TOLL-LIKE RECEPTOR 3 ANTAGONISTS

Field of the Invention

The present invention relates to Toll-Like Receptor 3 (TLR3) antibody antagonists, polynucleotides encoding TLR3 antibody antagonists or fragments thereof, and methods of making and using the foregoing.

Background of the Invention

Toll-like receptors (TLRs) regulate activation of the innate immune response and influence the development of adaptive immunity by initiating signal transduction cascades in response to bacterial, viral, parasitic, and in some cases, host-derived ligands (Lancaster *et al.*, J. Physiol. 563:945-955, 2005). The plasma membrane localized TLRs, TLR1, TLR2, TLR4 and TLR6 recognize ligands including protein or lipid components of bacteria and fungi. The predominantly intracellular TLRs, TLR3, TLR7 and TLR9 respond to dsRNA, ssRNA and unmethylated CpG DNA, respectively. Dysregulation of TLR signaling is believed to cause a multitude of problems, and therapeutic strategies are in development towards this axis (Hoffman *et al.*, Nat. Rev. Drug Discov. 4:879-880, 2005; Rezaei, Int. Immunopharmacol. 6:863-869, 2006; Wickelgren, Science 312:184-187, 2006). For example, antagonists of TLR4 and TLRs 7 and 9 are in clinical development for severe sepsis and lupus, respectively (Kanzler *et al.*, Nat. Med. 13:552-559, 2007).

TLR3 signaling is activated by dsRNA, mRNA or RNA released from necrotic cells during inflammation or virus infection. TLR3 activation induces secretion of interferons and pro-inflammatory cytokines and triggers immune cell activation and recruitement that are protective during certain microbial infections. For example, a dominant-negative TLR3 allele has been associated with increased susceptibility to Herpes Simplex encephalitis upon primary infection with HSV-1 in childhood (Zheng *et al.*, Science

317:1522-1527, 2007). In mice, TLR3 deficiency is associated with decreased survival upon coxsackie virus challenge (Richer *et al.*, PLoS One 4:e4127, 2009). However, uncontrolled or dysregulated TLR3 signaling has been shown to contribute to morbidity and mortality in certain viral infection models including West Nile, phlebovirus, vaccinia, and influenza A (Wang *et al.*, Nat. Med. 10:1366-1373, 2004; Gowen *et al.*, J. Immunol. 177:6301-6307, 2006; Hutchens *et al.*, J. Immunol. 180:483-491, 2008; Le Goffic *et al.*, PloS Pathog. 2:E53, 2006).

The crystal structures of the human and murine TLR3 extracellular domains have been determined ((Bell *et al.*, Proc. Natl. Acad. Sci. (USA), 102:10976-80, 2005; Choe, *et al.*, Science 309:581-585, 2005; Liu *et al.*, Science, 320:379-381, 2008). TLR3 adopts the overall shape of a solenoid horseshoe decorated by glycans and has 23 tandem units of leucine-rich repeat (LRR) motifs. The dsRNA binding sites have been mapped to two distinct regions (Liu *et al.*, Science, 320:379-81, 2008). The singaling assembly has been proposed to consist of 1 dsRNA and two TLR3 extracellular domains (Leonard *et al.*, Proc. Natl. Acad. Sci. (USA) 105: 258-263, 2008).

TLR3 has been shown to drive pathogenic mechanisms in a spectrum of inflammatory, immune-mediated and autoimmune diseases including, for example, septic shock (Cavassani *et al.*, J. Exp. Med. 205:2609-2621, 2008), acute lung injury (Murray *et al.*, Am. J. Respir. Crit. Care Med. 178:1227-1237, 2008), rheumatoid arthritis (Kim *et al.*, Immunol. Lett. 124:9-17, 2009; Brentano *et al.*, Arth. Rheum. 52:2656-2665, 2005), asthma (Sugiura *et al.*, Am. J. Resp. Cell Mol. Biol. 40:654-662, 2009; Morishima *et al.*, Int. Arch. Allergy Immunol. 145:163-174, 2008; Stowell *et al.*, Respir. Res. 10:43, 2009), inflammatory bowel disease such as Crohn's disease and ulcerative colitis (Zhou *et al.*, J. Immunol. 178:4548-4556, 2007; Zhou *et al.*, Proc. Natl. Acad. Sci. (USA) 104:7512-7515, 2007), autoimmune liver disease (Lang *et*

al., J. Clin. Invest. 116:2456-2463, 2006) and type I diabetes (Dogusan *et al.* Diabetes 57:1236-1245, 2008; Lien and Zipris, Curr. Mol. Med. 9:52-68, 2009). Furthermore, organ-specific increases in TLR3 expression have been shown to correlate with a number of pathological conditions driven by dysregulated local inflammatory responses such as in liver tissue in primary biliary cirrhosis (Takii *et al.*, Lab Invest. 85:908-920, 2005), rheumatoid arthritis joints (Ospelt *et al.*, Arthritis Rheum. 58:3684-3692, 2008), and nasal mucosa of allergic rhinitis patients (Fransson *et al.*, Respir. Res. 6:100, 2005).

In necrotic conditions, the release of intracellular content including endogenous mRNA triggers secretion of cytokines, chemokines and other factors that induce local inflammation, facilitate clearance of dead cell remnants and repair the damage. Necrosis often perpetuates inflammatory processes, contributing to chronic or exaggerated inflammation (Bergsbaken *et al.*, Nature Reviews 7:99-109, 2009). Activation of TLR3 at the site of necrosis may contribute to these aberrant inflammatory processes and generate a further pro-inflammatory positive feedback loop via the released TLR3 ligands. Thus, TLR3 antagonism may be beneficial in a variety of disorders involving chronic or exaggerated inflammation and/or necrosis.

Down-modulation of TLR3 activation may also represent a novel treatment strategy for oncologic indications including renal cell carcinomas and head and neck squamous cell carcinomas (Morikawa *et al.*, Clin. Cancer Res. 13:5703-5709, 2007; Pries *et al.*, Int. J. Mol. Med. 21:209-215, 2008). Furthermore, the $TLR3^{L423F}$ allele encoding a protein with reduced activity has been associated with protection against advanced "dry" age-related macular degeneration (Yang *et al.*, N. Engl. J. Med. 359:1456-1463, 2008), indicating that TLR3 antagonists may be beneficial in this disease.

Pathologies associated with inflammatory conditions and others, such as those associated with infections, have

significant health and economic impacts. Yet, despite advances in many areas of medicine, comparatively few treatment options and therapies are available for many of these conditions.

Thus, a need exists to suppress TLR3 activity to treat TLR3-associated conditions.

Brief Description of the Drawings

Fig. 1 shows the effect of anti-human TLR3 (huTLR3) mAbs in an NF-κB reporter gene assay.

Figs. 2A and 2B show the effect (% inhibition) or anti-huTLR3 mAbs in a BEAS-2B assay.

Figs. 3A and 3B show the effect of anti-huTLR3 mAbs in a NHBE assay.

Fig. 4 shows the effect of anti-huTLR3 mAbs in a PBMC assay.

Figs. 5A and 5B show the effect of anti-huTLR3 mAbs in a HASM assay.

Figs. 6A, 6B and 6C show the binding of anti-huTLR3 mAbs to TLR3 mutants.

Fig. 7A shows epitopes for mAb 15EVQ (black) and C1068 mAb (grey) (top image) and epitope for mAb 12QVQ/QSV (black, bottom image) superimposed on the structure of human TLR3 ECD. Fig. 7B shows localized H/D exchange perturbation map of TLR3 ECD protein complexed with mAb 15EVQ.

Figs. 8A and 8B show the effect of rat/mouse anti-mouse TLR3 mAb mAb 5429 (surrogate) in A) NF-κB and B) ISRE reporter gene assays.

Fig. 9 shows the effect of the surrogate mAbs (mAb 5429, mAb c1811) in the MEF CXCL10/IP-10 assay.

Fig. 10 shows specificity of binding of the surrogate mAb to TLR3. Top panel: isotype control; bottom panel: mAb c1811.

Fig. 11 shows effect of the surrogate mAbs on penH level in an AHR model.

Fig. 12 shows effect of the surrogate mAbs on total neutrophil numbers in BAL fluid in an AHR model.

Fig. 13 shows effect of the surrogate mAbs on CXCL10/IP-10 levels in BAL fluid in an AHR model.

Fig. 14 shows effect of the surrogate mAb on histopathology scores in a DSS model.

Fig. 15 shows effect of the surrogate mAb on A) histopathology scores and B) neutrophil influx in a T-cell transfer model.

Fig. 16 shows effect of the surrogate mAb on clinical scores in a CIA model.

Fig. 17 shows effect of the surrogate mAb on the clinical AUC scores in a CIA model.

Fig. 18 shows effect of the surrogate mAb on the survival of C57BL/6 mice following intranasal administration of influenza A/PR/8/34. mAb dosing began at day -1.

Fig. 19 shows effect of the surrogate mAb on clinical scores following influenza A/PR/8/34 administration. mAb dosing began at day -1.

Fig. 20 shows effect of the surrogate mAb on body weight over 14 days after administration of influenza A/PR/8/34. mAb dosing began at day -1.

Fig. 21 shows effect of the surrogate mAbs on blood glucose levels in (A) WT DIO and (B) TLR3KO DIO animals after glucose challenge.

Fig. 22 shows effect of the surrogate mAb on insulin levels in WT DIO animals.

Fig. 23 shows effect of mAb 15EVQ on (A) NTHi and (B) rhinovirus induced CXCL10/IP-10 and CCL5/RANTES levels in NHBE cells.

Fig. 24 shows effect of mAb 15EVQ on (A) sICAM-1 levels and (B) viability in HUVEC cells.

Fig. 25 shows survival of animals following administration of the surrogate mAb 3 days post infection with influenza A.

Fig. 26 shows clinical scores following administration of the surrogate mAb 3 days post infection with influenza A.

Fig. 27 shows body weight change of animals following administration of the surrogate mAb 3 days post infection with influenza A.

Fig. 28 shows the molecular structure of the quaternary complex of huTLR3 ECD with Fab 12QVQ/QSV, Fab 15EVQ and Fab c1068 in A. in ribbon and surface representations. The TLR3 ECD is in light gray with the N-terminus labeled N; all Fab molecules are shown in dark gray in ribbons representation. B. The epitopes are colored light gray and labeled on the TLR3 ECD as for the Fabs in A. In Figures 28, 29 and 30, the Fab 12QVQ/QSV, Fab c1068 and Fab 15EVQ are abbreviated to Fab12, Fab1068 and Fab15, respectively in the labels for clarity.

Fig 29. Shows a mechanism of neutralization by Fab 15EVQ. A. dsRNA:TLR3 signaling unit (SU) is shown with the Fab 15EVQ epitope highlighted (light gray) in one of the two TLR3 ECD (light and dark gray, and labeled TLR3). The dsRNA ligand is shown as a double helix in light gray. B. An illustration of Fab 15EVQ binding that sterically inhibited dsRNA binding and thus, inhibits the formation of the SU. Binding of Fab 15EVQ, which is higher affinity, will prevent the SU from forming or will disassemble the pre-formed SU.

Fig. 30 shows a mechanism of Fab 12QVQ/QSV and Fab c1068 and clustering of TLR3 signaling units (SU). A. Fab 12QVQ/QSV and Fab c1068 can bind (or co-bind) a single SU. B. Model for closest clustering of two SUs on a dsRNA of about 76 base pairs. The three epitopes are highlighted in different molecules for clarity. C. Binding of Fab 12QVQ/QSV and Fab c1068 prevents SU clustering due to steric clashes between the antibodies and neighboring SUs. The two left-pointing arrows qualitatively represent different degrees of separation of SUs due to the antibodies (bottom arrow for Fab 12QVQ/QSV and top arrow for Fab c1068).

Fig. 31 shows the correspondence between sequential, Kabat, and Chothia numbering for exemplary antibodies. The CDRs and HVs are highlighted in gray.

Fig. 32 shows alignment of VL of mAb 15EVQ with human Vk1 frameworks. Chothia hypervariable loops are underlined, paratope residues double underlined and the framework differences highlighted in gray. The Vκ1 genes are *01 alleles unless otherwise indicated. Residue numbering is sequential.

Fig. 33 shows alignment of VH of mAb 15EVQ with human Vh5 frameworks. Sequence features indicated as in Fig. 32.

Fig. 34 shows alignment of VL of mAb 12QVQ/QSV with human Vk3 frameworks. Sequence features indicated as in Fig. 32.

Fig. 35 shows alignment of VL and VH of mAb 15EVQ or mAb 12QVQ/QSV with human Jκ, Jλ or Jh frameworks. Sequence features indicated as in Fig. 32.

Summary of the Invention

One aspect of the invention is an isolated antibody or fragment thereof, wherein the antibody binds toll-like receptor 3 (TLR3) amino acid residues K416, K418, L440, N441, E442, Y465, N466, K467, Y468, R488, R489, A491, K493, N515, N516, N517, H539, N541, S571, L595, and K619 of SEQ ID NO: 2.

Another aspect of the invention is an isolated antibody or fragment thereof, wherein the antibody binds toll-like receptor 3 (TLR3) amino acid residues S115, D116, K117, A120, K139, N140, N141, V144, K145, T166, Q167, V168, S188, E189, D192, A195, and A219 of SEQ ID NO: 2.

Another aspect of the invention is an isolated antibody having a heavy chain variable region and a light chain variable region or fragment thereof, wherein the antibody binds TLR3 having an amino acid sequence shown in SEQ ID NO: 2 with the heavy chain variable region Chothia residues W33, F50, D52, D54, Y56, N58, P61, E95, Y97, Y100, and D100b and the light chain variable region Chothia residues Q27, Y32, N92, T93, L94, and S95.

Another aspect of the invention is an isolated antibody having a heavy chain variable region and a light chain

variable region or fragment thereof, wherein the antibody binds TLR3 having an amino acid sequence shown in SEQ ID NO: 2 with the heavy chain variable region Chothia residues N31a, Q52, R52b, S53, K54, Y56, Y97, P98, F99, and Y100, and the light chain variable region Chothia residues G29, S30, Y31, Y32, E50, D51, Y91, D92, and D93.

Another aspect of the invention is an isolated antibody reactive with TLR3, wherein the antibody has at least one of the following properties:

a. binds to human TLR3 with a Kd fo <10 nM;
b. reduces human TLR3 biological activity in an *in vitro* poly(I:C) NF-kB reporter gene assay >50% at 1 μg/ml;
c. inhibits >60% of IL-6 or CXCL10/IP-10 production from BEAS-2B cells stimulated with <100 ng/ml poly(I:C) at 10 μg/ml;
d. inhibits >50% of IL-6 or CXCL10/IP-10 production from BEAS-2B cells stimulated with <100 ng/ml poly(I:C) at 0.4 μg/ml;
e. inhibits >50% of IL-6 production from NHBE cells stimulated with 62.5 ng/ml poly(I:C) at 5 μg/ml;
f. inhibits >50% of IL-6 production from NHBE cells stimulated with 62.5 ng/ml poly(I:C)at 1 μg/ml;
g. inhibits >20% of poly(I:C)-induced IFN-γ, IL-6 or IL-12 production by PBMC cells at 1 μg/ml;
h. inhibits cynomologus TLR3 biological activity in an *in vitro* NF-kB reporter gene assay with IC50 < 10 μg/ml; or
i. inhibits cynomologus TLR3 biological activity in an *in vitro* ISRE reporter gene assay with IC50 < 5 μg/ml.

Another aspect of the invention is an isolated antibody reactive with TLR3 that competes for TLR3 binding with a monoclonal antibody, wherein the monoclonal antibody comprises the amino acid sequences of certain heavy chain

complementarity determining regions (CDRs) 1, 2 and 3, the amino acid sequences of certain light chain CDRs 1, 2 and 3, the amino acid sequences of certain heavy chain variable regions (VH) or the amino acid sequence of certain light chain variable regions (VL).

Another aspect of the invention is an isolated antibody reactive with TLR3 comprising both a heavy chain variable region and a light chain variable region and wherein the antibody comprises the amino acid sequences of certain heavy chain complementarity determining regions (CDRs) 1, 2 and 3 and the amino acid sequences of certain light chain CDRs 1, 2 and 3.

Another aspect of the invention is an isolated antibody reactive with TLR3 comprising both a heavy chain variable region and a light chain variable region and wherein the antibody comprises the amino acid sequences of certain heavy chain variable regions (VH) and the amino acid sequences of certain light chain variable regions (VL).

Another aspect of the invention is an isolated antibody reactive with TLR3 comprising both a heavy chain variable region and a light chain variable region and wherein the antibody comprises the amino acid sequence of certain heavy chains and the amino acid sequence of certain light chains.

Another aspect of the invention is an isolated antibody heavy chain comprising the amino acid sequence shown in SEQ ID NO: 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 124, 125, 126, 127, 128, 129, 159, 198, 200, 202, 164, 212, 213, 214, 215 or 216.

Another aspect of the invention is an isolated antibody light chain comprising the amino acid sequence shown in SEQ ID NO: 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 122, 123, 197, 199, 201, 163, 209, 210, 211, or 225.

Another aspect of the invention is an isolated antibody heavy chain comprising the amino acid sequence shown in SEQ

ID NO: 102, 130, 131, 132, 133, 134, 135, 160, 204, 206, 208, 220, 166 or 168.

Another aspect of the invention is an isolated antibody light chain comprising the amino acid sequence shown in SEQ ID NO: 155, 156, 157, 158, 203, 205, 207, 165, 167, or 227.

Another aspect of the invention is an isolated polynucleotide encoding an antibody heavy chain comprising the amino acid sequence shown in SEQ ID NO: 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 124, 125, 126, 127, 128, 129, 159, 198, 200, 202, 164, 212, 213, 214, 215 or 216.

Another aspect of the invention is an isolated polynucleotide encoding an antibody light chain comprising the amino acid sequence shown in SEQ ID NO: 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 122, 123, 197, 199, 201, 163, 209, 210, 211, or 225.

Another aspect of the invention is an isolated polynucleotide encoding an antibody heavy chain comprising the amino acid sequence shown in SEQ ID NO: 102, 130, 131, 132, 133, 134, 135, 160, 204, 206, 208, 220, 166 or 168.

Another aspect of the invention is an isolated polynucleotide encoding an antibody light chain comprising the amino acid sequence shown in SEQ ID NO: 155, 156, 157, 158, 203, 205, 207, 165, 167, or 227.

Another aspect of the invention is a pharmaceutical composition comprising the isolated antibody of the invention and a pharmaceutically acceptable carrier.

Another aspect of the invention is a vector comprising at least one polynucleotide of the invention.

Another aspect of the invention is a host cell comprising the vector of the invention.

Another aspect of the invention is a method of making an antibody reactive with TLR3 comprising culturing the host cell of the invention and recovering the antibody produced by the host cell.

Another aspect of the invention is a method of treating or preventing an inflammatory condition comprising administering a therapeutically effective amount of the isolated antibody of the invention to a patient in need thereof for a time sufficient to treat or prevent the inflammatory condition.

Another aspect of the invention is a method of treating or preventing a systemic inflammatory condition comprising administering a therapeutically effective amount of the isolated antibody of the invention to a patient in need thereof for a time sufficient to treat or prevent the systemic inflammatory condition.

Another aspect of the invention is a method of treating type II diabetes comprising administering a therapeutically effective amount of the isolated antibody of the invention to a patient in need thereof for a time sufficient to treat type II diabetes.

Another aspect of the invention is a method of treating hyperglycemia comprising administering a therapeutically effective amount of the isolated antibody of the invention to a patient in need thereof for a time sufficient to treat the hyperglycemia.

Another aspect of the invention is a method of treating hyperinsulinemia comprising administering a therapeutically effective amount of the isolated antibody of the invention to a patient in need thereof for a time sufficient to treat the insulin resistance.

Another aspect of the invention is a method of treating or preventing viral infections comprising administering a therapeutically effective amount of the isolated antibody of the invention to a patient in need thereof for a time sufficient to treat or prevent viral infections.

Detailed Description of the Invention

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

The term "antagonist" as used herein means a molecule that partially or completely inhibits, by any mechanism, an effect of another molecule such as a receptor or intracellular mediator.

As used herein, a "TRL3 antibody antagonist" or an antibody "reactive with TLR3" describes an antibody that is capable of, directly or indirectly, substantially counteracting, reducing or inhibiting TLR3 biological activity or TLR3 receptor activation. For example, an antibody reactive with TLR3 can bind directly to TLR3 and neutralize TLR3 activity, *i.e*, block TLR3 signaling to reduce cytokine and chemokine release or NF-κB activation.

The term "antibodies" as used herein is meant in a broad sense and includes immunoglobulin or antibody molecules including polyclonal antibodies, monoclonal antibodies including murine, human, human-adapted, humanized and chimeric monoclonal antibodies and antibody fragments.

In general, antibodies are proteins or peptide chains that exhibit binding specificity to a specific antigen. Intact antibodies are heterotetrameric glycoproteins, composed of two identical light chains and two identical heavy chains. Typically, each light chain is linked to a heavy chain by one covalent disulfide bond, while the number of disulfide linkages varies between the heavy chains of different immunoglobulin isotypes. Each heavy and light chain also has regularly spaced intrachain disulfide bridges. Each heavy chain has at one end a variable domain (variable region) (VH) followed by a number of constant domains (constant regions). Each light chain has a variable domain at one end (VL) and a constant domain at its other end; the constant domain of the light chain is aligned with the first constant domain of the heavy chain and the light chain

variable domain is aligned with the variable domain of the heavy chain. Antibody light chains of any vertebrate species can be assigned to one of two clearly distinct types, namely kappa (κ) and lambda (λ), based on the amino acid sequences of their constant domains.

Immunoglobulins can be assigned to five major classes, namely IgA, IgD, IgE, IgG and IgM, depending on the heavy chain constant domain amino acid sequence. IgA and IgG are further sub-classified as the isotypes IgA_1, IgA_2, IgG_1, IgG_2, IgG_3 and IgG_4.

The term "antibody fragments" means a portion of an intact antibody, generally the antigen binding or variable region of the intact antibody. Examples of antibody fragments include Fab, Fab', $F(ab')_2$ and Fv fragments, diabodies, single chain antibody molecules and multispecific antibodies formed from at least two intact antibodies.

An immunoglobulin light chain variable region or heavy chain variable region consists of a "framework" region interrupted by three "antigen-binding sites". The antigen-binding sites are defined using various terms as follows: (i) the term Complementarity Determining Regions (CDRs) is based on sequence variability (Wu and Kabat, J. Exp. Med. 132:211-250, 1970). Generally, the antigen-binding site has six CDRs; three in the VH (HCDR1, HCDR2, HCDR3), and three in the VL (LCDR1, LCDR2, LCDR3) (Kabat *et al.*, Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, Md., 1991). (ii) The term "hypervariable region", "HVR", or "HV" refers to the regions of an antibody variable domain which are hypervariable in structure as defined by Chothia and Lesk (Chothia and Lesk, Mol. Biol. 196:901-917, 1987). Generally, the antigen-binding site has six hypervariable regions, three in VH (H1, H2, H3) and three in VL (L1, L2, L3). Chothia and Lesk refer to structurally conserved HVs as "canonical structures". (iii) The "IMGT-CDRs" as proposed by Lefranc (Lefranc *et al.*, Dev. Comparat. Immunol. 27:55-77, 2003) are

based on the comparison of V domains from immunoglobulins and T-cell receptors. The International ImMunoGeneTics (IMGT) database (http://www_imgt_org) provides a standardized numbering and definition of these regions. The correspondence between CDRs, HVs and IMGT delineations is described in Lefranc *et al.*, Dev. Comparat. Immunol. 27:55-77, 2003. (iv) The antigen-binding site can also be delineated based on Specificity Determining Residue Usage (SDRU)(Almagro, Mol. Recognit. 17:132-143, 2004), where Specificity Determining Residues (SDR), refers to amino acid residues of an immunoglobulin that are directly involved in antigen contact. SDRU is a precise measure of a number and distribution of SDR for different types of antigens as defined by analyses of crystal structures of antigen-antibody complexes. (v) The antigen-binding site can also be defined as the antibody paratope residues identified from crystal structure of the antigen-antibody complex.

The term "composite sequences" as used herein means an antigen-binding site defined to include all amino acid residues delineated individually by Kabat, Chothia or IMGT, or any other suitable antigen-binding site delineation.

"Chothia residues" as used herein are the antibody VL and VH residues numbered according to Al-Lazikani (Al-Lazikani *et al.*, J. Mol. Biol. 273:927-48, 1997). Correspondence between the two most used numbering systems, Kabat (Kabat *et al.*, Sequences of Immunological Interest, 5th Ed. Public Health Service, NIH, Bethesda, MD, 1991) and Chothia (Chothia and Lesk, Mol. Biol. 196:901-17, 1987) in relation to sequential polypeptide numbering is shown in Figure 31 for exemplary antibodies of the invention.

"Framework" or "framework sequences" are the remaining sequences of a variable region other than those defined to be antigen-binding site. The framework is typically divided into four regions, FR1, FR2, FR3, and FR3, which form a scaffold for the three antigen-binding sites in each variable reigon. Because the antigen-binding site can be defined by

various terms as described above, the exact amino acid sequence of a framework depends on how the antigen-binding site was defined.

"A light chain variable region kappa 1 (Vκ1) framework" or "Vκ1" as used herein refers to a framework having an amino acid sequence encoded by any of the human Vκ1 functional genes or alleles thereof. Exemplary functional human Vk1 genes are IGKV1-5*01, IGKV1-6*01, IGKV1-8*01, IGKV1-9*01, IGKV1-12*01, IGKV1-13*02, IGKV1-16*01, IGKV1-17*01, IGKV1-27*01, IGKV1-33*01, IGKV1-37*01, IGKV1-39*01, IGKV1D-8*01, IGKV1D-12*01, IGKV1D-13*01, IGKV1D-16*01, IGKV1D-17*01, IGKV1D-33*01, IGKV1D-37*01, IGKV1D-39*01, IGKV1D-42*01, or IGKV1D-43*01. Nomenclature of the immunoglobulin genes is well known.

"A light chain variable region lambda 3 (Vλ3) framework" or "Vλ3" as used herein refers to a framework having an amino acid sequence encoded by any of the human Vλ3 functional genes or alleles thereof. Exemplary functional human Vλ3 genes are IGLV3-1*01, IGLV3-9*01, IGLV3-10*01, IGLV3-12*01, IGLV3-16*01, IGLV3-19*01, IGLV3-21*01, IGLV3-22*01, IGLV3-25*01, IGLV3-27*01, and IGLV3-32*01.

"A heavy chain variable region Vh5 framework" or "Vh5" as used herein refers to a framework having an amino acid sequence encoded by any of the human Vh5 functional genes or alleles thereof. Exemplary functional human Vh5 genes are IGHV5-51*01 and IGHV5-1*01.

"A heavy chain variable region Vh6 framework" or "Vh6" as used herein refers to a framework having an amino acid sequence encoded by any of the human Vh6 functional genes or alleles thereof. An exemplary functional human Vh6 gene is IGHV6-1*01.

"A light chain kappa J-region (Jκ) framework" or "Jκ" as used herein refers to a framework having an amino acid sequence encoded by any of the human Jκ functional genes or

alleles thereof. Exemplary functional human Vκ genes are IGKJ1, IGKJ2, IGKJ3, IGKJ4, and IGKJ5.

"A light chain lambda J-region (Jλ) framework" or "Jλ" as used herein refers to a framework having an amino acid sequence encoded by any of the human Jλ functional genes or alleles thereof. Exemplary functional human Jλ genes are IGLJ1, IGLJ2, IGLJ3, IGLJ4, IGLJ5, IGLJ6, and IGLJ7.

"A heavy chain J-region (Jh) framework" or "Jh" as used herein refers to a framework having an amino acid sequence encoded by any of the human Jh functional genes or alleles thereof. Exemplary functional human Jh genes are IGHJ1, IGHJ2, IGHJ3, IGHJ4, IGHJ5, and IGHJ6.

"Germline genes" or "antibody germline genes" as used herein are immunoglobulin sequences encoded by non-lymphoid cells that have not undergone the maturation process that leads to genetic rearrangement and mutation for expression of a particular immunoglobulin.

"Scaffold" as used herein refers to amino acid sequences of light or heavy chain variable regions encoded by human germline genes. Thus, the scaffold encompasses both the framework and the antigen-binding site.

The term "antigen" as used herein means any molecule that has the ability to generate antibodies either directly or indirectly. Included within the definition of "antigen" is a protein-encoding nucleic acid.

The term "homolog" means protein sequences having between 40% and 100% sequence identity to a reference sequence. Homologs of human TLR3 include polypeptides from other species that have between 40% and 100% sequence identity to a known human TLR3 sequence. Percent identity between two peptide chains can be determined by pairwise alignment using the default settings of the AlignX module of Vector NTI v.9.0.0 (Invitrogen, Carlsbad, CA). By "TLR3" is meant human TLR3 (huTLR3) and its homologs. The nucleotide and amino acid sequences of the full length huTLR3 are shown in SEQ ID NOs: 1 and 2, respectively. The nucleotide and

amino acid sequences of the huTLR3 extracellular domain (ECD) are shown in SEQ ID NOs: 3 and 4, respectively.

The term "substantially identical" as used herein means that the two antibody or antibody fragment amino acid sequences being compared are identical or have "insubstantial differences". Insubstantial differences are substitutions of 1, 2, 3, 4, 5 or 6 amino acids in an antibody or antibody fragment amino acid sequence. Amino acid sequences substantially identical to the sequences disclosed herein are also part of this application. In some embodiments, the sequence identity can be about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or higher. Percent identity can be determined as described above. Exemplary peptide chains being compared are heavy or light chain variable regions.

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

The term "inflammatory condition" as used herein means a localized response to cellular injury that is mediated in part by the activity of cytokines, chemokines, or inflammatory cells (*e.g.*, neutrophils, monocytes, lymphocytes, macrophages) which is characterized in most instances by pain, redness, swelling, and loss of tissue function. The term "inflammatory pulmonary condition" as used herein means an inflammatory condition affecting or associated with the lungs.

The term "monoclonal antibody" (mAb) as used herein means an antibody (or antibody fragment) obtained from a population of substantially homogeneous antibodies. Monoclonal antibodies are highly specific, typically being directed against a single antigenic determinant. The modifier "monoclonal" indicates the substantially homogeneous character of the antibody and does not require production of the antibody by any particular method. For example, murine mAbs can be made by the hybridoma method of Kohler *et al.*,

Nature 256:495-497, 1975. Chimeric mAbs containing a light chain and heavy chain variable region derived from a donor antibody (typically murine) in association with light and heavy chain constant regions derived from an acceptor antibody (typically another mammalian species such as human) can be prepared by the method disclosed in U.S. Pat. No. 4,816,567. Human-adapted mAbs having CDRs derived from a non-human donor immunoglobulin (typically murine) and the remaining immunoglobulin-derived parts of the molecule being derived from one or more human immunoglobulins can be prepared by techniques known to those skilled in the art such as that disclosed in U.S. Pat. No. 5,225,539. Human framework sequences useful for human-adaptation can be selected from relevant databases by those skilled in the art. Optionally, human-adapted mAbs can be further modified by incorporating altered framework support residues to preserve binding affinity by techniques such as those disclosed in Queen *et al.*, Proc. Natl. Acad. Sci. (USA), 86:10029-10032, 1989 and Hodgson *et al.*, Bio/Technology, 9:421, 1991.

Fully human mAbs lacking any non-human sequences can be prepared from human immunoglobulin transgenic mice by techniques referenced in, *e.g.*, Lonberg *et al.*, Nature 368:856-859, 1994; Fishwild *et al.*, Nature Biotechnology 14:845-851, 1996; and Mendez *et al.*, Nature Genetics 15:146-156, 1997. Human mAbs can also be prepared and optimized from phage display libraries by techniques referenced in, *e.g.*, Knappik *et al.*, J. Mol. Biol. 296:57-86, 2000; and Krebs *et al.*, J. Immunol. Meth. 254:67-84 2001. Fragments of antibodies e.g., Fab, F(ab')2, Fd, and dAb fragments may be produced by cleavage of the antibodies or by recombinant engineering. For example, Fab and F(ab')2 fragments may be generated by treating the antibodies with an enzyme such as pepsin.

The term "epitope" as used herein means a portion of an antigen to which an antibody specifically binds. Epitopes usually consist of chemically active (such as polar, non-

polar or hydrophobic) surface groupings of moieties such as amino acids or polysaccharide side chains and can have specific three-dimensional structural characteristics, as well as specific charge characteristics. An epitope can be linear in nature or can be a discontinous epitope, *e.g.*, a conformational epitope, which is formed by a spatial relationship between non-contiguous amino acids of an antigen rather than a linear series of amino acids. A conformational epitope includes epitopes resulting from folding of an antigen, where amino acids from differing portions of the linear sequence of the antigen come in close proximity in 3-dimensional space.

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

The term "specific binding" as used herein refers to antibody binding to a predetermined antigen with greater affinity than for other antigens or proteins. Typically, the antibody binds with a dissociation constant (K_D) of 10^{-7} M or less, and binds to the predetermined antigen with a K_D that is at least twofold less than its K_D for binding to a non-specific antigen (e.g., BSA, casein, or any other specified polypeptide) other than the predetermined antigen. The phrases "an antibody recognizing an antigen" and "an antibody specific for an antigen" are used interchangeably herein with the term "an antibody which binds specifically to an antigen" or "an antigen specific antibody" e.g. a TLR3 specific antibody. The dissociation constant can be measured using standard procedures as described below.

The term "TLR3 biological activity" or "TLR3 activation" as used herein refers to any activity occurring as a result of ligand binding to TLR3. TLR3 ligands include dsRNA, poly(I:C), and endogenous mRNA, *e.g.*, engodenous mRNA released from necrotic cells. An exemplary TLR3 activation results in activation of NF-κB in response to the TLR3 ligand. NF-κB activation can be assayed using a reporter-gene assay upon induction of the receptor with poly(I:C) (Alexopoulou *et al.*, Nature 413:732-738, 2001; Häcker *et al.*, EMBO J. 18:6973-6982, 1999). Another exemplary TLR3 activation results in activation of interferon response factors (IRF-3, IRF-7) in response to the TLR3 ligand. TLR3-mediated IRF activation can be assayed using a reporter gene driven by an interferon-stimulated response element (ISRE). Another exemplary TLR3 activation results in secretion of pro-inflammatory cytokines and chemokines, for example TNF-α, IL-6, IL-8, IL-12, CXCL5/IP-10 and RANTES. The release of cytokines and chemokines from cells, tissues or in circulation can be measured using well-known immunoassays, such as an ELISA immunoassay.

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

Amino acid	Three-letter code	One-letter code
Alanine	ala	A
Arginine	arg	R
Asparagine	asn	N
Aspartate	asp	D
Cysteine	cys	C
Glutamate	glu	E
Glutamine	gln	Q
Glycine	gly	G
Histidine	his	H
Isoleucine	ile	I
Leucine	leu	L
Lysine	lys	K

Methionine	met	M
Phenylalanine	phe	F
Proline	pro	P
Serine	ser	S
Threonine	thr	T
Tryptophan	trp	W
Tyrosine	tyr	Y
Valine	val	V

Compositions of matter

The present invention provides antibody antagonists capable of inhibiting TLR3 biological activity and uses of such antibodies. Such TLR3 antagonists may have the properties of binding TLR3 and inhibiting TLR3 activation. Exemplary mechanisms by which TLR3 activation may be inhibited by such antibodies include *in vitro*, *in vivo* or *in situ* inhibition of ligand binding to TLR3, inhibition of receptor dimerization, inhibition of TLR3 localization to the endosomal compartment, inhibition of kinase activity of downstream signaling pathways, or inhibition of TLR3 mRNA transcription. Other antibody antagonists capable of inhibiting TLR3 activation by other mechanisms are also within the scope of the various aspects and embodiments of the invention. These antagonists are useful as research reagents, diagnostic reagents and therapeutic agents.

Antibody diversity, in a natural system, is created by the use of multiple germline genes encoding variable regions and a variety of somatic events. The somatic events include recombination of variable gene segments with diversity (D) and joining (J) gene segments to make a complete VH region, and the recombination of variable and joining gene segments to make a complete VL region. The recombination process itself can be imprecise, resulting in the loss or addition of amino acids at the V(D)J junctions. These mechanisms of diversity occur in the developing B cell prior to antigen exposure. After antigenic stimulation, the expressed

antibody genes in B cells undergo somatic mutation. Based on the estimated number of germline gene segments, the random recombination of these segments, and random VH-VL pairing, up to 1.6×10^{7} different antibodies could be produced (Fundamental Immunology, 3rd ed. (1993), ed. Paul, Raven Press, New York, N.Y.). When other processes that contribute to antibody diversity (such as somatic mutation) are taken into account, it is thought that upwards of 10^{10} different antibodies could be generated (Immunoglobulin Genes, 2nd ed. (1995), eds. Jonio et al., Academic Press, San Diego, Calif.). Because of the many processes involved in generating antibody diversity, it is highly unlikely that independently derived monoclonal antibodies with the same antigen specificity will have identical amino acid sequences.

The invention provides novel antigen-binding sites and immunoglobulin chains derived from human immunoglobulin gene libraries. The structure for carrying an antigen-binding site is generally an antibody heavy or light chain or portion thereof, where the antigen-binding site is located to a naturally occurring antigen-binding site as determined as described above.

The invention provides an isolated antibody or fragment thereof reactive with TLR3 comprising both a heavy chain and a light chain variable region and wherein the antibody comprises the heavy chain complementarity determining region (CDR) amino acid sequences 1, 2 and 3 (HCDR1, HCDR2 and HCDR3) and the light chain complementarity determining region (CDR) amino acid sequences 1, 2 and 3 (LCDR1, LCDR2 and LCDR3) as shown in Table 1a.

Table 1a.

mAb no:	SEQ ID NO:					
	HCDR1	HCDR2	HCDR3	LCDR1	LCDR2	LCDR3
16	52	88	54	49	50	51
17	58	64	60	55	56	57
18	70	77	72	67	68	69
19	82	83	84	79	80	89
1	46	47	48	43	44	45
2	52	53	54	49	50	51
3	58	59	60	55	56	57
4	61	62	60	55	56	57
5	61	64	60	55	56	63
6	61	64	60	55	56	65
7	61	64	60	55	56	66
8	70	71	72	67	68	69
9	70	73	72	67	68	69
10	70	75	72	67	68	74
11	70	77	72	67	68	76
12	70	77	72	67	68	78
13	82	83	84	79	80	81
14	82	86	84	79	80	85
15*	82	86	84	79	80	87
15**	111	112	84	109	110	113
15-1	111	114	84	109	110	113
15-2	115	112	84	109	110	113
15-3	116	112	84	109	110	113
15-4	111	117	84	109	110	113
15-5	116	118	84	109	110	113
15-6	116	112	119	109	110	113
15-7	111	112	84	120	110	113
15-8	111	112	84	121	110	113
15-9	116	118	119	109	110	113
15-10	116	112	119	79	80	226
F17	61	192	60	55	56	191
F18	70	194	72	67	68	193
F19	82	196	84	79	80	195

15* CDRs defined by IMGT

15** CDRs defined as consensus

In certain embodiments the invention provides an isolated antibody or fragment reactive with TLR3 comprising both a heavy chain variable region and a light chain variable region and wherein the antibody comprises a HCDR2 amino acid sequence as shown in SEQ ID NO: 192, wherein the HCDR2 of SEQ ID NO: 192 is defined as shown in Formula (I):

Xaa_6-I-Xaa_7-Xaa_8-R-S-Xaa_9-W-Y-N-D-Y-A-V-S-V-K-S,

(I)

wherein

Xaa_6 may be Arg or Lys;

Xaa_7 may be Tyr, His or Ser;

Xaa_8 may be Met, Arg or Tyr; and

Xaa_9 may be Lys or Arg.

In other embodiments, the invention provides an isolated antibody or fragment reactive with TLR3 comprising both a heavy chain variable region and a light chain variable region and wherein the antibody comprises a HCDR2 amino acid sequence as shown in SEQ ID NO: 194, wherein the HCDR2 of SEQ ID NO: 194 is defined as shown in Formula (III):

I-I-Q $-Xaa_{15}$-R-S-K-W-Y-N-Xaa_{16}-Y-A-Xaa_{17}-S-V-K-S,

(III)

wherein

Xaa_{15} may be Lys, Thr or Ile;

Xaa_{16} may be Asn or Asp; and

Xaa_{17} may be Val or Leu.

In other embodiments, the invention provides an isolated antibody or fragment reactive with TLR3 comprising both a heavy chain variable region and a light chain variable region and wherein the antibody comprises a HCDR2 amino acid sequence as shown in SEQ ID NO: 196, wherein the HCDR2 of SEQ ID NO: 196 is defined as shown in Formula (V):

Xaa_{24}-I-D-P-S-D-S-Y-T-N-Y-Xaa_{25}-P-S-F-Q-G,

(V)

wherein

Xaa_{24} may be Phe or Arg; and

Xaa_{25} may be Ala or Ser.

In other embodiments, the invention provides an isolated antibody or fragment reactive with TLR3 comprising both a heavy chain variable region and a light chain variable region and wherein the antibody comprises a LCDR3 amino acid

sequence as shown in SEQ ID NO: 191, wherein the LCDR3 of SEQ ID NO: 191 is defined as shown in Formula (II):

$$Xaa_1\text{-}S\text{-}Y\text{-}D\text{—}Xaa_2\text{-}Xaa_3\text{-}Xaa_4\text{-}Xaa_5\text{-}T\text{-}V, \quad \text{(II)}$$

wherein

Xaa_1 may be Ala, Gln, Gly or Ser;

Xaa_2 may be Gly, Glu or Ser;

Xaa_3 may be Asp or Asn;

Xaa_4 may be Glu or Ser; and

Xaa_5 may be Phe, Ala or Leu.

In other embodiments, the invention provides an isolated antibody or fragment reactive with TLR3 comprising both a heavy chain variable region and a light chain variable region and wherein the antibody comprises a LCDR3 amino acid sequence as shown in SEQ ID NO: 193, wherein the LCDR3 of SEQ ID NO: 193 is defined as shown in Formula (IV):

$$Xaa_{10}\text{-}S\text{-}Y\text{-}D\text{—}Xaa_{11}\text{-}P\text{-}Xaa_{12}\text{-}Xaa_{13}\text{-}Xaa_{14}\text{-}V, \quad \text{(IV)}$$

wherein

Xaa_{10} may be Gln or Ser;

Xaa_{11} may be Thr, Glu or Asp;

Xaa_{12} may be Val or Asn;

Xaa_{13} may be Tyr or Phe; and

Xaa_{14} may be Ser, Asn or Gln.

In other embodiments, the invention provides an isolated antibody or fragment reactive with TLR3 comprising both a heavy chain variable region and a light chain variable region and wherein the antibody comprises a LCDR3 amino acid sequence as shown in SEQ ID NO: 195, wherein the LCDR3 of SEQ ID NO: 195 is defined as shown in Formula (VI):

$$Q\text{-}Q\text{-}Xaa_{18}\text{—}Xaa_{19}\text{-}Xaa_{20}\text{-}Xaa_{21}\text{-}Xaa_{22}\text{-}Xaa_{23}\text{-}T, \quad \text{(VI)}$$

wherein

Xaa_{18} may be Tyr, Gly or Ala;

Xaa_{19} may be Gly, Glu or Asn;

Xaa_{20} may be Ser or Thr;

Xaa_{21} may be Val, Ile or Leu;

Xaa_{22} may be Ser or Leu; and

Xaa_{23} may be Ile, Ser, Pro or Tyr.

The invention also provides an isolated antibody or fragment reactive with TLR3 having the heavy chain complementarity determining region (CDR) amino acid sequences 1,2 and 3 (HCDR1, HCDR2 and HCDR3) and light chain complementarity determining region (CDR) amino acid sequences 1, 2 and 3 (LCDR1, LCDR2 and LCDR3) as shown in Table 1a.

Antibodies whose antigen-binding site amino acid sequences differ insubstantially from those shown in Table 1a (SEQ ID NOs: 49-121 and 191-196) are encompassed within the scope of the invention. Typically, this involves one or more amino acid substitutions with an amino acid having similar charge, hydrophobic, or stereochemical characteristics. Additional substitutions in the framework regions, in contrast to antigen- binding sites may also be made as long as they do not adversely affect the properties of the antibody. Substitutions may be made to improve antibody properties, for example stability or affinity. One, two, three, four, five or six substitutions can be made to the antigen binding site. 1%, 2%, 3%, 4%, 5%, 10%, 15%, 20%, 25%, or 30% of the framework residues can be substituted, as long as the resulting antibody retains desired properties.

Conservative modifications will produce molecules having functional and chemical characteristics similar to those of the molecule from which such modifications are made. Substantial modifications in the functional and/or chemical characteristics of the molecules may be accomplished by selecting substitutions in the amino acid sequence that differ significantly in their effect on maintaining (1) the structure of the molecular backbone in the area of the substitution, for example, as a sheet or helical

conformation, (2) the charge or hydrophobicity of the molecule at the target site, or (3) the size of the molecule. For example, a "conservative amino acid substitution" may involve a substitution of a native amino acid residue with a nonnative residue such that there is little or no effect on the polarity or charge of the amino acid residue at that position. Furthermore, any native residue in the polypeptide may also be substituted with alanine, as has been previously described for alanine scanning mutagenesis (MacLennan *et al.*, Acta Physiol. Scand. Suppl. 643:55-67, 1998; Sasaki *et al.*, Adv. Biophys. 35:1-24, 1998). Desired amino acid substitutions (whether conservative or non-conservative) can be determined by those skilled in the art at the time such substitutions are desired. For example, amino acid substitutions can be used to identify important residues of the molecule sequence, or to increase or decrease the affinity of the molecules described herein. Exemplary amino acid substitutions are shown in Table 1b.

In certain embodiments, conservative amino acid substitutions also encompass non-naturally occurring amino acid residues which are typically incorporated by chemical peptide synthesis rather than by synthesis in biological systems. Amino acid substitutions can be done for example by PCR mutagenesis (US Pat. No. 4,683,195). Libraries of variants can be generated using well known methods, for example using random (NNK) or non-random codons, for example DVK codons, which encode 11 amino acids (ACDEGKNRSYW), and screening the libararies for variants with desired properties, as shown in Example 1. Table 1c shows substitutions made to three parent TLR3 antibody antagonists within the LCDR3 and HCDR2 regions to improve antibody properties.

Depending on delineation of the antigen-binding sites, the antigen-binding site residues of the antibodies of the invention and subsequently the framework residues may vary slightly for each heavy and light chain.

Table 1b.

Original residue	Exemplary substitutions	More Conservative substitutions
Ala (A)	Val, Leu, Ile	Val
Arg (R)	Lys, Gln, Asn	Lys
Asn (N)	Gln	Gln
Asp (D)	Glu	Glu
Cys (C)	Ser, Ala	Ser
Gln (Q)	Asn	Asn
Gly (G)	Pro, Ala	Ala
His (H)	Asn, Gln, Lys, Arg	Arg
Ile (I)	Leu, Val, Met, Ala, Phe, Norleucine	Leu
Leu (L)	Norleucine, Ile, Val, Met, Ala, Phe	Ile
Lys (K)	Arg, 1, 4 Diamino-butyric Acid, Gln, Asn	Arg
Met (M)	Leu, Phe, Ile	Leu
Phe (F)	Leu, Val, Ile, Ala, Tyr	Leu
Pro (P)	Ala	Gly
Ser (S)	Thr, Ala, Cys	Thr
Thr (T)	Ser	Ser
Trp (W)	Tyr, Phe	Tyr
Tyr (Y)	Trp, Phe, Thr, Ser	Phe
Val (V)	Ile, Met, Leu, Phe, Ala, Norleucine	Leu

Table 2a and 2b shows the antigen-binding site residues of exemplary antibodies of the invention delineated according to Kabat, Chothia and IMGT, and their composite sequences.

In other embodiments, the invention provides an isolated antibody or fragment reactive with TLR3 comprising both a heavy chain variable region and a light chain variable region and wherein the antibody comprises the amino acid sequences of the heavy chain variable (VH) and the light chain variable (VL) regions and also provides for each isolated heavy chain variable and light chain variable region as shown in Table 3a. F17, F18 and F19 represent antibody variants comprising consensus amino acid sequences for families 17, 18 and 19, respectively (see Example 1).

Table 1c.

Family 17 mAb	LCDR3										SEQ ID NO:
17	A	S	Y	D	G	D	E	F	T	V	
3											
4											
5	Q				E		S	A			
6	G				S	N	S	L			
7	S				S		S	L			
consensus	A,Q,G,S	S	Y	D	G,E,S	D,N	E,S	F,A,L	T	V	191

Family 17 mAb	HCDR2																		SEQ ID NO:
17	R	I	Y	M	R	S	K	W	Y	N	D	Y	A	V	S	V	K	S	
3			H	R															
4	K		S	Y			R												
5																			
6																			
7																			
consensus	R,K	I	Y,H,S	M,R,Y	R	S	K,R	W	Y	N	D	Y	A	V	S	V	K	S	192

5

Family 18A mAb	LCDR3											SEQ ID NO:
18	Q	S	Y	D	S	Q	F	S	F	G	V	
8												
9												
Family 18B												
mAb												
10	Q	S	Y	D	T	P	V	Y	S	V		
11	S				E		N	F	N			
12	S				D		N	F	Q			
consensus	Q,S	S	Y	D	T,E,D	P	V,N	Y,F	S,N,Q	V		193
	*consensus based on mAbs 10, 11, 12											

Family 18A, 18B mAb	HCDR2																		SEQ ID NO:
18	I	I	Q	K	R	S	K	W	Y	N	N	Y	A	V	S	V	K	S	
8				T							D								
9				I							D			L					
10																			
11																			
12																			
consensus	I	I	Q	K,T,I	R	S	K	W	Y	N	N,D	Y	A	V,L	S	V	K	S	194

Family 19 mAb	LCDR2									SEQ ID NO:
19	Q	Q	Y	G	S	V	S	I	T	
13			G	E	S	I	L	S		
14			A	E	T			P		
15			G	N	T	L		Y		
15-1			G	N	T	L		Y		
15-2			G	N	T	L		Y		
15-3			G	N	T	L		Y		
15-4			G	N	T	L		Y		
15-5			G	N	T	L		Y		
15-6			G	N	T	L		Y		
15-7			G	N	T	L		Y		
15-8			G	N	T	L		Y		
15-9			G	N	T	L		Y		
15-10			G	N	T	L		Y		
consensus	Q	Q	Y,G,A	G,E,N	S,T	V,I,L	S,L	I,S,P,Y	T	195

Family 19 mAb	HCDR2																	SEQ ID NO:
19	F	I	D	P	S	D	S	Y	T	N	Y	A	P	S	F	Q	G	
13																		
14																		
15																		
15.1	R																	
15.2																		
15.3																		
15.4												S						
15.5	R											S						
15.6																		
15.7																		
15-8																		
15-9	R											S						
15-10																		
consensus	F,R	I	D	P	S	D	S	Y	T	N	Y	A,S	P	S	F	Q	G	196

Although the embodiments illustrated in the Examples comprise pairs of variable regions, one from a heavy and one from a light chain, a skilled artisan will recognize that alternative embodiments may comprise single heavy or light chain variable regions. The single variable region can be used to screen for a second variable region capable of forming a two-domain specific antigen-binding fragment capable of, for example, binding to TLR3. The screening may be accomplished by phage display screening methods using for example hierarchical dual combinatorial approach disclosed in PCT Publ. No. WO92/01047. In this approach, an individual colony containing either a H or L chain clone is used to infect a complete library of clones encoding the other chain (L or H), and the resulting two-chain specific antigen-binding domain is selected in accordance with phage display techniques as described.

Table 2a.

mAb	CDR definition	HCDR1		HCDR2		HCDR3	
		SEQ ID	Sequence	SEQ ID	Sequence	SEQ ID	Sequence
14	IMGT	82	GYSFTNYW	86	IDPSDSYTNY	84	ARELYQGYMDTFDS
14	Kabat		NYWVG		FIDPSDSYTNYAPSFQ		ELYQGYMDTFDS
14	Chothia		GYSFT		PSDSYT		LYQGYMDTFD
14	Consensus	111	GYSFTNYWVG	112	FIDPSDSYTNYAPSFQ	84	ARELYQGYMDTFDS
15	IMGT	82	GYSFTNYW	86	IDPSDSYTNY	84	ARELYQGYMDTFDS
15	Kabat		NYWVG		FIDPSDSYTNYAPSFQ		ELYQGYMDTFDS
15	Chothia		GYSFT		PSDSYT		LYQGYMDTFD
15	Consensus	111	GYSFTNYWVG	112	FIDPSDSYTNYAPSFQ	84	ARELYQGYMDTFDS
15-1	IMGT	82	GYSFTNYW	86	IDPSDSYTNY	84	ARELYQGYMDTFDS
15-1	Kabat		NYWVG		RIDPSDSYTNYAPSFQ		ELYQGYMDTFDS
15-1	Chothia		GYSFT		PSDSYT		LYQGYMDTFD
15-1	Consensus	111	GYSFTNYWVG	114	RIDPSDSYTNYAPSFQ	84	ARELYQGYMDTFDS
15-2	IMGT	82	GYSFTNYW	86	IDPSDSYTNY	84	ARELYQGYMDTFDS
15-2	Kabat		NYWIG		FIDPSDSYTNYAPSFQ		ELYQGYMDTFDS
15-2	Chothia		GYSFT		PSDSYT		LYQGYMDTFD
15-2	Consensus	115	GYSFTNYWIG	112	FIDPSDSYTNYAPSFQ	84	ARELYQGYMDTFDS
15-3	IMGT	82	GYSFTNYW	86	IDPSDSYTNY	84	ARELYQGYMDTFDS
15-3	Kabat		NYWIS	86	FIDPSDSYTNYAPSFQ	84	ELYQGYMDTFDS
15-3	Chothia		GYSFT		PSDSYT		LYQGYMDTFD
15-3	Consensus	116	GYSFTNYWIS	112	FIDPSDSYTNYAPSFQ	84	ARELYQGYMDTFDS
15-4	IMGT	82	GYSFTNYW	86	IDPSDSYTNY	84	ARELYQGYMDTFDS
15-4	Kabat		NYWVG		FIDPSDSYTNYSPSFQ		ELYQGYMDTFDS
15-4	Chothia		GYSFT		PSDSYT		LYQGYMDTFD
15-4	Consensus	111	GYSFTNYWVG	117	FIDPSDSYTNYSPSFQ	84	ARELYQGYMDTFDS
15-5	IMGT	82	GYSFTNYW	86	IDPSDSYTNY	84	ARELYQGYMDTFDS
15-5	Kabat		NYWIS		RIDPSDSYTNYSPSFQ		ELYQGYMDTFDS
15-5	Chothia		GYSFT		PSDSYT		LYQGYMDTFD
15-5	Consensus	116	GYSFTNYWIS	118	RIDPSDSYTNYSPSFQ	84	ARELYQGYMDTFDS
15-6	IMGT	82	GYSFTNYW	86	IDPSDSYTNY		ARQLYQGYMDTFDS
15-6	Kabat		NYWIS		FIDPSDSYTNYAPSFQ		QLYQGYMDTFDS
15-6	Chothia		GYSFT		PSDSYT		LYQGYMDTFD
15-6	Consensus	116	GYSFTNYWIS	112	FIDPSDSYTNYAPSFQ	119	ARQLYQGYMDTFDS
15-7	IMGT	82	GYSFTNYW	86	IDPSDSYTNY	84	ARELYQGYMDTFDS
15-7	Kabat		NYWVG		FIDPSDSYTNYAPSFQ		ELYQGYMDTFDS
15-7	Chothia		GYSFT		PSDSYT		LYQGYMDTFD
15-7	Consensus	111	GYSFTNYWVG	112	FIDPSDSYTNYAPSFQ	84	ARELYQGYMDTFDS
15-8	IMGT	82	GYSFTNYW	86	IDPSDSYTNY	84	ARELYQGYMDTFDS
15-8	Kabat		NYWVG		FIDPSDSYTNYAPSFQ		ELYQGYMDTFDS
15-8	Chothia		GYSFT		PSDSYT		LYQGYMDTFD
15-8	Consensus	111	GYSFTNYWVG	112	FIDPSDSYTNYAPSFQ	84	ARELYQGYMDTFDS
15-9	IMGT	82	GYSFTNYW	86	IDPSDSYTNY	119	ARQLYQGYMDTFDS
15-9	Kabat		NYWIS		RIDPSDSYTNYSPSFQG		QLYQGYMDTFDS
15-9	Chothia		GYSFT		PSDSYT		LYQGYMDTFD
15-9	Consensus	116	GYSFTNYWIS	118	RIDPSDSYTNYSPSFQG	119	ARQLYQGYMDTFDS

In other embodiments, the invention provides an isolated antibody or fragment reactive with TLR3 comprising both a heavy chain variable region and a light chain variable region having amino acid sequences at least 95% identical to the variable region amino acid sequences shown in Table 3a.

In another aspect, the invention provides an isolated antibody having certain heavy chain and light chain amino acid sequences as shown in Table 3b.

Another aspect of the invention is isolated polynucleotides encoding any of the antibodies of the invention or their complement. Certain exemplary polynucleotides are disclosed herein, however, other polynucleotides which, given the degeneracy of the genetic code or codon preferences in a given expression system, encode the antibody antagonists of the invention are also within the scope of the invention.

Table 2b.

mAb	CDR definition	LCDR1		LCDR2		LCDR3	
		SEQ ID NO:	Sequence	SEQ ID NO:	Sequence	SEQ ID NO:	Sequence
14	IMGT	79	QSIGLY	80	AAS	85	QQAETVSPT
14	Kabat		RASQSIGLYLA		AASSLQS		QQAETVSPT
14	Chothia		SQSIGLY		AAS		AETVSP
14	Consensus	109	RASQSIGLYLA	110	AASSLQS	85	QQAETVSPT
15	IMGT	79	QSIGLY	80	AAS	87	QQGNTLSYT
15	Kabat		RASQSIGLYLA		AASSLQS		QQGNTLSYT
15	Chothia		SQSIGLY		AAS		GNTLSY
15	Consensus	109	RASQSIGLYLA	110	AASSLQS	113	QQGNTLSYT
15-1	IMGT	79	QSIGLY	80	AAS	87	QQGNTLSYT
15-1	Kabat		RASQSIGLYLA		AASSLQS		QQGNTLSYT
15-1	Chothia		SQSIGLY		AAS		GNTLSY
15-1	Consensus	109	RASQSIGLYLA	110	AASSLQS	113	QQGNTLSYT
15-2	IMGT	79	QSIGLY	80	AAS	87	QQGNTLSYT
15-2	Kabat		RASQSIGLYLA		AASSLQS		QQGNTLSYT
15-2	Chothia		SQSIGLY		AAS		GNTLSY
15-2	Consensus	109	RASQSIGLYLA	110	AASSLQS	113	QQGNTLSYT
15-3	IMGT	79	QSIGLY	80	AAS	87	QQGNTLSYT
15-3	Kabat		RASQSIGLYLA		AASSLQS		QQGNTLSYT
15-3	Chothia		SQSIGLY		AAS		GNTLSY
15-3	Consensus	109	RASQSIGLYLA	110	AASSLQS	113	QQGNTLSYT
15-4	IMGT	79	QSIGLY	80	AAS	87	QQGNTLSYT
15-4	Kabat		RASQSIGLYLA		AASSLQS		QQGNTLSYT
15-4	Chothia		SQSIGLY		AAS		GNTLSY
15-4	Consensus	109	RASQSIGLYLA	110	AASSLQS	113	QQGNTLSYT
15-5	IMGT	79	QSIGLY	80	AAS	87	QQGNTLSYT
15-5	Kabat		RASQSIGLYLA		AASSLQS		QQGNTLSYT
15-5	Chothia		SQSIGLY		AAS		GNTLSY
15-5	Consensus	109	RASQSIGLYLA	110	AASSLQS	113	QQGNTLSYT
15-6	IMGT	79	QSIGLY	80	AAS	87	QQGNTLSYT
15-6	Kabat		RASQSIGLYLA		AASSLQS		QQGNTLSYT
15-6	Chothia		SQSIGLY		AAS		GNTLSY
15-6	Consensus	109	RASQSIGLYLA	110	AASSLQS	113	QQGNTLSYT
15-7	IMGT		QSISSY	80	AAS	87	QQGNTLSYT
15-7	Kabat		RASQSISSYLA		AASSLQS		QQGNTLSYT
15-7	Chothia		SQSISSY		AAS		GNTLSY
15-7	Consensus	120	RASQSISSYLA	110	AASSLQS	113	QQGNTLSYT
15-8	IMGT	79	QSIGLY	80	AAS	87	QQGNTLSYT
15-8	Kabat		RASQSIGLYLN		AASSLQS		QQGNTLSYT
15-8	Chothia		SQSIGLY		AAS		GNTLSY
15-8	Consensus	121	RASQSIGLYLN	110	AASSLQS	113	QQGNTLSYT
15-9	IMGT	79	QSIGLY	80	AAS	87	QQGNTLSYT
15-9	Kabat		RASQSIGLYLA		AASSLQS		QQGNTLSYT
15-9	Chothia		SQSIGLY		AAS		GNTLSY
15-9	Consensus	109	RASQSIGLYLA	110	AASSLQS	113	QQGNTLSYT

Table 3a.

mAb no:	SEQ ID NO:	
	HV	LV
16	6	5
17	8	7
18	10	9
19	12	11
1	14	13
2	16	15
3	18	17
4	20	19
5	22	21
6	24	23
7	26	25
8	28	27
9	30	29
10	32	31
11	34	33
12	36	35
13	38	37
14	40	39
15	42	41

mAb no:	SEQ ID NO:	
	HV	LV
15-1	124	41
15-2	125	41
15-3	126	41
15-4	127	41
15-5	128	41
15-6	129	41
15-7	42	122
15-8	42	123
15-9	159	41
15-10	129	225
F17	198	197
F18	200	199
F19	202	201
c1811	164	163
9QVQ/QSV	212	209
10QVQ/QSV	213	210
12QVQ/QSV	214	211
14EVQ	215	39
15EVQ	216	41

Exemplary antibody antagonists may be antibodies of the IgG, IgD, IgG, IgA or IgM isotypes. Additionally, such antibody antagonists can be post-translationally modified by processes such as glycosylation, isomerization, deglycosylation or non-naturally occurring covalent modification such as the addition of polyethylene glycol (PEG) moieties (pegylation) and lipidation. Such modifications may occur *in vivo* or *in vitro*. For example, the antibodies of the invention can be conjugated to polyethylene glycol (PEGylated) to improve their pharmacokinetic profiles. Conjugation can be carried out by techniques known to those skilled in the art. Conjugation of therapeutic antibodies with PEG has been shown to enhance pharmacodynamics while not interfering with function. (Deckert *et al.*, Int. J. Cancer 87:382-390, 2000; Knight *et al.*, Platelets 15:409-418, 2004; Leong *et al.*, Cytokine

16:106-119, 2001; Yang *et al.*, Protein Eng. 16:761-770, 2003).

Table 3b.

mAb no:	Heavy chain	Light chain
	SEQ ID NO:	SEQ ID NO:
14	102	155
15	102	156
15-1	130	156
15-2	131	156
15-3	132	156
15-4	133	156
15-5	134	156
15-6	135	156
15-7	102	157
15-8	102	158
15-9	160	156
15-10	135	227
F17	204	203
F18	206	205
F19	208	207
14EVQ	220	155
15EVQ	220	156
5429	166	165
c1811	168	167

Pharmacokinetic properties of the antibodies of the invention could also be enhanced through Fc modifications by techniques known to those skilled in the art. For example, IgG4 isotype heavy chains contain a Cys-Pro-Ser-Cys (CPSC) motif in the hinge region capable of forming either inter- or intra-heavy chain disulfide bonds, *i.e.*, the two Cys residues in the CPSC motif may disulfide bond with the corresponding Cys residues in the other heavy chain (inter) or the two Cys residues within a given CPSC motif may disulfide bond with each other (intra). It is believed that *in vivo* isomerase enzymes are capable of converting inter-heavy chain bonds of

IgG4 molecules to intra-heavy chain bonds and *vice versa* (Aalberse and Schuurman, Immunology 105:9-19, 2002). Accordingly, since the heavy:light chain (H:L) pairs in those IgG4 molecules with intra-heavy chain bonds in the hinge region are not covalently associated with each other, they may dissociate into H:L monomers that then reassociate with H:L monomers derived from other IgG4 molecules forming bispecific, heterodimeric IgG4 molecules. In a bispecific IgG antibody the two Fabs of the antibody molecule differ in the epitopes that they bind. Substituting the Ser residue in the hinge region CPSC motif of IgG4 with Pro results in "IgG1-like behavior," *i.e.*, the molecules form stable disulfide bonds between heavy chains and therefore, are not susceptible to H:L exchange with other IgG4 molecules. In one embodiment, the antibodies of the invention will comprise an IgG4 Fc domain with a S to P mutation in the CPSC motif. The location of the CPSC motif is typically found at residue 228 of a mature heavy chain but can change depending on CDR lengths.

Further, sites can be removed that affect binding to Fc receptors other than an FcRn salvage receptor in the antibodies of the invention. For example, the Fc receptor binding regions involved in ADCC activity can be removed in the antibodies of the invention. For example, mutation of Leu234/Leu235 in the hinge region of IgG1 to L234A/L235A or Phe235/Leu236 in the hinge region of IgG4 to P235A/L236A minimizes FcR binding and reduces the ability of the immunoglobulin to mediate complement dependent cytotoxicity and ADCC. In one embodiment, the antibodies of the invention will comprise an IgG4 Fc domain with P235A/L236A mutations. The location of these residues identified above is typical in a mature heavy chain but can change depending on CDR lengths. Exemplary antibodies having P235A/L236A mutations are antibodies having heavy chain amino acid sequences shown in SEQ ID NOs: 218, 219 or 220.

Fully human, human-adapted, humanized and affinity-matured antibody molecules or antibody fragments are within the scope of the invention as are fusion proteins and chimeric proteins. Antibody affinity towards an antigen may be improved by rational design or random affinity maturation using well-known methods such as random or directed mutagenesis, or employing phage display libraries. For example, substitutions can be made to the Vernier Zone residues that mostly reside in the framework region or to the ""Affinity Determining Residues", ADRs, to modulate affinity of an antibody (US Pat. No. 6,639,055; PCT Publ. No. WO10/045340).

Fully human, human-adapted, humanized, affinity-matured antibody molecules or antibody fragments modified to improve stability, selectivity, cross-reactivity, affinity, immunogenicity or other desirable biological or biophysical property are within the scope of the invention. Stability of an antibody is influenced by a number of factors, including (1) core packing of individual domains that affects their intrinsic stability, (2) protein/protein interface interactions that have impact upon the HC and LC pairing, (3) burial of polar and charged residues, (4) H-bonding network for polar and charged residues; and (5) surface charge and polar residue distribution among other intra- and inter-molecular forces (Worn *et al.*, J. Mol. Biol., 305:989-1010, 2001). Potential structure destabilizing residues may be identified based upon the crystal structure of the antibody or by molecular modeling in certain cases, and the effect of the residues on antibody stability can be tested by generating and evaluating variants harboring mutations in the identified residues. One of the ways to increase antibody stability is to raise the thermal transition midpoint (Tm) as measured by differential scanning calorimetry (DSC). In general, the protein Tm is correlated with its stability and inversely correlated with its susceptibility to unfolding and denaturation in solution and the degradation processes that

depend on the tendency of the protein to unfold (Remmele *et al.*, Biopharm., 13:36-46, 2000). A number of studies have found correlation between the ranking of the physical stability of formulations measured as thermal stability by DSC and physical stability measured by other methods (Gupta *et al.*, AAPS PharmSci. 5E8, 2003; Zhang *et al.*, J. Pharm. Sci. 93:3076-3089, 2004; Maa *et al.*, Int. J. Pharm., 140:155-168, 1996; Bedu-Addo *et al.*, Pharm. Res., 21:1353-1361, 2004; Remmele *et al.*, Pharm. Res., 15:200-208, 1997). Formulation studies suggest that a Fab Tm has implication for long-term physical stability of a corresponding mAb. Differences in amino acids in either framework or within the antigen-binding sites could have significant effects on the thermal stability of the Fab domain (Yasui, *et al.*, FEBS Lett. 353:143-146, 1994).

The antibody antagonists of the invention may bind TLR3 with a K_d less than or equal to about 10^{-7}, 10^{-8}, 10^{-9}, 10^{-10}, 10^{-11} or 10^{-12} M. The affinity of a given molecule for TLR3, such as an antibody can be determined experimentally using any suitable method. Such methods may utilize Biacore or KinExA instrumentation, ELISA or competitive binding assays known to those skilled in the art.

Antibody antagonists binding a given TLR3 homolog with a desired affinity can be selected from libraries of variants or fragments by techniques including antibody affinity maturation. Antibody antagonists can be identified based on their inhibition of TLR3 biological activity using any suitable method. Such methods may utilize reporter-gene assays or assays measuring cytokine production using well known methods and as described in the application.

Another embodiment of the invention is a vector comprising at least one polynucleotide of the invention. Such vectors may be plasmid vectors, viral vectors, vectors for baculovirus expression, transposon based vectors or any other vector suitable for introduction of the polynucleotides

of the invention into a given organism or genetic background by any means.

Another embodiment of the invention is a host cell comprising any of the polynucleotides of the invention such as a polynucleotide encoding a polypeptide comprising an immunoglobulin heavy chain variable region having the amino acid sequence shown in SEQ ID NO: 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 124, 125, 126, 127, 128, 129, 159, 198, 200, 202, 164, 212, 213, 214, 215 or 216 or an immunoglobulin light chain variable region having the amino acid sequence shown in SEQ ID NO: 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 122, 123, 197, 199, 201, 163, 209, 210, 211, or 225.

Another embodiment of the invention is a host cell comprising a polynucleotide encoding a polypeptide comprising an immunoglobulin heavy chain having the amino acid sequence shown in SEQ ID NO: 102, 130, 131, 132, 133, 134, 135, 160, 204, 206, 208, 220, 166 or 168, or an immunoglobulin light chain having the amino acid sequence shown in SEQ ID NO: 155, 156, 157, 158, 203, 205, 207, 165, 167, or 227. Such host cells may be eukaryotic cells, bacterial cells, plant cells or archeal cells. Exemplary eukaryotic cells may be of mammalian, insect, avian or other animal origins. Mammalian eukaryotic cells include immortalized cell lines such as hybridomas or myeloma cell lines such as SP2/0 (American Type Culture Collection (ATCC), Manassas, VA, CRL-1581), NS0 (European Collection of Cell Cultures (ECACC), Salisbury, Wiltshire, UK, ECACC No. 85110503), FO (ATCC CRL-1646) and Ag653 (ATCC CRL-1580) murine cell lines. An exemplary human myeloma cell line is U266 (ATTC CRL-TIB-196). Other useful cell lines include those derived from Chinese Hamster Ovary (CHO) cells such as CHO-K1SV (Lonza Biologics, Walkersville, MD), CHO-K1 (ATCC CRL-61) or DG44.

Another embodiment of the invention is a method of making an antibody reactive with TLR3 comprising culturing a host cell of the invention and recovering the antibody

produced by the host cell. Methods of making antibodies and purifying them are well known in the art.

Another embodiment of the invention is a hybridoma cell line that produces an antibody of the invention.

Another embodiment of the invention is an isolated antibody or fragment thereof, wherein the antibody binds toll-like receptor 3 (TLR3) amino acid residues K416, K418, L440, N441, E442, Y465, N466, K467, Y468, R488, R489, A491, K493, N515, N516, N517, H539, N541, S571, L595, and K619 of SEQ ID NO: 2.

Another embodiment is an isolated antibody or fragment thereof, wherein the antibody binds toll-like receptor 3 (TLR3) amino acid residues S115, D116, K117, A120, K139, N140, N141, V144, K145, T166, Q167, V168, S188, E189, D192, A195, and A219 of SEQ ID NO: 2.

Several well known methodologies can be employed to determine the binding epitope of the antibodies of the invention. For example, when the structures of both individual components are known, *in silico* protein-protein docking can be carried out to identify compatible sites of interaction. Hydrogen-deuterium (H/D) exchange can be carried out with the antigen and antibody complex to map regions on the antigen that may be bound by the antibody. Segment and point mutagenesis of the antigen can be used to locate amino acids important for antibody binding. For large proteins such as TLR3, point mutagenesis mapping is simplified when the binding site is first localized to a region on the protein, such as by docking, segment mutagenesis or H/D exchange. When the structures of both individual components are known, *in silico* protein-protein docking can be carried out to identify compatible sites of interaction. Co-crystal structure of antibody-antigen complex can be used to identify residues contributing to the epitope and paratope.

Another embodiment of the invention is an isolated antibody or fragment thereof, wherein the antibody binds TLR3

having an amino acid sequence shown in SEQ ID NO: 2 with the heavy chain variable region Chothia residues W33, F50, D52, D54, Y56, N58, P61, E95, Y97, Y100, and D100b, and with the light chain variable region Chothia residues Q27, Y32, N92, T93, L94, and S95. The heavy chain paratope and the light chain paratope Chothia residues correspond to heavy chain residues W33, F50, D52, D55, Y57, N59, P62, E99, Y101, Y104, and D106 of SEQ ID NO: 216 and light chain residues Q27, Y32, N92, T93, L94, and S95 of SEQ ID NO: 41.

Another embodiment of the invention is an isolated antibody or fragment thereof, wherein the antibody binds TLR3 having an amino acid sequence shown in SEQ ID NO: 2 with the heavy chain variable region Chothia residues N31a, Q52, R52b, S53, K54, Y56, Y97, P98, F99, and Y100, and with the light chain variable region Chothia residues G29, S30, Y31, Y32, E50, D51, Y91, D92, and D93. The heavy chain paratope and the light chain paratope Chothia residues correspond to heavy chain residues N32, Q54, R56, S57, K58, Y60, Y104, P105, F106, and Y107 of SEQ ID NO: 214 and light chain residues G28, S29, Y30, Y31, E49, D50, Y90, D91, and D92 of SEQ ID NO: 211.

Isolated antibodies having certain paratope residues that bind TLR3 can be made by for example grafting the paratope residues into a suitable scaffold, assembling the engineered scaffolds into full antibodies, expressing the resulting antibodies, and testing the antibodies for binding to TLR3 or for an effect on TLR3 biological activity. Exemplary scaffolds are amino acid sequences of human antibody variable regions encoded by human germline genes. The scaffolds can be selected based on for example overall sequence homology, % identity between the paratope residues, or canonical structure class identity between the scaffold and an exemplary antibody, such as mAb 15EVQ or mAb 12QVQ/QSV. Human antibody germline genes are disclosed in, for example, Tomlinson et al., J. Mol. Biol 227:776-798, and at the International ImMunoGeneTics (IMGT) database

(http_://_www_imgt_org). Consensus human framework regions can also be used, e.g., as described in U.S. Pat. No. 6,300,064. Selection of suitable scaffold can be done for example according to methods described in PCT Publ. No. WO10/045340.

Exemplary human germline genes that can be used as scaffolds onto which the paratope residues are grafted are the genes encoded by the Vκ1, Vλ3, Vh5, Vh6, Jκ, Jλ, and the Jh frameworks. The germline J-regions are used in their entirety or in part to select FR4 sequences. For example, the mAb 15EVQ light chain paratope residues can be grafted to a Vκ1 framework encoded by IGKV1-39*01 that is joined directly to the J region sequence encoded by IGKJ1. Sequences from other Vκ1 genes can also be used, and the FR4 sequences of other Jκ genes can be substituted in place of IGKJ1. The mAb 15EVQ heavy chain paratope residues can be grafted to a Vh5 framework encoded by IGHV5-51*01, followed by about 11-13 residues, for example 12 residues, constituting HCDR3 and the FR4 sequence encoded by IGHJ1. The 11-13 residues span between the end of the FR3 region ("CAR") and the start of the FR4 region (WGQ for most JH regions) and include 4 defined paratope residues from mAb 15EVQ Vh. Sequences from other Vh5 genes can also be used, and the FR4 sequences of other Jh genes can be substituted in place of IGJH1. In another example, the mAb 12QVQ/QSV light chain paratope residues can be grafted to a Vλ3 framework encoded by IGLV3-1*01 that is joined directly to the J region sequence encoded by IGJL2. Sequences of other Vλ3 and Jλ genes can also be used. The length of LCDR3 is maintained at about 9-11 residues, for example 10 residues. These about 9-11 residues span between the end of the FR3 region ("YYC" for most V lambda scaffolds) and the start of the FR4 region ("FGG" for most JL regions) and include 3 defined paratope residues from mAb 12QVQ/QSV. The mAb 12QVQ/QSV heavy chain paratope residues can be grafted to a Vh6 framework encoded

by IGHV6-1*01, followed by about 9-11 residues, for example 10 residues, constituting HCDR3, and the FR4 sequence encoded by IGJH1. The about 9-11 residues span between the end of the FR3 region ("CAR") and the start of the FR4 region (WGQ for most JH regions) and include 4 defined paratope residues from mAb 12QVQ/QSV Vh. The FR4 sequences of other Jh genes can be substituted in place of IGHJ1. The binding to TLR3 and biological activity of the resulting antibody can be evaluated using standard methods. Alignments of the mAb 15EVQ and the mAb 12QVQ/QSV light chain variable regions and heavy chain variable regions with the exemplary Vκ1, Vh5, Vλ3, Vh6, Jκ, Jλ or Jh genes are shown in Figures 32 – 35. The paratope-grafted engineered antibodies can further be modified by substitutions of the Vernier Zone residues or the Affinity Determining Residues to improve antibody properties, for example affinity, as described above. As long as the paratope-grafted antibody retains binding to TLR3, the framework amino acid sequence in the paratope-grafted antibody may be 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical to the the mAb 15EVQ or 12QVQ/QSV framework sequences.

Sequences from the antigen-binding sites can be grafted in addition to the paratope residues using standard methods. For example, a complete HCDR3 or LCDR3 may be grafted.

Another aspect of the invention is an isolated antibody or fragment thereof reactive with TLR3 that competes for TLR3 binding with a monoclonal antibody, wherein the monoclonal antibody comprises the amino acid sequences of certain heavy chain complementarity determining regions (CDRs) 1, 2 and 3, the amino acid sequences of certain light chain CDRs 1, 2 and 3, the amino acid sequences of certain heavy chain variable regions (VH) or the amino acid sequence of certain light chain variable regions (VL). Examplary monoclonal antibodies of the invention are an isolated antibody comprising a heavy chain variable region having an amino acid sequence shown in SEQ ID NO: 216 and a light chain variable region amino acid

sequence shown in SEQ ID NO: 41, and an antibody comprising a heavy chain variable region having an amino acid sequence shown in SEQ ID NO: 214 and a light chain variable region amino acid sequence shown in SEQ ID NO: 211.

Competition between binding to TLR3 can be assayed *in vitro* using well known methods. For example, binding of MSD Sulfo-Tag™ NHS-ester –labeled antibody to TLR3 in the presence of an unlableled antibody can be assessed by ELISA. Exemplary antibodies of the invention are mAb 12, mAb 15 and mAb c1811 (see Table 3a). Previously described anti-TLR3 antibodies c1068 and its derivatives (described in PCT Publ. No. WO06/060513A2), TLR3.7 (eBiosciences, cat no 14-9039) and Imgenex IMG-315A (Imgenex IMG-315A; generated against human TLR3 amino acids amino acids 55-70, VLNLTHNQLRRLPAAN) do not compete with binding to TLR3 with mAbs 12, 15 or c1811 as shown in Example 5.

Another aspect of the invention is an isolated antibody reactive with TLR3, wherein the antibody has at least one of the following properties:

a. binds to human TLR3 with a Kd of <10 nM;
b. reduces human TLR3 biological activity in an *in vitro* poly(I:C) NF-kB reporter gene assay >50% at 1 μg/ml;
c. inhibits >60% of IL-6 or CXCL5/IP-10 production from BEAS-2B cells stimulated with <100 ng/ml poly(I:C) at 10 μg/ml;
d. inhibits >50% of IL-6 or CXCL5/IP-10 production from BEAS-2B cells stimulated with <100 ng/ml poly(I:C) at 0.4 μg/ml;
e. inhibits >50% of IL-6 production from NHBE cells stimulated with 62.5 ng/ml poly(I:C) at 5 μg/ml;
f. inhibits >50% of IL-6 production from NHBE cells stimulated with 62.5 ng/ml poly(I:C)at 1 μg/ml;
g. inhibits >20% of poly(I:C)-induced IFN-γ, IL-6 or IL-12 production by PBMC cells at 1 μg/ml.

h. inhibits cynomologus TLR3 biological activity in an *in vitro* NF-kB reporter gene assay with IC50 <10 μg/ml; or

i. inhibits cynomologus TLR3 biological activity in an *in vitro* ISRE reporter gene assay with IC50 <5 μg/ml.

Methods of Treatment

TLR3 antagonists of the invention, for example TLR3 antibody antagonists, can be used to modulate the immune system. While not wishing to be bound by any particular theory, the antagonists of the invention may modulate the immune system by preventing or reducing ligand binding to TLR3, dimerization of TLR3, TLR3 internalization or TLR3 trafficking. The methods of the invention may be used to treat an animal patient belonging to any classification. Examples of such animals include mammals such as humans, rodents, dogs, cats and farm animals. For example, the antibodies of the invention are useful in antagonizing TLR3 activity, in the treatment of inflammation, inflammatory and metabolic diseases and are also useful in the preparation of a medicament for such treatment wherein the medicament is prepared for administration in dosages defined herein.

Generally, inflammatory conditions, infection-associated conditions or immune-mediated inflammatory disorders that may be prevented or treated by administration of the TLR3 antibody antagonists of the invention include those mediated by cytokines or chemokines and those conditions which result wholly or partially from activation of TLR3 or signaling through the TLR3 pathway. Examples of such inflammatory conditions include sepsis-associated conditions, inflammatory bowel diseases, autoimmune disorders, inflammatory disorders and infection-associated conditions. It is also thought that cancers, cardiovascular and metabolic conditions, neurologic and fibrotic conditions can be prevented or treated by administration of the TLR3 antibody antagonists of the invention. Inflammation may affect a tissue or be systemic. Exemplary affected tissues are the respiratory tract, lung,

the gastrointestinal tract, small intestine, large intestine, colon, rectum, the cardiovascular system, cardiac tissue, blood vessels, joint, bone and synovial tissue, cartilage, epithelium, endothelium, hepatic or adipose tissue. Exemplary systemic inflammatory conditions are cytokine storm or hypercytokinemia, systemic inflammatory response syndrome (SIRS), graft versus host disease (GVHD), acute respiratory distress syndrome (ARDS), severe acute respiratory distress syndrome (SARS), catastrophic anti-phospholipid syndrome, severe viral infections, influenza, pneumonia, shock, or sepsis.

Inflammation is a protective response by an organism to fend off an invading agent. Inflammation is a cascading event that involves many cellular and humoral mediators. On one hand, suppression of inflammatory responses can leave a host immunocompromised; hovewer, if left unchecked, inflammation can lead to serious complications including chronic inflammatory diseases (*e.g.* asthma, psoriasis, arthritis, rheumatoid arthritis, multiple sclerosis, inflammatory bowel disease and the like), septic shock and multiple organ failure. Importantly, these diverse disease states share common inflammatory mediators, such as cytokines, chemokines, inflammatory cells and other mediators secreted by these cells.

TLR3 activation by its ligands poly(I:C), dsRNA or endogenous mRNA leads to activation of signaling pathways resulting in synthesis and secretion of pro-inflammatory cytokines, activation and recruitment of inflammatory cells, such as macrophages, granulocytes, neutrophils and eosinophils, cell death, and tissue destruction. TLR3 induces secretion of IL-6, IL-8, IL-12, TNF-α, MIP-1, CXCL5/IP-10 and RANTES, and other pro-inflammatory cytokines and chemokines implicated in immune cell recruitment and activation, thus contributing to tissue destruction in autoimmune and other inflammatory diseases. TLR3 ligand endogenous mRNA is released from necrotic cells during

inflammation, and may result in a positive feedback loop to activate TLR3 and perpetuate inflammation and further tissue damage. TLR3 antagonists, such as TLR3 antibody antagonists, may normalize cytokine secretion, reduce recruitment of inflammatory cells, and reduce tissue damage and cell death. Therefore, TLR3 antagonists have therapeutic potential to treat inflammation and a spectrum of inflammatory conditions.

One example of an inflammatory condition is sepsis-associated condition that may include systemic inflammatory response syndrome (SIRS), septic shock or multiple organ dysfunction syndrome (MODS). dsRNA released by viral, bacterial, fungal, or parasitic infection and by necrotic cells can contribute to the onset of sepsis. While not wishing to be bound by an particular theory, it is believed that treatment with TLR3 antagonists can provide a therapeutic benefit by extending survival times in patients suffering from sepsis-associated inflammatory conditions or prevent a local inflammatory event (*e.g.*, in the lung) from spreading to become a systemic condition, by potentiating innate antimicrobial activity, by demonstrating synergistic activity when combined with antimicrobial agents, by minimizing the local inflammatory state contributing to the pathology, or any combination of the foregoing. Such intervention may be sufficient to permit additional treatment (*e.g.*, treatment of underlying infection or reduction of cytokine levels) necessary to ensure patient survival. Sepsis can be modeled in animals, such as mice, by the adminstration of D-galactosamine and poly(I:C). In such models, D-galactosamine is a hepatotoxin which functions as a sepsis sensitizer and poly(I:C) is a sepsis-inducing molecule that mimics dsRNA and activates TLR3. TLR3 antagonist treatment may increase animal survival rates in a murine model of sepsis, and thus TLR3 antagonists may be useful in the treatment of sepsis.

Gastrointestinal inflammation is inflammation of a mucosal layer of the gastrointestinal tract, and encompasses

acute and chronic inflammatory conditions. Acute inflammation is generally characterized by a short time of onset and infiltration or influx of neutrophils. Chronic inflammation is generally characterized by a relatively longer period of onset and infiltration or influx of mononuclear cells. Mucosal layer may be mucosa of the bowel (including the small intestine and large intestine), rectum, stomach (gastric) lining, or oral cavity. Exemplary chronic gastrointestinal inflammatory conditions are inflammatory bowel disease (IBD), colitis induced by environmental insults (*e.g.*, gastrointestinal inflammation (*e.g.*, colitis) caused by or associated with (*e.g.*, as a side effect) a therapeutic regimen, such as administration of chemotherapy, radiation therapy, and the like), infections colitis, ischemic colitis, collagenous or lymphocytic colitis, necrotizing enterocolitis, colitis in conditions such as chronic granulomatous disease or celiac disease, food allergies, gastritis, infectious gastritis or enterocolitis (*e.g.*, Helicobacter pylori-infected chronic active gastritis) and other forms of gastrointestinal inflammation caused by an infectious agent.

Inflammatory bowel disease (IBD) includes a group of chronic inflammatory disorders of generally unknown etiology, *e.g.*, ulcerative colitis (UC) and Crohn's disease (CD). Clinical and experimental evidence suggest that the pathogenesis of IBD is multifactorial involving susceptibility genes and environmental factors. In inflammatory bowel diesase, the tissue damage results from an inappropriate or exaggerated immune response to antigens of the gut microflora. Several animal models for inflammatory bowel diseases exist. Some of the most widely used models are the 2,4,6-trinitrobenesulfonic acid/ethanol (TNBS)-induced colitis model or the oxazalone model, which induce chronic inflammation and ulceration in the colon (Neurath *et al.*, Intern. Rev. Immunol 19:51-62, 2000). Another model uses dextran sulfate sodium (DSS), which induces an acute

colitis manifested by bloody diarrhea, weight loss, shortening of the colon and mucosal ulceration with neutrophil infiltration. DSS-induced colitis is characterized histologically by infiltration of inflammatory cells into the lamina propria, with lymphoid hyperplasia, focal crypt damage, and epithelial ulceration (Hendrickson *et al.*, Clinical Microbiology Reviews 15:79-94, 2002). Another model involves the adoptive transfer of naïve $CD45RB^{high}$ CD4 T cells to RAG or SCID mice. In this model, donor naïve T cells attack the recipient gut causing chronic bowel inflammation and symptoms similar to human inflammatory bowel diseases (Read and Powrie, Curr. Protoc. Immunol. Chapter 15 unit 15.13, 2001). The administration of antagonists of the present invention in any of these models can be used to evaluate the potential efficacy of those antagonists to ameliorate symptoms and alter the course of diseases associated with inflammation in the gut, such as inflammatory bowel disease. Several treatment options for IBD are available, for example anti-TNF-α antibody therapies have been used for a decade to treat Crohn's disease (Van Assche *et al.*, Eur. J. Pharmacol. Epub Oct 2009). However, a significant percentage of patients are refractory to the current treatments (Hanauer et al., Lancet 359:1541-1549, 2002; Hanauer et al., Gastroenterology 130:323-333, 2006), and thus new therapies targeting refractory patient populations are needed.

Another example of an inflammatory condition is an inflammatory pulmonary condition. Exemplary inflammatory pulmonary conditions include infection-induced pulmonary conditions including those associated with viral, bacterial, fungal, parasite or prion infections; allergen-induced pulmonary conditions; pollutant-induced pulmonary conditions such as asbestosis, silicosis, or berylliosis; gastric aspiration-induced pulmonary conditions, immune dysregulation, inflammatory conditions with genetic predisposition such as as cystic fibrosis, and physical

trauma-induced pulmonary conditions, such as ventilator injury. These inflammatory conditions also include asthma, emphysema, bronchitis, chronic obstructive pulmonary disease (COPD), sarcoidosis, histiocytosis, lymphangiomyomatosis, acute lung injury, acute respiratory distress syndrome, chronic lung disease, bronchopulmonary dysplasia, community-acquired pneumonia, nosocomial pneumonia, ventilator - associated pneumonia, sepsis, viral pneumonia, influenza infection, parainfluenza infection, rotavirus infection, human metapneumovirus infection, respiratory syncitial virus infection and aspergillus or other fungal infections. Exemplary infection-associated inflammatory diseases may include viral or bacterial pneumonia, including severe pneumonia, cystic fibrosis, bronchitis, airway exacerbations and acute respiratory distress syndrome (ARDS). Such infection-associated conditions may involve multiple infections such as a primary viral infection and a secondary bacterial infection.

Asthma is an inflammatory disease of the lung that is characterized by airway hyperresponsiveness ("AHR"), bronchoconstriction, wheezing, eosinophilic or neutrophilic inflammation, mucus hypersecretion, subepithelial fibrosis, and elevated IgE levels. Patients with asthma experience "exacerbations", a worsening of symptoms, most commonly due to microbial infections of the respiratory tract (*e.g.* rhinovirus, influenza virus, Haemophilus influenza, etc.). Asthmatic attacks can be triggered by environmental factors (*e.g.* ascarids, insects, animals (*e.g.*, cats, dogs, rabbits, mice, rats, hamsters, guinea pigs and birds), fungi, air pollutants (*e.g.*, tobacco smoke), irritant gases, fumes, vapors, aerosols, chemicals, pollen, exercise, or cold air. Apart from asthma, several chronic inflammatory diseases affecting the lung are characterized by neutrophil infiltration to the airways, for example chronic obstructive pulmonary disease (COPD), bacterial pneumonia and cystic fibrosis (Linden *et al.*, Eur. Respir. J. 15:973-977, 2000;

Rahman *et al.*, Clin. Immunol. 115:268-276, 2005), and diseases such as COPD, allergic rhinitis, and cystic fibrosis are characterized by airway hyperresponsiveness (Fahy and O'Byrne, Am. J. Respir. Crit. Care Med. 163:822-823, 2001). Commonly used animal models for asthma and airway inflammation include the ovalbumin challenge model and methacholine sensitization models (Hessel *et al.*, Eur. J. Pharmacol. 293:401-412, 1995). Inhibition of cytokine and chemokine production from cultured human bronchial epithelial cells, bronchial fibroblasts or airway smooth muscle cells can also be used as *in vitro* models. The administration of antagonists of the present invention to any of these models can be used to evaluate the use of those antagonists to ameliorate symptoms and alter the course of asthma, airway inflammation, COPD and the like.

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

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

Arthritis, including osteoarthritis, rheumatoid arthritis, arthritic joints as a result of injury, and the like, are common inflammatory conditions which would benefit from the therapeutic use of anti-inflammatory proteins, such as the antagonists of the present invention. For example, rheumatoid arthritis (RA) is a systemic disease that affects the entire body and is one of the most common forms of arthritis. Since rheumatoid arthritis results in tissue damage, TLR3 ligands could be present at the site of the inflammation. Activation of TLR3 signaling may perpetuate inflammation and further tissue damage in the inflamed joint. Several animal models for rheumatoid arthritis are known in the art. For example, in the collagen-induced arthritis (CIA) model, mice develop chronic inflammatory arthritis that closely resembles human rheumatoid arthritis. Administration of the TLR3 antagonists of the present invention to the CIA model mice can be used to evaluate the use of these antagonists to ameliorate symptoms and alter the course of diseases.

Diabetes mellitus, diabetes, refers to a disease process derived from multiple causative factors and characterized by hyperglycemia (LeRoith *et al.*, (eds.), Diabetes Mellitus, Lippincott-Raven Publishers, Philadelphia, Pa. U.S.A. 1996), and all references cited therein. Uncontrolled hyperglycemia is associated with increased and premature mortality due to an increased risk for microvascular and macrovascular diseases, including nephropathy, neuropathy, retinopathy, hypertension, cerebrovascular disease and coronary heart disease. Therefore, control of glucose homeostasis is a critically important approach for the treatment of diabetes.

Underlying defects lead to a classification of diabetes into two major groups: type I diabetes (insulin dependent diabetes mellitus, IDDM), which arises when patients lack insulin-producing beta-cells in their pancreatic glands, and

type 2 diabetes (non-insulin dependent diabetes mellitus, NIDDM), which occurs in patients with an impaired beta-cell insulin secretion and/or resistance to insulin action.

Type 2 diabetes is characterized by insulin resistance accompanied by relative, rather than absolute, insulin deficiency. In insulin resistant individuals, the body secretes abnormally high amounts of insulin to compensate for this defect. When inadequate amounts of insulin are present to compensate for insulin resistance and adequately control glucose, a state of impaired glucose tolerance develops. In a significant number of individuals, insulin secretion declines further and the plasma glucose level rises, resulting in the clinical state of diabetes. Adipocity-associated inflammation has been stronly implicated in the development of insulin resistance, type 2 diabetes, dyslipidemia and cardiovascular disease. Obese adipose recruits and retains macrophages and can produce excessive pro-inflammatory cytokines including TNF-α and IL-6, free fatty acids and adipokines, which can interfere with insulin signaling and induce insulin resistance. TLR3 activation on macrophages may contribute to the pro-inflammatory status of the adipose. Several animal modes of insulin resistance are known. For example, in a diet-induced obesity model (DIO) animals develop hyperglycemia and insulin resistance accompanied by weight gain. Administration of TLR3 antagonists of the present invention to the DIO model can be used to evaluate the use of the antagonists to ameliorate complications associated with type 2 diabetes and alter the course of the disease.

Exemplary cancers may include at least one malignant disease in a cell, tissue, organ, animal or patient, including, but not limited to leukemia, acute leukemia, acute lymphoblastic leukemia (ALL), B-cell or T-cell ALL, acute myeloid leukemia (AML), chronic myelocytic leukemia (CML), chronic lymphocytic leukemia (CLL), hairy cell leukemia, myelodyplastic syndrome (MDS), a lymphoma, Hodgkin's disease,

a malignant lymphoma, non-Hodgkin's lymphoma, Burkitt's lymphoma, multiple myeloma, Kaposi's sarcoma, colorectal carcinoma, pancreatic carcinoma, renal cell carcinoma, breast cancer, nasopharyngeal carcinoma, malignant histiocytosis, paraneoplastic syndrome/hypercalcemia of malignancy, solid tumors, adenocarcinomas, squamous cell carcinomas, sarcomas, malignant melanoma, particularly metastatic melanoma, hemangioma, metastatic disease, cancer related bone resorption and cancer related bone pain.

Exemplary cardiovascular diseases may include cardiovascular disease in a cell, tissue, organ, animal, or patient, including, but not limited to, cardiac stun syndrome, myocardial infarction, congestive heart failure, stroke, ischemic stroke, hemorrhage, arteriosclerosis, atherosclerosis, restenosis, diabetic atherosclerotic disease, hypertension, arterial hypertension, renovascular hypertension, syncope, shock, syphilis of the cardiovascular system, heart failure, cor pulmonale, primary pulmonary hypertension, cardiac arrhythmias, atrial ectopic beats, atrial flutter, atrial fibrillation (sustained or paroxysmal), post perfusion syndrome, cardiopulmonary bypass inflammation response, chaotic or multifocal atrial tachycardia, regular narrow QRS tachycardia, specific arrhythmias, ventricular fibrillation, His bundle arrhythmias, atrioventricular block, bundle branch block, myocardial ischemic disorders, coronary artery disease, angina pectoris, myocardial infarction, cardiomyopathy, dilated congestive cardiomyopathy, restrictive cardiomyopathy, valvular heart diseases, endocarditis, pericardial disease, cardiac tumors, aordic and peripheral aneurysms, aortic dissection, inflammation of the aorta, occulsion of the abdominal aorta and its branches, peripheral vascular disorders, occulsive arterial disorders, peripheral atherosclerotic disease, thromboangitis obliterans, functional peripheral arterial disorders, Raynaud's phenomenon and disease, acrocyanosis, erythromelalgia, venous

diseases, venous thrombosis, varicose veins, arteriovenous fistula, lymphederma, lipedema, unstable angina, reperfusion injury, post pump syndrome and ischemia-reperfusion injury.

Exemplary neurological diseases may include neurologic disease in a cell, tissue, organ, animal or patient, including, but not limited to neurodegenerative diseases, multiple sclerosis, migraine headache, AIDS dementia complex, demyelinating diseases, such as multiple sclerosis and acute transverse myelitis; extrapyramidal and cerebellar disorders such as lesions of the corticospinal system; disorders of the basal ganglia or cerebellar disorders; hyperkinetic movement disorders such as Huntington's Chorea and senile chorea; drug-induced movement disorders, such as those induced by drugs which block CNS dopamine receptors; hypokinetic movement disorders, such as Parkinson's disease; Progressive supranucleo Palsy; structural lesions of the cerebellum; spinocerebellar degenerations, such as spinal ataxia, Friedreich's ataxia, cerebellar cortical degenerations, multiple systems degenerations (Mencel, Dejerine-Thomas, Shi-Drager, and Machado-Joseph); systemic disorders (Refsum's disease, abetalipoprotemia, ataxia, telangiectasia, and mitochondrial multisystem disorder); demyelinating core disorders, such as multiple sclerosis, acute transverse myelitis; and disorders of the motor unit such as neurogenic muscular atrophies (anterior horn cell degeneration, such as amyotrophic lateral sclerosis, infantile spinal muscular atrophy and juvenile spinal muscular atrophy); Alzheimer's disease; Down's Syndrome in middle age; Diffuse Lewy body disease; Senile Dementia of Lewy body type; Wernicke-Korsakoff syndrome; chronic alcoholism; Creutzfeldt-Jakob disease; Subacute sclerosing panencephalitis, Hallerrorden-Spatz disease and Dementia pugilistica.

Exemplary fibrotic conditions may include liver fibrosis (including but not limited to alcohol-induced cirrhosis, viral-induced cirrhosis, autoimmune-induced hepatitis); lung fibrosis (including but not limited to scleroderma,

idiopathic pulmonary fibrosis); kidney fibrosis (including but not limited to scleroderma, diabetic nephritis, glomerular nehpritis, lupus nephritis); dermal fibrosis (including but not limited to scleroderma, hypertrophic and keloid scarring, burns); myelofibrosis; neurofibromatosis; fibroma; intestinal fibrosis; and fibrotic adhesions resulting from surgical procedures. In such a method, the fibrosis can be organ specific fibrosis or systemic fibrosis. The organ specific fibrosis can be associated with at least one of lung fibrosis, liver fibrosis, kidney fibrosis, heart fibrosis, vascular fibrosis, skin fibrosis, eye fibrosis, bone marrow fibrosis or other fibrosis. The lung fibrosis can be associated with at least one of idiopathic pulmonary fibrosis, drug induced pulmonary fibrosis, asthma, sarcoidosis or chronic obstructive pulmonary disease. The liver fibrosis can be associated with at least one of cirrhosis, schistomasomiasis or cholangitis. The cirrhosis can be selected from alcoholic cirrhosis, post-hepatitis C cirrhosis, primary biliary cirrhosis. The cholangitis is sclerosing cholangitis. The kidney fibrosis can be associated with diabetic nephropathy or lupus glomeruloschelerosis. The heart fibrosis can be associated with myocardial infarction. The vascular fibrosis can be associated with postangioplasty arterial restenosis or atherosclerosis. The skin fibrosis can be associated with burn scarring, hypertrophic scarring, keloid, or nephrogenic fibrosing dermatopathy. The eye fibrosis can be associated with retro-orbital fibrosis, postcataract surgery or proliferative vitreoretinopathy. The bone marrow fibrosis can be associated with idiopathic myelofibrosis or drug induced myelofibrosis. The other fibrosis can be selected from Peyronie's disease, Dupuytren's contracture or dermatomyositis. The systemic fibrosis can be systemic sclerosis or graft versus host disease.

Administration/Pharmaceutical Compositions

The "therapeutically effective amount" of the agent effective in the treatment or prevention of conditions where suppression of TLR3 activity is desirable can be determined by standard research techniques. For example, the dosage of the agent that will be effective in the treatment or prevention of inflammatory condition such as asthma, Crohn's Disease, ulcerative colitis or rheumatoid arthritis can be determined by administering the agent to relevant animal models, such as the models described herein.

In addition, *in vitro* assays can optionally be employed to help identify optimal dosage ranges. Selection of a particular effective dose can be determined (*e.g.*, via clinical trials) by those skilled in the art based upon the consideration of several factors. Such factors include the disease to be treated or prevented, the symptoms involved, the patient's body mass, the patient's immune status and other factors known by the skilled artisan. The precise dose to be employed in the formulation will also depend on the route of administration, and the severity of disease, and should be decided according to the judgment of the practitioner and each patient's circumstances. Effective doses can be extrapolated from dose-response curves derived from *in vitro* or animal model test systems.

In the methods of the invention, the TLR3 antagonist may be administered singly or in combination with at least one other molecule. Such additional molecules may be other TLR3 antagonist molecules or molecules with a therapeutic benefit not mediated by TLR3 receptor signaling. Antibiotics, antivirals, palliatives and other compounds that reduce cytokine levels or activity are examples of such additional molecules.

The mode of administration for therapeutic use of the agent of the invention may be any suitable route that delivers the agent to the host. Pharmaceutical compositions of these agents are particularly useful for parenteral

administration, e.g., intradermal, intramuscular, intraperitoneal, intravenous, subcutaneous or intranasal.

The agent of the invention may be prepared as pharmaceutical compositions containing an effective amount of the agent as an active ingredient in a pharmaceutically acceptable carrier. The term "carrier" refers to a diluent, adjuvant, excipient, or vehicle with which the active compound is administered. Such pharmaceutical vehicles can be liquids, such as water and oils, including those of petroleum, animal, vegetable or synthetic origin, such as peanut oil, soybean oil, mineral oil, sesame oil and the like. For example, 0.4% saline and 0.3% glycine can be used. These solutions are sterile and generally free of particulate matter. They may be sterilized by conventional, well-known sterilization techniques (*e.g.*, filtration). The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, stabilizing, thickening, lubricating and coloring agents, etc. The concentration of the agent of the invention in such pharmaceutical formulation can vary widely, *i.e.*, from less than about 0.5%, usually at or at least about 1% to as much as 15 or 20% by weight and will be selected primarily based on required dose, fluid volumes, viscosities, etc., according to the particular mode of administration selected.

Thus, a pharmaceutical composition of the invention for intramuscular injection could be prepared to contain 1 ml sterile buffered water, and between about 1 ng to about 100 mg, *e.g.* about 50 ng to about 30 mg or more preferably, about 5 mg to about 25 mg, of a TLR3 antibody antagonist of the invention. Similarly, a pharmaceutical composition of the invention for intravenous infusion could be made up to contain about 250 ml of sterile Ringer's solution, and about 1 mg to about 30 mg and preferably 5 mg to about 25 mg of an antagonist of the invention. Actual methods for preparing parenterally administrable compositions are well known and

are described in more detail in, for example, "Remington's Pharmaceutical Science", 15th ed., Mack Publishing Company, Easton, PA.

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

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

Example 1

Identification and Derivation of Anti-huTLR3 Antagonist mAbs

The MorphoSys Human Combinatorial Antibody Library (HuCAL®) Gold phage display library (Morphosys AG, Martinsried, Germany) was used as a source of human antibody fragments and was panned against a purified TLR3 antigen generated from the expression of amino acids 1-703 of human TLR3 (huTLR3) (SEQ ID NO: 4) with a C-terminal poly-histidine tag and purified by immobilized metal affinity chromatography. Amino acids 1-703 correspond to the predicted extracellular domain (ECD) of huTLR3. Fab fragments (Fabs) that bound specifically to huTRL3 ECD were selected by presenting the TLR3 protein in a variety of ways so that a diverse set of antibody fragments could be identified, sequenced and confirmed as unique. From different panning strategies, 62 candidates (different V-region sequences) were identified as unique hTLR3 ECD binders.

The 62 candidates identified as huTLR3 ECD binders were screened for neutralizing activity in a range of cell-based assays relevant to identifying anti-inflammatory activity. Using preliminary activity data (see Example 2 below), four candidates (Fabs 16-19) defining families 16-19 were selected from the 62 as parents for CDR maturation of heavy chain CDR2

(HCDR2) and light chain CDR3 (LCDR3). One of the parental candidates (candidate 19) exhibited an N-linked glycosylation site in HCDR2; a Ser to Ala (S to A) mutation was made in this candidate to delete the site. Following CDR maturation of the four parental candidates, a total of 15 progeny candidates (candidates 1-15) were identified for further characterization as described in Example 2 below. A listing of the light and heavy chain variable regions present in each of the 19 candidates is shown in Table 3 above. The candidates are herein referred to as mAbs 1-19 or Fabs 1-19, depending whether they were Fabs or cloned as full length antibody chains (Example 3). Due to expression vector design, the mature amino termini of the variable regions for all candidates were QVE for heavy chain and DI for the light chain. The preferred sequences at these termini are those in the respective germline genes with high identity to the candidate sequences. For families 17 and 18 the germline sequences are QVQ for VH and SY for VL. For family 19, the sequences are EVQ for VH and DI for VL. The SY sequence is unique to the lambda subgroup 3 and there are reports of heterogeneity with either S or Y as the amino terminal residue. Thus, the QSV consensus terminus from the prominent lambda subgroup 1 was considered a more suitable replacement for DIE for VL of families 17 and 18. These changes were introduced into candidates 9, 10 and 12 from family 18 and candidates 14 and 15 from family 19. In this process, both the VH and VL regions of these antibodies were codon optimized. The amino acid sequences of the light chain variable region N-terminal germline variants of candidates 9, 10 and 11 are shown in SEQ ID NO:s 209-211, and the amino acid sequences of the heavy chain variable region N-terminal germline variants for candidates 9, 10, 12, 14, and 15 are shown in SEQ ID NO:s 212-216, respectively. The N-terminal variants of the candidates are herein referred to as candidate/mAb/Fab 9QVQ/QSV, 10QVQ/QSV, 12QVQ/QSV, 14EVQ or 15EVQ. The N-terminal germline variants were expressed as

mAbs and showed no effect on binding to TLR3 or in their ability to inhibit TLR3 biological activity when compared to their parent counterparts (data not shown).

Example 2

Determination of TLR3 Antagonist Activity *in vitro*

The 15 CDR-matured candidates described above were selected as potential human therapeutics and a range of binding and neutralizing activities were determined. The activity assays and results for the four parental Fabs, Fabs 16-19 and 15 CDR-matured Fabs, Fabs 1-15 or their non-germline V-region variants are described below.

Inhibition of NF-κB and ISRE Signaling Cascasde

293T cells were grown in DMEM and GlutaMax media (Invitrogen, Carlsbad, CA) supplemented with heat-inactivated FBS and transfected with 30 ng pNF-κB or ISRE firefly luciferase reporter plasmids, 13.5 ng pcDNA3.1 vector, 5 ng phRL-TK, and 1.5 ng pCDNA encoding FL TLR3 (SEQ ID NO: 2). The phRL-TK plasmid contains the *Renilla* luciferase gene driven by the HSV-1 thymidine kinase promoter (Promega, Madion, WI). TLR3 antibodies were incubated 30-60 min. before addition of poly(I:C) (GE Healthcare, Piscataway, NJ). The plates were incubated 6h or 24h at 37°C before the addition of the Dual-Glo luciferase reagent, and the plates were read on a FLUOstar plate reader. Normalized values (luciferase ratios) were obtained by dividing the firefly RLUs by the *Renilla* RLUs. Upon stimulation with the TLR3 agonist poly (I:C) (1 μg/ml), the NF-κB or ISRE signaling cascade stimulated firefly luciferase production was specifically inhibited by incubation of the cells with anti-TLR3 antibodies (0.4, 2.0 and 10 μg/ml) prior to stimulation. The results for the NF-κB assays are shown in Fig. 1 and are expressed as % inhibition of the Firefly/Renilla ratio with 5465 as the positive control (neutralizing anti-human TLR3 Mab) and an anti-human tissue factor mAb (859) as the human

IgG4 isotype control. >50% inhibition was achieved with mAb concentrations 0.4-10 μg/ml. c1068 and TLR3.7 inhibited about 38% and 8% of TLR3 biological activity at 10 μg/ml. Similar results were obtained with the ISRE reporter gene assay (data not shown).

Cytokine Release in BEAS-2B cells

BEAS-2B cells (SV-40 transformed normal human bronchial epithelial cell line) were seeded in a collagen type I coated dishes and incubated with or without anti-human TLR3 antibodies prior to addition of poly (I:C). Twenty-four hours after treatments, supernatants were collected and assayed for cytokine and chemokine levels using a custom multi-plex bead assay for detection of IL-6, IL-8, CCL-2/MCP-1, CCL5/RANTES, and CXCL10/IP-10. Results are shown in Fig. 2 as % inhibition of the individual cytokine/chemokine following mAb treatment at 0.4, 2.0 and 10 μg/ml. 5465 is a positive control; 859 is an isotype control.

Cytokine Release in NHBE cells

Cytokine release was also assayed in normal human bronchial epithelial (NHBE) cells (Lonza, Walkersville, MD). NHBE cells were expanded and transferred to collagen-coated dishes and incubated for 48 hours after which the media was removed and replenished with 0.2 ml of fresh media. The cells were then incubated with or without anti-human TLR3 mAbs 60 minutes prior to the addition of poly (I:C). Supernatants were collected after 24 hours and stored at -20°C or assayed immediately for IL-6 levels. Results are graphed in Fig. 3 as % inhibition of IL-6 secretion following mAb treatment using doses between 0.001 and 50 μg/ml. 5465 is a positive control, 859 is an isotype control. Most mAbs inhibited at least 50% of IL-6 production at <1 μg/ml, and achieved 75% inhibition at <5 μg/ml.

Cytokine Release in PBMC cells

Cytokine release was also assayed in human peripheral blood mononuclear cells (PBMC). Whole blood was collected from human donors into heparin collection tubes to which a Ficoll-Paque Plus solution was slowly layered underneath. The tubes were centrifuged and the PBMCs, that formed a white layer just above the Ficoll, were recovered and plated. The PBMCs were then incubated with or without anti-human TLR3 mAbs prior to the addition of 25 μg/ml poly(I:C). After 24 hrs, supernatants were collected and cytokine levels were determined using Luminex technology. Results are graphed in Fig. 4 as cumulative percentage inhibition of IFN-γ, IL-12 and IL-6 using a single dose of mAb (0.4 μg/ml) with 5465 is a positive control; hIgG4 is an isotype control.

Cytokine Release in HASM cells

Briefly, human airway smooth muscle (HASM) cells were incubated with or without anti-human TLR3 mAbs prior to the addition of a synergistic combination of 500 ng/ml poly(I:C) and 10 ng/ml TNF-α. After 24 hrs, supernatants were collected and cytokine levels were determined using Luminex technology. Results are graphed in Fig. 5 as levels of the chemokine CCL5/RANTES using three doses of mAb (0.4, 2 and 10 μg/ml). 5465 is a positive control; hIgG4 is an isotype control.

The results from the *in vitro* assays in human cells confirm the ability of the antibodies of the invention to reduce cytokine and chemokines release as a result of binding to huTLR3.

Example 3

Full-length Antibody Constructs

The four parental Fabs (candidate nos. 16-19) and 15 progeny Fabs (candidate nos. 1-15) heavy chains were cloned onto a human IgG4 background with a S229P Fc mutation. Candidates 9QVQ/QSV, 10QVQ/QSV, 12QVQ/QSV, 14EVQ or 15EVQ

were cloned onto a human IgG4 background with F235A/L236A and S229P Fc mutations.

The mature full-length heavy chain amino acid sequences are shown in SEQ ID NOs: 90-102 and 218-220 as follows:

Candidate	SEQ ID NO:
16	90
17	91
18	92
19	93
1	94
2	95
3	96
4	97
5, 6, 7	98
8	99
9	100
10, 11, 12	101
13, 14, 15	102
9EVQ	218
10EVQ, 12EVQ	219
14EVQ, 15EVQ	220

For expression, these heavy chain sequences can include an N-terminal leader sequence such as MAWVWTLLFLMAAAQSIQA (SEQ ID NO: 103). Exemplary nucleotide sequences encoding the heavy chain of candidates 14EVQ and 15EVQ with a leader sequence and the mature form (without a leader sequence) are shown in SEQ ID NOs: 104 and 105, respectively. Likewise, for expression, the light chain sequences of the antibodies of the invention can include an N-terminal leader sequence such as MGVPTQVLGLLLLWLTDARC (SEQ ID NO: 106). Exemplary nucleotide sequences encoding the light chain of codon optimized candidate 15 with a leader sequence and the mature

form (without a leader sequence) are shown in SEQ ID NOs: 107 and 108, respectively.

Example 4

Characterization of Anti-TLR3 mAb binding

EC50 values for the binding of the mAbs to human TLR3 extracellular domain (ECD) were determined by ELISA. Human TLR3 ECD protein was diluted to 2 μg/ml in PBS and 100 μl aliquots were dispensed to each well of a 96-well plate (Corning Inc., Acton, MA). After overnight incubation at 4°C, the plate was washed 3 times in wash buffer consisting of 0.05% Tween-20 (Sigma-Aldrich) in PBS. The wells were blocked with 200 μl blocking solution consisting of 2% I-Block (Applied Biosystems, Foster City, CA) and 0.05% Tween-20 in PBS. After blocking for 2 hours at room temperature the plate was washed 3 times followed by addition of serial

Table 4.

Candidate no.	EC50 (ng/ml)
1	17.18
2	53.12
3	23.42
4	12.77
5	19.94
6	19
7	16.13
8	18.58
9	22.61
10	15.84
11	26.33
12	25.59
13	23.51
14	33.59
15	32.64
16	43.66
17	13.8
18	9.68
19	66.54

dilutions of the anti-TLR3 mAb candidates 1 to 19 in blocking buffer. The anti-TLR3 mAbs were incubated for 2 hours at room temperature and washed 3 times. This was followed by addition of a peroxidase-conjugated sheep anti-human IgG (GE Healthcare, Piscataway, NJ) diluted 1:4000 in blocking buffer, incubated for 1 hour at room temperature followed by 3 washes in wash buffer. Binding was detected by 10-15 minute incubation in TMB-S (Fitzgerald Industries International, Inc., Concord, MA). The reaction was stopped with 25 µl 2N H_2SO_4 and absorbance read at 450 nm with subtraction at 650 nm using a SPECTRA Max spectrophotometer (Molecular Devices Corp., Sunnyvale, CA). EC50 values were determined by non-linear regression using GraphPad Prism software (GraphPad Software, Inc., San Diego, CA).

EC50 values were determined for binding to huTLR3 (Table 4) by incubating with 100 µl of 4-fold serial dilutions of mAbs from 2.5 µg/ml to 0.6 pg/ml. An anti-human tissue factor mAb 859 and hu IgG4κ were included as negative controls.

Binding affinity for huTLR3 ECD was also determined by Biacore analysis. The data (not shown) indicated that the mAbs 1-19 had a Kd for huTLR3 ECD of less than 10^{-8} M.

Example 5

Competitive Epitope Binding

Epitope binding experiments were performed to determine the anti-TLR3 antibody competition groups or "epitope bins".

For competitive ELISA, 5 µl (20 µg/ml) of purified human TLR3 ECD protein generated as described in Example 1 was coated on MSD HighBind plate (Meso Scale Discovery, Gaithersburg, MD) per well for 2 hr at room temperature. 150 µl of 5% MSD Blocker A buffer (Meso Scale Discovery) was added to each well and incubated for 2 hr at room temperature. Plates were washed three times with 0.1 M HEPES buffer, pH 7.4, followed by the addition of the mixture of

labeled anti-TLR3 mAb with different competitors. Labeled antibodies (10 nM) were incubated with increasing concentrations (1 nM to 2 μM) of unlabeled anti-TLR3 antibodies, and then added to the designated wells in a volume of 25 μl mixture. After 2-hour incubation with gentle shaking at room temperature, plates were washed 3 times with 0.1 M HEPES buffer (pH 7.4). MSD Read Buffer T was diluted with distilled water (4-fold) and dispensed at a volume of 150 μl/well and analyzed with a SECTOR Imager 6000. Antibodies were labeled with MSD Sulfo-Tag™ NHS-ester according to manufacturer's instructions (Meso Scale Discovery).

The following anti-TLR3 antibodies were evaluated: mAbs 1-19 obtained from a MorphoSys Human Combinatorial Antibody Library (shown in Table 3a); c1068 (described in WO06/060513A2), c1811 (rat anti-mouse TLR3 mAb produced by a hybridoma generated from rats immunized with mouse TLR3 protein), TLR3.7 (eBiosciences, San Diego, CA, cat no 14-9039) and IMG-315A (generated against human TLR3 amino acids amino acids 55-70 (VLNLTHNQLRRLPAAN) from Imgenex, San Diego, CA). For mAbs 9, 10, 12, 14 and 15, variants 9QVQ/QSV, 10QVQ/QSV, 12QVQ/QSV, 14EVQ or 15EVQ were used in this study.

Based on competiton assays, anti-TLR3 antibodies were assigned to five distinct bins. Bin A: mAbs 1, 2, 13, 14EVQ, 15EVQ, 16, 19; Bin B: mAbs 3, 4, 5, 6, 7, 8, 9QVQ/QSV, 10QVQ/QSV, 11, 12QVQ/QSV, 17, 18; Bin C: antibody Imgenex IMG-315A; Bin D: antibodies TLR3.7, c1068; and Bin E: antibody c1811.

Example 6

Epitope Mapping

Representative antibodies from distinct epitope bins as described in Example 5 were selected for further epitope mapping. Epitope mapping was performed using various approaches, including TLR3 segment swapping experiments,

mutagenesis, H/D exchange and *in silico* protein-protein docking (The Epitope Mapping Protocols, Methods in Molecular Biology, Volume 6, Glen E. Morris ed., 1996).

TLR3 segment swapping. TLR3 human-mouse chimeric proteins were used to locate gross antibody binding domains on TLR3. The human TLR3 protein extracellular domain was divided into three segments (aa 1-209, aa 210-436, aa 437-708 according to amino acid numbering based on human TLR3 amino acid sequence, GenBank Acc. No. NP_003256). MT5420 chimeric protein was generated by replacing human TLR3 amino acids 210-436 and 437-708 by corresponding mouse amino acids (mouse TLR3, GenBank Acc. No. NP_569054, amino acids 211-437 and 438-709). The MT6251 chimera was generated by replacing human amino acids at positions 437-708 by mouse TLR3 amino acids (mouse TLR3, GenBank Acc. No. NP_569054, amino acids 438-709). All constructs were generated in the pCEP4 vector (Life Technologies, Carslbad, CA) using standard cloning procedures. The proteins were transiently expressed in HEK293 cells as V5-His6 C-terminal fusion proteins, and purified as described in Example 1.

mAb c1068. mAb c1068 bound human TLR3 ECD with high affinity but did not bind well to murine TLR3. c1068 lost its ability to bind to both MT5420 and MT6251, demonstrating that the binding site was located within the amino acids 437-708 of the WT human TLR3 protein.

mAb 12QVQ/QSV. mAb 12QVQ/QSV bound both chimeras, indicating that the binding site for mAb 12QVQ/QSV was located within the amino acids 1-209 of the human TLR3 protein having a sequence shown in SEQ ID NO:2.

***In silico* protein-protein docking.** The crystal structure of mAb 15EVQ (see below) and the published human TLR3 structure (Bell *et al.*, J. Endotoxin Res. 12:375-378, 2006) were energy minimized in CHARMm (Brooks *et al.*, J. Computat. Chem. 4:187-217, 1983) for use as the starting models for docking. Protein docking was carried out with ZDOCKpro 1.0 (Accelrys, San Diego, CA), which is equivalent

to ZDOCK 2.1 (Chen and Weng, Proteins 51: 397-408, 2003) with an angular grid of 6 degrees. Known N-linked glycosylation site Asn residues in human TLR3 (Asn 52, 70, 196, 252, 265, 275, 291, 398, 413, 507 and 636) (Sun *et al.*, J. Biol. Chem. 281:11144-11151, 2006) were blocked from participating in the antibody-antigen complex interface by an energy term in the ZDOCK algorithm. 2000 initial poses were output and clustered and the docking poses were refined and rescored in RDOCK (Li *et al.*, Proteins 53:693-707, 2003). The 200 poses with the highest initial ZDOCK scores and 200 top RDOCK poses were visually inspected.

Crystallization of Fab 15EVQ was carried out by the vapor-diffusion method at 20°C (Benvenuti and Mangani, Nature Protocols 2:1633-51, 2007). The initial screening was set up using a Hydra robot in 96-well plates. The experiments were composed of droplets of 0.5 µl of protein solution mixed with 0.5 µl of reservoir solution. The droplets were equilibrated against 90 µl of reservoir solution. The Fab solution in 20 mM Tris buffer, pH 7.4, containing 50 mM NaCl was concentrated to 14.3 mg/ml using Amicon Ultra-5 kDa cells. The screening was performed with the Wizard I & II (Emerald BioSystems, Bainbridge Island, WA) and in-house crystallization screens. Fab 12QVQ/QSV was crystallized in a similar manner.

X-ray diffraction data were collected and processed using the Rigaku MicroMax™-007HF microfocus X-ray generator equipped with an Osmic™ VariMax™ confocal optics, Saturn 944 CCD detector, and an X-stream™ 2000 cryocooling system (Rigaku, Woodlands, TX). Diffraction intensities were detected over a 270° crystal rotation with the exposure time of 120 s per half-degree image. The X-ray data were processed with the program D*TREK (Rigaku). The structure was determined by the molecular replacement method using the program Phaser or CNX (Accelrys, San Diego, CA). Atomic positions and temperature factors were refined with REFMAC using all data in the resolution range 15-2.2 Å for Fab 15EVQ

and 50-1.9 Å for Fab 12QVQ/QSV. Water molecules were added at the (F_o-F_c) electron density peaks using the cut-off level of 3σ. All crystallographic calculations were performed with the CCP4 suite of programs (Collaborative Computational Project, Number 4. 1994. The CCP4 suite: programs for protein crystallography. Acta Crystallogr. D50:760-763). Model adjustments were carried out using the program COOT (Emsley et al., Acta Crystallogr. D60:2126-2132, 2004).

The resolved crystal structure of mAb 15EVQ showed that the antibody combining site was characterized by a number of negatively charged residues in the heavy chain (D52, D55, E99, D106 and D109). Thus, recognition between mAb 15EVQ and TLR3 most likely involved positively charged residues. The protein-protein docking simulations performed suggested that two large patches on TLR3 involving multiple positive charge residues showed good complementarity to the antibody. The residues on TLR3 in the interface of the TLR3 - anti-TLR3 antibody simulated complexes were R64, K182, K416, K467, Y468, R488, R489 and K493.

Mutagenesis studies. Single and combination point mutations were introduced into surface residues of TLR3 ECD in the regions identified above to contain the epitopes of mAb 12 and mAb 15EVQ and the mutant proteins were tested for antibody binding.

The nucleotide sequence encoding human TLR3 amino acids 1-703 (the ECD), (SEQ ID NO: 4; GenBank accession number NP_003256), was cloned using standard protocols. All mutants were generated by site directed mutagenesis using the Strategene Quickchange II XL kit (Stratagene, San Diego, CA) according to the manufacturer's protocol, using the oligonucleotides shown in Table 5a. Mutations were verified by DNA sequencing. The proteins were expressed under a CMV promoter as C-terminal His-tag fusions in HEK293 cells, and purified as described in Example 1.

Binding assays. The binding activity of mAb 12QVQ/QSV and mAb 15EVQ to human TLR3 and generated variants was

evaluated by ELISA. To expedite the process, mutants in the predicted mAb 15EVQ binding site were co-expressed in HEK cells by co-transfection of TLR3 ECD mutant containing a C-terminal His tag with mAb 12QVQ/QSV, followed by purification by metal affinity chromatography. The recovered sample was a complex of the TLR3 mutant with mAb 12. This approach was feasible because the mAb 12QVQ/QSV and mAb 15EVQ binding sites are distant from one another; and thus, point mutations at one site are unlikely to affect the epitope at the other site. These complexes were used in the ELISA binding assays. 5 µl per well of 20 µg/ml wild type TLR3 ECD or mutant proteins in PBS were coated on an MSD HighBind plate (Meso Scale Discovery, Gaithersburg, MD). The plates were incubated at room temperature for 60 min and blocked.

Table 5a. Sequences of the sense oligonucleiotides are shown. The anti-sense oligonucleotides with complementary sequences were used in the mutagenesis reaction.

Variant	Oligo	SeqID NO:
R64E	5' CCTTACCCATAATCAACTCGAGAGATTACCAGCCGCCAAC 3'	136
K182E	5'CAAGAGCTTCTATTATCAAACAATGAGATTCAAGCGCTAAAAAGTGAAG 3'	137
K416E	5' CCTTACACATACTCAACCTAACCGAGAATAAAATCTCAAAAATAG 3'	138
K467E/Y468A	5' GAAATCTATCTTTCCTACAACGAGGCCCTGCAGCTGACTAGGAACTC 3'	139
R488/R489/K493E	5' GCCTTCAACGACTGATGCTCGAGGAGGTGGCCCTTGAGAATGTGGATAGCTCTCCTTC 3'	140
T472S/R473T/N474S	5' GTACCTGCAGCTGTCTACGAGCTCCTTTGCCTTGGTCCC 3'	141
N196A	5' GAAGAACTGGATATCTTTGCCGCTTCATCTTTAAAAAAATTAGAGTTG 3'	169
Q167A	5' GTCATCTACAAAATTAGGAACTGCGGTTCAGCTGGAAAATCTCC 3'	170
K163E	5' CTCATAATGGCTTGTCATCTACAGAATTAGGAACTCAGGTTCAGC 3'	171
K147E	5' GAAAATTAAAAATAATCCCTTTGTCAAGCAGGAGAATTTAATCACATTAGATCTGTC 3'	172
K145E	5' GAAAATTAAAAATAATCCCTTTGTCGAGCAGAAGAATTTAATCACATTAG 3'	173
V144A	5' CAGAAAATTAAAAATAATCCCTTTGCAAAGCAGAAGAATTTAATCACATTAG 3'	174
N140A	5' CCAACTCAATCCAGAAAATTAAAGCTAATCCCTTTGTCAAGCAGAAG 3'	175
D116R	5' CAATGAGCTATCTCAACTTTCTCGTAAAACCTTTGCCTTCTGCAC 3'	176
D536K	5' GTCTTGAGAAACTAGAAATTCTCAAGTTGCAGCATAACAACTTAGCAC 3'	177
D536A	5' CTTGAGAAACTAGAAATTCTCGCATTGCAGCATAACAACTTAGCAC 3'	178
K619E	5' CTAAAGTCATTGAACCTTCAGGAGAATCTCATAACATCCGTTG 3'	179
K619A	5' CTCTAAAGTCATTGAACCTTCAGGCGAATCTCATAACATCCGTTGAG 3'	180
E570R	5' CCACATCCTTAACTTGAGGTCCAACGGCTTTGACGAG 3'	181
N541A	5' GAAATTCTCGATTTGCAGCATAACGCCTTAGCACGGCTCTGGAAAC 3'	182
Q538A	5' GAGAAACTAGAAATTCTCGATTTGGCGCATAACAACTTAGCACGGC 3'	183
H539E	5' CTAGAAATTCTCGATTTGCAGGAAAACAACTTAGCACGGCTCTG 3'	184
H539A	5' CTAGAAATTCTCGATTTGCAGGCTAACAACTTAGCACGGCTCTG 3'	185
N517A	5' CATTCTGGATCTAAGCAACAACGCCATAGCCAACATAAATGATGAC 3'	186
Y465A	5' GAAAATATTTTCGAAATCTATCTTTCCGCCAACAAGTACCTGCAGCTGAC 3'	187
R488E	5' GCCTTCAACGACTGATGCTCGAAAGGGTGGCCCTTAAAAATG 3'	188
R489E	5' CTTCAACGACTGATGCTCCGAGAGGTGGCCCTTAAAAATGTGG 3'	189
K467E	5' CGAAATCTATCTTTCCTACAACGAGTACCTGCAGCTGACTAG 3'	190

overnight in MSD Blocker A buffer (Meso Scale Discovery, Gaithersburg, MD) at 4°C. The following day the plates were washed and the MSD Sulfo-tag labeled mAb 15EVQ added at concentrations from 500 pM to 1 pM for 1.5 hours. After washes the labeled antibody was detected using MSD Read Buffer T and the plates were read using a SECTOR Imager 6000. To evaluate the binding activity of mAb 12QVQ/QSV to human TLR3 and variants, co-expression was carried out with mAb 15EVQ and binding ELISAs were performed as described for mAb 15EVQ, except that the detecting antibody was labeled mAb 12QVQ/QSV.

mAb 12QVQ/QSV: The binding site for mAb 12QVQ/QSV was located within the amino acids 1-209 of the human TLR3 protein as determined in the segment swap studies. The following TLR3 mutants were evaluated: D116R, N196A, N140A, V144A, K145E, K147E, K163E, and Q167A. The wild type TLR3 and V144A mutant showed comparable binding to mAb 12QVQ/QSV (Figure 6A). The antibody did not bind to TLR3 D116R mutant and had significantly reduced binding affinity to the K145E mutant. Thus, residues D116 and K145 which are closely apposed on the surface of TLR3 were identified as key epitope sites for mAb 12QVQ/QSV (Figure 7A).

The two critical residues of the mAb 12QVQ/QSV binding epitope were located near the face of the dsRNA binding site at the N-terminal segment of the TLR3 ectodomain (Pirher, *et al.*, Nature Struct. & Mol. Biol., 15:761-763, 2008). The complete epitope will contain other residues in the neighboring regions, which were not revealed by mutational analyses performed. Not wishing to be bound to any particular theory, it is believed that binding of mAb 12QVQ/QSV on its TLR3 epitope may directly or indirectly interfere with dsRNA binding on TLR3 ectodomain, thereby disrupting receptor dimerization and activation of downstream signaling pathways.

mAb 15EVQ: The following TLR3 mutants were evaluated: R64E, K182E, K416E, Y465A, K467E, R488E, R489E, N517A, D536A, D536K, Q538A, H539A, H539E, N541A, E570R, K619A, K619E, a double mutant K467E/Y468A, a triple mutant T472S/R473T/N474S, and a triple mutant R488E/R489E/K493E. The wild type TLR3, the R64E, K182E, K416E mutants and the triple mutant T472S/R473T/N474S showed comparable binding to mAb 15EVQ (Figure 6B and Table 5b). The antibody did not bind to TLR3 mutants K467E, R489E, K467E/Y468A and R488E/R489E/K493E (Figure 6B and 6C). The remaining variants showed intermediate binding with the R488E having the greatest effect. All of these mutants bound to mAb 12QVQ/QSV. These results showed that resides K467 and R489 were critical

determinants of the mAb 15EVQ epitope. Residue R488 also contributed to the epitope. These residues were closely apposed on the same surface of TLR3 (**Figure 7A**). The results also showed that residues Y465, Y468, N517, D536, Q538, H539, N541, E570, and K619, all on the same surface as K467, R488 and R489, contributed to the epitope. This conclusion was further supported by the H/D exchange studies with mAb 15EVQ. Figure 7A shows binding epitope sites for mAbs 12QVQ/QSV and 15EVQ (black) and C1068 mAb (grey) superimposed on the structure of human TLR3. The epitope for mAb 15EVQ covers residues Y465, K467, Y468, R488, R489, N517, D536, Q538, H539, N541, E570, and K619.

H/D Exchange studies. For H/D exchange, the procedures used to analyze the antibody perturbation were similar to that described previously (Hamuro *et al.*, J. Biomol. Techniques 14:171-182, 2003; Horn *et al.*, Biochemistry 45:8488-8498, 2006) with some modifications. Recombinant TLR3 ECD (expressed from *Sf9* cells with C-terminal His-tag and purified) was incubated in a deuterated water solution for predetermined times resulting in deuterium incorporation at exchangeable hydrogen atoms. The deuterated TLR3 ECD was captured on a column containing immobilized mAb 15EVQ and then washed with aqueous buffer. The back-exchanged TLR3 ECD protein was eluted from the column and localization of deuterium containing fragments was determined by protease digestion and mass spec analysis. As a reference control, TLR3 ECD sample was processed similarly except it was exposed to deuterated water only after capture on the antibody column and then washed and eluted in the same manner as the experimental sample. Regions bound to the antibody were inferred to be those sites relatively protected from exchange and thus contain a higher fraction of deuterium than the reference TLR3 ECD sample. About 80% of the protein could be mapped to specific peptides. Maps of H/D exchange perturbation of TLR3 ECD by mAb 15EVQ are shown in Figure 7B. Only the segment of TLR3 around the portion affected by mAb

15EVQ is shown for clarity. The remainder of the protein extending to the amino and carboxyl termini of TLR3 ECD was not affected appreciably.

The H/D exchange studies identified peptide segments $_{465}$YNKYLQL$_{471}$, $_{514}$SNNNIANINDDML$_{526}$ and $_{529}$LEKL$_{532}$ of SEQ ID NO: 2 as regions where exchange on TLR3 was particularly altered by binding to mAb 15EVQ. By its nature, H/D exchange is a linear mapping method and usually cannot define which residues within the peptide segment are most affected by antibody binding. However, the extensive overlap between the H/D exchange and mutational results gives added confidence that the surface shown in Figure 7A is the binding site for mAb 15EVQ. This binding site was in same linear amino acid sequence region as previously described for mAb c1068 (PCT Publ. no. WO06/060513A2) but it was found to be located on a completely non-overlapping surface (Figure 7A) in agreement with the lack of cross-competition between these antibodies.

The mAb 15EVQ binding epitope was spatially proximal to the dsRNA binding site at the C-terminal segment on TLR3 (Bell *et al.*, Proc. Natl. Acad. Sci. (USA) 103: 8792-8797, 2006; Ranjith-Kumar *et al.*, J Biol Chem, 282: 7668-7678, 2007; Liu *et al.*, Science, 320: 379-381, 2008). Not wishing to be bound to any particular theory, it is believed that binding of mAb 15EVQ on its TLR3 epitope causes steric clashes with a ligand dsRNA molecule and/or the dimer partner, preventing ligand binding and ligand-induced receptor dimerization.

Table 5b.

Variant	mAb 15	Variant	mAb 12
wt TLR3 ECD	+++	wt TLR3 ECD	+++
R64E	+++	D116R	-
K182E	+++	N140A	++
K416E	+++	V144A	+++
Y465A	++	K145E	+
K467E	-	K147E	++
R488E	+	K163E	++
R489E	-	Q167A	++
N517A	++	N196A	++
D536K	++		
D536A	++		
Q538A	++		
H539E	++		
H539A	++		
N541A	++		
E570R	++		
K619E	++		
K619A	++		
K467E/Y468A	-		
R488/R489/K493E	-		
T472S/R473T/N474S	+++		

Example 7

Generation of variants with enhanced thermal stability

Structure-based engineering was conducted to generate antibody variants with increased thermal stability, with simultaneous efforts to maintain the biological activity and minimize immunogenicity.

mAb 15EVQ was selected for engineering. To minimize immunogenicity, only germline mutations predicted to be beneficial based upon structural considerations were pursued. The VL and VH sequences of mAb 15EVQ (SEQ ID NO: 41 and SEQ ID NO: 216, respectively) were aligned with the human germline genes using BLAST searches. The closest germline

sequences identified were GenBank Acc. No. AAC09093 and X59318 for VH and VL, respectively. The following differences were identified between the germline VH, VL and those of the mAb 15EVQ VH and VL sequences: (VH) V34I, G35S, F50R, A61S, and Q67H; (VL) G30S, L31S, and A34N. The identified sequence differences were mapped onto the crystal structure of the mAb 15EVQ, and residues predicted to alter packing and interface interactions were selected for engineering. Based upon the crystal structure of the antibody (see Example 6), potential structure destabilizing residues were identified. (1) A small enclosed cavity was identified in the core of VH near V34. This cavity was large enough to accommodate a slightly larger sidechain such as Ile. (2) E99 of VH CDR3 was buried at the VH/VL interface without a H-bonding network. The negatively charged carboxylate group of E99 was in a generally hydrophobic environment with mostly van der Waals (vdw) contacts to neighboring residues. Burying a charge group is usually energetically unfavorable and thus has destabilizing effect. (3) F50 of VH is a VH/VL interface residue. Its aromatic sidechain is bulky and thus may have negative impact upon the pairing. H-bonding and *vdw* packing networks for the Fv were calculated and visually inspected in Pymol (www://_pymol_org). Buried cavities in the VH and VL domains were computed by Caver (Petrek *et al.*, BMC Bioinformatics, 7:316, 2006). All molecular graphics figures were prepared in Pymol. Mutations were made to the expression vectors encoding Fab fragments or IgG4 full human antibodies generated as described in Example 3 using standard cloning techniques using Quick Change II XL Site Directed Mutagenesis Kit (Stratagene, San Diego, CA), Change-IT Multiple Mutation Site Directed Mutagenesis Kit (USB Corporation, Cleveland, OH) or Quick Change II Site Directed Mutagenesis Kit (Stratagene, San Diego, CA). The reactions were performed according to each manufacturer's recommendations. The obtained clones were sequenced for verification, and the

resulting engineered variants were named mAbs 15-1 - 15-10 according to their modified heavy or light chain. Each variant chain (H or L) was expressed with the wild type mAb 15EVQ L or H chain to produce antibodies, except that the heavy chain for mAb 15-10 was from mAb 15-6. A listing of the SEQ ID NOs: for the CDRs, variable regions of light and heavy chains and full length heavy and light chains for mAb 15EVQ and its engineered variants is shown in Table 6. Table 7 shows primers for generation of each variant.

Table 6.

	SEQ ID NO:									
Candidate no:	HCDR1	HCDR2	HCDR3	LCDR1	LCDR2	LCDR3	LV	HV	Heavy IgG4	Light chain
15	111	112	84	109	110	113	41	216	220	156
15-1	111	114	84	109	110	113	41	124	130	156
15-2	115	112	84	109	110	113	41	125	131	156
15-3	116	112	84	109	110	113	41	126	132	156
15-4	111	117	84	109	110	113	41	127	133	156
15-5	116	118	84	109	110	113	41	128	134	156
15-6	116	112	119	109	110	113	41	129	135	156
15-7	111	112	84	120	110	113	122	42	102	157
15-8	111	112	84	121	110	113	123	42	102	158
15-9	116	118	119	109	110	113	41	159	160	156
15-10	116	112	119	109	110	226	225	129	135	227

Binding of mAbs 15-1 – 15-9 to TLR3 was evaluated by ELISA immunoassay. Human TLR3 ECD (100 µl of 2 µg/ml TLR3-ECD) was bound to a black Maxisorb plate (eBioscience) overnight at 4°C. The plates were washed and blocked, and diluted antibodies were aliquoted at 50 µl per well in duplicate onto the wells. The plate was incubated at RT for 2 hours shaking gently. Binding was detected using luminescence POD substrate (Roche Applied Science, Mannheim, Germany, Cat. No. 11 582 950 001) and goat anti-human Fc:HRP (Jackson ImmunoResearch, West Grove, PA, Cat. No. 109-035-098) and the plate was read in a SpectraMax plate reader (Molecular Devices, Sunnyvale, CA).

DSC experiments were performed on a MicroCal's Auto VP-capillary DSC system (MicroCal, LLC, Northampton, MA) in which temperature differences between the reference and sample cells were continuously measured, and calibrated to power units. Samples were heated from 10 °C to 95 °C at a heating rate of 60 °C/hour. The pre-scan time was 15 minutes and the filtering period was 10 seconds. The concentration used in the DSC experiments was about 0.5 mg/ml. Analysis of the resulting thermograms was performed using MicroCal Origin 7 software (MicroCal, LLC).

Table 7.

Candidate no:	Mutants	Primers	Seq ID NO:
15-1	HC: F50R	GCCTGGAGTGGATGGGCCGGATCGACCCCAGCG	142
		CGCTGGGGTCGATCCGGCCCATCCACTCCAGGC	143
15-2	HC: V34I	AGAGGTAACTCCCGTTGCGG	144
		GCATCTGGCGCACCCAGCCGATCCAGTAGTTGGTGAAG	145
15-3	HC: V34I/G35S	AGAGGTAACTCCCGTTGCGG	146
		GCATCTGGCGCACCCAGCTGATCCAGTAGTTGGTGAAG	147
15-4	HC: A61S/Q67H	AGAGGTAACTCCCGTTGCGG	144
		CGCTGATGGTCACGTGGCCCTGGAAGCTAGGGCTGTAGTTGGTGTAG	148
15-5	HC: F50R/V34I/G35S/ A61S/Q67H	CTTCACCAACTACTGGATCAGCTGGGTGCGCCAGATGC	149
		CGCTGATGGTCACGTGGCCCTGGAAGCTAGGGCTGTAGTTGGTGTAG	148
15-6	HC: V34I/G35S/E99Q	CGCCATGTACTACTGCGCCCGCCAGCTGTACCAGGGCTAC	150
		GTAGCCCTGGTACAGCTGGCGGGCGCAGTAGTACATGGCG	151
15-7	LC: G30S/L31S	GCCAGCCAGAGCATCAGCAGCTACCTGGCCTGGTACCAGC	152
		GCTGGTACCAGGCCAGGTAGCTGCTGATGCTCTGGCTGGC	153
15-8	LC: A34N	AGAGGTAACTCCCGTTGCGG	144
		CGGGCTTCTGCTGGTACCAGTTCAGGTAGCTGCTGATGCTCTG	154
15-9	HC: F50R/V34I/G35S /A61S/Q67H/E99Q	CGCCATGTACTACTGCGCCCGCCAGCTGTACCAGGGCTAC	150
		GTAGCCCTGGTACAGCTGGCGGGCGCAGTAGTACATGGCG	151
15-10	LC: S95P	CAGGGCAACACCCTGCCCTACACCTTCGGCCAG	228
		CTGGCCGAAGGTGTAGGGCAGGGTGTTGCCCTG	229

The thermal stability (Tm) of the generated variants was measured by DSC (Table 8). Binding of the antibody variants to TLR3 was comparable to that of the parental antibody.

Table 8. Summary of melting temperatures (T_M) of the variants and rationale for making them.

Candidate no:	Mutations		Rationale	TM (ºC)	ΔTM (ºC)
15EVQ		WT		64.7	0
15-1	HV	F50R	VH/VL interface	69.3	4.6
15-2	HV	V34I	VH core packing	66.9	2.2
15-3	HV	V34I/G35S	H-bonding, VH core packing	71.2	6.5
15-4	HV	A61S/Q67H	VH/VL packing, VH surface charge	65.4	0.7
15-5	HV	F50R/V34I/G35S/ A61S/Q67H	VH/VL interface, H-bonding, VH core	76.2	11.5
15-6	HV	V34I/G34S/E99Q	H-bonding, VH core packing, removal of	75	10.3
15-7	LV	G30S/L31S	L-CDR1 surface polar residues	63.1	-1.6
15-8	LV	A34N	VL/VH interface	64	-0.7
15-9	HV	F50R/V34I/G35S/ A61S/Q67H/E99Q	VH/VL interface, H-bonding, VH core	76	11.3
15-10	LV	S95P	Canonical structure stabilization	76.6	11.9

Example 8

Generation of a surrogate anti-TLR3 antibody

A chimeric antagonistic rat/mouse anti-mouse TLR3 antibody, herein named mAb 5429 was generated to evaluate effects of inhibiting TLR3 signaling in various *in vivo* models, as the humanized antibodies generated in Example 1 did not have sufficient specificity or antagonist activity for mouse TLR3. The surrogate chimeric mAb 5429 as well as its parent rat anti-mouse TLR3 antibody c1811 inhibited mouse TLR3 signaling *in vitro*, and *in vivo*, and ameliorated pathogenic mechanisms in several disease models in the mouse.

Data discussed below suggests a role for TLR3 in the induction and perpetuation of detrimental inflammation, and

contribute to the rationale for the therapeutic use of TLR3 antagonists and TLR3 antibody antagonists, for example acute and chronic inflammatory conditions including hypercytokinemia, asthma and airway inflammation, inflammatory bowel diseases and rheumatoid arthritis, viral infections, and type II diabetes.

Generation of the surrogate mAb 5429

CD rats were immunized with recombinant murine TLR3 ectodomain (amino acids 1-703 of seq ID NO: 162, GenBank Acc. No. NP_569054) generated using routine methods. Lymphocytes from two rats demonstrating antibody titers specific to murine TLR3 were fused to FO myeloma cells. A panel of monoclonal antibodies reactive to murine TLR3 were identified and tested for *in vitro* antagonist activity in the murine luciferase reporter and murine embryonic fibroblast assays. The hybridoma line C1811A was selected for further work. Functional variable region genes were sequenced from mAb c1811 secreted by the hybridoma. Cloned heavy chain and light chain variable region genes were then respectively inserted into plasmid expression vectors that provided coding sequences for generating a chimeric Rat/Balb C muIgG1/κ mAb designated as mAb 5429 using routine methods. The antibodies were expressed as described in Example 3. T he amino acid sequences of the mAb 5429 heavy and light chain variable regions are shown in SEQ ID NO:164 and SEQ ID NO: 163, respectively, and the heavy and light chain full length sequences are shown in SEQ ID NO:166 and SEQ ID NO: 165, respectively. The heavy and light chain full length sequences of mAb c1811 are shown in SEQ ID NO: 168 and SEQ ID NO: 167, respectively.

Characterization of mAb 5429

mAb 5429 was characterized in a panel of *in vitro* assays for its neutralizing ability on TLR3 signaling. The activity assays and results are described below.

Murine Luciferase Reporter Gene Assay

The murine TLR3 cDNA (SEQ ID NO: 161, GenBank Acc. No: NM_126166) was amplified by PCR from murine spleen cDNA (BD Biosciences, Bedford, MA), and cloned into the pCEP4 vector (Life Technologies, Carslbad, CA) using standard methods. 200 µl HEK293T cells were plated in 96 well white clear-bottom plates at a concentration of 4 x 10^4 cells/well in complete DMEM, and used the following day for transfections using Lipofectamine 2000 (Invitrogen Corp., Carslbad, CA) using 30 ng pNF-κB firefly luciferase (Stratagene, San Diego, CA) or 30 ng pISRE firefly luciferase (BD Biosciences, Bedford, MA), 5 ng phRL-TK control Renilla luciferase (Promega Corp., Madison, WI) reporter plasmids, 1.5 ng pCEP4 encoding the full-length murine TLR3, and 13.5 ng empty pcDNA3.1 vector (Life Technologies, Carslbad, CA) to bring the total DNA amount to 50 ng/well. 24 hours post-transfection, the cells were incubated for 30 minutes to 1 hour at 37°C with the anti-murine TLR3 antibodies in fresh serum-free DMEM before the addition of 0.1 or 1 µg/µl poly(I:C). The plates were harvested after 24 hours using the Dual-Glo Luciferase Assay System (Promega, Madison, WI). The relative light units were measured using a FLUOstar OPTIMA multi-detection reader with OPTIMA software (BMG Labtech GmbH, Germany). Normalized values (luciferase ratios) were obtained by dividing the firefly relative light units (RLUs) by the Renilla RLUs. mAb 5429 as well as its parent mAb c1811 and mAb 15 (Table 3a) reduced poly(I:C) - induced NF-kB and ISRE activation in a dose-dependent fashion (Figure 8A and 8B), demonstrating their abilities to antagonize the activity of TLR3. IC50s measured in the ISRE assay were 0.5, 22, and 0.7 µg/ml for mAb 5249, mAB 15 and mAb c1811, respectively.

Murine Embryonic Fibroblast (MEF) Assay

C57BL/6 MEF cells were obtained from Artis Optimus (Opti-MEF™ C57BL/6 - 0001). The cells were plated in 96-well

flat bottom plates (BD Falcon) at 20,000 cells/well in 200 µl MEF media (DMEM with glutamax, 10% heat inactivated-FBS, 1x NEAA, and 10 µg/ml gentamycin). All incubations were done at 37°C/5%CO_2. 24 hours after plating, mAb 5429 or mAb c1811 were added into wells. The plates were incubated with the mAbs for 1hr, after which Poly(I:C) was added at 1 µg/ml in each well. The supernatants were collected after a 24-hour incubation. Cytokine levels were determined using a bead kit (Invitrogen Corp., Carslbad, CA) to detect CXCL10/IP-10 following manufacturer's protocol. The results were graphed using GraphPad Prism Software. Both antibodies reduced poly(I:C)-induced CXCL10/IP-10 levels in a dose-dependent manner, demonstrating the abilities of these antibodies to antagonize endogenous TLR3 and inhibit TLR3 signaling (Figure 9).

Flow Cytometry- Surface Staining

C57BL/6 and TLR3 knockout (TLR3KO) (C57BL/6 background; female, 8-12 weeks of age, Ace Animals, Inc.), 10 per group, were dosed intraperitoneally with 1 ml of 3% Thioglycollate medium (Sigma) and 96 hrs later, the mice were euthanized and the peritoneum from each mouse was lavaged with 10 ml sterile PBS. Thioglycollate-elicited peritoneal macrophages were resuspended in PBS and cell viability was assessed using Trypan Blue staining. Cells were pelleted by centrifugation and resuspended in 250 µl FACS Buffer (PBS -Ca^{2+}-Mg^{2+}, 1% heat-inactivated FBS, 0.09% Sodium Azide) and were kept on wet ice. The CD16/32 reagent (eBioscience) was used at 10 µg/10^6 cells for 10 minutes to block Fc Receptors on the macrophages. The cells were distributed at 10^6 cells in 100 µl/well for surface staining. Alexa-Fluor 647 (Molecular Probes)-conjugated mAb c1811 and mAb 1679 (rat anti-mouse TLR3 antibody that had no TLR3 specificity, and thus used as an isotype control) were added at 0.25 µg/10^6 cells and incubated on ice in the dark for 30 minutes. The cells were washed and resuspended in 250 µl of FACS Buffer. The

viability stain, 7-AAD (BD Biosciences, Bedford, MA), was added at 5 µl/well no more than 30 minutes before acquisition of samples on FACS Calibur to detect a dead cell population. Samples were collected by the FACS Calibur using Cell Quest Pro Software. FCS Express was used to analyze the collected data by forming histograms.

The binding of mAb c1811 to murine thioglycollate-elicited peritoneal macrophages from C57BL/6 and TLR3KO mice were evaluated by flow cytometry to determine binding specificity. mAb 5429 was not used in this assay since the mouse Fc region of this chimeric antibody was expected to contribute to non-specific binding. mAb c1811 exhibited no binding to TLR3KO macrophages, and increased binding to the cell surfaces of C57BL/6 peritoneal macrophages, suggesting a specificity of the mAb for TLR3 (Figure 10). mAb 5429, having the same binding regions as mAb c1811, is assumed to have the same binding specificity as mAb c1811.

Example 9

TLR3 antibody antagonists protect from TLR3-mediated systemic inflammation

Model

The Poly(I:C)-induced systemic cytokine/chemokine model was used as a model of TLR3-mediated systemic inflammation. In this model, poly(I:C) (PIC) delivered intraperitoneally induced a systemic cytokine and chemokine response that was partially TLR3-mediated.

Female C57BL/6 mice (8-10 weeks old) or female TLR3KO mice (C57BL/6 background; 8-10 weeks old, Ace Animals, Inc.) were given mAb 5429 at 10, 20 or 50 mg/kg in 0.5 ml PBS, mAb c1811 at 2, 10 or 20 mg/kg in 0.5 ml PBS or 0.5 ml PBS alone (vehicle control) subcutaneously. 24 hours after antibody dosing, mice were given 50 µg poly(I:C) (Amersham Cat. No. 26-4732 Lot no. IH0156) in 0.1 ml PBS intraperitoneally. Retro-orbital blood was collected 1 and 4 hours after the poly(I:C) challenge. Serum was prepared from whole blood and

analyzed for cytokine and chemokine concentrations by Luminex.

Results

Poly(I:C) delivered intraperitoneally induced a systemic cytokine and chemokine response that was partially TLR3-mediated, as evidenced by the significantly reduced production of a panel of chemokines and cytokines in the TLR3KO animals (Table 9A). The TLR3-dependent poly(I:C)-induced mediators were IL-6, KC, CCL2/MCP-1 and TNF-α at 1 hr post-poly(I:C) challenge, and IL-1α, CCL5/RANTES and TNF-α at 4 hr post-poly(I:C) challenge. Both mAb c1811 and mAb 5429 significantly reduced levels of these TLR3-dependent mediators, demonstrating the ability of the antibodies to reduce TLR3 signaling *in vivo* (Table 9B). Values in Table 9 are shown as mean cytokine or chemokine concentrations in pg/ml of six animals/group ±SEM. These data suggest that TLR3 antagonism can be beneficial in reducing excess TLR3-mediated cytokine and chemokine levels in conditions such as cytokine storm or lethal shock.

Table 9A.

	C57BL/6		TLR3KO	
PIC	-	+	-	+
mAb 5429 (mg/kg)	-	-	-	-
mAb c1811 (mg/kg)	-	-	-	-
1 h PIC challenge				
TNFα	6.005± 0.32	319.4 ± 34.1*	9.13 ± 4.41	43.80 ± 10.13**
KC	129.3± 9.83	2357 ± 491.5*	152.0 ± 21.34	432.3 ± 90.66**
IL-6	40.91± 5.66	5317 ± 856.7*	120.1 ± 99.99	1214 ± 294.9**
MCP-1	84.67± 18.45	694.6 ± 127.8*	67.85 ± 34.16	249.9 ± 55.60**
4 h PIC challenge				
IL-1α	28.21± 17.78	796.7 ± 45.0*	13.94 ± 13.84	408.5 ± 29.91**
RANTES	20.87± 1.738	4511 ± 783.4*	36.01 ± 4.484	706.3 ± 84.36**
TNFα	0.10 ± 0	561.7 ± 81.84*	3.215 ± 3.115	305.8 ± 53.63**
	*p<0.001: One Way ANOVA to C57BL/6 PBS			
	**p<0.001 One Way ANOVA to C57BL/6 PIC			

Table 9B.

	C57BL/6					
PIC	+	+	+	+	+	+
mAb 5429 (mg/kg)	50	20	10	-	-	-
mAb c1811 (mg/kg)	-	-	-	20	10	2
1 h PIC challenge						
TNF-α	29.33 ± 3.78***	31.05 ± 1.59***	59.55 ± 12.71***	32.54 ± 3.89***	42.22 ± 7.04***	42.61 ± 10.58***
KC	466.3 ± 92.35***	440.3 ± 10.01***	744.6 ± 103.1**	637.3 ± 151.0***	944.2 ± 130.9**	919.3 ± 231.2**
IL-6	480.2 ± 62.88***	375.9 ± 46.14***	705.2 ± 149.8***	739.2 ± 113.3***	1047 ± 222***	1229 ± 378.4***
MCP-1	168.5 ± 15.04**	321.6 ± 206.7	219.2 ± 70.58*	184.0 ± 14.92**	278.3 ± 53.57	414.9 ± 97.17
4 h PIC challenge						
IL-1α	343.0 ± 33.01***	452.6 ± 94.86**	481.1 ± 121.0*	354.8 ± 45.43***	351.7 ± 68.85***	352.4 ± 39.60***
RANTES	1381 ± 169.7***	2439 ± 308.7**	1601 ± 398.9***	1303 ± 168.0***	1365 ± 474.1***	2209 ± 402.5**
TNF-α	100.1 ± 8.5***	205.1 ± 41.85***	226.1 ± 64.72***	138.9 ± 26.0***	121.6 ± 38.85***	223.8 ± 47.74***

***p<0.001, **p<0.01, *p<0.05: One Way ANOVA statistics were compared to the C57BL/6 + PIC group

Example 10

TLR3 antibody antagonists reduce airway hyperresponsiveness

Model

Airway hyperresponsiveness was induced by Poly(I:C).

Female C57BL/6 mice (12 weeks old) or female TLR3KO mice (C57BL/6 background; 12 weeks old, Ace Animals, Inc.) were anesthetized with isoflurane and several doses (10-100 µg) of poly(I:C) in 50 µl sterile PBS were administered intranasally. Mice received three administrations of poly(I:C)(or PBS) with a 24 hour rest period between each administration. 24 hours following the last poly(I:C)(or PBS) administration, lung function and airway hyperresponsiveness to methacholine were measured using whole body plethysmography (BUXCO system). The mice were placed into the whole body plethysmograph chamber and allowed to acclimate for at least 5 minutes. Following baseline readings, mice were exposed to increasing doses of nebulized methacholine (Sigma, St. Louis, MO). The nebulized methacholine was administered for 2 minutes, followed by a 5-minute data collection period, followed by a 10-minute rest

period before subsequent increasing-dose methacholine challenges. The increased airflow resistance was measured as Enhanced Pause (Penh) and is represented as the average Penh value over the 5-minute recording period (BUXCO system). Following lung function measurements, mice were euthanized and the lungs were cannulated. Bronchoalveolar lavages (BAL) were performed by injecting 1 ml of PBS into the lungs and retrieving the effluent. The lung tissues were removed and frozen. BAL fluids were centrifuged (1200 rpm, 10 min.) and the cell-free supernatants were collected and stored at -80°C until analysis. Cell pellets were resuspended in 200 µl PBS for total and differential cell counts. The multiplex assay was performed following the manufacturer's protocol and the Multiplex Immunoassay Kit (Millipore, Billercia, MA).

Results

Previous observations demonstrated that the intranasal administration of poly(I:C) induced a TLR3 -mediated impairment in lung function in mice with increased enhanced pause (PenH) measurement in whole body plethysmography (Buxco) at baseline and an increased responsiveness to aerosolized methacholine (an indicator of airway hyperesponsiveness) (PCT Publ. No. WO06/060513A2). This impairment in the lung function was associated with neutrophil recruitment into the lung, and increased levels of pro-inflammatory cytokines/chemokines in the lung. In this study, the effect of mAb 1811 and mAb 5429 was evaluated in poly(I:C)-induced impairment in lung function by administering each antibody at 50 mg/kg subcutaneously prior to poly(I:C) challenge.

TLR3-mediated impairment of lung function was significantly reduced by treatment of animals with TLR3 antibody antagonists prior to the poly(I:C) challenge. TLR3-mediated increases in baseline PenH and airway sensitivity to methacholine were prevented in the anti-TLR3 antibody-treated animals (Figure 11). Further, TLR3-mediated recruitment of

neutrophils into the mouse lung and generation of chemokines in the airways were reduced in the anti-TLR3 antibody - treated animals. The neutrophil numbers (Figure 12) and the CXCL10/IP-10 levels (Figure 13) were measured from the collected bronchoalveolar lavage fluid (BALF). The studies were repeated at least three times with similar results. Data shown in Figures 11, 12 and 13 are from one representative study. Each symbol represents a data point from one mouse, and the horizontal bars show group means. The study demonstrated that systemically-administed TLR3 antibody antagonists reached the lung, reduced TLR3-mediated impairment of lung function, neutrophil infiltration into the airway, chemokine generation and respiratory tract inflammation in the used model. Thus, TLR3 antagonists may be beneficial in the treatment or prevention of respiratory diseases characterized by airway hyperresponsiveness, such as asthma, allergic rhinitis, chronic obstructive pulmonary disease (COPD), and cystic fibrosis.

Example 11
TLR3 antibody antagonists protect from inflammatory bowel disease

Model

The DSS colitis Model was used as a model of inflammatory bowel disease.

Female C57BL/6 mice (<8 weeks old) or female TLR3KO mice (C57BL/6 background; <8 weeks old weighing between 16.5g and 18g, Ace Animals, Inc.) were fed gamma-irradiated food starting on day -1. DSS (Dextran sulfate) (MP Biomedicals, Aurora, OH, Catalog no: 160110; 35-50kDa; 18-20% Sulfur, Lot no. 8247J) was diluted in autoclaved acidified drinking water to a final concentration of 5%. The DSS-water was administered for 5 days, after which it was replaced with plain water. Mice were allowed to drink water ad libitum throughout the study. All water bottles were weighed every day to record water consumption. On days 0, 2, and 4 mice were dosed intraperitoneally with 5 mg/kg

(0.1 mg in 0.1 ml PBS) mAb 5429, mouse anti-TNF-α antibody, or PBS as a control. Mice were monitored daily throughout the study and were weighed on days 0 through 4 and day 7. Mice were euthanized on days 2 and 7 of the study. Abdominal cavities were opened and the ascending colons cut where they join the cecum. Colons were collected and fixed in 10% neutral buffered formalin. Colons were paraffin-embedded, sectioned and H&E stained (Qualtek Molecular Labs, Santa Barbara, CA). Colonic histopathological assessments were done in a blinded fashion by a veterinary pathologist as described below (PathoMetrix, San Jose, CA).

Histopathologic evaluation

Two segments of large intestine, colon and rectum were evaluated and scored for the following changes: (i) single cell necrosis; (ii) epithelial ulceration; (iii) epithelial sloughing; (iv) cryptal abscess; (v) cell proliferation; (vi) cryptal cell proliferation; (vii) granulation tissue formation in the lamina propria; (viii) granulation tissue in the submucosa; (ix) submucosal inflammatory cell infiltrate, neutrophil predominant; and (x) submucosal edema.

A single, overall score of severity was given based on the following standards:

0 - non-existent
1 - mild, focal or occasionally found
2 - mild, multifocal
3 - moderate, frequently found but in limited areas
4 - severe, frequently found in many areas or extensions of the tissue submitted
5 - very severe, extends to large portions of the tissue submitted

Results

Previous observations demonstrated that TLR3KO animals showed significantly reduced histopathology compared with wild type mice in a model of inflammatory bowel disease induced by DSS ingestion (PCT Publ. No. WO06/60513A2), thus suggesting that TLR3 signaling plays a role in the pathogenesis in this model. It has been reported that commensal bacterial RNA or mammalian RNA released from necrotic cells can act as endogenous ligands to stimulate TLR3 signaling (Kariko *et al.*, Immunity 23165-231175 2005; Kariko *et al.*, J. Biol. Chem. 279:12542-12550 2004), and therefore TLR3 stimulation by endogenous ligands in the gut may enhance and perpetuate inflammation in the DSS colitis model.

Disease severity was ameliorated in DSS-exposed animals upon treatment with anti-TLR3 antibodies, as assessed by compound histopathology scores (Figure 14). Figure 14 shows means, standard deviations and 95% confidence intervals for disease severity scores as horizontal bars. Significant reduction in the scores were observed in the wild type DSS-exposed animals treated with anti-TLR3 antibodies ($p < 0.05$) when compared to untreated wild type animals. DSS-exposed TLR3KO animals were protected from DSS-induced changes. DSS-exposed animals receiving anti-mouse TNF-α mAb demonstrated no improvement in histopathology in the DSS model. Therefore, the DSS model may be useful in evaluating therapeutics that may target the human patient population that is non-resposive to anti-TNF-α therapies, and neutralizing anti-TLR3 antibodies may have the potential to provide benefit to patients with inflammatory bowel disease who do not respond to anti-TNF-α therapies.

Model

The T cell Transfer Model was used as a model of inflammatory bowel disease. In this model, gut inflammation was induced in SCID mice by the transfer of a population of

regulatory T cell-devoid naïve T cells from immune-competent mice, which attack antigen-presenting cells in the gut mucosa.

Naïve T-cells ($CD4+CD45RB^{high}$ T cells) were injected intraperitoneally into SCID recipients to induce chronic colitis. Mice were given either PBS (500 μl/mouse intraperitoneally; vehicle control), mAb 5429 (0.1 mg/mouse intraperitoneally), or anti-TNF-α antibody (0.05 mg/mouse intraperitoneally; positive control) beginning 48 hours following transfer of T-cells and then twice weekly throughout the 8 week study. At 8 weeks following T-cell transfer (or when mice lost >15% of their original body weight) animals were euthanized and colons removed. Colons were fixed, paraffin-embedded and H&E stained. Histopathology (cell infiltration, crypt abscesses, epithelial erosion, goblet cell loss, and bowel wall thickening) was assessed quantitatively in a blinded fashion.

Results

Disease severity was ameliorated in animals that received T-cell transfer upon treatment with anti-TLR3 antibodies, as assessed by significant reduction in the histopathology sum of scores when compared to the control animals ($p<0.05$)(Figure 15A). For the sum of scores, crypt abscesses, ulceration, neutrophil influx, goblet cell loss, abnormal crypts, lamina propria inflammation and transmural involvement was assessed. Significant reduction was observed with crypt abscesses, ulceration and neutrophil influx (for all $p< 0.05$) (Figure 15B). Anti-TNF-α antibody was used as a positive control at doses known to provide optimal benefit.

Studies using two well known models of inflammatory bowel diseases, the DSS and the T-cell transfer model, demonstrated that systemically delivered TLR3 antibody antagonists reached the gut mucosa and reduced gastrointestinal tract inflammation induced through two

different pathogenic mechanisms. Thus, TLR3 antagonists may be beneficial for the treatment of inflammatory bowel diseases, including anti-TNF-α-refractory cases, and other immune-mediated pathologies in the gastrointestinal tract.

Example 12

TLR3 antibody antagonists protect from collagen-induced arthritis

Model

The collagen-induced arthritis (CIA) model was used as a model of rheumatoid arthritis.

Male B10RIII mice (6-8 weeks old, Jackson Labs) were divided into groups of 15 per group (arthritis groups) or 4 per group (control mice). Arthritis groups were anesthetized with Isoflurane and given injections of Type II collagen (Elastin Products) and Freund's complete adjuvant supplemented with M. tuberculosis (Difco) on days 0 and 15. On day 12, mice with developing type II collagen arthritis were randomized by body weight into treatment groups and were dosed subcutaneously (SC) on days 12, 17, and 22 (d12, d17, 2d2) with mAb 5429 (25 mg/kg), the negative control antibody CVAM (a recombinant mAb of no known specificity in the mouse) (5 mg/kg) or anti-TNF-α antibody (5 mg/kg, positive control). In addition, control groups of mice were treated with vehicle (PBS) or dexamethasone (0.5 mg/kg, Dex, reference compound) subcutaneously (SC) daily (QD) on days 12-25. Animals were observed daily from days 12 through 26. Fore and Hind paws were evaluated by a clinical scoring system (shown below). Animals were euthanized on study day 26 and histopathology was assessed in a blinded fashion (scoring system described below). Efficacy evaluation was based on animal body weights, and clinical arthritis scores. All animals survived to study termination.

Clinical scoring criteria for fore and hind paws

0 - normal

1 - hind or fore paw joint affected or minimal diffuse erythema and swelling

2 - hind or fore paw joints affected or mild diffuse erythema and swelling

3 - hind or fore paw joints affected or moderate diffuse erythema and swelling

4 - marked diffuse erythema and swelling, or =4 digit joints affected)

5 - severe diffuse erythema and severe swelling entire paw, unable to flex digits)

Histopathologic scoring methods for mouse joints with Type II collagen arthritis

When scoring paws or ankles from mice with lesions of type II collagen arthritis, severity of changes as well as number of individual joints affected were considered. When only 1-3 joints of the paws or ankles out of a possibility of numerous metacarpal/metatarsal/digit or tarsal/tibiotarsal joints were affected, an arbitrary assignment of a maximum score of 1, 2 or 3 for parameters below was given depending on severity of changes. If more than 2 joints were involved, the criteria below were applied to the most severely affected/majority of joints.

Clinical data for paw scores were analyzed using AUC for days 1-15, and % inhibition from controls were calculated.

Inflammation

0 - normal

1 - minimal infiltration of inflammatory cells in synovium and periarticular tissue of affected joints

2 - mild infiltration, if paws, restricted to affected joints

3 - moderate infiltration with moderate edema, if paws, restricted to affected joints

4 - marked infiltration affecting most areas with marked edema

5 - severe diffuse infiltration with severe edema

Pannus

0 - normal

1 - minimal infiltration of pannus in cartilage and subchondral bone

2 - mild infiltration with marginal zone destruction of hard tissue in affected joints

3 - moderate infiltration with moderate hard tissue destruction in affected joints

4 - marked infiltration with marked destruction of joint architecture, most joints

5 - severe infiltration associated with total or near total destruction of joint architecture, affects all joints

Cartilage Damage

0 - normal

1 - minimal to mild loss of toluidine blue staining with no obvious chondrocyte loss or collagen disruption in affected joints

2 – mild loss of toluidine blue staining with focal mild (superficial) chondrocyte loss and/or collagen disruption in affected joints

3 - moderate loss of toluidine blue staining with multifocal moderate (depth to middle zone) chondrocyte loss and/or collagen disruption in affected joints

4 - marked loss of toluidine blue staining with multifocal marked (depth to deep zone) chondrocyte loss and/or collagen disruption in most joints

5 - severe diffuse loss of toluidine blue staining with multifocal severe (depth to tide mark) chondrocyte loss and/or collagen disruption in all joints

Bone Resorption

0 - normal

1 - minimal with small areas of resorption, not readily apparent on low magnification, rare osteoclasts in affected joints

2 - mild with more numerous areas of, not readily apparent on low magnification, osteoclasts more numerous in affected joints

3 - moderate with obvious resorption of medullary trabecular and cortical bone without full thickness defects in cortex, loss of some medullary trabeculae, lesion apparent on low magnification, osteoclasts more numerous in affected joints

4 - marked with full thickness defects in cortical bone, often with distortion of profile of remaining cortical surface, marked loss of medullary bone, numerous osteoclasts, affects most joints

5 - severe with full thickness defects in cortical bone and destruction of joint architecture of all joints

Results

Dexamethasone (Dex) and anti-mouse TNF-α antibody was used as a positive control, PBS was used as vehicle control, and CVAM was used as a negative control antibody. All treatments were initiated on day 12 of the study, during the development of joint disease. Disease incidence for vehicle-treated disease control animals was 100% by study day 22. Negative control groups treated with vehicle or CVAM antibody had the highest clinical scores. Significantly reduced clinical scores were observed for the groups treated with Dex ($p<0.05$ for d18-d26), 5 mg/kg anti-TNF-α antibody ($p<0.05$ for d18-26), or 25 mg/kg mAb 5429 ($p<0.05$ for d18-d23 and d25-d26) (Figure 16). Clinical arthritis scores expressed as area under the curve (AUC) were significantly reduced by treatment with 25 mg/kg mAb 5429 (43% reduction), 5 mg/kg

anti-TNF-α antibody (52%), or Dex (69%) as compared to vehicle controls. Figure 17 shows means and standard deviations for AUC for each group.

Histopathological effects of the treatments were also assessed. Paw bone resorption was significantly decreased by treatment with 25 mg/kg mAb 5429 (47% decrease) as compared to vehicle controls. Positive control mice treated with 5 mg/kg anti-TNF-α antibody had significantly decreased paw inflammation (33%), cartilage damage (38%), and summed paw scores (37%). Treatment with Dex significantly reduced all paw histopathology parameters (73% reduction of summed scores).

These data demonstrate that TLR3 antibody antagonists improve clinical and histopathological disease symptoms in the CIA model, and suggest the use of TLR3 antagonists for treatment of rheumatoid arthritis.

Example 14

TLR3 antibody antagonists protect from acute lethal viral infections

Model

An influenza A virus challenge model was used as a model of acute lethal viral infection.

On Day -1, 4, 8, and 12, female C57BL/6 mice (12 weeks old) or female TLR3KO mice (C57BL/6 background; 12 weeks old, ACE Animals, inc., 15 mice per group) were dosed subcutaneously 20 mg/kg mAb 5429, or PBS alone. On day 0, the mice were anesthetized by isoflurane and were intranasally administered Influenza A/PR/8/34 virus (ATCC, Rockland, MD, Lot no. 218171), in 25 µl PBS (equivalent to $10^{5.55}$ CEID50). Animals were observed two times a day for changes in body weight and survival over the period of 14 days. A clinical scoring system was used to evaluate the level of disease progression and subtle improvements in response to Influenza A virus treatment.

Clinical scores

0 - normal, alert and reactive, no visible signs of illness

1 - ruffled coat, with or without slightly reduced ambulation

2 - ruffled coat, hunched posture when walking, reluctant ambulation, labored breathing

3 - ruffled coat, labored breathing, ataxia, tremor

4 - ruffled coat, inability to ambulate with gentle prodding, unconsciousness, feels cold to the touch

5 - found dead

Results

Survival, daily clinical scores, and changes in body weight were evaluated in the study. Both influenza A infected WT mice administered mAb 5429 (20 mg/kg) and influenza A infected TLR3KO not receiveing mAb 5429 demonstrated a statistically significant increase in survival ($p<0.001$ and $p<0.01$, respectively) when compared to C57BL/6 mice inoculated with the Influenza virus, indicating that antagonism or deficiency of TLR3 can prevent influenza - induced mortality (Figure 18). Clinical scores were significantly reduced in the group receiving 20 mg/kg mAb 5429, as well as in the TLR3KO group (Figure 19). The body weight of the mice was observed over a period of 14 days after influenza virus administration. Body weight decreased steadily in C57BL/6 mice dosed with Influenza A virus. However, both the C57BL/6 mice dosed with 20 mg/kg mAb 5429 and the TLR3KO mice demonstrated significantly greater body weight relative to the WT C57BL/6 mice inoculated with Influenza virus (Figure 20). These results demonstrated that TLR3 antibody antagonists reduced clinical symptoms and mortality in an acute lethal influenza viral infection model, and suggested that TLR3 antagonists may provide protection for humans in acute infectious states.

Example 15

TLR3 antibody antagonists improve hyperglycemia and reduce plasma insulin

Model

The Diet-induced obesity (DIO) model was used as a model of hyperglycemia and insulin resistance, and obesity.

C57BL/6 WT animals (about 3 weeks old, Jackson Labs) and TLR3KO animals (C57BL/6 background; about 3 weeks old, Ace Animals, Inc.) were maintained on a high fat diet for 12 to 16 weeks. Both TLR3KO and WT C57BL/6 mice were fed either with normal chow or high-fat diet (Purina TestDiet cat. no. 58126) consisting of 60.9% kcal fat and 20.8% kcal carbohydrates. Mice were maintained on a 12:12-h light-dark cycle, with water and food ad libitum. The weight of each mouse within each group was measured weekly. mAb 5429 was given intraperitoneally twice a week for the first week followed by once a week dosing for total of 7 weeks. Fasting retro-orbital blood serum samples were used for insulin measurements at the time points indicated. Glucose tolerance tests were performed by i.p administration of glucose at 1.0 mg/g body weight after overnight fast at week 7. In addition, fasting insulin and glucose levels were measured.

HOMA-IR was determined from the equation based on the levels of fasting glucose and insulin levels (12) using following equation: HOMA-IR = ((fasting glucose (mmol/l) x fasting insulin (mU/l))/ 22.5 (Wallace et al., Diabetes Care 27:1487-1495,, 2004). Fasting blood glucose (BG) was determined using glucose oxidase assay. Fasting insulin levels were determined using the insulin rat/mouse ELISA kit (Crystal Chem, cat. No. 90060).

Results

After 12-16 weeks on high fat diet, the WT DIO aimals were hyperglycemic and hyperinsulinemic. Glucose tolerance was improved in the WT DIO animals but not in the TLR3KO DIO animals upon treatment with mAb 5429. Significantly reduced blood glucose levels were observed in mAb 5429 treated animals post glucose challenge at 60, 90, 120, and 180 min when compared to control (PBS only) (Figure 21A). About 21% reduction in AUC was observed in the mAb 5429 treated WT DIO animals when compared to the WT DIO mice not receiveing the mAb. Fasting insulin levels were also reduced in the WT DIO animals treated with mAb 5429 (Figure 22). TLR3KO DIO animals showed no improvement in fasting insulin upon mAb 5429 treatment. Homeostatic model assessment (HOMA) analysis indicated improved insulin sensitivity in the WT DIO animals treated with mAb 5429, but not in the TLR3KO DIO animals. The HOMA-IR values were 14.0±9.8, 8.7±4.9, 9.0±3.0 for WT DIO, 5 mg/kg of WT DIO mAb 5429, and 20 mg/kg of WT DIO mAb 5429 animals, respectively. No effect was observed in TLR3KO DIO animals.

The study demonstrated that TLR3 antibody antagonists improved insulin resistance and reduced fasting glucose in the DIO model without weight loss, suggesting that TLR3 antagonists may be beneficial for the treatment of hyperglycemia, insulin resistance, and type II diabetes.

Example 16

TLR3 antibody antagonists protect from bacteria and virus-induced inflammatory responses

Reagents

Nontypeable *Haemophilus influenza* (NTHi) strains 35, isolated from a COPD patient with bacterial exacerbations, was obtained from Dr. T. F. Murphy (Buffalo VA Medical Center, Buffalo, NY). Human rhinovirus 16 was obtained from

the American Type Culture Collection (ATCC) with TCID(50)=2.8 x 10^7/ml.

NTHi stimulation assays

NHBE cells (Lonza, Wakersville, MD) were seeded in Microtest 96-well tissue culture plates (BD Biosciences, Bedford, MA) at 1 x 10^5/well. NTHi grown on agar plates for 16-20 hr were resuspended in growth medium at ~2 x 10^8 cfu/ml, treated with 100 µg/ml gentamycin for 30 min. and added at ~2 x 10^7/well to 96-well plates containing NHBEs. After 3 hours, supernatants were removed and replaced with fresh growth medium with or without antibodies (0.08 to 50 µg/ml final concentration). After additional 24 hr incubation, presence of cytokines and chemokines in cell supernatants was assayed in triplicate with a Cytokine 25-plex AB bead kit, Human (including IL-1β, IL-1RA, IL-2, IL-2R, IL-4, IL-5, IL-6, IL-7, IL-8, IL-10, IL12p40p70, IL-13, IL-15, IL-17, TNF-α, IFN-α, IFN-γ, GM-CSF, MIP-1α, MIP-1β, IP-10, MIG, Eotaxin, RANTES and MCP-1) (Life Technologies, Carslbad, CA) in the Luminex 100IS multiplex fluorescence analyzer and reader system (Luminex Corporation, Austin, TX).

Rhinovirus stimulation assays

NHBE cells were seeded in Microtest 96-well tissue culture plates (BD Biosciences, Bedford, MA) at 1 x 10^5 cells/well. The next day, antibodies (0.08 to 50 µg/ml final concentration) were added to NHBE or BEAS-2B cells and incubated for 1 hr, followed by addition of 10 µl/well of rhinovirus. After additional 24 hr incubation, presence of cytokines and chemokines in cell supernatants was assayed by luminex assays as described above.

Results

mAb 15EVQ inhibited NTHi induced IP-10/CXCL10 and RANTES/CCL5 production in a dose-dependent manner, while the control antibody, human IgG4 (Sigma, St. Louis, MO), showed

no inhibitory effect on NTHi stimulation (Figure 23A). mAb 15EVQ also inhibited rhinovirus induced CXCL10/IP-10 and CCL5/RANTES production (Figure 23B).

Example 17

TLR3 antibody antagonists suppress inflammatory responses in astroctyes

Methods

Normal human astrocytes from 2 donors (Lonza, Walkersville, MD) were plated in a 24 well plate at 75,000 cells/well and allowed to attach overnight. The next day, the astrocytes were treated with 200 ng/ml poly(I:C) and/or 10 μg/ml mAb 18 for 24 hours. Cytokines were measured by Luminex.

Results

Poly(I:C)- induced production of IL-6, IL-8, IL-12, IFN-α, IFN-γ, CXCL9/MIG, CCL3/MIP-1a, CCL4, CCL5/RANTES and CXCL10/IP-10 were inhibited by mAb 18, as shown in Table 10.

Table 10.

Donor 1	IL-6	IL-8	IL-12	IFN-α	IFN-γ
untreated	876.0 ± 36.8	539.7 ± 32. 6	16.6 ± 0.5	28.8 ± 1.5	12.3 ± 0.3
mAb 18	1011.9 ± 57.4	1401.9 ± 49.7	17.1 ± 0.5	31.6 ± 0.7	10.4 ± 0.2
Poly(I:C)	ol*	ol	30.3 ± 1.5	47.1 ± 3.1	35.9 ± 1.0
Poly(I:C) + mAb 18	2225.0 ± 108.1	6104.4 ± 259.9	16.8 + 0.9	30.5 ± 1.6	11.7 ± 0.6
Donor 2					
untreated	729.1 ± 7.1	248.2 ± 4.7	14 ± 0.5	19.5 ± 1.8	10.5 ± 0.5
mAb 18	779.0 ± 9.8	1132.6 ± 30.6	14.3 ± 0.6	20.8 ± 1.9	10.5 ± 0.1
Poly(I:C)	ol	ol	25.5 ± 0.4	36.3 ± 1.9	30.8 ± 0.9
Poly(I:C) + mAb 18	3393.3 ± 107.5	8660.4 ± 354.3	16.2 ± 0.3	24.7 ± 1.2	12.6 ± 0.3

Donor 1	CXCL9/MIG	CCL3/MIP-1a	CCL4	CCL5/RANTES	CXCL10/IP-10
untreated	12.6 ± 0.7	21 ± 0.9	14.8 ± 0.7	bl**	bl
mAb 18	14.8 ± 1.7	19.5 ± 1.5	14.8 ± 1.1	bl	bl
Poly(I:C)	78.3 ± 4.8	1569.3 ± 36.9	159.7 ± 12.7	788.2 ± 94.9	461.4 ± 10.3
Poly(I:C) + mAb 18	18.5 ± 1.6	31.2 ± 1.9	13.2 ± 0.9	bl	6.9 ± 0.5
Donor 2					
untreated	9.9 ± 1.6	12.3 ± 1.7	11.3 ± 0.3	bl	bl
mAb 18	8.9 ± 0.7	13.2 ± 1.5	11.1 ± 0.7	bl	bl
Poly(I:C)	62 ± 3.8	1552.9 ± 41.1	140.7 ± 4.8	546.8 ± 21.7	533.2 ± 15
Poly(I:C) + mAb 18	18.3 ± 2.7	66.6 ± 3.8	12.1 ± 0.8	bl	29.1 ± 6.2

*ol: over detection level

**bl: below detection level

Example 18

TLR3 antibody antagonists suppress inflammatory responses in endothelial cells

Methods

HUVEC cells (Lonza, Walkersville, MD) were cultured in serum-containing growth medium recommended by Lonza. Cells were resuspended in serum-free media (Lonza, Walkersville, MD), plated in 96-well plates at $3x10^5$ cells/ml, and incubated at 37°C, 5%CO2 for 24 hrs. Poly(I:C) (GE Healthcare, Piscataway, NJ) was added at increasing concentrations (1.5 to 100 μg/ml) and incubated for another 24 hours at 37°C. For cytokine inhibition assays, mAb 15EVQ was added to the cells at various concentrations (0 - 50 μg/ml) and incubated for 30

min, after which 20 μg/ml poly(I:C) was added for 24 hours. Cell supernatants were collected and cytokine levels were measured using the human cytokine 30-plex kit and Luminex MAP technology (Invitrogen Corp., Carslbad, CA). To measure sICAM-1 expession, the HUVEC cells were treated with 20 μg/ml poly(I:C) and various concentrations of mAb 15EVQ (0.8 - 50 μg/ml). The cell supernatants were analyzed for sICAM-1 expression by ELISA (R&D systems). Cell viability was measured using the CellTiterGlo kit (Promega, Madison, WI).

Results

HUVEC cells produced the following cytokines in response to poly(I:C): IL-1RA, IL-2, IL-2R, IL-6, IL-7, CXCL8/IL-8, IL-12 (p40/p70), IL-15, IL-17, TNF-α, IFN-α, IFN-γ, GM-CSF, CCL3/MIP-1α, CCL4/MIP-1β, CXCL10/IP-10, CCL5/RANTES, CCL2/MCP-1, VEGF, G-CSF, FGF-basic, and HGF (Table 11). mAb 15EVQ dose-dependently reduced levels of all cytokines induced by poly(I:C) (Table 12). The ability of mAb 15EVQ to reduce poly(I:C)-induced production of TNF-α, CCL2/MCP-1, CCL5/RANTES, and CXCL10/IP-10 suggested that inhibiton of TLR3-mediated activities may protect against leukocyte and T cell infiltration that can lead to atherosclerosis. Also, inhibition of VEGF by mAb 15EVQ suggested a potential benefit of TLR3 blockade in pathologies mediated by VEGF including angiogenesis in a variety of cancers and ocular diseases such as age-related macular degeneration.

TNF-α and IFN-γ function in leukocyte recruitment and increase the expression of adhesion molecules on the activated endothelium (Doukas *et al.*, Am. J. Pathol. 145:137-47, 1994; Pober *et al.*, Am. J. Pathol. 133:426-33, 1988). CCL2/MCP-1, CCL5/RANTES, and CXCL10/IP-10 have been implicated in monocyte and T cell recruitment and contribute to the development of atherosclerosis (Lundgerg *et al.*, Clin. Immunol. 2009). The generation of VEGF by endothelial cells has been linked to abnormal tissue growth or tumors in a

variety of cancers during angiogenesis (Livengood *et al.*, Cell. Immunol. 249:55-62, 2007).

Table 11.

Poly(I:C) μg/ml	IL-6	CXCL8/IL-8	CCL2/MCP-1
10	848.8 + 50.9	12876.0 + 2314.0	11813.4 + 1420.9
5	751.3 + 2.1	11363.7 + 108.2	11365.7 + 113.1
2.5	607.1 + 91.6	10961.5 + 2200.7	11607.3 + 2155.7
1.25	419.2 + 178.4	9631.5 + 3675.8	11690.9 + 3189.9
0.63	263.8 + 81.4	6231.9 + 1568.0	9075.6 + 1152.2
0.31	183.5 + 168.3	5257.9 + 1855.0	8106.8 + 1193.1
0.16	111.9 + 72.5	4057.6 + 1127.4	6619.8 + 1728.2
no poly(I:C)	0.00	1286.6 + 300.8	1360.1 + 245.4

Poly(I:C) μg/ml	IL-2R	IL-15	IL-17
100	784.4 + 45.4	61.3 + 12.5	43.8 + 5.3
50	718.6 + 56.8	61.3 + 12.5	47.6 + 0
25	735.7 + 23.4	56.7 + 18.9	58.3 + 4.9
12.5	650.5 + 29.8	38.8 + 6.5	39.8 + 10.9
6.25	643.4 + 39.9	34.2 + 0	32.1 + 0
3.13	681.8 + 24.3	38.8 + 6.5	43.8 + 5.3
1.56	578.6 + 10.5	29.4 + 6.7	36.1 + 5.6
no poly(I:C)	0.0	0.0	0.0

Poly(I:C) μg/ml	IFNα	CXCL10/IP-10	CCL4/MIP-1β
100	50.7 + 0	3803.1 + 185.5	234.5 + 19.7
50	44.9 + 1.7	2235.9 + 184.6	291.6 + 41.8
25	46.1 + 0	2403.0 + 271.9	278.7 + 4.7
12.5	41.2 + 3.5	2185.4 + 64.9	243.8 + 63.4
6.25	36.1 + 0	2100.0 + 288.1	201.9 + 46.2
3.13	40.0 + 1.8	3553.2 + 197.1	191.5 + 20.8
1.56	42.5 + 1.7	2064.3 + 242.1	165.3 + 16.3
no poly(I:C)	0.0	0.0	0.0

Poly(I:C) μg/ml	RANTES	TNFα	VEGF
100	6266.9 + 1708.7	12.8 + 3.2	581.1 + 181.4
50	2919.7 + 119.4	11.5 + 3.2	637.9 + 47.7
25	2805.1 + 176.7	9.8 + 2.8	700.3 + 62.5
12.5	2598.6 + 68.6	7.3 + 0.9	513.2 + 73.5
6.25	2449.2 + 830.6	6.9 + 1.4	440.4 + 29.5
3.13	3117.1 + 795.7	7.3 + 0.9	393.9 + 40.2
1.56	2481.0 + 719.3	6.0 + 1.8	358.4 + 74.8
no poly(I:C)	4.9 + 4.5	1.9 + 0.4	32.1 + 8.8

concentrations shown as pg/ml

Soluble Intercellular Adhesion Molecule 1 (sICAM-1) is generated by proteolytic cleavage and is a marker for endothelial cell activation. ICAM-1 plays a key role in leukocyte migration and activation and is upregulated on endothelial cells and epithelial cells during inflammation where it mediates adhesion to leukocytes via integrin molecules LFA-1 and Mac-1. Poly(I:C) activated the endothelial cells to upregulate sICAM-1 expression and the uregulation was reduced by treatment with mAb 15EVQ (Figure 24A).

Table 12.

mAb 15 (μg/ml)	50.00	10.00	2.00	0.40	0.08	0.016	0.003	0
PIC	+	+	+	+	+	+	+	-
IL-6	177.8 ± 5.6 *	214.6 + 3.6 *	359.2 + 57.6 *	727.2 + 50.5 *	10000 + 0	10000 + 0	10000 + 0	10000 + 0
CXCL8/IL-8	1040.7 ± 185.9	1765.9 + 97.1	6460.3 + 3684.4	57349.5 + 6293.4	72422.8 + 88279.2	47047.5 + 52393.1	76066.5 + 11354.1	96478.0 + 122298.4
CCL2/MCP-1	1187.7 ± 165.4 *	1955.4 + 72.7 *	9054.4 + 4110.9 *	20000 + 0.0	20000 + 0.0	20000 + 0.0	20000 + 0.0	20000 + 0.0
IL-2R	25.0 ± 35.3 *	0.0 + 0.0 *	312.3 + 137.6 *	521.5 + 5.5	664.7 + 9.8	661.2 + 14.8	698.4 + 57.6	654.2 + 14.8
IL-15	0.0 ± 0.0 *	0.0 + 0.0 *	0.0 + 0.0 *	4.1 + 0.0 *	38.8 + 6.5	43.4 + 0.0	38.8 + 6.5	43.4 + 0.0
IL-17	1.3 ± 1.8 *	11.8 + 16.8	11.8 + 16.8	27.9 + 6.0	47.4 + 10.4	54.3 + 20.2	40.0 + 0.0	51.2 + 5.1
IFNα	0.9 ± 1.3 *	0.9 + 1.3 *	19.0 + 7.7 *	36.1 + 0.0	44.9 + 1.7	41.2 + 3.5	47.3 + 1.7	40.0 + 1.8
CXCL10/IP-10	0.0 ± 0.0 *	58.1 + 2.6 *	633.0 + 471.6 *	1441.4 + 97.1	3023.8 + 166.1	2107.5 + 372.6	2346.4 + 226.1	2157.4 + 282.7
CCL4/MIP-1β	0.0 ± 0.0 *	0.0 + 0.0 *	2.9 + 4.1 *	62.1 + 7.2 *	176.6 + 21.3 *	227.5 + 19.9	248.3 + 19.4	281.7 + 37.5
RANTES	3.0 ± 0.0 *	15.4 + 4.5 *	201.1 + 169.1 *	952.4 + 41.1 *	2454.4 + 98.5 *	2698.1 + 88.6 *	2624.4 + 129.8 *	3459.7 + 181.8
TNFα	1.9 ± 0.4 *	1.6 + 0.0 *	2.2 + 0.0 *	3.4 + 0.0	6.3 + 0.5	8.5 + 0.0	7.6 + 1.4	6.9 + 2.3
VEGF	87.2 ± 8.7 *	28.6 + 8.7 *	88.3 + 52.1 *	156.1 + 6.4 *	479.6 + 14.1	544.6 + 8.3	533.5 + 70.2	607.3 + 29.9
	* Indicates significant p-values (less than 0.05) comparing mAb15 concentration vs. poly(I:C) alone Values are mean (pg/ml) ± SEM							

This suggested that TLR3 antibody antagonists can inhibit leukocyte trafficking and thus tissue damage caused by the influx of inflammatory cells.

For viability assays, HUVECs were cultured, plated and stimulated with poly(I:C) as described above. mAb 15EVQ dose-dependently restored poly(I:C)-induced reduction in HUVEC cell viability (Figure 24B).

Down-modulation of endothelial cell activation can suppress excessive immune cell infiltration and reduce tissue damage caused by cytokines that are increased during inflammatory conditions. Inflammation and overexpression of cytokines and adhesion molecules on endothelial cells are key contributors to developing atherosclerosis and hypertension. These data provide rationale for exploring the potential benefit of TLR3 antagonists for use in diseases of the blood vessels including vasculitides, and those featuring endothelial dysfunction. Another disease that is affected by inflammation and overexpressed cytokines is Kaposi's sarcoma (KS) that is common in immunosuppressed and HIV infected individuals and is caused by Kaposi's sarcoma herpes virus (KSHV). VEGF and cytokine production contribute to the survival of KS cells (Livengood *et al.*, Cell Immunol. 249:55-62, 2007). TLR3 antagonists could be beneficial at reducing

angiogenic risks associated with KS and other tumors and at preventing cell viability loss and protecting endothelial barrier integrity to prevent vascular leakage, a potentially serious condition associated with organ failure and life-threatening inflammatory conditions such as sepsis. TLR3 antagonism may also be beneficial in viral infections involving endothelial cell pathology such as the viral hemorrhagic fevers caused by members of the families flaviviridae (e.g. Dengue, yellow fever), filoviridae (Ebola, Marburg), bunyaviridae (e.g. Hantavirus, Nairovirus, Phlebovirus), and arenaviridae (e.g. Lujo, Lassa, Argentine, Bolivian, Venezuelan hemorrhagic fevers (Sihibamiya *et al.*, Blood 113:714-722, 2009).

Example 20
Cross-reactivity of TLR3 antibody antagonists with cynomolgus and murine TLR3

Activity against cynomolgus or murine TLR3 were assessed using the ISRE reporter gene assay as described in Example 2. The cynomolgus (SEQ ID NO: 217) and murine TLR3 cDNAs (SEQ ID NO: 161) were amplified from whole blood and cloned into the pCEP4 vector (Clontech), and expressed as described above. mAb 15EVQ had IC50s of 4.18 μg/ml and 1.74 μg/ml in the cyno NF-κB and ISRE assays, respectively, compared to IC50s of 0.44 and 0.65 μg/ml in the human TLR3 NF-kB and ISRE assays, respectively. Isotype control antibodies had no effect in these assays.

Example 21
Therapeutic dosing of TLR3 antibody antagonists protect from acute lethal viral infections

Example 14 descirbes prophylactic treatment (dosed on days -1, 4, 8, and 12) with TLR3 antibody antagonists against influenza A infection. This example demonstrates that therapeutic dosing of TLR3 antibody antagonists (day 3 after

influenza A infection after the onset of clinical symptoms) are efficacious in enhancing survival.

Model

An influenza A virus challenge model was used as a model of acute lethal viral infection as described in Example 14, except that dosing of animals with mAb 5249 was done 3 days post infection with influenza A, and the animals dosed were 8 weeks old. Anti-mouse IgG1 isotype control mAb was from BioLegend. The animals were dosed days 3, 7 and 11 post-infections with influenza A.

Survival, daily clinical scores, and changes in body weight were evaluated in the study. Both the C57Bl/6 mice administered mAb 5249 and the TLR3KO mice demonstrated a statistically significant increase in survival ($p < 0.028$ and $p < 0.001$, respectively) relative to the C57BL/6 mice inoculated with the anti-mouse IgG1 isotype control mAb and Influenza virus (Figure 25). The clinical scores were reduced (Figure 26) and the body weights incrased (Figure 27) in the C57BL/6 mice dosed with mAb 5249 and in the TLR3KO animals when compared with C57BL/6 mice dosed with anti-mouse IgG1 isotype control mAb and Influenza A. These results demonstrated that TLR3 antibody antagonists reduced clinical symptoms and mortality in an acute lethal influenza viral infection model, and suggested that TLR3 antagonists may provide protection for humans in acute infectious states.

Example 22

Epitopes and paratopes of TLR3 antibody antagonists by X-ray crystallography

The human TLR3 extracellular domain was crystallized in complex with Fabs of mAb 15EVQ, mAb 12QVQ/QSV and mAb c1068.

Methods

Expression and purification of proteins

The expression and purification of the TLR3 ECD (amino acids 1-703 of SEQ ID NO: 2) the three Fabs were as described above.

Preparation of the TLR3 ECD-three Fab quaternary complex

4 mg of human TLR3 ECD was mixed with 2.4 mg of each Fab and incubated at 4 °C for 3.5 h, corresponding to a molar ratio of 1 TLR3 ECD:1.1 Fab. The complex was purified by anion exchange chromatography on a MonoQ 5/50 GL column (GE Healthcare, Piscataway, NJ), equilibrated with 20 mM Tris pH 8.5, 10% glycerol (buffer A) and eluted with 20 mM Tris pH 8.5, 10% glycerol, 1 M NaCl (buffer B). Approximately 2.48 mg of complex in 1.74 mL was diluted to 10 mL with buffer A, loaded onto the column at 1 mL/min and eluted with a linear gradient of 0-40% B over 40 column volumes. Five consecutive purification runs were performed. Fractions from peak 1 were pooled, concentrated with an Amicon-15 mL Ultra-30000 MWCO and a Microcon 30000 MWCO to 14.49 mg/mL in 20 mM Tris pH 8.5, 27 mM NaCl, 10 % glycerol (Extinction coefficient: A_{280} (1 mg/mL) = 1.31).

Crystallization

Automated crystallization screening was performed using the Oryx4 automatic protein crystallization robot (Douglas Instruments) dispensing equal volumes of protein and reservoir solution in a sitting drop format using Corning plate 3550 (Corning Inc., Acton, MA). Initial screening was with Hampton Crystal Screen HT (HR2-130, Hampton Research, Aliso Viejo, CA). Small crystals from several conditions were used to generate seeds, which were then used in Microseed-Matrix Screening (MMS). Several rounds of refinement were performed that were based on conditions from the initial screening that gave small crystals. Reservoir conditions used for MMS were based on those that gave small crystals after refinement: 18-28% polyethylene glycol (PEG) 3350, 1M LiCl, pH4.5 and 2.0-2.9 M $(NH_4)_2SO_4$, 5% PEG400, pH 4.5, and explored pH and different additives. MMS crystallization screening was performed using the Oryx4 automatic protein crystallization robot (Douglas Instruments) by dispensing components in the following volume ratio: 1

protein solution: 0.25 seed stock: 0.75 reservoir solution. Crystals diffracting to ~10-Å resolution grew from 0.1 M Na acetate pH 4.5, 2.9 M $(NH_4)_2SO_4$, 5% methyl-pentane-diol (MPD) and 0.1 M Na acetate pH 4.5, 26% PEG3350, 1 M LiCl.

In an effort to improve the resolution of the crystals, MMS with the above conditions was combined with additive screening using selected components of the Hampton Additive Screen HR2-428 (Hampton Research, Aliso Viejo, CA) in the following volume ratio: 1 protein solution: 0.125 seed stock: 0.2 additive solution: 0.675 reservoir solution. X-ray quality crystals of the TLR3 ECD complexed with the Fabs, which diffract to ~ 5-Å resolution, were obtained after applying a combination of MMS and Additive screening from a solution containing 0.1 M Na acetate pH 4.5, 28% PEG 3350, 1 M LiCl, and 30 mM Gly-Gly-Gly.

X-ray data collection of TLR3 ECD quaternary complex

For X-ray data collection, a crystal (size ~1.0 x 0.5 x 0.1 mm^3) was soaked for a few seconds in a synthetic mother liquor (0.1 M Na acetate, pH 4.5, 28% PEG 3350, 1 M LiCl, 16% glycerol), and flash frozen in the stream of nitrogen at 100 K. X-ray diffraction data were collected and processed using a Rigaku MicroMax™-007HF microfocus X-ray generator equipped with an Osmic™ VariMax™ confocal optics, Saturn 944 CCD detector, and an X-stream™ 2000 cryocooling system (Rigaku, Woodlands, TX). Diffraction intensities were detected over a 250° crystal rotation with the exposure time of 1 min per half-degree image to the maximum resolution of 5 Å. The X-ray data were processed with the program D*TREK (Pflugrath, Acta Crystallographica Section D, 55:1718-1725, 1999). The crystal belongs to the monoclinic space group C2 with unit cell parameters: a = 214.90 Å, b = 142.08 Å, c = 125.04 Å, and β = 103.17°. The asymmetric unit contains 1 molecule of the complex. The X-ray data statistics are given in Table 13.

Table 13.

Data Collection		
Space group	C2	
Unit cell axes (Å)	214.90, 142.08, 125.04	
Unit cell angles (°)	90, 103.17, 90	
Resolution (Å)	30-5.0	(5.18-5.00)
No. unique reflections	15,877	(1589)
Completeness (%)	99.8	(99.6)
Redundancy	5.2	(4.9)
R_{merge} [a]	0.121	(0.312)
$\langle I/\sigma \rangle$	7.1	(2.9)
Structure refinement		
Resolution (Å)	29.4-5.0	
R_{cryst}/R_{free}(%)[b]	26.8/30.0	
No. of reflections		
Working set	15,792	
Test set (5% data)	788	
Rmsd from ideal values		
Bond length (Å)	0.007	
Bond angels (°)	0.744	
Number of protein atoms	15,442	
Ramachandran plot [c]		
Favored regions (%)	93.1	
Allowed (%)	98.8	
Disallowed (%)	1.2	

Structure Determination

The crystal structure of the TLR3 ECD - Fab 15EVQ - Fab 12QVQ/QSV - Fab c1068 was determined by molecular replacement using Phaser (Read, Acta Crystallogr. D. Biol. Crystallogr. 57:1373-1382, 2001). The search models were TLR3 ECD (Protein DataBank (PDB) structure ID 1ziw with all glycans removed, Choe *et al.*, Science 309:581-585, 2005) and the high resolution crystal structures of the three Fabs determined (See Table 13 for a summary of the crystal data and refinement statistics for these Fab structures). The elbow

angle of Fab 12QVQ/QSV was found to deviate significantly from that in the free form. A series of Fab 12QVQ/QSV models were generated by adjusting the elbow angle at ~5° intervals, one of which was found to agree well with the electron density. The structure refinement was carried with PHENIX (Adams *et al.*, J. Synchrotron Radiat. 11:53-55, 2004). The structure was refined as rigid body domains (each V or C domain) for the Fabs and 13 rigid segments (Definitions used in the refinement: 30-60,61-108,109-156,157-206,207-257,258-307,308-363,364-415,416-464,465-514,515-570,571-618,619-687) for the TLR3 ECD with one B factor for each Fab rigid body and a single B for the entire TLR3 ECD.

Translation/ Libration/ Screw (TLS) refinement was introduced for each of the Fab rigid bodies and TLR3 ECD was divided into 2 TLS segments at residue 330 of SEQ ID NO: 2. Glycan density was visible for 10 of the 15 N-glycosylation sites. Carbohydrate models from the crystal structure of the human TLR3 extracellular domain (Choe *et al.*, Science 309:581-585, 2005, PDB structure ID: 1ziw) were then added. The density for a short missing segment in TLR3 ECD (residues 337-342 of SEQ ID NO: 2) was visible after rigid body refinement, and it was filled in with the corresponding segment from the TLR3 extracellular structure 2a0z (Bell *et al.*, Proc. Natl. Acad. Sci. (USA) 102:10976-10980, 2005, PDB strucutre ID: 2a0z) . The C-terminus of TLR3 ECD contained additional density that matches that of 2a0z. This segment (647-703 of SEQ ID NO: 2) was then replaced with (residues 647-687) of 2a0w. Thus, the TLR3 ECD model was a hybrid between the TLR3 sturctures 1ziw and 2a0z and refined as 13 rigid body segments (amino acid range: 30-60,61-108,109-156,157-206,207-257,258-307,308-363,364-415,416-464,465-514,515-570,571-618,619-687).

The LCDR3 of Fab 12QVQ/QSV apparently adopted different conformation from its free form. Multi-start simulated annealing was carried out with standard parameters in PHENIX. The models of this LCDR3 were visually inspected in the

electron density map and the "best-matching" conformation was grafted onto the original model. The refinement process was monitored by R_{free} against 5% of the reflections set aside prior to initiating the calculations. In the final round, one B factor for each residue was included. Model inspection and manual rebuilding of the elbow regions of the Fabs and side chains at the protein-protein interfaces were done using COOT (Emsley *et al.*, Acta Crystallogr. D. Biol. Crystallogr. 60:2126-32, 2004). The final R_{cryst} and R_{free} were 26.8% and 30.0%, respectively, for all 15,792 independent reflections to 5.0 Å. The refinement statistics are given in Tables 13 and 14.

Results

The molecular structure of the TLR3 ECD-three Fab quaternary complex

The overall molecular structure of the complex is shown in Figure 28. In the asymmetric unit there is one TLR3 ECD and one molecule of each Fab. The structural model for TLR3 ECD includes all residues from 30 to 687 of huTLR3 (SEQ ID NO: 2). For the three Fabs, all residues from their respective unbound forms were included except solvent ions and water molecules. The TLR3 ECD molecule is very similar to the previously reported structures in overall topology (rmsd of 0.79 Å for 1ziw, 613 Cα's, and 1.37 Å for 2a0z, 595 Cα's). The Fab structures are all identical to their respective unbound forms except for LCDR3 of Fab 12QVQ/QSV as described in Methods as well as the elbow regions and some side chains at TLR3 ECD/Fab interfaces.

Table 14.

Data collection

	Fab 12QVQ/QSV		Fab 15EVQ		Fab c1068	
Space group	$P2_1$		$P2_1$		$P2_1$	
Cell dimensions						
a, b, c (Å)	75.83, 80.35, 83.06		54.68, 74.74, 64.99		82.48, 136.94, 83.25	
α, β, γ (°)	90, 115.24, 90		90, 103.69, 90		90, 114.95, 90	
Resolution (Å)	70-2.5	(2.59-2.50)	49-2.2	(2.28-2.20)	50-1.9	(2.0-1.9)
Unique reflections	27,785	(1653)	24,439	(1859)	117,490	(5916)
Completeness (%)	88.5	(53)	94.2	(72.8)	89.3	(45.2)
Redundancy	4	(1.8)	5.2	(4.3)	3.2	(2)
R_{merge} [a]	0.164	(0.297)	0.088	(0.445)	0.065	(0.264)
<I/σ> (unaveraged)	2.9	(1.2)	3.8	(1.4)	5.7	(1.6)

Structure Refinement

Resolution (Å)	15-2.5 (2.56-2.50)	15-2.2 (2.26-2.20)	75.38–1.90 (1.94–1.90)
R_{cryst}/R_{free}(%) [b]	19.7/25.4 (30.8/40.8)	19.3/26.9 (24.6/31.1)	20.4/27.7 (39.8/51.1)
No. of reflections			
Working set	26,723	23,308	111,413
Test set	882	1,008	5,917
Number of atoms			
Proteins	7,046	3,705	13,421
Solvent (water, etc.)	486	333	1,779
RMSD bond lengths (Å)	0.012	0.013	0.023
RMSD bond angles (°)	1.6	1.5	2
Ramachandran plot [c]			
Favored regions (%)	92.3	96.8	97.2
Allowed (%)	98.9	99.3	99.7
Disallowed (%)	1.1	0.7	0.3

Values for highest resolution shell are in ()'s.

[a] $R_{merge} = \Sigma|I - \langle I \rangle| / \Sigma I$, where I is the intensity of the measured reflection and <I> is the mean intensity of all measurements of this reflection.

[b] $R_{cryst} = \Sigma ||F_{obs}| - |F_{calc}|| / \Sigma |F_{obs}|$, where F_{obs} and F_{calc} are observed and calculated structure factors and R_{free} is calculated for a set of randomly chosen 5% of reflections prior to refinement.

[c] The Ramachandran plot was calculated with MolProbity (Davis, I.W., et al., Nucleic Acids Res, 32: W615-9, 2004).

The epitopes and the paratopes

The residues involved in binding between the TLR3 ECD and the three Fabs are shown in Figure 28B. Fab 12QVQ/QSV bound near the N-terminus of the TLR3 ECD. The conformational epitope was composed of residues from the TLR3 LRRs 3-7 (amino acids 100-221 of SEQ ID NO: 2). The binding of Fab 12QVQ/QSV buried approximately 928 $Å^2$ and 896 $Å^2$ on the

antigen and antibody, respectively. For Fab 12QVQ/QSV, the crystal structure identified following TLR3 (SEQ ID NO: 2) epitope residues: S115, D116, K117, A120, K139, N140, N141, V144, K145, T166, Q167, V168, S188, E189, D192, A195, and A219. For Fab 12QVQ/QSV, the crystal structure identified following paratope residues: light chain (SEQ ID NO: 211): G28, S29, Y30, Y31, E49, D50, Y90, D91, and D92. Heavy chain (SEQ ID NO: 214): N32, Q54, R56, S57, K58, Y60, Y104, P105, F106, and Y107.

Fab 15EVQ and Fab c1068 bound non-overlapping epitopes spanning LRRs 15-23 (amino acids 406-635 of SEQ ID NO: 2) near the C-terminus (Figure 28). Fab 15EVQ buried 1080 $Å^2$ and 1064 $Å^2$ on the antigen and antibody, respectively, whereas Fab c1068 buried 963 $Å^2$ and 914 $Å^2$ on the antigen and antibody, respectively. The epitope for Fab 15EVQ covers residues K416, K418, L440, N441, E442, Y465, N466, K467, Y468, R488, R489, A491, K493, N515, N516, N517, H539, N541, S571, L595 and K619 of TLR3 shown in SEQ ID NO: 2. For Fab 15EVQ, the crystal structure identified following paratope residues: light chain (SEQ ID NO: 41): Q27, Y32, N92, T93, L94, and S95. Heavy chain (SEQ ID NO: 216): W33, F50, D52, D55, Y57, N59, P62, E99, Y101, Y104, and D106.

For Fab c1068, the crystal structure identified following epitope residues on TLR3 (SEQ ID NO: 2): E446, T448, Q450, R453, R473, N474, A477, L478, P480, S498, P499, Q503, P504, R507, D523, D524, E527, E530, and K559. For Fab c1068, the crystal structure identified following paratope residues light chain: H30, N31, Y32, N50, E66, S67, G68 (glyc). Heavy chain: T30, T31, Y32, W33, H35, E50, N52, N54, N55, R57, N59, V99, M102, I103, and T104.

Mechanisms of neutralization and implication for TLR3 function

mAb 15EVQ: The mAb 15EVQ epitope contains TLR3 residues N517, H539 and N541, which overlap with the C-terminal dsRNA binding site (Bell et al., Proc. Natl. Acad. Sci. USA,

103:8792-7, 2006). Thus, by not wishing to be bound by any particulat theory, it is believed that the mAb 15EVQ competes for TLR3 binding against its ligand and prevents ligand-induced receptor dimerization, which is required for the formation of the signaling unit (Liu et al., Science 320:379-81, 2008). Figure 29 illustrates this direct competition mechanism for mAb 15EVQ. Depending upon the antibody concentration, this mechanism would lead to total inhibition of poly(I:C) or dsRNA induced TLR3 activation.

mAb 12QVQ/QSV and mAb c1068: As shown in Figure 30, these two antibodies do not have direct clashes with the dsRNA ligand. Thus, it is unlikely that they would neutralize TLR3 function in a similar mechanism to that of mAb 15EVQ. The Fab fragments are also oriented away from the ligand (Figure 30). Structurally, both mAb 12QVQ/QSV and Fab c1068 can bind to a signaling unit (SU) without disrupting its function. Sterically, it is unlikely that the two Fab fragments of a mAb molecule would be able to bind simultaneously the two TLR3 molecules in one SU, and thus prevent dsRNA mediated TLR3 dimerization. By not wishing to be bound by any particular theory, it is believed that binding of mAb 12QVQ/QSV or mAb c1068 to TLR3 prevents clustering of the signaling unit due to steric clashes between the antibodies and neighboring signaling units. Binding of TLR3 to dsRNA is not limited to the signaling unit defined by the dsRNA:TLR3 complex (Liu, et al., Science, 320: 379-81, 2008). It is possible that clustering of multiple SUs can lead to enhancement of signaling or that efficient TLR3 signaling requires this clustering. The positioning of mAb 12QVQ/QSV and mAb c1068 can block the clustering and result in neutralization of TLR3 activity. The maximal neutralization effects of antibodies would therefore be dependent upon the degree of separation of SUs due to antibody binding. As illustrated in Figure 30, mAb 12QVQ/QSV would cause larger separation than mAb c1068, and this could translate to greater potency of mAb 12QVQ/QSV. This is

consistent with observations that mAb c1068 and mAb 15EVQ can lead to ~50% and 100% TLR3 neutralization at saturation concentrations, respectively, and mAb 12QVQ/QSV exhibits intermediate activity. Thus, combined structural and TLR3 neturalization studies suggest a TLR3 signaling model in which the dsRNA:TLR3 signaling units cluster to achieve efficient signaling. mAb 12QVQ/QSV and mAb c1068 and also define a class of antibodies that can partially modulate TLR3 signaling without interfering with ligand binding or receptor dimerization.

CLAIMS

1. An isolated antibody or fragment thereof, wherein the antibody binds toll-like receptor 3 (TLR3) amino acid residues K416, K418, L440, N441, E442, Y465, N466, K467, Y468, R488, R489, A491, K493, N515, N516, N517, H539, N541, S571, L595, and K619 of SEQ ID NO: 2.
2. An isolated antibody or fragment thereof, wherein the antibody binds toll-like receptor 3 (TLR3) amino acid residues S115, D116, K117, A120, K139, N140, N141, V144, K145, T166, Q167, V168, S188, E189, D192, A195, and A219 of SEQ ID NO: 2.
3. An isolated antibody comprising a heavy chain variable region and a light chain variable region or fragment thereof, wherein the antibody binds TLR3 having an amino acid sequence shown in SEQ ID NO: 2 with the heavy chain variable region Chothia residues W33, F50, D52, D54, Y56, N58, P61, E95, Y97, Y100, and D100b and the light chain variable region Chothia residues Q27, Y32, N92, T93, L94, and S95.
4. The isolated antibody of claim 3, wherein the antibody has at least one of the following properties:
   a. binds to human TLR3 with a Kd of <10 nM;
   b. reduces human TLR3 biological activity in an *in vitro* poly(I:C) NF-κB reporter gene assay >50% at 1 μg/ml;
   c. inhibits >60% of IL-6 or CXCL10/IP-10 production from BEAS-2B cells stimulated with <100 ng/ml poly(I:C) at 10 μg/ml;
   d. inhibits >50% of IL-6 or CXCL10/IP-10 production from BEAS-2B cells stimulated with <100 ng/ml poly(I:C) at 0.4 μg/ml;
   e. inhibits >50% of IL-6 production from NHBE cells stimulated with 62.5 ng/ml poly(I:C) at 5 μg/ml;

f. inhibits >50% of IL-6 production from NHBE cells stimulated with 62.5 ng/ml poly(I:C) at 1 μg/ml;

g. inhibits >20% of poly(I:C)-induced IFN-γ, IL-6 or IL-12 production by PBMC at 1 μg/ml;

h. inhibits cynomologus TLR3 biological activity in an *in vitro* NF-kB reporter gene assay with IC50 <10 μg/ml; or

i. inhibits cynomologus TLR3 biological activity in an *in vitro* ISRE reporter gene assay with IC50 <5 μg/ml.

5. The isolated antibody of claim 3, wherein the antibody comprises a heavy chain complementarity determining region (CDR) 3 (HCDR3) that is 12 amino acids in length.

6. The isolated antibody of claim 3, wherein the antibody comprises the heavy chain complementarity determining regions (CDR) 1, 2 and 3 (HCDR1, HCDR2, HCDR3) having amino acid sequences at least 90% identical to the amino acid sequences shown in SEQ ID NO:s 82, 86 and 84, respectively, and the light chain complementarity determining regions 1, 2 and 3 (LCDR1, LCDR2, LCDR3) having amino acid sequences at least 90% identical to the amino acid sequences shown in SEQ ID NO:s 79, 80 and 87, respectively.

7. The isolated antibody of claim 3 comprising a light chain framework which is at least 90% identical to the amino acid sequence of a light chain variable region kappa 1 (Vκ1) framework (Vκ1) and a heavy chain framework which is at least 90% identical to the amino acid sequence of a heavy chain variable region Vh5 framework (Vh5).

8. The isolated antibody of claim 7, wherein the Vk1 framework is encoded by IGKV1-39*01 having an amino acid sequence shown in SEQ ID NO: 221, and the Vh5 framework is encoded by IGHV5-51*01 having an amino acid sequence shown in SEQ ID NO: 222.

9. An isolated antibody comprising a heavy chain variable region and a light chain variable region or fragment thereof, wherein the antibody binds TLR3 having an amino acid sequence shown in SEQ ID NO: 2 with the heavy chain variable region Chothia residues N31a, Q52, R52b, S53, K54, Y56, Y97, P98, F99, and Y100, and the light chain variable region Chothia residues G29, S30, Y31, Y32, E50, D51, Y91, D92, and D93.

10. The isolated antibody of claim 9, wherein the antibody has at least one of the following properties:
    a. binds to human TLR3 with a Kd of <10 nM;
    b. reduces human TLR3 biological activity in an *in vitro* poly(I:C) NF-κB reporter gene assay >50% at 1 μg/ml;
    c. inhibits >60% of IL-6 or CXCL10/IP-10 production from BEAS-2B cells stimulated with <100 ng/ml poly(I:C) at 10 μg/ml;
    d. inhibits >50% of IL-6 or CXCL10/IP-10 production from BEAS-2B cells stimulated with <100 ng/ml poly(I:C) at 0.4 μg/ml;
    e. inhibits >50% of IL-6 production from NHBE cells stimulated with 62.5 ng/ml poly(I:C) at 5 μg/ml;
    f. inhibits >50% of IL-6 production from NHBE cells stimulated with 62.5 ng/ml poly(I:C) at 1 μg/ml;
    g. inhibits >20% of poly(I:C)-induced IFN-γ, IL-6 or IL-12 production by PBMC at 1 μg/ml;

11. The isolated antibody of claim 9, wherein the antibody comprises a HCDR3 that is 10 amino acids in length and a LCDR3 that is 10 amino acids long.

12. The isolated antibody of claim 9, wherein the antibody comprises the heavy chain complementarity determining regions (CDR) 1, 2 and 3 (HCDR1, HCDR2, HCDR3) having amino acid sequences at least 90% identical to the amino acid sequences shown in SEQ ID

NO:s 70, 77 and 72, and the light chain complementarity determining regions 1, 2 and 3 (LCDR1, LCDR2, LCDR3) having amino acid sequences at least 90% identical to the amino acid sequences shown in SEQ ID NO:s 67, 68 and 78.

13. The isolated antibody of claim 9 comprising a light chain framework which is at least 90% identical to the amino acid sequence of a light chain variable region kappa 3 (Vλ3) framework (Vλ3) and a heavy chain framework which is at least 90% identical to the amino acid sequence of a heavy chain variable region Vh6 framework (Vh6).

14. The isolated antibody of claim 13, wherein the Vλ3 framework is encoded by IGLV3-1*01 having an amino acid sequence shown in SEQ ID NO: 223, and the Vh6 framework is encoded by IGHV6-1*01 having an amino acid sequence shown in SEQ ID NO: 224.

15. The isolated antibody or fragment of claim 1 or 9, wherein the antibody
    a. is fully human;
    b. is human-adapted;
    c. is conjugated to polyethylene glycol;
    d. is of an IgG4 isotype; or
    e. Fc domain comprises S229P, P235A or L236A mutations.

16. A pharmaceutical composition comprising the isolated antibody or fragment of claim 1 or 9 and a pharmaceutically acceptable carrier.

17. A method of treating an inflammatory condition comprising administering a therapeutically effective amount of the isolated antibody of claim 1 or 9 to a patient in need thereof for a time sufficient to treat or prevent the inflammatory condition.

18. The method of claim 17, wherein the inflammatory condition is an inflammatory pulmonary condition,

inflammatory bowel disease, autoimmune disease, systemic inflammatory condition, or rheumatoid arthritis.

19. The method of claim 18, wherein the inflammatory pulmonary condition is asthma, chronic obstructive pulmonary disease (COPD), airway hyperresponsiveness, or is induced by Nontypeable Haemophilus influenza.

20. The method of claim 18, wherein the systemic inflammatory condition is cytokine storm or hypercytokinemia, systemic inflammatory response syndrome (SIRS), graft versus host disease (GVHD), acute respiratory distress syndrome (ARDS), severe acute respiratory distress syndrome (SARS), catastrophic anti-phospholipid syndrome, severe viral infections, influenza, pneumonia, shock, or sepsis.

21. The method of claim 17, wherein the inflammatory condition is associated with gastronintestinal ulceration.

22. The method of claim 21, wherein the gastrointestinal ulceration is associated with infectious colitis, ischemic colitis, collagenous or lymphocytic colitis or necrotizing enterocolitis.

23. A method of treating type II diabetes, hyperglycemia or hyperinsulinemia comprising administering a therapeutically effective amount of the isolated antibody of claim 1 or 9 to a patient in need thereof for a time sufficient to treat type II diabetes, hyperglycemia or hyperinsulinemia.

24. A method of treating or preventing viral infections comprising administering a therapeutically effective amount of the isolated antibody of claim 1 or 9 to a patient in need thereof for a time sufficient to treat or prevent viral infections.

25. A method of claim 24, wherein the viral infection is influenza A virus infection.