ANTI-TREM-1 ANTIBODIES AND USES THEREOF

REFERENCE TO SEQUENCE LISTING SUBMITTED ELECTRONICALLY VIA EFS-WEB

[0001] The content of the electronically submitted sequence listing in ASCII text file (Name: 3338_092PC01_SeqListing.txt; Size: 106,162 bytes; and Date of Creation: March 27, 2019) filed with the application is herein incorporated by reference in its entirety.

BACKGROUND OF THE DISCLOSURE

[0002] TREM-1 is an activating receptor expressed on monocytes, macrophages, and neutrophils. These cells play a central role in chronic inflammatory diseases by releasing cytokines and other mediators that drive inflammation. TREM-1 mRNA and protein expression is up-regulated in patients with rheumatic arthritis (RA) and inflammatory bowel disease (IBD), and TREM-l-positive cells accumulate at sites of inflammation, correlating with disease severity. *See* Bouchon *et al.*, *Nature* 410:1103-1107 (2001); Schenk *et al.*, *Clin Invest* 117:3097-3106 (2007); and Kuai *et al.*, *Rheumatology* 48:1352-1358 (2009). Peptidoglycan-recognition-protein 1 (PGLYRP1) expressed primarily by activated neutrophils is a ligand for TREM-1 and mediate TREM-1 signaling upon binding..

[0003] *In vitro*, engagement of TREM-1 triggers secretion of pro-inflammatory cytokines including TNF, IL-8, and monocyte chemotactic protein-1. In addition, TREM-1 signaling synergizes with multiple Toll-like Receptors (TLRs) to further boost pro-inflammatory signals. In turn, this up-regulates expression of TREM-1, leading to a vicious cycle amplifying the inflammation. *See* Bouchon *et al.*, *J Immunol* 164:4991-4995 (2000). Increasing evidence indicates that TLRs contribute to the development and progression of chronic inflammatory diseases such as RA and IBD.

[0004] Humanized anti-TREM-1 mAbs that inhibit both human and cynomolgus TREM-1 function have been disclosed elsewhere. *See* WO 2013/120553 A1 and WO 2016/009086 A1. However, such antibodies either have viscosity profile that can hamper manufacturing process or have other issues that can limit their therapeutic potential (e.g., cytokine storm and ADCC). *See* Shire *et al.*, *J. Pharm. Sci.* 93:1390-1402 (2004); and Warncke *et al.*, *J Immunol.* 188:4405-11 (2012). Accordingly, there is a need for an anti-TREM-1 antibody that can specifically bind to and inhibit TREM-1 function but without the issues of the earlier anti-TREM-1 antibodies.

SUMMARY OF THE DISCLOSURE

[0005] Provided herein are isolated antibodies, such as monoclonal antibodies, in particular human (e.g., monoclonal) antibodies, that specifically bind triggering receptor expressed on myeloid cells-1 (TREM-1) and have desirable functional properties. In some embodiments, the antibody comprises a heavy chain variable region (VH), a light chain variable region (VL), and an IgG1 heavy

chain constant region, wherein the IgG1 heavy chain constant region comprises one or more amino acid substitutions compared to a wild-type IgG1 heavy chain constant region (SEQ ID NO: 9). In some embodiments, the antibody cross-competes with mAb 0318 for binding to blocking TREM-1 and comprises a heavy chain variable region (VH), a light chain variable region (VL), and an IgG1 heavy chain constant region, wherein the IgG1 heavy chain constant region comprises one or more amino acid substitutions compared to a wild-type IgG1 heavy chain constant region (SEQ ID NO: 9).

[0006] In some embodiments, the antibody binds to the same TREM-1 eptiope as mAb 0318. In some embodiments, the antibody specifically binds to a TREM-1 epitope comprising one or more amino acid residues selected from the group consisting of the D38, V39, K40, C41, D42, Y43, T44, L45, E46, K47, F48, A49, S50, S51, Q52, K53, A54, W55, Q56, Y90, H91, D92, H93, G94, L95, and L96 of SEQ ID NO: 1. In some embodiments, the antibody specifically binds to a TREM-1 epitope comprising amino acids D38 to L45, E46 to Q56, and/or Y90 to L96 of SEQ ID NO: 1.

[0007] In some embodiments, the IgG1 heavy chain constant region of the antibody disclosed herein comprises one or more amino acid substitutions selected from the group consisting of K214R, L234A, L235E, G237A, D356E, and L358M, per EU numbering. In some embodiments, the IgG1 heavy chain constant region comprises one or more amino acid substitutions selected from the group consisting of K214R, L234A, L235E, G237A, A330S, P331S, D356E, and L358M, per EU numbering. In some embodiments, the IgG1 heavy chain constant region comprises one or more amino acid substitutions selected from the group consisting of K214R, C226S, C229S, and P238S, per EU numbering. In some embodiments, the IgG1 heavy chain constant region comprises one or more amino acid substitutions selected from the group consisting of S131C, K133R, G137E, G138S, Q196K, I199T, N203D, K214R, C226S, C229S, and P238S, per EU numbering.

[0008] In some embodiments, the antibody disclosed herein comprises a heavy chain CDR1, CDR2, and CDR3 and a light chain CDR1, CDR2, and CDR3, wherein the heavy chain CDR3 comprises DMGIRRQFAY (SEQ ID NO: 26) or DMGIRRQFAY (SEQ ID NO: 26) except one or two substitutions. In some embodiments, the heavy chain CDR3 comprises DQGIRRQFAY (SEQ ID NO: 72).

[0009] In some embodiments, the antibody disclosed herein comprises a heavy chain CDR1, CDR2, and CDR3 and a light chain CDR1, CDR2, and CDR3, wherein the heavy chain CDR2 comprises RIRTKSSNYATYYAASVKG (SEQ ID NO: 25) or RIRTKSSNYATYYAASVKG (SEQ ID NO: 25) except one or two substitutions.

[0010] In some embodiments, the antibody disclosed herein comprises a heavy chain CDR1, CDR2, and CDR3 and a light chain CDR1, CDR2, and CDR3, wherein the heavy chain CDR1 comprises TYAMH (SEQ ID NO: 24) or TYAMH (SEQ ID NO: 24) except one or two substitutions.

[0011] In some embodiments, the antibody disclosed herein comprises a heavy chain CDR1, CDR2, and CDR3 and a light chain CDR1, CDR2, and CDR3, wherein the light chain CDR1 comprises RASQSVDTFDYSFLH (SEQ ID NO: 27) or RASQSVDTFDYSFLH (SEQ ID NO: 27)

except one or two substitutions. In some embodiments, the light chain CDR2 comprises RASNLES (SEQ ID NO: 28) or RASNLES (SEQ ID NO: 28) except one or two substitutions. In some embodiments, the light chain CDR3 comprises QQSNQDPYT (SEQ ID NO: 29) or QQSNQDPYT (SEQ ID NO: 29) except one or two substitutions.

[0012] In some embodiments, the VH of the antibody disclosed herein comprises an amino acid sequence which is at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to the amino acid sequence set forth as SEQ ID NO: 14. In somoe embodiments, the VL of the antibody disclosed herein comprises an amino acid sequence which is at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to the amino acid sequence set forth as SEQ ID NO: 15. In some embodiments, the VH and VL comprises SEQ ID NOs: 14 and 15, respectively.

[0013] In some embodiments, the antibody of the present disclosure comprises a heavy chain and a light chain, wherein the heavy chain comprises SEQ ID NO: 50, SEQ ID NO: 51, SEQ ID NO: 52, or SEQ ID NO: 53. In some embodiments, the light chain comprises SEQ ID NO: 54.

[0014] Provided herein is an isolated antibody which specifically binds to TREM-1, comprising a heavy chain CDR1, CDR2, CDR3; a light chain CDR1, CDR2, CDR3; and an IgG1 heavy chain constant region, wherein the heavy chain CDR1, CDR2, and CDR3 comprises TYAMH (SEQ ID NO: 24), RIRTKSSNYATYYAASVKG (SEQ ID NO: 25), and DMGIRRQFAY (SEQ ID NO: 26), respectively; wherein the light chain CDR1, CDR2, and CDR3 comprises RASQSVDTFDYSFLH (SEQ ID NO: 27), RASNLES (SEQ ID NO: 28), and QQSNQDPYT (SEQ ID NO: 29), respectively; and wherein the IgG1 heavy chain constant region comprises one or more amino acid substitutions selected from the group consisting of L234A, L235E, and G237A, per EU numbering.

[0015] Provided herein is an isolated antibody which specifically binds to TREM-1, comprising a heavy chain CDR1, CDR2, CDR3; a light chain CDR1, CDR2, CDR3; and an IgG1 heavy chain constant region, wherein the heavy chain CDR1, CDR2, and CDR3 comprises TYAMH (SEQ ID NO: 24), RIRTKSSNYATYYAASVKG (SEQ ID NO: 25), and DMGIRRQFAY (SEQ ID NO: 26), respectively; wherein the light chain CDR1, CDR2, and CDR3 comprises RASQSVDTFDYSFLH (SEQ ID NO: 27), RASNLES (SEQ ID NO: 28), and QQSNQDPYT (SEQ ID NO: 29), respectively; and wherein the IgG1 heavy chain constant region comprises amino acid substitutions selected from the group consisting of L234A, L235E, G237A, A330S, and P331S, per EU numbering.

[0016] Provided herein is an isolated antibody which specifically binds to TREM-1, comprising a heavy chain CDR1, CDR2, CDR3; a light chain CDR1, CDR2, CDR3; and an IgG1 heavy chain constant region, wherein the heavy chain CDR1, CDR2, and CDR3 comprises TYAMH (SEQ ID NO: 24), RIRTKSSNYATYYAASVKG (SEQ ID NO: 25), and DMGIRRQFAY (SEQ ID NO: 26), respectively; wherein the light chain CDR1, CDR2, and CDR3 comprises RASQSVDTFDYSFLH (SEQ ID NO: 27), RASNLES (SEQ ID NO: 28), and QQSNQDPYT (SEQ ID NO: 29), respectively;

and wherein the IgG1 heavy chain constant region comprises one or more amino acid substitutions selected from the group consisting of K214R, C226S, C229S, and P238S, per EU numbering.

[0017] Provided herein is an isolated antibody which specifically binds to TREM-1, comprising a heavy chain CDR1, CDR2, CDR3; a light chain CDR1, CDR2, CDR3; and an IgG1 heavy chain constant region, wherein the heavy chain CDR1, CDR2, and CDR3 comprises TYAMH (SEQ ID NO: 24), RIRTKSSNYATYYAASVKG (SEQ ID NO: 25), and DMGIRRQFAY (SEQ ID NO: 26), respectively; wherein the light chain CDR1, CDR2, and CDR3 comprises RASQSVDTFDYSFLH (SEQ ID NO: 27), RASNLES (SEQ ID NO: 28), and QQSNQDPYT (SEQ ID NO: 29), respectively; and wherein the IgG1 heavy chain constant region comprises one or more amino acid substitutions selected from the group consisting of S131C, K133R, G137E, G138S, Q196K, I199T, N203D, K214R, C226S, C229S, and P238S, per EU numbering.

[0018] In some embodiments, TREM-1 comprises an amino acid sequence of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, or SEQ ID NO: 7.

[0019] In some embodiments, the antibody of the present disclosure has a decreased binding affinity to FcγRI (CD64), FcγRIIA (CD32), FcγRIIB (CD32), FcγRIIIA (CD16a), FcγRIIIB (CD16b), or any combination thereof compared to an antibody comprising a heavy chain consisting of the amino acid sequence as set forth in SEQ ID NO: 76 and a light chain consisting of the amino acid sequence as set forth in SEQ ID NO: 54. In some embodiments, the antibody has a decreased binding affinity to FcγRI (CD64) by at least two fold, at least three fold, at least four fold, at least five fold, at least six fold, at least seven fold, at least eight fold, at least nine fold, or at least 10 fold compared to an antibody comprising a heavy chain consisting of the amino acid sequence as set forth in SEQ ID NO: 76 and a light chain consisting of the amino acid sequence as set forth in SEQ ID NO: 54.

[0020] In some embodiments, the antibody disclosed herein is less immunogenic compared to an antibody comprising a heavy chain consisting of the amino acid sequence as set forth in SEQ ID NO: 76 and a light chain consisting of the amino acid sequence as set forth in SEQ ID NO: 54. In some embodiments, the antibody does not agonize TREM-1 signaling upon binding to TREM-1 and in the absence of a stimulator. In some embodiments, the antibody does not induce expression of an inflammatory cytokine in immature dendritic cells (iDCs) when the cells are incubated in the presence of the antibody and in the absence of a stimulator compared to an antibody comprising a heavy chain consisting of the amino acid sequence as set forth in SEQ ID NO: 76 and a light chain consisting of the amino acid sequence as set forth in SEQ ID NO: 54.

[0021] In some embodiments, the antibody disclosed herein blocks the production of an inflammatory cytokine in a cell when the cells are activated in the presence of both the antibody and a stimulator. In some embodiments, the stimulator is a TREM-1 ligand. In some embodiments, the inflammatory cytokine is selected from a group consisting of IL-6, TNF-α, IL-8, IL-1β, IL-12, chitinase-3-like protein 1 (CHI3L1), and combinations thereof.

[0022] In some embodiments, the antibody of the present disclosure binds human FcRn, cynomolgus FcRn, and/or mouse FcRn in a pH dependent manner. In some embodiments, the antibody disclosed herein is more thermally stable compared to a reference antibody comprising a heavy chain consisting of the amino acid sequence as set forth in SEQ ID NO: 76 and a light chain consisting of the amino acid sequence as set forth in SEQ ID NO: 54, as measured by a Capillary Differential scanning calorimeter (CAP-DSC). In some embodiments, about 10% to 20%, about 20% to 30% (e.g., 24%), or about 30% to 40% of the antibody is reversible when it is heated to 77 ºC. In some embodiments, the antibody has a higher melting temperature (Tm) compared to an antibody comprising a heavy chain consisting of the amino acid sequence as set forth in SEQ ID NO: 76 and a light chain consisting of the amino acid sequence as set forth in SEQ ID NO: 54.

[0023] In some embodiments, the antibody disclosed herein has a viscosity of less than 5 cP, less than 4 cP, less than 3 cP, less than 2.5 cP, less than 2.4 cP, less than 2.3 cP, less than 2.2 cP, less than 2.1 cP, less than 2 cP, less than 1.9 cP, less than 1.8 cP, less than 1.7 cP, less than 1.6 cP, less than 1.5 cP, less than 1.4 cP, less than 1.3 cP, less than 1.2 cP, less than 1.1 cP, less than 1.0 cP, less than 0.9 cP, less than 0.8 cP, less than 0.7 cP, less than 0.6 cP, less than 0.5 cP, less than 0.4 cP, less than 0.3 cP, less than 0.2 cP, or less than 0.1 cP at a concentration of 80 mg/mL. In some embodiments, the antibody has a viscosity of less than 10 cP (e.g., 9 cP) at a concentration of 130 mg/mL.

[0024] In some embodiments, the antibody binds to human TREM-1 with of a K_D of less than 4 nM (e.g., 3.4 nM) as measured by Biacore. In some embodiments, the antibody binds to cynomolgus TREM-1 with a K_D of less than 1 nM (e.g., 0.91 nM), as measured by Biacore.

[0025] In some embodiments, the antibody is monomeric as observed by size-exclusion high-performance liquid chromatography (SE-HPLC). In some embodiments, the antibody exhibits minimal risk for fragmentation as observed by two-dimensional liquid chromatography-tandem mass spectrometry (2D-LC/MS) or intact mass analysis using liquid chromatography-tandem mass spectrometry (LC/MS). In some embodiments, the antibody has an isoelectric point of 8 to 9 (e.g., 8.75).

[0026] In some embodiments, the antibody is stable in a formulation comprising histidine, sucrose, arginine, and NaCl. In some embodiments, the antibody is stable for at least 2 months in a formulation comprising 20 mM histidine, 150 mM sucrose, 25 mM arginine, and 50 mM NaCl. In some embodiments, the formulation is at a pH of 6.0 and/or wherein the formulation is stored at 4°C, 25°C, or 40°C.

[0027] Also provided herein are bispecific molecules comprising an anti-TREM-1 antibody of the present disclosure, linked to a molecule having a second binding specificity.

[0028] Provided herein are nucleic acids encoding the antibody disclosed herein, vectors comprising the nucleic acids, and cells tramsformed with the vectors.

[0029] Provided herein are immunoconjugates comprising the anti-TREM-1 antibodies disclosed herein, linked to an agent.

[0030] Provided herein are compositions comprising anti-TREM-1 antibodies, or antigen binding portions thereof, bispecific molecules, or immunoconjugates described herein, and a carrier. Also provided herein are kits comprising the anti-TREM-1 antibodies, or antigen binding portions thereof, bispecific molecules, or immunoconjugates described herein, and instructions for use.

[0031] Provided herein is a method of inhibiting TREM-1 activity in a subject in need thereof, comprising administering the anti-TREM-1 antibody, the bispecific molecule, the nucleic acid, the vector, the cell, or the immunoconjugate of the present disclosure.

[0032] Provided herein is a method of treating an inflammatory disease or an autoimmune disease in a subject in need thereof, comprising administering the anti-TREM-1 antibody, the bispecific molecule, the nucleic acid, the vector, the cell, or the immunoconjugate of the present disclosure. In some embodiments, the inflammatory disease or the autoimmune disease is selected from the group consisting of an inflammatory bowel disease (IBD), Crohn's disease (CD), ulcerative colitis (UC), irritable bowel syndrome, rheumatoid arthritis (RA), psoriasis, psoriatic arthritis, systemic lupus erythematosus (SLE), lupus nephritis, vasculitis, sepsis, systemic inflammatory response syndrome (SIRS), type I diabetes, Grave's disease, multiple sclerosis (MS), autoimmune myocarditis, Kawasaki disease, coronary artery disease, chronic obstructive pulmonary disease, interstitial lung disease, autoimmune thyroiditis, scleroderma, systemic sclerosis, osteoarthritis, atopic dermatitis, vitiligo, graft versus host disease, Sjogrens's syndrome, autoimmune nephritis, Goodpasture's syndrome, chronic inflammatory demyelinating polyneuropathy, allergy, asthma, other autoimmune diseases that are a result of either acute or chronic inflammation, and any combinations thereof. In some embodiments, the method further comprises administering one or more additional therapeutics. In some embodiments, the additional therapeutics is an anti-IP-10 antibody or an anti-TNF-α antibody.

BRIEF DESCRIPTION OF THE DRAWINGS/FIGURES

[0033] FIGs. 1A and 1B shows that all the mAb 0318 variants bind to human and cynomolgus TREM-1 with similar affinity as the original mAb 0318 antibody (IgG4). FIG. 1A shows the binding affinity data for the 318-IgG1.3f variant to both human (top row) and cynomolgus (bottom row) TREM-1. FIG. 1B shows the binding affinity data for several different mAb 0318 variants to human TREM-1. The different variants shown include: (i) 318-IgG1.1f, (ii) 318-IgG1.3f, (iii) 318-IgG4-Aba, (iv) 318-IgG1-Aba, and (v) 318-IgG1.1f (M to Q mutant). The binding affinity data for the mAb 0318 antibody (IgG4 A and B) were provided for comparison purposes in FIG. 1B.

[0034] FIGs. 2A and 2B show the internalization of mAb 0318-IgG1.3f upon binding to TREM-1 expressed on CD14+ monocytes at various time points post-TREM-1 binding. In FIG. 2A, TREM-1 receptor expression was analyzed at 0, 6, and 24 hours post-binding. In FIG. 2B, TREM-1 receptor expression was analyzed at 0, 4, and 20 hours post-binding. FIG. 2B also provides data using the TREM26 antibody, which does not compete with the 0318 antibody variants for binding to TREM-1.

The TREM26 antibody was used to assess the fate of the TREM-1 receptor once it was internalized (e.g., whether it was degraded or recycled back to the surface).

[0035] FIG. 3 shows that the mAb 0318 variants do not agonize TREM-1 signaling as measured by the BWZ/hTREM-1 Reporter Cell Assay when a reporter cell line is incubated with ("Both") or without CHO-CD32 ("BWZ 36 only"). The variant antibodies shown include: (i) 318-IgG1.1f ("IgG1.1f"), (ii) 318-IgG1.3f ("IgG1.3f"), (iii) 318-IgG4-Aba ("FcAba-4"), (iv) 318-IgG1-Aba ("FcAba-1"). The MAB1278 antibody, a known agonist of TREM-1 signaling, was used as a positive control antibody (see inserted box). The 5C8 (isotype control) antibody was used as a negative control.

[0036] FIG. 4 shows potency of the different mAb 0318 variants at blocking TREM-1 mediated production of inflammatory cytokines by different human cells. The mAb 0318 antibody variants shown in FIG. 4 inhibit TREM-1 mediated release of inflammatory cytokines (e.g., TNF-α, IL-6, or IL-8) from different human cell types: PBMC, monocytes, neutrophils, and RBC-sedimented whole blood (i.e., majority of red blood cells removed using dextran-based RBC sedimentation protocol as described in the Examples). To produce the inflammatory cytokines, the cells were stimulated with either plate-bound PGRP1 and soluble peptidoglycan that lack TLR2 activity ("PGRP + PGN-Ecndss") or phorbol 12-myristate 13-acetate (PMA) stimulated neutrophils expressing PGRP1 ("PMA-Stim Neutrophil Endogenous PGRP"). The variant antibodies shown include: (i) 0318-IgG4, (ii) 0318-IgG1.3f, (iii) 0318-IgG1.1f, (iv) 0318-IgG1-Aba, and (v) 318-IgG4-Aba. "N/D" indicates that the expression level of the particular inflammatory cytokine was not determined.

[0037] FIGs. 5A and 5B show the potency of mAb 0318-IgG1.3f to block IL-8 production from whole blood after stimulation with PGN with or without PGRP1 in the presence of NOD2 inhibitor. FIG. 5A provides the inhibition data generated using the whole blood pharmacodynamics assay as described in the Examples. FIG. 5B provides the inhibition data generated using the whole blood intracellular cytokine assay as described in the Examples.

[0038] FIGs. 6A to 6C show the RNA expression levels of chitinase-3-like protein 1 ("CHI3L1") (FIG. 6A), IL-1β (FIG. 6B), and IL-6 (FIG. 6C) from whole blood stimulated in the presence of varying concentrations of mAb 0318-IgG1.3f (0-1 nM). Whole blood were collected from three different donors (#126, #290, and #322) and stimulated with soluble PGRP1 and soluble peptidoglycan that lack TLR2 activity ("Soluble PGRP + Soluble PGN-Ecndss"). In each of FIGs. 6A to 6C, the RNA expression levels (y-axis) are shown as both % inhibition (right column) and ΔΔCt (difference between the value of a reference gene and the value of the test sample) (left column). The different concentrations of the 0318-IgG1.3f antibody are shown on the x-axis.

[0039] FIG. 7 shows the viscosity-concentration profile of both the 318-IgG1.1f (square) and the 318-IgG1.3f (circle) variant antibodies. The viscosity profile was generated from dilution scheme using Rheosense m-VROC dynamic viscometer using a 3 point shear sweep for each point at constant

temperature. The solid line provides the best nonlinear curve fit for the data shown. The dotted line shows the maximum allowable viscosity level for efficacy.

[0040] FIG. 8 shows that both the 318-IgG1.1f and the 318-IgG1.3f variant antibodies have low to medium risk for immunogencity. VL6 (immunogenic IL-21R mAb) and KLH (keyhole limpet hemocyanin) were used as positive controls. Avastin was used as a negative control.

[0041] FIGs. 9A and 9B show that all the mAb 0318 variants are capable of binding to FcRn (human (black), cyno (white), and mouse (gray)) in a pH-dependent manner. FIG. 9A provides FcRn binding as % Rmax (maximum FcRn binding capacity). FIG. 9B provides the FcRn binding as sensorgrams. The 0318 antibody variants shown include: (i) IgG1-Aba, (ii) IgG4-Aba, (iii) IgG1.1f, and (iv) IgG1.3f. The mAb 0318 (IgG4) antibody is also shown for comparison purposes

[0042] FIGs. 10A and 10B show that all the mAb 0318 antibody variants demonstrate decreased binding to one or more of the human FcγRs (*i.e.*, CD64, CD32a-H131 variant, CD32a-R131 variant, CD32b, CD16a-V158 variant, and CD16B-NA2 variant). FIG. 10A shows the binding affinity as % Rmax (maximum FcγR capacity). FIG. 10B shows the sensorgrams. The 0318 antibody variants shown include: (i) IgG1-Aba, (ii) IgG4-Aba, (iii) IgG1.1f, and (iv) IgG1.3f. The mAb 0318 (IgG4) antibody is shown for comparison purposes. 1F4-hIgG1f antibody, which is known to bind to multiple FcγRs, was used as a control.

[0043] FIGs. 11A to 11I show that the 0318 variant antibodies are not agonistic on their own (i.e., in the absence of a stimulus), as measured by the release of different inflammatory cytokines (e.g., IL-6, TNF-α, and IL-12) when cultured with immature-dendritic cells. FIGs. 11A, 11B, and 11C provide the amount of IL-6 produced for immature-dendritic cells isolated from donors D179, D276, and D341, respectively. FIGs. 11D, 11E, and 11F provide the amount of TNF-α produced for immature-dendritic cells isolated from donors D179, D276, and D341, respectively. FIGs. 11G, 11H, and 11I provide the amount of IL-12 produced for immature-dendritic cells isolated from donors D179, D276, and D341, respectively. The 0318 antibody variants shown include: (i) IgG1.1f, (ii) IgG1.3f, and (iii) IgG1-Aba. The dosages (μg/mL) of the antibodies used are shown in parentheses. The immature-dendritic cells were cultured with the anti-TREM-1 antibody variants with and without CHO cells expressing membrane CD32a (to stimulate Fc cross-linking). PGRP+PGN, CD40L trimer ("Trimer"), and Pfizer's anti-CD40 agonist antibody ("CP870") were used as positive controls. The isotype antibody ("CHIL-6") was used as a negative control. The dotted line shows the lowest limit of detection for the assay.

[0044] FIG. 12 shows the pharmacokinetics of single dose mAb 0318-IgG1.3f variant in cynomolgus monkey following subcutaneous administration. Each of the animals received one of the following doses: (i) 0.1 mg/kg (n=4) ("1"), (ii) 0.5 mg/kg (n=4) ("2"), (iii) 2 mg/kg (n=3) ("3"), or (iv) 10 mg/kg (n=4) ("4"). Data are shown as mean ± standard deviation.

[0045] FIG. 13 shows target-mediated drug disposition schematic used to describe the pharmacokinetic (PK), pharmacodynamics (PD), and receptor occupancy (RO) data in cynomolgus monkey.

[0046] FIGs. 14A and 14B show the total TREM-1 receptor density on monocytes (FIG. 14A) and granulocytes (FIG. 14B) following single dose (subcutaneous (sc) or intravenous (iv) administration) of mAb 0318-IgG1.3f variant in cynomolgous monkey. The TREM-1 receptor density is shown as a percentage of the TREM-1 receptor density prior to administration of the antibody. Each of the animals received one of the following doses: (a) 0.1 mg/kg (sc) (n=4) ("A"), (b) 0.5 mg/kg (n=4) (sc) ("B"), (c) 2 mg/kg (n=3) (sc) ("C"), (d) 2 mg/kg (n=3) (iv) ("D"), or (e) 10 mg/kg (n=4) (sc) ("E"). Data are shown as mean ± standard deviation.

[0047] FIGs. 15A and 15B show the TREM-1 receptor occupancy on monocytes (FIG. 15A) and granulocytes (FIG. 15B) following single dose of mAb 0318-IgG1.3f variant in cynomolgous monkey. The receptor occupancy data is shown as a percentage of the total TREM-1 receptor expressed on the cells. Each of the animals received one of the following doses: (a) 0.1 mg/kg (sc) (n=4) ("A"), (b) 0.5 mg/kg (n=4) (sc) ("B"), (c) 2 mg/kg (n=3) (sc) ("C"), (d) 2 mg/kg (n=3) (iv) ("D"), or (e) 10 mg/kg (n=4) (sc) ("E"). Data are shown as mean ± standard deviation. The dotted line shows 85% receptor occupancy.

[0048] FIGs. 16A and 16B show the observed (open circle) and model-predicted (solid line) PK (upper left panel), PD (upper right panel), RO (bottom left panel), and total surface TREM-1 receptor expression (bottom right panel) following a single dose of mAb 0318-IgG1.3f variant in cynomolgus monkey described by a 2-compartment PK model with TMDD in central compartment. In FIG. 16A, each of the monkey received a single dose of 0.1 mg/kg of the antibody subcutaneously. In FIG. 16B, the animals received a single dose of 10 mg/kg of the antibody subcutaneously.

DETAILED DESCRIPTION OF DISCLOSURE

[0049] In order that the present description can be more readily understood, certain terms are first defined. Additional definitions are set forth throughout the detailed description.

[0050] It is to be noted that the term "a" or "an" entity refers to one or more of that entity; for example, "a nucleotide sequence," is understood to represent one or more nucleotide sequences. As such, the terms "a" (or "an"), "one or more," and "at least one" can be used interchangeably herein.

[0051] Furthermore, "and/or" where used herein is to be taken as specific disclosure of each of the two specified features or components with or without the other. Thus, the term "and/or" as used in a phrase such as "A and/or B" herein is intended to include "A and B," "A or B," "A" (alone), and "B" (alone). Likewise, the term "and/or" as used in a phrase such as "A, B, and/or C" is intended to encompass each of the following aspects: A, B, and C; A, B, or C; A or C; A or B; B or C; A and C; A and B; B and C; A (alone); B (alone); and C (alone).

[0052] It is understood that wherever aspects are described herein with the language "comprising," otherwise analogous aspects described in terms of "consisting of" and/or "consisting essentially of" are also provided.

[0053] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this disclosure is related. For example, the Concise Dictionary of Biomedicine and Molecular Biology, Juo, Pei-Show, 2nd ed., 2002, CRC Press; The Dictionary of Cell and Molecular Biology, 3rd ed., 1999, Academic Press; and the Oxford Dictionary Of Biochemistry And Molecular Biology, Revised, 2000, Oxford University Press, provide one of skill with a general dictionary of many of the terms used in this disclosure.

[0054] Units, prefixes, and symbols are denoted in their Système International de Unites (SI) accepted form. Numeric ranges are inclusive of the numbers defining the range. Unless otherwise indicated, nucleotide sequences are written left to right in 5' to 3' orientation. Amino acid sequences are written left to right in amino to carboxy orientation. The headings provided herein are not limitations of the various aspects of the disclosure, which can be had by reference to the specification as a whole. Accordingly, the terms defined immediately below are more fully defined by reference to the specification in its entirety.

[0055] The term "about" is used herein to mean approximately, roughly, around, or in the regions of. When the term "about" is used in conjunction with a numerical range, it modifies that range by extending the boundaries above and below the numerical values set forth. In general, the term "about" can modify a numerical value above and below the stated value by a variance of, e.g., 10 percent, up or down (higher or lower).

[0056] The term "triggering receptor expressed on myeloid cells 1" (also known as TREM1, TREM-1, and CD354) refers to a receptor that is expressed on monocytes, macrophages, and neutrophils. Primary ligand for TREM-1 include peptidoglycan-recognition-protein 1 (PGLYRP1), which belongs to a family of peptidoglycan (PGN) binding proteins (PGRPs). When activated, TREM-1 associates with the ITAM-containing signaling adaptor protein, DAP12. Downstream signalling may include activation of the NFAT transcription factor, causing an up-regulation of pro-inflammatory cytokine production. The term "TREM-1" includes any variants or isoforms of TREM-1 which are naturally expressed by cells. Accordingly, in some embodiments, antibodies described herein can cross-react with TREM-1 from species other than human (e.g., cynomolgus TREM-1).

[0057] Three isoforms of human TREM-1 have been identified. Isoform 1 (Accession No. NP_061113.1; SEQ ID NO: 1) consists of 234 amino acids and represents the canonical sequence. Isoform 2 (Accession No. NP_001229518.1; SEQ ID NO: 2) consists of 225 amino acids and differ from the canonical sequence at amino acid residues 201-234. The amino acid residues encode part of the transmembrane domain and the cytoplasmic domain. Isoform 3 (Accession No. NP_001229519; SEQ ID NO: 3) consists of 150 amino acids, and is soluble. It lacks amino acid residues 151-234,

which encode the transmembrane domain, the cytoplasmic domain, and part of the extracellular domain. The amino acid residues 138-150 also differ from the canonical sequence described above.

[0058] Below are the amino acid sequences of the three known human TREM-1 isoforms.

(A) Human TREM-1 isoform 1 (Accession No. NP_061113.1; SEQ ID NO: 1; encoded by the nucleotide sequence having Accession No. NM_018643; SEQ ID NO: 4):

MRKTRLWGLLWMLFVSELRAATKLTEEKYELKEGQTLDVKCDYTLEKFASSQKAWQIIRDGEMPKTLA
CTERPSKNSHPVQVGRIILEDYHDHGLLRVRMVNLQVEDSGLYQCVIYQPPKEPHMLFDRIRLVVTKG
FSGTPGSNENSTQNVYKIPPTTTKALCPLYTSPRTVTQAPPKSTADVSTPDSEINLTNVTDIIRVPVF
NIVILLAGGFLSKSLVFSVLFAVTLRSFVP (signal sequence is underlined);

(B) Human TREM-1 isoform 2 (Accession No. NP_001229518.1; SEQ ID NO: 2; encoded by the nucleotide sequence having Accession No. NM_001242589; SEQ ID NO: 5):

MRKTRLWGLLWMLFVSELRAATKLTEEKYELKEGQTLDVKCDYTLEKFASSQKAWQIIRDGEMPKTLA
CTERPSKNSHPVQVGRIILEDYHDHGLLRVRMVNLQVEDSGLYQCVIYQPPKEPHMLFDRIRLVVTKG
FSGTPGSNENSTQNVYKIPPTTTKALCPLYTSPRTVTQAPPKSTADVSTPDSEINLTNVTDIIRYSFQ
VPGPLVWTLSPLFPSLCAERM (signal sequence is underlined);

(C) Human TREM-1 isoform 3 (Accession No. NP_001229519; SEQ ID NO: 3; encoded by the nucleotide sequence having Accession No. NM_001242590; SEQ ID NO: 6):

MRKTRLWGLLWMLFVSELRAATKLTEEKYELKEGQTLDVKCDYTLEKFASSQKAWQIIRDGEMPKTLA
CTERPSKNSHPVQVGRIILEDYHDHGLLRVRMVNLQVEDSGLYQCVIYQPPKEPHMLFDRIRLVVTKG
FRCSTLSFSWLVDS (signal sequence is underlined).

[0059] Cynomolgus TREM-1 protein (Accession No. XP_001082517; SEQ ID NO: 7) is predicted to have the following amino acid sequence:

MRKTRLWGLLWMLFVSELRATTELTEEKYEYKEGQTLEVKCDYALEKYANSRKAWQKMEGKMPKILAK
TERPSENSHPVQVGRITLEDYPDHGLLQVQMTNLQVEDSGLYQCVIYQHPKESHVLFNPICLVVTKGS
SGTPGSSENSTQNVYRTPSTTAKALGPRYTSPRTVTQAPPESTVVVSTPGSEINLTNVTDIIRVPVFN
IVIIVAGGFLSKSLVFSVLFAVTLRSFGP (signal sequence is underlined).

[0060] The present disclosure relates to antibodies that specifically bind and block the function of TREM-1. The antibodies block TREM-1 function by reducing/blocking TREM-1 activation and downstream signaling.

[0061] The anti-TREM-1 antibodies of the present disclosure block TREM-1 signaling by means of one or a combination of several different mechanisms, blocking TREM-1 directly or indirectly. In one embodiment, the antibodies prevent the natural ligand of TREM-1, peptidoglycan recognition protein 1 (PGLYRP1), from creating a functional complex with TREM-1. In another embodiment, the antibodies block TREM-1 by preventing individual TREM-1 molecules from forming dimers or multimers. In some embodiments, the TREM-1 dimerization or multimerization is reduced or prevented by anti-TREM-1 antibodies that are capable of binding to a portion of TREM-1 that would otherwise reside in the interface of a TREM-1 dimer, thus preventing individual TREM-1 molecules

from associating with one another. In other embodiments, the TREM-1 dimerization or multimerization is reduced or prevented by anti-TREM-1 antibodies that interfere with the interaction of TREM-1 with its ligand.

[0062] In some embodiments, the anti-TREM-1 antibodies can block PGLYRP1-induced activation of TREM-1. PGLYRP1, a highly conserved, 196 amino acid long protein consisting of a signal peptide and a peptidoglycan binding domain, is expressed in neutrophils and released upon their activation. The amino acid sequence of PGLYRP1 (Accession No. NP_005082.1; SEQ ID NO: 8) is provided below:

MSRRSMLLAWALPSLLRLGAAQETEDPACCSPIVPRNEWKALASECAQHLSLPLRYVVVSHTAGSSCN
TPASCQQQARNVQHYHMKTLGWCDVGYNFLIGEDGLVYEGRGWNFTGAHSGHLWNPMSIGISFMGNYM
DRVPTPQAIRAAQGLLACGVAQGALRSNYVLKGHRDVQRTLSPGNQLYHLIQNWPHYRSP (signal sequence is underlined).

[0063] Accordingly, in some embodiments, the anti-TREM-1 antibodies of the present disclosure down-regulate or block the release of proinflammatory cytokines from myeloid cells (e.g., dendritic cells and monocytes). In some embodiments, the anti-TREM-1 antibodies block the release of TNF-α, MIP-1beta, MCP-1, IL-1beta, GM-CSF, IL-6 and/or IL-8 from macrophages, neutrophils, synovial tissue cells and/or a reporter cell, as disclosed herein.

[0064] While the controlled release of inflammatory cytokines in response to foreign antigens can be beneficial (e.g., mounting an effective adaptive immune response), too much inflammatory cytokine release can have dire consequences. For instance, one common and toxic clinical complication that have been observed with the *in vivo* administration of certain antibodies against cell surface immune receptors (e.g., anti-human CD3 antibodies such as OKT3) is the cytokine release syndrome (CRS), which is associated with the excessive release of various cytokines (e.g., TNF-alpha, IFN-gamma, and IL-2) into the circulation. CRS can occur as a result of the simultaneous binding of the antibodies to its cognate antigen (e.g., CD3 on T cells) (via the variable region of the antibody) and the Fc receptors (e.g., FcγRs) and/or complement receptors (via the constant region of the antibody) on the accessory cells (e.g., antigen presenting cells). This interaction results in the activation of the cells (e.g., T cells and/or the accessory cells) and the release of various cytokines that produce a systemic inflammatory response characterized by hypotension, pyrexia, and rigors. Other symptoms of CRS include fever, chills, nausea, vomiting, and dyspnea.

[0065] In addition to blocking the PGLYRP1-induced production of inflammatory cytokines, in one embodiment, the anti-TREM-1 antibodies of the present disclosure reduces the incidence of or results in no incidence of cytokine release syndrome when administered to a subject in need thereof. In some embodiments, the anti-TREM-1 antibodies do not induce the expression of inflammatory cytokines by cells (e.g., dendritic cells) when the cells are incubated in the presence of the antibody alone, compared to an antibody comprising a heavy chain consisting of the amino acid sequence as set forth in SEQ ID NO: 76 and a light chain consisting of the amino acid sequence as set forth in SEQ

ID NO: 54. In some embodiments, the anti-TREM-1 antibodies have decreased binding to one or more FcγRs, which can help reduce the onset of CSR.

[0066] In some embodiments, the anti-TREM-1 antibodies of the present disclosure bind both human TREM-1 and TREM-1 from another species. The term "TREM-1", as used herein, thus encompasses any naturally occurring form of TREM-1 which can be derived from any suitable organism. For example, TREM-1 for use as described herein can be vertebrate TREM-1, such as mammalian TREM-1, such as TREM-1 from a primate (such as a human, a chimpanzee, a cynomolgus monkey, or a rhesus monkey); a rodent (such as a mouse or a rat), a lagomorph (such as a rabbit), or an artiodactyl (such a cow, sheep, pig or camel). In certain embodiments, TREM-1 is SEQ ID NO: 1 (human TREM-1, isoform 1). The TREM-1 can be a mature form of TREM-1, such as a TREM-1 protein that has undergone post-translational processing within a suitable cell. Such a mature TREM-1 protein can, for example, be glycosylated. The TREM-1 can be a full length TREM-1 protein.

[0067] In some embodiments, the anti-TREM-1 antibodies of the present disclosure are monoclonal antibodies, in the sense that they are directly or indirectly derived from a single clone of a B lymphocyte. In some embodiments, the anti-TREM-1 antibodies are produced, screened, and purified using, for example, the methods described in the Examples of International Publ. No. WO 2013/120553. In brief, a suitable mouse such as a TREM-1 or TREM- l/TREM-3 knock-out (KO) mouse are immunized with TREM-1, a cell expressing TREM-1, or a combination of both. In another embodiment, the anti-TREM-1 antibodies are polyclonal antibodies, in the sense that they are mixture of monoclonal antibodies as disclosed herein.

[0068] In some embodiments, the anti-TREM-1 antibodies of the current disclosure are recombinantly expressed in prokaryotic or eukaryotic cells. In some embodiments, the prokaryotic cell is *E. coli*. In certain embodiments, the eukaryotic is a yeast, insect, or mammalian cell, such as a cell derived from an organism that is a primate (such as a human, a chimpanzee, a cynomolgus monkey or a rhesus monkey), a rodent (such as a mouse or a rat), a lagomorph (such as a rabbit) or an artiodactyl (such a cow, sheep, pig or camel). Suitable mammalian cell lines include, but are not limited to, HEK293 cells, CHO cells, and HELA cells. The anti-TREM-1 antibodies as disclosed herein can also be produced by means of other methods known to the person skilled in the art, such as a phage display or a yeast display. Once produced, the antibodies can be screened for binding to, for example, full length TREM-1 or mutants thereof using the methods described in the Examples of International Publ. No. WO 2013/120553.

[0069] The term "antibody" as used herein refers to a protein, derived from a germline immunoglobulin sequence, which is capable of specifically binding to an antigen (TREM-1) or a portion thereof. The term includes full length antibodies of any class or isotype (that is, IgA, IgE, IgG, IgM and/or IgY) and any single chain or fragment thereof. An antibody that specifically binds to an antigen, or portion thereof, may bind exclusively to that antigen, or portion thereof, or it may bind to a

limited number of homologous antigens, or portions thereof.Full-length antibodies usually comprise at least four polypeptide chains: two heavy (H) chains and two light (L) chains that are interconnected by disulfide bonds. One immunoglobulin sub-class of particular pharmaceutical interest is the IgG family. In humans, the IgG class may be sub-divided into 4 sub-classes: IgG1, IgG2, IgG3 and IgG4, based on the sequence of their heavy chain constant regions. The light chains can be divided into two types, kappa and lambda, based on differences in their sequence composition. IgG molecules are composed of two heavy chains, interlinked by two or more disulfide bonds, and two light chains, each attached to a heavy chain by a disulfide bond. A heavy chain may comprise a heavy chain variable region (VH) and up to three heavy chain constant (CH) regions: CH1, CH2 and CH3. A light chain may comprise a light chain variable region (VL) and a light chain constant region (CL). VH and VL regions can be further subdivided into regions of hypervariability, termed complementarity determining regions (CDRs), interspersed with regions that are more conserved, termed framework regions (FR). VH and VL regions are typically composed of three CDRs and four FRs, arranged from amino-terminus to carboxy-terminus in the following order: FR1, CDR1, FR2, CDR2, FR3, CDR3, FR4. The hypervariable regions of the heavy and light chains form a binding domain that is capable of interacting with an antigen, whilst the constant region of an antibody may mediate binding of the immunoglobulin to host tissues or factors, including but not limited to various cells of the immune system (effector cells), Fc receptors and the first component (C1q) of the classical complement system. Antibodies of the current invention may be isolated. The term "isolated antibody" refers to an antibody that has been separated and/or recovered from (an)other component(s) in the environment in which it was produced and/or that has been purified from a mixture of components present in the environment in which it was produced. Certain antigen-binding fragments of antibodies may be suitable in the context of the current invention, as it has been shown that the antigen-binding function of an antibody can be performed by fragments of a full-length antibody.

[0070] The term "antigen-binding portion" of an antibody refers to one or more fragment(s) of an antibody that retain the ability to specifically bind to an antigen, such as TREM-1, as described herein. Examples of antigen-binding fragments include Fab, Fab', F(ab)2, F(ab')2, F(ab)S, Fv (typically the VL and VH domains of a single arm of an antibody), single-chain Fv (scFv; *see, e.g.*, Bird *et al.*, *Science* 242:42S-426 (1988); Huston *et al.*, *PNAS* 85: 5879-5883 (1988)), dsFv, Fd (typically the VH and CH1 domain), and dAb (typically a VH domain) fragments; VH, VL, VhH, and V-NAR domains; monovalent molecules comprising a single VH and a single VL chain; minibodies, diabodies, triabodies, tetrabodies, and kappa bodies (*see, e.g.,* Ill *et al.*, *Protein Eng* 10:949-57 (1997)); camel IgG; IgNAR; as well as one or more isolated CDRs or a functional paratope, where the isolated CDRs or antigen-binding residues or polypeptides can be associated or linked together so as to form a functional antibody fragment. Various types of antibody fragments have been described or reviewed in, *e.g.*, Holliger and Hudson, *Nat Biotechnol* 2S :1126-1136 (2005) ; International Publ. No. WO 2005/040219, and U.S. Publ. Nos. 2005/0238646 and 2002/0161201. These antibody

fragments may be obtained using conventional techniques known to those of skill in the art, and the fragments may be screened for utility in the same manner as intact antibodies.

[0071] A "human" antibody (HuMAb) refers to an antibody having variable regions in which both the framework and CDR regions are derived from human germline immunoglobulin sequences. Furthermore, if the antibody contains a constant region, the constant region also is derived from human germline immunoglobulin sequences. The anti-TREM-1 antibodies described herein can include amino acid residues not encoded by human germline immunoglobulin sequences (*e.g.,* mutations introduced by random or site-specific mutagenesis *in vitro* or by somatic mutation *in vivo*). However, the term "human antibody", as used herein, is not intended to include antibodies in which CDR sequences derived from the germline of another mammalian species, such as a mouse, have been grafted onto human framework sequences. The terms "human" antibodies and "fully human" antibodies are used synonymously.

[0072] A "humanized" antibody refers to a human/non-human chimeric antibody that contains one or more sequences (CDR regions or parts thereof) that are derived from a non-human immunoglobulin. A humanised antibody is, thus, a human immunoglobulin (recipient antibody) in which at least residues from a hyper-variable region of the recipient are replaced by residues from a hyper-variable region of an antibody from a non-human species (donor antibody) such as from a mouse, rat, rabbit or non-human primate, which have the desired specificity, affinity, sequence composition and functionality. In some instances, FR residues of the human immunoglobulin are replaced by corresponding non-human residues. An example of such a modification is the introduction of one or more so-called back-mutations, which are typically amino acid residues derived from the donor antibody. Humanization of an antibody may be carried out using recombinant techniques known to the person skilled in the art (*see, e.g.*, Antibody Engineering, Methods in Molecular Biology, vol. 248, edited by Benny K. C. Lo). A suitable human recipient framework for both the light and heavy chain variable domain may be identified by, for example, sequence or structural homology. Alternatively, fixed recipient frameworks may be used, e.g., based on knowledge of structure, biophysical and biochemical properties. The recipient frameworks can be germline derived or derived from a mature antibody sequence. CDR regions from the donor antibody can be transferred by CDR grafting. The CDR grafted humanised antibody can be further optimised for e.g. affinity, functionality and biophysical properties by identification of critical framework positions where re-introduction (backmutation) of the amino acid residue from the donor antibody has beneficial impact on the properties of the humanized antibody. In addition to donor antibody derived backmutations, the humanized antibody can be engineered by introduction of germline residues in the CDR or framework regions, elimination of immunogenic epitopes, site-directed mutagenesis, affinity maturation, etc.

[0073] Furthermore, humanized antibodies can comprise residues that are not found in the recipient antibody or in the donor antibody. These modifications are made to further refine antibody

performance. In general, a humanised antibody will comprise at least one - typically two - variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and in which all or substantially all of the FR residues are those of a human immunoglobulin sequence. The humanised antibody can, optionally, also comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin. The term "humanised antibody derivative" refers to any modified form of the humanised antibody, such as a conjugate of the antibody and another agent or antibody.

[0074] The term "recombinant human antibody," as used herein, includes all human antibodies that are prepared, expressed, created or isolated by recombinant means, such as (a) antibodies isolated from an animal (*e.g.,* a mouse) that is transgenic or transchromosomal for human immunoglobulin genes or a hybridoma prepared therefrom, (b) antibodies isolated from a host cell transformed to express the antibody, *e.g.,* from a transfectoma, (c) antibodies isolated from a recombinant, combinatorial human antibody library, and (d) antibodies prepared, expressed, created or isolated by any other means that involve splicing of human immunoglobulin gene sequences to other DNA sequences. Such recombinant human antibodies comprise variable and constant regions that utilize particular human germline immunoglobulin sequences are encoded by the germline genes, but include subsequent rearrangements and mutations which occur, for example, during antibody maturation. As known in the art (*see*, *e.g.,* Lonberg *Nature Biotech.* 23(9): 1117- 1125 (2005)), the variable region contains the antigen binding domain, which is encoded by various genes that rearrange to form an antibody specific for a foreign antigen. In addition to rearrangement, the variable region can be further modified by multiple single amino acid changes (referred to as somatic mutation or hypermutation) to increase the affinity of the antibody to the foreign antigen. The constant region will change in further response to an antigen (*i.e.,* isotype switch). Therefore, the rearranged and somatically mutated nucleic acid molecules that encode the light chain and heavy chain immunoglobulin polypeptides in response to an antigen cannot have sequence identity with the original nucleic acid molecules, but instead will be substantially identical or similar (*i.e.,* have at least 80% identity).

[0075] A "chimeric antibody" refers to an antibody in which the variable regions are derived from one species and the constant regions are derived from another species, such as an antibody in which the variable regions are derived from a mouse antibody and the constant regions are derived from a human antibody.

[0076] In one embodiment, the anti-TREM-1 antibodies of the current disclosure are IgG antibodies. An "IgG antibody", *e.g.*, a human IgG1, as used herein has, in certain embodiments, the structure of a naturally occurring IgG antibody, *i.e.*, it has the same number of heavy and light chains and disulfide bonds as a naturally occurring IgG antibody of the same subclass. For example, the TREM-1 IgG1 antibody consists of two heavy chains (HCs) and two light chains (LCs), wherein the two heavy chains and light chains are linked by the same number and location of disulfide bridges that

occur in naturally occurring IgG1antibody (unless the antibody has been mutated to modify the disulfide bridges).

[0077] As used herein, "isotype" refers to the antibody class (*e.g.,* IgG1, IgG2, IgG3, IgG4, IgM, IgA1, IgA2, IgD, and IgE antibody) that is encoded by the heavy chain constant region genes.

[0078] "Allotype" refers to naturally occurring variants within a specific isotype group, which variants differ in a few amino acids (*see, e.g.,* Jefferis *et al.*, *mAbs* 1:1 (2009)). Anti-TREM-1 antibodies described herein can be of any allotype. In some embodiments, the anti-TREM-1 antibodies are of "IgG1.3f" allotype, which comprises one or more amino acid substitutions selected from the group consisting of L234A, L235E, and G237A, per EU numbering, as compared to a wild-type IgG1 isotype (e.g., SEQ ID NO: 9). In other embodiments, the anti-TREM-1 antibodies are of "IgG1.1f" allotype, which comprises one or more amino acid substitutions selected from the group consisting of L234A, L235E, G237A, A330S, and P331S, per EU numbering, as compared to a wild-type IgG1 isotype (e.g., SEQ ID NO: 9). In certain embodiments, the anti-TREM-1 antibodies are of "IgG1-Aba" allotype, which comprises one or more amino acid substitutions selected from the group consisting of K214R, C226S, C229S, and P238S, per EU numbering, as compared to a wild-type IgG1 isotype (e.g., SEQ ID NO: 9). In further embodiments, the anti-TREM-1 antibodies are of "IgG4-Aba" allotype, which comprises the CH1 domain of a wild-type IgG4 isotype (e.g., SEQ ID NO: 10) and CH2 and CH3 domains of IgG1. In some embodiments, the IgG4-Aba allotype antibody comprises one or more amino acid substitutions selected from the group consisting of S131C, K133R, G137E, G138S, Q196K, I199T, N203D, K214R, C226S, C229S, and P238S, per EU numbering, as compared to a wild-type IgG1 isotype (e.g., SEQ ID NO: 9).

[0079] 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."

[0080] An "isolated antibody," as used herein, is intended to refer to an antibody that has been separated and/or recovered from (an)other component(s) in the environment in which it was produced and/or that has been purified from a mixture of components present in the environment in which it was produced.

[0081] An "effector function" refers to the interaction of an antibody Fc region with an Fc receptor or ligand, or a biochemical event that results therefrom. Exemplary "effector functions" include C1q binding, complement dependent cytotoxicity (CDC), Fc receptor binding, FcγR-mediated effector functions such as ADCC and antibody dependent cell-mediated phagocytosis (ADCP), and downregulation of a cell surface receptor (*e.g.,* the B cell receptor; BCR). Such effector functions generally require the Fc region to be combined with a binding domain (*e.g.,* an antibody variable domain). In one embodiment, the anti-TREM-1 antibodies of the current disclosure comprise Fc regions that do not bind to one or more FcγRs and therefore, lack effector function (i.e., effectorless).

[0082] An "Fc receptor" or "FcR" is a receptor that binds to the Fc region of an immunoglobulin. FcRs that bind to an IgG antibody comprise receptors of the FcγR family, including allelic variants and alternatively spliced forms of these receptors. The FcγR family consists of three activating (FcγRI, FcγRIII, and FcγRIV in mice; FcγRIA, FcγRIIA, and FcγRIIIA in humans) and one inhibitory (FcγRIIB) receptor. Various properties of human FcγRs are known in the art. The majority of innate effector cell types coexpress one or more activating FcγR and the inhibitory FcγRIIB, whereas natural killer (NK) cells selectively express one activating Fc receptor (FcγRIII in mice and FcγRIIIA in humans) but not the inhibitory FcγRIIB in mice and humans. Human IgG1 binds to most human Fc receptors and is considered equivalent to murine IgG2a with respect to the types of activating Fc receptors that it binds to.

[0083] An "Fc region" (fragment crystallizable region) or "Fc domain" or "Fc" refers to the C-terminal region of the heavy chain of an antibody that mediates the binding of the immunoglobulin to host tissues or factors, including binding to Fc receptors located on various cells of the immune system (*e.g.,* effector cells) or to the first component (C1q) of the classical complement system. Thus, an Fc region comprises the constant region of an antibody excluding the first constant region immunoglobulin domain (*e.g.,* CH1 or CL).

[0084] In IgG, the Fc region comprises immunoglobulin domains CH2 and CH3 and the hinge between CH1 and CH2 domains. Although the definition of the boundaries of the Fc region of an immunoglobulin heavy chain might vary, as defined herein, the human IgG heavy chain Fc region is defined to stretch from an amino acid residue D221 for IgG1, V222 for IgG2, L221 for IgG3 and P224 for IgG4 to the carboxy-terminus of the heavy chain, wherein the numbering is according to the EU index as in Kabat. The CH2 domain of a human IgG Fc region extends from amino acid 237 to amino acid 340, and the CH3 domain is positioned on C-terminal side of a CH2 domain in an Fc region, *i.e.,* it extends from amino acid 341 to amino acid 447 or 446 (if the C-terminal lysine residue is absent) or 445 (if the C-terminal glycine and lysine residues are absent) of an IgG. As used herein, the Fc region can be a native sequence Fc, including any allotypic variant, or a variant Fc (*e.g.,* a non-naturally occurring Fc). Fc can also refer to this region in isolation or in the context of an Fc-comprising protein polypeptide such as a "binding protein comprising an Fc region," also referred to as an "Fc fusion protein" (*e.g.,* an antibody or immunoadhesion).

[0085] A "native sequence Fc region" or "native sequence Fc" comprises an amino acid sequence that is identical to the amino acid sequence of an Fc region found in nature. Native sequence human Fc regions include a native sequence human IgG1 Fc region; native sequence human IgG2 Fc region; native sequence human IgG3 Fc region; and native sequence human IgG4 Fc region as well as naturally occurring variants thereof. Native sequence Fc include the various allotypes of Fcs (*see, e.g.,* Jefferis *et al.*, *mAbs* 1: 1 (2009)).

[0086] A "variant sequence Fc region" or "non-naturally occurring Fc" comprises a modification, typically to alter one or more of its functional properties, such as serum half-life, complement

fixation, Fc-receptor binding, protein stability and/or antigen-dependent cellular cytotoxicity, or lack thereof, among others. In some embodiments, the anti-TREM-1 antibodies of the present disclosure can be chemically modified (e.g., one or more chemical moieties can be attached to the antibody) or be modified to alter its glycosylation, again to alter one or more functional properties of the antibody. In one embodiment, the anti-TREM-1 antibody is an IgG1 isotype and carries a modified Fc domain comprising one or more, and perhaps all of the following mutations that will result in decreased affinity to certain Fc receptors (L234A, L235E, and G237A) and in reduced C1q-mediated complement fixation (A330S and P331S), respectively (residue numbering according to the EU index).

[0087] The terms "hinge," "hinge domain," "hinge region," and "antibody hinge region" refer to the domain of a heavy chain constant region that joins the CH1 domain to the CH2 domain and includes the upper, middle, and lower portions of the hinge (Roux *et al.*, *J Immunol* 161:4083 (1998)). The hinge provides varying levels of flexibility between the binding and effector regions of an antibody and also provides sites for intermolecular disulfide bonding between the two heavy chain constant regions. As used herein, a hinge starts at Glu216 and ends at Gly237 of all IgG isotypes (Roux *et al.*, *J Immunol* 161:4083 (1998)). The sequencse of wildtype IgG1, IgG2, IgG3, and IgG4 hinges are known in the art (e.g., International PCT publication no. WO 2017/087678). In one embodiment, the hinge region of CH1 of the anti-TREM-1 antibodies is modified such that the number of cysteine residues in the hinge region is altered, e.g., increased or decreased. This approach is described further for instance in U.S. Pat. No. 5,677,425.

[0088] The constant region may be modified to stabilize the antibody, e.g., to reduce the risk of a bivalent antibody separating into two monovalent VH-VL fragments. For example, in an IgG4 constant region, residue S228 (residue numbering according to the EU index) may be mutated to a proline (P) residue to stabilize inter heavy chain disulphide bridge formation at the hinge (*see, e.g.*, Angal *et al.*, *Mol Immunol.* 30: 105-8(1995)). Antibodies or fragments thereof can also be defined in terms of their complementarity-determining regions (CDRs). The term "complementarity-determining region" or "hypervariable region", when used herein, refers to the regions of an antibody in which amino acid residues involved in antigen binding are situated. The region of hypervariability or CDRs can be identified as the regions with the highest variability in amino acid alignments of antibody variable domains. Databases can be used for CDR identification such as the Kabat database, the CDRs e.g., being defined as comprising amino acid residues 24-34 (CDR1), 50-59 (CDR2) and 89-97 (CDR3) of the light-chain variable domain, and 31-35 (CDR1), 50-65 (CDR2) and 95-102 (CDR3) in the heavy-chain variable domain; (Kabat et al. 1991 ; Sequences of Proteins of Immunological Interest, Fifth Edition, U.S. Department of Health and Human Services, NIH Publication No. 91-3242) Alternatively CDRs can be defined as those residues from a "hypervariable loop" (residues 26-33 (L1), 50-52 (L2) and 91-96 (L3) in the light-chain variable domain and 26-32 (H1), 53-55 (H2) and 96-101 (H3) in the heavy-chain variable domain (Chothia and Lesk, *J. Mol. Biol* 196 : 901-917

(1987)). Typically, the numbering of amino acid residues in this region is performed by the method described in Kabat et al., supra. Phrases such as "Kabat position", "Kabat residue", and "according to Kabat" herein refer to this numbering system for heavy chain variable domains or light chain variable domains. Using the Kabat numbering system, the actual linear amino acid sequence of a peptide may contain fewer or additional amino acids corresponding to a shortening of, or insertion into, a framework (FR) or CDR of the variable domain. For example, a heavy chain variable domain may include amino acid insertions (residue 52a, 52b and 52c according to Kabat) after residue 52 of CDR H2 and inserted residues (e.g. residues 82a, 82b, and 82c, etc. according to Kabat) after heavy chain FR residue 82. The Kabat numbering of residues may be determined for a given antibody by alignment at regions of homology of the sequence of the antibody with a "standard" Kabat numbered sequence.

[0089] The term "epitope" or "antigenic determinant" refers to a site on an antigen (*e.g.,* TREM-1) to which an immunoglobulin or antibody specifically binds, *e.g.,* as defined by the specific method used to identify it. Epitopes can be formed both from contiguous amino acids (usually a linear epitope) or noncontiguous amino acids juxtaposed by tertiary folding of a protein (usually a conformational epitope). Epitopes formed from contiguous amino acids are typically, but not always, retained on exposure to denaturing solvents, whereas epitopes formed by tertiary folding are typically lost on treatment with denaturing solvents. An epitope typically includes at least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 or 15 amino acids in a unique spatial conformation. Methods for determining what epitopes are bound by a given antibody (*i.e.,* epitope mapping) are well known in the art and include, for example, immunoblotting and immunoprecipitation assays, wherein overlapping or contiguous peptides from (*e.g.,* from TREM-1) are tested for reactivity with a given antibody (*e.g.,* anti-TREM-1 antibody). Methods of determining spatial conformation of epitopes include techniques in the art and those described herein, for example, x-ray crystallography, antigen mutational analysis, 2-dimensional nuclear magnetic resonance and HDX-MS (*see*, *e.g.,* Epitope Mapping Protocols in Methods in Molecular Biology, Vol. 66, G. E. Morris, Ed. (1996)).

[0090] The term "binds to the same epitope" with reference to two or more antibodies means that the antibodies bind to the same segment of amino acid residues, as determined by a given method. Techniques for determining whether antibodies bind to the "same epitope on TREM-1" with the antibodies described herein include, for example, epitope mapping methods, such as, x-ray analyses of crystals of antigen:antibody complexes which provides atomic resolution of the epitope and hydrogen/deuterium exchange mass spectrometry (HDX-MS). Other methods monitor the binding of the antibody to antigen fragments or mutated variations of the antigen where loss of binding due to a modification of an amino acid residue within the antigen sequence is often considered an indication of an epitope component. In addition, computational combinatorial methods for epitope mapping can also be used. These methods rely on the ability of the antibody of interest to affinity isolate specific

short peptides from combinatorial phage display peptide libraries. Antibodies having the same VH and VL or the same CDR1, 2 and 3 sequences are expected to bind to the same epitope.

[0091] Antibodies that "compete with another antibody for binding to a target" refer to antibodies that inhibit (partially or completely) the binding of the other antibody to the target. Whether two antibodies compete with each other for binding to a target, *i.e.,* whether and to what extent one antibody inhibits the binding of the other antibody to a target, can be determined using known competition experiments, *e.g.*, BIACORE® surface plasmon resonance (SPR) analysis. In certain embodiments, an antibody competes with, and inhibits binding of another antibody to a target by at least 50%, 60%, 70%, 80%, 90% or 100%. The level of inhibition or competition can be different depending on which antibody is the "blocking antibody" (*i.e.,* the cold antibody that is incubated first with the target). Competition assays can be conducted as described, for example, in Ed Harlow and David Lane, Cold Spring Harb Protoc ; 2006; doi: 10.1101/pdb.prot4277 or in Chapter 11 of "Using Antibodies" by Ed Harlow and David Lane, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, USA 1999. Two antibodies "cross-compete" if antibodies block each other both ways by at least 50%, *i.e.*, regardless of whether one or the other antibody is contacted first with the antigen in the competition experiment.

[0092] As used herein, the terms "specific binding," "selective binding," "selectively binds," and "specifically binds," refer to antibody binding to an epitope on a predetermined antigen. Typically, the antibody (i) binds with an equilibrium dissociation constant (K_D) of approximately less than 10^{-7} M, such as approximately less than 10^{-8} M, 10^{-9} M or 10^{-10} M or even lower when determined by, *e.g.,* surface plasmon resonance (SPR) technology in a BIACORE® 2000 instrument using the predetermined antigen, *e.g.,* recombinant human TREM-1, as the analyte and the antibody as the ligand, or Scatchard analysis of binding of the antibody to antigen positive cells, and (ii) binds to the predetermined antigen with an affinity that is at least two-fold greater than its affinity for binding to a non-specific antigen (*e.g.,* BSA, casein) other than the predetermined antigen or a closely-related antigen. Accordingly, an antibody that "specifically binds to human TREM-1" refers to an antibody that binds to soluble or cell bound human TREM-1 with a K_D of 10^{-7} M or less, such as approximately less than 10^{-8} M, 10^{-9} M or 10^{-10} M or even lower. An antibody that "cross-reacts with cynomolgus TREM-1" refers to an antibody that binds to cynomolgus TREM-1 with a K_D of 10^{-7} M or less, such as approximately less than 10^{-8} M, 10^{-9} M or 10^{-10} M or even lower. In certain embodiments, such antibodies that do not cross-react with TREM-1 from a non-human species exhibit essentially undetectable binding against these proteins in standard binding assays.

[0093] The term "binding specificity" herein refers to the interaction of a molecule such as an antibody, or fragment thereof, with a single exclusive antigen, or with a limited number of highly homologous antigens (or epitopes). In contrast, antibodies that are capable of specifically binding to TREM-1 are not capable of binding dissimilar molecules. Antibodies according to the invention may not be capable of binding Nkp44, the Natural killer cell p44-related protein.

[0094] The specificity of an interaction and the value of an equilibrium binding constant can be determined directly by well-known methods. Standard assays to evaluate the ability of ligands (such as antibodies) to bind their targets are known in the art and include, for example, ELISAs, Western blots, RIAs, and flow cytometry analysis. The binding kinetics and binding affinity of the antibody also can be assessed by standard assays known in the art, such as SPR.

[0095] Competitive binding assays for determining whether two antibodies compete or cross-compete for binding include: competition for binding to myeloid cells expressing TREM-1, *e.g.,* by flow cytometry, such as described in the Examples. Other methods include: SPR (*e.g.,* BIACORE®), solid phase direct or indirect radioimmunoassay (RIA), solid phase direct or indirect enzyme immunoassay (EIA), sandwich competition assay (*see* Stahli *et al.*, *Methods in Enzymology* 9:242 (1983)); solid phase direct biotin-avidin EIA (*see* Kirkland *et al.*, *J. Immunol.* 137:3614 (1986)); solid phase direct labeled assay, solid phase direct labeled sandwich assay (*see* Harlow and Lane, Antibodies: A Laboratory Manual, Cold Spring Harbor Press (1988)); solid phase direct label RIA using 1-125 label (*see* Morel *et al.*, *Mol. Immunol.* 25(1):7 (1988)); solid phase direct biotin-avidin EIA (Cheung *et al.*, *Virology* 176:546 (1990)); and direct labeled RIA. (Moldenhauer *et al.*, *Scand. J. Immunol.* 32:77 (1990)).

[0096] As used herein, the term "bin" is defined using a reference antibody. If a second antibody is unable to bind to an antigen at the same time as the reference antibody, the second antibody is said to belong to the same "bin" as the reference antibody. In this case, the reference and the second antibody competitively bind the same part of an antigen and are coined "competing antibodies". If a second antibody is capable of binding to an antigen at the same time as the reference antibody, the second antibody is said to belong to a separate "bin". In this case, the reference and the second antibody do not competitively bind the same part of an antigen and are coined "non-competing antibodies".

[0097] Antibody "binning" does not provide direct information about the epitope. Competing antibodies, i.e., antibodies belonging to the same "bin" can have identical epitopes, overlapping epitopes, or even separate epitopes. The latter is the case if the reference antibody bound to its epitope on the antigen takes up the space required for the second antibody to contact its epitope on the antigen ("steric hindrance"). Non-competing antibodies generally have separate epitopes.

[0098] The term "binding affinity" herein refers to a measurement of the strength of a non-covalent interaction between two molecules, e.g. an antibody, or fragment thereof, and an antigen. The term "binding affinity" is used to describe monovalent interactions (intrinsic activity).

[0099] The binding affinity between two molecules, e.g. an antibody, or fragment thereof, and an antigen, through a monovalent interaction may be quantified by determination of the equilibrium dissociation constant (K_D). In turn, K_D can be determined by measurement of the kinetics of complex formation and dissociation, e.g. by the SPR method. The rate constants corresponding to the association and the dissociation of a monovalent complex are referred to as the association rate

constant k_a (or k_{on}) and dissociation rate constant k_d (or k_{0ff}), respectively. $K_D$is related to k_a and k_d through the equation $K_D = k_d / k_a$. Following the above definition, binding affinities associated with different molecular interactions, such as comparison of the binding affinity of different antibodies for a given antigen, may be compared by comparison of the K_D values for the individual antibody/antigen complexes.

[0100] As used herein, the term "high affinity" for an IgG antibody refers to an antibody having a K_D of 10^{-8} M or less, 10^{-9} M or less, or 10^{-10} M or less for a target antigen. However, "high affinity" binding can vary for other antibody isotypes. For example, "high affinity" binding for an IgM isotype refers to an antibody having a K_D of 10^{-10} M or less, or 10^{-8} M or less.

[0101] The term "EC_{50}" in the context of an *in vitro* or *in vivo* assay using an antibody or antigen binding fragment thereof, refers to the concentration of an antibody or an antigen-binding portion thereof that induces a response that is 50% of the maximal response, *i.e.,* halfway between the maximal response and the baseline.

[0102] The term "naturally-occurring" as used herein as applied to an object refers to the fact that an object can be found in nature. For example, a polypeptide or polynucleotide sequence that is present in an organism (including viruses) that can be isolated from a source in nature and which has not been intentionally modified by man in the laboratory is naturally- occurring.

[0103] A "polypeptide" refers to a chain comprising at least two consecutively linked amino acid residues, with no upper limit on the length of the chain. One or more amino acid residues in the protein can contain a modification such as, but not limited to, glycosylation, phosphorylation or disulfide bond formation. A "protein" can comprise one or more polypeptides.

[0104] The term "nucleic acid molecule," as used herein, is intended to include DNA molecules and RNA molecules. A nucleic acid molecule can be single-stranded or double-stranded, and can be cDNA.

[0105] "Conservative amino acid substitutions" refer to substitutions of an amino acid residue with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (*e.g.,* lysine, arginine, histidine), acidic side chains (*e.g.,* aspartic acid, glutamic acid), uncharged polar side chains (*e.g.,* glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine, tryptophan), nonpolar side chains (*e.g.,* alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine), beta-branched side chains (*e.g.,* threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). In certain embodiments, a predicted nonessential amino acid residue in an anti-TREM-1 antibody is replaced with another amino acid residue from the same side chain family. Methods of identifying nucleotide and amino acid conservative substitutions which do not eliminate antigen binding are well-known in the art (*see*, *e.g.,* Brummell *et al.*, *Biochem.* 32: 1180-1187 (1993); Kobayashi *et al. Protein Eng.* 12(10):879-884 (1999); and Burks *et al. Proc. Natl. Acad. Sci. USA* 94:412-417 (1997)).

[0106] For nucleic acids, the term "substantial homology" indicates that two nucleic acids, or designated sequences thereof, when optimally aligned and compared, are identical, with appropriate nucleotide insertions or deletions, in at least about 80% of the nucleotides, at least about 90% to 95%, or at least about 98% to 99.5% of the nucleotides. Alternatively, substantial homology exists when the segments will hybridize under selective hybridization conditions, to the complement of the strand.

[0107] For polypeptides, the term "substantial homology" indicates that two polypeptides, or designated sequences thereof, when optimally aligned and compared, are identical, with appropriate amino acid insertions or deletions, in at least about 80% of the amino acids, at least about 90% to 95%, or at least about 98% to 99.5% of the amino acids.

[0108] The percent identity between two sequences is a function of the number of identical positions shared by the sequences (*i.e.,* % homology = # of identical positions/total # of positions x 100), taking into account the number of gaps, and the length of each gap, which need to be introduced for optimal alignment of the two sequences. The comparison of sequences and determination of percent identity between two sequences can be accomplished using a mathematical algorithm, as described in the non-limiting examples below.

[0109] The percent identity between two nucleotide sequences can be determined using the GAP program in the GCG software package (available at worldwideweb.gcg.com), using a NWSgapdna.CMP matrix and a gap weight of 40, 50, 60, 70, or 80 and a length weight of 1, 2, 3, 4, 5, or 6. The percent identity between two nucleotide or amino acid sequences can also be determined using the algorithm of E. Meyers and W. Miller (*CABIOS*, 4: 11-17 (1989)) which has been incorporated into the ALIGN program (version 2.0), using a PAM120 weight residue table, a gap length penalty of 12 and a gap penalty of 4. In addition, the percent identity between two amino acid sequences can be determined using the Needleman and Wunsch (*J. Mol. Biol.* (48):444-453 (1970)) algorithm which has been incorporated into the GAP program in the GCG software package (available at worldwideweb.gcg.com), using either a Blossum 62 matrix or a PAM250 matrix, and a gap weight of 16, 14, 12, 10, 8, 6, or 4 and a length weight of 1, 2, 3, 4, 5, or 6.

[0110] The nucleic acid and protein sequences described herein can further be used as a "query sequence" to perform a search against public databases to, for example, identify related sequences. Such searches can be performed using the NBLAST and XBLAST programs (version 2.0) of Altschul, *et al.* (1990) *J. Mol. Biol.* 215:403-10. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to the nucleic acid molecules described herein. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to the protein molecules described herein. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.*, (1997) *Nucleic Acids Res.* 25(17):3389-3402. When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (*e.g.,* XBLAST and NBLAST) can be used. *See* worldwideweb.ncbi.nlm.nih.gov.

[0111] The nucleic acids can be present in whole cells, in a cell lysate, or in a partially purified or substantially pure form. A nucleic acid is "isolated" or "rendered substantially pure" when purified away from other cellular components or other contaminants, *e.g.,* other cellular nucleic acids (*e.g.,* the other parts of the chromosome) or proteins, by standard techniques, including alkaline/SDS treatment, CsCl banding, column chromatography, agarose gel electrophoresis and others well known in the art. *See*, F. Ausubel, *et al.*, ed. Current Protocols in Molecular Biology, Greene Publishing and Wiley Interscience, New York (1987).

[0112] Nucleic acids, *e.g.,* cDNA, can be mutated, in accordance with standard techniques to provide gene sequences. For coding sequences, these mutations, can affect amino acid sequence as desired. In particular, DNA sequences substantially homologous to or derived from native V, D, J, constant, switches and other such sequences described herein are contemplated (where "derived" indicates that a sequence is identical or modified from another sequence).

[0113] The term "vector," as used herein, is intended to refer to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid," which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (*e.g.,* bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.,* non-episomal mammalian vectors) can be integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "recombinant expression vectors" (or simply, "expression vectors") In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector. However, also included are other forms of expression vectors, such as viral vectors (*e.g.,* replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

[0114] The term "recombinant host cell" (or simply "host cell"), as used herein, is intended to refer to a cell that comprises a nucleic acid that is not naturally present in the cell, and can be a cell into which a recombinant expression vector has been introduced. It should be understood that such terms are intended to refer not only to the particular subject cell but to the progeny of such a cell. Because certain modifications can occur in succeeding generations due to either mutation or environmental influences, such progeny cannot, in fact, be identical to the parent cell, but are still included within the scope of the term "host cell" as used herein.

[0115] As used herein, the term "linked" refers to the association of two or more molecules. The linkage can be covalent or non-covalent. The linkage also can be genetic (*i.e.,* recombinantly fused).

Such linkages can be achieved using a wide variety of art recognized techniques, such as chemical conjugation and recombinant protein production.

[0116] As used herein, "administering" refers to the physical introduction of a composition comprising a therapeutic agent to a subject, using any of the various methods and delivery systems known to those skilled in the art. Different routes of administration for the anti-TREM-1 antibodies described herein include intravenous, intraperitoneal, intramuscular, subcutaneous, spinal or other parenteral routes of administration, for example by injection or infusion. The phrase "parenteral administration" as used herein means modes of administration other than enteral and topical administration, usually by injection, and includes, without limitation, intravenous, intraperitoneal, intramuscular, intraarterial, intrathecal, intralymphatic, intralesional, intracapsular, intraorbital, intracardiac, intradermal, transtracheal, subcutaneous, subcuticular, intraarticular, subcapsular, subarachnoid, intraspinal, epidural and intrasternal injection and infusion, as well as *in vivo* electroporation. Alternatively, an antibody described herein can be administered via a non-parenteral route, such as a topical, epidermal or mucosal route of administration, for example, intranasally, orally, vaginally, rectally, sublingually or topically. Administering can also be performed, for example, once, a plurality of times, and/or over one or more extended periods.

[0117] As used herein, the terms "inhibits" or "blocks" (*e.g.,* referring to inhibition/blocking of binding of TREM-1 ligand to TREM-1 on cells) are used interchangeably and encompass both partial and complete inhibition/blocking. In some embodiments, the anti-TREM-1 antibody inhibits binding of TREM-1 ligand to TREM-1 by at least about 50%, for example, about 60%, 70%, 80%, 90%, 95%, 99%, or 100%, determined, *e.g.,* as further described herein. In some embodiments, the anti-TREM-1 antibody inhibits binding of TREM-1 ligand to TREM-1 by no more than 50%, for example, by about 40%, 30%, 20%, 10%, 5% or 1%, determined, *e.g.,* as further described herein.

[0118] The terms "treat," "treating," and "treatment," as used herein, refer to any type of intervention or process performed on, or administering an active agent to, the subject with the objective of reversing, alleviating, ameliorating, inhibiting, or slowing down or preventing the progression, development, severity or recurrence of a symptom, complication, condition or biochemical indicia associated with a disease or enhancing overall survival. Treatment can be of a subject having a disease or a subject who does not have a disease (*e.g.,* for prophylaxis).

[0119] The term "effective dose" or "effective dosage" is defined as an amount sufficient to achieve or at least partially achieve a desired effect. A "therapeutically effective amount" or "therapeutically effective dosage" of a drug or therapeutic agent is any amount of the drug that, when used alone or in combination with another therapeutic agent, promotes disease regression evidenced by a decrease in severity of disease symptoms, an increase in frequency and duration of disease symptom-free periods, or a prevention of impairment or disability due to the disease affliction. A therapeutically effective amount or dosage of a drug includes a "prophylactically effective amount" or a "prophylactically effective dosage", which is any amount of the drug that, when administered alone

or in combination with another therapeutic agent to a subject at risk of developing a disease or of suffering a recurrence of disease, inhibits the development or recurrence of the disease. The ability of a therapeutic agent to promote disease regression or inhibit the development or recurrence of the disease can be evaluated using a variety of methods known to the skilled practitioner, such as in human subjects during clinical trials, in animal model systems predictive of efficacy in humans, or by assaying the activity of the agent in *in vitro* assays.

[0120] The term "patient" includes human and other mammalian subjects that receive either prophylactic or therapeutic treatment.

[0121] As used herein, the term "subject" includes any human or non-human animal. For example, the methods and compositions described herein can be used to treat a subject having cancer. The term "non-human animal" includes all vertebrates, *e.g.,* mammals and non-mammals, such as non-human primates, sheep, dog, cow, chickens, amphibians, reptiles, etc.

[0122] As used herein, the terms "ug" and "uM" are used interchangeably with "μg" and "μM," respectively.

[0123] Various aspects described herein are described in further detail in the following subsections.

I. Anti-TREM-1 Antibodies

[0124] Described herein are antibodies, e.g., fully human antibodies, which are characterized by particular functional features or properties. For example, the antibodies of the present disclosure specifically bind human TREM-1, and more specifically, a particular domain (*e.g.*, a functional domain) within the extracellular domain of human TREM-1. In one embodiment, the antibodies specifically bind to the site on TREM-1 to which the TREM-1 ligand (e.g., PGLYRP1) binds. In certain embodiments, the antibodies are antagonist antibodies, i.e., they inhibit or suppress the activity of TREM-1 (i.e., do not agonize upon binding) on cells, e.g., monocytes, macrophages, and neutrophils. In some embodiments, the anti-TREM-1 antibodies cross-react with TREM-1 from one or more non-human primates, such as cynomolgus TREM-1. In some embodiments, the anti-TREM-1 antibodies block the production of inflammatory cytokines (e.g., IL-6, TNF-α, IL-8, IL-1β, IL-12, and combinations thereof) by cells (e.g., macrophages, dendritic cells, neutrophils) upon activation. In other embodiments, the anti-TREM-1 antibodies comprise Fc regions that do not bind to one or more FcγRs. In further embodiments, the anti-TREM-1 antibodies do not induce the release of proinflammatory cytokines by myeloid cells (e.g., dendritic cells) and, thereby reduce or prevent the onset of inflammatory cytokine storm after the administration of the anti-TREM-1 antibodies to a subject in need thereof.

[0125] In some embodiments, the particular anti-TREM-1 antibodies described herein are antibodies, *e.g.,* monoclonal, recombinant, and/or human antibodies, that cross-compete with mAb

0318 for binding to human TREM-1. In some embodiments, the anti-TREM-1 antibodies also cross-compete with mAb 0318 for binding to cynomolgus TREM-1. In other words, the anti-TREM-1 antibodies of the present disclosure belong to the same "bin" as mAb 0318 in certain embodiments.

[0126] The mAb 0318 antibody has a heavy chain variable region (VH) comprising SEQ ID NO: 14 and a light chain variable region (VL) comprising SEQ ID NO: 15. *See* International Publ. No. 2016/009086. The mAb 0318 also has a heavy chain CDR1, CDR2, and CDR3, which correspond to amino acids 31-35, 50-68, and 101-110 of SEQ ID NO: 14, respectively. The light chain CDR1, CDR2, and CDR3 of the mAb 0318 antibody correspond to amino acids 24-38, 54-60, and 93-101 of SEQ ID NO: 15.

[0127] Accordingly, in some embodiments, the anti-TREM-1 antibody of the present disclosure comprises a VH and VL of SEQ ID NOs: 14 and 15, respectively. In another embodiment, the VH of the anti-TREM-1 antibody comprises a CDR1 sequence of amino acids 31-35 (TYAMH) of SEQ ID NO: 14, wherein one of the amino acids can be substituted by a different amino acid. In certain embodiments, the VH of the anti-TREM-1 antibody comprises a CDR2 sequence of amino acids 50-68 (RIRTKSSNYATYYAASVKG) of SEQ ID NO: 14, wherein one, two, or three of the amino acids can be substituted by a different amino acid. In some embodiments, the VH of the anti-TREM-1 antibody comprises a CDR3 sequence of amino acids 101-110 (DMGIRRQFAY) of SEQ ID NO: 14, wherein one, two, or three of the amino acids can be substituted by a different amino acid.

[0128] In some embodiments, the VL of the anti-TREM-1 antibody comprises a CDR1 sequence of amino acids 24-38 (QQSNQDPYT) of SEQ ID NO: 15, wherein one, two, or three of the amino acids can be substituted by a different amino acid. In other embodiments, the VL of the anti-TREM-1 antibody comprises a CDR2 sequence of amino acids 54-60 (RASNLES) of SEQ ID NO: 15, wherein one or two of the amino acids can be substituted with a different amino acid. In some embodiments, the VL of the anti-TREM-1 antibody comprises a CDR3 sequence of amino acids 93-101 (QQSNQDPYT) of SEQ ID NO: 15, wherein one or two of the amino acids can be substituted with a different amino acid.

[0129] Methionine residues in CDRs of antibodies can be oxidized, resulting in potential chemical degradation and consequent reduction in potency of the antibody. Accordingly, the anti-TREM-1 antibodies disclosed herein can have one or more methionine residues in the heavy and/or light chain CDRs replaced with amino acid residues which do not undergo oxidative degradation. In some embodiments, the methionine residues within the heavy chain CDR1 and CDR3 are replaced with amino acid residues that do not undergo oxidative degradation (e.g., glutamine or leucine). Accordingly, in one embodiment, the VH of the anti-TREM-1 antibody comprises a CDR3 sequence of amino acids 101-110 (DQGIRRQFAY) of SEQ ID NO: 81or amino acids 101-110 (DLGIRRQFAY) of SEQ ID NO: 82. In other embodiments, the VH of the anti-TREM-1 antibody comprises a CDR1 sequence of amino acids 31-35 (TYAQH) of SEQ ID NO: 83 or amino acids 31-

35 (TYALH) of SEQ ID NO: 84. Similarly, in some embodiments, deamidation sites can be removed from the anti-TREM-1 antibodies, particularly in the CDRs.

[0130] In some embodiments, the VH and VL of the anti-TREM-1 antibody comprises a VH and VL sequences of anti-TREM-1 antibodies disclosed in International Publ. No. WO 2017/152102 A2, which is hereby incorporated by reference in its entirety. In some embodiments, the VL of the anti-TREM-1 antibody comprises a CDR1 sequence selected from the group consisting of SEQ ID NOs: 9-27 from WO 2017/152102, a CDR2 sequence selected from the group consisting of SEQ ID NOs: 28-40 from WO 2017/152102, and/or a CDR3 sequence selected from the group consisting of SEQ ID NOs: 41-119 from WO 2017/152102. In one embodiment, the VH of the anti-TREM-1 antibody comprises a CDR1 sequence selected from the group consisting of SEQ ID NOs: 120-143 from WO 2017/152102, a CDR2 sequence selected from the group consisting of SEQ ID NOs: 144-172 from WO 2017/152102, and/or a CDR3 sequence selected from the group consisting of SEQ ID NOs: 173-247 from WO 2017/152102.

[0131] In some embodiments, the anti-TREM-1 antibodies of the present disclosure comprise CDR and/or variable region sequences that have at least 80% identity (e.g., at least 85%, at least 95%, at least 95%, or at least 99% identity) to the CDR and/or variable region sequences of the mAb 0318 antibody.

[0132] In some embodiments, the anti-TREM-1 antibodies comprise a heavy chain variable region (VH) and a light chain variable region (VL) comprising SEQ ID NOs: 14 and 15, respectively. In some embodiments, the anti-TREM-1 antibodies comprise a heavy chain (HC) and a light chain (LC), wherein the HC comprises SEQ ID NO: 50, SEQ ID NO: 51, SEQ ID NO: 52, or SEQ ID NO: 53. In some embodiments, the LC comprises SEQ ID NO: 54.

[0133] In some embodiments, the anti-TREM-1 antibodies of the present disclosure comprise a heavy chain variable region (VH) selected from the group consisting of SEQ ID NOs: 396-475 from WO 2017/152102 and/or a light chain variable region (VL) selected from the group consisting of SEQ ID NOs: 316-395 from WO 2017/152102.

[0134] In some embodiments, the anti-TREM-1 antibody comprises a heavy chain and a light chain, wherein the heavy chain and light chain comprises aminthe o acid sequences as shown in Table 7. In some embodiments, the anti-TREM-1 antibody comprises a heavy chain and a light chain, wherein the heavy chain comprises the amino acid sequence set forth as SEQ ID NO: 50 and the light chain comprises the amino acid sequence set forth as SEQ ID NO: 54. In some embodiments, the anti-TREM-1 antibody comprises a heavy chain and a light chain, wherein the heavy chain comprises the amino acid sequence set forth as SEQ ID NO: 51 and the light chain comprises the amino acid sequence set forth as SEQ ID NO: 54. In some embodiments, the anti-TREM-1 antibody comprises a heavy chain and a light chain, wherein the heavy chain comprises the amino acid sequence set forth as SEQ ID NO: 52 and the light chain comprises the amino acid sequence set forth as SEQ ID NO: 54. In some embodiments, the anti-TREM-1 antibody comprises a heavy chain and a light chain, wherein

the heavy chain comprises the amino acid sequence set forth as SEQ ID NO: 53 and the light chain comprises the amino acid sequence set forth as SEQ ID NO: 54.

[0135] Heavy and light chains comprising an amino acid sequence that is at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identical to any of the heavy or light chains set forth herein, *e.g.*, SEQ ID NOs: 50 to 54 can be used for forming the anti-TREM-1 antibodies having the desired characteristics, *e.g.*, those further described herein.

[0136] In some embodiments, the anti-TREM-1 antibody of the present disclosure comprises a heavy chain and a light chain, wherein the heavy chain comprises an amino acid sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to the amino acid sequence set forth as SEQ ID NO: 50, 51, 52, or 53 and wherein the light chain comprises an amino acid sequence that is at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to the amino acid sequence set forth as SEQ ID NO: 54.

[0137] In some embodiments, the anti-TREM1 antibody comprises a heavy chain constant region, wherein the heavy chain constant region comprises one or more amino acid substitutions selected from the group consisting of K214R, L234A, L235E, G237A, D356E, L358M, and any combination thereof per EU numbering. In some embodiments, the anti-TREM-1 antibody comprises a heavy chain constant region, wherein the heavy chain constant region comprises one or more amino acid substitutions selected from the group consisting of K214R, L234A, L235E, G237A, A330S, P331S, D356E, L358M, and any combination thereofper EU numbering. In some embodiments, the anti-TREM-1 antibody comprises a heavy chain constant region, wherein the heavy chain constant region comprises one or more amino acid substitutions selected from the group consisting of K214R, C226S, C229S, P238S, and any combination thereof per EU numbering. In some embodiments, the anti-TREM-1 antibody comprises a heavy chain constant region, wherein the heavy chain constant region comprises one or more amino acid substitutions selected from the group consisting of S131C, K133R, G137E, G138S, Q196K, I199T, N203D, K214R, C226S, C229S, P238S, and any combination thereof per EU numbering.

[0138] In one embodiment, the anti-TREM-1 antibody is capable of binding variants of human TREM-1 (e.g., TREM-1 isoforms 2 and 3, SEQ ID NOs: 2 and 3, respectively), as determined using, e.g., surface plasmon resonance. In another embodiment, the anti-TREM-1 antibody is capable of binding cynomolgus TREM-1 (SEQ ID NO: 7), as determined using, e.g., surface plasmon resonance.

[0139] In some embodiments, anti-TREM-1 antibodies described herein bind to human TREM-1 with high affinity, *e.g.*, as determined by BIACORE™ (*e.g.*, as described in the Examples), with a K_D of 10^{-7} M or less, 10^{-8} M or less, 10^{-9} M (1 nM) or less, 10^{-10} M or less, 10^{-11} M or less, 10^{-12} M or less, 10^{-12} M to 10^{-7} M, 10^{-11} M to 10^{-7} M, 10^{-10} M to 10^{-7} M, or 10^{-9} M to 10^{-7} M. In some embodiments, anti-TREM-1 antibodies described herein bind to cyno TREM-1, *e.g.*, as determined by BIACORE™ (*e.g.*, as described in the Examples), with a K_D of 10^{-7} M or less, 10^{-8} M or less, 10^{-9} M or less, 10^{-10} M

or less, 10^{-11} M or less, 10^{-12} M or less, 10^{-12} M to 10^{-7} M, 10^{-11} M to 10^{-7} M, 10^{-10} M to 10^{-7} M, or 10^{-9} M to 10^{-7} M.

[0140] In one embodiment, the antibodies of the present disclosure bind anti-TREM-1 at one or more of the same epitopes as the mAb 0318 antibody. In some embodiments, the anti-TREM-1 antibody is capable of specifically binding (i) at least one amino acid residue selected from the group consisting of the A21, T22, K23, L24, T25, E26, and any combination thereof and (ii) at least one amino acid residue selected from the group consisting of the A49, S50, S51, Q52, K53, A54, W55, Q56, 157, 158, R59, D60, G61, E62, M63, P64, K65, T66, L67, A68, C69, T70, E71, R72, P73, S74, K75, N76, S77, H78, P79, V80, Q81, V82, G83, R84, 185, and any combination thereof and (iii) at least one amino acid residue selected from the group consisting of the C113, V114, 1115, Y116, Q117, P118, P119, and any combination thereof of human TREM-1 (e.g., Isoform 1, SEQ ID NO: 1). See WO 2016/009086.

[0141] In one embodiment, the anti-TREM-1 antibody is capable of specifically binding to amino acids D38 to F48 of SEQ ID NO: 1 (human TREM-1), as determined using, e.g., HX-MS or X-ray diffraction. In some embodiments, the anti-TREM-1 antibody has an epitope comprising one, two, three, four, five, six, seven, or all of the amino acid residues D38, V39, K40, C41, D42, Y43, T44, and L45 of SEQ ID NO: 1 (human TREM-1) and one, two, or all of the amino acid residues selected from the group consisting of the E46, K47, and F48 of SEQ ID NO: 1 (human TREM-1), as determined using, e.g., HX-MS or X-ray diffraction. In certain embodiments, the anti-TREM-1 antibody has an epitope comprising one, two, three, or all of the amino acid residues selected from the group consisting of the D42, E46, D92, and H93 of SEQ ID NO: 1 (human TREM-1), as determined using variants of TREM-1 and surface plasmon resonance.

[0142] In one embodiment, the anti-TREM-1 antibody of the present disclosure has an epitope comprising at least the amino acid residues E46 and/or D92 of SEQ ID NO: 1 (human TREM-1), as determined using variants of TREM-1 and surface plasmon resonance. In another embodiment, the anti-TREM-1 antibody comprises one, two, or all of the amino acid residues selected from the group consisting of L31, 186, and V101 of SEQ ID NO: 1 (human TREM-1). In certain embodiments, the anti-TREM-1 antibody is capable of specifically binding a polypeptide comprising amino acid residues E19 to L26 of cynomolgus monkey TREM-1 (SEQ ID NO : 7), as determined using, e.g., HX-MS or X-ray diffraction.

[0143] In one embodiment, the anti-TREM-1 antibody is capable of specifically binding human TREM-1, wherein the epitope of the antibody comprises one, two, three, four, five, six, seven, eight, nine, or all of the amino acid residues selected from the group consisting of the V39, K40, C41, D42, Y43, L45, E46, K47, F48, and A49 of SEQ ID NO: 1.

[0144] In one embodiment, the anti-TREM-1 antibody is capable of specifically binding human TREM-1, wherein the epitope of the antibody comprises the D42 of SEQ ID NO : 1. In other embodiments, the anti-TREM-1 antibody is capable of specifically binding human TREM-1, wherein

the epitope of the antibody comprises the E46 of SEQ ID NO: 1. In some embodiments, the epitope of the antibody can comprise the V39, C41, D42, Y43, L45 of SEQ ID NO: 1. In further embodiments, The epitope of the antibody can comprise the E46, K47 and A49 of SEQ ID NO: 1. In a specific embodiment, the epitope of the anti-TREM-1 antibody can further comprise the F48 of SEQ ID NO: 1.

[0145] In some embodiments, the anti-TREM-1 antibody has a viscosity profile similar to that of the mAb 0318 antibody. In some embodiments, the anti-TREM-1 antibody of the present disclosure has a viscosity of less than 5 cP, less than 4 cP, less than 3 cP, less than 2.5 cP, less than 2.4 cP, less than 2.3 cP, less than 2.2 cP, less than 2.1 cP, less than 2 cP, less than 1.9 cP, less than 1.8 cP, less than 1.7 cP, less than 1.6 cP, less than 1.5 cP, less than 1.4 cP, less than 1.3 cP, less than 1.2 cP, less than 1.1 cP, less than 1.0 cP, less than 0.9 cP, less than 0.8 cP, less than 0.7 cP, less than 0.6 cP, less than 0.5 cP, less than 0.4 cP, less than 0.3 cP, less than 0.2 cP, or less than 0.1 cP at a concentration of 80 mg/mL. In some embodiments, the anti-TREM-1 antibody has a a viscosity of less than 10 cP (e.g., 9 cP) at a concentration of 130 mg/mL.

[0146] In some embodiments, the anti-TREM-1 antibody of the present disclosure comprises mutations, wherein one or more negatively charged residues in the light CDR1 and CDR3 regions of the antibody are substituted with uncharged residues. In some embodiments, the anti-TREM-1 antibody comprises a substitution at one or more of amino acid residues D1, D30, D33, D74, D98, E27, and E97 of SEQ ID NO: 15 with an amino acid residue selected from the group consisting of glycine, alanine, serine, asparagine, glutamine, threonine, cysteine, and tyrosine. These mutations are referred to herein as "charge patch" mutations.

[0147] In some embodiments, the anti-TREM-1 antibody of the present disclosure comprises mutations in the Fab-Fab interaction area of SEQ ID NO: 14 to reduce Fab-Fab dimerization. It was previously shown with the mAb 0318 antibody that because antibodies comprise two Fabs, multimerization could impact viscosity. These mutations are referred to as "Fab- Fab interaction" mutations. In certain embodiments, the anti-TREM-1 antibody comprises a mutation at any one of residues Y32, R52, S55, S56, N57, A59, M102, I104 and R106 of SEQ ID NO: 14 or F32, D33, Y34, Y53, R54, and D98 of SEQ ID NO 15 with an amino acid residue selected from the group consisting of glycine, alanine, serine, asparagine, glutamine, threonine, cysteine, lysine, arginine, tryptophan, histidine and tyrosine.

[0148] In one embodiment, the anti-TREM-1 antibody as disclosed herein comprises a mutation at position 32 of SEQ ID NO: 15, wherein the phenylalanine is mutated to an mino acid selected from amino acid residues glycine, serine, threonine, cysteine, alanine, valine, leucine, isoleucine, and methionine. Such mutation is based on the observation that an Ala substitution in position Y90 of SEQ ID NO: 1 improved the affinity of SEQ ID NO: 3 to TREM-1. The Y90 was found to interact with a phenylalanine residue of SEQ ID NO: 15. Mutation of SEQ ID NO: 15 in order to improve the Fab-TREM-1 interaction are referred to as "Fab- TREM-1 interaction" mutations. Provided herein are

anti-TREM-1 antibodies whose variable regions are linked (e.g., covalently linked or fused) to an Fc, *e.g.,* an IgG1, IgG2, IgG3 or IgG4 Fc, which can be of any allotype or isoallotype, *e.g.,* for IgG1: G1m, G1m1(a), G1m2(x), G1m3(f), G1m17(z); for IgG2: G2m, G2m23(n); for IgG3: G3m, G3m21(g1), G3m28(g5), G3m11(b0), G3m5(b1), G3m13(b3), G3m14(b4), G3m10(b5), G3m15(s), G3m16(t), G3m6(c3), G3m24(c5), G3m26(u), G3m27(v); and for K: Km, Km1, Km2, Km3 (*see*, *e.g.,* Jeffries *et al.* (2009) mAbs 1:1). In some embodiments, the variable regions of the anti-TREM-1 antibodies disclosed herein are linked to an effectorless or mostly effectorless Fc, *e.g.*, IgG1. In some embodiments, the variable regions of the anti-TREM-1 antibodies are linked to an Fc that has reduced binding or is incapable of binding to one or more FcγRs.

[0149] In one embodiment, the VH domain of the anti-TREM-1 antibody described herein can be fused to the constant domain of a human IgG (*i.e.*, Fc), *e.g.,* IgG1, IgG2, IgG3, or IgG4, which is either naturally-occurring or modified, *e.g.,* as further described herein. For example, a VH domain can comprise the amino acid sequence of any VH domain described herein fused to a human IgG, *e.g.,* an IgG1, constant region, such as the following wild-type human IgG1 constant domain amino acid sequence:

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSS
LGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW
QQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 9) or that of an allotypic variant of SEQ ID NO: 9 and have the following amino acid sequences:

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSS
LGTQTYICNVNHKPSNTKVDK**R**VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
PREPQVYTLPPSR**E**E**M**TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW
QQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 77; allotype specific amino acid residues are in bold and underlined).

[0150] In one embodiment, the VH domain of the anti-TREM-1 antibody described herein can comprise the amino acid sequence of any VH domain described herein fused to an effectorless constant region, *e.g.*, the following effectorless human IgG1 constant domain amino acid sequences:

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSS
LGTQTYICNVNHKPSNTKVDK**R**VEPKSCDKTHTCPPCPAPE<u>AE</u>G<u>A</u>PSVFLFPPKPKDTLMISRTPEVTCVVVDVS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP<u>SS</u>IEKTISKAKGQ
PREPQVYTLPPSR**E**E**M**TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW
QQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 78; "IgG1.1f," comprising substitutions L234A, L235E, G237A, A330S and P331S, per EU numbering, which are underlined)

or

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSS
LGTQTYICNVNHKPSNTKVDK**R**VEPKSCDKTHTCPPCPAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
PREPQVYTLPPSR**E**E**M**TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW
QQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 79; "IgG1.3f", comprising substitutions L234A, L235E and G237A, per EU numbering, which are underlined).

[0151] For example, an allotypic variant of IgG1 comprises an K97R, D239E, and/or L241M (underlined and bolded above) and numbering according to that in SEQ ID NOs: 77-79. Within the full length heavy region and according to EU numbering, these amino acid substitutions are numbered K214R, D356E, and L358M. In some embodiments, the constant region of an anti-TREM-1 antibody further comprises one or more mutations or substitutions at amino acids L117, A118, G120, A213, and P214 (underlined above) as numbered in SEQ ID NO: 77-79, or L234, A235, G237, A330 and P331, per EU numbering. In further embodiments, the constant region of the anti-TREM-1 antibody comprises one or more mutations or substitutions at amino acids L117A, A118E, G120A, A213S, and P214S of SEQ ID NO: 77-79, or L234A, L235E, G237A, A330S and P331S, per EU numbering. The constant region of the anti-TREM-1 antibody may also comprise one or more mutations or substitutions L117A, A118E and G120A of SEQ ID NO: 9, or L234A, L235E and G237A, per EU numbering.

[0152] In some embodiments, the VH domain of the anti-TREM-1 antibodies described herein comprises the amino acid sequence of any VH domain described herein fused to an IgG1 constant domain comprising the following amino acid sequences:

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSS
LGTQTYICNVNHKPSNTKVDK**R**VEPKSCDKTHTSPPSPAPELLGGSSVFLFPPKPKDTLMISRTPEVTCVVVDVS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW
QQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 11; "IgG1-Aba", comprising substitutions K214R, C226S, C229S, and P238S, per EU numbering, which are underlined); or

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSS
LGTKTYTCNVDHKPSNTKVDK**R**VEPKSCDKTHTSPPSPAPELLGGSSVFLFPPKPKDTLMISRTPEVTCVVVDVS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW
QQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 12; "IgG4-Aba", comprising substitutions S131C, K133R, G137E, G138S, Q196K, I199T, N203D, K214R, C226S, C229S, and P238S, per EU numbering, which are underlined).

[0153] A VL domain described herein can be fused to the constant domain of a human Kappa or Lambda light chain. For example, a VL domain of a anti-TREM-1 antibody can comprise the amino acid sequence of any VL domain described herein fused to the following human IgG1 kappa light chain amino acid sequence:

RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLS KADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 13)

[0154] In certain embodiments, the heavy chain constant region comprises a lysine or another amino acid at the C-terminus, *e.g.,* it comprises the following last amino acids: LSPGK (SEQ ID NO: 48) in the heavy chain. In certain embodiments, the heavy chain constant region is lacking one or more amino acids at the C-terminus, and has, *e.g.,* the C-terminal sequence LSPG (SEQ ID NO: 49) or LSP.

[0155] In one embodiment, the variable region of the anti-TREM-1 antibody is linked to an effectorless or mostly effector less Fc. In certain embodiments, the variable region of the anti-TREM-1 antibody is linked to a Fc selected from the group consisting of IgG1.1f, IgG1.3f, IgG1-Aba, and IgG4-Aba, as described herein.

[0156] Generally, variable regions described herein can be linked to an Fc comprising one or more modification, typically to alter one or more functional properties of the antibody, such as Fc receptor binding, inflammatory cytokine release, serum half-life, complement fixation, and/or antigen-dependent cellular cytotoxicity. Furthermore, an antibody described herein can be chemically modified (*e.g.,* one or more chemical moieties can be attached to the antibody) or be modified to alter its glycosylation, to alter one or more functional properties of the antibody. Each of these embodiments is described in further detail below. The numbering of residues in the Fc region is that of the EU index of Kabat.

[0157] The Fc region encompasses domains derived from the constant region of an immunoglobulin (*e.g.*, IgG1, IgG2, IgG3, IgG4, and other classes such as IgA, IgD, IgE and IgM), including a fragment, analog, variant, mutant or derivative of the constant region. The constant region of an immunoglobulin is defined as a naturally- occurring or synthetically-produced polypeptide homologous to the immunoglobulin C-terminal region, and can include a CH1 domain, a hinge, a CH2 domain, a CH3 domain, or a CH4 domain, separately or in combination.

[0158] Ig molecules interact with multiple classes of cellular receptors. For example IgG molecules interact with three classes of Fcγ receptors (FcγR) specific for the IgG class of antibody, namely FcγRI, FcγRII, and FcγRIII. The important sequences for the binding of IgG to the FcγR receptors have been reported to be located in the CH2 and CH3 domains. The serum half-life of an antibody is influenced by the ability of that antibody to bind to an Fc receptor (FcR).

[0159] In one embodiment, the Fc region of the anti-TREM-1 antibodies is a variant Fc region, *e.g.,* an Fc sequence that has been modified (*e.g.,* by amino acid substitution, deletion and/or insertion) relative to a parent Fc sequence (*e.g.,* an unmodified Fc polypeptide that is subsequently modified to generate a variant), to provide desirable structural features and/or biological activity.

[0160] For example, one can make modifications in the Fc region in order to generate an Fc variant that (a) has increased or decreased antibody-dependent cell-mediated cytotoxicity (ADCC), (b) increased or decreased complement mediated cytotoxicity (CDC), (c) has increased or decreased

affinity for C1q and/or (d) has increased or decreased affinity for a Fc receptor relative to the parent Fc. Such Fc region variants will generally comprise at least one amino acid modification in the Fc region. Combining amino acid modifications is thought to be particularly desirable. For example, the variant Fc region can include two, three, four, five, etc. substitutions therein, *e.g.,* of the specific Fc region positions identified herein.

[0161] A variant Fc region can also comprise a sequence alteration wherein amino acids involved in disulfide bond formation are removed or replaced with other amino acids. Such removal can avoid reaction with other cysteine-containing proteins present in the host cell used to produce the anti-TREM-1 antibodies described herein. Even when cysteine residues are removed, single chain Fc domains can still form a dimeric Fc domain that is held together non-covalently. In other embodiments, the Fc region can be modified to make it more compatible with a selected host cell. For example, one can remove the PA sequence near the N-terminus of a typical native Fc region, which can be recognized by a digestive enzyme in E. coli such as proline iminopeptidase. In other embodiments, one or more glycosylation sites within the Fc domain can be removed. Residues that are typically glycosylated (*e.g.,* asparagine) can confer cytolytic response. Such residues can be deleted or substituted with unglycosylated residues (*e.g.,* alanine). In other embodiments, sites involved in interaction with complement, such as the C1q binding site, can be removed from the Fc region. For example, one can delete or substitute the EKK sequence of human IgG1. In certain embodiments, sites that affect binding to Fc receptors can be removed, preferably sites other than salvage receptor binding sites. In other embodiments, an Fc region can be modified to remove an ADCC site. ADCC sites are known in the art; *see, e.g.*, Sarmay *et al.*, *Molec. Immunol.* 29 (5): 633-9 (1992) with regard to ADCC sites in IgG1. Specific examples of variant Fc domains are disclosed, for example, in WO 97/34631 and WO 96/32478.

[0162] In one embodiment, the hinge region of Fc is modified such that the number of cysteine residues in the hinge region is altered, *e.g.,* increased or decreased. This approach is described further in U.S. Patent No. 5,677,425 by Bodmer *et al.* The number of cysteine residues in the hinge region of Fc is altered to, for example, facilitate assembly of the light and heavy chains or to increase or decrease the stability of the antibody. In one embodiment, the Fc hinge region of an antibody is mutated to decrease the biological half-life of the antibody. More specifically, one or more amino acid mutations are introduced into the CH2-CH3 domain interface region of the Fc-hinge fragment such that the antibody has impaired Staphylococcyl protein A (SpA) binding relative to native Fc-hinge domain SpA binding. This approach is described in further detail in U.S. Patent No. 6,165,745 by Ward *et al.*

[0163] In yet other embodiments, the Fc region is altered by replacing at least one amino acid residue with a different amino acid residue to alter the effector function(s) of the antibody. For example, one or more amino acids selected from amino acid residues 234, 235, 236, 237, 297, 318, 320, 322, 330, and/or 331 can be replaced with a different amino acid residue such that the antibody

has an altered affinity for an effector ligand but retains the antigen-binding ability of the parent antibody. The effector ligand to which affinity is altered can be, for example, an Fc receptor or the C1 component of complement. This approach is described in further detail in U.S. Patent Nos. 5,624,821 and 5,648,260, both by Winter *et al.*

[0164] In another example, one or more amino acids selected from amino acid residues 329, 331 and 322 can be replaced with a different amino acid residue such that the antibody has altered C1q binding and/or reduced or abolished complement dependent cytotoxicity (CDC). This approach is described in further detail in U.S. Patent Nos. 6,194,551 by Idusogie *et al.*

[0165] In another example, one or more amino acid residues within amino acid positions 231 and 239 are altered to thereby alter the ability of the antibody to fix complement. This approach is described further in PCT Publication WO 94/29351 by Bodmer *et al.*

[0166] In yet another example, the Fc region can be modified to decrease antibody dependent cellular cytotoxicity (ADCC) and/or to decrease the affinity for an Fcγ receptor by modifying one or more amino acids at the following positions: 234, 235, 236, 238, 239, 240, 241 , 243, 244, 245, 247, 248, 249, 252, 254, 255, 256, 258, 262, 263, 264, 265, 267, 268, 269, 270, 272, 276, 278, 280, 283, 285, 286, 289, 290, 292, 293, 294, 295, 296, 298, 299, 301, 303, 305, 307, 309, 312, 313, 315, 320, 322, 324, 325, 326, 327, 329, 330, 331, 332, 333, 334, 335, 337, 338, 340, 360, 373, 376, 378, 382, 388, 389, 398, 414, 416, 419, 430, 433, 434, 435, 436, 437, 438 or 439. Exemplary substitutions include 236A, 239D, 239E, 268D, 267E, 268E, 268F, 324T, 332D, and 332E. Exemplary variants include 239D/332E, 236A/332E, 236A/239D/332E, 268F/324T, 267E/268F, 267E/324T, and 267E/268F/324T. Other modifications for enhancing FcγR and complement interactions include but are not limited to substitutions 298 A, 333A, 334A, 326A, 2471, 339D, 339Q, 280H, 290S, 298D, 298V, 243L, 292P, 300L, 396L, 3051, and 396L. These and other modifications are reviewed in Strohl, 2009, Current Opinion in Biotechnology 20:685-691.

[0167] Other Fc modifications that can be made to Fcs are those for reducing or ablating binding to FcγR and/or complement proteins, thereby reducing or ablating Fc-mediated effector functions such as ADCC, ADCP, and CDC. Exemplary modifications include but are not limited substitutions, insertions, and deletions at positions 234, 235, 236, 237, 267, 269, 325, 328, 330, and/or 331 (*e.g.,* 330 and 331), wherein numbering is according to the EU index. Exemplary substitutions include but are not limited to 234A, 235E, 236R, 237A, 267R, 269R, 325L, 328R, 330S, and 331S (*e.g.,* 330S, and 331S), wherein numbering is according to the EU index. An Fc variant can comprise 236R/328R. Other modifications for reducing FcγR and complement interactions include substitutions 297A, 234A, 235A, 237A, 318A, 228P, 236E, 268Q, 309L, 330S, 331 S, 220S, 226S, 229S, 238S, 233P, and 234V, as well as removal of the glycosylation at position 297 by mutational or enzymatic means or by production in organisms such as bacteria that do not glycosylate proteins. These and other modifications are reviewed in Strohl, 2009, *Current Opinion in Biotechnology* 20:685-691.

[0168] Optionally, the Fc region can comprise a non-naturally occurring amino acid residue at additional and/or alternative positions known to one skilled in the art (*see, e.g.,* U.S. Pat. Nos. 5,624,821; 6,277,375; 6,737,056; 6,194,551; 7,317,091; 8,101,720; International Publ. Nos. WO 00/42072; WO 01/58957; WO 02/06919; WO 04/016750; WO 04/029207; WO 04/035752; WO 04/074455; WO 04/099249; WO 04/063351; WO 05/070963; WO 05/040217, WO 05/092925, and WO 06/0201 14).

[0169] The affinities and binding properties of an Fc region for its ligand can be determined by a variety of *in vitro* assay methods (biochemical or immunological based assays) known in the art including but not limited to, equilibrium methods (*e.g.,* enzyme-linked immunoabsorbent assay (ELISA), or radioimmunoassay (RIA)), or kinetics (*e.g.,* BIACORE analysis), and other methods such as indirect binding assays, competitive inhibition assays, fluorescence resonance energy transfer (FRET), gel electrophoresis and chromatography (*e.g.,* gel filtration). These and other methods can utilize a label on one or more of the components being examined and/or employ a variety of detection methods including but not limited to chromogenic, fluorescent, luminescent, or isotopic labels. A detailed description of binding affinities and kinetics can be found in Paul, W. E., ed., Fundamental immunology, 4th Ed., Lippincott-Raven, Philadelphia (1999), which focuses on antibody-immunogen interactions.

[0170] In certain embodiments, the anti-TREM-1 antibodies of the present disclosure comprise an Fc that has reduced binding or is incapable of binding to FcγRs. In some embodiments, the anti-TREM-1 antibody has a decreased binding affinity to FcγRI (CD64), FcγRIIA (CD32), FcγRIIB (CD32), FcγRIIIA (CD16a), FcγRIIIB (CD16b), or any combination thereof compared to an antibody comprising a heavy chain consisting of the amino acid sequence as set forth in SEQ ID NO: 76 and a light chain consisting of the amino acid sequence as set forth in SEQ ID NO: 54. In some embodiments, the anti-TREM-1 antibody has a decreased binding affinity to FcγRI (CD64) by at least two fold, at least three fold, at least four fold, at least five fold, at least six fold, at least seven fold, at least eight fold, at least nine fold, or at least 10 fold compared to an antibody comprising a heavy chain consisting of the amino acid sequence as set forth in SEQ ID NO: 76 and a light chain consisting of the amino acid sequence as set forth in SEQ ID NO: 54.

[0171] In some embodiments, the anti-TREM-1 antibodies comprise an IgG1 Fc variant comprising: (a) one or more amino acid substitutions selected from the group consisting of L234A, L235E, G237A, and any combination thereof, per EU numbering; (b) one or more amino acid substitutions selected from the group consisting of L234A, L235E, G237A, A330S, P331S, and any combination thereof per EU numbering; (c) one or more amino acid substitutions selected from the group consisting of K214R, C226S, C229S, P238S, and any combination thereof per EU numbering; or (d) one or more amino acid substitutions selected from the group consisting of S131C, K133R, G137E, G138S, Q196K, I199T, N203D, K214R, C226S, C229S, P238S, and any combination thereof per EU numbering.

[0172] In some embodiments, the anti-TREM-1 antibody, as disclosed herein, has (a) an IgG1 isotype and comprises one or more amino acid substitutions in the Fc region at an amino acid residue selected from the group consisting of: N297A, N297Q, D270A, D265A, L234A, L235A, C226S, C229S, P238S, E233P, L234V, P238A, A327Q, A327G, P329A, K322A, L234F, L235E, P331S, T394D, A330L, M252Y, S254T, T256E, , L328E, P238D, S267E, L328F, E233D, G237D, H268D, P271G, A330R, and any combination thereof, wherein the numbering of the residues is according to EU or Kabat numbering, or comprises an amino acid deletion in the Fc region at a position corresponding to glycine 236; (b) an IgG2 isotype and comprises one or more amino acid substitutions in the Fc region at an amino acid residue selected from the group consisting of: P238S , V234A, G237A, H268A, H268Q, H268E, V309L, N297A, N297Q, A330S, P331S, C232S, C233S, M252Y, S254T, T256E, and any combination thereof, wherein the numbering of the residues is according to EU or Kabat numbering; or (c) an IgG4 isotype and comprises one or more amino acid substitutions in the Fc region at an amino acid residue selected from the group consisting of: E233P, F234V, L234A/F234A, L235A, G237A, E318A, S228P, L236E, S241P, L248E, T394D, M252Y, S254T, T256E, N297A, N297Q, and any combination thereof, wherein the numbering of the residues is according to EU or Kabat numbering. In some embodiments, (a) the Fc region further comprises one or more additional amino acid substitutions at an amino acid residue selected from the group consisting of A330L, L234F; L235E, P331S, and any combination thereof, wherein the numbering of the residues is according to EU or Kabat numbering; (b) the Fc region further comprises one or more additional amino acid substitutions at a position selected from the group consisting of M252Y, S254T,T256E, and any combination thereof, wherein the numbering of the residues is according to EU or Kabat numbering; or (c) the Fc region further comprises a S228P amino acid substitution according to EU or Kabat numbering. See WO 2017/152102.

[0173] In certain embodiments, an Fc is chosen that has reduced complement fixation. An exemplary Fc, *e.g.,* IgG1 Fc, with reduced complement fixation has the following two amino acid substitutions: A330S and P331S.

[0174] In certain embodiments, an Fc is chosen that has essentially no effector function, *i.e.,* it has reduced binding to FcγRs and reduced complement fixation. An exemplary Fc, *e.g.,* IgG1 Fc, that is effectorless comprises the following five mutations: L234A, L235E, G237A, A330S and P331S.

II. Antibody Physical Properties

[0175] Anti-TREM-1 antibodies, e.g., those described herein, have some or all of the physical characteristics of the specific anti-TREM-1 antibodies described herein, such as the characteristics described in the Examples.

[0176] Glycosylation sites, particularly within the variable regions, can result in increased immunogenicity of the antibody or an alteration of the pK of the antibody due to altered antigen

binding (Marshall *et al.*, (1972) *Annu Rev Biochem* 41:673-702; Gala and Morrison (2004) *J. Immunol* 172:5489-94; Wallick *et al.*, (1988) *J Exp Med* 168: 1099-109; Spiro (2002) Glycobiology 12:43R-56R; Parekh *et al.*, (1985) *Nature* 316:452-7; Mimura *et al.*, (2000) *Mol Immunol* 37:697-706). Glycosylation has been known to occur at motifs containing an N-X-S/T sequence. In some embodiments, the anti-TREM-1 antibodies of the present disclosure do not contain or have reduced variable region glycosylation. This can be achieved either by selecting antibodies that do not contain the glycosylation motif in the variable region or by mutating residues within the glycosylation region. Accordingly, in some embodiments, the anti-TREM-1 antibody as disclosed herein are less less immunogenic compared to an antibody comprising a heavy chain consisting of the amino acid sequence as set forth in SEQ ID NO: 76 and a light chain consisting of the amino acid sequence as set forth in SEQ ID NO: 54.

[0177] In some embodiments, the anti-TREM-1 antibodies do not contain asparagine isomerism sites. The deamidation of asparagine can occur on N-G or D-G sequences and result in the creation of an isoaspartic acid residue that introduces a kink into the polypeptide chain and decreases its stability (isoaspartic acid effect).

[0178] Each antibody will have a unique isoelectric point (pi), which generally falls in the pH range between 6 and 9.5. The pi for an IgG1 antibody typically falls within the pH range of 7-9.5 and the pi for an IgG4 antibody typically falls within the pH range of 6-8. There is speculation that antibodies with a pi outside the normal range can have some unfolding and instability under *in vivo* conditions. Thus, the anti-TREM-1 antibodies, as disclosed herein, can contain a pi value that falls in the normal range (e.g., 8-9). This can be achieved either by selecting antibodies with a pi in the normal range or by mutating charged surface residues.

[0179] Each antibody will have a characteristic melting temperature, with a higher melting temperature indicating greater overall stability *in vivo* (Krishnamurthy R and Manning M C (2002) *Curr Pharm Biotechnol* 3:361-71). Generally, the T_Mi (the temperature of initial unfolding) can be greater than 60 °C, greater than 65 °C, or greater than 70 °C. In some embodiments, the anti-TREM-1 antibodies of the present disclosure have a higher melting temperature compared to an antibody comprising a heavy chain consisting of the amino acid sequence as set forth in SEQ ID NO: 76 and a light chain consisting of the amino acid sequence as set forth in SEQ ID NO: 54. Accordingly, in some embodiments, the anti-TREM-1 antibodies of the present disclosure are thermally stable compared to a reference antibody comprising a heavy chain consisting of the amino acid sequence as set forth in SEQ ID NO: 76 and a light chain consisting of the amino acid sequence as set forth in SEQ ID NO: 54, as measured by, *e.g.*, a Capillary Differential scanning calorimeter (CAP-DSC). The melting point of an antibody can be measured using differential scanning calorimetry (Chen *et al.*, (2003) *Pharm Res* 20: 1952-60; Ghirlando *et al.*,(1999) *Immunol Lett* 68:47-52) or circular dichroism (Murray *et al.*, (2002) *J. Chromatogr Sci* 40:343-9). In some embodiments, about 10% to 20%, about 20% to 30% (e.g., 24%), or about 30% to 40% of the antibody is reversible when it is heated to 77 °C.

[0180] In some embodiments, the anti-TREM-1 antibodies of the present disclosure do not degrade rapidly. Degradation of an antibody can be measured using capillary electrophoresis (CE) and MALDI-MS (Alexander A J and Hughes D E (1995) *Anal Chem* 67:3626-32).

[0181] In some embodiments, the anti-TREM-1 antibodies, as disclosed herein, have minimal aggregation effects, which can lead to the triggering of an unwanted immune response and/or altered or unfavorable pharmacokinetic properties. Generally, antibodies are acceptable with aggregation of 25% or less, 20% or less, 15% or less, 10% or less, or 5% or less. Aggregation can be measured by several techniques, including size-exclusion column (SEC), high performance liquid chromatography (HPLC), and dynamic light scattering (DLS). In some embodiments, the anti-TREM-1 antibodies of the present disclosure are monomeric as observed by size-exclusion high-performance liquid chromatography (SE-HPLC). In some embodiments, the anti-TREM-1 antibodies exhibit minimal risk for fragmentation as observed by two-dimensional liquid chromatography-tandem mass spectrometry (2D-LC/MS) or intact mass analysis using liquid chromatography-tandem mass spectrometry (LC/MS).

III. Nucleic Acids, Vectors, and Cells

[0182] Another aspect described herein pertains to nucleic acid molecules that encode the anti-TREM-1 antibodies described herein. The nucleic acids can be present in whole cells, in a cell lysate, or in a partially purified or substantially pure form. A nucleic acid is "isolated" or "rendered substantially pure" when purified away from other cellular components or other contaminants, *e.g.,* other cellular nucleic acids (*e.g.,* other chromosomal DNA, *e.g.,* the chromosomal DNA that is linked to the isolated DNA in nature) or proteins, by standard techniques, including alkaline/SDS treatment, CsCl banding, column chromatography, restriction enzymes, agarose gel electrophoresis and others well known in the art. *See*, F. Ausubel, *et al.*, ed. (1987) Current Protocols in Molecular Biology, Greene Publishing and Wiley Interscience, New York. A nucleic acid described herein can be, for example, DNA or RNA and can or cannot contain intronic sequences. In some embodiments, the nucleic acid is a cDNA molecule.

[0183] Nucleic acids described herein can be obtained using standard molecular biology techniques. For antibodies expressed by hybridomas (*e.g.,* hybridomas prepared from transgenic mice carrying human immunoglobulin genes as described further below), cDNAs encoding the light and heavy chains of the antibody made by the hybridoma can be obtained by standard PCR amplification or cDNA cloning techniques. For antibodies obtained from an immunoglobulin gene library (*e.g.,* using phage display techniques), nucleic acid encoding the antibody can be recovered from the library.

[0184] In some embodiments, the nucleic acids described herein are those encoding the VH and VL sequences of the anti-TREM-1 antibodies of the present disclosure. Exemplary DNA sequences encoding the VH and VL sequences are set forth in SEQ ID NOs: 58-61 and 62-65, respectively.

[0185] A method for making an anti-TREM-1 antibody as disclosed herein can comprise expressing the heavy chain and the light chains in a cell line comprising the nucleotide sequences encoding the heavy and light chains with a signal peptide, *e.g.*, SEQ ID NOs: 58-61 and 62-65, respectively. Host cells comprising these nucleotide sequences are encompassed herein.

[0186] Once DNA fragments encoding VH and VL segments are obtained, these DNA fragments can be further manipulated by standard recombinant DNA techniques, for example to convert the variable region genes to full-length antibody chain genes, to Fab fragment genes or to a scFv gene. In these manipulations, a VL- or VH-encoding DNA fragment is operatively linked to another DNA fragment encoding another protein, such as an antibody constant region or a flexible linker. The term "operatively linked", as used in this context, is intended to mean that the two DNA fragments are joined such that the amino acid sequences encoded by the two DNA fragments remain in-frame.

[0187] The isolated DNA encoding the VH region can be converted to a full-length heavy chain gene by operatively linking the VH-encoding DNA to another DNA molecule encoding heavy chain constant regions (hinge, CH1, CH2 and/or CH3). The sequences of human heavy chain constant region genes are known in the art (*see, e.g.*, Kabat, E. A., *et al.* (1991) Sequences of Proteins of Immunological Interest, Fifth Edition, U.S. Department of Health and Human Services, NIH Publication No. 91-3242) and DNA fragments encompassing these regions can be obtained by standard PCR amplification. The heavy chain constant region can be an IgG1, IgG2, IgG3, IgG4, IgA, IgE, IgM or IgD constant region, for example, an IgG2 and/or IgG 4 constant region. For a Fab fragment heavy chain gene, the VH-encoding DNA can be operatively linked to another DNA molecule encoding only the heavy chain CH1 constant region.

[0188] The isolated DNA encoding the VL region can be converted to a full-length light chain gene (as well as a Fab light chain gene) by operatively linking the VL-encoding DNA to another DNA molecule encoding the light chain constant region, CL. The sequences of human light chain constant region genes are known in the art (*see, e.g.*, Kabat, E. A., *et al.* (1991) Sequences of Proteins of Immunological Interest, Fifth Edition, U.S. Department of Health and Human Services, NIH Publication No. 91-3242) and DNA fragments encompassing these regions can be obtained by standard PCR amplification. The light chain constant region can be a kappa or lambda constant region.

[0189] Another aspect described herein pertains to cells (*e.g.*, host cells) expressing (*e.g.*, recombinantly) anti-TREM-1 antibodies described herein and related polynucleotides and expression vectors. Provided herein are also vectors comprising polynucleotides comprising nucleotide sequences encoding anti-TREM-1 antibodies or a fragment thereof. In some embodiments, the vectors can be

used for recombinantly expressing anti-TREM-1 antibodies described herein in host cells, *e.g.*, in mammalian cells. In some embodiments, the vectors can be used for gene therapy.

[0190] Suitable vectors for the disclosure include expression vectors, viral vectors, and plasmid vectors. In some embodiments, the vector is a viral vector.

[0191] As used herein, an expression vector refers to any nucleic acid construct which contains the necessary elements for the transcription and translation of an inserted coding sequence, or in the case of an RNA viral vector, the necessary elements for replication and translation, when introduced into an appropriate host cell. Expression vectors can include plasmids, phagemids, viruses, and derivatives thereof.

[0192] Expression vectors of the disclosure can include polynucleotides encoding the antibody or antigen binding portin thereof described herein. In some embodiments, the coding sequences for the antibody or antigen binding portin thereof is operably linked to an expression control sequence. As used herein, two nucleic acid sequences are operably linked when they are covalently linked in such a way as to permit each component nucleic acid sequence to retain its functionality. A coding sequence and a gene expression control sequence are said to be operably linked when they are covalently linked in such a way as to place the expression or transcription and/or translation of the coding sequence under the influence or control of the gene expression control sequence. Two DNA sequences are said to be operably linked if induction of a promoter in the 5' gene expression sequence results in the transcription of the coding sequence and if the nature of the linkage between the two DNA sequences does not (1) result in the introduction of a frame-shift mutation, (2) interfere with the ability of the promoter region to direct the transcription of the coding sequence, or (3) interfere with the ability of the corresponding RNA transcript to be translated into a protein. Thus, a gene expression sequence would be operably linked to a coding nucleic acid sequence if the gene expression sequence were capable of effecting transcription of that coding nucleic acid sequence such that the resulting transcript is translated into the desired antibody or antigen binding portin thereof.

[0193] Viral vectors include, but are not limited to, nucleic acid sequences from the following viruses: retrovirus, such as Moloney murine leukemia virus, Harvey murine sarcoma virus, murine mammary tumor virus, and Rous sarcoma virus; lentivirus; adenovirus; adeno-associated virus; SV40-type viruses; polyomaviruses; Epstein-Barr viruses; papilloma viruses; herpes virus; vaccinia virus; polio virus; and RNA virus such as a retrovirus. One can readily employ other vectors well-known in the art. Certain viral vectors are based on non-cytopathic eukaryotic viruses in which non-essential genes have been replaced with the gene of interest. Non-cytopathic viruses include retroviruses, the life cycle of which involves reverse transcription of genomic viral RNA into DNA with subsequent proviral integration into host cellular DNA. Retroviruses have been approved for human gene therapy trials. Most useful are those retroviruses that are replication-deficient (i.e., capable of directing synthesis of the desired proteins, but incapable of manufacturing an infectious particle). Such genetically altered retroviral expression vectors have general utility for the high efficiency

transduction of genes in vivo. Standard protocols for producing replication-deficient retroviruses (including the steps of incorporation of exogenous genetic material into a plasmid, transfection of a packaging cell line with plasmid, production of recombinant retroviruses by the packaging cell line, collection of viral particles from tissue culture media, and infection of the target cells with viral particles) are provided in Kriegler, M., Gene Transfer and Expression, A Laboratory Manual, W.H. Freeman Co., New York (1990) and Murry, E. J., Methods in Molecular Biology, Vol. 7, Humana Press, Inc., Cliffton, N.J. (1991).

[0194] In some embodiments, the virus is an adeno-associated virus, a double-stranded DNA virus. The adeno-associated virus can be engineered to be replication-deficient and is capable of infecting a wide range of cell types and species. It further has advantages such as heat and lipid solvent stability; high transduction frequencies in cells of diverse lineages, including hematopoietic cells; and lack of superinfection inhibition thus allowing multiple series of transductions. Reportedly, the adeno-associated virus can integrate into human cellular DNA in a site-specific manner, thereby minimizing the possibility of insertional mutagenesis and variability of inserted gene expression characteristic of retroviral infection. In addition, wild-type adeno-associated virus infections have been followed in tissue culture for greater than 100 passages in the absence of selective pressure, implying that the adeno-associated virus genomic integration is a relatively stable event. The adeno-associated virus can also function in an extrachromosomal fashion.

IV. Immunoconjugates

[0195] The present disclosure also provides immunoconjugates comprising any of the anti-TREM-1 antibodies disclosed herein. In some embodiments, the immunoconjugate comprises an antibody or an antigen binding portion linked to an agent. In some embodiments, the immunoconjugate comprises a bispecific molecule disclosed herein linked to an agent (e.g., as therapeutic agent or a diagnostic agent).

[0196] For diagnostic purposes, appropriate agents are detectable labels that include radioisotopes, for whole body imaging, and radioisotopes, enzymes, fluorescent labels and other suitable antibody tags for sample testing. The detectable labels that can be linked to any anti-TREM-1 antibody described herein can be any of the various types used currently in the field of *in vitro* diagnostics, including particulate labels including metal sols such as colloidal gold, isotopes such as I^{125} or Tc^{99} presented for instance with a peptidic chelating agent of the N_2S_2, N_3S or N_4 type, chromophores including fluorescent markers, luminescent markers, phosphorescent markers and the like, as well as enzyme labels that convert a given substrate to a detectable marker, and polynucleotide tags that are revealed following amplification such as by polymerase chain reaction. Suitable enzyme labels include horseradish peroxidase, alkaline phosphatase and the like. For instance, the label can be the enzyme alkaline phosphatase, detected by measuring the presence or formation of

chemiluminescence following conversion of 1,2 dioxetane substrates such as adamantyl methoxy phosphoryloxy phenyl dioxetane (AMPPD), disodium 3-(4-(methoxyspiro{l,2-dioxetane-3,2'-(5'-chloro)tricyclo{3.3.1.1 3,7}decan}-4-yl) phenyl phosphate (CSPD), as well as CDP and CDP-STAR® or other luminescent substrates well-known to those in the art, for example the chelates of suitable lanthanides such as Terbium(III) and Europium(III). The detection means is determined by the chosen label. Appearance of the label or its reaction products can be achieved using the naked eye, in the case where the label is particulate and accumulates at appropriate levels, or using instruments such as a spectrophotometer, a luminometer, a fluorimeter, and the like, all in accordance with standard practice.

[0197] In some embodiments, conjugation methods result in linkages which are substantially (or nearly) non-immunogenic, *e.g.,* peptide- (*i.e.,* amide-), sulfide-, (sterically hindered), disulfide-, hydrazone-, and ether linkages. These linkages are nearly non-immunogenic and show reasonable stability within serum (*see, e.g.,* Senter, P. D., *Curr. Opin. Chem. Biol.* 13 (2009) 235-244; WO 2009/059278; WO 95/17886).

[0198] Depending on the biochemical nature of the moiety and the antibody, different conjugation strategies can be employed. In case the moiety is naturally-occurring or recombinant of between 50 to 500 amino acids, there are standard procedures in text books describing the chemistry for synthesis of protein conjugates, which can be easily followed by the skilled artisan (*see, e.g.,* Hackenberger, C. P. R., and Schwarzer, D., Angew. *Chem. Int. Ed. Engl.* 47 (2008) 10030-10074). In some embodiments the reaction of a maleinimido moiety with a cysteine residue within the antibody or the moiety is used. This is an especially suited coupling chemistry in case *e.g.,* a Fab or Fab'-fragment of an antibody is used. Alternatively, in some embodiments, coupling to the C-terminal end of the antibody or moiety is performed. C-terminal modification of a protein, *e.g.,* of a Fab-fragment, can be performed as described (Sunbul, M. and Yin, J., *Org. Biomol. Chem.* 7 (2009) 3361-3371).

[0199] In general, site specific reaction and covalent coupling is based on transforming a natural amino acid into an amino acid with a reactivity which is orthogonal to the reactivity of the other functional groups present. For example, a specific cysteine within a rare sequence context can be enzymatically converted in an aldehyde (*see* Frese, M. A., and Dierks, T., *ChemBioChem.* 10 (2009) 425-427). It is also possible to obtain a desired amino acid modification by utilizing the specific enzymatic reactivity of certain enzymes with a natural amino acid in a given sequence context (*see, e.g.,* Taki, M. *et al.*, *Prot. Eng. Des. Sel.* 17 (2004) 119-126; Gautier, A. *et al. Chem. Biol.* 15 (2008) 128-136; and Protease-catalyzed formation of C— N bonds is used by Bordusa, F., Highlights in Bioorganic Chemistry (2004) 389-403). Site specific reaction and covalent coupling can also be achieved by the selective reaction of terminal amino acids with appropriate modifying reagents.

[0200] The reactivity of an N-terminal cysteine with benzonitrils (*see* Ren, H. *et al.*, *Angew. Chem. Int. Ed. Engl.* 48 (2009) 9658-9662) can be used to achieve a site-specific covalent coupling.

[0201] Native chemical ligation can also rely on C-terminal cysteine residues (Taylor, E. Vogel; Imperiali, B, *Nucleic Acids and Molecular Biology* (2009), 22 (Protein Engineering), 65-96).

[0202] US6437095 B1 describes a conjugation method which is based on the faster reaction of a cysteine within a stretch of negatively charged amino acids with a cysteine located in a stretch of positively charged amino acids.

[0203] The moiety can also be a synthetic peptide or peptide mimic. In case a polypeptide is chemically synthesized, amino acids with orthogonal chemical reactivity can be incorporated during such synthesis (see *e.g.,* de Graaf, A. J. *et al.*, *Bioconjug. Chem.* 20 (2009) 1281-1295). Since a great variety of orthogonal functional groups is at stake and can be introduced into a synthetic peptide, conjugation of such peptide to a linker is standard chemistry.

[0204] In order to obtain a mono-labeled polypeptide, the conjugate with 1:1 stoichiometry can be separated by chromatography from other conjugation side-products. This procedure can be facilitated by using a dye labeled binding pair member and a charged linker. By using this kind of labeled and highly negatively charged binding pair member, mono conjugated polypeptides are easily separated from non-labeled polypeptides and polypeptides which carry more than one linker, since the difference in charge and molecular weight can be used for separation. The fluorescent dye can be useful for purifying the complex from un-bound components, like a labeled monovalent binder.

[0205] In some embodiments, the moiety attached to an anti-TREM-1 antibody is selected from the group consisting of a binding moiety, a labeling moiety, and a biologically active moiety.

[0206] Anti-TREM-1 antibodies described herein can also be conjugated to a therapeutic agent to form an immunoconjugate such as an antibody-drug conjugate (ADC). Suitable therapeutic agents include antimetabolites, alkylating agents, DNA minor groove binders, DNA intercalators, DNA crosslinkers, histone deacetylase inhibitors, nuclear export inhibitors, proteasome inhibitors, topoisomerase I or II inhibitors, heat shock protein inhibitors, tyrosine kinase inhibitors, antibiotics, and anti-mitotic agents. In the ADC, the antibody and therapeutic agent preferably are conjugated via a linker cleavable such as a peptidyl, disulfide, or hydrazone linker. In some embodiments, the linker is a peptidyl linker such as Val-Cit, Ala-Val, Val-Ala-Val, Lys-Lys, Pro-Val-Gly-Val-Val (SEQ ID NO: 80), Ala-Asn-Val, Val-Leu-Lys, Ala-Ala-Asn, Cit-Cit, Val-Lys, Lys, Cit, Ser, or Glu. The ADCs can be prepared as described in U.S. Pat. Nos. 7,087,600; 6,989,452; and 7,129,261; PCT Publications WO 02/096910; WO 07/038658; WO 07/051081; WO 07/059404; WO 08/083312; and WO 08/103693; U.S. Patent Publications 20060024317; 20060004081; and 20060247295.

[0207] Anti-TREM-1 antibodies, *e.g.,* those described herein, can also be used for detecting TREM-1, such as human TREM-1, *e.g.,* human TREM-1 in tissues or tissue samples. The antibodies can be used, *e.g.,* in an ELISA assay or in flow cytometry. In some embodiments, an anti-TREM-1 antibody is contacted with cells, *e.g.,* cells in a tissue, for a time appropriate for specific binding to occur, and then a reagent, *e.g.,* an antibody that detects the anti-TREM-1 antibody, is added. Exemplary assays are provided in the Examples. The anti-TREM-1 antibody can be a fully human

antibody, or it can be a chimeric antibody, such as an antibody having human variable regions and murine constant regions or a portion thereof. Exemplary methods for detecting TREM-1, *e.g.,* human TREM-1, in a sample (cell or tissue sample) comprise (i) contacting a sample with an anti-TREM-1 antibody, for a time sufficient for allowing specific binding of the anti-TREM-1 antibody to TREM-1 in the sample, and (2) contacting the sample with a detection reagent, *e.g.,* an antibody, that specifically binds to the anti-TREM-1 antibody, such as to the Fc region of the anti-TREM-1 antibody, to thereby detect TREM-1 bound by the anti-TREM-1 antibody. Wash steps can be included after the incubation with the antibody and/or detection reagent. Anti-TREM-1 antibodies for use in these methods do not have to be linked to a label or detection agents, as a separate detection agent can be used.

[0208] Other uses for anti-TREM-1 antibodies, *e.g.,* as monotherapy or combination therapy, are provided elsewhere herein, *e.g.,* in the section pertaining to combination treatments.

V. Bispecific Molecules

[0209] Anti-TREM-1 antibodies described herein can be used for forming bispecific molecules. An anti-TREM-1 antibody, or antigen-binding portions thereof, can be derivatized or linked to another functional molecule, *e.g.,* another peptide or protein (*e.g.,* another antibody or ligand for a receptor) to generate a bispecific molecule that binds to at least two different binding sites or target molecules. For example, an anti-TREM-1 antibody can be linked to an antibody or scFv that binds specifically to any protein that can be used as potential targets for combination treatments, such as the proteins described herein (*e.g.,* antibodies to IP-10 or TNF-α). The antibody described herein can in fact be derived or linked to more than one other functional molecule to generate multispecific molecules that bind to more than two different binding sites and/or target molecules; such multispecific molecules are also intended to be encompassed by the term "bispecific molecule" as used herein. To create a bispecific molecule described herein, an antibody described herein can be functionally linked (*e.g.,* by chemical coupling, genetic fusion, noncovalent association or otherwise) to one or more other binding molecules, such as another antibody, antibody fragment, peptide or binding mimetic, such that a bispecific molecule results.

[0210] Accordingly, provided herein are bispecific molecules comprising at least one first binding specificity for TREM-1 and a second binding specificity for a second target epitope. In some embodiments described herein in which the bispecific molecule is multispecific, the molecule can further include a third binding specificity.

[0211] In some embodiments, the bispecific molecules described herein comprise as a binding specificity at least one antibody, or an antibody fragment thereof, including, *e.g.,* an Fab, Fab', F(ab')2, Fv, or a single chain Fv (scFv). The antibody can also be a light chain or heavy chain dimer,

or any minimal fragment thereof such as a Fv or a single chain construct as described in Ladner *et al.* U.S. Patent No. 4,946,778.

[0212] While human monoclonal antibodies are preferred, other antibodies which can be employed in the bispecific molecules described herein are murine, chimeric and humanized monoclonal antibodies.

[0213] The bispecific molecules described herein can be prepared by conjugating the constituent binding specificities using methods known in the art. For example, each binding specificity of the bispecific molecule can be generated separately and then conjugated to one another. When the binding specificities are proteins or peptides, a variety of coupling or cross-linking agents can be used for covalent conjugation. Examples of cross-linking agents include protein A, carbodiimide, N-succinimidyl-S-acetyl-thioacetate (SATA), 5,5'-dithiobis(2-nitrobenzoic acid) (DTNB), o-phenylenedimaleimide (oPDM), N-succinimidyl-3-(2-pyridyldithio)propionate (SPDP), and sulfosuccinimidyl 4-(N-maleimidomethyl) cyclohaxane-1-carboxylate (sulfo-SMCC) (*see*, *e.g.*, Karpovsky *et al.* (1984) *J. Exp. Med.* 160: 1686; Liu, MA *et al.* (1985) *Proc. Natl. Acad. Sci. USA* 82:8648). Other methods include those described in Paulus (1985) *Behring Ins. Mitt.* No. 78, 118-132; Brennan *et al.* (1985) *Science* 229:81-83), and Glennie *et al.* (1987) *J. Immunol.* 139: 2367-2375). Some conjugating agents are SATA and sulfo-SMCC, both available from Pierce Chemical Co. (Rockford, IL).

[0214] When the binding specificities are antibodies, they can be conjugated via sulfhydryl bonding of the C-terminus hinge regions of the two heavy chains. In some embodiments, the hinge region is modified to contain an odd number of sulfhydryl residues, preferably one, prior to conjugation.

[0215] Alternatively, both binding specificities can be encoded in the same vector and expressed and assembled in the same host cell. This method is particularly useful where the bispecific molecule is a mAb x mAb, mAb x Fab, mAb x $(scFv)_2$, Fab x $F(ab')_2$ or ligand x Fab fusion protein. A bispecific antibody can comprise an antibody comprising an scFv at the C-terminus of each heavy chain. A bispecific molecule described herein can be a single chain molecule comprising one single chain antibody and a binding determinant, or a single chain bispecific molecule comprising two binding determinants. Bispecific molecules can comprise at least two single chain molecules. Methods for preparing bispecific molecules are described for example in U.S. Patent Number 5,260,203; U.S. Patent Number 5,455,030; U.S. Patent Number 4,881,175; U.S. Patent Number 5,132,405; U.S. Patent Number 5,091,513; U.S. Patent Number 5,476,786; U.S. Patent Number 5,013,653; U.S. Patent Number 5,258,498; and U.S. Patent Number 5,482,858.

[0216] Binding of the bispecific molecules to their specific targets can be confirmed using art-recognized methods, such as enzyme-linked immunosorbent assay (ELISA), radioimmunoassay

[0217] (RIA), FACS analysis, bioassay (*e.g.*, , growth inhibition), or Western Blot assay. Each of these assays generally detects the presence of protein-antibody complexes of particular interest by employing a labeled reagent (*e.g.*, , an antibody) specific for the complex of interest.

VI. Kits

[0218] Provided herein are kits comprising one or more anti-TREM-1 antibodies described herein, or antigen-binding portions thereof, bispecific molecules, or immunoconjugates thereof. In some embodiments, provided herein is a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions described herein, such as one or more antibodies provided herein or an antigen-binding portion thereof, optional an instructing for use. In some embodiments, the kits contain a pharmaceutical composition described herein and any prophylactic or therapeutic agent, such as those described herein.

VII. Compositions and Formulations

[0219] Further provided herein are compositions (e.g., pharmaceutical compositions) and formulations comprising one or more of the anti-TREM-1 antibodies (including polynucleotides, vectors, and cells that encode and/or express the anti-TREM-1 antibodies) disclosed herein. For example, in one embodiment, the present disclosure provides a pharmaceutical composition comprising one or more anti-TREM-1 antibodies as disclosed herein, formulated together with a pharmaceutically acceptable carrier.

[0220] As used herein, "pharmaceutically acceptable carrier" includes any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like that are physiologically compatible. In some embodiments, the carrier is suitable for intravenous, intramuscular, subcutaneous, parenteral, spinal or epidermal administration (*e.g.*, by injection or infusion). Depending on the route of administration, the active compound, *i.e.*, antibody, immunoconjugate, or bispecific molecule, can be coated in a material to protect the compound from the action of acids and other natural conditions that can inactivate the compound.

[0221] Accordingly, one object of the present disclosure is to provide a pharmaceutical formulation, which improves the stability of the anti-TREM-1 antibodies and thus, allows for their long-term storage. In some embodiments, the pharmaceutical formulation disclosed herein comprises: (a) an anti-TREM-1 antibody; (b) a buffering agent; (c) a stabilizing agent; (d) a salt; (e) a bulking agent; and/or (f) a surfactant. In some embodiments, the pharmaceutical formulation is stable for at least 1 month, at least 2 months, at least 3 months, at least 6 months, at least 1 year, at least 2 years, at least 3 years, at least 5 years or more. In some embodiments, the formulation is stable when stored at 4°C, 25°C, or 40°C.

Buffering Agent

[0222] Buffering agents useful for the present invention can be a weak acid or base used to maintain the acidity (pH) of a solution near a chosen value after the addition of another acid or base. Suitable buffering agents can maximize the stability of the pharmaceutical formulations by maintaining pH control of the formulation. Suitable buffering agents can also ensure physiological compatibility or optimize solubility. Rheology, viscosity and other properties can also dependent on the pH of the formulation. Common buffering agents include, but are not limited to, histidine, citrate, succinate, acetate and phosphate. In some embodiments, a buffering agent comprises histidine (e.g., L-histidine) with isotonicity agents and potentially pH adjustment with an acid or a base known in the art. In certain embodiments, the buffering agent is L- histidine. In certain embodiments, the pH of the formulation is maintained between about 2 and about 10, or between about 4 and about 8.

Stabilizing Agent

[0223] Stabilizing agents are added to a pharmaceutical product in order to stabilize that product. Such agents can stabilize proteins in a number of different ways. Common stabilizing agents include, but are not limited to, amino acids such as glycine, alanine, lysine, arginine, or threonine, carbohydrates such as glucose, sucrose, trehalose, raffmose, or maltose, polyols such as glycerol, mannitol, sorbitol, cyclodextrins or destrans of any kind and molecular weight, or PEG. In one aspect of the invention, the stabilizing agent is chosen in order to maximize the stability of FIX polypeptide in lyophilized preparations. In certain embodiments, the stabilizing agent is sucrose and/or arginine.

Bulking Agent

[0224] Bulking agents can be added to a pharmaceutical product in order to add volume and mass to the product, thereby facilitating precise metering and handling thereof. Common bulking agents include, but are not limited to, lactose, sucrose, glucose, mannitol, sorbitol, calcium carbonate, or magnesium stearate.

Surfactant

[0225] Surfactants are amphipathic substances with lyophilic and lyophobic groups. A surfactant can be anionic, cationic, zwitterionic, or nonionic. Examples of nonionic surfactants include, but are not limited to, alkyl ethoxylate, nonylphenol ethoxylate, amine ethoxylate, polyethylene oxide, polypropylene oxide, fatty alcohols such as cetyl alcohol or oleyl alcohol, cocamide MEA, cocamide DEA, polysorbates, or dodecyl dimethylamine oxide. In some embodiments, the surfactant is polysorbate 20 or polysorbate 80.

[0226] In some embodiments, the pharmaceutical formulation of the present disclosure comprises:

(a) about 0.25 mg/mL to 250 mg/mL (e.g., 10 to 200 mg/mL) of an anti-TREM-1 antibody;

(b) about 20 mM histidine;

(c) about 150 mM sucrose;

(d) about 25 mM arginine; and

(e) about 50 mM NaCl.

[0227] The formulation can further comprise one or more of a buffer system, a preservative, a tonicity agent, a chelating agent, a stabilizer and/or a surfactant, as well as various combinations thereof. The use of preservatives, isotonic agents, chelating agents, stabilizers and surfactants in pharmaceutical compositions is well-known to the skilled person. Reference may be made to Remington: The Science and Practice of Pharmacy, 19th edition, 1995.

[0228] In some embodiments, the pharmaceutical formulation is an aqueous formulation. Such a formulation is typically a solution or a suspension, but may also include colloids, dispersions, emulsions, and multi-phase materials. The term "aqueous formulation" is defined as a formulation comprising at least 50% w/w water. Likewise, the term "aqueous solution" is defined as a solution comprising at least 50 % w/w water, and the term "aqueous suspension" is defined as a suspension comprising at least 50 % w/w water.

[0229] In some embodiments, the pharmaceutical formulation is a freeze-dried formulation, to which the physician or the patient adds solvents and/or diluents prior to use.

[0230] Pharmaceutical compositions described herein also can be administered in combination therapy, *i.e.,* combined with other agents. For example, the combination therapy can include a anti-anti-TREM-1 antibody described herein combined with at least one other therapeutic agent. Examples of therapeutic agents that can be used in combination therapy can include other compounds, drugs, and/or agents used for the treatment of a disease or disorder (e.g., an inflammatory disorder). Such compounds, drugs, and/or agents can include, for example, anti-inflammatory drugs or antibodies that block or reduce the production of inflammatory cytokines. In some embodiments, therapeutic agents can include an anti-IP-10 antibody, an anti-TNF-α antibody (e.g., adalimumab (HUMIRA®), golimumab (SIMPONI®), infliximab (REMICADE®), certolizumab pegol (CIMZIA®)), interferon beta-1a (e.g., AVONEX®, REBIF®), interferon beta-1b (e.g., BETASERON®, EXTAVIA®), glatiramer acetate (e.g., COPAXONE®, GLATOPA®), mitoxantrone (e.g., NOVANTRONE®), non-steroidal anti-inflammatory drugs (NSAIDs), analgesics, corticosteroids, and combinations thereof.

[0231] The pharmaceutical compounds described herein can include one or more pharmaceutically acceptable salts. A "pharmaceutically acceptable salt" refers to a salt that retains the desired biological activity of the parent compound and does not impart any undesired toxicological effects (see *e.g.,* Berge, S.M., *et al.* (1977) *J. Pharm. Sci.* 66: 1-19). Examples of such salts include acid addition salts and base addition salts. Acid addition salts include those derived from nontoxic inorganic acids, such as hydrochloric, nitric, phosphoric, sulfuric, hydrobromic, hydroiodic, phosphorous and the like, as well as from nontoxic organic acids such as aliphatic mono- and dicarboxylic acids, phenyl- substituted alkanoic acids, hydroxy alkanoic acids, aromatic acids, aliphatic and aromatic sulfonic acids and the like. Base addition salts include those derived from alkaline earth metals, such as sodium, potassium, magnesium, calcium and the like, as well as from nontoxic organic amines, such as N,N'-dibenzylethylenediamine, N-methylglucamine, chloroprocaine, choline, diethanolamine, ethylenediamine, procaine and the like.

[0232] A pharmaceutical composition described herein can also include a pharmaceutically acceptable anti-oxidant. Examples of pharmaceutically acceptable antioxidants include: (1) water soluble antioxidants, such as ascorbic acid, cysteine hydrochloride, sodium bisulfate, sodium metabisulfite, sodium sulfite and the like; (2) oil-soluble antioxidants, such as ascorbyl palmitate, butylated hydroxyanisole (BHA), butylated hydroxytoluene (BHT), lecithin, propyl gallate, alpha-tocopherol, and the like; and (3) metal chelating agents, such as citric acid, ethylenediamine tetraacetic acid (EDTA), sorbitol, tartaric acid, phosphoric acid, and the like.

[0233] Examples of suitable aqueous and nonaqueous carriers that can be employed in the pharmaceutical compositions described herein include water, ethanol, polyols (such as glycerol, propylene glycol, polyethylene glycol, and the like), and suitable mixtures thereof, vegetable oils, such as olive oil, and injectable organic esters, such as ethyl oleate. Proper fluidity can be maintained, for example, by the use of coating materials, such as lecithin, by the maintenance of the required particle size in the case of dispersions, and by the use of surfactants.

[0234] These compositions can also contain adjuvants such as preservatives, wetting agents, emulsifying agents and dispersing agents. Prevention of presence of microorganisms can be ensured both by sterilization procedures, supra, and by the inclusion of various antibacterial and antifungal agents, for example, paraben, chlorobutanol, phenol sorbic acid, and the like. It can also be desirable to include isotonic agents, such as sugars, sodium chloride, and the like into the compositions. In addition, prolonged absorption of the injectable pharmaceutical form can be brought about by the inclusion of agents which delay absorption such as aluminum monostearate and gelatin.

[0235] Pharmaceutically acceptable carriers include sterile aqueous solutions or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion. The use of such media and agents for pharmaceutically active substances is known in the art. Except insofar as any conventional media or agent is incompatible with the active compound, use thereof in the pharmaceutical compositions described herein is contemplated. A pharmaceutical composition can comprise a preservative or can be devoid of a preservative. Supplementary active compounds can be incorporated into the compositions.

[0236] Therapeutic compositions typically must be sterile and stable under the conditions of manufacture and storage. The composition can be formulated as a solution, microemulsion, liposome, or other ordered structure suitable to high drug concentration. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. In many cases, the compositions can include isotonic agents, for example, sugars, polyalcohols such as mannitol, sorbitol, or sodium chloride in the composition. Prolonged absorption of the injectable compositions

can be brought about by including in the composition an agent that delays absorption, for example, monostearate salts and gelatin.

[0237] Sterile injectable solutions can be prepared by incorporating the active compound in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by sterilization microfiltration. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle that contains a basic dispersion medium and the required other ingredients from those enumerated herein. In the case of sterile powders for the preparation of sterile injectable solutions, some methods of preparation are vacuum drying and freeze-drying (lyophilization) that yield a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

[0238] The amount of active ingredient which can be combined with a carrier material to produce a single dosage form will vary depending upon the subject being treated, and the particular mode of administration. The amount of active ingredient which can be combined with a carrier material to produce a single dosage form will generally be that amount of the composition which produces a therapeutic effect. Generally, out of one hundred percent, this amount will range from about 0.01 percent to about ninety-nine percent of active ingredient, from about 0.1 percent to about 70 percent, or from about 1 percent to about 30 percent of active ingredient in combination with a pharmaceutically acceptable carrier.

[0239] Dosage regimens are adjusted to provide the optimum desired response (*e.g.,* a therapeutic response). For example, a single bolus can be administered, several divided doses can be administered over time or the dose can be proportionally reduced or increased as indicated by the exigencies of the therapeutic situation. It is especially advantageous to formulate parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units suited as unitary dosages for the subjects to be treated; each unit contains a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier. The specification for the dosage unit forms described herein are dictated by and directly dependent on (a) the unique characteristics of the active compound and the particular therapeutic effect to be achieved, and (b) the limitations inherent in the art of compounding such an active compound for the treatment of sensitivity in individuals.

[0240] For administration of a anti-TREM-1 antibody, *e.g.,* described herein, the dosage ranges from about 0.0001 to 100 mg/kg, and more usually 0.01 to 5 or 10 mg/kg, of the host body weight. For example dosages can be 0.3 mg/kg body weight, 1 mg/kg body weight, 3 mg/kg body weight, 5 mg/kg body weight or 10 mg/kg body weight or within the range of 1- 10 mg/kg. An exemplary treatment regime entails administration once per week, once every two weeks, once every three weeks, once every four weeks, once a month, once every 3 months or once every three to 6 months. Exemplary dosage regimens for a anti-TREM-1 antibody described herein include 1 mg/kg body

weight or 3 mg/kg body weight via intravenous administration, with the antibody being given using one of the following dosing schedules: (i) every four weeks for six dosages, then every three months; (ii) every three weeks; (iii) 3 mg/kg body weight once followed by 1 mg/kg body weight every three weeks.

[0241] In some embodiments, the anti-TREM-1 antibody is administered at a flat dose (flat dose regimen). In other embodiments, the anti-TREM-1 antibody is administered at a fixed dose with another antibody. In certain embodiments, the anti-TREM-1 antibody is administered at a dose based on body weight.

[0242] In some methods, two or more monoclonal antibodies with different binding specificities are administered simultaneously, in which case the dosage of each antibody administered falls within the ranges indicated. Antibody is usually administered on multiple occasions. Intervals between single dosages can be, for example, weekly, monthly, every three months or yearly. Intervals can also be irregular as indicated by measuring blood levels of antibody to the target antigen in the patient. In some methods, dosage is adjusted to achieve a plasma antibody concentration of about 1-1000 μg/ml and in some methods about 25-300 μg/ml.

[0243] An antibody can be administered as a sustained release formulation, in which case less frequent administration is required. Dosage and frequency vary depending on the half-life of the antibody in the patient. In general, human antibodies show the longest half-life, followed by humanized antibodies, chimeric antibodies, and nonhuman antibodies. The dosage and frequency of administration can vary depending on whether the treatment is prophylactic or therapeutic. In prophylactic applications, a relatively low dosage is administered at relatively infrequent intervals over a long period of time. Some patients continue to receive treatment for the rest of their lives. In therapeutic applications, a relatively high dosage at relatively short intervals is sometimes required until progression of the disease is reduced or terminated, and until the patient shows partial or complete amelioration of symptoms of disease. Thereafter, the patient can be administered a prophylactic regime.

[0244] Actual dosage levels of the active ingredients in the pharmaceutical compositions described herein can be varied so as to obtain an amount of the active ingredient which is effective to achieve the desired therapeutic response for a particular patient, composition, and mode of administration, without being toxic to the patient. The selected dosage level will depend upon a variety of pharmacokinetic factors including the activity of the particular compositions described herein employed, or the ester, salt or amide thereof, the route of administration, the time of administration, the rate of excretion of the particular compound being employed, the duration of the treatment, other drugs, compounds and/or materials used in combination with the particular compositions employed, the age, sex, weight, condition, general health and prior medical history of the patient being treated, and like factors well known in the medical arts.

[0245] A composition described herein can be administered via one or more routes of administration using one or more of a variety of methods known in the art. As will be appreciated by the skilled artisan, the route and/or mode of administration will vary depending upon the desired results. Routes of administration for the anti-TREM-1 antibodies described herein can include intravenous, intramuscular, intradermal, intraperitoneal, subcutaneous, spinal or other parenteral routes of administration, for example by injection or infusion. The phrase "parenteral administration" as used herein means modes of administration other than enteral and topical administration, usually by injection, and includes, without limitation, intravenous, intramuscular, intraarterial, intrathecal, intracapsular, intraorbital, intracardiac, intradermal, intraperitoneal, transtracheal, subcutaneous, subcuticular, intraarticular, subcapsular, subarachnoid, intraspinal, epidural and intrasternal injection and infusion.

[0246] Alternatively, an antibody described herein could potentially be administered via a non-parenteral route, such as a topical, epidermal or mucosal route of administration, for example, intranasally, orally, vaginally, rectally, sublingually or topically.

[0247] The active compounds can be prepared with carriers that will protect the compound against rapid release, such as a controlled release formulation, including implants, transdermal patches, and microencapsulated delivery systems. Biodegradable, biocompatible polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid. Many methods for the preparation of such formulations are patented or generally known to those skilled in the art. *See*, *e.g.,* Sustained and Controlled Release Drug Delivery Systems, J.R. Robinson, ed., Marcel Dekker, Inc., New York, 1978.

[0248] Therapeutic compositions can be administered with medical devices known in the art. For example, in a particular embodiment, a therapeutic composition described herein can be administered with a needleless hypodermic injection device, such as the devices disclosed in U.S. Patent Nos. 5,399,163; 5,383,851; 5,312,335; 5,064,413; 4,941,880; 4,790,824; or 4,596,556. Examples of well-known implants and modules for use with anti-TREM-1 antibodies described herein include: U.S. Patent No. 4,487,603, which discloses an implantable micro-infusion pump for dispensing medication at a controlled rate; U.S. Patent No. 4,486,194, which discloses a therapeutic device for administering medicaments through the skin; U.S. Patent No. 4,447,233, which discloses a medication infusion pump for delivering medication at a precise infusion rate; U.S. Patent No. 4,447,224, which discloses a variable flow implantable infusion apparatus for continuous drug delivery; U.S. Patent No. 4,439,196, which discloses an osmotic drug delivery system having multi-chamber compartments; and U.S. Patent No. 4,475,196, which discloses an osmotic drug delivery system. These patents are incorporated herein by reference. Many other such implants, delivery systems, and modules are known to those skilled in the art.

[0249] In some embodiments, the anti-TREM-1 antibodies described herein can be formulated to ensure proper distribution *in vivo*. For example, the blood-brain barrier (BBB) excludes many highly

hydrophilic compounds. To ensure that the therapeutic compounds described herein cross the BBB (if desired, *e.g.,* for brain cancers), they can be formulated, for example, in liposomes. For methods of manufacturing liposomes, see, *e.g.,* U.S. Patents 4,522,811; 5,374,548; and 5,399,331. The liposomes can comprise one or more moieties which are selectively transported into specific cells or organs, thus enhance targeted drug delivery (see, *e.g.,* V.V. Ranade (1989) *J. Clin. Pharmacol.* 29:685). Exemplary targeting moieties include folate or biotin (see, *e.g.,* U.S. Patent 5,416,016 to Low *et al.*); mannosides (Umezawa *et al.*, (1988) *Biochem. Biophys. Res. Commun.* 153: 1038); antibodies (P.G. Bloeman *et al.* (1995) *FEBS Lett.* 357: 140; M. Owais *et al.* (1995) *Antimicrob. Agents Chemother.* 39: 180); surfactant protein A receptor (Briscoe *et al.* (1995) *Am. J. Physiol.* 1233: 134); pl20 (Schreier *et al.* (1994) *J. Biol. Chem.* 269:9090); see also K. Keinanen; M.L. Laukkanen (1994) *FEBS Lett.* 346: 123; J.J. Killion; I.J. Fidler (1994) *Immunomethods* 4:273.

VIII. Uses and Methods

[0250] The anti-TREM-1 antibodies of the present disclosure and the compositions comprising such antibodies (*e.g.*, pharmaceutical composition, formulations, polynucleotides, vectors, and cells) can be used for the treatment of an inflammatory disease (*e.g.*, by inhibiting TREM-1 activity).

[0251] Accordingly, in one aspect, the present disclosure provides methods for treating an inflammatory disease in a subject in need thereof, comprising administering a therapeutically effective dose of the anti-TREM-1 antibody to the subject. Examples of inflammatory diseases that can be treated with the present anti-TREM-1 antibodies include, but not limited to, inflammatory bowel disease (IBD), Crohn's disease (CD), ulcerative colitis (UC), irritable bowel syndrome, rheumatoid arthritis (RA), psoriasis, psoriatic arthritis, systemic lupus erythematosus (SLE), lupus nephritis, type I diabetes, Grave's disease, multiple sclerosis (MS), autoimmune myocarditis, Kawasaki disease, coronary artery disease, chronic obstructive pulmonary disease, interstitial lung disease, autoimmune thyroiditis, scleroderma, systemic sclerosis, osteoarthritis, atopic dermatitis, vitiligo, graft versus host disease, Sjogrens's syndrome, autoimmune nephritis, Goodpasture's syndrome, chronic inflammatory demyelinating polyneuropathy, allergy, asthma and other autoimmune diseases that are a result of either acute or chronic inflammation.

[0252] In one embodiment, the anti-TREM-1 antibodies are suitable for use in the treatment of individuals with inflammatory bowel disease. Inflammatory Bowel Disease (IBD) is a disease that may affect any part of the gastrointestinal tract from mouth to anus, causing a wide variety of symptoms. IBD primarily causes abdominal pain, diarrhoea (which may be bloody), vomiting or weight loss, but may also cause complications outside of the gastrointestinal tract such as skin rashes, arthritis, inflammation of the eye, fatigue and lack of concentration. Patients with IBD can be divided into two major classes, those with ulcerative colitis (UC) and those with Crohn's disease (CD). CD generally involves the ileum and colon, it can affect any region of the intestine but is often

discontinuous (focused areas of disease spread throughout the intestine). UC always involves the rectum (colonic) and is more continuous. In CD, the inflammation is transmural, resulting in abscesses, fistulas and strictures, whereas in UC, the inflammation is typically confined to the mucosa. There is no known pharmaceutical or surgical cure for Crohn's disease, whereas some patients with UC can be cured by surgical removal of the colon. Treatment options are restricted to controlling symptoms, maintaining remission and preventing relapse. Efficacy in inflammatory bowel disease in the clinic may be measured as a reduction in the Crohn's Disease Activity Index (CDAI) score for CD which is scoring scale based on laboratory tests and a quality of life questionnaire. In animal models, efficacy is mostly measured by increase in weight and also a disease activity index (DAI), which is a combination of stool consistency, weight and blood in stool.

[0253] In one embodiment, the anti-TREM-1 antibodies of the present disclosure are suitable for use in the treatment of individuals with rheumatoid arthritis. Rheumatoid arthritis (RA) is a systemic disease that affects nearly if not all of the body and is one of the most common forms of arthritis. It is characterized by inflammation of the joint, which causes pain, stiffness, warmth, redness and swelling. This inflammation is a consequence of inflammatory cells invading the joints, and these inflammatory cells release enzymes that may digest bone and cartilage. As a result, this inflammation can lead to severe bone and cartilage damage and to joint deterioration and severe pain, among other physiologic effects. The involved joint can lose its shape and alignment, resulting in pain and loss of movement. There are several animal models for rheumatoid arthritis known in the art. For example, in the collagen-induced arthritis (CIA) model, mice develop an inflammatory arthritis that resembles human rheumatoid arthritis. Since CIA shares similar immunological and pathological features with RA, this makes it a suitable model for screening potential human anti-inflammatory compounds. Efficacy in this model is measured by decrease in joint swelling. Efficacy in RA in the clinic is measured by the ability to reduce symptoms in patients which is measured as a combination of joint swelling, erythrocyte sedimentation rate, C-reactive protein levels and levels of serum factors, such as anti-citrullinated protein antibodies.

[0254] In one embodiment, the anti-TREM-1 antibodies as disclosed herein are suitable suitable for use in the treatment of individuals with psoriasis. Psoriasis is a T-cell mediated inflammatory disorder of the skin that can cause considerable discomfort. It is a disease for which there is currently no cure and it affects people of all ages. Although individuals with mild psoriasis can often control their disease with topical agents, more than one million patients worldwide require ultraviolet light treatments or systemic immunosuppressive therapy. Unfortunately, the inconvenience and risks of ultraviolet radiation and the toxicities of many therapies limit their long-term use. Moreover, patients usually have recurrence of psoriasis, and in some cases rebound shortly after stopping immunosuppressive therapy. A recently developed model of psoriasis based on the transfer of CD4+ T cells mimics many aspects of human psoriasis and therefore can be used to identify compounds suitable for use in treatment of psoriasis (Davenport *et al.*, *Internat. Immunopharmacol* 2 : 653-672,

2002). Efficacy in this model is a measured by reduction in skin pathology using a scoring system. Similarly, efficacy in patients is measured by a decrease in skin pathology.

[0255] In one embodiment, the anti-TREM-1 antibodies are suitable for use in the treatment of individuals with psoriatic arthritis. Psoriatic arthritis (PA) is a type of inflammatory arthritis that occurs in a subset of patients with psoriasis. In these patients, the skin pathology/symptoms are accompanied by a joint swelling similar to that seen in rheumatoid arthritis. It features patchy, raised, red areas of skin inflammation with scaling. Psoriasis often affects the tips of the elbows and knees, the scalp, the navel and around the genital areas or anus. Approximately 10% of patients who have psoriasis also develop an associated inflammation of their joints.

[0256] In terms of the present disclosure, prophylactic, palliative, symptomatic and/or curative treatments may represent separate aspects of the disclosure. An antibody of the invention can be administered parenterally, such as intravenously, such as intramuscularly, such as subcutaneously. Alternatively, an antibody of the invention can be administered via a non-parenteral route, such as perorally or topically. An antibody of the invention can be administered prophylactically. An antibody of the invention can be administered therapeutically (on demand).

[0257] The following examples are offered by way of illustration and not by way of limitation. The contents of all references cited throughout this application are expressly incorporated herein by reference.

EXAMPLES

Example 1: Analysis of the Interaction Kinetics for the 318 Antibody Variants to both Human and Cynolmogus TREM-1 by Surface Plasmon Resonance

[0258] The binding kinetics of the mAb 0318 variants towards human TREM-l-Fc (hTREM-1) and cynomolgus TREM-l-Fc (cTREM-1) were determined. Binding studies were performed on a ProteOn Analyzer (BioRad) that measures molecular interactions in real time through surface plasmon resonance. Experiments were run at 25°C and the samples were stored at 15°C in the sample compartment. The signal (RU, response units) reported by the ProteOn is directly correlated to the mass on the individual sensor chip surfaces in the six parallel flow cells. Anti-human Fc monoclonal or anti-murine Fc polyclonal antibody from Biacore human or mouse Fc capture kits were immobilized in horizontal direction onto flow cells of a GLM sensor chip according to the manufacturer's instructions. The final immobilization level of capture antibody was approximately 2600- 6000 RU in each experiment. The capture of purified monoclonal mouse or recombinantly expressed anti-hTREM-1 antibodies was conducted by diluting the antibodies to 5-10 nM into running buffer (10 mM Hepes 0,15 M NaCI, 5 mM EDTA, 0.05% surfactant P20, pH 7.4) followed by injection in vertical direction at 30 µl/min for 60 sec, creating reference interspots adjacent to all flow cells with only anti-Fc antibody immobilized. This typically resulted in final capture levels of test

antibodies of approximately 100-300 RU and Rmax values of analyte of 30-90 RU. Binding of hTREM-1 or cTREM-1 proteins was conducted by injecting analyte (antigen) over all flow cells in horizontal direction to allow for comparative analyses of binding to different captured anti-TREM-1 antibodies relative to binding to the reference interspot. hTREM-1 or cTREM-1 proteins were diluted serially 1 :3 to 1.2-100 nM or into running buffer, injected at 100 µl/min for 250 s and allowed to dissociate for 600s. The GLM surface was regenerated after each injection cycle of analyte via two 18 s injections of 10 mM Glycine, pH 1.7 and 50 mM NaOH at 100 µl/min. This regeneration step removed the anti-TREM-1 antibody and any bound TREM- 1 protein from the immobilized capture antibody surface and allowed for the subsequent binding of the next interaction sample pair. The regeneration procedure did not remove the directly immobilized anti-Fc capture antibody from the chip surface.

[0259] Binding affinity between antibodies and the antigen was quantified by determination of the equilibrium dissociation constant (K_D) determined by measurement of the kinetics of complex formation and dissociation. The rate constants corresponding to the association and the dissociation of a monovalent complex such as k_a (association rate) and k_d (dissociation rate) were retrieved by fitting data to 1:1 Langmuir model using the ProteOn evaluation software for data analysis. K_D is related to k_a and k_d through the equation $K_D = k_d / k_a$.

[0260] Binding curves were processed by double referencing (subtraction of reference surface signals as well as blank buffer injections over captured anti-TREM-1 antibodies) prior to data analysis. This allowed correction for instrument noise, bulk shift and drift during sample injections.

[0261] As shown in FIG. 1A and 1B, the mAb 0318 variants (i.e., 318-IgG1.1f, 318-IgG1.3f, 318-IgG4-Aba, and 318-IgG1-Aba) were all found to have similar affinity towards human TREM-l-Fc as mAb 0318-IgG4. The 0318-IgG1.3f variant also bound to cynomolgus TREM-1, albeit with slightly reduced affinity as compared to human TREM-1. *See* FIG. 1A.

Example 2: Internalization Analysis of mAb 0318-IgG1.3f upon Binding to TREM-1 Receptor

[0262] The mAb 0318-IgG1.3f variant antibody was tested for its internalization in primary human monocytes using both laser scanning confocal microscopy (data not shown) and Amnis ImageStream® Imaging Flow Cytometry Analysis. As shown in FIG. 2A, at 0 hours, TREM-1 is expressed primarily on the surface of the monocytes. However, by 24 hours after antibody binding, a significant percentage (~36%) of the TREM-1 receptor (as evidenced by 0318-IgG1.3f staining) has been internalized, suggesting that upon mAb 0318-IgG1.3f antibody binding, the entire antibody-receptor complex is internalized within the cell.

[0263] Next, to determine the fate of the TREM-1 receptor once it has been internalized, the TREM26 antibody (cat. No. 314902, Biolegend; See US20150274825 at paragraph [0005]) was used for comparison. The TREM26 antibody does not compete with the 0318 antibody variants described

in the present disclosure. As shown in FIG. 2B, compared to 0 hours, there was a significant reduction in TREM26+ expression (~51%) at the 20 hour time point. There was also a significant reduction (4 fold) in TREM26+ MFI (mean fluorescence index) at the 20 hour time point (post mAb 0318-IgG1.3f treatment), suggesting that the TREM-1 receptor is degraded upon internalization. This loss of TREM-1 receptor expression upon antibody exposure is reversible, however, once the antibody is removed (data not shown).

Example 3: Analysis of the mAb 0318 Variants to Efficiently Block TREM-1 Activation Using the BWZ/hTREM-1 Reporter Cell Assay

[0264] The ability of the anti-TREM-1 mAb 0318 variants to inhibit human TREM-1 signaling was determined using the BWZ.36/hTREM-1DAP12:NFAT-LacZ cell line (herein also referred to as the "BWZ/hTREM-1 reporter cell") assay as described in, for example, U.S. Pat. No. 9,550,830 B2 and International Publ. No. WO 2016/009086 A1. Briefly, approximately 40,000 hTREM-1/BWZ.36 cells/well were plated in a clear bottom, black 96 well plate in the presence of 75 ng/ml PGLYRP1 (SEQ ID NO: 8) with 2.5 μg/ml PGN-ECndi (Cat. no. tlrl-kipgn, Invivogen San Diego, Calif., USA) to provide a sub-maximal positive signal, or alternatively in the presence of a sub-maximal level (1 μg/ml) of plastic adsorbed anti TREM-1 monoclonal antibody (Cat. no. MAB1278, R&D Systems, Minneapolis, Minn., USA) to provide a positive signal.

[0265] The mAb 0318 variants (i.e., 0318-IgG1.3f; 0318-IgG1.1f; 0318-IgG1-Aba; and 0318-IgG4-Aba) were titered into the assay starting at 10 μg/ml, with 5 serial 2-fold dilutions. The assay was incubated overnight at 37°C, subsequently developed with Beta Glo (Cat. no. E4740, Promega Madison, Wis., USA), as per the Beta Glo protocol, and luminescence was recorded. Data was plotted showing Beta Glo relative luminescent units vs test antibody concentration. Non-neutralizing negative control mIgG1 (Cat. no. MAB002, R&D Systems Minneapolis, Minn., USA) and neutralizing positive control polyclonal goat anti hPGLYRP1 antibody (Cat. no. AF2590, R &D Systems, Minneapolis, Minn., USA) were run on each assay plate. The MAB1278 antibody (cat. no. MAB1278, R&D Systems; See US20150274825 at paragraph [0005]), a known agonist of TREM-1 signaling, was also used as a positive control (see inserted box).

[0266] As shown in FIG. 3, all the mAb 0318 variants were potent at inhibiting human TREM-1 signaling as observed previously with the mAb 0318 IgG4 antibody in International Publ. No. WO 2016/009086 A1.

Example 4: *In vitro* analysis of the potency of the mAb 0318 antibody variants at inhibiting TREM-1 mediated production of inflammatory cytokines by different primary human cells

[0267] To further assess the antagonistic properties of the anti-TREM-1 mAb 0318 variants, their potency to block the release of various inflammatory cytokines (e.g., TNF-α, IL-6, or IL-8) from

activated human primary cells was assessed. Primary monocytes, neutrophils, and peripheral blood mononuclear cells (PBMCs) were isolated from human whole blood and stimulated with plate-bound PGRP1 and soluble peptidoglycan (PGN-ECndss; a form of peptidoglycan without the TLR2 activity).

[0268] As shown in FIG. 4, all the mAb 0318 variants (i.e., IgG1.3f, IgG1.1f, IgG1-Aba, and IgG4-Aba) were all potent (IC_{50} values in the ~10-20 pM range) at inhibiting TREM-1 mediated release of TNF-α from PBMC and monocytes. The potency of these mAb 0318 variants were similar to that observed with the mAb 0318-IgG4 antibody. The mAb 0318-IgG1.3f antibody was also potent in inhibiting IL-6 production (IC_{50} value of ~32 pM). For neutrophils, the mAb 0318-IgG1.3f variant appeared to be better compared to the mAb 0318-IgG4 antibody at blocking TREM-1 mediated IL-8 production from neutrophils. (*See* FIG. 4).

[0269] As further demonstration of the antagonistic properties of the anti-TREM-1 mAb 0318 antibody variants, a monocyte-neutrophil co-culture assay was also used. Neutrophil-associated PGRP1 when co-cultured with monocytes can ligate TREM-1 receptors, resulting in monocyte-derived TNF-α production. As shown in FIG. 4, all the mAb 0318 antibody variants effectively blocked this endogenous activation (IC_{50} values ranging from 19-44 pM). Similar results were observed with RBC-sedimented whole blood. (*See* FIG. 4).

Example 5: *In Vitro* Analysis of the Potency of mAb 0318-IgG1.3f to Block IL-8 Production from Stimulated Whole Blood

[0270] One of the major challenges towards the development of a whole blood pharmacodynamics (PD) assay to measure the antagonistic properties of the anti-TREM-1 antibody variants is the high background resulting from the PGN stimulation. To help address this issue, whole blood was stimulated with pre-complexed PGRP1+PGN in the presence of NOD2 inhibitor (to block background cytokines produced by NOD2 stimulation by PGN). IL-8 levels were measured using the standard ligand binding pharmacodynamics assay (HTRF®) (FIG. 5A) or an intracellular cytokine staining (ICS) assay (FIG. 5B).

[0271] As shown in FIGs. 5A and 5B, the 0318-IgG1.3f antibody effectively blocked the TREM-1 mediated IL-8 production with percent inhibition ranging from about 60-90% (see FIG. 5A). The observed IC50 values (mean value of 12 pM with HTRF and 19.6 pM with ICS) were similar to that observed with other functional assays (e.g., see Example 4).

Example 6: *In Vitro* Analysis of the Potency of mAb 0318-IgG1.3f to Block mRNA Expression of Different Inflammatory Mediators in Stimulated Whole Blood

[0272] To additionally demonstrate the antagonistic properties of mAb 0318-IgG1.3f, the expression levels of select inflammatory mediators (i.e., chitinase-3-like protein 1 ("CHI3L1"), IL1β, and IL6) were measured measured by Real-Time PCR (qPCR). Briefly, human whole blood collected in EDTA tubes from three normal healthy volunteers (donor #126, 290, and 322) was stimulated with pre-complexed hPGRP1 (50 µg/ml) and PGN-ECndss (10 µg/ml) (Invivogen tlrl-ksspgn) overnight in the presence of varying concentrations of mAb 0318-IgG1.3f (0-1 nM). Following stimulation, the plasma was removed and frozen for cytokine measurements. The mRNA was isolated from the samples using the MagMax-96 Blood Isolation Kit (ThermoFisher AM1837) according to the manufacturer's protocol. The isolated mRNA was then converted to cDNA utilizing the SuperScript VILO Master Mix (Thermo Fisher 11755250). Next, qPCR was performed using the following probes: HPRT1 (Hs99999909_m1) (Thermo Fisher 4351370), CHI3L1 (Hs01072228_m1) (Thermo Fisher 4331182), IL1β (Hs00174097_m1) (Thermo Fisher 4331182), and IL6 (Hs00985639_m1) (Thermo Fisher 4331182) and TaqMan Fast Universal Master Mix (2x) (Thermo Fisher 4366072). Gene expression values were normalized to HPRT1 and ΔΔCT values were generated. Results were then plotted and IC_{50} values were determined.

[0273] As shown in FIGs. 6A-6C and in agreement with the earlier Examples, mAb 0318-IgG1.3f was able to inhibit the TREM-1 mediated expression of different inflammatory mediators in human whole blood. The inhibition appeared to be dose dependent. TheIC50 values are shown in Table 1 below.

[0274] Collectively, the above results demonstrate that the mAb 0318 antibody variants described in the present disclosure are antagonistic and can effectively block TREM-1 mediated production of inflammatory cytokines from various human cells.

Table 1.

Cell Type	Inflammatory Mediator	Stimulus	mAb 0318-IgG1.3f IC50 (pM)
Whole Blood	CHI3L1 RNA	Soluble PGRP + Soluble PGN-Ecndss	4.58±5.60 (N=3)
	IL1b RNA		11.15±16.01 (N=3)
	IL6 RNA		97.66±125.63 (N=3)

Example 7: Viscosity of the mAb 0318 Variants

[0275] Sample was buffer exchanged and dialyzed into the formulation of choice (20mM histidine, 150mM sucrose, 25mM arginine, 50mM sodium chloride, pH 6.0), followed by concentration using Amicon Ultra centrifugal molecular weight cutoff filters. Aggregation state of the samples was measured to by size exclusion chromatography to control for potential changes in

monomericity upon concentration, which were not observed. Concentration-dependent viscosity was determined using a RheoSense m-VROC solution viscometer using a 3 point ascending shear sweep for each concentration measured. Concentration was determined by measuring absorbance at 280nm by nanoDrop using dilution series and extrapolation.

[0276] As shown in FIG. 7, both the 318-IgG1.1f and 318-IgG1.3f variants had similar viscosity profile. At a concentration of about 130 mg/mL, the 0318-IgG1.3f variant had a viscosity value of about 9 cP. Such viscosity profile closely mirrored that observed previously with mAb 0318-IgG4 (*see* International Publ. No. WO 2016/009086).

Example 8: Immunogenicity Potential of the mAb 0318 Variants

[0277] As shown in FIG. 8 and Table 2 (below), the 318-IgG1.1f and 318-IgG1.3f variants had low to medium risk for immunogenicity in human patients. Only about 22-30% of the donor had immunogenic responses (as measured by *in vitro* $CD4^+$ T cell proliferation) to these antibodies. The immunogenicity for the 0318-IgG1-Aba and 0318-IgG4-Aba variants was 10% and 42.5%, respectively. *See* Table 2 (below). In contrast, the mAb 0318-IgG4 was much more immunogenic (55%) in human patients. KLH (keyhole limpet hemocyanin) and VL6 (IL-21R mAb), which were used as positive controls, were highly immunogenic in the human patients (100% and 40%, respectively).

Table 2.

Assay	Cohort	0318 Variant	Conc. (mg/mL)	Host Cell	EU/mg	% Monomer	Assay Conc. (ug/mL)	% Immunogenicity
PBMC	40	IgG4	161	UCOE CHO	<0.001	97.9	150	55.0
PBMC	40	IgG1-Aba	145	UCOE CHO	<0.001	97.3	150	10.0
PBMC	40	IgG1.1f	170	UCOE CHO	<0.006	98.6	150	22.5
PBMC	40	IgG4-Aba	5	HEK	<0.02	98.9	150	42.5
PBMC	40	IgG1.3f	4.6	HEK	<0.02	99.5	150	30.0

Example 9: Binding Analysis of the mAb 0318 Variants to FcRn Using Surface Plasmon Resonance (SPR)

[0278] To determine whether the different mAb 0318 variants were able to bind to FcRn, the FcRn receptors (mouse, human, and cyno) were immobilized onto a BIAcore CM5-biosensor chip (GE Healthcare Bioscience, Uppsala, Sweden) via amine coupling to a level of 400 Response Unites (RU). The assay was carried out at room temperature with PBS, 0.05 % Tween-20™ pH 6.0 (GE Healthcare Bioscience) as running and dilution buffer. The different mAb 0318 variants (200 nM)

were injected at a flow rate of 50 μL/min at room temperature at pH 6.0. Association time was 180 seconds, dissociation phase (also at pH 6.0) took 360 seconds. Regeneration of the chip surface back to baseline was reached by a short injection of 50 mM Tris, pH 8.0, and 150 mM NaCl. Evaluation of SPR-data was performed by comparison of the biological response signal height at 180 seconds after injection and at 300 seconds after injection. The corresponding parameters are the RU max level (180 seconds after injection) and late stability (300 seconds after end of injection).

[0279] As shown in FIGs. 9A and 9B, the mAb 0318 antibody variants (IgG1-Aba mod, IgG4-Aba mod, IgG1.1f, and IgG1.3f) were all able to bind to human, mouse, and cyno FcRn in a pH dependent manner. This was also true for the mAb 0318 antibody (IgG4).

Example 10: Binding Analysis of the mAb 0318 Variants to One or More FcγRs

[0280] As discussed earlier, the in vivo administration of antibodies to certain cell surface immune receptors has the potential for inducing cytokine release, which can result in the induction of a common and toxic clinical complication known as the cytokine release syndrome (CRS). Because of the concern that FcγR engagement could lead to potential TREM-1 agonistic activity via cross-linking, mAb 0318-IgG4 was re-engineered into one of the variant formats described in the present disclosure (i.e., IgG1.1f, IgG1.3f, IgG1-Aba, or IgG4-Aba). Then, the ability of the 0318 antibody variants to bind to different FcγRs was assessed.

[0281] As shown in FIGs. 10A and 10B, the 318-IgG1.1f and 318-IgG1.3f variants had minimal binding to all of the FcγRs (i.e., FcγRI (CD64), FcγRIIA (CD32a-H131 and CD32a-R131 variants), FcγRIIB (CD32b), FcγRIIIA (CD16a-V158 variant), and FcγRIIIB (CD16b-NA2 variant)). The 318-IgG1-Aba and 318-IgG4-Aba variants did not bind to FcγRIIA, FcγRIIB, FcγRIIIA, and FcγRIIIB but did bind to FcγRI. In contrast, mAb 0318 (IgG4) showed significant binding to all of the FcγRs.

Example 11: Analysis of the Induction of Inflammatory Cytokines by the mAb 0318 Variants

[0282] To further determine if the *in vivo* treatment with the mAb 0318 variants poses a risk of cytokine release syndrome, whole blood was collected from 8 human donors and the monocytes were isolated. Then, the monocytes were differentiated into immature dendritic cells by plating the monocytes ($4x10^6$ cells/well) and culturing them in a differentiation media containing IL-4 and GM-CSF (100 ng/mL). At around days 2-3 post-plating, approximately half of the differentiation media was replaced with fresh media. At day 7, the cells were harvested and the differentiation efficiency was assessed by analyzing CD14 expression on the cells using flow cytometer. Next, the immature dendritic cells were plated onto a flat bottom plate ($0.8x10^5$ cells/well) and the mAb 0318 variants were added to respective wells (with or without CHO-CD32a). Immature dendritic cells stimulated with PGRP + PGN were used as a positive control. The cells were then incubated overnight at 37°C.

The next day, supernatants were harvested from the wells and the amount of TNF-α,IL-6, and IL-12 produced was assessed using an ELISA assay.

[0283] The results from representative donors are shown in FIGs. 11A to 11I.The addition of the different mAb 0318 variants (0318-IgG1.1f, 0318-IgG1.3f, and 0318-IgG1.1 Aba) resulted in minimal IL-6 (FIGs. 11A, 11B, and 11C), TNF-α (FIGs. 11D, 11E, and 11F), and IL-12 (FIGs. 11G, 11H, and 11I) production by the immature dendritic cells. These results, along with those from Example 9, demonstrate that the anti-TREM-1 antibodies disclosed herein have a low risk of inducing a cytokine release syndrome when administered to patients *in vivo*.

Example 12: Additional Characteristics of the mAb 0318 Variants

[0284] Biophysical characteristics of the 0318-IgG1.3f variant are provided in Table 3 (below).

Table 3. Biophysical Characteristics of anti-TREM-1 0318-IgG1.3f Antibody

Property	**Method**	**Results**
Identity	LC-MS	Intact Mass confirmed
	LC-MS/MS peptide map	Sequence confirmed by Lys-C peptide map (95.4% recovery; Glycosylation occupancy of 99.7%)
Purity/Homogeneity	SEC	96.3% monomer, 3.6% HMW
	SEC-MALS	Main Peak is 95% monomer & homogeneous (145 kDa)
	LC-MS	G0F (23.3%), G1F (51.3%), G2F (17.3%), SG2F (2.1%), S2G2F (1.0%)
	Capillary isoelectric focusing (cIEF)	Main Peak pI = 8.75 (55%); Acidic variants = 29.5% & Basic variants = 15.5%
	SDS-PAGE	Reduced: 2 predominant bands of ~50 kDa & 25 kDa Non-Reduced: Predominant band of ~150 kDa with minor fragments of ~98 kDa, 75 kDa, 50 kDa, 25 kDa (artifacts of SDS-running conditions)
Affinity	SPR (Biacore)	**huTREM1:** K_D = 0.91 nM; k_{on} = 1.4 E+06 (1/Ms); k_{off} = 1.3 E-3 (1/s) **CynoTREM1:** K_D = 3.4 nM; k_{on} = 4.0 E+05 (1/Ms); k_{off} = 1.4 E-3 (1/s)
Thermal Stability	DSC	T_m1 = 66.2°C; T_m2 = 78.4°C; T_m3 = 83.2°C
		Reversibility at 77°C = 24%
FcγR/FcRn Interaction	SPR (Biacore)	Demonstrates decreased binding to all FcγRs
		Expected pH dependent FcRn binding comparable to wild-type IgG1 mAbs

[0285] The biophysical properties of the mAb 0318-IgG1.3f variant are favorable for clinical development. The identity of the antibody was confirmed by mass spectrometry analysis (Intact Mass Analysis & Peptide Mapping). The antibody was > 96% monomeric as tested by size exclusion chromatography. A single N-glycosylation site was confirmed at N301 on the heavy chain with a glycan profile matching the glycan profile of CHO-expressed monoclonal antibodies (G0F, G1F, and G2F). Thermal stability (T_m1 = 66.2°C; T_m2 = 78.4°C; T_m3 = 83.2°C) and thermal reversibility (24% at 77°C) of the mAb 0318-IgG1.3f was within the range for a typical human IgG1.3 monoclonal antibody.

[0286] Stability characteristics of the mAb 0318-IgG1.3f variant are provided in Table 4 (below).

Table 4. Stability of the Anti-TREM-1 0318-IgG1.3f Antibody

Property	**Method(s)**	**Results**
Freeze/Thaw (2 h @ -80°C, 4 h @ RT x 3)	UV, SEC, DLS, iCIEF	No freeze/thaw stability risk revealed
Solubility/Concentration Profile	UV, SEC	>150 mg/mL in formulation buffer (20 mM histidine, 150 mM sucrose, 50 mM sodium chloride, 25 mM arginine, pH 6.0)
pH Screen for Conformational and Colloidal Stability	Optim2 (Tm and Tagg onset)	Optimal conformational stability = pH 6-8 Optimal colloidal stability = pH 5-6
Buffer and Excipient Screening	Optim2 (Tm and Tagg onset)	Stabilizers: sucrose, sorbitol, arginine (high concentration), glycerol
Accelerated Stability 150 mg/mL 12 w @ 4°C, 25°C, and 40° C in the formulation (20 mM histidine, 150 mM sucrose, 50 mM sodium chloride, 25 mM arginine, pH 6.0)	SEC, cIEF, HIC, LC-MS/MS (peptide mapping), LC/MS (intact mass), 2D-LC/MS (fragments), Biacore, bioassay, UV-Vis, DLS	12 w @ 40°C = 1.2%/month increase in HMW 2.4%/month increase in LMW 12 w @ 40°C = Increase in Rh and Pd 12 w @ 40°C = 11%/month increase in acidic variants 12 w @ 40°C = 3%/month VSNK deamidation
Viscosity Assessment	Determine concentration-viscosity profile	Solution reaches 9 cP at ~130 mg/mL, with predicted viscosity of 12 cP at 150 mg/mL

[0287] No physical stability issues were observed during freeze-thaw stress (3 cycles) at 150 mg/mL in the described formulation (20 mM histidine, 150 mM sucrose, 50 mM sodium chloride, 25 mM arginine, pH 6.0). Forced degradation studies in the studied formulation at 150 mg/mL were set up at 4, 25, and 40°C (up to 3 months). CDR chemical modifications remained low throughout all temperature conditions and did not affect activity, as determined by SPR. VSNK deamidation was below expectations compared with other monoclonal antibodies on the IgG1.3f framework (3%/month increase at 40°C storage), changes to which were time and temperature dependent. All other chemical modifications (oxidation, deamidation, isomerization) also remained low as monitored during the stability studies. Of note, storage at 40°C indicates a formation of both HMW and LMW

variants (demonstrating 1.2%/month and 2.4%/month, respectively). The observed changes were time and temperature dependent, such that HMW increased 0.25%/month, which LMW remained unchanged under 4°C storage over the study period. The low LMW formation under 40°C storage was characterized by 2D-LC/MS with high resolution accurate mass measurements as the cumulative species of 1 Fab loss, as well as the Fab arm, putatively at a conserved sequence in the upper hinge region.

Example 13: PK/TK/PD Study for the mAb 0318-IgG1.3f Variant in Cynomolgus Monkeys

[0288] A single-dose pharmacokinetic (PK), toxicokinetic (TK), and pharmacodynamics (PD) study was conducted in Cynomolgus monkeys for the anti-TREM-1 0318-IgG1.3f antibody. Some of the animals received 2 mg/kg of the 0318-IgG1.3f antibody intravenously (n=3). Other animals received one of the following doses of the 0318-IgG1.3f antibody subcutaneously: (i) 0 mg/kg (i.e., control) (n=4), (ii) 0.1 mg/kg (n=4), (iii) 0.5 mg/kg (n=4), (iv) 2 mg/kg (n=3), or (v) 10 mg/kg (n=4). Upon antibody administration, pharmacokinetics, anti-drug antibodies (ADA), TREM-1 receptor occupancy (RO), and ex vivo pharmacodynamics responses were examined at pre-determined time points.

Pharmacokinetics (PK)

[0289] To assess the pharmacokinetics, serum concentrations of the 0318-IgG1.3f antibody were assessed in the animals with a ligand binding assay using a biotinylated recombinant TREM-1 protein as the capture reagent and a commercial polyclonal goat-anti-TREM-1 antibody as the detection reagent.

[0290] As shown in FIG. 12, the pharmacokinetics of the 0318-IgG1.3f antibody was determined to be non-linear between 0.1 and 10 mg/kg, predominantly due to target mediated clearance (i.e., internalization and degradation of the antibody upon binding to TREM-1 receptor; *see* Example 2).

[0291] Non-compartmental analysis based PK parameters are presented in Tables 5 (intravenous administration) and 6 (subcutaneous administration). Briefly, a 100-fold increase in dose resulted in 830-fold increase in serum exposures (AUCs). *See* Table 6. Clearance following 2 mg/kg IV dose was 0.1 ± 0.02 mL/h/kg and similar to other IgG1 based mAbs in monkeys. *See* Table 4. The Vss at 36 ± 5 mL/kg, was similar to plasma volume indicating limited extravascular distribution. The half-life of the 0318-IgG1.3f antibody increased from 2 days for 0.1 mg/kg dose to 10 days at 2 and 10 mg/kg (single subcutaneous dose administration). *See* Table 6. The bioavailability of the 0318-IgG1.3f antibody following the subcutaneous administration (2 mg/kg) was high at 84%.

Table 5. PK Parameters of mAb 0318-IgG1.3f in Cynomolgus Monkey after Single IV Dose

mAb 0318-IgG1.3f IV-PK Parameters in Cynomolgus Monkeys	
Dose (mg/kg)	2

N	3
Vss (mL/kg)	36 ± 5
CL (mL/h/kg)	0.1 ± 0.02
$T_{1/2}$ (days)	10 ± 2
AUC_{last} (μM*h)	116 ± 20
ADA Positive/Total Examined	3/3 (1/3)*

* Number of monkeys out of total examined that showed persistent ADA.

Table 5. PK Parameters of mAb 0318-IgG1.3f in Cynomolgus Monkeys after Single SC Dose

mAb 0318-IgG1.3f SC-PK Parameters in Cynomolgus Monkeys				
Dose (mg/kg)	0.1	0.5	2	10
N	4	4	3	4
Cmax (nM)	13 ± 4	50 ± 3	189 ± 22	1419 ± 93
Tmax (h)	24	48	168 ± 96	84 ± 24
AUC_{last} (μM*h)	1 ± 0.2	15 ± 1	94 ± 13	649 ± 64
$T_{1/2}$ (days)	2 ± 0.4	4 ± 2	10 ± 5	10 ± 3
SC Bioavailability			84%	
ADA positive/Total Examined	3/4 (2/4)*	4/4 (2/4)*	3/3 (2/3)*	3/4 (1/4)*

* Number of monkeys out of total examined that showed persistent ADA.

Anti-Drug Antibodies (ADA)

[0292] While serum ADA were detected in most monkeys (16 out of 18) following single dose (regardless of the route of administration), exposure of the 0318-IgG1.3f antibody and TREM-1 receptor occupancy (RO) was not compromised in majority of ADA positive animals. *See* Tables 4 and 5. Accelerated decline in terminal exposure of the 0318-IgG1.3f antibody that was accompanied with formation of ADA was observed only in two monkeys (one in 0.1 mg/kg dose-group at day 7 and one in 0.5 mg/kg dose-group at day 21). Since ADA affected exposure in these two monkeys in the terminal phase, corresponding data points were eliminated for PK analysis.

TREM-1 Receptor Occupancy (RO) and Total TREM-1 Receptor Levels

[0293] Next, the occupancy of the TREM-1 receptors expressed on peripheral blood monocytes and granulocytes were assessed. As shown in FIGs. 15A and 15B, for all doses tested, the percentage of TREM-1 receptors that were occupied (i.e., bound to the anti-TREM-1 antibodiy) were similar between the monocytes and the granulocytes. Moreover, the duration of receptor occupancy appeared to be dependent on the dose of the 0318-IgG1.3f antibody administered to the animals. At 0.5 mg/kg, there was ≥ 85% RO observed for up to 2 weeks post antibody administration. In contrast, with the 2 and 10 mg/kg, ≥ 85% of the TREM-1 receptors remained occupied for at least 1 month post administration.

[0294] Following the 0318-IgG1.3f antibody dosing, the total TREM-1 receptor levels were reduced on both monocytes and granulocytes. *See* FIGs. 14A and 14B. As discussed earlier, this reduction is presumably due to increased receptor turnover following antibody binding. The decrease

in surface TREM-1 receptor expression was reversible and the duration of surface receptor loss was correlated with duration of receptor occupancy at least at the dose-levels examined.

[0295] Levels of soluble TREM-1 (sTREM-1) appeared to increase 10- to 50-fold following single dose of the mAb 0318 mAb-IgG1.3f variant in all dose groups tested. (Data not shown). It is unclear if the increase in sTREM-1 levels was related to the anti-TREM-1 antibody administration or to the general handling of the animals during the course of the study. In any case, since drug concentrations far exceeded (>1000 fold) sTREM-1 levels, the soluble target is not anticipated to effect binding of the mAb 0318 mAb-IgG1.3f variant to cell surface TREM-1.

Example 14: PK/TK/PD Study for the mAb 0318-IgG1.3f Variant in Cynomolgus Monkeys Described by a 2-Compartment PK Model with TMDD in Central Compartment

[0296] Monkey PK, RO, total receptor levels, and PD data were described using a 2-compartment PK model with saturable target-mediated drug disposition (TMDD) in the central compartment to accommodate for the observed non-linear PK (*see* Example 12 and FIG. 13). A direct-effect inhibitory model was used to describe the PD response. This model was able to effectively capture the time course of PK/RO/PD observed in the monkeys. The observed (open circle) and model-predicted endpoints (solid line) are provided in FIGs. 16A (0.1 mg/kg subcutaneous dosing) and 16B (10 mg/kg subcutaneous dosing). Table 7 provides the estimated PK/PD parameters. When serum exposures of the mAb 0318-IgG1.3f variant and TREM-1 RO data were pooled from all monkeys, a concentration-dependent increase in RO was observed. *See* FIGs. 16A and 16B. An Emax model used to describe the concentration-RO relationship, estimated in vivo RO EC_{50} to be 1.6 ± 0.2 nM.

Table 7. Parameter Estimates of PK/PD Model Used to Describe Monkey PK/TK/PD Data and Projected Human Parameter Estimates

PK Parameters	Description	Cyno-Model Estimate (CV%)	Projected Human Estimate
Ka (h-1)	Absorption rate constant	0.049 (15)	0.049
V1 (mL/kg)	Volume of distribution of central compartment	22 (5)	22
Ke (h-1)	Elimination rate constant from central compartment	0.003 (10)	0.0019
K12 (h-1)	Distribution rate constants	0.024 (14)	0.015
K21 (h-1)		0.022 (7)	0.014
F (%)	SC bioavailability	80 (5)	80
Kdeg (h-1)	Target turnover rate constant	0.09 (20)	0.09
Kint (h-1)	Target-mAb complex internalization rate constant	0.39 (18)	0.39
R0 (nmol/kg)	Baseline target level in central compartment	0.024 (22)	0.024
KD (nM)	mAb affinity for TREM-1	0.64 (12)	0.24

Koff (h-1)	mAb off-rate from TREM-1	0.37 (7)	0.30
IC50 (nM)	Concentration to inhibit PGN+PGRP mediated ex-vivo TREM-1 stimulation by 50%	1.9 (92)	0.1
E0 (%)	Basal PGN+PGRP mediated ex-vivo TREM-1 stimulation (pre-dose)	100 (fixed)	100

Table 8.

SEQ ID	Description	Sequences
50	318-IgG1.3f Heavy Chain	EVQLVESGGGLVQPGGSLKLSCAASGFTFSTYAMHWVRQASGKGLEWVGRIRTKSSNYATYYAAS VKGRFTISRDDSKNTAYLQMNSLKTEDTAVYYCTRDMGIRRQFAYWGQGTLVTVSSASTKGPSVF PLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSS SLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAEGAPSVFLFPPKPKDTLMISRT PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
51	318-IgG1.1f Heavy Chain	EVQLVESGGGLVQPGGSLKLSCAASGFTFSTYAMHWVRQASGKGLEWVGRIRTKSSNYATYYAAS VKGRFTISRDDSKNTAYLQMNSLKTEDTAVYYCTRDMGIRRQFAYWGQGTLVTVSSASTKGPSVF PLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSS SLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAEGAPSVFLFPPKPKDTLMISRT PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC KVSNKALPSSIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
52	318-IgG1-Aba Heavy Chain	EVQLVESGGGLVQPGGSLKLSCAASGFTFSTYAMHWVRQASGKGLEWVGRIRTKSSNYATYYAAS VKGRFTISRDDSKNTAYLQMNSLKTEDTAVYYCTRDMGIRRQFAYWGQGTLVTVSSASTKGPSVF PLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSS SLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAEGAPSVFLFPPKPKDTLMISRT PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
53	318-IgG4-Aba Heavy Chain	EVQLVESGGGLVQPGGSLKLSCAASGFTFSTYAMHWVRQASGKGLEWVGRIRTKSSNYATYYAAS VKGRFTISRDDSKNTAYLQMNSLKTEDTAVYYCTRDMGIRRQFAYWGQGTLVTVSSASTKGPSVF PLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSS SLGTKTYTCNVDHKPSNTKVDKRVEPKSCDKTHTSPPSPAPELLGGSSVFLFPPKPKDTLMISRT PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
54	318-IgG1.3f, IgG1.1f, IgG1-Aba, IgG4-Aba Light Chain	DIVLTQSPDSLAVSLGERATINCRASQSVDTFDYSFLHWYQQKPGQPPKLLIYRASNLESGVPDR FSGSGSGTDFTLTISSLQAEDVAVYYCQQSNQDPYTFGQGTKLEIKRTVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKV YACEVTHQGLSSPVTKSFNRGEC

[0297] This PCT application claims the priority benefit of U.S. Provisional Application No. 62/651,605, filed April 2, 2018, which is herein incorporated by reference in its entirety.