** MVC# SEQ ID NO:	**IL-17A** **IC_{50} nM**	**IL-17A/F** **IC_{50} nM**	**IL-17F** **IC_{50} nM**	**IL-23** **IC_{50} nM**
339.15.3.6 mAb Hybridoma line lot E10915	N/A	N/A	9.8	0.34	0.32	Not Done
IL23.4 mAb IgG4.1 - BDC Lot PC-1413-32	SEQ ID NO:107	SEQ ID NO:109	Not Done	Not Done	Not Done	0.029
23/17VCV7 IgG1.1	MVC1108 SEQ ID NO:111	MVC1107 SEQ ID NO:113	24	13	5.9	0.053
23/17VCV8 IgG1.1	MVC1110 SEQ ID NO:115	MVC1109 SEQ ID NO:117	2.4	0.34	0.31	2.6

PDGF-C/PDGF-D and PDGFRα/PDGFβ VCVFc Bispecific Antibodies Bioassay Activity; Normal Human Lung Fibroblasts (NHLF) Proliferation Assay Results

[00244] PDGF-C and PDGF-D induce proliferation of the NHLF cells in a dose dependent manner with a sub maximal concentration determined to be 0.1nM for PDGF-C and 6nM for PDGF-D. Table 20 and Table 21 present IC_{50} data for the PDGF-C/PDGF-D or PDGFRα/PDGFRβ VCVFc bispecific antibody described herein.

PDGF-C/PDGF-D VCVFc Bispecific Antibody Table

Table 20

Name	**Heavy Chain** MVC# SEQ ID NO:	**Light Chain** MVC# SEQ ID NO:	**PDGFC IC_{50} nM**	**PDGFD IC_{50} nM**
PDGFC mAb Hybridoma Lot-E2826	N/A	N/A	.083	Not Done
PDGFD mAb Hybridoma Lot-E4342	N/A	N/A	Not Done	3.5
C/DVCV1 IgG1.1	MVC1112 SEQ ID NO:119	MVC1111 SEQ ID NO:121	0.090	20

PDGFRα/PDGFRβ VCVFc Bispecific Antibody Table

Table 21

Name	**Heavy Chain** MVC# SEQ ID NO:	**Light Chain** MVC# SEQ ID NO:	**PDGFC % Inhibition**	**PDGFD % Inhibition**
PDGFRα mAb Hybridoma Lot-C5161	N/A	N/A	100%	30%
PDGFRβ mAb Hybridoma Lot-C8938	N/A	N/A	50%	100%
α/βVCV2 IgG1.1	MVC1118 SEQ ID NO:123	MVC1117 SEQ ID NO:125	70%	100%

IL-23/IL-17A/F VCVFc Bispecific Antibodies Bioassay Activity; Primary Human Fibroblast Assay to Measure Human IL-17A, IL-17A/F, and IL-17F Activity by IL-6 Induction

[00245] The bioassay was pertextured as described in Example 3 hereinabove.

IL-23/IL-17A/F VCVFc Bispecific Antibodies Bioassay Activity; Primary Human Fibroblast Assay Results

[00246] Human IL-17A, IL-17A/F and IL-17F induce human IL-6 production in a dose dependent manner with an EC_{50} concentration determined to be 0.08nM for IL-17A, 25nM for IL-17A/F and 25nM for IL-17F. Anti-human IL-23/IL-17A/F VCVFc bispecific antibody 23/17VCV2 (SEQ ID NO:91 and SEQ ID NO:93). Table 22 presents example IC_{50} data for the IL-23/IL-17A/F VCVFc bispecific antibody described herein.

Table 22

Profile		**23/17VCV2 IgG1.1** SEQ ID NO:91 SEQ ID NO:93	**339-134 mAbIgG1.1** SEQ ID NO:64 SEQ ID NO:66	**IL23.6(7B7) mAbIgG1.1** SEQ ID NO:68 SEQ ID NO:17
Cellular Potency Hu. primary fibroblast cells (HFFF) IC_{50}	IL-17A EC_{50} = 0.08 nM	0.3 nM	2 nM	Not Done
	IL-17AF EC_{50} = 25 nM	26 nM	22 nM	Not Done
	IL-17F EC_{50} = 25 nM	25 nM	23 nM	Not Done
Cellular potency Primary T cell assay IC_{50}	IL-23 EC_{50} = 0.02 nM	0.4 nM	Not Done	0.02 nM

IL-23/IL-17A/F VCVFc Bispecific Antibodies Co-Binding Activity; Primary Human Fibroblast Assay to measure the inhibition of human IL-17A, IL-7A/F, or IL-F while simultaneously bound to human IL-23. The Primary Human T Cell Phospho-STAT3 Assay to measure the inhibition of human IL-23 while simultaneously bound to human IL-17A, IL-7A/F, or IL-17F.

[00247] The primary human fibroblast assay was run in the presence of excess amounts of IL-23 at 30nM. The primary human T cell phospho-STAT3 assay was run in the presence of excess amounts of IL-17A, IL-17A/F, and IL-17F at 30nM.

IL-23/IL-17A/F VCVFc Bispecific Antibodies Bioassay Co-Binding Results

[00248] Bispecific antibody 23/17VCV2 (SEQ ID NO:91 and SEQ ID NO:93) when examined in the presence of human IL-23 did not interfere with human IL-17A, IL-17A/F, IL-17F inhibition. Bispecific antibody 23/17VCV2 when examined in the presence of human IL-17A, IL-17A/F, IL-17F did not interfere with human IL-23 inhibition.

Measurement of Binding Affinities of IL-23/IL-17A/F VCVFc Bispecific Antibodies to Human IL-17A, IL-17A/F, IL-17F, and Human IL-23 Via Surface Plasmon Resonance (Biacore)

[00249] Binding activities were determined as described in Example 3 hereinabove.

IL-23/IL-17A/F VCVFc Bispecific Antibodies Biacore Activity

[00250] The results of the binding experiments with human IL-17A, IL-17A/F, and IL-17F are shown in Tables 23, 24, and 25, respectively. The results of the binding experiments with the human IL-23/IL-12B heterodimer are shown in Table 26.

IL-23/IL-17A/F VCVFc Bispecific Antibodies Binding Affinity for IL-17A

Table 23

Bispecific Antibody	**k_{a1} ($M^{-1}s^{-1}$)**	**k_{d1} (s^{-1})**	**K_{D1} (M)**	**K_{D1} (nM)**
339-134 mAb IgG1.1 SEQ ID NO:64 SEQ ID NO:66	2.E+06	3.E-03	1.E-9	1.0
23/17VCV2 IgG1.1 SEQ ID NO:91 SEQ ID NO:93	3.8E+06	3.4E-03	8.9E-10	0.9

Bispecific Antibody	k_{a1} ($M^{-1}s^{-1}$)	k_{d1} (s^{-1})	K_{D1} (M)	K_{D1} (nM)
23/17VCV4 IgG4.1 SEQ ID NO:97 SEQ ID NO:93	5.4E+06	5.4E+03	1.0E+09	1.0
23/17VCV6 IgG1.1 SEQ ID NO:103 SEQ ID NO:105	4.0E+06	4.7E+03	1.2E+09	1.2

IL-23/IL-17A/F VCVFc Bispecific Antibodies Binding Affinity for IL-17A/F

Table 24

Bispecific Antibody	k_{a1} ($M^{-1}s^{-1}$)	k_{d1} (s^{-1})	K_{D1} (M)	K_{D1} (nM)
339-134 mAb IgG1.1 SEQ ID NO:64 SEQ ID NO:66	2.E+06	5.E-04	2.E-10	0.2
23/17VCV2 IgG1.1 SEQ ID NO:91 SEQ ID NO:93	1.8E+06	7.1E-04	3.9E-10	0.4
23/17VCV4 IgG4.1 SEQ ID NO:97 SEQ ID NO:93	1.5E+06	7.7E+04	5.1E+10	0.5
23/17VCV6 IgG1.1 SEQ ID NO:103 SEQ ID NO:105	1.2E+06	7.9E+04	6.6E+10	0.7

IL-23/IL-17A/F VCVFc Bispecific Antibodies Binding Affinity for IL-17F

Table 25

Bispecific Antibody	k_{a1} ($M^{-1}s^{-1}$)	k_{d1} (s^{-1})	K_{D1} (M)	K_{D1} (nM)
339-134 mAb IgG1.1 SEQ ID NO:64 SEQ ID NO:66	2.E+06	2.E-04	1.E-10	0.1
23/17VCV2 IgG1.1 SEQ ID NO:91 SEQ ID NO:93	2.4E+06	5.1E-04	2.1E-10	0.2
23/17VCV4 IgG4.1 SEQ ID NO:97 SEQ ID NO:93	2.2E+06	3.5E+04	1.6E+10	0.2
23/17VCV6 IgG1.1 SEQ ID NO:103 SEQ ID NO:105	3.4E+06	1.2E+04	3.5E+11	0.04

IL-23/IL-17A/F VCVFc Bispecific Antibodies Binding Affinity for IL23/IL-12B

Table 26

Antibody or Bispecific Antibody	k_{a1} ($M^{-1}s^{-1}$)	k_{d1} (s^{-1})	K_{D1} (M)	K_{D1} (nM)
7B7Mab SEQ ID NO:68 SEQ ID NO:17	3.E+05	2.E-04	7.E-10	0.7
23/17VCV2 IgG1.1 SEQ ID NO:91 SEQ ID NO:93	4.7E+04	2.1E-04	4.5E-09	4.5

Antibody or Bispecific Antibody	k_{a1} ($M^{-1}s^{-1}$)	k_{d1} (s^{-1})	K_{D1} (M)	K_{D1} (nM)
23/17VCV4 IgG4.1 SEQ ID NO:97 SEQ ID NO:93	No Binding	No Binding	No Binding	No Binding
23/17VCV6 IgG1.1 SEQ ID NO:103 SEQ ID NO:105	5.6E+04	1.1E+04	2.0E+09	2.0

Simultaneous Co-binding of IL-17A/F and IL-23 to the IL-23/IL-17A/F VCVFc Bispecific Antibodies Via Surface Plasmon Resonance (Biacore)

[00251] This assay was performed as described in Example 3 hereinabove.

Simultaneous Co-binding of IL-17A/F and IL-23 to the IL-23/IL-17A/F VCVFc Bispecific Antibodies Via Surface Plasmon Resonance (Biacore) Results

[00252] Bispecific antibody 23/17VCV2 (SEQ ID NO:91 and SEQ ID NO:93) was able to simultaneously co-bind both human IL-23 and human IL-17A/F, demonstrating that both arms of the bispecific antibodies were functional.

Example 7

IL-23p19 Epitope Mapping

[00253] The analysis described in this Example 7 aims to identify the epitopic residues on IL-23p19 for which the IL-23p19 antibody (7B7 antibody or Mab, 7B7 Fab and biAb3, all of which have a heavy chain variable domain as shown in SEQ ID NO:7 and light chain variable domain as shown in SEQ ID NO:9) binds. Fab 7B7, 7B7 antibody and biAb3 have all been used in the binding studies at various stages because they are interchangeable as far as their epitope on IL-23p19.

Proteolytic Digest and Peptide Data on Epitope

[00254] Mass spectrometry epitope sequence analysis of the IL-23p19 antibody was based on both epitope extraction and epitope excision methods. (Parker et al., "MALDI/MS-based epitope mapping of antigens bound to immobilized antibodies", *Mol. Biotechnol.*, 20(1):49-62 (Jan. 2002)). In both cases the IL-23p19 antibody was directly immobilized via primary amines of the antibody on surface-activated beads at an average density of 2 mg mAb per 1 ml bed volume. Peptides from IL-23 his-tag antigen were generated with or without reduction and alkylation. Reduction of the antigen IL-23 was performed by incubating with 50 mM dithiothreitol in PBS and 4M guanidine HCl for 1 hour at 37 °C. This was followed by alkylation with 100 mM iodoacetamide for 30 minutes at room temperature. Reduced and alkylated IL-23 was dialyzed against PBS overnight prior to fragmentation. For epitope extraction, antigen peptides were generated by proteolytic digestion with the endoproteinases trypsin, chymotrypsin, lys-C, arg-C, asp-N and or glu-C with an enzyme to antigen ratio of up to 2% (w/w). Incubations were performed at 37 °C with incubation times ranging from 2 hours to overnight. The resulting peptides were mixed with antibody resin at room temperature for 30 minutes. This resin was then washed three times to remove any non-specifically bound peptides. All digestion, incubation, and wash steps were performed in PBS pH 7. The same protocol was followed for epitope excision except that the intact antigen was incubated with the antibody for 30 minutes at room temperature prior to enzymatic digestion. In both methods antibody bound peptides were eluted and analyzed on ESI-MS.

[00255] These data indicate that IL-23p19 antibody has a discontinuous epitope comprised of three peptide regions in IL-23p19. Synthetic peptides were generated to further examine these three peptide regions, and their binding was tested and analyzed by both ELISA and mass spectrometry. Based on these observations, it is suggested that the following peptides represent the sequences of the IL-23p19 antibody epitope:

Peptide 1: WQRLLLRFKILR (residues 156-167 of SEQ ID NO:6)

Peptide 2: SAHPLVGHMDLR (residues 46-57 of SEQ ID NO:6)

Peptide 3: IHQGLIFYEKLLGSDIFTGEPSLLP (residues 93-117 of SEQ ID NO:6).

IL-23 Epitope Mapping by HDX-MS

[00256] Hydrogen/deuterium exchange mass spectrometry (HDX-MS) method probes protein conformation and conformational dynamics in solution by monitoring the rate and extent of deuterium exchange of backbone amide hydrogen atoms. The level of HDX

depends on the solvent accessibility of backbone amide hydrogen atoms and the conformation of the protein. The mass increase of the protein upon HDX can be precisely measured by MS. When this technique is paired with enzymatic digestion, structural features at the peptide level can be resolved, enabling differentiation of surface exposed peptides from those folded inside. Typically, the deuterium labeling and subsequent quenching experiments are performed, followed by online pepsin digestion, peptide separation, and MS analysis. Prior to epitope mapping of BMS-986113 in IL-23 by HDX-MS, non-deuteriated experiments were performed to generate a list of common peptic peptides for IL-23 (4.4 mg/mL) and IL-23/BMS-986113 (1:1 molar ratio, 4.4 mg/mL & 3.36 mg/mL), achieving a sequence coverage of 97% for IL-23. In this experiment, 10 mM phosphate buffer (pH 7.0) was used during the labeling step, followed by adding quenching buffer (200 mM phosphate buffer with 1.5M GdnCl and 0.5M TCEP, pH 2.5, 1:1, v/v). For epitope mapping experiments, 5 μL of each sample (IL-23 or IL-23/BMS-986113 (1:1 molar ratio)) was mixed with 65 μL HDX labeling buffer (10 mM phosphate buffer in D_2O, pD 7.0) to start the labeling reactions at room temperature (~25 °C). The reactions were carried out for different periods of time: 20 sec, 1 min, 10 min, 60 min and 240 min. By the end of each labeling reaction period, the reaction was quenched by adding quenching buffer (1:1, v/v) and the quenched sample was injected into Waters HDX-MS system for analysis. The observed common peptic peptides were monitored for their deuterium uptake levels in the absence/presence of BMS-986113. The same protocol was followed for epitope mapping of anti-IL-23 7B7 Fab (4.91 mg/mL) in IL-23 by HDX-MS.

[00257] Epitope mapping of anti-IL-23 7B7 Fab in complex with IL-23 and biAb3 with IL-23 indicate that biAb3 has a discontinuous epitope comprised of five peptide regions in IL-23p19. Based on relative deuterium uptake levels, five peptide regions can be ranked as region 1 > 2 > 3 > 4 > 5 with region 1 having the most significant changes in deuterium uptakes and region 5 having the least significant changes in deuterium uptakes. The five peptide regions on IL-23p19 as determined by HDX-MS for the IL-23p19 antibody were determined as follows:

Region 1: PDSPVGQL (residues 117-124 of SEQ ID NO:6);

Region 2: IFTGEPSLL (residues 108-116 of SEQ ID NO:6);

Region 3: KILRSLQAF (residues 164-172 of SEQ ID NO:6);

Region 4: QQLSQKLCTLAWSAHPLVGHMD (residues 34-55 of SEQ ID NO:6); and

Region 5: CLQRIHQGLIFYEKLLG (residues 89-105 of SEQ ID NO:6).

Computational Epitope Prediction and Design of Alanine Shave Mutants

[00258] Alanine shave mutagenesis is a strategy for mutating multiple residues in the same construct to alanine to remove the amino acid side chains in epitope of binding (Wells, J.A., "Systemic mutational analyses of protein-protein interfaces", *Enzym.*, 202:390-411 (1991)). Multiple sources of information on the involvement of residues in a potential epitope with the 7B7 Fab and biAb3 were combined to produce a targeted list of regional alanine shave mutants. The residues contained in the overlapping regions between both the HDX (see above in this Example 7) and the proteolytic digest peptide mapping (see above in this Example 7) were mapped onto the sequence of the IL-23p19 domain and three linear regions of common residues were identified as Regions A, B and C. Region A corresponds to amino acid residues 33-59 of SEQ ID NO:6. Region B corresponds to amino acid residues 89-125 of SEQ ID NO:6. Region C corresponds to amino acid residues 144-173 of SEQ ID NO:6. In order to calculate the residues whose side chains are exposed (solvent accessible surface area, SASA) and would therefore be located on the protein surface of the p19 domain of IL-23, an in-house structure of the IL-23 heterodimer was used. For each residue in the p19 domain of IL-23 the ratio of accessible surface to the standard exposed surface for the amino acid type was calculated and residues were grouped into bins. Residues were placed in accessibility bins as follows: <30%, 30-40%, 40-50%, 50-60%, 60-70%, 70-80%, > 90% exposed. The standard residue accessibilities for each amino acid type were calculated in the extended tripeptide Gly-X-Gly. The second calculation performed was ODA (Optimal Docking Area) which is useful for predicting likely protein-protein interaction surfaces. The method identifies optimal surface patches with the lowest docking desolvation energy. The ODA was calculated for the p19 domain of IL-23 and these results used to prioritize residues for mutagenesis.

[00259] Residues in these three regions (A, B, C) were prioritized based upon a high score in both the ODA and SASA calculations and also weighted based on the extent of hydrogen-deuterium exchange relative to the uncomplexed IL-23 (peptide #1 >#2>#3>#4>#5). Regions with non-identity to mouse were cloned as mouse swap mutants, instead of alanine shave mutants, which did not show an impact on binding in small scale

testing. With the exception of M7 which contains a linear sequence of residues in an extended loop, residues were then combined into non-linear epitopes based on mapping them to the X-ray crystallographic structure of IL-23 (M5, M6, M8). Additional backup mutants were generated with the sub-epitopes of predominantly linear residues (M9, M10, M11). The alanine shave mutants designed by this method are shown below in Table 27.

Table 27: Alanine Shave Mutants of IL-23p19

Name	Region Mutated	IL-23p19 (SEQ ID NO:6) Residues Mutated to Alanine
M5	A and B	H53A, M54A, E112A, L116A and D118A
M6	A and C	T42A, W45A, H48A, F163A and Q170A
M7	C	W142A, E143A, T144A, Q145A and Q146A
M8	A, B and C	H53A, E112A, Q154A and W156A
M9	B	L116A, D118A and Q123A
M10	A	H53A, M54A, D55A and F163A
M11	C	W142A, T144A and Q146A

Cloning, Expression and Purification of IL-23 Epitope Mapping Alanine Mutants

[00260] Non-tagged wild-type IL-23 p40 subunit entry vector construct was generated by PCR and the fidelity of the PCR fragment was confirmed by sequencing. The transient expression construct was generated by Gateway LR recombination and sequence confirmed. The His-tagged wild-type IL-23 p19 subunit construct and all mutant constructs were generated by PCR and cloned into the transient expression vector directly. The fidelity of all PCR fragments was confirmed by sequencing. To generate the wild-type control, non-tagged wild-type IL-23 P40 subunit was co-expressed with the His-tagged wild-type P19 subunit transiently in HEK293-6E cells at 4 L scale for IL-23 complex purification. Briefly, HEK293-6E cells at 1×10^6 cells/ml were transfected with expression plasmids/PEI complex at the ratio of 0.5 (p19)/0.5 (p40)/1.5 (PEI). Tryptone N1 feed was added 24 hours later and cells harvested on 120 hours post transfection. The conditioned media was filtered with 0.2 μM filters. Seven His-tagged IL-23 p19 mutant constructs were co-transfected with the non-tagged wild-type IL-23 p40 subunit at the 30 ml scale following the same transfection protocol described above. The conditioned media were transferred for analysis and the expression of all mutants was confirmed by anti-His Western-blot. Based on preliminary binding results, mutants M5, M7, M9, and M10 were selected and scaled up at 2 L scale with

the same transfection protocol. The wild-type was also scaled up at 2L. The scale-ups of wild-type and mutants of IL-23 at 2 liters of HEK cells were harvested and the supernatants were concentrated and buffer exchanged to PBS by tangential flow filtration with a 10 kDa membrane. The proteins were then purified by immobilized nickel affinity chromatography. The wild-type was eluted with 40mM imidazole and then buffer exchanged by desalting gel filtration chromatography to PBS (5.6mM Na_2HPO_4, 1.1mM KH_2PO_4, 154mM NaCl, pH 7.4). The purity of the wild-type was determined by SDS-PAGE to be >95%. The mutants were washed with 40mM imidazole followed by elution at 500 mM Imidazole. The elution pools were then buffer exchanged by dialysis to PBS (7mM Na_2HPO_4, 3mM NaH_2PO_4, 130mM NaCl, pH 7.1). The purity of the mutants was determined by SDS-PAGE to be >95%. Single alanine mutants of his-tagged IL-23p19 at key residues identified by alanine shave mutagenesis were generated by gene synthesis and then cloned into the transient transfection vector. Expression and purification were similar to the alanine shave mutants with the exception of M35A which was an affinity purified.

Biacore Binding Analysis of IL-23 Mutants to the IL-23p19 Antibody

[00261] The binding of the 30mL small scale expression of all seven (7) alanine mutants (see Table 27) was measured by surface Plasmon resonance (SPR, Biacore)) on a BIACORE® T100 in PBST (7mM Na_2HPO_4, 3mM NaH_2PO_4, 130mM NaCl, 0.05% Tween 20, pH 7.4) at 25 °C. The relevant antibodies and receptors were captured at a level of about 60 RUs by protein A immobilized at 2000 RUs on a CM5 sensor chip. In addition to the biAb3, Merck's IL-23 p19 mAb (7G10) and STELARA® (IL-12/IL-23 p40 mAb) were used as controls for domain binding. In addition, the commercial receptors for IL-23 were used as controls: hIL-23R-Fc and hIL-12Rβ1-Fc (both from R&D Systems). The supernatants were diluted 1:5 into PBST and injected at 30μL /min over the mAb or receptor surface for 3 minutes and, after a dissociation time, regenerated with 10mM Glycine, pH 2.0. Binding to a reference surface of Protein A without any captured antibody was subtracted from all specific binding curves before analysis. The results shown in Fig. 9 show the response 10 seconds before the end of the injection.

[00262] The Biacore results demonstrate that the IL-23 alanine shave mutants maintain binding to the p40 specific antibody and the p19 specific IL-23 receptor (except for M8 which potentially describes the receptor binding site). Binding of another IL-23p19 mAb and IL-12Rβ1-Fc was also performed and is consistent with the results of Fig. 9. The M5 mutant shows a dramatic loss of binding to 7B7 Mab while M9 & M10 show partial loss of

binding to 7B7 Mab (see Fig. 10). M7 does not show any impact to binding to the antibody or controls. Therefore, these four mutants were chosen for scale-up and purification, the three mutants that lose binding to the IL-23p19 antibody (7B7 antibody or Mab, 7B7 Fab and biAb3, all of which have a heavy chain variable domain as shown in SEQ ID NO:7 and light chain variable domain as shown in SEQ ID NO:9) and the M7 as a control.

[00263] Biacore analysis of the purified mutants used the same assay format as the supernatants except that the wild-type and mutant IL-23 was diluted to 25 nM and serially titrated 1:2 down to 1.5nM. All results obtained with the purified IL-23 mutants confirmed the data obtained with the expression supernatants. The data were fit to a 1:1 Langmuir binding model to determine the Kd values shown in Fig. 10 and Table 28. The 1-2 RU of reference subtracted binding observed for M5 binding to the IL-23p19 antibody (7B7 antibody or Mab, 7B7 Fab and biAb3, all of which have a heavy chain variable domain as shown in SEQ ID NO:7 and light chain variable domain as shown in SEQ ID NO:9) was simulated using the BIAsimulation software 2.1 using the average Rmax determined from kinetic analysis of M9 & M10. The affinity was estimated to be ≥330μM with a 1500 fold weaker Kd than wild-type as shown in Table 28.

Table 28. Biacore Kinetic Analysis of IL-23 Alanine Mutants Binding IL-23p19 Antibody

	7B7 mab			BiAb3	STELARA®	Merck 7G10
Variant	Kd (nM)	Kd-shift (from WT)	ΔΔG (kcal/mole)	ΔΔG (kcal/mole)	ΔΔG (kcal/mole)	ΔΔG (kcal/mole)
WT	0.14	NA	NA	NA	NA	NA
M5	≥ 300	1500	4.6	3.8	0.1	1.9
M7	0.4	3	0.5	NM	0.1	0.2
M9	25	140	2.9	2.3	0.1	0.2
M10	43	230	3.2	2.3	0.3	0.4

[00264] Biacore analysis of single alanine mutants was performed to confirm the non-linear epitope demonstrated by the M5, M9, and M10 alanine shave mutants. Most single alanine mutants in the three linear regions A, B, and C showed no change in binding to the 7B7 mAb or biAb3. Only three of the fourteen single alanine mutant of IL-23 tested

showed a significant decrease in binding affinity greater than 1 kcal/mole. The affinity and the ΔΔG values for the key residues overlapping between alanine shave mutants M5, M9, and M10 shown in Table 29 and demonstrate that one major residue in linear region B and two residues in linear region A contribute predominantly to the binding energy of the IL-23p19 antibody-IL-23 complex.

Table 29. Biacore Kinetic Analysis of IL-23 Single Alanine Mutants Binding IL-23p19 Antibody

	7B7 mab			BiAb3	STELARA®	Merck 7G10
Variant	Kd (nM)	Kd-shift (from WT)	ΔΔG (kcal/mole)	ΔΔG (kcal/mole)	ΔΔG (kcal/mole)	ΔΔG (kcal/mole)
WT	0.14	NA	NA	NA	NA	NA
His53 (region A)	0.2	0	0.2	0.2	0.3	0
Met 54 (region A)	6.8	48	2.3	2.2	0.3	1.0
Asp55 (region A)	9.6	68	2.5	2.3	0.5	0.7
Glu112 (region B)	0.7	5	0.9	1.2	0.3	1.7
Leu116 (region B)	46	330	3.4	3.0	0.5	0.2
Asp118 (region B)	0.1	0	0	-0.4	-0.3	-0.3

IL-23 Induced STAT3 Phosphorylation in BaF3/huIL-23Rα/huIL-12Rβ1 Transfectants

[00265] A murine bone marrow derived cell line (BaF3) was stably transfected with human IL-23Rα and human IL-12Rβ1 full length receptors and cloned. IL-23 induction of phosphorylation of STAT3 was monitored by ELISA for IL-23 Alanine shave mutants. BaF3/huIL-23Rα/huIL-12Rβ1 (clone 6) cells were washed three times with assay media before being plated at 50,000 cells per well in 96-well round-bottom tissue culture plates.

BaF3/huIL-23Rα/huIL-12Rβ1 cells respond to IL-23 in a dose dependant manner by phosphorylation of STAT3. To assess antibody inhibition of IL-23 signaling, an EC_{50} concentration of 20pM IL-23 was premixed with three-fold serial dilutions of each antibody from 33 nM to 0.56 pM and incubated at 37 °C for 15 minutes in assay media prior to addition to the cells. Following pre-incubation, treatments were added in duplicate to plates containing cells and incubated at 37 °C for 15 minutes to stimulate phosphorylation of STAT3. Stimulation was stopped with the addition of ice-cold wash buffer and cells lysed according to manufacturer's instructions (Bio-Rad Laboratories Cell Lysis kit, Cat #171-304012). Phosphorylated STAT3 levels were determined by ELISA (Bio-Rad Laboratories Phospho-$STAT3^{(Tyr705)}$ kit, Cat #171-V22552) according to manufacturer's instructions. Data was analyzed and IC_{50} values were calculated using GraphPad Prism 4 software. All the IL-23 Alanine shave mutants and all the IL-23 Alanine single mutants are active and equal potent as wt IL-23 (untagged and tagged) at inducing pSTAT3 activity on BaF3/huIL-23Rα/huIL-12Rβ1 transfectants (Table 30). Results for biAb3, STELARA® (IL-12/IL-23 p40 mAb), and Merck's IL-23p19 antibody (7G10) inhibition of IL-23 Alanine shave mutant induced pSTAT3 are shown in Table 31. biAb3 neutralizes the biological activity of wt IL-23 and IL-23 M7 Alanine shave mutant with equal potency, M9 and M10 with reduced potency, and does not neutralize the biological activity of M5 on BaF3/huIL-23Rα/huIL-12Rβ1 transfectants. STELARA® IL-12 p40 mAb neutralizes the biological activity of wt IL-23 and all the IL-23 Alanine shave mutants with equal potency on BaF3/huIL-23Rα/huIL-12Rβ1 transfectants. Positive control Merck IL-23 p19 mAb (7G10) neutralizes the biological activity of wt IL-23, M7, M9 and M10 Alanine shave mutants with equal potency and does not neutralize the biological activity of M5 on BaF3/huIL-23Rα/huIL-12Rβ1 transfectants.

Table 30. EC_{50} values for IL-23 Alanine shave mutants and IC_{50} Values for biAb3, STELARA® (IL-12/IL-23 p40 mAb), and Merck's IL-23p19 antibody (7G10) inhibition of IL-23 Alanine shave mutants induced pSTAT3 in BaF3/huIL-23Rα/huIL-12Rβ1 transfectants

Antibody	wt human IL-23	IL-23 M5	IL-23 M7	IL-23 M9	IL-23 M10
None (EC_{50})	21 pM	26 pM	21 pM	33 pM	19 pM
biAb3	19 pM	NA	17 pM	2400 pM	5300 pM
STELARA®	79 pM	62 pM	59 pM	67 pM	71 pM
Merck 7G10	380 pM	NA	310 pM	260 pM	350 pM

[00266] Single IL-23p19 mutations (H53A, M54A and D55A) were constructed and IC_{50} Values for 7B7, STELARA® (IL-12 /IL-23p40 mAb), and Merck's IL-23p19 antibody (7G10) (Table 31) to inhibit the single IL-23p19 mutated polypeptides to induce pSTAT3 in BaF3/huIL-23Rα/huIL-12Rβ1 transfectants was determined. The 7B7 mAb neutralizes the biological activity of IL-23 Alanine single mutants H53A, E112A, and D118A with equal potency, M54A and D55A mutants with significantly reduced potency, and does not neutralize the biological activity of L116A mutant compared to wt IL-23 on BaF3/huIL-23Rα/huIL-12Rβ1 transfectants (Table 31). STELARA® IL-12 p40 mAb neutralizes the biological activity of all the IL-23 Alanine single mutants with equal potency compared to wt IL-23 on BaF3/huIL-23Rα/huIL-12Rβ1 transfectants. Merck IL-23 p19 mAb neutralizes the biological activity of all the IL-23 Alanine single mutants with equal potency compared to wt IL-23 on BaF3/huIL-23Rα/huIL-12Rβ1 transfectants, except for IL-23 E112A mutant which it does not neutralize.

Table 31: IC_{50} Values for 7B7, STELARA® (IL-12 /IL-23p40 mAb), and Merck's IL-23p19 Antibody (7G10) to Inhibit IL-23p19 Single Mutations (H53A, M54A and D55A) to Induce pSTAT3 in BaF3/huIL-23Rα/huIL-12Rβ1 Transfectants

Antibody	IL-23 wt IC_{50} (nM)	IL-23 H53A IC_{50} (nM)	IL-23 M54A IC_{50} (nM)	IL-23 D55A IC_{50} (nM)	IL-23 E112A IC_{50} (nM)	IL-23 L116A IC_{50} (nM)	IL-23 D118A IC_{50} (nM)
7B7/biAb3	0.020	0.015	0.71	1.2	0.025	>3	0.012
STELARA® p40	0.067	0.078	0.081	0.077	0.033	0.054	0.052
Merck 7G10	0.18	0.19	0.27	0.18	>3	0.24	0.22

[00267] Taking all these results together, 7B7 mAb inhibition of IL-23 requires amino acids residues M54, D55, and L116, but does not require amino acid residues H53, E112, or D118. STELARA® and Merck antibodies were able inhibit the IL-23 Alanine single mutants M54A, D55A and L116A with no loss in activity, suggesting the loss in activity seen with IL-23 M54, D55 and L116 Alanine mutants are specific to the 7B7 mAb and the biAb3.

Oligomeric State Analysis of IL-23 Mutants and 7B7 Fab Complexes

[00268] To confirm the oligomeric state of the heterodimeric IL-23 mutants and their ability to complex with the 7B7 Fab, the proteins were studied by analytical size-exclusion chromatography (SEC-MALS) separation using an AGILENT® 1100 series HPLC fitted with a diode-array absorbance detector, on a Shodex Protein KW-803 column in buffer (0.1 um filtered) containing 200 mM K_2PO_4 (pH 6.8 with HCl), 150mM NaCl, and 0.02% sodium azide, at a flow rate of 0.5mL/min. A Wyatt Technology MINIDAWN™ TREOS® laser light scattering instrument was plumbed downstream from the HPLC, followed by a Wyatt OPTILAB® T-REX™ differential refractometer. Sixty (60) μg of each IL-23 sample was injected after filtering at a concentration of 10.3μM. For complex formation, 60μg of the 7B7 Fab was premixed with a 6% molar excess and incubated with the IL-23 protein at a concentration of 10.9μM at room temperature for at 3-6 hours before chromatographic separation. Particulates were removed from protein samples with a spin filter (NANOSEP® MF, 0.2μm, Pall Corporation) prior to injection. Data were analyzed with ASTRA® 6 (Wyatt) and Chemstation (Agilent). All mutants were mostly monomeric, similar to the wild-type. The M5 mutant did not show significant complex formation after pre-incubation with the Fab and eluted close to where the M5 IL-23 alone elutes demonstrating that little if any complex was formed in the 10μM concentration range of this experiment. M7 complexed and eluted similar to the wild-type. The M9 and M10 mutants form complex at these concentrations, but the mass was somewhat less than that of the wild-type and the retention time was slightly later than the wild-type and M7, suggesting that their affinity for 7B7 was weaker than the wild-type and M7. SEC-MALS analysis of the 14 single alanine mutants showed that all were mostly monomeric, similar to the wild-type, and only the L116A mutant showed a late-shifted elution time and a slight reduction in the expected mass of the complex suggesting that the affinity of the IL-23 for the 7B7 Fab was reduced. These results are consistent with the Biacore shift in Kd for these L116A. The effect of the reduced affinity of the complex of D54A and M55A with the Fab was not able to be resolved under the conditions of this assay.

Differential Scanning Calorimetry of IL-23 Mutants

[00269] The thermal stability profile for the wild type and mutant IL-23 heterodimers was measured by differential scanning calorimetry (DSC) using a MICROCAL® VP-capillary DSC instrument. 0.7 mg/ml protein samples in PBS (7mM

Na_2HPO_4, 3mM NaH_2PO_4, 130mM NaCl, pH 7.1) were scanned from 10-100 °C at 90o/hr, and the resulting thermograms were subjected to a buffer blank subtraction and fitting procedure. The denaturation of each molecule was characterized by two unfolding transitions and the fitted transition midpoint (Tm) values of each transition were within 1-4 °C of the wild type. The results show that none of the alanine shave mutants nor the 14 single alanine mutants show significant thermal destabilization relative to the wild type.

Fourier Transform Infrared Spectroscopy (FT-IR) Analysis of IL-23 Mutants

[00270] Secondary structure comparison of the alanine shave mutants and wild type of IL-23 was performed using a FT-IR spectroscopy on Biotools Prota FT-IR instrument with CaF_2 windows with a pathlength of ~7 μm and a Ne-He laser at 632.8nm. Data were collected with a resolution of 2 cm^{-1} and analyzed with Prota/Bomem-GRAMS/31 AI software. Duplicate measurements were made for each sample and the method variability is about 3%. Secondary structure content was calculated using Amide I peak as it is structure sensitive. Approximately an equal quantity of α-Helix and β-sheet was observed in all IL-23 samples as indicated by peaks at 1637 cm-1 for α-Helix and peak at 1637 cm-1 as well as shoulder at 1687 cm-1 for β-sheet. Overall no significant difference in FT-IR spectrum and calculated secondary structure result was observed in the alanine shave mutants compared to the wild type IL-23.

Circular Dichroism (CD) Analysis of IL-23 Mutants

[00271] Secondary structure comparison of the alanine shave mutants and wild type of IL-23 using CD spectroscopy was performed using a Jasco J-815 Spectrophotometer. The spectra were collected at 0.25 mg/mL IL-23 protein concentration in PBS pH7.1 using a 1mm path length cells at 25 °C from 300-190 nm with a data interval of 0.1nm, a 50 nm/min scanning speed, a 1nm bandwidth, and 2 accumulations. Overall no significant difference in secondary structure profile was observed in the alanine shave mutants compared to the wild type IL-23 using circular dichroism.

Nuclear Magnetic Resonance (NMR) Spectroscopy Analysis of IL-23 Mutants

[00272] Proton NMR is a highly sensitive technique that allows one to assess the conformational state at atomic detail. 1D ^1H NMR spectra were acquired for each of four mutant (M5, M7, M9, M10) and wild type IL23 proteins. All proteins were dialyzed simultaneously against NMR buffer (PBS in 8% D_2O/92% H_2O) to eliminate potential

differences resulting from sample preparation. In addition, ^{1}H signal intensities were corrected for differences in protein concentration by normalizing to the wild type spectrum. All NMR data was collected at 32 °C on a Bruker Avance 3 spectrometer operating at 600 MHz. 1D NMR spectra were acquired using the standard bruker pulse sequence (ZG) optimized for solvent and excipient suppression using the Watergate, WET, and Water flipback selective excitation pulse schemes. Two thousand forty-eight (2048) scans were signal averaged for each spectrum. Cosine squared apodization was applied prior to Fourier transformation, and a first order polynomial baseline correction was used to flatten the appearance of the baseline. Examination of each of the spectra for the individual proteins reveals that each mutant protein was properly folded, as evidenced by the well-dispersed resonances in both the high field (< 0.5 ppm) and low field (>6.5 ppM) regions of the spectra. The high field methyl resonances indicated the presence of an intact hydrophobic core; the downfield amide protons reflected the existence of well-formed secondary structure (alpha helices and beta sheets). Comparison of the spectra with that for wild type IL23 indicated a very close match, precluding the existence of large conformational changes in the protein structure induced by the amino acid substitutions. In addition, the NMR results also indicated that extra loss in activity in M5 is unlikely due to an extra large disruption in structural integrity at the mutation sites in M5. The fact that M5 was considerably closer to the wild-type protein by principle component analysis than M9 suggests, that the following M5-mutations which are missing in M9, *i.e.*, H53A, M54A and E112A do not cause much of a disruption in the M5-structure. It was also observed that mutants M7 & M9 which contain the elimination of an aromatic residue appeared most similar to each other in the principle component analysis. All single mutants appear similar to wild-type with the exception of D118A and M54A, however other controls demonstrate that these mutants maintain stability and activity similar to wild-type.

Summary of IL-23 Epitope Analysis

[00273] The methods of Alanine Shave and Single Mutagenesis have been used to map the epitope of hIL-23 for the 7B7 Fab contained in both the 7B7 Fab, 7B7 antibody and biAb3. The targeted mutagenesis strategy was performed using epitope information generated by proteolytic digest LCMS analysis, peptide binding, hydrogen/deuterium exchange mass spectrometry, solvent accessible surface area calculations and docking algorithm calculations. Small scale screening by SPR and scale-up of select purified mutants demonstrated a specific epitope for 7B7/biAb3 binding hIL-23. The M5 mutant shows dramatic decrease in binding

to 7B7/biAb3, while maintaining functional activity, binding to p40 and p19 specific reagents, monomeric oligomeric state, thermal stability, and secondary structural features similar to the wild-type. The M5 mutant showed a dramatic loss of binding to 7B7/biAb3 while M9 & M10, which each contained two of the same mutated residues as M5, each show partial loss of binding to 7B7/biAb3. The affinity of the M5 IL-23 mutant was ≥ 300nM for 7B7/biAb3 which is approximately 1,500-fold weaker than wild-type IL-23 demonstrating that the residues in the M5 mutant define the epitope for 7B7/biAb3 binding to IL-23. Thus, the data suggests that the 7B7/biAb3 antibody binds to a discontinuous epitope on the p19 subunit of IL-23. This discontinuous epitope on IL-23p19 comprises at least two epitope regions (region A (amino acid residues 33-59 of SEQ ID NO:6) and region B (amino acid residues 89-125 of SEQ ID NO:6)). Specifically, with respect to the first epitope or region A of IL-23p19, amino acid residues 54 (Met) and 55 (Asp) of SEQ ID NO:6 contribute a significant amount of binding energy to 7B7/biAb3's ability to bind IL-23p19. With respect to the second epitope or region B of IL-23p19, amino acid residue 116 (Leu) is the primary residue within Region B energetically contributing to 7B7/biAb3's ability to bind IL-23p19.

Example 8

Marmoset EAE Model

Background and Rationale

[00274] Multiple sclerosis (MS) is a chronic autoimmune, inflammatory, neurodegenerative disease of the central nerve system (CNS) characterized by a loss of myelin in the brain and spinal cord. Although the mechanisms underlying disease initiation are not clearly understood, the disease processes that contribute to clinical progression of multiple sclerosis are inflammation, demyelination, and axonal loss, or neurodegeneration. Macrophages and microglia are the main immune cells of the CNS. These cells, as well as T cells, neutrophils, astrocytes, and microglia, can contribute to the immune-related pathology of, e.g., multiple sclerosis. Furthermore, T cell reactivity/autoimmunity to several myelin proteins, including myelin basic protein (MBP), proteolipid protein (PLP), myelin oligodendrocyte protein (MOG), and perhaps other myelin proteins, have been implicated in the induction and perpetuation of disease state and pathology of multiple sclerosis. This interaction of autoreactive T cells and myelin proteins can result in the release of proinflammatory cytokines, including TNF-alpha, IFN-gamma, and IL-17, among others. Additional consequences are the proliferation of T cells, activation of B cells and macrophages, upregulation of chemokines and adhesion molecules, and the disruption of the

blood-brain barrier. The ensuing pathology is a loss of oligodendrocytes and axons, and the formation of a demyelinated "plaque". The plaque consists of a lesion in which the myelin sheath is now absent and the demyelinated axons are embedded within glial scar tissue. Demyelination can also occur as the result of specific recognition and opsinization of myelin antigens by autoantibodies, followed by complement- and/or activated macrophage-mediated destruction. It is this axonal loss and neurodegeneration that is thought to be primarily responsible for the irreversible neurological impairment that is observed in progressive multiple sclerosis.

[00275] Multiple sclerosis (MS) is classified into four types, characterized by the disease's progression.

[00276] (1) *Relapsing-remitting MS* (RRMS). RRMS is characterized by relapse (attacks of symptom flare-ups) followed by remission (periods of recovery). Symptoms may vary from mild to severe, and relapses and remissions may last for days or months. More than 80 percent of people who have MS begin with relapsing-remitting cycles.

[00277] (2) *Secondary-progressive MS* (SPMS). SPMS often develops in people who have relapsing-remitting MS. In SPMS, relapses and partial recoveries occur, but the disability doesn't fade away between cycles. Instead, it progressively worsens until a steady progression of disability replaces the cycles of attacks.

[00278] (3) *Primary-progressive MS* (PPMS). PPMS progresses slowly and steadily from its onset. There are no periods of remission and symptoms generally do not decrease in intensity. About 15 percent of people who have MS have PPMS.

[00279] (4) *Progressive-relapsing MS* (PRMS). In this relatively rare type of MS, people experience both steadily worsening symptoms and attacks during periods of remission.

[00280] Mayo Clinic (located on the internet at mayoclinic.org/multiple-sclerosis/types).

[00281] There is a large amount of clinical and pathological heterogeneity in the course of human multiple sclerosis. Symptoms most often begin between the ages of 18 and 50 years old, but can begin at any age. The clinical symptoms of multiple sclerosis can vary from mild vision disturbances and headaches, to blindness, severe ataxia and paralysis. The majority of the patients (approximately 70 – 75%) have relapsing-remitting multiple sclerosis, in which disease symptoms can recur within a matter of hours to days, followed by a much slower recovery; the absence of symptoms during stages of remission is not uncommon. The incidence and frequency of relapses and remissions can vary greatly, but as

time progresses, the recovery phases can be incomplete and slow to occur. This worsening of disease in these cases is classified as secondary-progressive multiple sclerosis, and occurs in approximately 10 - 15% of multiple sclerosis patients. Another 10 – 15% of patients are diagnosed with primary-progressive multiple sclerosis, in which disease symptoms and physical impairment progress at a steady rate throughout the disease process.

[00282] Both IL-23 and IL-17 are overexpressed in the central nervous system of humans with multiple sclerosis and in mice undergoing an animal model of multiple sclerosis, experimental autoimmune encephalomyelitis (EAE). The overexpression is observed in mice when the EAE is induced by either myelin oligodendrocyte glycoprotein (MOG) 35-55 peptide- or proteolipid peptide (PLP). Furthermore, neutralization of either IL-23/p19 or IL-17 results in amelioration of EAE symptoms in mice (Park et al, Nat Immunol. 6:1133 (2005); and Chen et al, J Clin Invest. 116:1317 (2006)).

Methods

[00283] Experimental autoimmune encephalomyelitis (EAE) is a well-characterized and reproducible animal model which replicates certain aspects of MS. EAE is inducible in rodents and non-human primates, such as the common marmoset. Genain, C. P. and Hauser, S. L., "Creation of a model for multiple sclerosis in Callithrix jacchus marmosets," J. Mol. Med., 75:187–197 (1997). In marmoset EAE, animals are immunized with a recombinant human myelin oligodendrocyte glycoprotein (rHuMOG) to induce the development of a disease closely resembling human multiple sclerosis. Published studies of this model have employed MOG emulsified in complete Freund's adjuvant (CFA) as the immunogen, in a single inoculation. Our early attempts to induce EAE in the marmoset using the published methodology led to onset of clinical symptoms between 23 to 142 days after MOG injection (data not shown). Since this timeline was considered to be too long for pre-clinical efficacy studies, a modified protocol employing an initial priming dose followed by a booster immunization to induce disease was employed. Using the prime/boost protocol as described in this study, we evaluated the activity of a surrogate bispecific antibody having an IL-17A/F binding entity and an IL-23 binding entity in this non-human primate model of EAE. The surrogate bispecific antibody was a biAbFabL (see Fig. 2), having the same IL-17 A/F binding entity as biAb-1, biAb-2, biAb-3 and biAb-4, while having a surrogate IL-23 binding entity as the IL-23 binding entity of biAb-3, for example, has reduced affinity for marmoset IL-23p19. Accordingly, an alternative IL-23 binding entity was utilized in the surrogate bispecific antibody. The alternative IL-23 binding entity utilized in the surrogate

bispecific antibody was the same IL-23 binding entity identified as IL-23 mAb in Fig. 13 and Fig. 14.

[00284] For induction of EAE, rHuMOG (BlueSky Biotech, Worcester, MA) was diluted in sterile PBS to 0.66 mg/ml and then emulsified with an equal volume of incomplete Freund's adjuvant (IFA, Sigma #F5506) containing 5 mg/mL of M. tuberculosis H37 RA (Difco # 231141). 300 µL of the final CFA/MOG mixture (containing 0.33 mg/mL of MOG and 2.5 mg/ml of H37RA) was injected at 2 sites on the shaved shoulder area of each animal (150 µl x 2 injection sites). All marmosets were immunized with CFA/MOG on the same day (Day 0).

[00285] On Day 21, the animals received a booster immunization of IFA/MOG, (prepared as above but without the H37 RA) injected at 2 injection sites over the shaved lumbar/hip area. Marmosets were anesthetized with Ketamine (15 mg/kg) via IM injection for the prime and boost inoculations.

[00286] The surrogate IL-23/17 AF bAb (IgG4.1k) was formulated in 20mM succinic acid, 150mM arginine buffer (pH 5.6). Dosing was started 1 day prior to the priming inoculation with CFA/MOG. Animals were given either placebo (PBS, SC, 2x/week) or IL-23/17 AF bAb (7 mg/kg, SC, 2x/week). Other treatment groups included BMS-938790 (IL-23 adnectin; 3 mg/kg, SC, 2x/week), ADX_PRD1651 (IL-23/17 binectin, 10 mg/kg, SC, 2x/week), and a surrogate IL-23 mAb IgG4.1 (IL-23.15-g4P, 9 mg/kg, SC, 2x/week). Doses were administered on Tuesdays and Fridays throughout the study period. Individual body weights were recorded weekly and animals were dosed based on individual body weight. All SC doses were administered into the flank area following topical swabbing with alcohol. The dose sites were alternated (left or right side) for each dose administration. Treatment groups at the start of the study consisted of 8 animals per group (mixed males and females). Animals were conscious and hand-restrained at the time of drug injection.

[00287] Visual assessments of disease status were made daily beginning on Day 12. Assessments were made and recorded by consensus of two investigators. Clinical scores were based on a modification of published disease score as described in Table 32 below.

Table 32 – Marmoset EAE clinical scoring system

0 = No Clinical signs
0.5 = reduced alertness/slow movements, or losing appetite
1.0 = weight loss >10% (initial wt. at beginning of study Day 0)

1.5 = unilateral or bilateral visual defects, dissociated gaze abnormalities
2.0 = vision impairment and/or balance is weak, ataxia, or abnormal gait
2.5 = mono or paraparesis of front or back limbs and/or sensory loss and/or brain stem syndrome
3.0 = hemi- or paraplegia (paralysis of the posterior half of one side) (can also include 1 leg and 1 hand paralysis at same time)
4.0 = quadriplegia
5.0 = moribund or spontaneous death

Results

[00288] The number of animals with signs/symptoms of EAE disease per groups was as follows:

[00289] *Group A* (PBS): 5 of 7 marmosets (71%) showed EAE-like disease and/or neurologic dysfunction at some point during the study. Disease presentation consisted of blindness and paralysis.

[00290] *Group B* (IL-23 adnectin, BMS-938790): 1 of 6 marmosets (17%) showed EAE-like disease. Disease presentation consisted of progressive blindness and paralysis.

[00291] *Group C* (IL-23/17 binectin, ADX_PRD1651): 6 of 7 marmosets (86%) showed EAE-like disease. However, 3 of the animals showed evidence of EAE signs/symptoms on only a single observation day.

[00292] *Group D* (IL-23 mAb): 3 of 6 marmosets (50%) showed EAE-like disease. Blindness was prevalent.

[00293] *Group E* (IL-23/17 AF bAb): 4 of 8 marmosets (50%) showed EAE-like disease; 3 of these 4 animals had transient symptoms with a "positive" score on only a single observation day. Disease consisted of mostly mild symptoms such as slow movement or reduced alertness.

[00294] Compared to the disease incidence in Group A (PBS), the difference in disease incidence in each of the other treatment groups was not statistically significant ($p>0.05$, Fisher's Exact Test).

[00295] A small subset of animals in the study did develop more severe signs/symptoms of EAE, with several marmosets requiring euthanasia to comply with pre-established humane endpoints. The number of animals in each group requiring euthanasia was as follows: Group A (2); Group B (1); Group C (1); Group D (0); Group E (0).

[00296] Animals that were euthanized for humane reasons as a result of EAE symptoms were assigned a clinical severity score of "4" at the time of euthanasia which was carried throughout the remainder of the study for the purpose of calculating a group mean clinical severity score. Fig. 12 depicts the mean clinical severity score for each treatment group over the course of the study. Group A (PBS) reached a peak score of approximately 1.6 by the end of the study. All other groups displayed lower mean clinical scores, with Group E (IL-23/17 AF bAb) showing only a brief period (~1wk) when any signs of EAE disease were evident. Due to the limited numbers of animals in each group and the inter-animal variability in EAE disease scores among animals within a group, none of the differences between Group A (PBS) and the other treatment groups was statistically significant (Mann-Whitney U Test).

[00297] In summary, this study showed a trend toward reduced disease severity and reduced disease incidence in the marmoset EAE model by several of the compounds evaluated. Overall, the animals treated with IL-23/17 AF bAb (IgG4.1k) appeared to experience the most beneficial outcome (Fig. 12), though the differences between groups were not statistically significant. The finding that the animals treated with the IL-23/17 AF bAb were better protected than the animals treated with just the IL-23 mAb, suggests that dual targeting of both the IL-23 and IL-17AF pathways will result in greater efficacy in the treatment of human diseases in which these cytokine pathways play a role, including but not limited to multiple sclerosis.

Post-Mortem MRI

[00298] At the end of the study, the surviving marmosets were submitted for necropsy. The skull cap was removed and the brain was fixed in situ in formalin for 3 weeks. To assess lesions in white matter and the optic tracks, T2W and proton density MRI scans were conducted with the Bruker Biospec 7T system with a 72mm Quad RF coil, using the following parameters: Total scan time ~ 15 - 20 mins per sample, 23 axial images were collected, TR/TE = 5000/20ms, slice thickness = 1.2mm, FOV = 4cm, matrix = 256x256, in-plane resolution = 156mm^2.

[00299] Scans were reviewed and semi-quantitative interpretations were performed by consensus reading of 3 radiologists after review of all MRI images for each group of animals. Lesion scoring was based on lesion count in the white matter covering the entire brain. Optic nerve scoring was based on swelling and increased signal intensity reflecting inflammation in the optic tract and nerve.

[00300] Overall, a significant ($p < 0.05$) reduction in lesion load was observed for the IL-23/17 AF bAb group compared to the vehicle group (Fig. 13). The optic tract score was also significantly lower in the IL-23/17 AF bAb group compared to vehicle (Fig. 14). None of the other treatment groups were significantly different than vehicle-treated group for either of these MRI measurements. Thus, consistent with the clinical disease scores, the group of animals treated with the IL-23/17 AF bAb had the lowest mean MRI values again suggesting that dual targeting of both the IL-23 and IL-17AF pathways will result in greater efficacy in the treatment of diseases in humans.

Example 9

IL-17A and IL-17F Epitope Mapping

[00301] The analysis described in this Example 9 aims to identify the epitopic residues on IL-17A and IL-17F for which the IL-17A/F binding entity of biAb3 (heavy chain variable domain as shown in SEQ ID 13 and light chain variable domains as shown in SEQ ID NO:9) binds.

[00302] The strategy to identify the key differences between the epitope of the biAb3 and the mouse parent (339.15.5.3) utilized X-ray crystallography, site-directed mutagenesis, in-silico mutagenesis, and binding and functional assays to analyze the mutants. The heavy chain variable domain of the IL-17A/F binding entity of biAb3 is a humanized version of the heavy chain variable domain of clone 339.15.5.3, clone 339.15.3.6 or clone 339.15.5.3. The heavy chain CDR residues of the IL-17A/F binding entity of biAb3 and clone 339.15.5.3, clone 339.15.3.6 or clone 339.15.5.3 are identical. However, the two mAbs differ in the framework region of their heavy chain variable domains. The two mAbs have different light chains therefore the residues of IL-17 in contact with the light chain of each mAb was the focus of this study.

X-ray crystallography

[00303] IL17A Fab complex and IL17F Fab complex crystallography was performed to determine the contact interface residues for contact surface modeling for epitope / paratope residue predictions, and buried surface determination. The three-dimensional structures were also used for Protein Mutant energetic calculations based on modeled crystal structure complexes.

[00304] The Fabs of each antibody were cloned and expressed periplasmically in E.coli strain BL21 (humanized 339-134) or BL21 Star (BiAb). Purification for both included

IMAC followed by SEC. Both IL-17A and IL-17F were expressed in E.coli strain W3110 as inclusion bodies and refolded, followed by a several step purification.

[00305] The Fab derived from the IL-17 arms of the biAb3 (heavy chain variable domain of SEQ ID NO:13 and heavy chain CH1 domain of SEQ ID NO:15; and a light chain of SEQ ID NO:17) and the Fab derived from the humanized lead of the parent (humanized anti-human IL-17A/F antibody 339-134 mAb (SEQ ID NO:65 and SEQ ID NO:67) were complexed with either human IL-17A or IL-17F. Complex formation of either IL-17A or IL-17F with the BiAb3 and the humanized anti-human IL-17A/F antibody 339-134 mAb was monitored by SEC.

[00306] Co-crystals of each of the four complexes were generated by broad screening followed by optimization of crystallization conditions. A data set on each sample was collected at the APS LS-CAT beamlines.

Table 33 - Summary of X-ray crystallography dataset resolution.

Complex	Resolution
IL-17A A2999F/Parent Fab A3052F	2.85 Å
IL-17F A2768F/Parent Fab A3052F	3.75 Å
IL-17A A2999F/Lead Fab A3185F	3.4 Å
IL-17F A2768F/Lead Fab A3185F	4.25 Å

[00307] Each structure was determined by molecular replacement using Phaser MR from the CCP4 suite. The IL-17A search model was derived from PDB ID 2VXS. The IL-17F search model was taken from PDB ID 1JPY. For each Fab, search models were generated for the constant and variable domains using the humanized Fab from PDB ID 3IDX with the hypervariable loops deleted. The final models were obtained after iterative rounds of refinement in REFMAC5 and manual model building in Coot. In addition, additional rounds of refinement and map generation in Autobuster were performed for model building and refinement of all of the lower resolution structures. Crystallographic statistics for data collection and refinement are shown for the humanized parental Fab structures in Table 34 and the humanized lead Fab structures in Table 35. Each structure was assessed for geometry using MolProbity which had been downloaded to run on an internal server.

Table 34 - Crystallographic statistics for the humanized parental Fab A3052F in complex with either IL-17A or IL-17F

	IL-17A/Parent Fab A3052F		IL-17F/Parent Fab A3052F	
	Overall	**Highest shell**	**Overall**	**Highest shell**
Crystal ID	238318e7		238699f10	
Unique puck ID	oyg0-1		apa7-6	
Collection date	1-Nov-2012		18-Dec-2012	
$\Delta\phi$	0.5°		1.0°	
Images	71-260 (95°)		1-180 (180°)	
Wavelength	0.97856 Å		0.97856 Å	
Space Group	$P3_221$		$C2$	
Unit Cell	$a = b = 141.9$ Å, $c = 91.2$ Å $\alpha = \beta = 90°$, $\gamma = 120°$		$a = 226.1$ Å, $b = 62.3$ Å, $c = 117.3$ Å $\alpha = \gamma = 90°$, $\beta = 104.4°$	
Solvent content	70%		60%	
V_m	4.1 Å^3/Da		3.1 Å^3/Da	
Resolution	50-2.85 Å	2.91-2.85	50-3.75 Å	3.84-3.75
I/σ	18.2	2.3	16.7	2.0
Completeness	99.1%	99.3%	97.4%	97.2%
R_{merge}	0.062	0.538	0.066	0.709
Multiplicity	5.9	6.0	3.4	3.5
Reflections	24,828	1821	16,223	1198
Mosaicity	0.4		0.3-0.8	
Refinement				
R	0.269		0.251	
R_{free}	0.309		0.300	
Validation				
Ramachandran favored	91.9%		86.8%	
Ramachandran outliers	1.0%		3.6%	
Rotamer outliers	3.2%		10.3%	
Clash score	3.78 (100th)		10.08 (97th)	
Molprobity score	2.04 (99th)		2.92 (91st)	

Table 35 - Crystallographic statistics for the humanized lead Fab A3185F alone or in complex with IL-17A or IL-17F

	Lead Fab A3185F		**IL-17A/Lead Fab A3185F**		**IL-17F/Lead Fab A3185F**	
	Overall	**Highest shell**	**Overall**	**Highest shell**	**Overall**	**Highest shell**
Crystal ID	243072a6		240719f6		238860g7	
Unique puck ID	koc5-3		jsm6-5		cum1-2	
Beamline	APS 21 ID-D		APS 21 ID-D		APS 21 ID-G	
Collection date	18-April-2013		18-April-2013		30-Nov-2012	
$\Delta\phi$	1.0°		1.0°		0.5°	
Images	1-257 (257°)		1-180 (180°)		1-180 (180°)	
Wavelength	0.93005 Å		0.93005 Å		0.97856 Å	
Space Group	*C*2		$C222_1$		$P2_1$	
Unit Cell	*a* = 92.1 Å, *b* = 60.1 Å, *c* = 73.0 Å, α = γ = 90°, β = 94.9°		*a* = 54.6 Å, *b* = 83.6 Å, *c* = 248.9 Å, α = β = γ = 90°		*a* = 115.0 Å, *b* = 61.8 Å, *c* = 124.9 Å, α = γ = 90°, β = 92.3°	
Solvent content	39%		51%		64%	
V_m	2.0 $Å^3$/Da		2.5 $Å^3$/Da		3.4 $Å^3$/Da	
Resolution	50-2.1 Å	2.14-2.10 Å	50-3.4 Å	3.48-3.40 Å	50-4.25 Å	4.35-4.25 Å
I/σ	13.2	3.9	18.6	3.1	13.7	2.8
Completeness	99.6%	99.4%	98.1%	97.5%	98.2%	98.9%
R_{merge}	0.108	0.450	0.090	0.583	0.066	0.556
Multiplicity	5.2	5.3	4.5	4.9	3.6	3.7
Reflections	23,262	1708	9200	653	12,522	931
Mosaicity	0.3		0.5		0.3	
Refinement						
R	0.175		0.243		0.285	
R_{free}	0.227		0.313		0.347	
Validation						
Ramachandran favored	97.3%		94.1%		92.5%	
Ramachandran outliers	0.0%		0.8%		1.4%	
Rotamer outliers	0.8%		5.3%		4.4%	
Clash score	2.91 (99^{th})		3.40 (100^{th})		3.98 (100^{th})	
Molprobity score	1.22 (100^{th})		2.08 (100^{th})		2.14 (100^{th})	

[00308] Each Fab primarily bound to one half-site of the IL-17 homodimer primarily through its heavy chain, and to a lesser extent through the light chain. Differences in binding of the humanized parent and humanized lead Fab appear consistent with higher affinity of the humanized lead Fab.

[00309] Globally, each of the IL-17/BMS Fab complexes exhibited the same overall structure in which one Fab recognized one half-site of the IL-17 homodimer (Fig. 15). Thus, the binding stoichiometry is shown crystallographically to be two (2) Fabs to one (1) IL-17 homodimer (or two (2) Fabs to two (2) IL-17 protomers). The majority of the interactions with the interleukin are formed by the heavy chain with the hypervariable loop3 (or complementary determining region CDR3) forming the heart of the antibody-antigen interaction. In addition, a number of residues of CRD2 of the heavy chain interact with the

interleukin. CDR1 of the heavy chain does not appear to interact with the interleukin significantly. For the light chain, CDR3 is involved in the recognition of IL-17. CDR1 of the light chain also appears to provide a weak, longer range binding interaction.

[00310] The crystal structure coordinates were used to define the contact interface as previously described (S. Sheriff., "Some Methods for Examining the Interaction between Two Molecules," Immunomethods, 3:191-196 (1993)), where a minimal definition, defined as residues in contact, was derived from the program CONTACSYM (Sheriff, S., Hendrickson, W.A., and Smith, J.L. (1987). Structure of Myohemerythrin in the Azidomet State at 1.7/1.3 Å Resolution. J. Mol. Biol. 197, 273-296.). A maximal definition of the interface, defined as residues at least partially buried by the interaction, was derived from Program MS (Connolly, M.L. (1983). Analytical Molecular Surface Calculation. J. Appl. Crystallogr. 16, 548-558).

Table 36 – Contact and Buried Interface Residues of Complexes

IL17 Type	IL17A (SEQ ID NO:2)		IL17F (SEQ ID NO:4)			
mAb Type	Humanized Parent	Humanized Lead	Humanized Parent		Humanized Lead	
Resolution	2.85 Å	3.4 Å	3.75 Å		4.2 Å	
Chain			A	B	A	B
		Asn 75	Asn 83		Asn 83	Asn 83
	Ala 92	Ala 92	Ala 100	Ala 100	Ala 100	Ala 100
	*Lys 93	*Lys 93	*Gln 101	*Gln 101	*Gln 101	*Gln 101
	*Cys 94	*Cys 94	*Cys 102	*Cys 102	*Cys 102	*Cys 102
	*Arg 95	*Arg 95	*Arg 103	*Arg 103	*Arg 103	*Arg 103
	*His 96	*His 96	*Asn 104	*Asn 104	*Asn 104	*Asn 104
	*Leu 97	*Leu 97	*Leu 105	*Leu 105	*Leu 105	*Leu 105
	*Gly 98					Gly 106
	Asp 103					
				Lys 113	Lys 113	
	*Val 106	Val 106	*Glu 114	*Glu 114	*Glu 114	Glu 114
	Asp 107	Asp 107	Asp 115	Asp 115	Asp 115	Asp 115
	*Tyr 108	*Tyr 108	*Ile 116	*Ile 116	*Ile 116	*Ile 116
	*His 109	*His 109	Ser 117	*Ser 117	*Ser 117	*Ser 117
					Met 118	Met 118
	*Asn 111	*Asn 111	*Asn 119	*Asn 119	*Asn 119	*Asn 119
	*Ser 112	*Ser 112	*Ser 120	*Ser 120	*Ser 120	*Ser 120
	*Val 113	*Val 113	*Val 121	*Val 121	*Val 121	*Val 121
	*Pro 114	*Pro 114	Pro 122	Pro 122	*Pro 122	*Pro 122
			*Gln 124	Gln 124		*Gln 124
	Ser 141	Ser 141	Thr 149	Thr 149	Thr 149	Thr 149
	Val 147	*Val 147	Val 155	Val 155	Val 155	
		Thr 148	Thr 156	Thr 156	Thr 156	Thr 156
	*Pro 149	*Pro 149	*Pro 157	*Pro 157	*Pro 157	*Pro 157
	*Ile 150	*Ile 150	*Val 158	*Val 158		Val 158
	*Val 151	*Val 151				
	His 152	*His 152				
	His 153	His 153				

Residues with an asterick (*) are in contact at the complex interface.

Residues lacking an asterick are completely buried in the complex contact interface.

[00311] The main interaction of the Fab with IL-17A (SEQ ID NO:2) appears to be to residues L97 and a stretch of residues from H109-N111 (Fig. 15). I100, G98, N111, S112, V113, and P114 are conserved between IL-17A and IL-17F (amino acid residues I100, G98, N111, S112, V113, and P114 of SEQ ID NO:2 or IL-17A correspond to amino acid residues I108, G106, N119, S120, V121, and P122 of SEQ ID NO:4 or IL-17F). Thus, after obtaining

this initial structure, it was expected that the humanized parent Fab A3052F would bind IL-17F in essentially an identical manner as that observed with IL-17A. However, near these residues there are several residues which differ between IL-17A (SEQ ID NO:2) and IL-17F (SEQ ID NO:4), such as K93 in IL-17A (Q101 in 17F), H95 in IL-17A (N104 in 17F), Y108 in IL-17A (I116 in 17F), and H109 in IL-17A (S117 in 17F). The C-terminus of IL-17A (SEQ ID NO:2) also appears to weakly interact with the Fab through residues P149 and I150, which correspond to residues P157 and V158 of IL-17F (SEQ ID NO:4). However, the differences between IL-17A and IL-17F would not be expected to alter the global antibody-antigen interaction significantly.

[00312] In comparison with the 2.85 Å resolution of the humanized parent Fab, the 3.4 Å resolution of the humanized lead Fab exhibits very similar interactions between the heavy chain and the interleukin as expected given the same sequence for the heavy chain. In contrast, the light chains between these two Fabs are completely different and as expected, these residues coordinate the interleukin in a different manner. The biAb Fab has one fewer residue in CDR3 which allows the loop to stretch out over the interleukin, allowing the backbone oxygen of G93 (G93 of SEQ ID NO:9 or G4 of SEQ ID NO:27) of the biAb Fab to form a direct hydrogen bond with the backbone nitrogen of Y108 of SEQ ID NO:2 (IL-17A). The same atom (backbone oxygen of N91 of SEQ ID NO:67 in the humanized parent Fab) was 2.3 Å away from the location in the parent Fab and was unable to hydrogen bond with the interleukin. Furthermore, the change of WN to YG allows Y33 of CDR1 (Y33 of SEQ ID NO:9) to approach the interleukin by 5.1 Å relative to its position in the lower affinity parent Fab thereby gaining additional packing interactions with H109 of IL-17A (SEQ ID NO:2). Finally, Y96 (Y96 of SEQ ID NO:9) of the biAb Fab may form a hydrogen bond with N106 (N106 of SEQ ID NO:13) of the heavy chain, assisting to align it in a hydrogen bond with the Y108 (Y108 of SEQ ID NO:2) backbone oxygen of the interleukin (IL-17A). Overall, these changes in the interface of CDR3 of the biAb Fab appear consistent with its higher affinity and have been tested by site-directed mutagenesis as shown below.
Unfortunately, crystal structures were not obtained for a complex consisting of the mouse parental Fab with either IL-17A or IL-17F. This suggests that the conditions for optimizing the interactions of these complexes are different from those used for successful crystallization of the humanized parental and lead Fabs.

[00313] In addition to interpretation of individual residue contacts, another measure of the differences in the humanized parent Fab vs. the biAb bound to the interleukin can be captured by calculating the total surface area buried by the interacting regions of the

IL17/Fab complexes. This analysis was carried out using the MS algorithm for the IL-17A Fab complexes, as they were the highest resolution, and should provide the most reliable comparison. The two structures with IL-17F were over 3.5 Å and not considered reliable for this analysis. The parental Fab buried 720 $Å^2$ on IL-17A, while the biAb Fab buried 820 $Å^2$ (see Table 37). This difference (100 $Å^2$) in surface area is supported by the measured increased binding affinity of the lead Ab for IL-17A. Interestingly, the surface area of due to an extended side chain conformation for many amino acids is less than 100 $Å^2$ (A,N,D,C,G,L,P,S,T,V), see *Atlas of Protein Side-Chain Interactions V1.* Singh and Thornton 1992, 6-11). So, in aggregate by this measurement, the binding epitope difference on IL-17A for the lead vs. the parental structures might be described as approximately one (1) residue equivalent.

Table 37 – Surface Area

	Complex	
	IL-17A / Parent	IL-17A / Lead
Resolution	2.85 Å	3.4 Å
Buried on IL-17A	720	820
Buried on FAB	740	830

Computational Epitope Prediction and Design of Alanine Shave Mutants

[00314] To provide detailed characterization of the different contributions of IL-17A and IL-17F epitope residues to the binding kinetics of the Parental and Lead Fabs, residues in the binding interfaces identified by X-ray crystallography were selected for site specific mutation to further distinguish differences between the binding of the human parent mAb and biAb.

[00315] A variety of criteria for selection of individual and multiple mutations on a single molecule were employed to select a set of representative and informative mutants to test. Crystal structures of IL-17A/Parental Fab, IL-17F/Lead Fab, described earlier herein were used to inform selection of residues to mutate. Residues at the ligand- Fab interaction interface were selected, while focusing on residues in contact with Fab light chain residues. Regions of poor definition in the crystal structure for one Fab but not the other were also selected because t his may suggest a difference in residue mobility within the complex in parent vs. biAb. In addition, residue positions where homologous IL-17 A/F residues differ were also selected because this may indicate tolerance to change for Fab binding, or may contribute to different binding affinities relative to the parental and biAb Fabs. The interface

was modeled with the proposed mutants to look for differences in energetics in complex with parental vs. biAb Fabs. Clusters of contact residues (alanine shave mutants) were combined to generate mutants with additive or synergistic changes in binding affinity. The mutants of each interleukin which were generated for experimental analysis are shown in Table 38 and 39.

Table 38: IL-17A mutants

IL17A-WT	Residues 24-155 of SEQ ID NO:2
IL17A-M1	N105A, Y108A, H109A
IL17A-M2	L97A, Y108A, N111A
IL17A-M3	K61A
IL17A-M4	K61A, S64A, R69A
IL17A-M5	N105A
IL17A-M6	Y108A
IL17A-M7	H109A
IL17A-M8	V106A, D107A
IL17A-M9	I150A, V151A
IL17A-M10	Y108A, H109A, V151A, H152A
IL17A-M11	Y108A, V151A
IL17A-M12	H109A, I150A, H152A

Table 39: IL-17F mutants

IL17F-WT	Residues 31-163 of SEQ ID NO:4
IL17F-M1	L105A, I116A, N119A
IL17F-M2	K113A, E114A, I116A
IL17F-M3	S69A, R72A, R77A
IL17F-M4	S69A
IL17F-M5	R72A
IL17F-M6	K113A
IL17F-M7	E114A
IL17F-M8	I116A
IL17F-M9	D115A, S117A
IL17F-M10	V158A, I159A

Cloning & Expression of IL-17A & F epitope mapping alanine mutants

[00316] The mutant constructs of IL-17A and IL-17F were generated by gene synthesis and then cloned into the transient transfection vector for expression in HEK293-6E cells. 30mL cultures of HEK293-6E cells at 1×10^6 cells/ml were transfected with expression plasmids/PEI complex and cells harvested on 120 hours post transfection.

Biacore concentration analysis of IL-17A&F mutants

[00317] The concentration of each alanine mutant of IL-17A and IL-17F in the HEK harvest supernatants was quantitated by the level of capture on an anti-his Fab Biacore sensor surface. Protein A and huIgG surfaces were also immobilized as controls to assess non-specific binding of supernatants (no non-specific binding was observed). The concentration in each supernatant was quantitated using a standard curve of purified IL-17A-his or IL-17F-his ranging from 80ug/mL to 0.039 ug/mL. The calibration curve was fit to a linear curve for the data from 0.3125 to 0.0039ug/mL. The supernatants were run at 1:20, 1:60 and 1:180 dilution to allow multiple measurements in the linear range of the standard curve.

[00318] IL-17A mutant 8 had significantly reduced expression (only about 10% of the expression level of the wild-type). IL-17F mutants M2, M3, M7, and M9 had significantly reduced expression. The M9 mutant of IL-17F was virtually undetectable while the IL-17F M2 and M7 mutants were at less than 5% of the wild-type expression level.

Table 40: Expression levels of IL-17A and IL-17F constructs in HEK supernatants

IL-17 variant	µg/mL expression level in HEK supernatants
IL17A-WT	7.2
IL17A-M1	6.3
IL17A-M2	13.0
IL17A-M3	15.3
IL17A-M4	18.6
IL17A-M5	10.3
IL17A-M6	11.7
IL17A-M7	12.4
IL17A-M8	0.6
IL17A-M9	13.6
IL17A-M10	14.8
IL17A-M11	13.2
IL17A-M12	12.1
IL17F-WT	13.6
IL17F-M1	16.2
IL17F-M2	0.3
IL17F-M3	1.4
IL17F-M4	12.2
IL17F-M5	6.8
IL17F-M6	7.1
IL17F-M7	0.3
IL17F-M8	10.3
IL17F-M9	<0.1
IL17F-M10	15.0

IL-17 Bioassay (NIH/3T3/KZ170 NF-κB Luciferase Reporter assay)

[00319] A murine fibroblast cell line (NIH/3T3, ATCC# CRL-1658) was stably transfected with an NF-κB luciferase reporter designated KZ170 and cloned out. NIH/3T3/KZ170 clone 1 cells were seeded at 10,000 cells/well in 96-well white opaque luciferase plates and incubated overnight at 37°C. The following day serial dilutions of recombinant human IL-17A, IL-17F, IL-17A Alanine mutants, and IL-17F Alanine mutants, using the Biacore determined concentrations, were made up in assay media and added to the plates containing the cells and incubated at 37°C for 4 hours. Following incubation the media was removed and cells lysed before being read on the Berthold Centro XS^3 Luminometer using flash substrate according to manufactures instructions. Increases in mean fluorescence intensity (via activation of the NF-κB luciferase reporter) were indicative of an IL-17A or IL-17F receptor-ligand interaction. EC_{50} (effective concentration at 50 percent) values were calculated using GraphPad Prism®4 software for each IL-17A and IL-17F Alanine mutant.

All of the IL-17A mutants show cell functional activity, though some have lost a few fold in activity with respect to wild-type (Fig. 16). All IL-17F mutants except M3 show cell functional activity, though 3 of the mutants (M2, M5, M10) show significantly reduced activity (Fig. 17).

Biacore binding analysis of IL-17A&F mutants for binding to the BiAb3 and other related antibodies

[00320] The antibodies used for the Biacore binding assay were the biAb3 (heavy chain variable domain as shown in SEQ ID NO:7 and light chain variable domain as shown in SEQ ID NO:9) and the mouse parent antibody 339.15.5.3 (which contains the same variable region sequences as 339.15.3.5 and 339.15.3.6). Isotyping using the IsoStrip Mouse Monoclonal Antibody Isotyping Kit (Roche, Indianapolis, IN, USA) demonstrates that the 339.15.5.3 antibody is the IgG2a/kappa just like the 339.15.3.5 used for humanization. No sequence or isotype differences have been determined between 339.15.3.5 and 339.15.5.3.

[00321] The binding of the supernatants from the 30mL expression of all 12 IL-17A and 10 IL-17F alanine mutants and a wild-type control supernatant for each (see Table 41 and Table 42) was measured by surface Plasmon resonance (SPR, Biacore)) on a Biacore T100 in HBS-EP (10mM HEPES, 3mM EDTA, 150mM NaCl, 0.05% Tween 20, pH 7.4) at 25°C. The relevant antibodies and receptors were captured at a level of about 150-250 RUs by protein A immobilized at 3000 RUs on a CM5 sensor chip. In addition to the biAb3 and the parent mAb (339.15.3.5), other anti-IL-17 mAbs were used as controls for domain binding. In addition, the commercial receptor for IL-17A was used as a control: hIL-17RA-Fc (from R&D Systems) though a suitable IL-17RC reagent was not identified for this assay. The supernatants were diluted based on the anti-his quantitation determined concentration into HBS-EP at a concentration of 9 nM and diluted serially 1:3 and injected at 30uL/min over the mAb or receptor surface for 90 seconds and, after a dissociation time, regenerated with 10mM Glycine, pH 1.5. IL-17A M2 and IL-17F M1 were also run at higher concentration (in the 400-500 nM range at the expression level of the supernatant) because little to no binding signal was observed for the biAb captured surface. Binding to a reference surface of Protein A without any captured antibody was subtracted from all specific binding curves before analysis. All titration curves were fit to a 1:1 Langmuir binding model to determine the Kd values shown in Fig. 18 and Tables 41 and 42.

[00322] The Biacore results demonstrate that the IL-17A mutants M1, M2, M6, M10, and M11 show a reduction in binding affinity for the BiAb and contain residues that

contribute to the binding epitope differences compared with the parent antibody. Most of these mutants show a 3-15 fold reduction (45-fold for M1) in binding to the IL-17RA-Fc likely because the receptor binding site has been altered. However, the cellular potency was maintained within a few fold for all mutants that impacted the BiAb3 interaction suggesting that these receptor disruptions are not significant for function.

[00323] The IL-17F mutants M1, M2, M7, and M8 show a reduction in binding affinity for the biAb however these same mutants show a similar reduced binding affinity for the parent antibody indicating that the epitope change between parent and biAb in IL-17A does not translate to IL-17F. These four mutants maintain potency in the cell functional assay similar to wild-type IL-17F, however many of the other mutants do not which limits our interpretation of the IL-17F mutagenesis.

Table 41: Biacore Kinetic Analysis of IL-17A Alanine Mutants Binding biAb3 and mouse parent antibodies

	biAb3			mouse parent		
Variant	Kd (nM)	Kd-shift (from WT)	ΔΔG (kcal/mole)	Kd (nM)	Kd-shift (from WT)	ΔΔG (kcal/mole)
WT	0.05	none	0	0.03	none	0
M1	0.23	4.5	0.9	0.02	none	-0.3
M2	>1uM	>20,000	>5.9	>1uM	>35,000	>6.2
M3	0.05	none	0	0.02	none	-0.4
M4	0.09	2	0.4	0.02	none	-0.3
M5	0.04	none	-0.2	0.01	none	-0.9
M6	0.11	2.2	0.5	0.02	none	-0.3
M7	0.04	none	-0.2	0.01	none	-0.4
M8	0.05	none	0	0.03	none	0.1
M9	0.04	none	-0.1	0.01	none	-0.4
M10	0.3	5.7	1.0	0.02	none	-0.3
M11	0.11	2.2	0.5	0.01	none	-0.4
M12	0.06	none	0.1	0.02	none	-0.3

Table 42: Biacore Kinetic Analysis of IL-17F Alanine Mutants Binding biAb3 and mouse parent antibodies

	biAb3			Mouse parent		
Variant	Kd (nM)	Kd-shift (from WT)	ΔΔG (kcal/mole)	Kd (nM)	Kd-shift (from WT)	ΔΔG (kcal/mole)
WT	0.08	none	0	0.005	none	0
M1	>1uM	>12,000	>5.6	>1uM	>100,000	>7.3
M2	0.7	9.0	1.3	0.01	2	0.5
M3	0.15	2.0	0.4	<0.001	none	-1.3
M4	0.08	none	0	<0.001	none	-0.8
M5	0.11	none	0.2	<0.001	none	-2.1
M6	0.08	none	0	<0.001	none	-1.6
M7	0.55	7.0	1.2	0.03	5.9	1.1
M8	0.2	2.5	0.6	0.02	3.7	0.8
M9	NM	NM	NM	NM	NM	NM
M10	0.09	none	0	<0.001	none	-1.6

NM - not measured because the mutant was not expressed at detectable levels.

In Silico Mutagenesis

[00324] Energetic analyses were preformed for the IL-17A-Parent Fab, IL-17A-Lead Fab, and IL-17F-Lead Fab. Because the X-ray structures of the complexes were incomplete protein modeling was used to complete the structural models by building in the missing amino acid side chains using standard protocols (Maestro protein preparation wizard and Prime side chain modeling). The structural models were then used to calculate interaction energies for wildtype protein (IL-17A or IL-17F) or mutant IL-17 molecules with the Fabs. The interaction energies are a measure of the calculated affinity of the Fab towards the IL-17 (treated as ligand). In order to calculate the stability and delta-stability of mutant proteins the software MOE (ver. 2012.10, Chemical Computing Group) was used. The Residue Scanning protocol was used to perform computational site-directed mutagenesis to generate mutations and perform the affinity and stability calculations.

[00325] A comparison of the computational predicted binding energies with the calculated ΔΔG values determined from the Biacore affinities for IL-17A mutants are shown in Fig. 19. The IL-17A mutants identified in Fig. 19 are mislabeled. The SEQ ID NO:2 numbering of IL-17A mutants identified in Fig. 19 are one less than they should be. The mutants are as identified as in Table 38. For example, N104A, Y107A and H108A should be N105A, Y108A and H109A and so on across the Figure. This comparison shows that the trend across the panel of mutants for the Biacore energetics are in agreement with the computational energetic prediction of the binding interface. Analysis of the IL-17A binding to the mouse parent were not possible because that complex failed to crystallize and an acceptable model could not be generated. An attempt to generate results for IL-17F mutants binding to the BiAb3 produced inconsistent results, likely because the structures used for these were at poor resolution and missing necessary residue information.

Summary of IL-17A&F Epitope Mapping

[00326] The strategy to identify the key differences between the epitope of the BiAb3 and the mouse parent (339.15.5.3) utilized X-ray crystallography, site-directed mutagenesis, in-silico mutagenesis, and binding and functional assays to analyze the mutants. The two mAbs differ in their light chain therefore the residues in contact with the light chain of each mAb were the focus of this study.

[00327] The IL-17A mutagenesis resulted in a panel of mutants with good expression and reasonable cellular potency. A significant change in the ΔΔG for binding to the biAb3 was measured for all mutants that contain Y108A with a 0.5 kcal/mole change measured for the Y108A single point mutant. These changes in ΔΔG were not observed for

binding to the mouse parent antibody indicating that the Y108 is new residue in the epitope of IL-17A for the biAb3 compared with the mouse parent mAb. The energetic data is consistent with the interface analysis of the crystal structures showing that this residue is interacting with the light chain which is different in biAb3 compared with the mouse parent and that Y108A is brought into closer proximity to the biAb3 due to differences in the CDR3 of the biAb3 light chain compared with the mouse parent. The only IL-17A mutant shown here that impacts the binding of the mouse parent antibody is one that interacts with a heavy chain residue indicating that the light chain does not play much of a role in binding of the mouse parent antibody to IL-17A.

[00328] The IL-17F mutagensis resulted in a panel of mutants with more variable and lower expression levels and significant losses in potency. The crystal structures obtained for IL-17F were also at poorer resolution than the IL-17A structures. This suggests that IL-17F is not as amenable to mutagenesis and potentially more dynamic in nature. However, the mutants with reduced binding to the biAb3 also reduced binding to the mouse parent mAb. And, all of the these mutants with reduced mAb binding were of reasonable potency and lower, but sufficient, expression levels for the analysis.

[00329] From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for purposes of illustration, various modifications may be made without deviating from the spirit and scope of the invention. Accordingly, the invention is not limited except as by the appended claims.

CLAIMS

What is claimed is:

1. A bispecific antibody comprising an IL-17A/F binding entity and an IL-23 binding entity, wherein the IL-17A/F binding entity comprises two pairs of immunoglobulin chains, each pair having one light and one heavy chain, and the IL-23 binding entity comprises two Fab fragments each comprising a light chain and the C_{H1} and variable regions of a heavy chain, and the Fab fragments of the IL-23 binding entity are linked to the C-termini of the heavy chains of the IL-17A/F binding entity, or to the N-termini of the light chains and the heavy chains of the IL-17A/F binding entity.

2. A bispecific antibody comprising an IL-17A/F binding entity and an IL-23 binding entity, wherein the IL-23 binding entity comprises two pairs of immunoglobulin chains, each pair having one light and one heavy chain, and the IL-17A/F binding entity comprises two Fab fragments each comprising a light chain and the C_{H1} and variable regions of a heavy chain, and the Fab fragments of the IL-17A/F binding entity are linked to the C-termini of the heavy chains of the IL-23 binding entity, or to the N-termini of the light chains and the heavy chains of the IL-23 binding entity.

3. The bispecific antibody of Claim 1 or 2 wherein the IL-17A/F binding entity and the IL-23 binding entity are linked by peptide linkers.

4. The bispecific antibody of Claim 3 wherein the linker comprises the amino acid sequence of SEQ ID NO:12.

5. A bispecific antibody comprising an IL-17A/F binding entity and an IL-23 binding entity, wherein the IL-17A/F binding entity comprises a light chain and an IL-17A/F heavy chain, and the IL-23 binding entity comprises a light chain and an IL-23 heavy chain.

6. The bispecific antibody of Claim 1, 2 or 5 wherein the light chains of the IL-17A/F binding entity and the IL-23 binding entity comprise a variable domain

comprising a CDR1 having the amino acid sequence of SEQ ID NO:22, a CDR2 having the amino acid sequence of SEQ ID NO:23, and a CDR3 having the sequence of SEQ ID NO:24.

7. The bispecific antibody of Claim 1, 2 or 5 wherein the light chains of the IL-17A/F binding entity and the IL-23 binding entity comprise a variable domain comprising the amino acid sequence of SEQ ID NO:9.

8. The bispecific antibody of Claim 1, 2 or 5 wherein the light chains of the IL-17A/F binding entity and the IL-23 binding entity comprise a constant domain comprising the amino acid sequence of SEQ ID NO:10.

9. The bispecific antibody of Claim 1, 2 or 5 wherein the light chains of the IL-17A/F binding entity and the IL-23 binding entity comprise a variable domain comprising the amino acid sequence of SEQ ID NO:9 and a constant domain comprising the amino acid sequence of SEQ ID NO:10.

10. The bispecific antibody of Claim 1 or 2 wherein the heavy chains of the IL-17A/F binding entity comprise a variable domain comprising a CDR1 having the amino acid sequence of SEQ ID NO:25, a CDR2 having the amino acid sequence of SEQ ID NO:26, and a CDR3 having the amino acid sequence of SEQ ID NO:27.

11. The bispecific antibody of Claim 5 wherein the IL-17A/F heavy chain comprises a variable domain comprising a CDR1 having the amino acid sequence of SEQ ID NO:25, a CDR2 having the amino acid sequence of SEQ ID NO:26, and a CDR3 having the amino acid sequence of SEQ ID NO:27.

12. The bispecific antibody of Claim 1 or 2 wherein the heavy chains of the IL-17A/F binding entity comprise a variable domain comprising the amino acid sequence of SEQ ID NO:13.

13. The bispecific antibody of Claim 5 wherein the IL-17A/F heavy chain comprises a variable domain comprising the amino acid sequence of SEQ ID NO:13.

14. The bispecific antibody of Claim 1 wherein the heavy chains of the IL-17A/F binding entity comprise a constant domain comprising the amino acid sequence of SEQ ID NO:11.

15. The bispecific antibody of Claim 2 wherein the heavy chains of the IL-17A/F binding entity comprise a C_{H1} region comprising the amino acid sequence of SEQ ID NO:15.

16. The bispecific antibody of Claim 5 wherein the IL-17A/F heavy chain comprises a C_{H1} region comprising the amino acid sequence of SEQ ID NO:15.

17. The bispecific antibody of Claim 1 or 2 wherein the heavy chains of the IL-23 binding entity comprise a variable domain comprising a CDR1 having the amino acid sequence of SEQ ID NO:19, a CDR2 having the amino acid sequence of SEQ ID NO:20, and a CDR3 having the amino acid sequence of SEQ ID NO:21.

18. The bispecific antibody of Claim 5 wherein the IL-23 heavy chain comprises a variable domain comprising a CDR1 having the amino acid sequence of SEQ ID NO:19, a CDR2 having the amino acid sequence of SEQ ID NO:20, and a CDR3 having the amino acid sequence of SEQ ID NO:21.

19. The bispecific antibody of Claim 1 or 2 wherein the heavy chains of the IL-23 binding entity comprise a variable domain comprising the amino acid sequence of SEQ ID NO:7.

20. The bispecific antibody of Claim 5 wherein the IL-23 heavy chain comprises a variable domain comprising the amino acid sequence of SEQ ID NO:7.

21. The bispecific antibody of Claim 2 wherein the heavy chains of the IL-23 binding entity comprise a constant domain comprising the amino acid sequence of SEQ ID NO:8 or the amino acid sequence of residues 1-326 of SEQ ID NO:8.

22. The bispecific antibody of Claim 5 wherein the IL-23 heavy chain comprises a constant domain comprising the amino acid sequence of SEQ ID NO:8 or the amino acid sequence of residues 1-326 of SEQ ID NO:8.

23. The bispecific antibody of Claim 1 wherein the heavy chains of the IL-23 binding entity comprise a C_{H1} region comprising the amino acid sequence of SEQ ID NO:14.

24. A bispecific antibody comprising a pair of heavy chains each comprising an amino acid sequence selected from the group consisting of SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:74 and SEQ ID NO:84, and a pair of light chains each comprising the amino acid sequence of SEQ ID NO:17; or a pair of heavy chains each comprising the amino acid sequence of SEQ ID NO:77 and a pair of light chains each comprising the amino acid sequence of SEQ ID NO:79.

25. The bispecific antibody of Claim 24 comprising a pair of heavy chains each comprising the amino acid sequence of SEQ ID NO:74 and a pair of light chains each comprising the amino acid sequence of SEQ ID NO:17.

26. A bispecific antibody comprising an IL-17A/F binding entity and an IL-23 binding entity, wherein the IL-17A/F binding entity comprises a light chain comprising the amino acid sequence of SEQ ID NO:17 and an IL-17A/F heavy chain comprising the amino acid sequence of SEQ ID NO:80, and the IL-23 binding entity comprises a light chain comprising the amino acid sequence of SEQ ID NO:17 and an IL-23 heavy chain comprising the amino acid sequence of SEQ ID NO:60.

27. A bispecific antibody comprising a first binding entity and a second binding entity wherein the first binding entity is an antibody comprising two pairs of immunoglobulin chains; the second binding entity is a Fv unit comprising a heavy chain variable domain and a light chain variable domain; the Fv unit of the second binding entity is positioned between the Fab region and the hinge region of the antibody of the first binding entity; and the Fv unit of the second binding entity is linked to the Fab region of the antibody of the first binding entity.

28. The bispecific antibody of Claim 27 wherein the first binding entity is a lymphocyte antigen, cytokine, cytokine receptor, growth factor, growth factor receptor, interleukin or interleukin receptor and the second binding entity is a lymphocyte antigen, cytokine, cytokine receptor, growth factor, growth factor receptor, interleukin or interleukin receptor.

29. The bispecific antibody of Claim 27 wherein the first binding entity is an IL-23 binding entity and the second binding entity is an IL-17A/F binding entity, or the first binding entity is an IL-17A/F binding entity and the second binding entity is an IL-23 binding entity.

30. The bispecific antibody of Claim 29 wherein the heavy chain variable domain of the Fv unit of the second binding entity is linked to the C_{H1} region of the Fab fragment of the antibody of the first binding entity by a first peptide linker molecule, and the light chain variable domain of the Fv unit of the second binding entity is linked to the light chain constant domain of the Fab fragment of the antibody of the first binding entity by a second peptide linker.

31. The bispecific antibody of Claim 30 wherein the first peptide linker has the amino acid sequence of SEQ ID NO:12 or SEQ ID NO:86, and the second peptide linker has the amino acid sequence of SEQ ID NO:12 or SEQ ID NO:85.

32. The bispecific antibody of Claim 29 wherein the Fv unit of the second binding entity has a light chain variable domain comprising a CDR1 having the amino acid sequence of SEQ ID NO:22, a CDR2 having the amino acid sequence of SEQ ID NO:23, and a CDR3 having the amino acid sequence of SEQ ID NO:24.

33. The bispecific antibody of Claim 29 wherein the Fv unit of the second binding entity has a light chain variable domain comprising the amino acid sequence of SEQ ID NO:9.

34. The bispecific antibody of Claim 29 wherein the Fv unit is an IL-23 binding entity comprising a heavy chain variable domain comprising a CDR1 having the

amino acid sequence of SEQ ID NO:19, a CDR2 having the amino acid sequence of SEQ ID NO:20, and a CDR3 having the amino acid sequence of SEQ ID NO:21.

35. The bispecific antibody of Claim 29 wherein the Fv unit is an IL-23 binding entity comprising a heavy chain variable domain comprising the amino acid sequence of SEQ ID NO:7.

36. The bispecific antibody of Claim 29 wherein the Fv unit is an IL-17A/F binding entity comprising a heavy chain variable domain comprising a CDR1 having the amino acid sequence of SEQ ID NO:25, a CDR2 having the amino acid sequence of SEQ ID NO:26, and a CDR3 having the amino acid sequence of SEQ ID NO:27.

37. The bispecific antibody of Claim 29 wherein the Fv unit is an IL-17A/F binding entity comprising a heavy chain variable domain comprising the amino acid sequence of SEQ ID NO:13.

38. A bispecific antibody comprising a pair of heavy chains each comprising the amino acid sequence of SEQ ID NO:87 and a pair of light chains each comprising the amino acid sequence of SEQ ID NO:89, or a pair of heavy chains each comprising the amino acid sequence of SEQ ID NO:91 and a pair of light chains each comprising the amino acid sequence of SEQ ID NO:93, or a pair of heavy chains each comprising the amino acid sequence of SEQ ID NO:95 and a pair of light chains each comprising the amino acid sequence of SEQ ID NO:89, or a pair of heavy chains each comprising the amino acid sequence of SEQ ID NO:97 and a pair of light chains each comprising the amino acid sequence of SEQ ID NO:93, or a pair of heavy chains each comprising the amino acid sequence of SEQ ID NO:99 and a pair of light chains each comprising the amino acid sequence of SEQ ID NO:101, or a pair of heavy chains each comprising the amino acid sequence of SEQ ID NO:103 and a pair of light chains each comprising the amino acid sequence of SEQ ID NO:105, or a pair of heavy chains each comprising the amino acid sequence of SEQ ID NO:111 and a pair of light chains each comprising the amino acid sequence of SEQ ID NO:113, or a pair of heavy chains each comprising the amino acid sequence of SEQ ID NO:115 and a pair of light chains each comprising the amino acid sequence of SEQ ID NO:117.

39. An isolated monoclonal antibody or antigen-binding fragment thereof that specifically binds to IL-17A (SEQ ID NO:2) and IL-17F (SEQ ID NO:4) comprising a heavy chain variable domain and a light chain variable domain, wherein the heavy chain variable domain comprises the amino acid residues of SEQ ID NO:13 and a light chain variable domain comprises the amino acid residues of SEQ ID NO:9.

40. The isolated monoclonal antibody of Claim 39, wherein the antibody comprises a human constant region.

41. The isolated monoclonal antibody of Claim 40, wherein the isotype of the heavy chain is IgG1, IgG2, IgG3 or IgG4.

42. The isolated monoclonal antibody of Claim 41, wherein the IgG4 heavy chain has a Serine to Proline mutation at position 241 according to Kabat.

43. The isolated monoclonal antibody of Claim 39, wherein the heavy chain comprises the amino acid residues of SEQ ID NOs:16, 18, 28, 29 or 74.

44. The isolated monoclonal antibody of Claim 39, wherein the light chain comprises the amino acid residues of SEQ ID NO:17.

45. The isolated monoclonal antibody of Claim 39, wherein the heavy chain comprises the amino acid residues of SEQ ID NOs:16, 18, 28, 29 or 74, and the light chain comprises the amino acid residues of SEQ ID NO:17.

46. A bispecific antibody comprising the antibody of Claim 39.

47. An isolated monoclonal antibody or antigen-binding fragment thereof that specifically binds to IL-23p19 (SEQ ID NO:6) comprising a heavy chain variable domain and a light chain variable domain, wherein the heavy chain variable domain comprises the amino acid residues of SEQ ID NO:7, and wherein the light chain variable domain comprises the amino acid residues of SEQ ID NO:9.

48. The isolated monoclonal antibody of Claim 47, wherein the antibody comprises a human constant region.

49. The isolated monoclonal antibody of Claim 48, wherein the isotype of the heavy chain is IgG1, IgG2, IgG3 or IgG4.

50. The isolated monoclonal antibody of Claim 49, wherein the IgG4 heavy chain has a Serine to Proline mutation at position 241 according to Kabat.

51. The isolated monoclonal antibody of Claim 47, wherein the heavy chain comprises the amino acid residues of SEQ ID NOs:16, 18, 28, 29 or 74.

52. The isolated monoclonal antibody of Claim 47, wherein the light chain comprises the amino acid residues of SEQ ID NO:17.

53. The isolated monoclonal antibody of Claim 47, wherein the heavy chain comprises the amino acid residues of SEQ ID NOs:16, 18, 28, 29 or 74, and the light chain comprises the amino acid residues of SEQ ID NO:17.

54. An isolated bispecific antibody comprising the antibody of Claim 39.

55. An isolated bispecific antibody comprising a first binding entity and a second binding entity wherein the first binding entity is an antibody comprising two pairs of immunoglobulin chains and the second binding entity comprises a single domain antibody, wherein the single domain antibody of the second binding entity is positioned between the C_{H1} region of the Fab fragment and the hinge of the first binding entity.

56. The isolated bispecific antibody of Claim 55, wherein the second binding entity is linked to the first binding entity by a linker molecule.

57. The isolated bispecific antibody of Claim 56, wherein the linker molecule is $(G_4S)_2$.

58. The isolated bispecific antibody of Claim 56, wherein the linker molecule is the amino acid residues of SEQ ID NO:86.

59. The isolated bispecific antibody of Claim 56, wherein the first binding entity is a lymphocyte antigen, cytokine, cytokine receptor, growth factor, growth factor receptor, interleukin or interleukin receptor and the second binding entity is a lymphocyte antigen, cytokine, cytokine receptor, growth factor, growth factor receptor, interleukin or interleukin receptor.

60. An isolated nucleic acid encoding the heavy chain or the light chain of the bispecific antibody as in any one of Claims 1, 2, 5, 24, 26, 27 and 55.

61. An isolated nucleic acid encoding the heavy chain or the light chain of the antibody according to Claim 39 or 47.

62. An expression vector comprising the following operably linked elements:

a transcription promoter;

a polynucleotide encoding the heavy chain of the bispecific antibody of Claim 1; and

a transcription terminator.

63. An expression vector comprising the following operably linked elements:

a transcription promoter;

a polynucleotide encoding the light chain of the bispecific antibody of Claim 1; and

a transcription terminator.

64. A recombinant host cell comprising the expression vectors of Claims 62 and 63, wherein the cell expresses the heavy chain and light chain.

65. An expression vector comprising the following operably linked elements:

a transcription promoter;

a first polynucleotide encoding the heavy chain of the bispecific antibody of Claim 1;

a second polynucleotide encoding the light chain of the bispecific antibody of Claim 1; and

a transcription terminator.

66. An expression vector comprising the following operably linked elements:

a first transcription promoter;

a first polynucleotide encoding the heavy chain of the bispecific antibody of Claim 1; and

a first transcription terminator; and

a second transcription promoter;

a second polynucleotide encoding the light chain of the bispecific antibody of Claim 1; and

a second transcription terminator.

67 A recombinant host cell comprising the expression vector of Claim 65 or Claim 66, wherein the cell expresses the heavy chain and light chain.

68. An expression vector comprising the following operably linked elements:

a transcription promoter;

a polynucleotide encoding the heavy chain of the bispecific antibody of Claim 2; and

a transcription terminator.

69. An expression vector comprising the following operably linked elements:

a transcription promoter;

a polynucleotide encoding the light chain of the bispecific antibody of Claim 2; and

a transcription terminator.

70. A recombinant host cell comprising the expression vectors of Claims 68 and 69, wherein the cell expresses the heavy chain and light chain.

71. An expression vector comprising the following operably linked elements:

a transcription promoter;

a first polynucleotide encoding the heavy chain of the bispecific antibody of Claim 2;

a second polynucleotide encoding the light chain of the bispecific antibody of Claim 2; and

a transcription terminator.

72. An expression vector comprising the following operably linked elements:

a first transcription promoter;

a first polynucleotide encoding the heavy chain of the bispecific antibody of Claim 2; and

a first transcription terminator; and

a second transcription promoter;

a second polynucleotide encoding the light chain of the bispecific antibody of Claim 2; and

a second transcription terminator.

73. A recombinant host cell comprising the expression vector of Claim 71 or Claim 72, wherein the cell expresses the heavy chain and light chain.

74. An expression vector comprising the following operably linked elements:

a transcription promoter;

a polynucleotide encoding the heavy chain of the bispecific antibody of Claim 5; and

a transcription terminator.

75. An expression vector comprising the following operably linked elements:

a transcription promoter;

a polynucleotide encoding the light chain of the bispecific antibody of Claim 5; and

a transcription terminator.

76. A recombinant host cell comprising the expression vectors of Claims 74 and 75, wherein the cell expresses the heavy chain and light chain.

77. An expression vector comprising the following operably linked elements:

a transcription promoter;

a first polynucleotide encoding the heavy chain of the bispecific antibody of Claim 5;

a second polynucleotide encoding the light chain of the bispecific antibody of Claim 5; and

a transcription terminator.

78. An expression vector comprising the following operably linked elements:

a first transcription promoter;

a first polynucleotide encoding the heavy chain of the bispecific antibody of Claim 5; and

a first transcription terminator; and

a second transcription promoter;

a second polynucleotide encoding the light chain of the bispecific antibody of Claim 5; and

a second transcription terminator.

79. A recombinant host cell comprising the expression vector of Claim 77 or Claim 78, wherein the cell expresses the heavy chain and light chain.

80. An expression vector comprising the following operably linked elements:

a transcription promoter;

a polynucleotide encoding the heavy chain of the bispecific antibody of Claim 24; and

a transcription terminator.

81. An expression vector comprising the following operably linked elements:

a transcription promoter;

a polynucleotide encoding the light chain of the bispecific antibody of Claim 24; and

a transcription terminator.

82. A recombinant host cell comprising the expression vectors of Claims 80 and 81, wherein the cell expresses the heavy chain and light chain.

83. An expression vector comprising the following operably linked elements:

a transcription promoter;

a first polynucleotide encoding the heavy chain of the bispecific antibody of Claim 24;

a second polynucleotide encoding the light chain of the bispecific antibody of Claim 24; and

a transcription terminator.

84. An expression vector comprising the following operably linked elements:

a first transcription promoter;

a first polynucleotide encoding the heavy chain of the bispecific antibody of Claim 24; and

a first transcription terminator; and

a second transcription promoter;

a second polynucleotide encoding the light chain of the bispecific antibody of Claim 24; and

a second transcription terminator.

85. A recombinant host cell comprising the expression vector of Claim 83 or Claim 84, wherein the cell expresses the heavy chain and light chain.

86. An expression vector comprising the following operably linked elements:

a transcription promoter;

a polynucleotide encoding the heavy chain of the bispecific antibody of Claim 27; and

a transcription terminator.

87. An expression vector comprising the following operably linked elements:

a transcription promoter;

a polynucleotide encoding the light chain of the bispecific antibody of Claim 27; and

a transcription terminator.

88. A recombinant host cell comprising the expression vectors of Claims 86 and 87, wherein the cell expresses the heavy chain and light chain.

89. An expression vector comprising the following operably linked elements:

a transcription promoter;

a first polynucleotide encoding the heavy chain of the bispecific antibody of Claim 27;

a second polynucleotide encoding the light chain of the bispecific antibody of Claim 27; and

a transcription terminator.

90. An expression vector comprising the following operably linked elements:

a first transcription promoter;

a first polynucleotide encoding the heavy chain of the bispecific antibody of Claim 27; and

a first transcription terminator; and

a second transcription promoter;

a second polynucleotide encoding the light chain of the bispecific antibody of Claim 27; and

a second transcription terminator.

91. A recombinant host cell comprising the expression vector of Claim 89 or Claim 90, wherein the cell expresses the heavy chain and light chain.

92. An expression vector comprising the following operably linked elements:

a transcription promoter;

a polynucleotide encoding the heavy chain of the bispecific antibody of Claim 55; and

a transcription terminator.

93. An expression vector comprising the following operably linked elements:

a transcription promoter;

a polynucleotide encoding the light chain of the bispecific antibody of Claim 55; and

a transcription terminator.

94. A recombinant host cell comprising the expression vectors of Claims 92 and 93, wherein the cell expresses the heavy chain and light chain.

95. An expression vector comprising the following operably linked elements:

a transcription promoter;

a first polynucleotide encoding the heavy chain of the bispecific antibody of Claim 55;

a second polynucleotide encoding the light chain of the bispecific antibody of Claim 55; and

a transcription terminator.

96. An expression vector comprising the following operably linked elements:

a first transcription promoter;

a first polynucleotide encoding the heavy chain of the bispecific antibody of Claim 55; and

a first transcription terminator; and

a second transcription promoter;

a second polynucleotide encoding the light chain of the bispecific antibody of Claim 55; and

a second transcription terminator.

97. A recombinant host cell comprising the expression vector of Claim 95 or Claim 96, wherein the cell expresses the heavy chain and light chain.

98. An expression vector comprising the following operably linked elements:

a transcription promoter;

a polynucleotide encoding the heavy chain of the antibody of Claim 39; and

a transcription terminator.

99. An expression vector comprising the following operably linked elements:

a transcription promoter;

a polynucleotide encoding the light chain of the antibody of Claim 39; and

a transcription terminator.

100. A recombinant host cell comprising the expression vectors of Claims 98 and 99, wherein the cell expresses the heavy chain and light chain.

101. An expression vector comprising the following operably linked elements:

a transcription promoter;

a first polynucleotide encoding the heavy chain of the antibody of Claim 39;

a second polynucleotide encoding the light chain of the antibody of Claim 39; and

a transcription terminator.

102. An expression vector comprising the following operably linked elements:

a first transcription promoter;

a first polynucleotide encoding the heavy chain of the antibody of Claim 39; and

a first transcription terminator; and

a second transcription promoter;

a second polynucleotide encoding the light chain of the antibody of Claim 39; and

a second transcription terminator.

103. A recombinant host cell comprising the expression vector of Claim 101 or Claim 102, wherein the cell expresses the heavy chain and light chain.

104. An expression vector comprising the following operably linked elements:

a transcription promoter;

a polynucleotide encoding the heavy chain of the antibody of Claim 47; and

a transcription terminator.

105. An expression vector comprising the following operably linked elements:

a transcription promoter;

a polynucleotide encoding the light chain of the antibody of Claim 47; and

a transcription terminator.

106. A recombinant host cell comprising the expression vectors of Claims 104 and 105, wherein the cell expresses the heavy chain and light chain.

107. An expression vector comprising the following operably linked elements:

a transcription promoter;

a first polynucleotide encoding the heavy chain of the antibody of Claim 47;

a second polynucleotide encoding the light chain of the antibody of Claim 47; and

a transcription terminator.

108. An expression vector comprising the following operably linked elements:

a first transcription promoter;

a first polynucleotide encoding the heavy chain of the antibody of Claim 47; and

a first transcription terminator; and

a second transcription promoter;

a second polynucleotide encoding the light chain of the antibody of Claim 47; and

a second transcription terminator.

109. A recombinant host cell comprising the expression vector of Claim 107 or Claim 108, wherein the cell expresses the heavy chain and light chain.

110. A method of producing the bispecific antibody of Claim 1, the method comprising:

culturing the cell according to Claim 64 or Claim 67; and
isolating the bispecific antibody produced by the cell.

111. A method of producing the bispecific antibody of Claim 2, the method comprising:

culturing the cell according to Claim 70 or Claim 73; and
isolating the bispecific antibody produced by the cell.

112. A method of producing the bispecific antibody of Claim 5, the method comprising:

culturing the cell according to Claim 76 or Claim 79; and
isolating the bispecific antibody produced by the cell.

113. A method of producing the bispecific antibody of Claim 24, the method comprising:

culturing the cell according to Claim 82 or Claim 85; and
isolating the bispecific antibody produced by the cell.

114. A method of producing the bispecific antibody of Claim 27, the method comprising:

culturing the cell according to Claim 88 or Claim 91; and
isolating the bispecific antibody produced by the cell.

115. A method of producing the bispecific antibody of Claim 55, the method comprising:

culturing the cell according to Claim 94 or Claim 97; and
isolating the bispecific antibody produced by the cell.

116. A method of producing the antibody of Claim 39, the method comprising:

culturing the cell according to Claim 100 or Claim 103; and
isolating the bispecific antibody produced by the cell.

117. A method of producing the antibody of Claim 47, the method comprising:

culturing the cell according to Claim 106 or Claim 109; and

isolating the bispecific antibody produced by the cell.

118. The method of Claim 110, wherein the cell is a prokaryotic cell.

119. The method of Claim 118, wherein the prokaryotic cell is an *E. coli* cell.

120. The method of Claim 110, wherein the cell is a eukaryotic cell.

121. The method of Claim 120, wherein the eukaryotic cell is a mammalian cell.

122. The method of Claim 121, wherein the mammalian cell is selected from the group consisting of a VERO, HeLa, Chinese Hamster Ovary (CHO), W138, BHK, COS-7 and MDCK cell.

123. The method of Claim 120, wherein the eukaryotic cell is a yeast cell.

124. The method of Claim 123, wherein the yeast cell is a *Saccharomyces cerevisiae* cell or a *Pichia pastoris* cell.

125. The method of Claim 111, wherein the cell is a prokaryotic cell.

126. The method of Claim 125, wherein the prokaryotic cell is an *E. coli* cell.

127. The method of Claim 111, wherein the cell is a eukaryotic cell.

128. The method of Claim 127, wherein the eukaryotic cell is a mammalian cell.

129. The method of Claim 128, wherein the mammalian cell is selected from the group consisting of a VERO, HeLa, Chinese Hamster Ovary (CHO), W138, BHK, COS-7 and MDCK cell.

130. The method of Claim 127, wherein the eukaryotic cell is a yeast cell.

131. The method of Claim 130, wherein the yeast cell is a *Saccharomyces cerevisiae* cell or *Pichia pastoris* cell.

132. The method of Claim 111, wherein the cell is a prokaryotic cell.

133. The method of Claim 132, wherein the prokaryotic cell is an *E. coli* cell.

134. The method of Claim 111, wherein the cell is a eukaryotic cell.

135. The method of Claim 134, wherein the eukaryotic cell is a mammalian cell.

136. The method of Claim 135, wherein the mammalian cell is selected from the group consisting of a VERO, HeLa, Chinese Hamster Ovary (CHO), W138, BHK, COS-7 and MDCK cell.

137. The method of Claim 134, wherein the eukaryotic cell is a yeast cell.

138. The method of Claim 137, wherein the yeast cell is a *Saccharomyces cerevisiae* cell or *Pichia pastoris* cell.

139. The method of Claim 112, wherein the cell is a prokaryotic cell.

140. The method of Claim 139, wherein the prokaryotic cell is an *E. coli* cell.

141. The method of Claim 112, wherein the cell is a eukaryotic cell.

142. The method of Claim 141, wherein the eukaryotic cell is a mammalian cell.

143. The method of Claim 142, wherein the mammalian cell is selected from the group consisting of a VERO, HeLa, Chinese Hamster Ovary (CHO), W138, BHK, COS-7 and MDCK cell.

144. The method of Claim 141, wherein the eukaryotic cell is a yeast cell.

145. The method of Claim 144, wherein the yeast cell is a *Saccharomyces cerevisiae* cell or *Pichia pastoris* cell.

146. The method of Claim 113, wherein the cell is a prokaryotic cell.

147. The method of Claim 146, wherein the prokaryotic cell is an *E. coli* cell.

148. The method of Claim 113, wherein the cell is a eukaryotic cell.

149. The method of Claim 148, wherein the eukaryotic cell is a mammalian cell.

150. The method of Claim 149, wherein the mammalian cell is selected from the group consisting of a VERO, HeLa, Chinese Hamster Ovary (CHO), W138, BHK, COS-7 and MDCK cell.

151. The method of Claim 148, wherein the eukaryotic cell is a yeast cell.

152. The method of Claim 151, wherein the yeast cell is a *Saccharomyces cerevisiae* cell or *Pichia pastoris* cell.

153. The method of Claim 114, wherein the cell is a prokaryotic cell.

154. The method of Claim 153, wherein the prokaryotic cell is an *E. coli* cell.

155. The method of Claim 114, wherein the cell is a eukaryotic cell.

156. The method of Claim 155, wherein the eukaryotic cell is a mammalian cell.

157. The method of Claim 156, wherein the mammalian cell is selected from the group consisting of a VERO, HeLa, Chinese Hamster Ovary (CHO), W138, BHK, COS-7 and MDCK cell.

158. The method of Claim 155, wherein the eukaryotic cell is a yeast cell.

159. The method of Claim 158, wherein the yeast cell is a *Saccharomyces cerevisiae* cell or *Pichia pastoris* cell.

160. The method of Claim 115, wherein the cell is a prokaryotic cell.

161. The method of Claim 160, wherein the prokaryotic cell is an *E. coli* cell.

162. The method of Claim 115, wherein the cell is a eukaryotic cell.

163. The method of Claim 162, wherein the eukaryotic cell is a mammalian cell.

164. The method of Claim 163, wherein the mammalian cell is selected from the group consisting of a VERO, HeLa, Chinese Hamster Ovary (CHO), W138, BHK, COS-7 and MDCK cell.

165. The method of Claim 162, wherein the eukaryotic cell is a yeast cell.

166. The method of Claim 165, wherein the yeast cell is a *Saccharomyces cerevisiae* cell or *Pichia pastoris* cell.

167. A method of treating a disease characterized by elevated expression of one or more of IL-17A, IL-17F and IL-23 in a mammal in need of such treatment comprising administering a therapeutically effective amount of the bispecific antibody according to Claim 1, 2, 5, 24, 26, 27, 37 or 55, or the antibody according to Claim 39 or 47 to said mammal.

168. The method of Claim 167, wherein the disease is multiple sclerosis (MS), irritable bowel syndrome (IBS), inflammatory bowel disease (IBD) such as ulcerative colitis and Crohn's disease, atopic dermatitis, contact dermatitis, systemic sclerosis, systemic lupus erythematosus (SLE), antineutrophil cytoplasmic antibodies (ANCA)-associated vasculitis (AAV), giant cell arteritis, multiple sclerosis (MS) (e.g., relapsing-remitting multiple sclerosis, secondary-progressive multiple sclerosis, primary-progressive multiple sclerosis and/or progressive-relapsing multiple sclerosis), colitis, endotoxemia, arthritis, rheumatoid arthritis (RA), osteoarthritis, Sjögren's syndrome, psoriasis, psoriatic arthritis, adult respiratory disease (ARD), septic shock, multiple organ failure, inflammatory lung injury such as idiopathic pulmonary fibrosis, asthma, chronic obstructive pulmonary disease (COPD), airway hyper-responsiveness, chronic bronchitis, allergic asthma, eczema, *Helicobacter pylori* infection, intraabdominal adhesions and/or abscesses as results of peritoneal inflammation (*e.g.*, from infection, injury, etc.), nephrotic syndrome, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome, organ allograft rejection, graft vs. host disease (GVHD), lupus nephritis, IgA nephropathy, diabetic kidney disease, minimal change disease (lipoid nephrosis), focal segmental glomerulosclerosis (FSGS), nephrogenic systemic fibrosis (NSF), nephrogenic fibrosing dermopathy, fibrosing cholestatic hepatitis, eosinophilic fasciitis (Shulman's syndrome), scleromyxedema (popular mucinosis), scleroderma, lichen sclerosusetatrophicus, POEMs syndrome (Crow-Fukase syndrome, Takatsuki disease or PEP syndrome), nephrotic syndrome, graft-versus-host-disease (GVHD), graft-versus-host-disease (GVHD) (from a transplant, such as blood, bone marrow, kidney, pancreas, liver, orthotopic liver, lung, heart, intestine, small intestine, large intestine, thymus, allogeneic stem cell, reduced-intensity allogeneic, bone, tendon, cornea, skin, heart valves, veins, arteries, blood vessels, stomach and testis), lytic bone disease (*e.g.*, multiple myeloma-induced lytice bone disease), cystic fibrosis, age-related mascular degeneration

(AMD; *e.g.*, wet AMD and dry AMD), liver fibrosis, pulmonary fibrosis, atherosclerosis, cardiac ischemia/reperfusion injury, heart failure, myocarditis, cardiac fibrosis, adverse myocardial remodeling, transplant rejection, streptococcal cell wall (SCW)-induced arthritis, gingivitis/periodontitis, herpetic stromal keratitis, gluten-sensitive enteropathy restenosis, Kawasaki disease, or an immune mediated renal disease.

169. A method for inhibiting inflammation in a mammal in need of such treatment comprising administering a therapeutically effective amount of the bispecific antibody according to Claim 1, 2, 5, 24, 26, 27, 37 or 55, or the antibody according to Claim 39 or 47 to said mammal.

170. The method of Claim 169 wherein the inflammation is associated with a disease selected from the group consisting of multiple sclerosis (MS) (e.g., relapsing-remitting multiple sclerosis, secondary-progressive multiple sclerosis, primary-progressive multiple sclerosis and/or progressive-relapsing multiple sclerosis), irritable bowel syndrome (IBS), inflammatory bowel disease (IBD) such as ulcerative colitis and Crohn's disease, atopic dermatitis, contact dermatitis, systemic sclerosis, systemic lupus erythematosus (SLE), antineutrophil cytoplasmic antibodies (ANCA)-associated vasculitis (AAV), giant cell arteritis, multiple sclerosis (MS), colitis, endotoxemia, arthritis, rheumatoid arthritis (RA), osteoarthritis, Sjögren's syndrome, psoriasis, psoriatic arthritis, adult respiratory disease (ARD), septic shock, multiple organ failure, inflammatory lung injury such as idiopathic pulmonary fibrosis, asthma, chronic obstructive pulmonary disease (COPD), airway hyper-responsiveness, chronic bronchitis, allergic asthma, eczema, *Helicobacter pylori* infection, intraabdominal adhesions and/or abscesses as results of peritoneal inflammation (*e.g.*, from infection, injury, etc.), nephrotic syndrome, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome, organ allograft rejection, graft vs. host disease (GVHD), lupus nephritis, IgA nephropathy, diabetic kidney disease, minimal change disease (lipoid nephrosis), focal segmental glomerulosclerosis (FSGS), nephrogenic systemic fibrosis (NSF), nephrogenic fibrosing dermopathy, fibrosing cholestatic hepatitis, eosinophilic fasciitis (Shulman's syndrome), scleromyxedema (popular mucinosis), scleroderma, lichen sclerosusetatrophicus, POEMs syndrome (Crow-Fukase syndrome, Takatsuki disease or PEP syndrome), nephrotic syndrome, graft-versus-host-disease (GVHD), graft-versus-host-disease (GVHD) (from a transplant, such as blood, bone marrow, kidney, pancreas, liver, orthotopic liver, lung, heart, intestine, small intestine, large intestine, thymus, allogeneic stem cell,

reduced-intensity allogeneic, bone, tendon, cornea, skin, heart valves, veins, arteries, blood vessels, stomach and testis), lytic bone disease (*e.g.*, multiple myeloma-induced lytice bone disease), cystic fibrosis, age-related mascular degeneration (AMD; *e.g.*, wet AMD and dry AMD), liver fibrosis, pulmonary fibrosis, atherosclerosis, cardiac ischemia/reperfusion injury, heart failure, myocarditis, cardiac fibrosis, adverse myocardial remodeling, transplant rejection, streptococcal cell wall (SCW)-induced arthritis, gingivitis/periodontitis, herpetic stromal keratitis, gluten-sensitive enteropathy restenosis, Kawasaki disease, and an immune mediated renal disease.

171. A composition comprising the bispecific antibody according to Claim 1, 2, 5, 24, 26, 27, 37 or 55, or the antibody according to Claim 39 or 47 and a pharmaceutically acceptable carrier.

172. A method of treating a disease characterized by elevated expression of one or more of IL-17A, IL-17F and IL-23 in a mammal in need of such treatment comprising administering a therapeutically effective amount of the composition according to Claim 171 to said mammal.

173. The method according to Claim 172, wherein the disease is multiple sclerosis (MS) (e.g., relapsing-remitting multiple sclerosis, secondary-progressive multiple sclerosis, primary-progressive multiple sclerosis and/or progressive-relapsing multiple sclerosis), irritable bowel syndrome (IBS), inflammatory bowel disease (IBD) such as ulcerative colitis and Crohn's disease, atopic dermatitis, contact dermatitis, systemic sclerosis, systemic lupus erythematosus (SLE), antineutrophil cytoplasmic antibodies (ANCA)-associated vasculitis (AAV), giant cell arteritis, multiple sclerosis (MS), colitis, endotoxemia, arthritis, rheumatoid arthritis (RA), osteoarthritis, Sjögren's syndrome, psoriasis, psoriatic arthritis, adult respiratory disease (ARD), septic shock, multiple organ failure, inflammatory lung injury such as idiopathic pulmonary fibrosis, asthma, chronic obstructive pulmonary disease (COPD), airway hyper-responsiveness, chronic bronchitis, allergic asthma, eczema, *Helicobacter pylori* infection, intraabdominal adhesions and/or abscesses as results of peritoneal inflammation (*e.g.*, from infection, injury, etc.), nephrotic syndrome, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome, organ allograft rejection, graft vs. host disease (GVHD), lupus nephritis, IgA nephropathy, diabetic kidney disease, minimal change disease (lipoid nephrosis), focal segmental glomerulosclerosis (FSGS), nephrogenic

systemic fibrosis (NSF), nephrogenic fibrosing dermopathy, fibrosing cholestatic hepatitis, eosinophilic fasciitis (Shulman's syndrome), scleromyxedema (popular mucinosis), scleroderma, lichen sclerosusetatrophicus, POEMs syndrome (Crow-Fukase syndrome, Takatsuki disease or PEP syndrome), nephrotic syndrome, graft-versus-host-disease (GVHD), graft-versus-host-disease (GVHD) (from a transplant, such as blood, bone marrow, kidney, pancreas, liver, orthotopic liver, lung, heart, intestine, small intestine, large intestine, thymus, allogeneic stem cell, reduced-intensity allogeneic, bone, tendon, cornea, skin, heart valves, veins, arteries, blood vessels, stomach and testis), lytic bone disease (*e.g.*, multiple myeloma-induced lytice bone disease), cystic fibrosis, age-related mascular degeneration (AMD; *e.g.*, wet AMD and dry AMD), liver fibrosis, pulmonary fibrosis, atherosclerosis, cardiac ischemia/reperfusion injury, heart failure, myocarditis, cardiac fibrosis, adverse myocardial remodeling, transplant rejection, streptococcal cell wall (SCW)-induced arthritis, gingivitis/periodontitis, herpetic stromal keratitis, gluten-sensitive enteropathy restenosis, Kawasaki disease, or an immune mediated renal disease.

174. A method for inhibiting inflammation in a mammal in need of such treatment comprising administering a therapeutically effective amount of the composition according to Claim 171 to said mammal.

175. The method according to Claim 174, wherein the inflammation is associated with a disease selected from the group consisting of multiple sclerosis (MS) (e.g., relapsing-remitting multiple sclerosis, secondary-progressive multiple sclerosis, primary-progressive multiple sclerosis and/or progressive-relapsing multiple sclerosis), irritable bowel syndrome (IBS), inflammatory bowel disease (IBD) such as ulcerative colitis and Crohn's disease, atopic dermatitis, contact dermatitis, systemic sclerosis, systemic lupus erythematosus (SLE), antineutrophil cytoplasmic antibodies (ANCA)-associated vasculitis (AAV), giant cell arteritis, multiple sclerosis (MS), colitis, endotoxemia, arthritis, rheumatoid arthritis (RA), osteoarthritis, Sjögren's syndrome, psoriasis, psoriatic arthritis, adult respiratory disease (ARD), septic shock, multiple organ failure, inflammatory lung injury such as idiopathic pulmonary fibrosis, asthma, chronic obstructive pulmonary disease (COPD), airway hyper-responsiveness, chronic bronchitis, allergic asthma, eczema, *Helicobacter pylori* infection, intraabdominal adhesions and/or abscesses as results of peritoneal inflammation (*e.g.*, from infection, injury, etc.), nephrotic syndrome, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome, organ allograft rejection, graft vs.

host disease (GVHD), lupus nephritis, IgA nephropathy, diabetic kidney disease, minimal change disease (lipoid nephrosis), focal segmental glomerulosclerosis (FSGS), nephrogenic systemic fibrosis (NSF), nephrogenic fibrosing dermopathy, fibrosing cholestatic hepatitis, eosinophilic fasciitis (Shulman's syndrome), scleromyxedema (popular mucinosis), scleroderma, lichen sclerosusetatrophicus, POEMs syndrome (Crow-Fukase syndrome, Takatsuki disease or PEP syndrome), nephrotic syndrome, graft-versus-host-disease (GVHD), graft-versus-host-disease (GVHD) (from a transplant, such as blood, bone marrow, kidney, pancreas, liver, orthotopic liver, lung, heart, intestine, small intestine, large intestine, thymus, allogeneic stem cell, reduced-intensity allogeneic, bone, tendon, cornea, skin, heart valves, veins, arteries, blood vessels, stomach and testis), lytic bone disease (*e.g.*, multiple myeloma-induced lytice bone disease), cystic fibrosis, age-related mascular degeneration (AMD; *e.g.*, wet AMD and dry AMD), liver fibrosis, pulmonary fibrosis, atherosclerosis, cardiac ischemia/reperfusion injury, heart failure, myocarditis, cardiac fibrosis, adverse myocardial remodeling, transplant rejection, streptococcal cell wall (SCW)-induced arthritis, gingivitis/periodontitis, herpetic stromal keratitis, gluten-sensitive enteropathy restenosis, Kawasaki disease, and an immune mediated renal disease.

176. The bispecific antibody as in any one of Claims 1, 2 and 26, wherein the IL-17A/F binding entity binds:

(a) an IL-17A homodimer with a binding affinity (K_{D1}) of at least 1 x 10^{-9} M, at least 5 x 10^{-9} M, at least 1 x 10^{-10} M, at least 5 x 10^{-10} M, at least 8 x 10^{-10} M or at least at least 1 x 10^{-11} M;

(b) an IL-17F homodimer with a binding affinity (K_{D1}) of at least 1 x 10^{-9} M, at least 5 x 10^{-9} M, at least 1 x 10^{-10} M, at least 2 x 10^{-10} M, at least 3 x 10^{-10} M, at least 4 x 10^{-10} M, at least 5 x 10^{-10} M or at least 1 x 10^{-11} M; and/or

(c) an IL-17A/F heterodimer with a binding affinity (K_{D1}) of at least 1 x 10^{-8} M, at least 5 x 10^{-8} M, at least 1 x 10^{-9} M, at least 2 x 10^{-9} M, at least 3 x 10^{-9} M, at least 4 x 10^{-9} M, at least 5 x 10^{-9} M, at least 6 x 10^{-9} M, at least 7 x 10^{-9} M, at least 9 x 10^{-9} M, at least 1 x 10^{-10} M or at least 5 x 10^{-10} M, and

wherein the binding affinity is measured by surface plasmon resonance, such as Biacore.

177. The bispecific antibody as in any one of Claims 1, 2 and 26, wherein the IL-23 binding entity binds IL-23p19 with a binding affinity (K_{D1}) of at least 1 x 10^{-9} M, at

least 5 x 10^{-9} M, at least 1 x 10^{-10} M, at least 2 x 10^{-10} M, at least 3 x 10^{-10} M, at least 4 x 10^{-10} M, at least 5 x 10^{-10}, at least 6 x 10^{-10}, at least 7 x 10^{-10}, at least 8 x 10^{-10} or at least 9 x 10^{-10}, at least 1 x 10^{-11}, wherein the binding affinity is measured by surface plasmon resonance, such as Biacore.

178. The bispecific antibody as in any one of Claims 1, 2 and 26, wherein the IL-17A/F binding entity binds:

(a) an IL-17A homodimer with a binding affinity (K_{D1}) of at least 1 x 10^{-9} M, at least 5 x 10^{-9} M, at least 1 x 10^{-10} M, at least 5 x 10^{-10} M, at least 8 x 10^{-10} M or at least at least 1 x 10^{-11} M;

(b) an IL-17F homodimer with a binding affinity (K_{D1}) of at least 1 x 10^{-9} M, at least 5 x 10^{-9} M, at least 1 x 10^{-10} M, at least 2 x 10^{-10} M, at least 3 x 10^{-10} M, at least 4 x 10^{-10} M, at least 5 x 10^{-10} M or at least 1 x 10^{-11} M; and/or

(c) an IL-17A/F heterodimer with a binding affinity (K_{D1}) of at least 1 x 10^{-8} M, at least 5 x 10^{-8} M, at least 1 x 10^{-9} M, at least 2 x 10^{-9} M, at least 3 x 10^{-9} M, at least 4 x 10^{-9} M, at least 5 x 10^{-9} M, at least 6 x 10^{-9} M, at least 7 x 10^{-9} M, at least 9 x 10^{-9} M, at least 1 x 10^{-10} M or at least 5 x 10^{-10} M; and

wherein the IL-23 binding entity binds IL-23p19 with a binding affinity (K_{D1}) of at least 1 x 10^{-9} M, at least 5 x 10^{-9} M, at least 1 x 10^{-10} M, at least 2 x 10^{-10} M, at least 3 x 10^{-10} M, at least 4 x 10^{-10} M, at least 5 x 10^{-10}, at least 6 x 10^{-10}, at least 7 x 10^{-10}, at least 8 x 10^{-10} or at least 9 x 10^{-10}, at least 1 x 10^{-11}; and

wherein the binding affinity is measured by surface plasmon resonance, such as Biacore.

179. The bispecific antibody as in any one of Claims 1, 2 and 26, wherein the IL-17A/F binding entity neutralizes or inhibits (a) IL-17A induction of G-CSF in primary human small airway epithelial cells (SAEC) with an IC_{50} of 0.5 pm or less; (b) IL-17F induction G-CSF in primary human small airway epithelial cells (SAEC) with an IC_{50} of 2.0 nM or less, 1.5 nM or less, 1.4 nM or less, 1.3 nM or less, 1.2 nM or less, 1.1 nM or less, or 1.0 nM or less; and/or (c) IL-17A/F induction G-CSF in primary human small airway epithelial cells (SAEC) with an IC_{50} of 1.3 nM or less, 1.2 nM or less, 1.1 nM or less, 1.0 nM or less, 0.9 nM or less, 0.8 nM or less, 0.7 nM or less, 0.6 nM or less, or 0.5 nM or less.

180. The bispecific antibody as in any one of Claims 1, 2 and 26, wherein the IL-17A/F binding entity neutralizes or inhibits (a) IL-17A induction of IL-6 in human primary fibroblast cells (HFFF) with an IC_{50} of 0.5 nM or less, 0.4 nM or less, 0.3 nM or less, 0.2 nM or less, 0.1 nM or less, 0.09 nM or less, 0.08 nM or less, 0.07 nM or less, 0.06 nM or less, 0.05 nM or less, 0.04 nM or less, 0.03 nM or less, 0.02 nM or less, or 0.01 nM or less; (b) IL-17F induction of IL-6 in human primary fibroblast cells (HFFF) with an IC_{50} of 30 nM or less, 28 nM or less, 26 nM or less, 25 nM or less, 22 nM or less, 20 nM or less, 19 nM or less, 18 nM or less, 17 nM or less, 16 nM or less, 15 nM or less, 14 nM or less, 13 nM or less, 12 nM or less, 11 nM or less, or 10 nM or less; and/or (c) IL-17A/F induction of IL-6 in human primary fibroblast cells (HFFF) with an IC_{50} of 30 nM or less, 28 nM or less, 26 nM or less, 22 nM or less, 20 nM or less, 18 nM or less, 17 nM or less, 16 nM or less, 15 nM or less, 14 nM or less, 13 nM or less, 12 nM or less, 11 nM or less, 10 nM or less, 9.5 nM or less, 9.4 nM or less, 9.3 nM or less, 9.2 nM or less, 9.1 nM or less, or 9.0 nM or less.

181. The bispecific antibody as in any one of Claims 1, 2 and 26, wherein the IL-23 binding entity neutralizes or inhibits (a) IL-23 induced IL-17A and IL-17F production in murine splenocytes with an IC_{50} of 0.5 nM or less, 0.4 nM or less, 0.3 nM or less, 0.2 nM or less, 0.1 nM or less, 0.09 nM or less, 0.08 nM or less, 0.07 nM or less, or 0.06 nM or less.

182. The bispecific antibody as in any one of Claims 1, 2 and 26, wherein the IL-23 binding entity neutralizes or inhibits IL-23 induced STAT3 phosphorylation in activated primary human T cells with an IC_{50} of 0.1 nM or less, 0.2 nM or less, 0.3 nM or less, 0.4 nM or less, 0.5 nM or less, 0.8 nM or less, 0.9 nM or less, 0.01 nM or less, 0.02 nM or less, 0.03 nM or less, 0.04 nM or less, or 0.05 nM or less.

183. The monoclonal antibody or antigen-binding fragment thereof according to Claim 27, wherein the antibody or antigen-binding fragment binds:

(a) an IL-17A homodimer with a binding affinity (K_{D1}) of at least 1×10^{-9} M, at least 5×10^{-9} M, at least 1×10^{-10} M, at least 5×10^{-10} M, at least 8×10^{-10} M or at least at least 1×10^{-11} M;

(b) an IL-17F homodimer with a binding affinity (K_{D1}) of at least 1×10^{-9} M, at least 5×10^{-9} M, at least 1×10^{-10} M, at least 2×10^{-10} M, at least 3×10^{-10} M, at least 4×10^{-10} M, at least 5×10^{-10} M or at least 1×10^{-11} M; and/or

(c) an IL-17A/F heterodimer with a binding affinity (K_{D1}) of at least 1 x 10^{-8} M, at least 5 x 10^{-8} M, at least 1 x 10^{-9} M, at least 2 x 10^{-9} M, at least 3 x 10^{-9} M, at least 4 x 10^{-9} M, at least 5 x 10^{-9} M, at least 6 x 10^{-9} M, at least 7 x 10^{-9} M, at least 9 x 10^{-9} M, at least 1 x 10^{-10} M or at least 5 x 10^{-10} M, and

wherein the binding affinity is measured by surface plasmon resonance, such as Biacore.

184. The monoclonal antibody or antigen-binding fragment thereof according to Claim 27, wherein the antibody or antigen-binding fragment neutralizes or inhibits (a) IL-17A induction of G-CSF in primary human small airway epithelial cells (SAEC) with an IC_{50} of 0.5 pm or less; (b) IL-17F induction G-CSF in primary human small airway epithelial cells (SAEC) with an IC_{50} of 2.0 nM or less, 1.5 nM or less, 1.4 nM or less, 1.3 nM or less, 1.2 nM or less, 1.1 nM or less, or 1.0 nM or less; and/or (c) IL-17A/F induction G-CSF in primary human small airway epithelial cells (SAEC) with an IC_{50} of 1.3 nM or less, 1.2 nM or less, 1.1 nM or less, 1.0 nM or less, 0.9 nM or less, 0.8 nM or less, 0.7 nM or less, 0.6 nM or less, or 0.5 nM or less.

185. The monoclonal antibody or antigen-binding fragment thereof according to Claim 27, wherein the antibody or antigen-binding fragment neutralizes or inhibits (a) IL-17A induction of IL-6 in human primary fibroblast cells (HFFF) with an IC_{50} of 0.5 nM or less, 0.4 nM or less, 0.3 nM or less, 0.2 nM or less, 0.1 nM or less, 0.09 nM or less, 0.08 nM or less, 0.07 nM or less, 0.06 nM or less, 0.05 nM or less, 0.04 nM or less, 0.03 nM or less, 0.02 nM or less, or 0.01 nM or less; (b) IL-17F induction of IL-6 in human primary fibroblast cells (HFFF) with an IC_{50} of 30 nM or less, 28 nM or less, 26 nM or less, 25 nM or less, 22 nM or less, 20 nM or less, 19 nM or less, 18 nM or less, 17 nM or less, 16 nM or less, 15 nM or less, 14 nM or less, 13 nM or less, 12 nM or less, 11 nM or less, or 10 nM or less; and/or (c) IL-17A/F induction of IL-6 in human primary fibroblast cells (HFFF) with an IC_{50} of 30 nM or less, 28 nM or less, 26 nM or less, 22 nM or less, 20 nM or less, 18 nM or less, 17 nM or less, 16 nM or less, 15 nM or less, 14 nM or less, 13 nM or less, 12 nM or less, 11 nM or less, 10 nM or less, 9.5 nM or less, 9.4 nM or less, 9.3 nM or less, 9.2 nM or less, 9.1 nM or less, or 9.0 nM or less.

186. The monoclonal antibody or antigen-binding fragment of Claim 47, wherein the antibody or antigen-binding fragment binds IL-23p19 with a binding affinity

(K_{D1}) of at least 1 x 10^{-9} M, at least 5 x 10^{-9} M, at least 1 x 10^{-10} M, at least 2 x 10^{-10} M, at least 3 x 10^{-10} M, at least 4 x 10^{-10} M, at least 5 x 10^{-10}, at least 6 x 10^{-10}, at least 7 x 10^{-10}, at least 8 x 10^{-10} or at least 9 x 10^{-10}, at least 1 x 10^{-11}, wherein the binding affinity is measured by surface plasmon resonance, such as Biacore.

187. The monoclonal antibody or antigen-binding fragment of Claim 47, wherein the antibody or antigen-binding fragment neutralizes or inhibits (a) IL-23 induced IL-17A and IL-17F production in murine splenocytes with an IC_{50} of 0.5 nM or less, 0.4 nM or less, 0.3 nM or less, 0.2 nM or less, 0.1 nM or less, 0.09 nM or less, 0.08 nM or less, 0.07 nM or less, or 0.06 nM or less.

188. The monoclonal antibody or antigen-binding fragment of Claim 47, wherein the antibody or antigen-binding fragment neutralizes or inhibits IL-23 induced STAT3 phosphorylation in activated primary human T cells with an IC_{50} of 0.1 nM or less, 0.2 nM or less, 0.3 nM or less, 0.4 nM or less, 0.5 nM or less, 0.8 nM or less, 0.9 nM or less, 0.01 nM or less, 0.02 nM or less, 0.03 nM or less, 0.04 nM or less, or 0.05 nM or less.

189. An isolated antibody or antigen-binding fragment thereof which specifically binds IL-23p19, wherein the antibody or antigen-binding fragment binds a discontinuous epitope on IL-23p19 comprising a first epitope and a second epitope, wherein the first epitope consists of at least one of amino acid residues 33-59 of SEQ ID NO:6 and the second epitope consists of at least one of amino acid residues 89-125 of SEQ ID NO:6.

190. The antibody or antigen-binding fragment of Claim 189, wherein the antibody or antigen-binding fragment binds to at least amino acid residue 54 of SEQ ID NO:6 of the first epitope.

191. The antibody or antigen-binding fragment of Claim 189, wherein the antibody or antigen-binding fragment binds to at least amino acid residue 55 of SEQ ID NO:6 of the first epitope.

192. The antibody or antigen-binding fragment of Claim 189, wherein the antibody or antigen-binding fragment binds to at least amino acid residues 54 and 55 of SEQ ID NO:6 of the first epitope.

193. The antibody or antigen-binding fragment of Claim 189, wherein the antibody or antigen-binding fragment binds to at least at amino acid residue 116 of SEQ ID NO:6 of the second epitope.

194. The antibody or antigen-binding fragment of Claim 189, wherein the antibody or antigen-binding fragment binds to at least amino acid residues 54 and 55 of SEQ ID NO:6 of the first epitope, and to least amino acid residue 116 of SEQ ID NO:6 of the second epitope.

195. The antibody or antigen-binding fragment of Claim 189, wherein the antigen or antigen-binding fragment is a bispecific antibody or bispecific antigen-binding fragment.

196. The antibody or antigen-binding fragment of any one of claims 189-195, wherein the discontinuous epitope on IL-23p19 is determined by at least one of proteolytic digest, hydrogen/deuterium exchange mass spectrometry and alanine mutagenesis.

197. The antibody or antigen-binding fragment of any one of claims 189-195, wherein the discontinuous epitope on IL-23p19 is determined by proteolytic digest.

198. The antibody or antigen-binding fragment of any one of claims 189-195, wherein the discontinuous epitope on IL-23p19 is determined by hydrogen/deuterium exchange mass spectrometry or alanine mutagenesis.

199. The antibody or antigen-binding fragment of any one of claims 189-195, wherein the discontinuous epitope on IL-23p19 is determined by alanine mutagenesis.

200. An isolated antibody or antigen-binding fragment thereof which specifically binds IL-23p19, wherein the antibody or antigen-binding fragment binds a discontinuous epitope on IL-23p19 comprising a first epitope and a second epitope, wherein the antibody or antigen-binding fragment binds to at least amino acid residues 54 and 55 of SEQ ID NO:6 of the first epitope, and to least amino acid residue 116 of SEQ ID NO:6 of the second epitope.

201. The antibody or antigen-binding fragment of claim 200, wherein the antigen or antigen-binding fragment is a bispecific antibody or bispecific antigen-binding fragment.

202. The antibody or antigen-binding fragment of claim 200 or 201, wherein the discontinuous epitope on IL-23p19 is determined by at least one of proteolytic digest, hydrogen/deuterium exchange mass spectrometry and alanine mutagenesis.

203. The antibody or antigen-binding fragment of claim 200 or 201, wherein the discontinuous epitope on IL-23p19 is determined by proteolytic digest.

204. The antibody or antigen-binding fragment of claim 200 or 201, wherein the discontinuous epitope on IL-23p19 is determined by hydrogen/deuterium exchange mass spectrometry or alanine mutagenesis.

205. The antibody or antigen-binding fragment of claim 200 or 201, wherein the discontinuous epitope on IL-23p19 is determined by alanine mutagenesis.

206. The antibody or antigen-binding fragment of Claim 196, wherein the antigen or antigen-binding fragment is a bispecific antibody or bispecific antigen-binding fragment.

207. An isolated IL-17A/F binding entity which specifically binds IL-17A at an epitope comprising at least amino acid residue 108 (Tyr) of SEQ ID NO:2, wherein the IL-17A/F binding entity is a monoclonal antibody or antigen-binding fragment thereof.

208. The IL-17A/F binding entity of Claim 207, wherein the epitope on IL-17A is determined by alanine mutagenesis.

209. The IL-17A/F binding entity of Claim 207, wherein the epitope on IL-17A is determined by X-ray crystallography.

210. The IL-17A/F binding entity of Claim 207, wherein the epitope on IL-17A is determined by alanine mutagenesis and X-ray crystallography.

211. The IL-17A/F binding entity as in any one of Claims 207-210, wherein the IL-17A epitope is a continuous or a discontinuous epitope.

212. An isolated IL-17A/F cross-reactive monoclonal antibody or antigen-binding fragment thereof, wherein the antibody or antigen-binding fragment thereof binds IL-17A at an epitope comprising at least amino acid residue 108 (Tyr) of SEQ ID NO:2.

213. The monoclonal antibody or antigen-binding fragment thereof of Claim 212, wherein the epitope on IL-17A is determined by alanine mutagenesis.

214. The monoclonal antibody or antigen-binding fragment thereof of Claim 212, wherein the epitope on IL-17A is determined by X-ray crystallography.

215. The monoclonal antibody or antigen-binding fragment thereof as in any one of Claims 212-214, wherein the IL-17A epitope is a continuous or a discontinuous epitope.

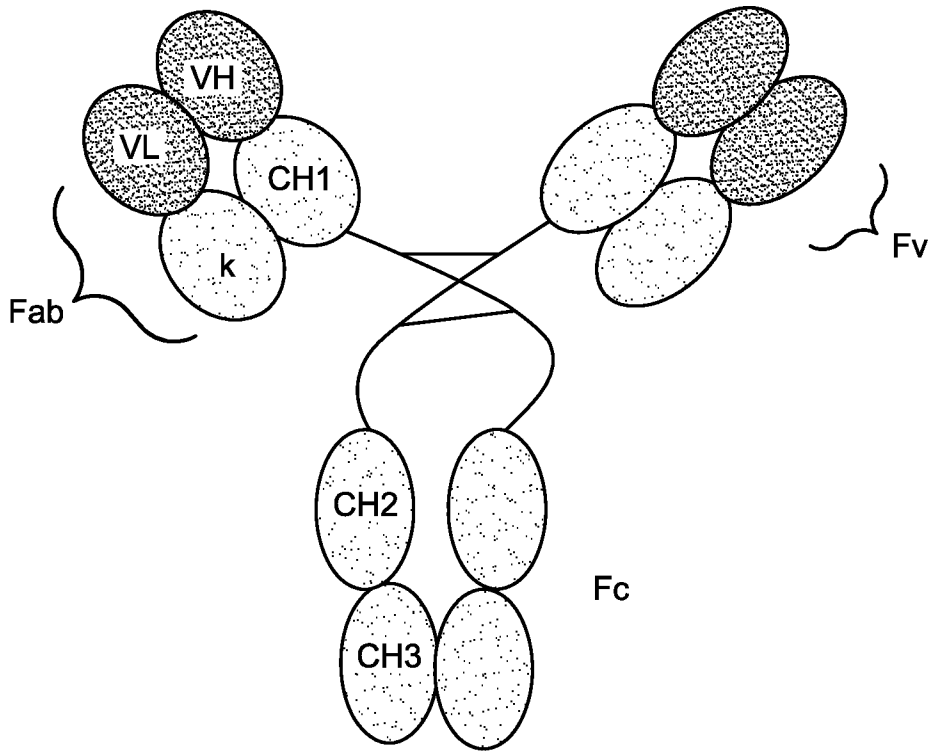

FIG. 1

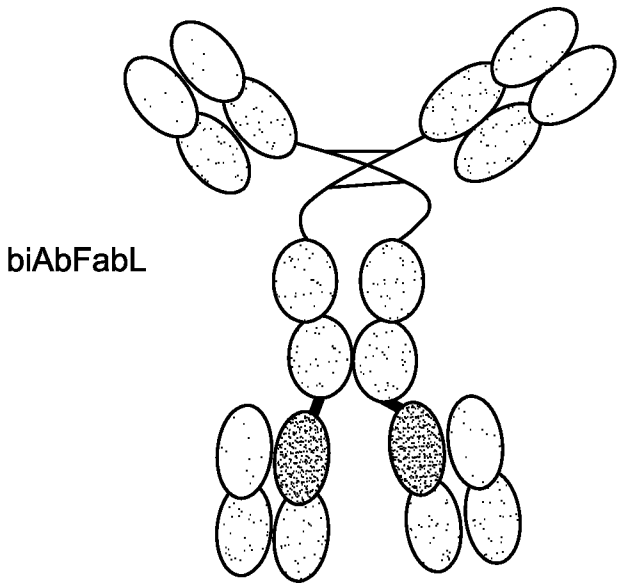

FIG. 2

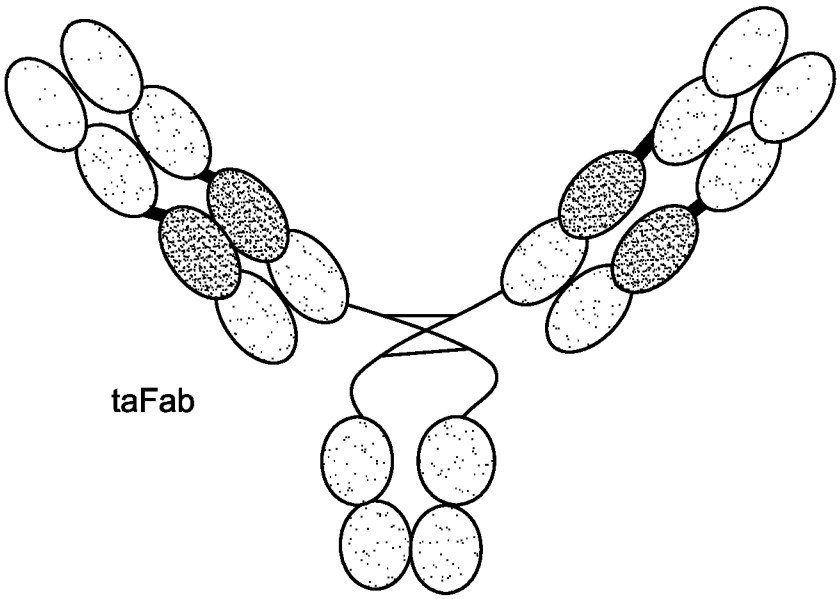

FIG. 3

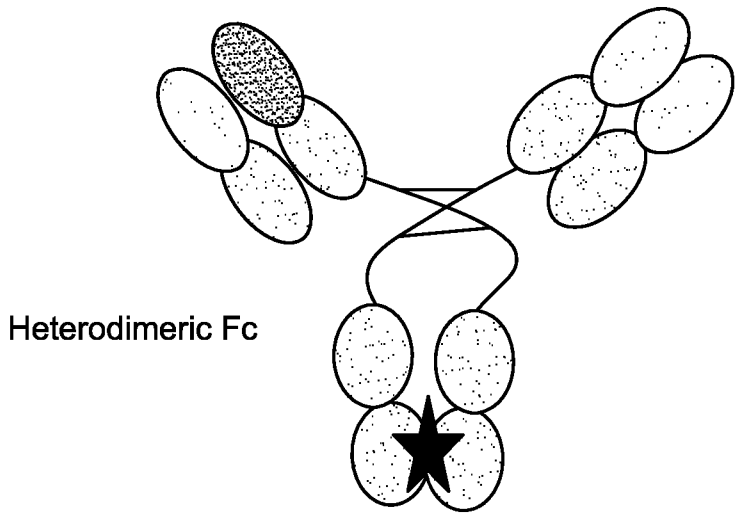

FIG. 4

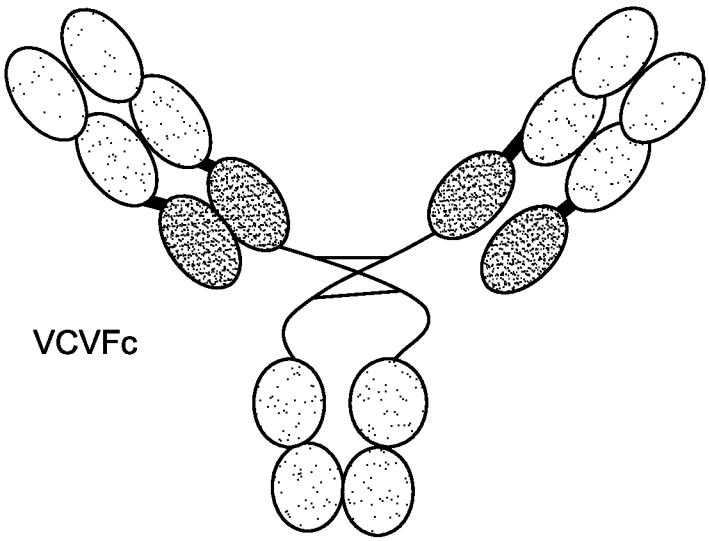

FIG. 5

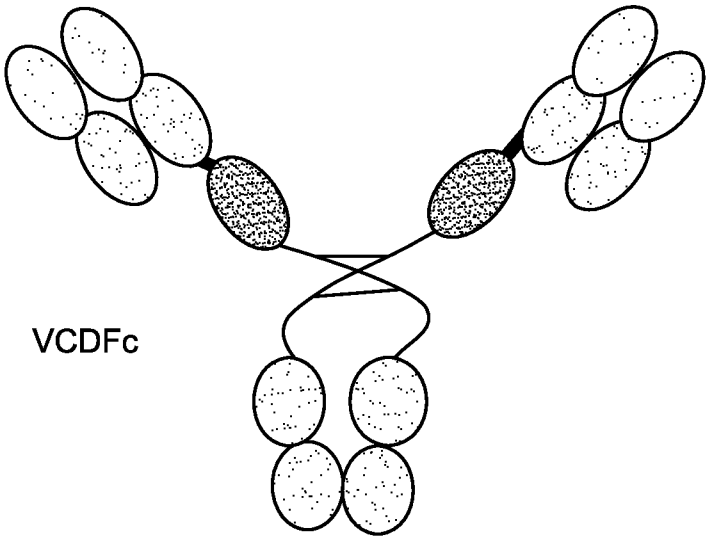

FIG. 6

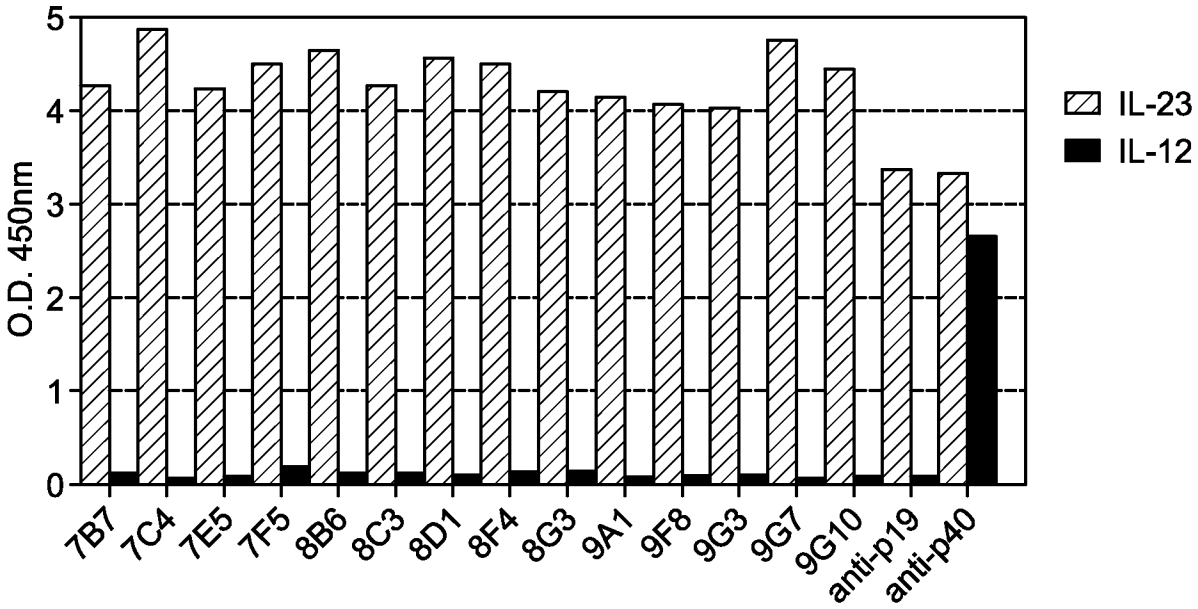
O.D. 450nm
0
1
2
3
4
5
IL-23
IL-12
7B7
7C4
7E5
7F5
8B6
8C3
8D1
8F4
8G3
9A1
9F8
9G3
9G7
9G10
anti-p19
anti-p40

FIG. 7

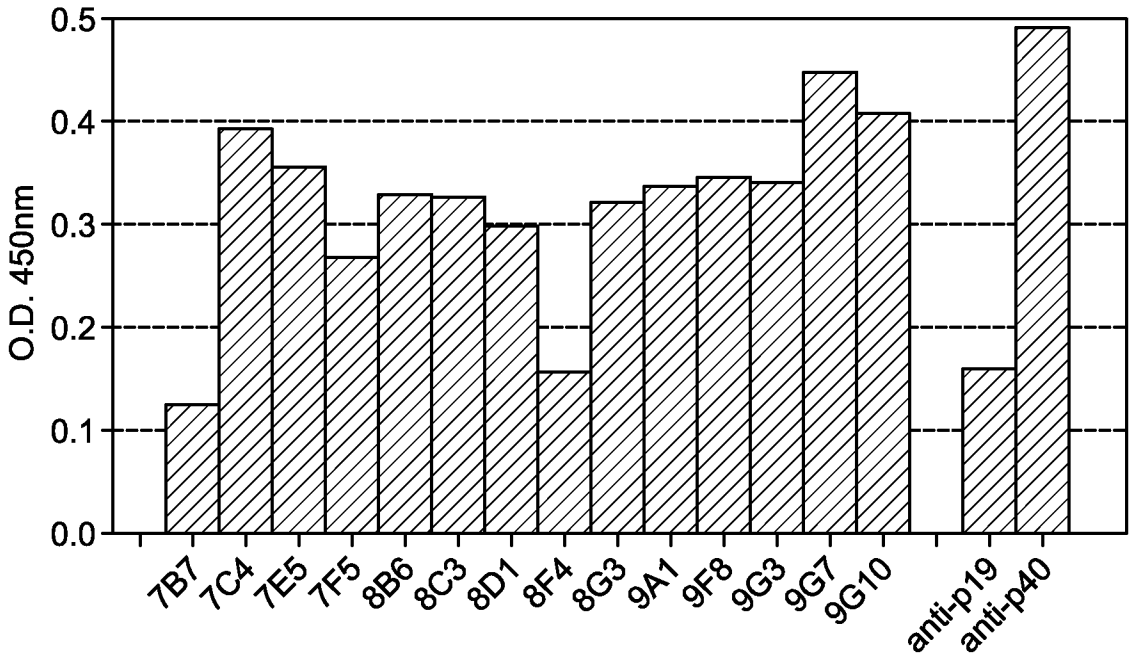
O.D. 450nm
0.0
0.1
0.2
0.3
0.4
0.5
7B7
7C4
7E5
7F5
8B6
8C3
8D1
8F4
8G3
9A1
9F8
9G3
9G7
9G10
anti-p19
anti-p40

FIG. 8

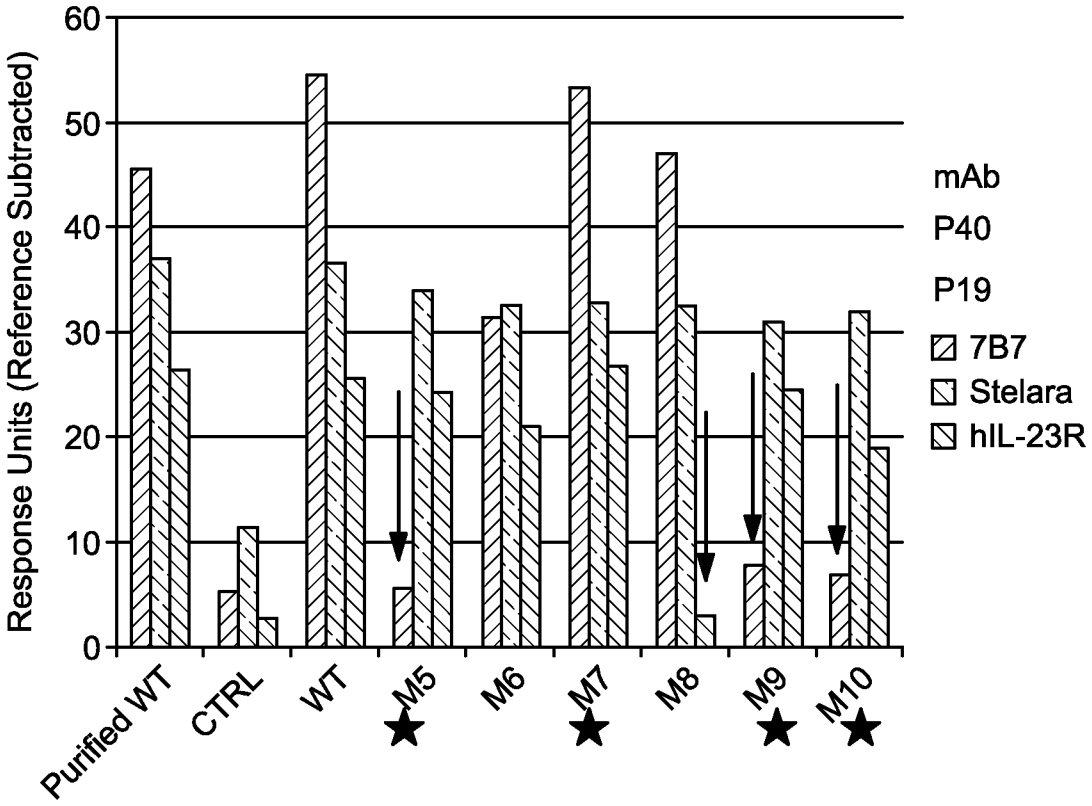
Response Units (Reference Subtracted)
60
50
40
30
20
10
0
Purified WT
CTRL
WT
M5
M6
M7
M8
M9
M10
mAb
P40
P19
7B7
Stelara
hIL-23R

FIG. 9

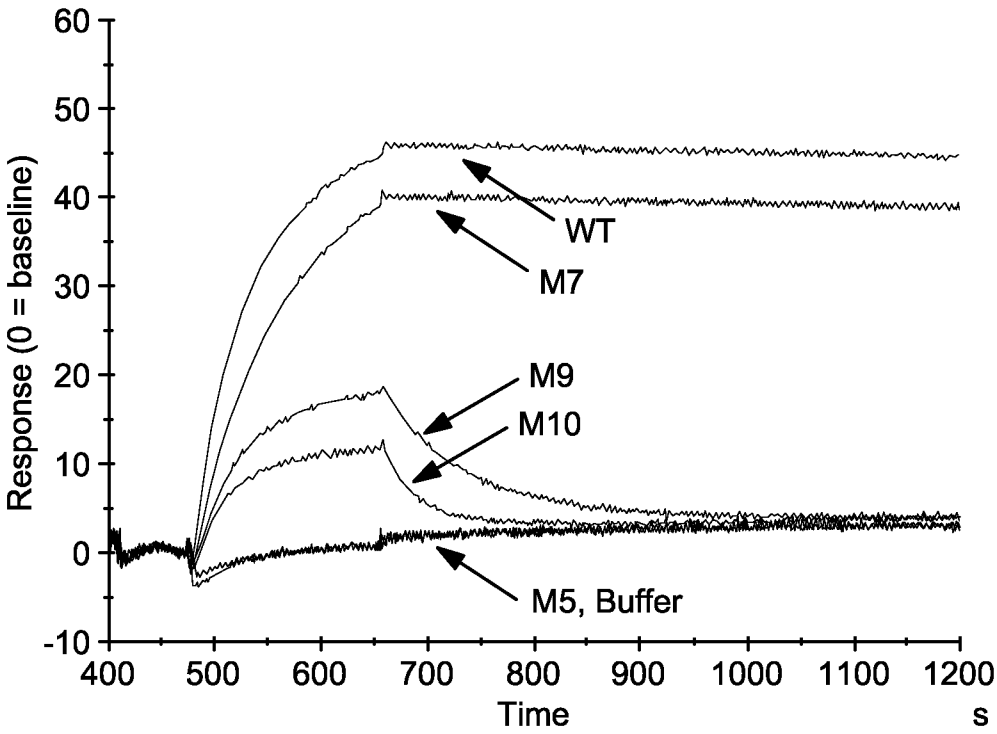
Response (0 = baseline)
60
50
40
30
20
10
0
-10
400
500
600
700
800
900
1000
1100
1200
Time
s
WT
M7
M9
M10
M5, Buffer

FIG. 10

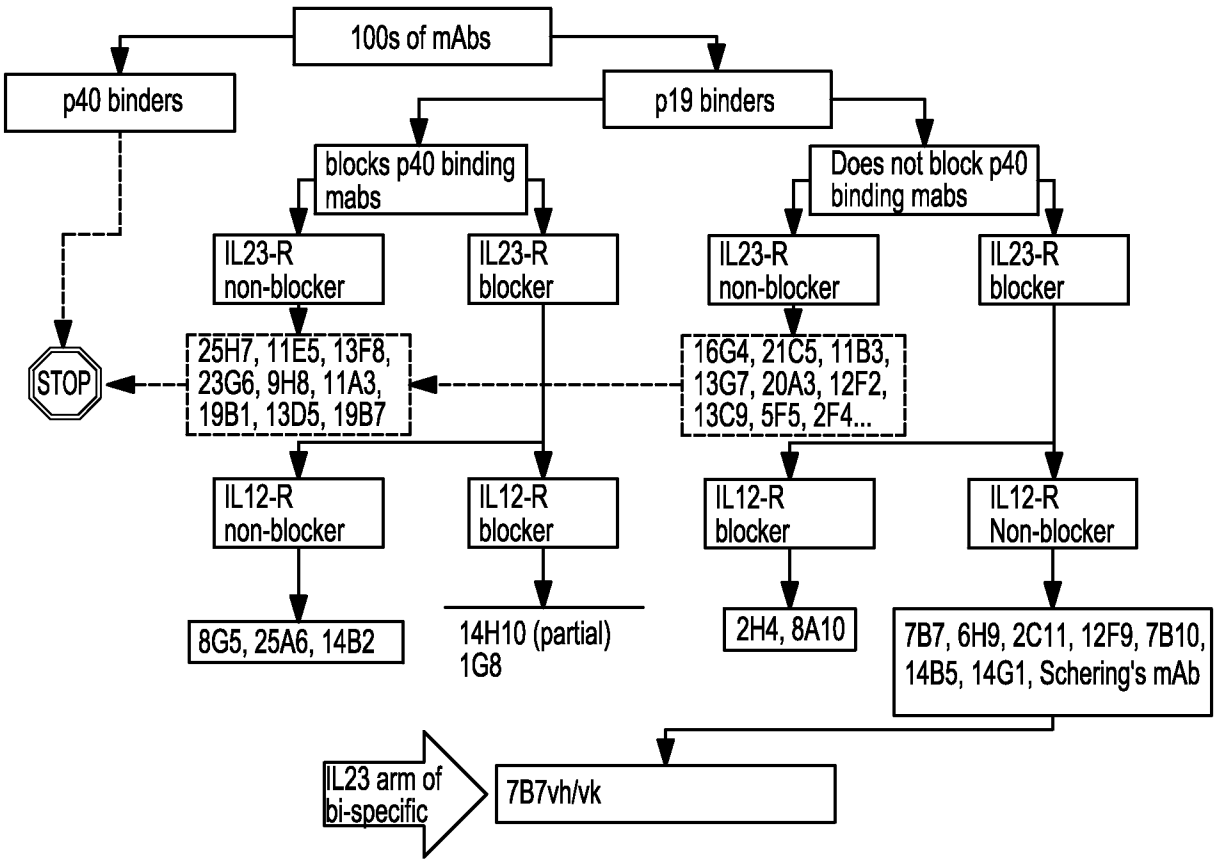
100s of mAbs
p40 binders
p19 binders
blocks p40 binding mabs
Does not block p40 binding mabs
IL23-R non-blocker
IL23-R blocker
IL23-R non-blocker
IL23-R blocker
STOP
25H7, 11E5, 13F8, 23G6, 9H8, 11A3, 19B1, 13D5, 19B7
16G4, 21C5, 11B3, 13G7, 20A3, 12F2, 13C9, 5F5, 2F4...
IL12-R non-blocker
IL12-R blocker
IL12-R blocker
IL12-R Non-blocker
8G5, 25A6, 14B2
14H10 (partial) 1G8
2H4, 8A10
7B7, 6H9, 2C11, 12F9, 7B10, 14B5, 14G1, Schering's mAb
IL23 arm of bi-specific
7B7vh/vk

FIG. 11

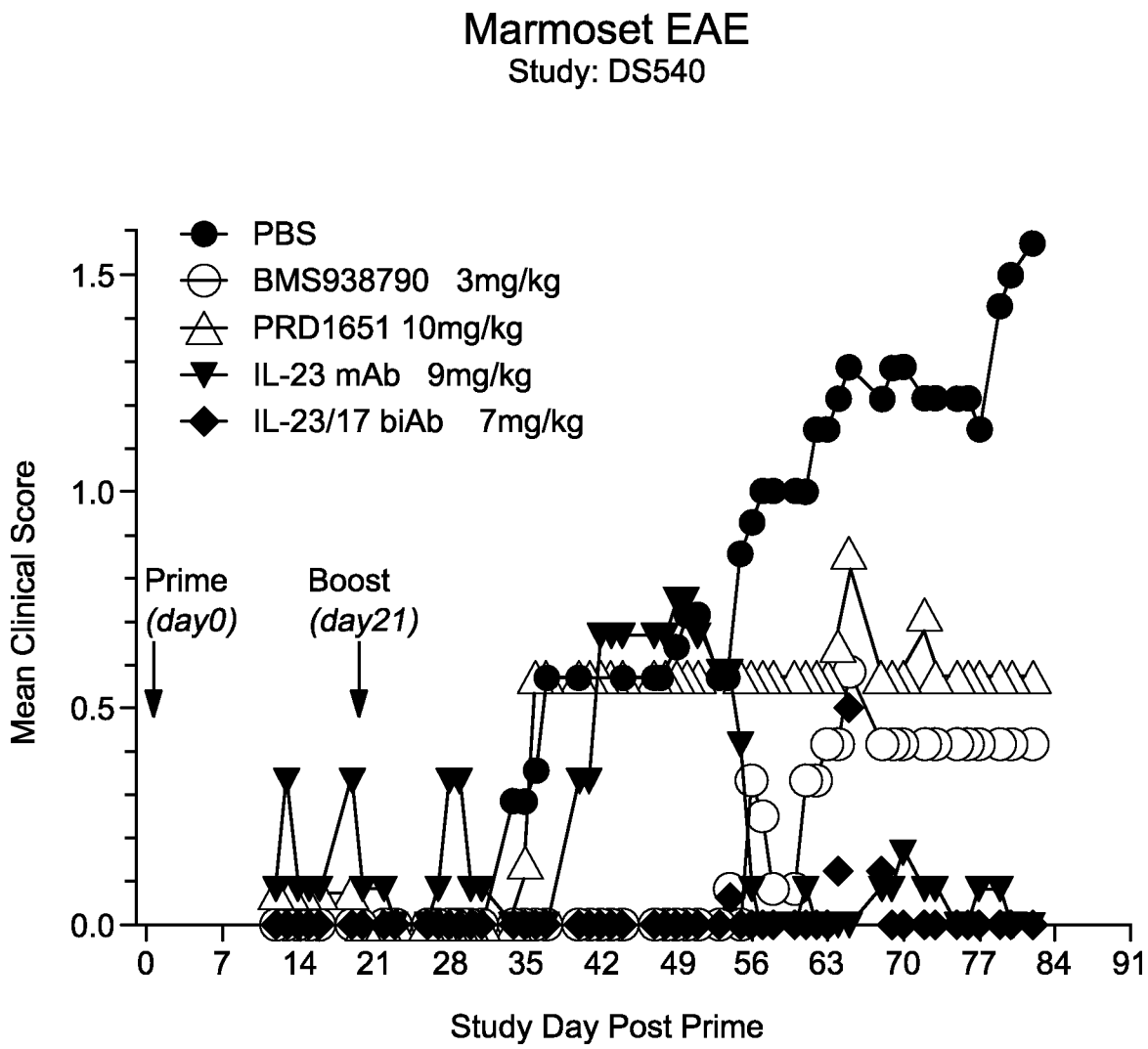
Marmoset EAE
Study: DS540
PBS
BMS938790 3mg/kg
PRD1651 10mg/kg
IL-23 mAb 9mg/kg
IL-23/17 biAb 7mg/kg
Mean Clinical Score
1.5
1.0
0.5
0.0
Prime
(day0)
Boost
(day21)
0
7
14
21
28
35
42
49
56
63
70
77
84
91
Study Day Post Prime

FIG. 12

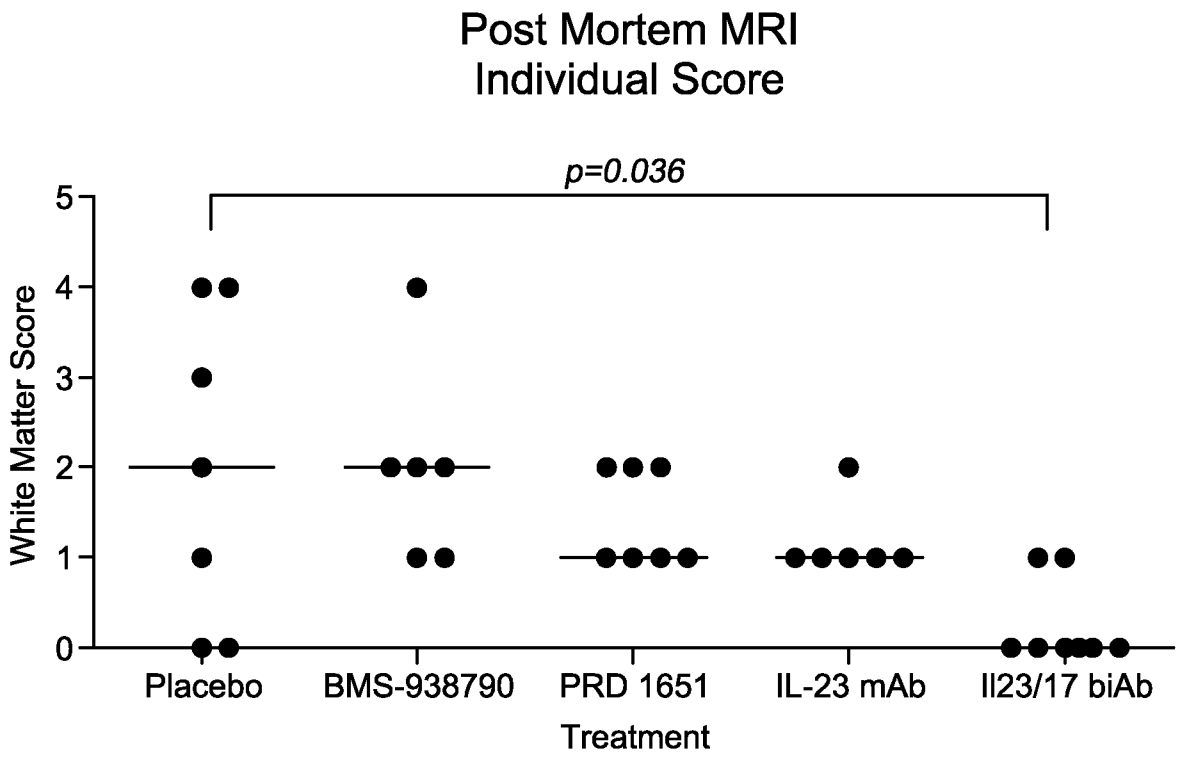
Post Mortem MRI
Individual Score
p=0.036
White Matter Score
5
4
3
2
1
0
Placebo
BMS-938790
PRD 1651
IL-23 mAb
Il23/17 biAb
Treatment

FIG. 13

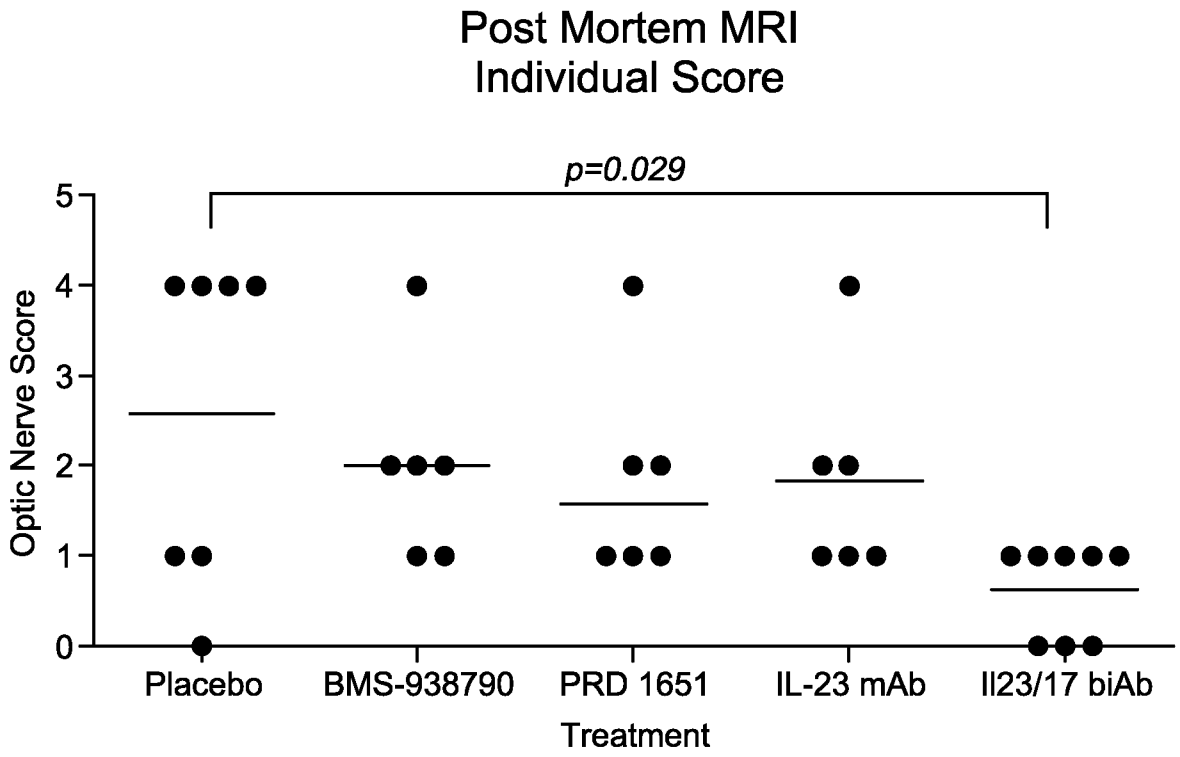
Post Mortem MRI
Individual Score
p=0.029
Optic Nerve Score
5
4
3
2
1
0
Placebo
BMS-938790
PRD 1651
IL-23 mAb
Il23/17 biAb
Treatment

FIG. 14

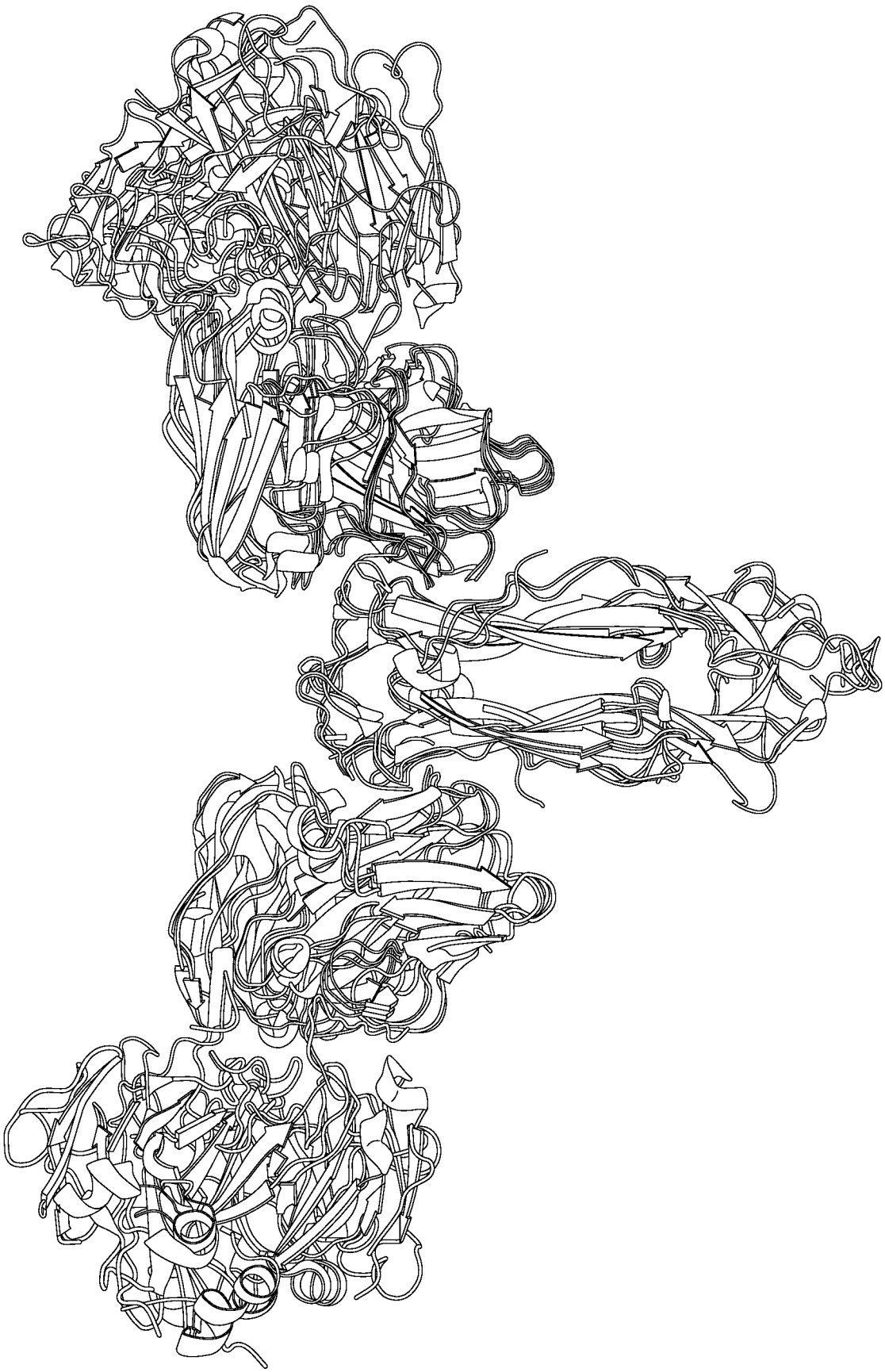

FIG. 15

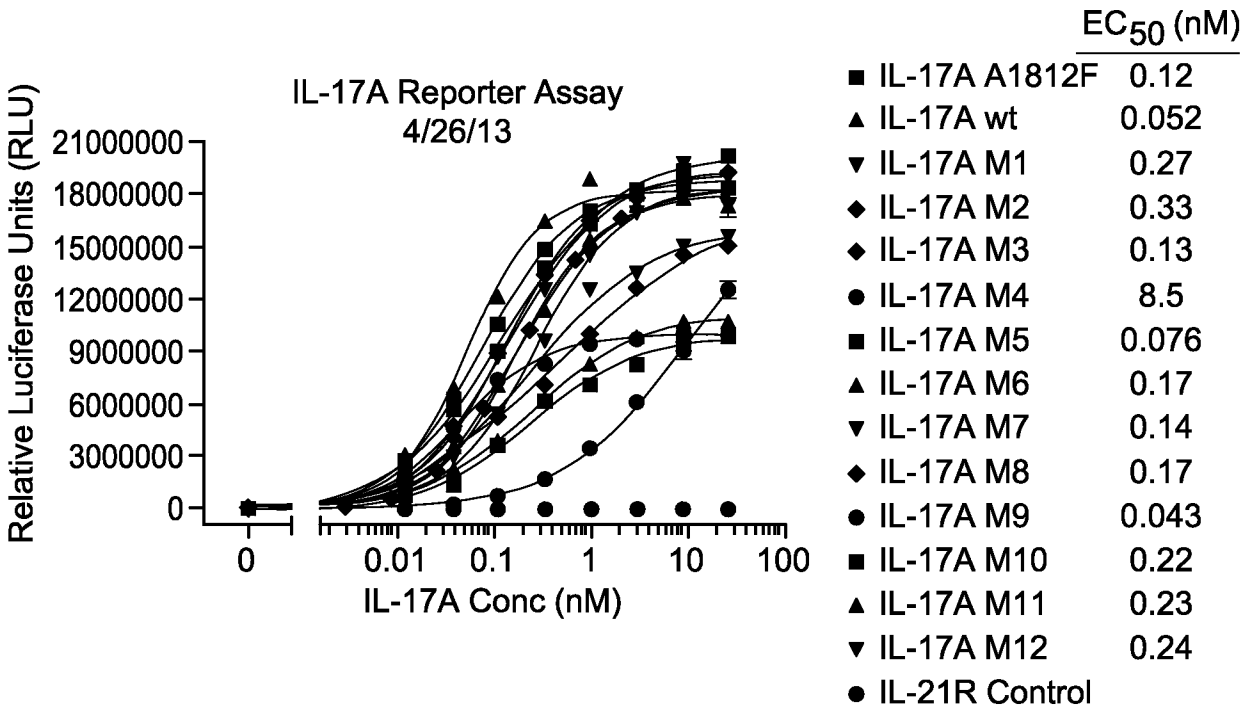
IL-17A Reporter Assay
4/26/13
Relative Luciferase Units (RLU)
21000000
18000000
15000000
12000000
9000000
6000000
3000000
0
0
0.01
0.1
1
10
100
IL-17A Conc (nM)
EC50 (nM)
IL-17A A1812F 0.12
IL-17A wt 0.052
IL-17A M1 0.27
IL-17A M2 0.33
IL-17A M3 0.13
IL-17A M4 8.5
IL-17A M5 0.076
IL-17A M6 0.17
IL-17A M7 0.14
IL-17A M8 0.17
IL-17A M9 0.043
IL-17A M10 0.22
IL-17A M11 0.23
IL-17A M12 0.24
IL-21R Control

FIG. 16

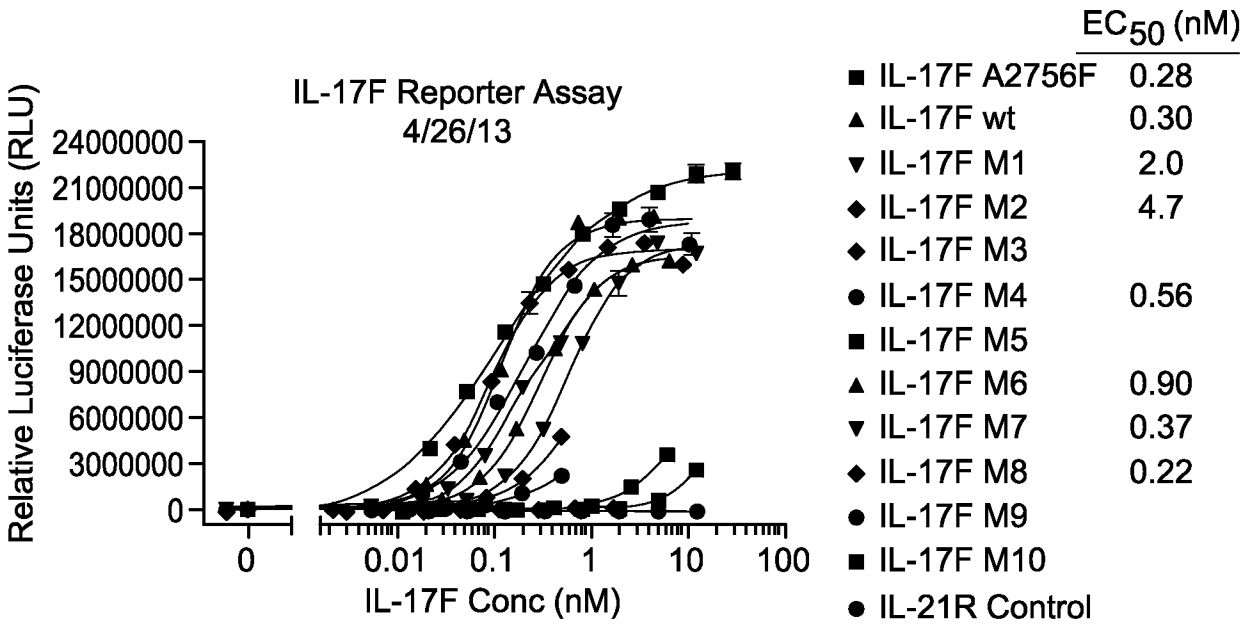
IL-17F Reporter Assay
4/26/13
Relative Luciferase Units (RLU)
24000000
21000000
18000000
15000000
12000000
9000000
6000000
3000000
0
0
0.01
0.1
1
10
100
IL-17F Conc (nM)
EC50 (nM)
IL-17F A2756F 0.28
IL-17F wt 0.30
IL-17F M1 2.0
IL-17F M2 4.7
IL-17F M3
IL-17F M4 0.56
IL-17F M5
IL-17F M6 0.90
IL-17F M7 0.37
IL-17F M8 0.22
IL-17F M9
IL-17F M10
IL-21R Control

FIG. 17

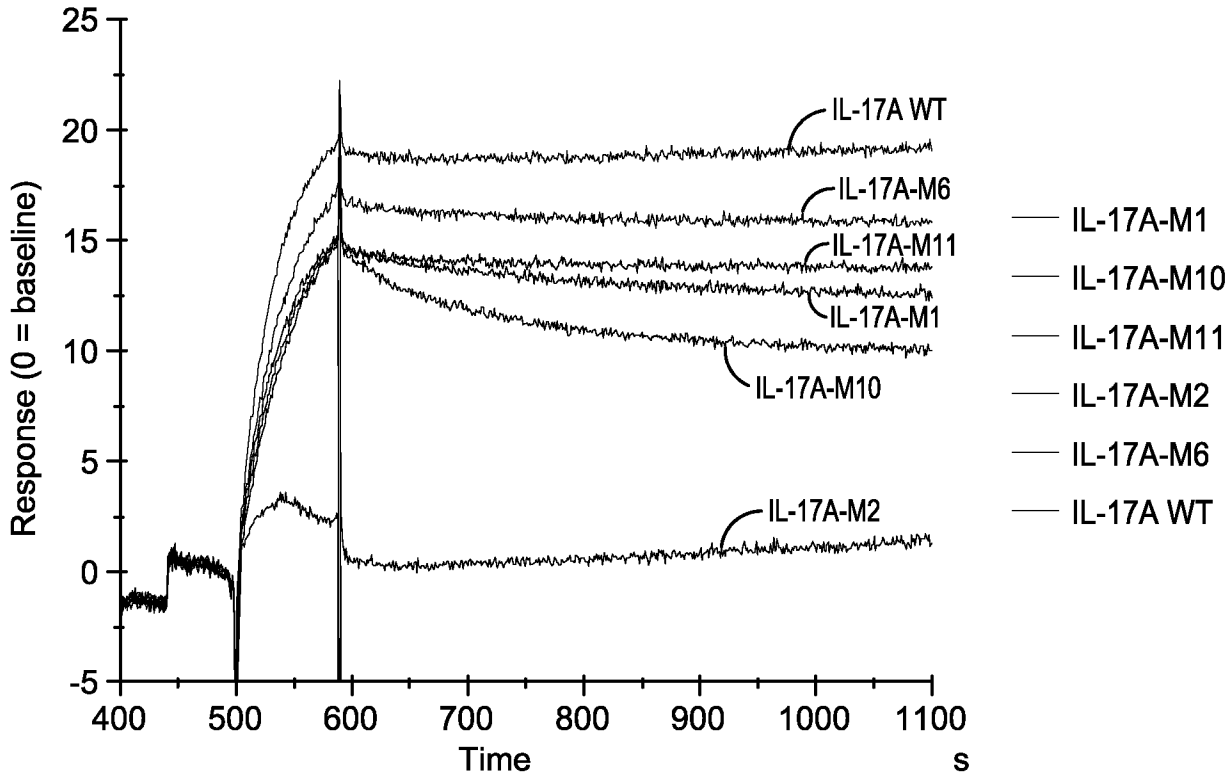
25
20
15
10
5
0
-5
Response (0 = baseline)
400
500
600
700
800
900
1000
1100
Time
s
IL-17A WT
IL-17A-M6
IL-17A-M11
IL-17A-M1
IL-17A-M10
IL-17A-M2
IL-17A-M1
IL-17A-M10
IL-17A-M11
IL-17A-M2
IL-17A-M6
IL-17A WT

FIG. 18

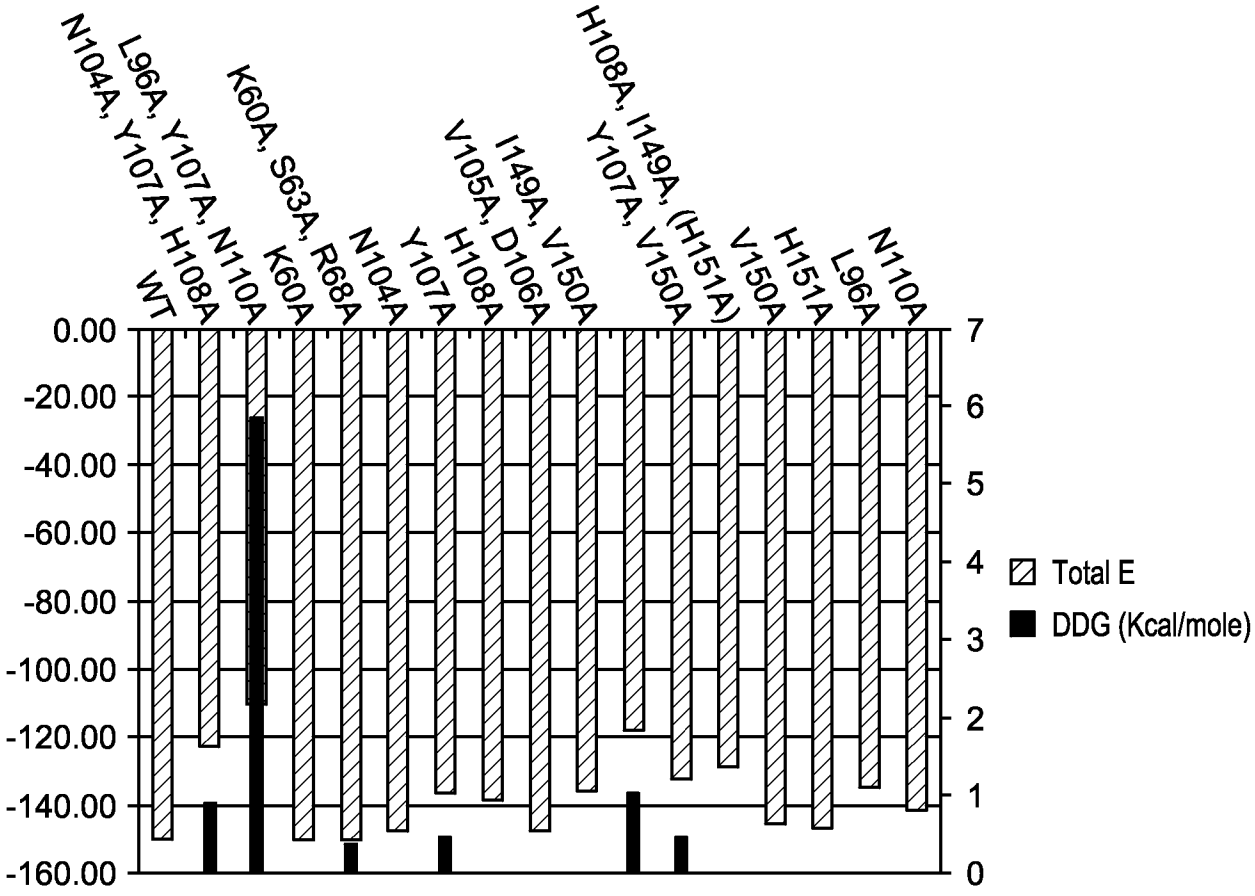
WT
N104A, Y107A, H108A
L96A, Y107A, N110A
K60A
K60A, S63A, R68A
N104A
Y107A
H108A
V105A, D106A
I149A, V150A
H108A, I149A, (H151A)
Y107A, V150A
V150A
H151A
L96A
N110A
0.00
-20.00
-40.00
-60.00
-80.00
-100.00
-120.00
-140.00
-160.00
7
6
5
4
3
2
1
0
Total E
DDG (Kcal/mole)

FIG. 19