(54) Title: COMPOSITIONS AND METHODS OF INHIBITING MASP-1, MASP-2 AND/OR MASP-3 FOR TREATMENT OF PAROXYSMAL NOCTURNAL HEMOGLOBINURIA
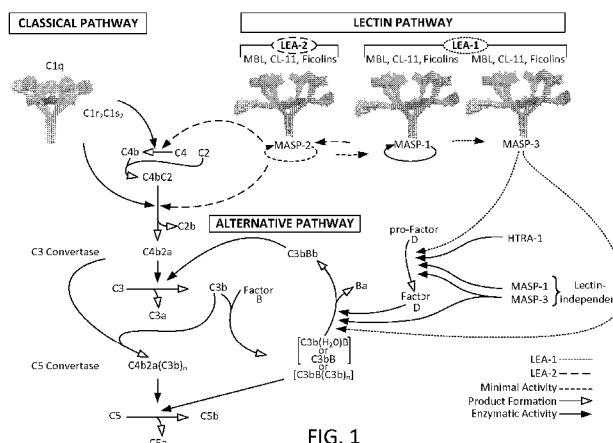
FIG. 1

(57) Abstract: Provided are methods and compositions for inhibiting MASP-3-dependent complement activation in a subject suffering from paroxysmal nocturnal hemoglobinuria by administering to the subject a composition comprising an amount of a MASP-3 inhibitory agent in an amount effective to inhibit MAS P-3-depencien! complement activation. Also provided are methods and compositions for increasing the survival of red blood cells in a subject suffering from paroxysmal nocturnal hemoglobinuria by administering to the subject a composition comprising an amount of at least one of a MASP-1 inhibitory agent and/or a MAS P-3 inhibitory agent effective to increase the survival of red blood cells. The subject may be administered a MASP-2 inhibitory agent and a MASP-1 inhibitory agent, a MASP-2 inhibitory agent and a MASP-3 inhibitory agent, administered, a MASP-3 inhibitory agent and a MASP-1 inhibitory agent, or a MASP-1 inhibitory agent, a MASP-2 inhibitory agent and a MASP-3 inhibitory agent.

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COMPOSITIONS AND METHODS OF INHIBITING MASP-1 AND/OR MASP-2 AND/OR MASP-3 FOR THE TREATMENT OF PAROXYSMAL NOCTURNAL HEMOGLOBINURIA

CROSS-REFERENCE TO RELATED APPLICATION

This application claims the benefit of Application No. 61/621,461 filed April 6, 2012.

STATEMENT REGARDING SEQUENCE LISTING

The sequence listing associated with this application is provided in text format in lieu of a paper copy and is hereby incorporated by reference into the specification. The name of the text file containing the sequence listing is MP_1_0146_PCT_Sequence_20130327_ST25.txt. The text file is 85 KB; was created on April 1, 2013; and is being submitted via EFS-Web with the filing of the specification.

BACKGROUND

The complement system provides an early acting mechanism to initiate, amplify and orchestrate the immune response to microbial infection and other acute insults (M.K. Liszewski and J.P. Atkinson, 1993, in *Fundamental Immunology*, Third Edition, edited by W.E. Paul, Raven Press, Ltd., New York), in humans and other vertebrates. While complement activation provides a valuable first-line defense against potential pathogens, the activities of complement that promote a protective immune response can also represent a potential threat to the host (K.R. Kalli, et al., *Springer Semin. Immunopathol. 15*:417-431, 1994; B.P. Morgan, *Eur. J. Clinical Investig. 24*:219-228, 1994). For example, C3 and C5 proteolytic products recruit and activate neutrophils. While indispensable for host defense, activated neutrophils are indiscriminate in their release of destructive enzymes and may cause organ damage. In addition, complement activation may cause the deposition of lytic complement components on nearby host cells as well as on microbial targets, resulting in host cell lysis.

The complement system has also been implicated in the pathogenesis of numerous acute and chronic disease states, including: myocardial infarction, stroke, ARDS, reperfusion injury, septic shock, capillary leakage following thermal burns,

postcardiopulmonary bypass inflammation, transplant rejection, rheumatoid arthritis, multiple sclerosis, myasthenia gravis, and Alzheimer's disease. In almost all of these conditions, complement is not the cause but is one of several factors involved in pathogenesis. Nevertheless, complement activation may be a major pathological mechanism and represents an effective point for clinical control in many of these disease states. The growing recognition of the importance of complement-mediated tissue injury in a variety of disease states underscores the need for effective complement inhibitory drugs. To date, Eculizumab (Solaris®), an antibody against C5, is the only complement-targeting drug that has been approved for human use. Yet, C5 is one of several effector molecules located "downstream" in the complement system, and blockade of C5 does not inhibit activation of the complement system. Therefore, an inhibitor of the initiation steps of complement activation would have significant advantages over a "downstream" complement inhibitor.

Currently, it is widely accepted that the complement system can be activated through three distinct pathways: the classical pathway, the lectin pathway, and the alternative pathway. The classical pathway is usually triggered by a complex composed of host antibodies bound to a foreign particle (*i.e.*, an antigen) and thus requires prior exposure to an antigen for the generation of a specific antibody response. Since activation of the classical pathway depends on a prior adaptive immune response by the host, the classical pathway is part of the acquired immune system. In contrast, both the lectin and alternative pathways are independent of adaptive immunity and are part of the innate immune system.

The activation of the complement system results in the sequential activation of serine protease zymogens. The first step in activation of the classical pathway is the binding of a specific recognition molecule, C1q, to antigen-bound IgG and IgM molecules. C1q is associated with the C1r and C1s serine protease proenzymes as a complex called C1. Upon binding of C1q to an immune complex, autoproteolytic cleavage of the Arg-Ile site of C1r is followed by C1r-mediated cleavage and activation of C1s, which thereby acquires the ability to cleave C4 and C2. C4 is cleaved into two fragments, designated C4a and C4b, and, similarly, C2 is cleaved into C2a and C2b. C4b fragments are able to form covalent bonds with adjacent hydroxyl or amino groups and generate the C3 convertase (C4b2a) through noncovalent interaction with the C2a fragment of activated C2. C3 convertase (C4b2a) activates C3 by proteolytic cleavage

into C3a and C3b subcomponents leading to generation of the C5 convertase (C4b2a3b), which, by cleaving C5 leads to the formation of the membrane attack complex (C5b combined with C6, C7, C8 and C-9, also referred to as "MAC") that can disrupt cellular membranes resulting in cell lysis. The activated forms of C3 and C4 (C3b and C4b) are covalently deposited on the foreign target surfaces, which are recognized by complement receptors on multiple phagocytes.

Independently, the first step in activation of the complement system through the lectin pathway is also the binding of specific recognition molecules, which is followed by the activation of associated serine protease proenzymes. However, rather than the binding of immune complexes by C1q, the recognition molecules in the lectin pathway comprise a group of carbohydrate-binding proteins (mannan-binding lectin (MBL), H-ficolin, M-ficolin, L-ficolin and C-type lectin CL-11), collectively referred to as lectins. See J. Lu et al., *Biochim. Biophys. Acta 1572*:387-400, (2002); Holmskov et al., *Annu. Rev. Immunol.* 21:547-578 (2003); Teh et al., *Immunology 101*:225-232 (2000)). See also J. Luet et al., *Biochim Biophys Acta* 1572:387-400 (2002); Holmskov et al, *Annu Rev Immunol* 21:547-578 (2003); Teh et al., *Immunology* 101:225-232 (2000); Hansen et al, *J. Immunol* 185(10):6096-6104 (2010).

Ikeda et al. first demonstrated that, like C1q, MBL could activate the complement system upon binding to yeast mannan-coated erythrocytes in a C4-dependent manner (Ikeda et al., *J. Biol. Chem. 262*:7451-7454, (1987)). MBL, a member of the collectin protein family, is a calcium-dependent lectin that binds carbohydrates with 3-and 4-hydroxy groups oriented in the equatorial plane of the pyranose ring. Prominent ligands for MBL are thus D-mannose and N-acetyl-D-glucosamine, while carbohydrates not fitting this steric requirement have undetectable affinity for MBL (Weis et al., *Nature* 360:127-134, (1992)). The interaction between MBL and monovalent sugars is extremely weak, with dissociation constants typically in the single-digit millimolar range. MBL achieves tight, specific binding to glycan ligands by avidity, i.e., by interacting simultaneously with multiple monosaccharide residues located in close proximity to each other (Lee et al., *Archiv. Biochem. Biophys.* 299:129-136, (1992)). MBL recognizes the carbohydrate patterns that commonly decorate microorganisms such as bacteria, yeast, parasites and certain viruses. In contrast, MBL does not recognize D-galactose and sialic acid, the penultimate and ultimate sugars that usually decorate "mature" complex glycoconjugates present on mammalian plasma and cell surface glycoproteins. This

binding specificity is thought to promote recognition of "foreign" surfaces and help protect from "self-activation." However, MBL does bind with high affinity to clusters of high-mannose "precursor" glycans on N-linked glycoproteins and glycolipids sequestered in the endoplasmic reticulum and Golgi of mammalian cells (Maynard et al., *J. Biol. Chem.* *257*:3788-3794, (1982)). In addition, it has been shown that MBL can bind the polynucleotides, DNA and RNA, which may be exposed on necrotic and apoptotic cells (Palaniyar et al., *Ann. N.Y. Acad. Sci.,* 1010:467-470 (2003); Nakamura et al., *J. Leuk. Biol.* 86:737-748 (2009)). Therefore, damaged cells are potential targets for lectin pathway activation via MBL binding.

The ficolins possess a different type of lectin domain than MBL, called the fibrinogen-like domain. Ficolins bind sugar residues in a Ca^{++}-independent manner. In humans, three kinds of ficolins (L-ficolin, M-ficolin and H-ficolin) have been identified. The two serum ficolins, L-ficolin and H-ficolin, have in common a specificity for N-acetyl-D-glucosamine; however, H-ficolin also binds N-acetyl-D-galactosamine. The difference in sugar specificity of L-ficolin, H-ficolin, CL-11, and MBL means that the different lectins may be complementary and target different, though overlapping, glycoconjugates. This concept is supported by the recent report that, of the known lectins in the lectin pathway, only L-ficolin binds specifically to lipoteichoic acid, a cell wall glycoconjugate found on all Gram-positive bacteria (Lynch et al., *J. Immunol. 172*:1198-1202, (2004)). In addition to acetylated sugar moieties, the ficolins can also bind acetylated amino acids and polypeptides (Thomsen et al., *Mol. Immunol.* 48(4):369-81 (2011)). The collectins (i.e., MBL) and the ficolins bear no significant similarity in amino acid sequence. However, the two groups of proteins have similar domain organizations and, like C1q, assemble into oligomeric structures, which maximize the possibility of multisite binding.

The serum concentrations of MBL are highly variable in healthy populations and this is genetically controlled by polymorphisms/mutations in both the promoter and coding regions of the MBL gene. As an acute phase protein, the expression of MBL is further upregulated during inflammation. L-ficolin is present in serum at concentrations similar to those of MBL. Therefore, the L-ficolin branch of the lectin pathway is potentially comparable to the MBL arm in strength. MBL and ficolins can also function as opsonins, which allow phagocytes to target MBL- and ficolin-decorated surfaces (see Jack et al., *J Leukoc Biol.,* 77(3):328-36 (2004), Matsushita and Fujita, *Immunobiology,*

205(4-5):490-7 (2002), Aoyagi et al., *J Immunol*, 174(1):418-25(2005). This opsonization requires the interaction of these proteins with phagocyte receptors (Kuhlman et al., *J. Exp. Med. 169*:1733, (1989); Matsushita et al., *J. Biol. Chem. 271*:2448-54, (1996)), the indentity of which has not been established.

Human MBL forms a specific and high-affinity interaction through its collagen-like domain with unique C1r/C1s-like serine proteases, termed MBL-associated serine proteases (MASPs). To date, three MASPs have been described. First, a single enzyme "MASP" was identified and characterized as the enzyme responsible for the initiation of the complement cascade (i.e., cleaving C2 and C4) (Matsushita et al., *J Exp Med* 176(6):1497-1502 (1992); Ji et al., *J. Immunol. 150*:571-578, (1993)). It was subsequently determined that the MASP activity was, in fact, a mixture of two proteases: MASP-1 and MASP-2 (Thiel et al., *Nature 386*:506-510, (1997)). However, it was demonstrated that the MBL-MASP-2 complex alone is sufficient for complement activation (Vorup-Jensen et al., *J. Immunol. 165*:2093-2100, (2000)). Furthermore, only MASP-2 cleaved C2 and C4 at high rates (Ambrus et al., *J. Immunol. 170*:1374-1382, (2003)). Therefore, MASP-2 is the protease responsible for activating C4 and C2 to generate the C3 convertase, C4b2a. This is a significant difference from the C1 complex of the classical pathway, where the coordinated action of two specific serine proteases (C1r and C1s) leads to the activation of the complement system. In addition, a third novel protease, MASP-3, has been isolated (Dahl, M.R., et al., *Immunity 15*:127-35, 2001). MASP-1 and MASP-3 are alternatively spliced products of the same gene.

MASPs share identical domain organizations with those of C1r and C1s, the enzymatic components of the C1 complex (Sim et al., *Biochem. Soc. Trans. 28*:545, (2000)). These domains include an N-terminal C1r/C1s/sea urchin VEGF/bone morphogenic protein (CUB) domain, an epidermal growth factor-like domain, a second CUB domain, a tandem of complement control protein domains, and a serine protease domain. As in the C1 proteases, activation of MASP-2 occurs through cleavage of an Arg-Ile bond adjacent to the serine protease domain, which splits the enzyme into disulfide-linked A and B chains, the latter consisting of the serine protease domain.

MBL can also associate with an alternatively spliced form of MASP-2, known as MBL-associated protein of 19 kDa (MAp19) or small MBL-associated protein (sMAP), which lacks the catalytic activity of MASP-2. (Stover, *J. Immunol. 162*:3481-90, (1999); Takahashi et al., *Int. Immunol. 11*:859-863, (1999)). MAp19 comprises the first two

domains of MASP-2, followed by an extra sequence of four unique amino acids. The function of Map19 is unclear (Degn et al., *J Immunol. Methods*, 2011). The MASP-1 and MASP-2 genes are located on human chromosomes 3 and 1, respectively (Schwaeble et al., *Immunobiology 205*:455-466, (2002)).

Several lines of evidence suggest that there are different MBL-MASP complexes and a large fraction of the MASPs in serum is not complexed with MBL (Thiel,et al., *J. Immunol. 165*:878-887, (2000)). Both H- and L-ficolin bind to all MASPs and activate the lectin complement pathway, as does MBL (Dahl et al., *Immunity 15*:127-35, (2001); Matsushita et al., *J. Immunol. 168*:3502-3506, (2002)). Both the lectin and classical pathways form a common C3 convertase (C4b2a) and the two pathways converge at this step.

The lectin pathway is widely thought to have a major role in host defense against infection in the naïve host. Strong evidence for the involvement of MBL in host defense comes from analysis of patients with decreased serum levels of functional MBL (Kilpatrick, *Biochim. Biophys. Acta 1572*:401-413, (2002)). Such patients display susceptibility to recurrent bacterial and fungal infections. These symptoms are usually evident early in life, during an apparent window of vulnerability as maternally derived antibody titer wanes, but before a full repertoire of antibody responses develops. This syndrome often results from mutations at several sites in the collagenous portion of MBL, which interfere with proper formation of MBL oligomers. However, since MBL can function as an opsonin independent of complement, it is not known to what extent the increased susceptibility to infection is due to impaired complement activation.

In contrast to the classical and lectin pathways, no initiators of the alternative pathway have previously been found to fulfill the recognition functions that C1q and lectins perform in the other two pathways. Currently it is widely accepted that the alternative pathway spontaneously undergoes a low level of turnover activation, which can be readily amplified on foreign or other abnormal surfaces (bacteria, yeast, virally infected cells, or damaged tissue) that lack the proper molecular elements that keep spontaneous complement activation in check. There are four plasma proteins directly involved in the activation of the alternative pathway: C3, factors B and D, and properdin.

Although there is extensive evidence implicating both the classical and alternative complement pathways in the pathogenesis of non-infectious human diseases, the role of the lectin pathway is just beginning to be evaluated. Recent studies provide evidence that

activation of the lectin pathway can be responsible for complement activation and related inflammation in ischemia/reperfusion injury. Collard et al. (2000) reported that cultured endothelial cells subjected to oxidative stress bind MBL and show deposition of C3 upon exposure to human serum (Collard et al., *Am. J. Pathol. 156*:1549-1556, (2000)). In addition, treatment of human sera with blocking anti-MBL monoclonal antibodies inhibited MBL binding and complement activation. These findings were extended to a rat model of myocardial ischemia-reperfusion in which rats treated with a blocking antibody directed against rat MBL showed significantly less myocardial damage upon occlusion of a coronary artery than rats treated with a control antibody (Jordan et al., *Circulation 104*:1413-1418, (2001)). The molecular mechanism of MBL binding to the vascular endothelium after oxidative stress is unclear; a recent study suggests that activation of the lectin pathway after oxidative stress may be mediated by MBL binding to vascular endothelial cytokeratins, and not to glycoconjugates (Collard et al., *Am. J. Pathol. 159*:1045-1054, (2001)). Other studies have implicated the classical and alternative pathways in the pathogenesis of ischemia/reperfusion injury and the role of the lectin pathway in this disease remains controversial (Riedermann, N.C., et al., *Am. J. Pathol. 162*:363-367, 2003).

Recent studies have shown that MASP-1 and MASP-3 convert the alternative pathway activation enzyme factor D from its zymogen form into its enzymatically active form (see Takahashi M. et al., *J Exp Med* 207(1):29-37 (2010); Iwaki et al., J. Immunol. 187:3751-58 (2011)). The physiological importance of this process is underlined by the absence of alternative pathway functional activity in plasma of MASP-1/3-deficient mice. Proteolytic generation of C3b from native C3 is required for the alternative pathway to function. Since the alternative pathway C3 convertase (C3bBb) contains C3b as an essential subunit, the question regarding the origin of the first C3b via the alternative pathway has presented a puzzling problem and has stimulated considerable research.

C3 belongs to a family of proteins (along with C4 and α-2 macroglobulin) that contain a rare posttranslational modification known as a thioester bond. The thioester group is composed of a glutamine whose terminal carbonyl group forms a covalent thioester linkage with the sulfhydryl group of a cysteine three amino acids away. This bond is unstable and the electrophilic glutamyl-thioester can react with nucleophilic moieties such as hydroxyl or amino groups and thus form a covalent bond with other molecules. The thioester bond is reasonably stable when sequestered within a

hydrophobic pocket of intact C3. However, proteolytic cleavage of C3 to C3a and C3b results in exposure of the highly reactive thioester bond on C3b and, following nucleophilic attack by adjacent moieties comprising hydroxyl or amino groups, C3b becomes covalently linked to a target. In addition to its well-documented role in covalent attachment of C3b to complement targets, the C3 thioester is also thought to have a pivotal role in triggering the alternative pathway. According to the widely accepted "tick-over theory", the alternative pathway is initiated by the generation of a fluid-phase convertase, iC3Bb, which is formed from C3 with hydrolyzed thioester (iC3; C3(H_2O)) and factor B (Lachmann, P.J., et al., *Springer Semin. Immunopathol.* 7:143-162, (1984)). The C3b-like C3(H_2O) is generated from native C3 by a slow spontaneous hydrolysis of the internal thioester in the protein (Pangburn, M.K., et al., *J. Exp. Med.* 154:856-867, 1981). Through the activity of the C3(H_2O)Bb convertase, C3b molecules are deposited on the target surface thereby initiating the alternative pathway.

Prior to the instant discovery described herein, very little was known about the initiators of activation of the alternative pathway. Activators were thought to include yeast cell walls (zymosan), many pure polysaccharides, rabbit erythrocytes, certain immunoglobulins, viruses, fungi, bacteria, animal tumor cells, parasites, and damaged cells. The only feature common to these activators is the presence of carbohydrate, but the complexity and variety of carbohydrate structures has made it difficult to establish the shared molecular determinants which are recognized. It has been widely accepted that alternative pathway activation is controlled through the fine balance between inhibitory regulatory components of this pathway, such as factor H, factor I, DAF, and CR1, and properdin, the latter of which is the only positive regulator of the alternative pathway (see Schwaeble W.J. and Reid K.B., *Immunol Today* 20(1):17-21 (1999)).

In addition to the apparently unregulated activation mechanism described above, the alternative pathway can also provide a powerful amplification loop for the lectin/classical pathway C3 convertase (C4b2a) since any C3b generated can participate with factor B in forming additional alternative pathway C3 convertase (C3bBb). The alternative pathway C3 convertase is stabilized by the binding of properdin. Properdin extends the alternative pathway C3 convertase half-life six to ten fold. Addition of C3b to the alternative pathway C3 convertase leads to the formation of the alternative pathway C5 convertase.

All three pathways (i.e., the classical, lectin and alternative) have been thought to converge at C5, which is cleaved to form products with multiple proinflammatory effects. The converged pathway has been referred to as the terminal complement pathway. C5a is the most potent anaphylatoxin, inducing alterations in smooth muscle and vascular tone, as well as vascular permeability. It is also a powerful chemotaxin and activator of both neutrophils and monocytes. C5a-mediated cellular activation can significantly amplify inflammatory responses by inducing the release of multiple additional inflammatory mediators, including cytokines, hydrolytic enzymes, arachidonic acid metabolites, and reactive oxygen species. C5 cleavage leads to the formation of C5b-9, also known as the membrane attack complex (MAC). There is now strong evidence that sublytic MAC deposition may play an important role in inflammation in addition to its role as a lytic pore-forming complex.

In addition to its essential role in immune defense, the complement system contributes to tissue damage in many clinical conditions. Thus, there is a pressing need to develop therapeutically effective complement inhibitors to prevent these adverse effects.

SUMMARY

In one aspect, the present invention provides a method of inhibiting MASP-3-dependent complement activation in a subject suffering from paroxysmal nocturnal hemoglobinuria (PNH). The method includes the step of administering to the subject a composition comprising an amount of a MASP-3 inhibitory agent effective to inhibit MASP-3-dependent complement activation. In some embodiments, the method further comprises administering to the subject a composition comprising a MASP-2 inhibitory agent.

In another aspect, the present invention provides a pharmaceutical composition comprising at least one inhibitory agent, wherein the at least one inhibitory agent comprises a MASP-2 inhibitory agent and a MASP-3 inhibitory agent and a pharmaceutically acceptable carrier.

In another aspect, the present invention provides a pharmaceutical composition comprising a MASP-3 inhibitory agent that binds to a portion of MASP-1 (SEQ ID NO: 10: full-length) and that also binds to a portion of MASP-3 (SEQ ID NO:8) and a pharmaceutical carrier.

In another aspect, the present invention provides a pharmaceutical composition comprising a MASP-3 inhibitory agent that binds to a portion of MASP-2 (SEQ ID NO: 5: full-length) and that also binds to a portion of MASP-3 (SEQ ID NO:8) and a pharmaceutical carrier.

In another aspect, the present invention provides a pharmaceutical composition comprising a MASP-3 inhibitory agent that binds to a portion of MASP-1 (SEQ ID NO: 10: full-length) and that also binds to a portion of MASP-2 (SEQ ID NO:5) and a pharmaceutical carrier.

In another aspect, the present invention provides a pharmaceutical composition comprising a MASP-3 inhibitory agent that binds to a portion of MASP-1 (SEQ ID NO: 10 full length), that binds to a portion of MASP-2 (SEQ ID NO: 5: full-length) and that also binds to a portion of MASP-3 (SEQ ID NO:8) and a pharmaceutical carrier.

As described herein, the pharmaceutical compositions of the invention can be used in accordance with the methods of the invention.

These and other aspects and embodiments of the herein described invention will be evident upon reference to the following detailed description and drawings. All of the U.S. patents, U.S. patent application publications, U.S. patent applications, foreign patents, foreign patent applications and non-patent publications referred to in this specification are incorporated herein by reference in their entirety, as if each was incorporated individually.

DESCRIPTION OF THE DRAWINGS

The foregoing aspects and many of the attendant advantages of this invention will become more readily appreciated as the same become better understood by reference to the following detailed description, when taken in conjunction with the accompanying drawings, wherein:

FIGURE 1 illustrates a new understanding of the lectin and alternative pathways;

FIGURE 2 is a schematic diagram adapted from Schwaeble et al., *Immunobiol* 205:455-466 (2002), as modified by Yongqing et al., *BBA* 1824:253 (2012), illustrating the MASP-2 and MAp19 protein domains and the exons encoding the same;

FIGURE 3 is a schematic diagram adapted from Schwaeble et al., *Immunobiol* 205:455-466 (2002), as modified by Yongqing et al., *BBA* 1824:253 (2012), illustrating the MASP-1, MASP-3 and MAp44 protein domains and the exons encoding the same;

FIGURE 4 shows an alignment of the amino acid sequences of the MASP-1, MASP-2 and MASP-3 proteins and indicates consensus regions therebetween;

FIGURE 5 shows an alignment of the amino acid sequences of the MASP-1, MASP-2 and MASP-3 Alpha chains;

FIGURE 6 shows an alignment of the amino acid sequences of the MASP-1, MASP-2 and MASP-3 Beta Chains;

FIGURE 7A shows a pairwise alignment of the amino acid sequences of the MASP-1 and MASP-2 Protease Domains (Beta-chains);

FIGURE 7B shows a pairwise alignment of the amino acid sequences of the MASP-1 and MASP-3 Protease Domains (Beta-chains);

FIGURE 7C shows a pairwise alignment of the amino acid sequences of the MASP-2 and MASP-3 Protease Domains (Beta-chains);

FIGURE 8 is a Kaplan-Meyer plot graphically illustrating the percent survival of MASP-2 KO and WT mice after administration of an infective dose of 2.6×10^7 cfu of *N. meningitidis* serogroup A Z2491, demonstrating that MASP-2 deficient mice are protected from *N. meningitidis* induced mortality, as described in Example 1;

FIGURE 9 is a Kaplan-Meyer plot graphically illustrating the percent survival of MASP-2 KO and WT mice after administration of an infective dose of 6×10^6 cfu of *N. meningitidis* serogroup B strain MC58, demonstrating that MASP-2 deficient mice are protected from *N. meningitidis* induced mortality, as described in Example 1;

FIGURE 10 graphically illustrates the log cfu/mL of *N. meningitidis* serogroup B strain MC58 per mL of blood recovered from MASP-2 KO and WT mice at different time points after i.p. infection with 6×10^6 cfu of *N. meningitidis* serogroup B strain MC58 (n=3 at different time points for both groups of mice), demonstrating that although the MASP-2 KO mice were infected with the same dose of *N. meningitidis* serogroup B strain MC58 as the WT mice, the MASP-2 KO mice have enhanced clearance of bacteremia as compared to WT, as described in Example 1;

FIGURE 11 graphically illustrates the average illness score of MASP-2 KO and WT mice at 3, 6, 12 and 24 hours after infection with 6×10^6 cfu of *N. meningitidis* serogroup B strain MC58, demonstrating that the MASP-2-deficient mice showed much lower illness scores at 6 hours, 12 hours, and 24 hours after infection, as compared to WT mice, as described in Example 1;

FIGURE 12 is a Kaplan-Meyer plot graphically illustrating the percent survival of mice after administration of an infective dose of 4×10^6 cfu of *N. meningitidis* serogroup B strain MC58, followed by administration 3 hours post-infection of either inhibitory MASP-2 antibody (1 mg/kg) or control isotype antibody, demonstrating that MASP-2 antibody is effective to treat and improve survival in subjects infected with N. *meningitidis,* as described in Example 2;

FIGURE 13 graphically illustrates the log cfu/mL of viable counts of *N. meningitidis* serogroup B strain MC58 recovered at different time points in the human sera samples shown in TABLE 5 taken at various time points after incubation with *N. meningitidis* serogroup B strain MC58, as described in Example 3;

FIGURE 14 graphically illustrates the log cfu/mL of viable counts of *N. meningitidis* serogroup B-MC58 recovered at different time points in the human sera samples shown in TABLE 7, showing that complement-dependent killing of *N. meningitidis* in human 20% (v/v) serum is MASP-3 and MBL-dependent, as described in Example 3;

FIGURE 15 graphically illustrates the log cfu/mL of viable counts of *N. meningitidis* serogroup B-MC58 recovered at different time points in the mouse sera samples shown in TABLE 9, showing that the MASP-2 -/- knockout mouse (referred to as "MASP-2 -/-") serum has a higher level of bactericidal activity for N. meningitidis than WT mouse serum, whereas in contrast, the MASP-1/3 -/- mouse serum does not have any bactericidal activity, as described in Example 3;

FIGURE 16 graphically illustrates the kinetics of C3 activation under lectin pathway-specific conditions (1% plasma) in WT, C4-/-, MASP-1/3-/-, Factor B-/- and MASP-2-/- mouse sera, as described in Example 4;

FIGURE 17 graphically illustrates the level of alternative pathway-driven (AP-driven) C3b deposition on zymosan-coated microtiter plates under "traditional" alternative pathway-specific (AP-specific) conditions (*i.e.* BBS/EGTA/Mg^{++} without Ca^{++}) as a function of serum concentration in serum samples obtained from MASP-3-deficient, C4-deficient and MBL-deficient human subjects, as described in Example 4;

FIGURE 18 graphically illustrates the level of AP-driven C3b deposition on zymosan-coated microtiter plates under "traditional" AP-specific conditions (*i.e.,* BBS/EGTA/Mg^{++} without Ca^{++}) as a function of time in 10% human serum samples

obtained from MASP-3-deficient, C4-deficient and MBL-deficient human subjects, as described in Example 4;

FIGURE 19A graphically illustrates the level of C3b deposition on mannan-coated microtiter plates as a function of serum concentration in serum samples obtained from WT, MASP-2-deficient, and MASP-1/3-deficient mice under "traditional" AP-specific conditions (*i.e.* BBS/EGTA/Mg^{++} without Ca^{++}) or under physiological conditions allowing both the lectin pathway and the alternative pathway (AP) to function (BBS/Mg^{++}/Ca^{++}), as described in Example 4;

FIGURE 19B graphically illustrates the level of C3b deposition on zymosan-coated microtiter plates as a function of serum concentration in serum samples obtained from WT, MASP-2-deficient, and MASP-1/3-deficient mice under traditional AP-specific conditions (*i.e.* BBS/EGTA/Mg^{++} without Ca^{++}) or under physiological conditions allowing both the lectin pathway and the alternative pathway to function (BBS/Mg^{++}/Ca^{++}), as described in Example 4;

FIGURE 19C graphically illustrates the level of C3b deposition on *S. pneumoniae* D39-coated microtiter plates as a function of serum concentration in serum samples obtained from WT, MASP-2-deficient, and MASP-1/3-deficient mice under traditional AP-specific conditions (*i.e.* BBS/EGTA/Mg^{++} without Ca^{++}) or under physiological conditions allowing both the lectin pathway and the alternative pathway to function (BBS/Mg^{++}/Ca^{++}), as described in Example 4;

FIGURE 20A graphically illustrates the results of a C3b deposition assay in highly diluted sera carried out on mannan-coated microtiter plates under traditional AP-specific conditions (*i.e.* BBS/EGTA/Mg^{++} without Ca^{++}) or under physiological conditions allowing both the lectin pathway and the alternative pathway to function (BBS/Mg^{++}/Ca^{++}), using serum concentrations ranging from 0 % up to 1.25%, as described in Example 4;

FIGURE 20B graphically illustrates the results of a C3b deposition assay carried out on zymosan-coated microtiter plates under traditional AP-specific conditions (*i.e.* BBS/EGTA/Mg^{++} without Ca^{++}) or under physiological conditions allowing both the lectin pathway and the alternative pathway to function (BBS/Mg^{++}/Ca^{++}), using serum concentrations ranging from 0 % up to 1.25%, as described in Example 4;

FIGURE 20C graphically illustrates the results of a C3b deposition assay carried out on *S. pneumoniae* D39-coated microtiter plates under traditional AP-specific

conditions (*i.e.* BBS/EGTA/Mg^{++} without Ca^{++}) or under physiological conditions allowing both the lectin pathway and the alternative pathway to function (BBS/Mg^{++}/Ca^{++}), using serum concentrations ranging from 0 % up to 1.25%, as described in Example 4;

FIGURE 21 graphically illustrates the level of hemolysis (as measured by hemoglobin release of lysed mouse erythrocytes (Crry/C3-/-) into the supernatant measured by photometry) of mannan-coated murine erythrocytes by human serum under physiological conditions (*i.e.*, in the presence of Ca^{++}) over a range of serum dilutions in serum from MASP-3-/-, heat inactivated normal human serum (HI NHS), MBL-/-, NHS + MASP-2 monoclonal antibody and NHS control, as described in Example 5;

FIGURE 22 graphically illustrates the level of hemolysis (as measured by hemoglobin release of lysed mouse erythrocytes (Crry/C3-/-) into the supernatant measured by photometry) of mannan-coated murine erythrocytes by human serum under physiological conditions (*i.e.*, in the presence of Ca^{++}) over a range of serum concentration in serum from MASP-3-/-, heat inactivated (HI) NHS, MBL-/-, NHS + MASP-2 monoclonal antibody and NHS control, as described in Example 5;

FIGURE 23 graphically illustrates the level of hemolysis (as measured by hemoglobin release of lysed WT mouse erythrocytes into the supernatant measured by photometry) of non-coated murine erythrocytes by human serum under physiological conditions (*i.e.*, in the presence of Ca^{++}) over a range of serum concentrations in serum from 3MC (MASP-3-/-), heat inactivated (HI) NHS, MBL-/-, NHS + MASP-2 monoclonal antibody and NHS control, as described in Example 5;

FIGURE 24 graphically illustrates hemolysis (as measured by hemoglobin release of lysed mouse erythrocytes (CD55/59-/-) into the supernatant measured by photometry) of non-coated murine erythrocytes by human serum under physiological conditions (*i.e.*, in the presence of Ca^{++}) over a range of serum concentrations in serum from heat inactivated (HI) NHS, MBL-/-, NHS + MASP-2 monoclonal antibody and NHS control, as described in Example 5;

FIGURE 25 graphically illustrates hemolysis (as measured by hemoglobin release of lysed rabbit erythrocytes into the supernatant measured by photometry) of mannan-coated rabbit erythrocytes by MASP-1/3-/- mouse serum and WT control mouse serum under physiological conditions (*i.e.*, in the presence of Ca^{++}) over a range of serum concentrations, as described in Example 6;

FIGURE 26 graphically illustrates the level of C3b deposition (OD 405 nm) on a zymosan-coated microtiter plate as a function of serum concentration in serum samples from factor D-/-, MASP-2-/- and WT mouse sera in a C3 deposition assay carried out under AP-specific conditions, as described in Example 7;

FIGURE 27 graphically illustrates the level of C3b deposition (OD 405 nm) on a zymosan-coated microtiter plate as a function of serum concentration in serum samples from factor D-/-; MASP-2-/- and WT mouse sera in a C3 deposition assay carried out under physiological conditions (in the presence of Ca^{++}), as described in Example 7;

FIGURE 28 graphically illustrates the level of C3b deposition (OD 405 nm) on a zymosan-coated microtiter plate as a function of serum incubation time (minutes) in mouse serum samples obtained from factor D-/-; factor B-/-; plus and minus MASP-2 monoclonal antibody in a C3b deposition assay carried out under physiological conditions (in the presence of Ca^{++}), as described in Example 7;

FIGURE 29A graphically illustrates lectin pathway specific C4b deposition on a zymosan-coated microtiter plate, measured *ex vivo* in undiluted serum samples taken from mice (n=3 mice/group) at various time points after subcutaneous dosing of either 0.3 mg/kg or 1.0 mg/kg of the mouse MASP-2 MoAb, as described in Example 13;

FIGURE 29B graphically illustrates the time course of lectin pathway recovery for three weeks following a single intraperitoneal administration of mouse MASP-2 MoAb at 0.6 mg/kg in mice, as described in Example 13;

FIGURE 30A is a FACS histogram of MASP-3 antigen/antibody binding for clone M3J5, as described in Example 15;

FIGURE 30B is a FACS histogram of MASP-3 antigen/antibody binding for clone M3M1, as described in Example 15;

FIGURE 31 graphically illustrates a saturation binding curve of clone M3J5 (Clone 5) for the MASP-3 antigen, as described in Example 15;

FIGURE 32A is an amino acid sequence alignment of the VH regions of M3J5, M3M1, D14 and 1E10 to the chicken DT40 VH sequence, wherein dots represent amino acid identity with the DT40 sequence and dashes indicate spaces introduced to maximize the alignment, as described in Example 15;

FIGURE 32B is an amino acid sequence alignment of the VL regions of M3J5, M3M1, D14 and 1E10 to the chicken DT40 VL sequence, wherein dots represent amino

acid identity with the DT40 sequence and dashes indicate spaces introduced to maximize the alignment, as described in Example 15;

FIGURE 33 is a bar graph showing the inhibitory activity of the mAb1E10 in the Wieslab Complement System Screen, MBL Pathway in comparison to the positive serum provided with the assay kit, as well as an isotype control antibody, demonstrating that mAb1E10 partial inhibits LEA-2-dependent activation, (via inhibition of MASP-1-dependent activation of MASP-2), whereas the isotype control antibody does not, as described in Example 15;

FIGURE 34 graphically illustrates the level of C3b deposition for 1% normal human serum plus isotype control, SGMI-1Fc or SGMI-2Fc over a concentration range of 0.15 to 1000 nM, demonstrating that both SGMI-1Fc and SGMI-2Fc inhibited C3b deposition from normal serum in mannan-coated ELISA wells, with IC_{50} values of approximately 27nM and 300nM, respectively, as described in Example 16;

FIGURE 35A provides the results of flow cytometry analysis for C3b deposition on heat-killedS *Staphylococcus aureus*, demonstrating that in normal human serum in the presence of EDTA, which is known to inactivate the lectin and alternative pathways, no C3b deposition was observed (panel 1), in normal human serum treated with Mg^{++}/EGTA, alternative pathway-driven C3b deposition is observed (panel 2), and as shown in panel 3, 4 and 5, in factor B-depleted, factor D-depleted and properdin (factor P)-depleted serum, respectively, no alternative pathway driven C3b deposition is observed, as described in Example 17;

FIGURE 35B provides the results of flow cytometry analysis for C3b deposition on heat-killed *S. aureus*, demonstrating that, as in EDTA-treated normal serum (panel 1), AP-driven C3b deposition is absent in 3MC serum in the presence of Mg^{++}/EGTA (panel 3), whereas panels 4 and 5 show that active full length rMASP-3 (panel 4) and active rMASP-3 (CCP1-CCP2-SP) (panel 5) both restore AP-driven C3b deposition in 3MC serum to levels observed in normal serum treated with Mg^{++}/EGTA (panel 2), neither inactive rMASP-3 (S679A) (panel 6) nor wild type rMASP-1 (panel 7) can restore AP-driven C3b deposition in 3MC serum, as described in Example 17;

FIGURE 36 shows the results of a Western blot analysis to determine factor B cleavage in response to *S. aureus* in 3MC serum in the presence or absence of rMASP-3, demonstrating that the normal human serum in the presence of EDTA (negative control, lane 1) demonstrates very little Factor B cleavage relative to normal human serum in the

presence of Mg^{++}/EGTA, shown in lane 2 (positive control), as further shown in lane 3, 3MC serum demonstrates very little Factor B cleavage in the presence of Mg^{++}/EGTA. However, as shown in lane 4, Factor B cleavage is restored by the addition and pre-incubation of full-length, recombinant MASP-3 protein to the 3MC serum, as described in Example 17;

FIGURE 37 shows Comassie staining of a protein gel in which Factor B cleavage is analyzed, demonstrating that Factor B cleavage is most optimal in the presence of C3, MASP-3 and pro-factor D (lane 1), and as shown in lanes 4 and 5, either MASP-3 or pro-factor D alone are able to mediate Factor B cleavage, as long as C3 is present, as described in Example 17;

FIGURE 38 graphically illustrates the mean fluorescent intensities (MFI) of C3b staining of *S. aureus* obtained from mAbD14 (which binds MASP-3), mAb1A5 (negative control antibody) and an isotype control antibody plotted as a function of mAb concentration in 3MC serum in the presence of rMASP-3, demonstrating that mAbD14 inhibits MASP-3-dependent C3b deposition in a concentration-dependent manner, as described in Example 17;

FIGURE 39 shows Western blot analysis of pro-factor D substrate cleavage, wherein compared to pro-factor D alone (lane 1) or the inactive full length recombinant MASP-3 (S679A; lane 3) or MASP-1 (S646A; lane 4), full length wild type recombinant MASP-3 (lane2) and MASP-1 (lane 5) either completely or partially cleave pro-factor D to generate mature factor D, as described in Example 18;

FIGURE 40 is a Western blot showing the inhibitory activity of the MASP-3 binding mAbs D14 (lane 2) and M3M1 (lane 3) on MASP-3-dependent pro-factor D cleavage in comparison to a control reaction containing only MASP-3 and pro-factor D (no mAb, lane 1), as well as a control reaction containing a mAb obtained from the DTLacO library that binds MASP-1, but not MASP-3 (lane 4), as described in Example 18;

FIGURE 41 graphically illustrates the level of AP-driven C3b deposition on zymosan-coated microtiter plates as a function of serum concentration in serum samples obtained from MASP-3-deficient (3MC), C4-deficient and MBL-deficient subjects, demonstrating that MASP-3-deficient sera from Patient 2 and Patient 3 have residual AP activity at high serum concentrations (25%, 12.5%, 6.25% serum concentrations), but a

significantly higher AP_{50} (i.e., 8.2% and 12.3% of serum needed to achieve 50% of maximum C3 deposition), as described in Example 19;

FIGURE 42 graphically illustrates the level of AP-driven C3b deposition on zymosan-coated microtiter plates under "traditional" AP-specific conditions (i.e., $BBS/EGTA/Mg^{++}$ without Ca^{++}) as a function of time in 10% human serum samples obtained from MASP-3 deficient, C4-deficient and MBL-deficient human subjects, as described in Example 19;

FIGURE 43 graphically illustrates the percent hemolysis (as measured by hemoglobin release of lysed rabbit erythrocytes into the supernatant measured by photometry) of mannan-coated rabbit erythrocytes over a range of serum concentrations in serum from two normal human subjects (NHS) and from two 3MC patients (Patient 2 and Patient 3), measured in the absence of Ca^{++}, demonstrating that MASP-3 deficiency reduces the percentage of complement-mediated lysis of mannan-coated erythrocytes as compared to normal human serum, as described in Example 19;

FIGURE 44 graphically illustrates the level of AP-driven C3b deposition on zymosan-coated microtiter plates as a function of the concentration of recombinant full length MASP-3 protein added to serum samples obtained from human 3MC Patient 2 (MASP-3$^{-/-}$), demonstrating that, compared to the negative control inactive recombinant MASP-3 (MASP-3A; S679A), active recombinant MASP-3 protein reconstitutes AP-driven C3b deposition on zymosan-coated plates in a concentration-dependent manner, as described in Example 19;

FIGURE 45 graphically illustrates the percent hemolysis (as measured by hemoglobin release of lysed rabbit erythrocytes into the supernatant measured by photometry) of mannan-coated rabbit erythrocytes over a range of serum concentrations in (1) normal human serum (NHS); (2) 3MC patient serum; (3) 3MC patient serum plus active full length recombinant MASP-3 (20 µg/ml); and (4) heat-inactivated human serum (HIS), measured in the absence of Ca^{++}, demonstrating that the percent lysis of rabbit erythrocytes is significantly increased in 3MC serum containing rMASP-3 as compared to the percent lysis in 3MC serum without recombinant MASP-3 (p=0.0006), as described in Example 19;

FIGURE 46 graphically illustrates the percentage of rabbit erythrocyte lysis in 7% human serum from 3MC Patient 2 and from 3MC Patient 3 containing active recombinant MASP-3 at a concentration range of 0 to 110 µg/ml (in BBS/ Mg^{++}/EGTA, demonstrating

that the percentage of rabbit erythrocyte lysis increases with the amount of recombinant MASP-3 in a concentration-dependent manner, as described in Example 19; and

FIGURE 47 graphically illustrates the level of LEA-2-driven C3b deposition on Mannan-coated ELISA plates as a function of the concentration of human serum diluted in BBS buffer, for serum from a normal human subject (NHS), from two 3MC patients (Patient 2 and Patient 3), from the parents of Patient 3 and from a MBL-deficient subject.

DESCRIPTION OF SEQUENCE LISTING

SEQ ID NO:1 human MAp19 cDNA

SEQ ID NO:2 human MAp19 protein (with leader)

SEQ ID NO:3 human MAp19 protein (mature)

SEQ ID NO:4 human MASP-2 cDNA

SEQ ID NO:5 human MASP-2 protein (with leader)

SEQ ID NO:6 human MASP-2 protein (mature)

SEQ ID NO:7 human MASP-3 cDNA

SEQ ID NO:8 human MASP-3 protein (w/leader)

SEQ ID NO:9 human MASP-1 cDNA

SEQ ID NO:10 human MASP-1 protein (w/leader)

SEQ ID NO:11 human MAp44 protein (w/leader)

SEQ ID NO:12 rat MASP-2 cDNA

SEQ ID NO:13 rat MASP-2 protein (with leader)

SEQ ID NO:14 DNA encoding 17D20_dc35VH21N11VL (OMS646) heavy chain variable region (VH) (without signal peptide)

SEQ ID NO:15 17D20_dc35VH21N11VL (OMS646) heavy chain variable region (VH) polypeptide

SEQ ID NO:16 17N16mc heavy chain variable region (VH) polypeptide

SEQ ID NO:17 17D20_dc21N11VL (OMS644) light chain variable region (VL) polypeptide

SEQ ID NO:18 DNA encoding 17N16_dc17N9 (OMS641) light chain variable region (VL) (without signal peptide)

SEQ ID NO:19 17N16_dc17N9 (OMS641) light chain variable region (VL) polypeptide

SEQ ID NO:20: scFv daughter clone 17N16m_d17N9 full length polypeptide

SEQ ID NO:21: scFv daughter clone 17D20m_d3521N11 full length polypeptide

SEQ ID NO:22: scFv daughter clone 17N16m_d17N9 DNA encoding full length polypeptide (without signal peptide)

SEQ ID NO:23: scFv daughter clone 17D20m_d3521N11 DNA encoding full length polypeptide (without signal peptide)

SEQ ID NO:24: parent DTLacO heavy chain variable region (VH) polypeptideSEQ ID NO:25: MASP-3 specific clone M3J5 heavy chain variable region (VH) polypeptide

SEQ ID NO:26: MASP-3 specific clone M3M1 heavy chain variable region (VH) polypeptide

SEQ ID NO:27: parent DTLacO light chain variable region (VL) polypeptide

SEQ ID NO:28: MASP-3 specific clone M3J5 light chain variable region (VL) polypeptide

SEQ ID NO:29: MASP-3 specific clone M3M1 light chain variable region (VL) polypeptide

SEQ ID NO:30: MASP-3 clone D14 heavy chain variable region (VH) polypeptide

SEQ ID NO:31: MASP-3 clone D14 light chain variable region (VL) polypeptide

SEQ ID NO:32: MASP-1 clone 1E10 heavy chain variable region (VH) polypeptide

SEQ ID NO:33: MASP-1 clone 1E10 light chain variable region (VL) polypeptide

SEQ ID NO:34 SGMI-1 peptide

SEQ ID NO:35 SGMI-2 peptide

SEQ ID NO:36 human IgG1-Fc polypeptide;

SEQ ID NO:37 peptide linker #1 (12aa);

SEQ ID NO:38: peptide linker #2 (10aa);

SEQ ID NO:39: nucleic acid encoding polypeptide fusion comprising the human IL-2-signal sequence, SGMI-1, linker#1, and human IgG1-Fc;

SEQ ID NO:40: mature polypeptide fusion comprising SGMI-1, linker#1 and human IgG1-Fc (SGMI-1Fc);

SEQ ID NO:41: nucleic acid encoding polypeptide fusion comprising the human IL-2-signal sequence, SGMI-2, linker#1 and human IgG1-Fc;

SEQ ID NO:42: mature polypeptide fusion comprising SGMI-2, linker#1 and human IgG1-Fc (SGMI-2Fc).

DETAILED DESCRIPTION

I.   DEFINITIONS

Unless specifically defined herein, all terms used herein have the same meaning as would be understood by those of ordinary skill in the art of the present invention. The following definitions are provided in order to provide clarity with respect to the terms as they are used in the specification and claims to describe the present invention.

As used herein, the lectin pathway effector arm 1 ("LEA-1") refers to lectin-dependent activation of factor B and factor D by MASP-3.

As used herein, the lectin pathway effector arm 2 ("LEA-2") refers to MASP-2-dependent complement activation.

As used herein, the term "MASP-3-dependent complement activation" comprises two components: (i) lectin MASP-3-dependent activation of factor B and factor D, encompassed in LEA-1-mediated complement activation, occurs in the presence of Ca^{++}, commonly leading to the conversion of C3bB to C3bBb and of pro-factor D to factor D; and (ii) lectin-independent conversion of factor B and factor D, which can occur in the absence of Ca^{++}, commonly leading to the conversion of C3bB to C3bBb and of pro-factor D to factor D. LEA-1-mediated complement activation and lectin-independent conversion of factor B and factor D have been determined to cause opsonization and/or lysis. While not wishing to be bound by any particular theory, it is believed that only when multiple C3b molecules associate and bind in close proximity, the C3bBb C3 convertase changes its substrate specificity and cleaves C5 as the alternative pathway C5 convertase termed C3bBb(C3b)n.

As used herein, the term "MASP-2-dependent complement activation", also referred to herein as LEA-2-mediated complement activation, comprises MASP-2 lectin-dependent activation, which occurs in the presence of Ca^{++}, leading to the formation of the lectin pathway C3 convertase C4b2a and upon accumulation of the C3 cleavage product C3b subsequently to the C5 convertase C4b2a(C3b)n, which has been determined to cause opsonization and/or lysis.

As used herein, the term "traditional understanding of the alternative pathway" also referred to as the "traditional alternative pathway" refers to the alternative pathway

prior to the instant discovery described herein, *i.e.,* complement activation that is triggered, for example, by zymosan from fungal and yeast cell walls, lipopolysaccharide (LPS) from Gram negative outer membranes, and rabbit erythrocytes, as well as from many pure polysaccharides, viruses, bacteria, animal tumor cells, parasites and damaged cells, and which has traditionally been thought to arise from spontaneous proteolytic generation of C3b from complement factor C3. As used herein, activation of the "traditional alternative pathway", also referred to herein as the "alternative pathway", is measured in Mg^{++}/EGTA buffer (*i.e.,* in the absence of Ca^{++}).

As used herein, the term "lectin pathway" refers to complement activation that occurs via the specific binding of serum and non-serum carbohydrate-binding proteins including mannan-binding lectin (MBL), CL-11 and the ficolins (H-ficolin, M-ficolin, or L-ficolin). As described herein, the inventors have discovered that the lectin pathway is driven by the two effector arms, lectin pathway effector arm 1 (LEA-1), which is now known to be MASP-3-dependent, and lectin pathway effector arm 2 (LEA-2), which is MASP-2-dependent. As used herein, activation of the lectin pathways are assessed using Ca^{++} containing buffers.

As used herein, the term "classical pathway" refers to complement activation that is triggered by antibody bound to a foreign particle and requires binding of the recognition molecule C1q.

As used herein, the term "HTRA-1" refers to the serine peptidase High-temperature requirement serine protease A1.

As used herein, the term "MASP-3 inhibitory agent" refers to any agent that directly or indirectly inhibits MASP-3-dependent complement activation, including agents that bind to or directly interact with MASP-3, including MASP-3 antibodies and MASP-3 binding fragments thereof, natural and synthetic peptides, competitive substrates, small-molecules, expression inhibitors and isolated natural inhibitors, and also encompasses peptides that compete with MASP-3 for binding to another recognition molecule (e.g., MBL, CL-11, H-ficolin, M-ficolin, or L-ficolin) in the lectin pathway. In one embodiment, the MASP-3 inhibitory agent is specific to MASP-3, and does not bind to MASP-1 or MASP-2. An inhibitory agent that directly inhibits MASP-3 can be referred to as a direct MASP-3 inhibitory agent (e.g., a MASP-3 antibody), while an inhibitory agent that indirectly inhibits MASP-3 can be referred to as an indirect MASP-3 inhibitory agent (e.g., a MASP-1 antibody that inhibits MASP-3 activation). An example

of a direct MASP-3 inhibitory agent is a MASP-3 specific inhibitory agent, such as a MASP-3 inhibitory agent that specifically binds to a portion of MASP-3 (SEQ ID NO:8) with a binding affinity of at least 10 times greater than to other components in the complement system. In one embodiment, a MASP-3 inhibitory agent indirectly inhibits MASP-3 activity, such as, for example, an inhibitor of MASP-3 activation, including an inhibitor of MASP-1-mediated MASP-3 activation (e.g., a MASP-1 antibody or MASP-1 binding fragments thereof, natural and synthetic peptides, small-molecules, expression inhibitors and isolated natural inhibitors, and also encompasses peptides that compete with MASP-1 for binding to MASP-3). In another embodiment, a MASP-3 inhibitory agent inhibits MASP-3-mediated maturation of factor D. In another embodiment, a MASP-3 inhibitory agent inhibits MASP-3-mediated activation of factor B. MASP-3 inhibitory agents useful in the method of the invention may reduce MASP-3-dependent complement activation by greater than 10%, such as greater than 20%, greater than 50%, or greater than 90%. In one embodiment, the MASP-3 inhibitory agent reduces MASP-3-dependent complement activation by greater than 90% (i.e., resulting in MASP-3 complement activation of only 10% or less). It is expected that MASP-3 inhibition will block, in full or in part, both LEA-1-related lysis and opsonization and lectin-independent conversion of factor B and factor D-related lysis and opsonization.

As used herein, the term "MASP-1 inhibitory agent" refers to any agent that binds to or directly interacts with MASP-1 and inhibits at least one of (i) MASP-3-dependent complement activation and/or (ii) MASP-2-dependent complement activation and/or (iii) lectin-independent or lectin-dependent MASP-1-mediated maturation of factor D, wherein the lectin-dependent MASP-1 maturation of factor D involves direct activation of factor D, including MASP-1 antibodies and MASP-1 binding fragments thereof, natural and synthetic peptides, small-molecules, expression inhibitors and isolated natural inhibitors, and also encompasses peptides that compete with MASP-1 for binding to another recognition molecule (e.g., MBL, CL-11, H-ficolin, M-ficolin, or L-ficolin) in the lectin pathway. In one embodiment, MASP-1 inhibitory agents useful in the method of the invention reduce MASP-3-dependent complement activation by greater than 10%, such as greater than 20%, greater than 50%, or greater than 90%. In one embodiment, the MASP-1 inhibitory agent reduces MASP-3-dependent complement activation by greater than 90% (i.e., resulting in MASP-3 complement activation of only 10% or less). In another embodiment, MASP-1 inhibitory agents useful in the method of the invention

reduce MASP-2-dependent complement activation by greater than 10%, such as greater than 20%, greater than 50%, or greater than 90%. In one embodiment, the MASP-1 inhibitory agent reduces MASP-2-dependent complement activation by greater than 90% (i.e., resulting in MASP-2 complement activation of only 10% or less).

In another embodiment, MASP-1 inhibitory agents useful in the method of the invention reduce both MASP-3-dependent complement activation (LEA-1), lectin-independent conversion of factor B and factor D, and MASP-2-dependent complement activation (LEA-2) by greater than 10%, such as greater than 20%, greater than 50%, or greater than 90%. In one embodiment, the MASP-1 inhibitory agent reduces MASP-3-dependent complement activation (LEA-1), lectin-independent conversion of factor B and factor D, and MASP-2-dependent complement activation (LEA-2) by greater than 90% (i.e., resulting in MASP-3 complement activation of only 10% or less and MASP-2 complement activation of only 10% or less).

An example of a direct MASP-1 inhibitory agent is a MASP-1-specific inhibitory agent, such as a MASP-1 inhibitory agent that specifically binds to a portion of MASP-1 (SEQ ID NO:10) with a binding affinity of at least 10 times greater than to other components in the complement system. In many instances, given that MASP-1 can activate MASP-3, and given the MASP-1 can activate MASP-2, inhibition of MASP-1 would be expected to be effective in inhibiting MASP-3 and/or MASP-2. In some instances, however, inhibition of either MASP-1 or MASP-3 or MASP-2 may be a preferred embodiment relative to inhibition of the other MASP targets. For example, in the setting of *Staphylococcus aureus (S. aureus)* infection, MASP-3 has been shown to be activated and is responsible for *S. aureus* opsonization in the absence of MASP-1 (see Iwaki D. et al., *J Immunol* 187(7):3751-8 (2011)). Therefore, in the treatment of paroxysmal nocturnal hemoglobinuria (PNH), for example, it might be advantageous to directly inhibit MASP-1 rather than MASP-3, thereby reducing the potential susceptibility to *S. aureus* during LEA-1-inhibitory treatment of PNH.

As used herein, the term "MASP-2 inhibitory agent" refers to any agent that binds to or directly interacts with MASP-2 and inhibits at least one of (i) MASP-2-dependent complement activation and/or (ii) MASP-1-dependent complement activation, including MASP-2 antibodies and MASP-2 binding fragments thereof, natural and synthetic peptides, small-molecules, expression inhibitors and isolated natural inhibitors, and also encompasses peptides that compete with MASP-2 for binding to another recognition

molecule (e.g., MBL, CL-11, H-ficolin, M-ficolin, or L-ficolin) in the lectin pathway. MASP-2 inhibitory agents useful in the method of the invention may reduce MASP-2-dependent complement activation by greater than 10%, such as greater than 20%, greater than 50%, or greater than 90%. In one embodiment, the MASP-2 inhibitory agent reduces MASP-2-dependent complement activation by greater than 90% (i.e., resulting in MASP-2 complement activation of only 10% or less). An example of a direct MASP-2 inhibitory agent is a MASP-2-specific inhibitory agent, such as a MASP-2 inhibitory agent that specifically binds to a portion of MASP-2 (SEQ ID NO:5) with a binding affinity of at least 10 times greater than to other components in the complement system.

As used herein, the term "antibody" encompasses antibodies and antibody fragments thereof, derived from any antibody-producing mammal (e.g., mouse, rat, rabbit, and primate including human), or from a hybridoma, phage selection, recombinant expression or transgenic animals (or other methods of producing antibodies or antibody fragments"), that specifically bind to a target polypeptide, such as, for example, MASP-1, MASP-2 or MASP-3 polypeptides or portions thereof. It is not intended that the term "antibody" limited as regards to the source of the antibody or the manner in which it is made (e.g., by hybridoma, phage selection, recombinant expression, transgenic animal, peptide synthesis, etc). Exemplary antibodies include polyclonal, monoclonal and recombinant antibodies; pan-specific, multispecific antibodies (e.g., bispecific antibodies, trispecific antibodies); humanized antibodies; murine antibodies; chimeric, mouse-human, mouse-primate, primate-human monoclonal antibodies; and anti-idiotype antibodies, and may be any intact antibody or fragment thereof. As used herein, the term "antibody" encompasses not only intact polyclonal or monoclonal antibodies, but also fragments thereof (such as dAb, Fab, Fab', F(ab')$_2$, Fv), single chain (ScFv), synthetic variants thereof, naturally occurring variants, fusion proteins comprising an antibody portion with an antigen-binding fragment of the required specificity, humanized antibodies, chimeric antibodies, and any other modified configuration of the immunoglobulin molecule that comprises an antigen-binding site or fragment (epitope recognition site) of the required specificity.

A "monoclonal antibody" refers to a homogeneous antibody population wherein the monoclonal antibody is comprised of amino acids (naturally occurring and non-naturally occurring) that are involved in the selective binding of an epitope. Monoclonal antibodies are highly specific for the target antigen. The term "monoclonal antibody"

encompasses not only intact monoclonal antibodies and full-length monoclonal antibodies, but also fragments thereof (such as Fab, Fab', F(ab')$_2$, Fv), single chain (ScFv), variants thereof, fusion proteins comprising an antigen-binding portion, humanized monoclonal antibodies, chimeric monoclonal antibodies, and any other modified configuration of the immunoglobulin molecule that comprises an antigen-binding fragment (epitope recognition site) of the required specificity and the ability to bind to an epitope. It is not intended to be limited as regards the source of the antibody or the manner in which it is made (*e.g.*, by hybridoma, phage selection, recombinant expression, transgenic animals, etc.). The term includes whole immunoglobulins as well as the fragments etc. described above under the definition of "antibody".

As used herein, the term "antibody fragment" refers to a portion derived from or related to a full-length antibody, such as, for example, a MASP-1, MASP-2 or MASP-3 antibody, generally including the antigen binding or variable region thereof. Illustrative examples of antibody fragments include Fab, Fab', F(ab)$_2$, F(ab')$_2$ and Fv fragments, scFv fragments, diabodies, linear antibodies, single-chain antibody molecules and multispecific antibodies formed from antibody fragments.

As used herein, a "single-chain Fv" or "scFv" antibody fragment comprises the V_H and V_L domains of an antibody, wherein these domains are present in a single polypeptide chain. Generally, the Fv polypeptide further comprises a polypeptide linker between the V_H and V_L domains, which enables the scFv to form the desired structure for antigen binding.

As used herein, a "chimeric antibody" is a recombinant protein that contains the variable domains and complementarity-determining regions derived from a non-human species (e.g., rodent) antibody, while the remainder of the antibody molecule is derived from a human antibody.

As used herein, a "humanized antibody" is a chimeric antibody that comprises a minimal sequence that conforms to specific complementarity-determining regions derived from non-human immunoglobulin that is transplanted into a human antibody framework. Humanized antibodies are typically recombinant proteins in which only the antibody complementarity-determining regions are of non-human origin (including antibodies generated from phage display or yeast).

As used herein, the term "mannan-binding lectin" ("MBL") is equivalent to mannan-binding protein ("MBP").

As used herein, the "membrane attack complex" ("MAC") refers to a complex of the terminal five complement components (C5b combined with C6, C7, C8 and C9) that inserts into and disrupts membranes (also referred to as C5b-9).

As used herein, "a subject" includes all mammals, including without limitation humans, non-human primates, dogs, cats, horses, sheep, goats, cows, rabbits, pigs and rodents.

As used herein, the amino acid residues are abbreviated as follows: alanine (Ala;A), asparagine (Asn;N), aspartic acid (Asp;D), arginine (Arg;R), cysteine (Cys;C), glutamic acid (Glu;E), glutamine (Gln;Q), glycine (Gly;G), histidine (His;H), isoleucine (Ile;I), leucine (Leu;L), lysine (Lys;K), methionine (Met;M), phenylalanine (Phe;F), proline (Pro;P), serine (Ser;S), threonine (Thr;T), tryptophan (Trp;W), tyrosine (Tyr;Y), and valine (Val;V).

In the broadest sense, the naturally occurring amino acids can be divided into groups based upon the chemical characteristic of the side chain of the respective amino acids. By "hydrophobic" amino acid is meant either Ile, Leu, Met, Phe, Trp, Tyr, Val, Ala, Cys or Pro. By "hydrophilic" amino acid is meant either Gly, Asn, Gln, Ser, Thr, Asp, Glu, Lys, Arg or His. This grouping of amino acids can be further subclassed as follows. By "uncharged hydrophilic" amino acid is meant either Ser, Thr, Asn or Gln. By "acidic" amino acid is meant either Glu or Asp. By "basic" amino acid is meant either Lys, Arg or His.

As used herein the term "conservative amino acid substitution" is illustrated by a substitution among amino acids within each of the following groups: (1) glycine, alanine, valine, leucine, and isoleucine, (2) phenylalanine, tyrosine, and tryptophan, (3) serine and threonine, (4) aspartate and glutamate, (5) glutamine and asparagine, and (6) lysine, arginine and histidine.

The term "oligonucleotide" as used herein refers to an oligomer or polymer of ribonucleic acid (RNA) or deoxyribonucleic acid (DNA) or mimetics thereof. This term also covers those oligonucleobases composed of naturally-occurring nucleotides, sugars and covalent internucleoside (backbone) linkages as well as oligonucleotides having non-naturally-occurring modifications.

As used herein, an "epitope" refers to the site on a protein (e.g., a human MASP-3 protein) that is bound by an antibody. "Overlapping epitopes" include at least one (e.g.,

two, three, four, five, or six) common amino acid residue(s), including linear and non-linear epitopes.

As used herein, the terms "polypeptide," "peptide," and "protein" are used interchangeably and mean any peptide-linked chain of amino acids, regardless of length or post-translational modification. The MASP proteins (MASP-1, MASP-2 or MASP-3) described herein can contain or be wild-type proteins or can be variants that have not more than 50 (e.g., not more than one, two, three, four, five, six, seven, eight, nine, ten, 12, 15, 20, 25, 30, 35, 40, or 50) conservative amino acid substitutions. Conservative substitutions typically include substitutions within the following groups: glycine and alanine; valine, isoleucine, and leucine; aspartic acid and glutamic acid; asparagine, glutamine, serine and threonine; lysine, histidine and arginine; and phenylalanine and tyrosine.

The human MASP-1 protein (set forth as SEQ ID NO:10), human MASP-2 protein (set forth as SEQ ID NO:5) and human MASP-3 protein (set forth as SEQ ID NO:8) described herein also include "peptide fragments" of the proteins, which are shorter than full-length and/or immature (pre-pro) MASP proteins, including peptide fragments of a MASP protein include terminal as well internal deletion variants of the protein. Deletion variants can lack one, two, three, four, five, six, seven, eight, nine, ten, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acid segments (of two or more amino acids) or noncontiguous single amino acids. In some embodiments, the human MASP-1 protein can have an amino acid sequence that is, or is greater than, 70 (e.g., 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, or 100) % identical to the human MASP-1 protein having the amino acid sequence set forth in SEQ ID NO: 10.

In some embodiments, the human MASP-3 protein can have an amino acid sequence that is, or is greater than, 70 (e.g., 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, or 100) % identical to the human MASP-3 protein having the amino acid sequence set forth in SEQ ID NO: 8.

In some embodiments, the human MASP-2 protein can have an amino acid sequence that is, or is greater than, 70 (e.g., 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, or 100) % identical to the human MASP-2 protein having the amino acid sequence set forth in SEQ ID NO: 5.

In some embodiments, peptide fragments can be at least 6 (e.g., at least 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 250, 300, 350, 400, 450, 500, or 600 or more) amino acid residues in length (e.g., at least 6 contiguous amino acid residues in any one of SEQ ID NOS: 5, 8 or 10). In some embodiments, an antigenic peptide fragment of a human MASP protein is fewer than 500 (e.g., fewer than 450, 400, 350, 325, 300, 275, 250, 225, 200, 190, 180, 170, 160, 150, 140, 130, 120, 110, 100, 95, 90, 85, 80, 75, 70, 65, 60, 55, 50, 49, 48, 47, 46, 45, 44, 43, 42, 41, 40, 39, 38, 37, 36, 35, 34, 33, 32, 31, 30, 29, 28, 27, 26, 25, 24, 23, 22, 21, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, or 6) amino acid residues in length (e.g., fewer than 500 contiguous amino acid residues in any one of SEQ ID NOS: 5, 8 or 10).

In some embodiments, in the context of generating an antibody that binds MASP-1, MASP-2 and/or MASP-3, the peptide fragments are antigenic and retain at least 10% (e.g., at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 50%, at least 55%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, at least 99%, at least 99.5%, or 100% or more) of the ability of the full-length protein to induce an antigenic response in a mammal (see below under "Methods for Producing an Antibody").

Percent (%) amino acid sequence identity is defined as the percentage of amino acids in a candidate sequence that are identical to the amino acids in a reference sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity. Alignment for purposes of determining percent sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN, ALIGN-2 or Megalign (DNASTAR) software. Appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full-length of the sequences being compared can be determined by known methods.

In representative embodiments, the human MASP-1 protein (SEQ ID NO:10) is encoded by the cDNA sequence set forth as SEQ ID NO:9; the human MASP-2 protein (SEQ ID NO:5) is encoded by the cDNA sequence set forth as SEQ ID NO:4; and the human MASP-3 protein (SEQ ID NO:8) is encoded by the cDNA sequence set forth as SEQ ID NO:7. Those skilled in the art will recognize that the cDNA sequences disclosed

in SEQ ID NO:9, SEQ ID NO:4 and SEQ ID NO:7 represent a single allele of human MASP-1, MASP-2 and MASP-3, respectively, and that allelic variation and alternative splicing are expected to occur. Allelic variants of the nucleotide sequences shown in SEQ ID NO:9, SEQ ID NO:4 and SEQ ID NO:7, including those containing silent mutations and those in which mutations result in amino acid sequence changes, are within the scope of the present invention. Allelic variants of the MASP-1, MASP-2 or MASP-3 sequence can be cloned by probing cDNA or genomic libraries from different individuals according to standard procedures, or may be identified by homology comparison search (e.g., BLAST searching) of databases containing such information.

II.   THE LECTIN PATHWAY: A NEW UNDERSTANDING

i.   Overview: the Lectin pathway has been redefined

As described herein, the inventors have made the surprising discovery that the lectin pathway of complement has two effector arms to activate complement, both driven by lectin pathway activation complexes formed of carbohydrate recognition components (MBL, CL-11 and ficolins): i) the effector arm formed by the lectin pathway-associated serine proteases MASP-1 and MASP-3, referred to herein as "lectin pathway effector arm 1" or "LEA-1"; and (ii) the MASP-2 driven activation effector arm, referred to herein as "lectin pathway effector arm 2", or "LEA-2". Both LEA-1 and LEA-2 can effect lysis and/or opsonization.

It has also been determined that lectin-independent conversion of factor B by MASP-3 and lectin-independent conversion of factor D by HTRA-1, MASP-1 and MASP-3, which both can occur in the absence of Ca^{++}, commonly lead to the conversion of C3bB to C3bBb and of pro-factor D to factor D. Therefore, inhibiting MASP-3 can inhibit both LEA-1 and the lectin-independent activation of factor B and/or factor D, which can result in the inhibition of lysis and/or opsonization.

FIGURE 1 illustrates this new understanding of the pathways of complement activation. As shown in FIGURE 1, LEA-1 is driven by lectin-bound MASP-3, which can activate the zymogen of factor D to its active form and/or cleave the C3b- or C3b($H_2$0)-bound factor B, leading to conversion of the C3bB zymogen complex into its enzymatically active form C3bBb. Activated factor D, generated by MASP-3, can also convert the C3bB or C3b($H_2$0) zymogen complexes into their enzymatically active form.

MASP-1 is capable of rapid self-activation, whereas MASP-3 is not. In many cases, MASP-1 is the activator of MASP-3.

While in many examples lectins (i.e., MBL, CL-11 or ficolins) can direct activity to cellular surfaces, **FIGURE 1** also outlines the lectin-independent functions of MASP-3, MASP-1, and HTRA-1 in factor B activation and/or factor D maturation. As with the lectin-associated form of MASP-3 in LEA-1, the lectin-independent form of MASP-3 is capable of mediating conversion of C3bB or C3b(H$_2$0) to C3bBb (see also **FIGURES 36** and **37**) and pro-factor D to factor D (see **FIGURE 39**). MASP-1 (see also **FIGURE 39**) and the non-MASP-related protein HTRA-1 can also activate factor D (Stanton et al., *Evidence That the HTRA1 Interactome Influences Susceptibility to Age-Related Macular Degeneration*, presented at The Association for Research in Vision and Ophthalmology 2011 conference on May 4, 2011) in a manner in which no lectin component is required.

Thus, MASP-1 (via LEA-1 and lectin-independent forms), MASP-3 (via LEA-1 and lectin-independent forms), and HTRA-1 (lectin-independent only) are capable of either direct or indirect activation at one or more points along a MASP-3 - factor D - factor B axis. In doing so, they generate C3bBb, the C3 convertase of the alternative pathway, and they stimulate the production and deposition of C3b on microbial surfaces. C3b deposition plays a critical role in opsonization, labeling the surfaces of microbes for destruction by host phagocytic cells, such as macrophages. As an example herein (**FIGURE 35**), MASP-3 is critical for opsonization of *S. aureus*. C3b deposition occurs rapidly on *S. aureus* exposed to human serum in a MASP-3-dependent fashion (**FIGURE 35**).

The contributions of LEA-1 and the lectin-independent functions of MASP-3, MASP-1, or HTRA-1 are not limited to opsonization, however. As diagrammed in **FIGURE 1**, these three components can also cause cell lysis by indirect or direct activation of factor B, and the production of C3b. These components form complexes that generate the alternative pathway C5 convertase, C3bBb(C3b)$_n$. As described further herein, the requirement for MASP-3 and MBL, but not MASP-2 (and, therefore, not LEA-2 in this example), in the lysis of *N. meningitidis* (see **FIGURES 13, 14** and **15**) demonstrates a role for LEA-1 in lysis. In summary, the opsonization results obtained from the *S. aureus* studies and the lysis results observed in the *N. meningitidis* studies support the role of LEA-1 in both processes (as diagrammed in **FIGURE 1**). Furthermore, these studies demonstrate that both opsonization and lysis can result from

the conversion of C3bB or C3b(H₂0) and/or of pro-factor D to factor D; therefore, both processes can be outcomes of the lectin-independent roles of MASP-3, MASP-1, or HTRA-1. Thus, the model developed by the inventors in **FIGURE 1** supports the use of inhibitors of principally MASP-3, but also MASP-1 and/or HTRA-1, to block opsonization and/or lysis and to treat pathologies caused by dysregulation of these processes.

1. Lectin Pathway Effector Arm (LEA-1)

The first effector arm of the lectin pathway, LEA-1, is formed by the lectin pathway-associated serine proteases MASP-1 and MASP-3. As described herein, the inventors have now shown that, in the absence of MASP-3 and in the presence of MASP-1, the alternative pathway is not effectively activated on surface structures. These results demonstrate that MASP-3 plays a previously undisclosed role in initiating the alternative pathway, and this is confirmed using the MASP-3-deficient 3MC serum obtained from patients with the rare 3MC autosomal recessive disorder (Rooryck C, et al., Nat Genet. 43(3):197-203 (2011)) with mutations that render the serine protease domain of MASP-3 dysfunctional. Based on these novel findings, it is expected that complement activation involving the alternative pathway, as conventionally defined, is MASP-3-dependent. In fact, MASP-3, and its activation of LEA-1, may represent the hitherto elusive initiator of the alternative pathway.

As further described in Examples 1-4 herein, in MASP-2-deficient sera, the inventors observed a higher activity of lectin-dependent alternative pathway activation resulting in a higher bactericidal activity (*i.e.,* lytic activity) against *N. meningitidis.* While not wishing to be bound by any particular theory, it is believed that in absence of MASP-2, MASP-1-bearing carbohydrate recognition complexes are more likely to bind close to MASP-3-bearing carbohydrate recognition complexes to activate MASP-3. It is known that, in many instances, activation of MASP-3 is dependent on MASP-1 activity, as MASP-3 is not an auto-activating enzyme and very often requires the activity of MASP-1 to be converted from its zymogen form into its enzymatically active form. MASP-1 (like MASP-2) is an auto-activating enzyme, while MASP-3 does not auto-activate and, in many instances, needs the enzymatic activity of MASP-1 to be converted into its enzymatically active form. *See,* Zundel S, et al., *J Immunol.,* 172(7):4342-50 (2004). In absence of MASP-2, all lectin pathway recognition complexes are either loaded with MASP-1 or MASP-3. Therefore, the absence of MASP-2 facilitates the MASP-1-

mediated conversion of MASP-3 into its enzymatically active form. Once MASP-3 is activated, activated MASP-3 initiates alternative pathway activation, now referred to as "LEA-1" activation, through a MASP-3-mediated conversion of C3bB to C3bBb and/or conversion of pro-factor D to factor D. C3bBb, also referred to as the alternative pathway C3 convertase, cleaves additional C3 molecules yielding deposition of opsonic C3b molecules. If several C3b fragments bind in close proximity to the C3bBb convertase complex, this results in the formation of the alternative pathway C5 convertase C3bBb(C3b)n, which promotes formation of MAC. Additionally, C3b molecules deposited on the surface form new sites for factor B binding, which can now be cleaved by factor D and/or MASP-3 to form additional sites where alternative pathway C3 and C5 convertase complexes can be formed. This latter process is needed for effective lysis and does not require lectins once the initial C3b deposition has occurred. A recent publication (Iwaki D. et al., *J Immunol* 187(7):3751-8 (2011)) as well as data generated from the inventors (**FIGURE 37**) demonstrate that the alternative pathway C3 convertase zymogen complex C3bB is converted into its enzymatically active form by activated MASP-3. The inventors now have discovered that the MASP-3-mediated cleavage of factor B represents a subcomponent of the newly described LEA-1, which promotes lectin-dependent formation of the alternative pathway C3 convertase C3bBb.

2. Lectin Pathway Effector Arm (LEA-2)

The second effector arm of the lectin pathway, LEA-2, is formed by the lectin pathway-associated serine protease MASP-2. MASP-2 is activated upon binding of the recognition components to their respective pattern, and may also be activated by MASP-1, and subsequently cleaves the complement component C4 into C4a and C4b. After the binding of the cleavage product C4b to plasma C2, C4b-bound C2 becomes substrate of a second MASP-2-mediated cleavage step which converts C4b-bound C2 into the enzymatically active complex C4bC2a and a small C2b cleavage fragment. C4b2a is the C3-converting C3 convertase of the lectin pathway, converting the abundant plasma component C3 into C3a and C3b. C3b binds to any surface in close proximity via a thioester bond. If several C3b fragments bind in close proximity to the C3 convertase complex C4b2a, this convertase alters its specificity to convert C5 into C5b and C5a, forming the C5 convertase complex C4b2a(C3b)n. While this C5 convertase can initiate formation of MAC, this process is thought to be insufficiently effective to promote lysis on its own. Rather, the initial C3b opsonins produced by LEA-2 form the nucleus for the

formation of new alternative pathway C3 convertase and C5 convertase sites, which ultimately lead to abundant MAC formation and lysis. This latter event is mediated by factor D activation of factor B associated with LEA-2-formed C3b, and hence is dependent on LEA-1 by virtue of the essential role for MASP-1 in the maturation of factor D. There is also a MASP-2-dependent C4-bypass activation route to activate C3 in the absence of C4, which plays an important role in the pathophysiology of ischemia-reperfusion injury, since C4-deficient mice are not protected from ischemia-reperfusion injury while MASP-2-deficient mice are (Schwaeble et al., *PNAS*, 2011 *supra*). LEA-2 is also tied to the coagulation pathway, involving the cleavage of prothrombin to thrombin (common pathway) and also the cleavage of factor XII (Hageman factor) to convert into its enzymatically active form XIIa. Factor XIIa in turn cleaves factor XI to XIa (intrinsic pathway). The intrinsic pathway activation of the clotting cascade leads to fibrin formation, which is of critical importance for thrombus formation.

FIGURE 1 illustrates the new understanding of the lectin pathway and alternative pathway based on the results provided herein. **FIGURE 1** delineates the role of LEA-2 in both opsonization and lysis. While MASP-2 is the initiator of "downstream" C3b deposition (and resultant opsonization) in multiple lectin-dependent settings physiologically (**FIGURES 20A, 20B, 20C**), it also plays a role in lysis of serum-sensitive bacteria. As illustrated in **FIGURE 1**, the proposed molecular mechanism responsible for the increased bactericidal activity of MASP-2-deficient or MASP-2-depleted serum/plasma for serum-sensitive pathogens such as *N. meningitidis* is that, for the lysis of bacteria, lectin pathway recognition complexes associated with MASP-1 and MASP-3 have to bind in close proximity to each other on the bacterial surface, thereby allowing MASP-1 to cleave MASP-3. In contrast to MASP-1 and MASP-2, MASP-3 is not an auto-activating enzyme, but, in many instances, requires activation/cleavage by MASP-1 to be converted into its enzymatically active form.

As further shown in **FIGURE 1**, activated MASP-3 can then cleave C3b-bound factor B on the pathogen surface to initiate the alternative activation cascade by formation of the enzymatically active alternative pathway C3 and C5 convertases C3bBb and C3bBb(C3b)n, respectively. MASP-2-bearing lectin-pathway activation complexes have no part in the activation of MASP-3 and, in the absence of or after depletion of MASP-2, all-lectin pathway activation complexes will either be loaded with MASP-1 or MASP-3. Therefore, in the absence of MASP-2, the likelihood is markedly increased that on the

microbial surface MASP-1- and MASP-3-bearing lectin-pathway activation complexes will come to sit in close proximity to each other, leading to more MASP-3 being activated and thereby leading to a higher rate of MASP-3-mediated cleavage of C3b-bound factor B to form the alternative pathway C3 and C5 convertases C3bBb and C3bBb(C3b)n on the microbial surface. This leads to the activation of the terminal activation cascades C5b-C9 that forms the Membrane Attack Complex, composed of surface-bound C5b associated with C6, C5bC6 associated with C7, C5bC6C7 associated with C8, and C5bC6C7C8, leading to the polymerization of C9 that inserts into the bacterial surface structure and forms a pore in the bacterial wall, which will lead to osmolytic killing of the complement-targeted bacterium.

The core of this novel concept is that the data provided herein clearly show that the lectin pathway activation complexes drive the following two distinct activation routes, as illustrated in **FIGURE 1**:

i) LEA-1: A MASP-3-dependent activation route that initiates and drives activation of complement by generating the alternative pathway convertase C3bBb through initial cleavage and activation of factor B on activator surfaces, which will then catalyze C3b deposition and formation of the alternative pathway convertase C3bBb. The MASP-3-driven activation route plays an essential role in the opsonization and lysis of microbes and drives the alternative pathway on the surface of bacteria, leading to optimal rates of activation to generate membrane attack complexes; and

ii) LEA-2: A MASP-2-dependent activation route leading to the formation of the lectin pathway C3 convertase C4b2a and, upon accumulation of the C3 cleavage product C3b, subsequently to the C5 convertase C4b2a(C3b)n. In the absence of complement C4, MASP-2 can form an alternative C3 convertase complex which involves C2 and clotting factor XI.

In addition to its role in lysis, the MASP-2-driven activation route plays an important role in bacterial opsonization leading to microbes being coated with covalently bound C3b and cleavage products thereof (i.e., iC3b and C3dg), which will be targeted for the uptake and killing by C3 receptor-bearing phagocytes, such as granulocytes, macrophages, monocytes, microglia cells and the reticuloendothelial system. This is the most effective route of clearance of bacteria and microorganisms that are resistant to complement lysis. These include most of the gram-positive bacteria.

In addition to LEA-1 and LEA-2, there is the potential for lectin-independent activation of factor D by MASP-3, MASP-1 and/or HTRA-1, and there is also the potential for lectin-independent activation of factor B by MASP-3.

While not wishing to be bound by any particular theory, it is believed that each of (i) LEA-1, (ii) LEA-2 and (iii) lectin-independent activation of factor B and/or factor D lead to opsonization and/or the formation of MAC with resultant lysis.

   ii.   Background of MASP-1, MASP-2 and MASP-3

Three mannan-binding lectin-associated serine proteases (MASP-1, MASP-2 and MASP-3) are presently known to be associated in human serum with the mannan-binding lectin (MBL). Mannan-binding lectin is also called 'mannose-binding protein' or 'mannose-binding lectin' in the recent literature. The MBL–MASP complex plays an important role in innate immunity by virtue of the binding of MBL to carbohydrate structures present on a wide variety of microorganisms. The interaction of MBL with specific arrays of carbohydrate structures brings about the activation of the MASP proenzymes which, in turn, activate complement by cleaving the complement components C4 and C2 to form the C3 convertase C4b2b (Kawasaki *et al.*, *J. Biochem* 106:483-489 (1989); Matsushita & Fujita, *J. Exp Med.* 176:1497-1502 (1992); Ji *et al.*, *J. Immunol* 150:571-578 (1993)).

The MBL-MASP proenzyme complex was, until recently, considered to contain only one type of protease (MASP-1), but it is now clear that there are two other distinct proteases (i.e., MASP-2 and MASP-3) associated with MBL (Thiel *et al.*, *Nature* 386:506-510 (1997); Dahl *et al.*, *Immunity* 15:127-135 (2001)), as well as an additional serum protein of 19 kDa, referred to as "MAp19" or "sMAP" (Stover *et al.*, *J. Immunol* 162:3481-3490 (1999); Stover *et al.*, *J. Immunol* 163:6848-6859 (1999); Takahashi *et al.*, *Int. Immunol* 11:859-63 (1999)).

MAp19 is an alternatively spliced gene product of the structural gene for MASP-2 and lacks the four C-terminal domains of MASP-2, including the serine endopeptidase domain. The abundantly expressed truncated mRNA transcript encoding MAp19 is generated by an alternative splicing/polyadenylation event of the MASP-2 gene. By a similar mechanism, the MASP-1/3 gene gives rise to three major gene products, the two serine proteases MASP-1 and MASP-3 and a truncated gene product of 44 kDa referred to as "MAp44" (Degn *et al.*, *J. Immunol* 183(11):7371-8 (2009); Skjoedt *et al.*, *J Biol Chem* 285:8234-43 (2010)).

MASP-1 was first described as the P-100 protease component of the serum Ra-reactive factor, which is now recognized as being a complex composed of MBL plus MASP (Matsushita *et al.*, *Collectins and Innate Immunity*, (1996); Ji *et al.*, *J Immunol* 150:571-578 (1993). The ability of an MBL-associated endopeptidase within the MBL-MASPs complex to act on the complement components C4 and C2 in a manner apparently identical to that of the C1s enzyme within the C1q–(C1r)$_2$–(C1s)$_2$ complex of the classical pathway of complement suggests that there is a MBL–MASPs complex which is functionally analogous to the C1q–(C1r)$_2$–(C1s)$_2$ complex. The C1q–(C1r)$_2$–(C1s)$_2$ complex is activated by the interaction of C1q with the Fc regions of antibody IgG or IgM present in immune complexes. This brings about the autoactivation of the C1r proenzyme which, in turn, activates the C1s proenzyme which then acts on complement components C4 and C2.

The stoichiometry of the MBL-MASPs complex differs from the one found for the C1q–(C1r)$_2$–(C1s)$_2$ complex in that different MBL oligomers appear to associate with different proportions of MASP-1/MAp19 or MASP-2/MASP-3 (Dahl *et al.*, Immunity 15:127-135 (2001). The majority of MASPs and MAp19 found in serum are not complexed with MBL (Thiel *et al.*, *J Immunol* 165:878-887 (2000)) and may associate in part with ficolins, a recently described group of lectins having a fibrinogen-like domain able to bind to N-acetylglucosamine residues on microbial surfaces (Le *et al.*, *FEBS Lett* 425:367 (1998); Sugimoto *et al.*, *J. Biol Chem* 273:20721 (1998)). Among these, human L-ficolin, H-ficolin and M-ficolin associate with MASPs as well as with MAp19 and may activate the lectin pathway upon binding to the specific carbohydrate structures recognized by ficolins (Matsushita *et al.*, *J Immunol* 164:2281-2284 (2000); Matsushita *et al.*, *J Immunol* 168:3502-3506 (2002)). In addition to the ficolins and MBL, an MBL-like lectin collectin, called CL-11, has been identified as a lectin pathway recognition molecule (Hansen et al. *J Immunol* 185:6096-6104 (2010); Schwaeble et al. *PNAS* 108:7523-7528 (2011)). There is overwhelming evidence underlining the physiological importance of these alternative carbohydrate recognition molecules and it is therefore important to understand that MBL is not the only recognition component of the lectin activation pathway and that MBL deficiency is not to be mistaken for lectin-pathway deficiency. The existence of possibly an array of alternative carbohydrate-recognition complexes structurally related to MBL may broaden the spectrum of microbial structures that initiate a direct response of the innate immune system via activation of complement.

All lectin pathway recognition molecules are characterized by a specific MASPs-binding motif within their collagen-homologous stalk region (Wallis et al. *J. Biol Chem* 279:14065-14073 (2004)). The MASP-binding site in MBLs, CL-11 and ficolins is characterized by a distinct motif within this domain: Hyp-Gly-Lys-Xaa-Gly-Pro, where Hyp is hydroxyproline and Xaa is generally an aliphatic residue. Point mutations in this sequence disrupt MASP binding.

1. **Respective structures, sequences, chromosomal localization and splice variants**

FIGURE 2 is a schematic diagram illustrating the domain structure of the MASP-2 polypeptide (SEQ ID NO:5) and MAp19 polypeptide (SEQ ID NO:2) and the exons encoding the same. FIGURE 3 is a schematic diagram illustrating the domain structure of the MASP-1 polypeptide (SEQ ID NO:10), MASP-3 polypeptide (SEQ ID NO:8) and MAp44 polypeptide (SEQ ID NO:11) and the exons encoding the same. As shown in FIGURES 2 and 3, the serine proteases MASP-1, MASP-2 and MASP-3 consist of six distinct domains arranged as found in C1r and C1s; *i.e.*, (I) an N-terminal C1r/C1s/sea urchin VEGF/bone morphogenic protein (or CUBI) domain; (II) an epidermal growth factor (EGF)-like domain; (III) a second CUB domain (CUBII); (IV and V) two complement control protein (CCP1 and CCP2) domains; and (VI) a serine protease (SP) domain.

The cDNA-derived amino acid sequences of human and mouse MASP-1 (Sato *et al.*, *Int Immunol* 6:665-669 (1994); Takada *et al.*, *Biochem Biophys Res Commun* 196:1003-1009 (1993); Takayama *et al.*, *J. Immunol* 152:2308-2316 (1994)), human, mouse, and rat MASP-2 (Thiel *et al.*, *Nature* 386:506-510 (1997); Endo *et al.*, *J Immunol* 161:4924-30 (1998); Stover *et al.*, *J. Immunol* 162:3481-3490 (1999); Stover *et al.*, *J. Immunol* 163:6848-6859 (1999)), as well as human MASP-3 (Dahl *et al.*, *Immunity* 15:127-135 (2001)) indicate that these proteases are serine peptidases having the characteristic triad of His, Asp and Ser residues within their putative catalytic domains (Genbank Accession numbers: human MASP-1: BAA04477.1; mouse MASP-1: BAA03944; rat MASP-1: AJ457084; Human MASP-3:AAK84071; mouse MASP-3: AB049755, as accessed on Genbank on 2/15/2012, each of which is hereby incorporated herein by reference).

As further shown in FIGURES 2 and 3, upon conversion of the zymogen to the active form, the heavy chain (alpha, or A chain) and light chain (beta, or B chain) are split

to yield a disulphide-linked A-chain and a smaller B-chain representing the serine protease domain. The single-chain proenzyme MASP-1 is activated (like proenzyme C1r and C1s) by cleavage of an Arg-Ile bond located between the second CCP domain (domain V) and the serine protease domain (domain VI). Proenzymes MASP-2 and MASP-3 are considered to be activated in a similar fashion to that of MASP-1. Each MASP protein forms homodimers and is individually associated with MBL and the ficolins in a Ca^{++}-dependent manner.

2. MASp-1/3

The human MASP-1 polypeptide (SEQ ID NO:10) and MASP-3 polypeptide (SEQ ID NO:8) arise from one structural gene (Dahl *et al.*, *Immunity* 15:127-135 (2001), which has been mapped to the 3q27–28 region of the long arm of chromosome 3 (Takada *et al.*, *Genomics* 25:757-759 (1995)). The MASP-3 and MASP-1 mRNA transcripts are generated from the primary transcript by an alternative splicing/polyadenylation process. The MASP-3 translation product is composed of an alpha chain, which is common to both MASP-1 and MASP-3, and a beta chain (the serine protease domain), which is unique to MASP-3. As shown in **FIGURE 3**, the human MASP-1 gene encompasses 18 exons. The human MASP-1 cDNA (set forth as SEQ ID NO:9) is encoded by exons 2, 3, 4, 5, 6, 7, 8, 10, 11, 13, 14, 15, 16, 17 and 18. As further shown in **FIGURE 3**, the human MASP 3 gene encompasses twelve exons. The human MASP-3 cDNA (set forth as SEQ ID NO:7) is encoded by exons 2, 3, 4, 5, 6, 7, 8, 10, 11 and 12. An alternative splice results in a protein termed MBL-associated protein 44 ("MAp44)," (set forth as SEQ ID NO:11), arising from exons 2, 3, 4, 5, 6, 7, 8 and 9.

The human MASP-1 polypeptide (SEQ ID NO: 10 from Genbank BAA04477.1) has 699 amino acid residues, which includes a leader peptide of 19 residues. When the leader peptide is omitted, the calculated molecular mass of MASP-1 is 76,976 Da. As shown in **FIGURE 3**, the MASP-1 amino acid sequence contains four N-linked glycosylation sites. The domains of the human MASP-1 protein (with reference to SEQ ID NO:10) are shown in **FIGURE 3** and include an N-terminal C1r/C1s/sea urchin VEFG/bone morphogenic protein (CUBI) domain (aa 25-137 of SEQ ID NO:10), an epidermal growth factor-like domain (aa 139-181 of SEQ ID NO:10), a second CUB domain (CUBII) (aa 185-296 of SEQ ID NO:10), as well as a tandem of complement control protein (CCP1 aa 301-363 and CCP2 aa 367-432 of SEQ ID NO:10) domains and a serine protease domain (aa 449-694 of SEQ ID NO:10).

The human MASP-3 polypeptide (SEQ ID NO:8, from Genbank AAK84071) has 728 amino acid residues, which includes a leader peptide of 19 residues. When the leader peptides are omitted, the calculated molecular mass of MASP-3 is 81,873 Da. As shown in **FIGURE 3**, there are seven N-linked glycosylation sites in MASP-3. The domains of the human MASP-3 protein (with reference to SEQ ID NO:8) are shown in **FIGURE 3** and include an N-terminal C1r/C1s/sea urchin VEGF/bone morphogenic protein (CUBI) domain (aa 25-137 of SEQ ID NO:8), an epidermal growth factor-like domain (aa 139-181 of SEQ ID NO:8), a second CUB domain (CUBII) (aa 185-296 of SEQ ID NO:8), as well as a tandem of complement control protein (CCP1 aa 301-363 and CCP2 aa 367-432 of SEQ ID NO:8) domains and a serine protease domain (aa 450-711 of SEQ ID NO:8).

The MASP-3 translation product is composed of an alpha chain (heavy chain), containing the CUB-1-EGF-CUB-2-CCP-1-CCP-2 domains (alpha chain: aa 1-448 of SEQ ID NO:8) which is common to both MASP-1 and MASP-3, and a light chain (beta chain: aa 449-728 of SEQ ID NO:8), containing the serine protease domain, which is unique to MASP-3 and MASP-1.

3. MASP-2

The human MASP-2 gene is located on chromosome 1p36.3-2 (Stover *et al.*, *Cytogenet and Cell Genet* 84:148-149 (1999) and encompasses twelve exons, as shown in **FIGURE 2**. MASP-2 (SEQ ID NO:5) and MAp19 (SEQ ID NO:2) are encoded by transcripts of a single structural gene generated by alternative splicing/polyadenylation (Stover *et al.*, Genes and Immunity 2:119-127 (2001)). The human MASP-2 cDNA (SEQ ID NO:4) is encoded by exons 2, 3, 4, 6, 7, 8, 9, 10, 11 and 12. The 20 kDa protein termed MBL-associated protein 19 ("MAp19", also referred to as "sMAP") (SEQ ID NO:2), encoded by (SEQ ID NO:1) arises from exons 2, 3, 4 and 5. MAp19 is a nonenzymatic protein containing the N-terminal CUB1-EGF region of MASP-2 with four additional residues (EQSL) derived from exon 5 as shown in **FIGURE 2**.

The MASP-2 polypeptide (SEQ ID NO:5) has 686 amino acid residues, which includes a leader peptide of 15 residues that is cleaved off after secretion, resulting in the mature form of human MASP-2 (SEQ ID NO:6). As shown in **FIGURE 2**, the MASP-2 amino acid sequence does not contain any N-linked glycosylation sites. The MASP-2 polypeptide exhibits a molecular structure similar to MASP-1, MASP-3, and C1r and C1s, the proteases of the C1 complement system. The domains of the human MASP-2 protein (numbered with reference to SEQ ID NO:5) are shown in **FIGURE 2** and include

an N-terminal C1r/C1s/sea urchin VEGF/bone morphogenic protein (CUBI) domain (aa 24-136 of SEQ ID NO:5), an epidermal growth factor-like domain (aa 138-180 of SEQ ID NO:5), a second CUB domain (CUBII) (aa 184-295 of SEQ ID NO:5), as well as a tandem of complement control protein (CCP1 aa 300-359 and CCP2 aa 364-431 of SEQ ID NO:5) domains and a serine protease domain (aa 445-682 of SEQ ID NO:5).

As shown in **FIGURE 2**, the MASP-2 polypeptide has an alpha chain (heavy chain) containing the CUB-1-EGF-CUB-2-CCP-1-CCP-2 domains (alpha chain: aa 1-443 of SEQ ID NO:5) and a beta chain (light chain) containing the serine protease domain (beta chain: aa 444-686). The CUB-1, EGF and CUB-2 domains are required for dimerization and the CUB-1, EGF, CUB-2 and CCP-1 domains contain the binding site for MBP. As described in Wallis et al., *J. Biol Chem* 279:14065-14073 (2004), each MASP-2 dimer binds to two MBL subunits.

4. Comparison of MASP-1, MASP-2 and MASP-3 amino acid sequences

FIGURE 4 is an amino acid alignment of the protein sequences of MASP-1 (SEQ ID NO:10), MASP-2 (SEQ ID NO:6) and MASP-3 (SEQ ID NO:8), showing the CUBI, EGF, CUBII, CCP1, CCP2 domains and conserved catalytic triad residues (H, D, S) in the serine protease (SP) domains. The symbol "." indicates an identical amino acid sequence.

FIGURE 5 is an amino acid alignment of the alpha chain sequences, including the CUBI-EGF-CUBII-CCP1-CCP2, of MASP-1 (alpha chain: aa 1-447 of SEQ ID NO:10) MASP-2 (alpha chain: aa 1-443 of SEQ ID NO:5) and MASP-3 (alpha chain: aa 1-448 of SEQ ID NO:8). There are numerous patches of identity in the CUBI, EGF, and CUBII domains, as indicated by dotted boxes in **FIGURE 5**. The CCP1 and CCP2 domains are indicated by the dark shaded boxes. The overall percent identity between the alpha chains of human MASP1/3 and human MASP-2 is provided below in TABLE 1.

FIGURE 6 is an amino acid alignment of the beta chain sequences (including the serine protease domains) of MASP-1 (beta chain: aa 448-699 of SEQ ID NO:10), MASP-2 (beta chain: aa 444-686 of SEQ ID NO:5) and MASP-3 (beta chain: aa 449-728 of SEQ ID NO:8). **FIGURE 7A** shows a pairwise amino acid alignment between the beta chain sequences of MASP-1 (beta chain: aa 448-699 of SEQ ID NO:10) and MASP-2 (beta chain: aa 444-686 of SEQ ID NO:5). **FIGURE 7B** shows a pairwise amino acid alignment between the beta chain sequences of MASP-1 (beta chain: aa 448-699 of SEQ ID NO:10) and MASP-3 (beta chain: aa 449-728 of SEQ ID NO:8). **FIGURE 7C** shows

a pairwise amino acid alignment between the beta chain sequences of MASP-2 (beta chain: aa 444-686 of SEQ ID NO:5) and MASP-3 (beta chain: aa 449-728 of SEQ ID NO:8). The regions of identity in **FIGURES 5-7** are shown as dotted boxes surrounding the identical amino acids (shown as "." Symbol).

The percent identity between the alpha and beta chains of the human MASP-1, MASP-2 and MASP-3 proteins is provided in **TABLE 1** below.

TABLE 1: Percent Identity between human MASP proteins

	% Identity Between A Chains			% Identity Between B Chains		
	MASP-1	MASP-2	MASP-3	MASP-1	MASP-2	MASP-3
MASP-1	100%	45.6%	98%	100%	27%	27%
MASP-2	45.6%	100%	45.4%	27%	100%	28.6%
MASP-3	98%	45.4%	100%	27%	28.6%	100%

With regard to the alpha chains (heavy chains), as indicated above in **TABLE 1**, the MASP-1 and MASP-3 alpha chains are identical (except for the 15 amino acid sequence at 3' end). The overall % identity between the MASP-2 and MASP-3 alpha chain is 45.4%, with numerous patches of identity in the CUBI-EGF-CUBII domains, as shown in **FIGURE 5**.

With regard to the beta chains (light chains), the overall percent identity between the three beta chains is low, in the range of 27% to 28%. However, although overall identity between the three B-chains is low, there are numerous patches of identity, as shown in **FIGURE 6**. As further shown in **FIGURES 7A-C**, identical patches of sequence are more broadly distributed between MASP-2 and 3 than between 1 and 2 or 1 and 3.

All the cysteine residues present in MASP-2, MASP-3, C1r and C1s align with equivalent residues in MASP-1; however, MASP-1 has two cysteine residues (at positions 465 and 481 in the L chain) that are not found in the MASP-2, MASP-3, C1r and C1s. These two cysteine residues in MASP-1 are in the expected positions used to form the 'histidine-loop' disulfide bridge as found in trypsin and chymotrypsin. This suggests that MASP-2, MASP-3, C1r, and C1s may have evolved, by gene duplication and divergence, from MASP-1 (Nonaka & Miyazawa, *Genome Biology* 3 Reviews 1001.1-1001.5 (2001)).

5. Respective biological functions/activities, including relevant human genetic data

The role of the MBL/Ficolin–MASPs complexes in innate immunity is mediated via the calcium-dependent binding of the C-type lectin domains (present in the MBL molecule) or via the binding of the fibrinogen-like domains (present in the ficolin molecule) to carbohydrate structures found on yeast, bacteria, viruses, and fungi. This recognition phase brings about the activation of the proenzyme MASP-2, which then mimics the action of the activated C1s within the C1q–(C1r)2–(C1s)2 complex by cleaving C4 and C2 to form the C3 convertase C4b2b. This allows deposition of C4b and C3b on target pathogens and thus promotes killing and clearance through phagocytosis.

Evidence in the recent literature suggests that the lectin pathway activation complex only requires the activity of MASP-2 to cleave C4 and C2: i) the reconstitution of a minimal lectin-pathway activation complex using recombinant MBL and recombinantly expressed MASP-2 appears to be sufficient to effectively cleave both C4 and C2 *in vitro* (Vorup-Jensen *et al.*, *J. Immunol* 165:2093-2100 (2000); Rossi *et al.*, *J Biol Chem* 276:40880-40887 (2001); Ambrus et al., *J Immunol* 170:1374-1382 (2003); Gál et al, *J Biol Chem* 280:33435-33444 (2005)); while ii) the serum of mice with a gene-targeted deficiency of MASP-2 is devoid of any lectin pathway functional activity (Schwaeble *et al.*, *PNAS* 108:7523-7528 (2011)). Recently, a genetically determined deficiency of MASP-2 was described (Stengaard-Pedersen et al., *New Eng. J. Med.* 349:554-560, (2003)). The mutation of a single nucleotide leads to an Asp-Gly exchange in the CUB1 domain and renders MASP-2 incapable of binding to MBL.

In addition, the functional characterization of sera of mice deficient of both MASP-1 and MASP-3 shows that lectin pathway activity is slower, but not absent when comparing sera of wild-type and MASP-1/MASP-3 knockout (MASP-1/3$^{-/-}$) mice under physiological conditions (Takahashi *et al.*, *J. Immunol* 180:6132-6138 (2008); Schwaeble et al., *PNAS* (2011)). These studies suggest that in contrast to the classical pathway effector endopeptidase C1s, activation of MASP-2 does not essentially involve or require the activity of any of the other MBL-associated serine endopeptidases (*i.e.*, MASP-1 or MASP-3) and that the proteolytic activity of MASP-2 suffices to translate binding of the carbohydrate recognition molecules of the lectin pathway (*i.e.*, MBL, ficolins or CL-11) into complement activation. However, more recent studies have demonstrated that while MASP-2 does have the capacity to autoactivate, the catalytic rate of MASP-1 activation

of the MASP-2 zymogen exceeds that of MASP-2 cleavage of its own zymogen form by about 85,000 fold (Héja et al., *PNAS* 106:10498-503 (2011); Megyeri et al., *J. Biol. Chem.* 288(13):8922-34 (2013)). Therefore, it is likely that the primary activator of MASP-2 in physiological settings is MASP-1. As judged by the size of the fragments of C4 generated, and the functional C3 convertase activity generated, it seems likely that the activated MASP-2 cleaves C4 and C2 in an identical manner to that carried out by activated C1s, *i.e,.* at a single arginyl bond (Arg76 Ala77) within the alpha-chain of C4 and at a single arginyl bond (Arg223 Lys224) within the proenzyme chain of C2. It has also been reported that the mouse MASP (in the form of the mouse MBL–MASP complex designated Ra-reactive factor) can, unlike C1s, cleave the alpha-chain of complement component C3 to yield the biologically active fragments C3a and C3b (Ogata *et al, J. Immunol* 154:2351-2357 (1995)). If this were to take place in the human system, it would require the cleavage of a single arginyl bond (Arg77 Ser78) within the alpha-chain of C3. Activated MASP-2, like activated C1s, is unable to cleave complement component C5. The proteolytic activities of MASP-1 and MASP-2 are inhibited by C1-Inhibitor (Matsushita *et al., J Immunol* 165:2637-2642 (2000) whereas C1-Inhibitor does not react with MASP-3 (Dahl *et al., Immunity* 15:127-135 (2001); Zundel et al., *J Immunol* 172:4342-4350 (2004)).

The biological functions of MASP-1 and MASP-3 have been slow to emerge. The substrate specificity and the physiological role of MASP-1 have been a subject of debate since its discovery. Numerous potential substrates have been identified during the recent years. It was suggested that MASP-1 can cleave native C3 slowly and this direct cleavage of C3 may initiate the complement cascade perhaps with the contribution of the alternative pathway (Matsushita et al., *J Immunol* 165:2637-2642 (2000)). Later it was shown that recombinant MASP-1 cleaves the inactive (thioester hydrolyzed) form of C3 which is unproductive in terms of initiating the complement cascade (Ambrus et al., *J Immunol* 170:1374-1382 (2003)). The lack of lectin pathway activity in the serum dilutions of MASP-2-deficient mice unequivocally proved that the MASP-1-driven C3-bypass mechanism does not exist (Schwaeble et al., *PNAS* 108:7523-7528 (2011)). The complement components that are cleaved by MASP-1 with considerable efficiency are C2 (Rossi et al., *J Biol Chem* 276:40880-40887 (2001); Ambrus et al., *J Immunol* 170:1374-1382 (2003)) and the zymogen form of factor D (Takahashi et al., *J Exp Med* 207:29-37 (2010)). As for the ability of MASP-1 to cleave C2, it is plausible therefore that MASP-1

can augment the C3-convertase (C4b2a)-forming ability of MASP-2 via C2 cleavage. This suggestion is supported by the observation that the activity of the lectin pathway is diminished in MASP-1-depleted human serum and in the serum of MASP-1/3-deficient mice (Takahashi et al., *J Immunol* 180:6132-6138 (2008)), which observation also suggests that MASP-1 has a role in activating MASP-2. Moreover, while every C4b deposited by MBL-MASPs complex can form C4b2a convertase, only one out of four C4b deposited by the classical pathway C1 complex can do the same (Rawal et al., *J Biol Chem* 283 (12):7853-63 (2008)).

MASP-1 also cleaves MASP-2 and MASP-3 (Megyeri M., et al, J Biol Chem. 2013 Mar 29;288(13):8922-34). Recent experiments suggest that although MASP-2 can autoactivate, MASP-1 is the primary activator of zymogen MASP-2. The activation of MASP-2 was delayed in the serum of MASP-1 knockout mice (Takahashi et al., *J Immunol* 180: 6132-6138 (2008)) and a similar result was obtained when the activity of MASP-1 was blocked by a specific inhibitor in normal human serum (Kocsis et al., *J Immunol* 185(7):4169-78 (2010)). Moreover, Degn et al. (*J. Immunol.* 189(8): 3957-69 (2012)) found MASP-1 to be critical for MASP-2 activation and subsequent C4 cleavage in human serum. The catalytic rate for the conversion of zymogen MASP-2 to active MASP-2 is more than 85,000-fold greater than the rate by which MASP-2 can autoactivate (Megyeri et al., *J. Biol. Chem.* 288:8922–8934 (2013); Héja et al., *J. Biol. Chem.* 287(24):20290-300 (2012); Héja et al., *PNAS* 109:10498-503 (2012)).

Recent discoveries have also linked MASP-1 to the alternative pathway. MASP-1 can convert zymogen factor D into its enzymatically active form (**FIGURE 39**; Takahashi et al., *J Exp Med* 207:29-37 (2010)). Furthermore, MASP-1 activates the zymogen form of MASP-3 (Megyeri et al., *J. Biol. Chem.* 288:8922–8934 (2013); Degn et al. *J. Immunol.* 189(8): 3957-69 (2012)), which itself can activate zymogen factor D (**FIGURE 39**) as well as cleave factor B, another essential component of the alternative pathway, to its active form (Iwaki et al., *J. Immunol.* 187:3751-58 (2011)). The conversion of pro-factor D and pro-factor B, however, is likely to be independent of the activation state of LEA-2 and may occur through non-complex-bound MASP-1.

Several lines of evidence indicate that MASP-1 is a thrombin-like enzyme and is important in activation of the coagulation pathway. MASP-1 can cleave several substrates of thrombin including fibrinogen (Hajela K. et al., *Immunobiology* 205(4-5):467-75 (2002)), factor XIII (Krarup et al., *Biochim Biophys Acta* 1784(9):1294-1300

(2008)) and protease-activated receptor 4 (PAR4) (Megyeri et al., *J Immunol* 183(5):3409-16 (2009)). Moreover, antithrombin in the presence of heparin is a more efficient inhibitor of MASP-1 than C1-inhibitor (Dobó et al., *J Immunol* 183:1207-1214 (2009)). The connection between the complement and the coagulation pathway is also underlined by the observation that MASP-2 is able to activate prothrombin (Krarup A. et al., *PLoS One* 2(7):e623 (2007)). Limited coagulation represents an ancient type of innate immunity when the spreading of invading pathogens is prevented by the fibrin clot. The releasing fibrinopeptide B has proinflammatory activity. The MASP-1-mediated cleavage of PAR4 activates the endothelial cells-initiating inflammatory reaction (Megyeri et al., *J Immunol* 183(5):3409-16 (2009)).

MASP-3 has no proteolytic activity towards C4, C2 or C3 substrates. Conversely, MASP-3 was reported to act as an inhibitor of the lectin pathway (Dahl et al., *Immunity* 15:127-135 (2001)). This conclusion may have come about because in contrast to MASP-1 and MASP-2, MASP-3 is not an autoactivating enzyme (Zundel S. et al., *J Immunol* 172:4342-4350 (2004); Megyeri et al., *J. Biol. Chem.* 288:8922–8934 (2013).

Recently, evidence for possible physiological functions of MASP-1 and MASP-3 emerged from transgenic mouse studies using a mouse strain with a combined MASP-1 and MASP-3 deficiency. While MASP-1/3-knockout mice have a functional lectin pathway (Schwaeble et al., *PNAS* 108:7523-7528 (2011)), they appear to lack alternative pathway activity (Takahashi et al., *JEM* 207(1):29-37 (2010)). Lack of alternative pathway activity appears to be due to a processing defect of complement factor D, which is necessary for alternative pathway activity. In MASP-1/3 knockout mice, all factor D is circulating as a proteolytically inactive pro-form, whereas in the serum of normal mice, substantially all of factor D is in the active form. Biochemical analysis suggested that MASP-1 may be able to convert complement factor D from its zymogen form into its enzymatically active form (**FIGURE 39**; Takahashi et al., *JEM* 207(1):29-37 (2010)). MASP-3 also cleaves pro-factor D zymogen and produce active factor D *in vitro* (**FIGURE 39**; Takahashi et al., *JEM* 207(1):29-37 (2010)). Factor D is present as an active enzyme in circulation in normal individuals, and MASP-1 and MASP-3, as well as HTRA-1, may be responsible for this activation. Furthermore, mice with combined MBL and ficolin deficiencies still produce normal levels of factor D and have a fully functional alternative pathway. Thus, these physiological functions of MASP-1 and MASP-3 do not necessarily involve lectins, and are thus unrelated to the lectin pathway. Recombinant

mouse and human MASP-3 also appear to cleave factor B and support C3 deposition on *S. aureus in vitro* (**FIGURE 36**; Iwaki D. et al., *J Immunol* 187(7):3751-8 (2011)).

An unexpected physiological role for MASP-3 has emerged from recent studies of patients with 3MC syndrome (previously designated the Carnevale, Mingarelli, Malpuech, and Michels syndrome; OMIM # 257920). These patients display severe developmental abnormalities, including cleft palate, cleft lip, cranial malformations and mental retardation. Genetic analysis identified 3MC patients that were homozygous for a dysfunctional MASP-3 gene (Rooryck et al., *Nat Genet.* 43(3):197-203 (2011)). Another group of 3MC patients was found to be homozygous for a mutation in the MASP-1 gene that leads to the absence of functional MASP-1 and MASP-3 proteins. Yet another group of 3MC patients lacked a functional CL-11 gene. (Rooryck et al., *Nat Genet.* 43(3):197-203 (2011)). Thus, the CL-11 MASP-3 axis appears to play a role during embryonic development. The molecular mechanisms of this developmental pathway are unclear. It is unlikely, however, to be mediated by a conventional complement-driven process since individuals with deficiencies of common complement components C3 do not develop this syndrome. Thus, prior to the discovery of the instant inventors, as described herein, a functional role for MASP-3 in lectin-dependent complement activation was previously not established.

The structures of the catalytic fragment of MASP-1 and MASP-2 have been determined by X-ray crystallography. Structural comparison of MASP-1 protease domain with those of other complement proteases revealed the basis of its relaxed substrate specificity (Dobó et al., *J. Immunol* 183:1207-1214 (2009)). While the accessibility of the substrate binding groove of MASP-2 is restricted by surface loops (Harmat et al., *J Mol Biol* 342:1533-1546 (2004)), MASP-1 has an open substrate binding pocket which resembles that of trypsin rather than other complement proteases. A thrombin-like property of the MASP-1 structure is the unusually large 60 amino acid loop (loop B) which may interact with substrates. Another interesting feature of the MASP-1 structure is the internal salt bridge between the S1 Asp189 and Arg224. A similar salt bridge can be found in the substrate binding pocket of factor D, which can regulate its protease activity. C1s and MASP-2 have almost identical substrate specificities. Surprisingly, some of the eight surface loops of MASP-2, which determine the substrate specificities, have quite different conformations compared to those of C1s. This means that the two functionally related enzymes interact with the same substrates in a different

manner. The structure of zymogen MASP-2 shows an inactive protease domain with disrupted oxyanion hole and substrate binding pocket (Gál et al., *J Biol Chem* 280:33435-33444 (2005)). Surprisingly, zymogen MASP-2 shows considerable activity on a large protein substrate, C4. It is likely that the structure of zymogen MASP-2 is quite flexible, enabling the transition between the inactive and the active forms. This flexibility, which is reflected in the structure, may play a role in the autoactivation process.

Northern blot analysis indicates that liver is the major source of MASP-1 and MASP-2 mRNA. Using a 5' specific cDNA probe for MASP-1, major MASP-1 transcript was seen at 4.8 kb and a minor one at approximately 3.4 kb, both present in human and mouse liver (Stover et al., *Genes Immunity* 4:374-84 (2003)). MASP-2 mRNA (2.6 kb) and MAp19 mRNA (1.0 kb) are abundantly expressed in liver tissue. MASP-3 is expressed in the liver, and also in many other tissues, including neuronal tissue (Lynch N. J. et al., *J Immunol* 174:4998-5006 (2005)).

A patient with a history of infections and chronic inflammatory disease was found to have a mutated form of MASP-2 that fails to form an active MBL–MASP complex (Stengaard-Pedersen et al., *N Engl J Med* 349:554-560 (2003)). Some investigators have determined that deficiency of MBL leads to a tendency to frequent infections in childhood (Super *et al.*, *Lancet* 2:1236-1239 (1989); Garred *et al.*, *Lancet* 346:941-943 (1995) and a decreased resistance to HIV infection (Nielsen *et al.*, *Clin Exp Immunol* 100:219-222 (1995); Garred *et al.*, *Mol Immunol* 33 (suppl 1):8 (1996)). However, other studies have not demonstrated a significant correlation of low MBL levels with increased infections (Egli et al., PLoS One. 8(1):e51983(2013); Ruskamp et al., J Infect Dis. 198(11):1707-13 (2008); Israëls et al., Arch Dis Child Fetal Neonatal Ed. 95(6):F452-61 (2010)). While the literature is mixed, deficiency, or non-utilization, of MASP may have an adverse effect on an individual's ability to mount immediate, non-antibody-dependent defense against certain pathogens.

  iii. <u>Supporting data for the new understanding, underscoring traditional assay</u> <u>conditions that are devoid of Ca^{++} and results obtained using a more</u> <u>physiological set of conditions that include Ca^{++}.</u>

Several independent lines of strong experimental evidence are provided herein pointing to the conclusion that the lectin pathway activation route of complement activates complement via two independent effector mechanisms: i) LEA-2: a MASP-2-

driven path that mediates complement-driven opsonisation, chemotaxis (Schwaeble et al., *PNAS* 108:7523-7528 (2011)), and cell lysis, and ii) LEA-1: a novel MASP-3-dependent activation route that initiates complement activation by generating the alternative pathway convertase C3bBb through cleavage and activation of factor B on activator surfaces, which will then catalyze C3b deposition and formation of the alternative pathway convertase C3bBb, which can result in cell lysis as well as microbial opsonization. In addition, as described herein, separate lectin-independent activation of factor B and/or factor D by MASP-1, MASP-3, or HTRA-1, or a combination of any the three, can also lead to complement activation via the alternative pathway.

A lectin pathway-dependent MASP-3-driven activation of the alternative pathway appears to contribute to the well-established factor D-mediated cleavage of C3b-bound factor B to achieve optimal activation rates for complement-dependent lysis through the terminal activation cascade to lyse bacterial cells through the formation of C5b-9 membrane attack complexes (MAC) on the cellular surface (**FIGURES 14-15**). This rate-limited event appears to require optimal coordination as it is defective in the absence of MASP-3 functional activity as well as in the absence of factor D functional activity. As described in Examples 1-4 herein, the inventors discovered this MASP-3-dependent lectin pathway function when studying the phenotype of MASP-2 deficiency and MASP-2 inhibition in experimental mouse models of *N. menigitidis* infection. Gene-targeted, MASP-2-deficient mice and wild-type mice treated with antibody-based MASP-2 inhibitors were highly resistant to experimental *N. meningitidis* infection (see **FIGURES 8-12**). When the infectious dose was adjusted to give approximately 60% mortality in the wild-type littermates, all of the MASP-2-deficient or MASP-2-depleted mice cleared the infection and survived (see **FIGURE 8** and **FIGURE 12**). This extremely high degree of resistance was reflected in a significant increase of serum bactericidal activity in MASP-2-deficient or MASP-2-depleted mouse serum. Further experiments showed that this bactericidal activity was dependent on alternative pathway-driven bacterial lysis. Mouse sera deficient of factor B, or factor D, or C3 showed no bactericidal activity towards *N. meningitidis*, indicating that the alternative pathway is essential for driving the terminal activation cascade. A surprising result was that mouse sera deficient of MBL-A and MBL-C (both being the lectin-pathway recognition molecules that recognize *N. meningitidis*) as well as mouse sera deficient of the lectin pathway-associated serine proteases MASP-1 and MASP-3 had lost all bacteriolytic activity towards *N. meningitidis*

(FIGURE 15). A recent paper (Takahashi M. et al., *JEM* 207: 29-37 (2010)) and work presented herein (FIGURE 39) demonstrate that MASP-1 can convert the zymogen form of factor D into its enzymatically active form and may in part explain the loss of lytic activity through the absence of enzymatically active factor D in these sera. This does not explain the lack of bactericidal activity in MBL-deficient mice since these mice have normal enzymatically active factor D (Banda et al., *Mol Imunol* 49(1-2):281-9 (2011)). Remarkably, when testing human sera from patients with the rare 3MC autosomal recessive disorder (Rooryck C, et al., Nat Genet. 43(3):197-203) with mutations that render the serine protease domain of MASP-3 dysfunctional, no bactericidal activity against *N. meningitidis* was detectable (n.b.: These sera have MASP-1 and factor D, but no MASP-3).

The hypothesis that human serum requires lectin pathway-mediated MASP-3-dependent activity to develop bactericidal activity is further supported by the observation that MBL-deficient human sera also fail to lyse *N. meningitidis* (FIGURES 13-14). MBL is the only human lectin-pathway recognition molecule that binds to this pathogen. Since MASP-3 does not auto-activate, the inventors hypothesize that the higher bacteriolytic activity in MASP-2-deficient sera could be explained by a favored activation of MASP-3 through MASP-1 since, in the absence of MASP-2, all lectin-pathway activation complexes that bind to the bacterial surface will be loaded with either MASP-1 or MASP-3. Since activated MASP-3 cleaves both factor D (FIGURE 39) and factor B to generate their respective enzymatically active forms *in vitro* (FIGURE 37 and Iwaki D., et al., *J. Immunol.*187(7):3751-3758 (2011)), the most likely function of MASP-3 is to facilitate the formation of the alternative pathway C3 convertase (i.e., C3bBb).

While the data for the lectin-dependent role are compelling, multiple experiments suggest that MASP-3 and MASP-1 are not necessarily obligated to function in a complex with lectin molecules. Experiments such as that shown in FIGURE 35B demonstrate the ability of MASP-3 to activate the alternative pathway (as demonstrated by C3b deposition on *S. aureus*) under conditions (i.e., the presence of EGTA) in which complexes with lectin would not be present. FIGURE 35A demonstrates that deposition under these conditions is dependent upon factor B, factor D, and factor P, all critical components of the alternative pathway. Addtionally, factor D activation by MASP-3 and MASP-1 (FIGURE 39), and factor B activation by MASP-3 (FIGURE 37) can occur *in vitro* in the absence of lectin. Finally, hemolysis studies of mouse erythrocytes in the presence of

human serum demonstrate a clear role for both MBL and MASP-3 for cell lysis. However, the deficiency of MBL does not completely reproduce the severity of the deficiency of MASP-3, in contrast to what would be expected if all functional MASP-3 were complexed with MBL. Thus, the inventors do not wish to be constrained by the notion that all of the roles for MASP-3 (and MASP-1) demonstrated herein can be attributed solely to function associated with lectin.

The identification of the two effector arms of the lectin pathway, as well as the possible lectin-independent functions of MASP-1, MASP-3, and HTRA-1, represent novel opportunities for therapeutic interventions to effectively treat defined human pathologies caused by excessive complement activation in the presence of microbial pathogens or altered host cells or metabolic deposits. As described herein, the inventors have now discovered that in the absence of MASP-3 and in the presence of MASP-1, the alternative pathway is not activated on surface structures (see **FIGURES 17-18, 35B, 41-42, 45-46**). Since the alternative pathway is important in driving the rate-limiting events leading to bacterial lysis as well as cell lysis (Mathieson PW, et al., *J Exp Med* 177(6):1827-3 (1993)), our results demonstrate that activated MASP-3 plays an important role in the lytic activity of complement. As shown in **FIGURES 14-15, 21-23, 43-44, and 46-47**, in serum of 3MC patients lacking MASP-3 but not MASP-1, the lytic terminal activation cascade of complement is defective. The data shown in **FIGURES 14** and **15** demonstrate a loss of bacteriolytic activity in absence of MASP-3 and/or MASP-1/MASP-3 functional activity. Likewise, the loss of hemolytic activity in MASP-3-deficient human serum (**FIGURES 21-23, 43-44** and **46-47**), coupled with the ability to reconstitute hemolysis by adding recombinant MASP-3 (**FIGURES 46-47**), strongly supports the conclusion that activation of the alternative pathway on target surfaces (which is essential to drive complement-mediated lysis) depends on the presence of activated MASP-3. Based on the new understanding of the lectin pathway detailed above, alternative pathway activation of target surfaces is thus dependent upon LEA-1, and/or lectin-independent activation of factor B and/or factor D, which is also mediated by MASP-3, and therefore, agents that block MASP-3-dependent complement activation will prevent alternative pathway activation on target surfaces.

The disclosure of the essential role of MASP-3-dependent initiation of alternative pathway activation implies that the alternative pathway is not an independent, stand-alone pathway of complement activation as described in essentially all current medical

textbooks and recent review articles on complement. The current and widely held scientific view is that the alternative pathway is activated on the surface of certain particulate targets (microbes, zymosan, and rabbit erythrocytes) through the amplification of spontaneous "tick-over" C3 activation. However, the absence of any alternative pathway activation in sera of MASP-1 and MASP-3 double-deficient mice and human 3MC patient serum on both zymosan-coated plates and two different bacteria (*N. meningitidis* and *S. aureus*), and the reduction of hemolysis of erythrocytes in MASP-3-deficient sera from human and mouse indicate that initiation of alternative pathway activation on these surfaces requires functional MASP-3. The required role for MASP-3 may be either lectin-dependent or –independent, and leads to formation of the alternative pathway C3 convertase and C5 convertase complexes, i.e. C3bBb and C3bBb(C3b)n, respectively. Thus, the inventors here disclose the existence of a previously elusive initiation routes for the alternative pathway. This initiation route is dependent upon (i) LEA-1, a newly discovered activation arm of the lectin pathway, and/or (ii) lectin-independent roles of the proteins MASP-3, MASP-1, and HTRA-1.

III.   **THE ROLE OF MASP-2 AND MASP-3 IN PAROXYSMAL NOCTURNAL HEMOGLOBINURIA AND THERAPEUTIC METHODS USING MASP-2 AND MASP-3 INHIBITORY AGENTS**

   i.   Overview of PNH

Paroxysmal nocturnal hemoglobinuria (PNH), sometimes also referred to as Marchiafava-Micheli syndrome, is an acquired, potentially life-threatening disease of the blood. PNH may develop on its own, referred to as "primary PNH" or in the context of other bone marrow disorders such as aplastic anemia, referred to as "secondary PNH." The majority of cases are primary PNH. PNH is characterized by complement-induced destruction of red blood cells (hemolysis), low red blood cell counts (anemia), thrombosis and bone marrow failure. Laboratory findings in PNH show changes consistent with intravascular hemolytic anemia: low hemoglobin, raised lactate dehydrogenase, raised reticulocyte counts (immature red cells released by the bone marrow to replace the destroyed cells), raised bilirubin (a breakdown product of hemoglobin), in the absence of autoreactive RBC-binding antibodies as a possible cause.

The hallmark of PNH is the chronic complement-mediated hemolysis caused by the unregulated activation of terminal complement components, including the membrane

attack complex, on the surface of circulating RBCs. PNH RBCs are subject to uncontrolled complement activation and hemolysis due to the absence of the complement regulators CD55 and CD59 on their surface (Lindorfer, M.A., et al., *Blood* 115(11):2283-91 (2010), Risitano, et al., *Mini-Reviews in Medicinal Chemistry*, 11:528-535 (2011)). CD55 and CD59 are abundantly expressed on normal RBCs and control complement activation. CD55 acts as a negative regulator of the alternative pathway, inhibiting the assembly of the alternative pathway C3 convertase (C3bBb) complex and accelerating the decay of preformed convertase, thus blocking the formation of the membrane attack complex (MAC). CD59 inhibits the complement membrane attack complex directly by binding the C5b678 complex and preventing C9 from binding and polymerizing.

While hemolysis and anemia are the dominant clinical features of PNH, the disease is a complex hematologic disorder that further includes thrombosis and bone marrow failure as part of the clinical findings (Risitano et al, *Mini Reviews in Med Chem* 11:528-535 (2011)). At the molecular level, PNH is caused by the abnormal clonal expansion of hematopoietic stem cells lacking a functional PIG A gene. PIG A is an X-linked gene encoding a glycosyl-phosphatidyl inositol transferase required for the stable surface expression of GPI-anchored class A glycoproteins, including CD55 and CD59. For reasons that are presently under investigation, hematopoietic stem cells with a dysfunctional PIG A gene that arise as the result of spontaneous somatic mutations can undergo clonal expansion to the point where their progeny constitute a significant portion of the peripheral hematopoietic cell pool. While both erythrocyte and lymphocyte progeny of the mutant stem cell clone lack CD55 and CD59, only the RBCs undergo overt lysis after they enter the circulation.

Current treatment for PNH includes blood transfusion for anemia, anticoagulation for thrombosis and the use of the monoclonal antibody eculizumab (Soliris®), which protects blood cells against immune destruction by inhibiting the complement system (Hillmen P. et al., *N. Engl. J. Med.* 350(6):552-559 (2004)). Eculizumab (Soliris®) is a humanized monoclonal antibody that targets the complement component C5, blocking its cleavage by C5 convertases, thereby preventing the production of C5a and the assembly of MAC. Treatment of PNH patients with eculizumab has resulted in a reduction of intravascular hemolysis, as measured by lactate dehydrogenase (LDH), leading to hemoglobin stabilization and transfusion independence in about half of the patients (Risitano et al, *Mini-Reviews in Medicinal Chemistry*, 11(6) (2011)). While nearly all

patients undergoing therapy with eculizumab achieve normal or almost normal LDH levels (due to control of intravascular hemolysis), only about one third of the patients reach a hemoglobin value about 11gr/dL, and the remaining patients on eculizumab continue to exhibit moderate to severe (i.e., transfusion-dependent) anemia, in about equal proportions (Risitano A.M. et al., *Blood* 113:4094-100 (2009)). As described in Risitano et al., *Mini-Reviews in Medicinal Chemistry* 11:528-535 (2011), it was demonstrated that PNH patients on eculizumab contained large amounts of C3 fragments bound to their PNH erythrocytes (while untreated patients did not). This finding lead to the recognition that in Soliris treated PNH patients, PNH RBCs that are no longer hemolyzed due to C5 blockade now can accumulate copious amounts of membrane-bound C3 fragments, which operate as opsonins, resulting in their entrapment in the reticuloendothelial cells through specific C3 receptors and subsequent extravascular hemolysis. Thus, while preventing intravascular hemolysis and the resulting sequelae, eculizumab therapy simply diverts the disposition of these RBCs from intravascular to extravascular hemolysis, resulting in substantial residual untreated anemia in many patients (Risitano A.M. et al., *Blood* 113:4094-100 (2009)). Therefore, therapeutic strategies in addition to the use of eculizumab are needed for those patients developing C3-fragment-mediated extravascular hemolysis, because they continue to require red cell transfusions. Such C3 fragment targeting approaches have demonstrated utility in experimental systems (Lindorfer et al., *Blood* 115:2283-91, 2010).

    ii.   <u>Complement-initiating mechanisms in PNH</u>

The causal link between defective surface expression of the negative complement regulators CD55 and CD59 in PNH, combined with the effectiveness of eculizumab in preventing intravascular hemolysis, clearly define PNH as a condition mediated by the complement system. While this paradigm is widely accepted, the nature of the events initiating complement activation, and the complement activation pathway(s) involved remain unresolved. Because CD55 and CD59 negatively regulate the terminal amplification steps in the complement cascade common to all complement initiation pathways, deficiency of these molecules will lead to exaggerated formation and membrane integration of membrane attack complexes, regardless of whether complement activation is initiated by the lectin pathway, by the classical pathway or by spontaneous turnover of the alternative pathway. Thus, in PNH patients, any complement activation events that lead to C3b deposition on the RBC surface can trigger subsequent

amplification and pathological hemolysis (intravascular and/or extravascular) and precipitate a hemolytic crisis. A clear mechanistic understanding of the molecular events triggering hemolytic crisis in PNH patients has remained elusive. Because no complement initiating event is overtly evident in PNH patients undergoing a hemolytic crisis, the prevailing view is that complement activation in PNH may occur spontaneously owing to low level "tick-over" activation of the alternative pathway, which is subsequently magnified by inappropriate control of terminal complement activation due to lack of CD55 and CD59.

However, it is important to note that in its natural history, PNH usually develops or is exacerbated after certain events, such as an infection or an injury (Risitano, *Biologics* 2:205-222 (2008)), which have been shown to trigger complement activation. This complement activation response is not dependent on prior immunity of the host towards the inciting pathogen, and hence likely does not involve the classical pathway. Rather, it appears that this complement activation response is initiated by lectin binding to foreign or "altered self" carbohydrate patterns expressed on the surface of microbial agents or damaged host tissue. Thus, the events precipitating hemolytic crisis in PNH are tightly linked to complement activation initiated via lectins. This makes it very likely that lectin activation pathways provide the initiating trigger that ultimately leads to hemolysis in PNH patients.

Using well-defined pathogens that activate complement via lectins as experimental models to dissect the activation cascades at the molecular level, we demonstrate that, depending on the inciting microbe, complement activation can be initiated by either LEA-2 or LEA-1, leading to opsonization and/or lysis. This same principle of dual responses (i.e., opsonization and/or lysis) to lectin initiation events will likely also apply to other types of infectious agents, or to complement activation by lectins following tissue injury to the host, or other lectin-driven complement activation events that may precipitate PNH. On the basis of this duality in the lectin pathway, we infer that LEA-2- and/or LEA-1-initiated complement activation in PNH patients promotes opsonization and/or lysis of RBCs with C3b and subsequent extravascular and intravascular hemolysis. Therefore, in the setting of PNH, inhibition of both LEA-1 and LEA-2 would be expected to address both intravascular and extravascular hemolysis, providing a significant advantage over the C5 inhibitor eculizumab.

It has been determined that exposure to *S. pneumoniae* preferentially triggers lectin-dependent activation of LEA-2, which leads to opsonization of this microbe with C3b. Since *S. pneumonia* is resistant to MAC-mediated lysis, its clearance from circulation occurs through opsonisation with C3b. This opsonization and subsequent removal from circulation is LEA-2-dependent, as indicated by compromised bacterial control in MASP-2-deficient mice and in mice treated with MASP-2 monoclonal antibodies (PLOS Pathog., 8: e1002793. (2012)).

In exploring the role of LEA-2 in the innate host responses to microbial agents, we tested additional pathogens. A dramatically different outcome was observed when *Neisseria meningitidis* was studied as a model organism. *N. meningitidis* also activates complement via lectins, and complement activation is required for containment of *N. meningitidis* infections in the naïve host. However, LEA-2 plays no host protective functional role in this response: As shown in **FIGURES 8** and **9**, blockade of LEA-2 through genetic ablation of MASP-2 does not reduce survival following infection with *N. meningitidis*. To the contrary, LEA-2 blockade by MASP-2 ablation significantly improved survival (**FIGURES 8** and **9**) as well as illness scores (**FIGURE 11**) in these studies. LEA-2 blockade by administration of MASP-2 antibody yielded the same result (**FIGURE 12**), eliminating secondary or compensatory effects in the knockout-mouse strain as a possible cause. These favorable outcomes in LEA-2-ablated animals were associated with a more rapid elimination of *N. meningitidis* from the blood (**FIGURE 10**). Also, as described herein, incubation of *N. meningitidis* with normal human serum killed *N. meningitidis* (**FIGURE 13**). Addition of a functional monoclonal antibody specific for human MASP-2 that blocks LEA-2, but not administration of an isotype control monoclonal antibody, may enhance this killing response. Yet, this process depends on lectins and at least a partially functional complement system, as MBL-deficient human serum or heat-inactivated human serum was unable to kill *N. meningitidis* (**FIGURE 13**). Collectively, these novel findings suggest that *N. meningitidis* infections in the presence of a functional complement system are controlled by a lectin-dependent but LEA-2-independent pathway of complement activation.

The hypothesis that LEA-1 may be the complement pathway responsible for lectin-dependent killing of *N. meningitidis* was tested using a serum specimen from a 3MC patient. This patient was homozygous for a nonsense mutation in exon 12 of the MASP-1/3 gene. As a result, this patient lacked a functional MASP-3 protein, but was

otherwise complement sufficient (exon 12 is specific for the MASP-3 transcript; the mutation has no effect on MASP-1 function or expression levels) (see *Nat Genet* 43(3):197-203 (2011)). Normal human serum efficiently kills *N. meningitidis*, but heat-inactivated serum deficient in MBL (one of the recognition molecules for the Lectin pathway) and MASP-3-deficient serum were unable to kill *N. meningitidis* (**FIGURE 14**). Thus, LEA-1 appears to mediate *N. meningitidis* killing. This finding was confirmed using serum samples from knockout mouse strains. While complement containing normal mouse serum readily killed *N. meningitidis*, MBL-deficient or MASP-1/3-deficient mouse serum was as ineffective as heat-inactivated serum that lacks functional complement (**FIGURE 15**). Conversely, MASP-2-deficient serum exhibited efficient killing of *N. meningitidis*.

These findings provide evidence for a hitherto unknown duality in the lectin pathway by revealing the existence of separate LEA-2 and LEA-1 pathways of lectin-dependent complement activation. In the examples detailed above, LEA-2 and LEA-1 are non-redundant and mediate distinct, functional outcomes. The data suggest that certain types of lectin pathway activators (including, but not limited to *S. pneumonia*) preferentially initiate complement activation via LEA-2 leading to opsonization, while others (exemplified by *N. meningitidis*) preferentially initiate complement activation via LEA-1 and promote cytolytic processes. The data do not, however, necessarily limit LEA-2 to opsonization and LEA-1 to cytolytic processes, as both pathways in other settings can mediate opsonization and/or lysis.

In the context of lectin-dependent complement activation by *N. meningitidis*, LEA-2 and LEA-1 arms appear to compete with each other, as blockade of LEA-2 enhanced LEA-1-dependent lytic destruction of the organism *in vitro* (**FIGURE 15**). As detailed above, this finding can be explained by the increased likelihood of lectin MASP-1 complexes residing in close proximity to lectin MASP-3 complexes in the absence of MASP-2, which will enhance LEA-1 activation and thus promote more effective lysis of *N. meningitides*. Because lysis of *N. meningitidis* is the main protective mechanism in the naïve host, blockade of LEA-2 *in vivo* increases *N. meningitidis* clearance and leads to enhanced killing.

While the examples discussed above illustrate opposing effects of LEA-2 and LEA-1 with respect to outcomes following infection with *N. meningitidis*, there may be other settings where both LEA-2 and LEA-1 may synergize to produce a certain outcome.

As detailed below, in other situations of pathological complement activation via lectins such as those present in PNH, LEA-2- and LEA-1-driven complement activation may cooperate in a synergistic manner to contribute to the overall pathology of PNH. In addition, as described herein, MASP-3 also contributes to the lectin-independent conversion of factor B and factor D, which can occur in the absence of Ca^{++}, commonly leading to the conversion of C3bB to C3bBb and of pro-factor D to factor D, which may further contribute to the pathology of PNH.

iii.   Biology and expected functional activity in PNH

This section describes the inhibitory effects of LEA-2 and LEA-1 blockade on hemolysis in an *in vitro* model of PNH. The findings support the utility of LEA-2-blocking agents (including, but not limited to, antibodies that bind to and block the function of MASP-2) and LEA-1-blocking agents (including, but not limited to, antibodies that bind to and block the function of MASP-1-mediated activation of MASP-3, MASP-3, or both) to treat subjects suffering from one or more aspects of PNH, and also the use of inhibitors of LEA-2 and/or LEA-1, and/or MASP-3-dependent, lectin-independent complement activation (including MASP-2 inhibitors, MASP-3 inhibitors, and dual- or bispecific MASP-2/MASP-3 or MASP-1/MASP-2 inhibitors, and pan-specific MASP-1/MASP-2/MASP-3 inhibitors) to ameliorate the effects of C3-fragment-mediated extravascular hemolysis in PNH patients undergoing therapy with a C5-inhibitor such as eculizumab.

iv.   MASP-2 inhibitors to block opsonization and extravascular hemolysis of
        PNH RBCs through the reticuloendothelial system

As detailed above, PNH patients become anemic owing to two distinct mechanisms of RBC clearance from circulation: intravascular hemolysis via activation of the membrane attack complex (MAC), and extravascular hemolysis following opsonization with C3b and subsequent clearance following complement receptor binding and uptake by the reticuloendothelial system. The intravascular hemolysis is largely prevented when a patient is treated with eculizumab. Because eculizumab blocks the terminal lytic effector mechanism that occurs downstream of both the complement-initiating activation event as well as the ensuing opsonization, eculizumab does not block extravascular hemolysis (Risitano A.M. et al., *Blood* 113:4094-100 (2009)). Instead, RBCs that would have undergone hemolysis in untreated PNH patients now can accumulate activated C3b proteins on their surface, which augments uptake by the

reticuloendothelial system and enhances their extravascular hemolysis. Thus, eculizumab treatment effectively diverts RBC disposition from intravascular hemolysis to potential extravascular hemolysis. As a result, some eculizumab-treated PNH patients remain anemic. It follows that agents that block complement activation upstream and prevent the opsonization of PNH RBCs may be particularly suitable to block the extravascular hemolysis occasionally seen with eculizumab.

The microbial data presented here suggest that LEA-2 is often the dominant route for lectin-dependent opsonization. Furthermore, when lectin-dependent opsonization (measured as C3b deposition) was assessed on three prototypic lectin activation surfaces (mannan, **FIGURE 19A**; zymosan, **FIGURE 19B**, and *S. pneumonia*; **FIGURE 19C**), LEA-2 appears to be the dominant route for lectin-dependent opsonization under physiologic conditions (i.e., in the presence of Ca^{++} wherein all complement pathways are operational). Under these experimental conditions, MASP-2-deficient serum (which lacks LEA-2) is substantially less effective in opsonizing the test surfaces than WT serum. MASP-1/3-deficient serum (which lacks LEA-1) is also compromised, though this effect is much less pronounced as compared to serum lacking LEA-2. The relative magnitude of the contributions of LEA-2 and LEA-1 to lectin-driven opsonization is further illustrated in **FIGURES 20A – 20C**. While the alternative pathway of complement has been reported to support opsonization of lectin activating surfaces in the absence of lectin pathway or classical pathway (Selander et al., *J Clin Invest* 116(5):1425-1434 (2006)), the alternative pathway in isolation (measured under Ca^{++}-free assay conditions) appears substantially less effective than the LEA-2- and LEA-1-initiated processes described herein. By extrapolation, these data suggest that opsonization of PNH RBCs may also be preferentially initiated by LEA-2 and, to a lesser extent, by LEA-1 (possibly amplified by the alternative pathway amplification loop), rather than the result of lectin-independent alternative pathway activation. Therefore, LEA-2 inhibitors may be expected to be most effective at limiting opsonization and preventing extravascular hemolysis in PNH. However, recognition of the fact that lectins other than MBL, such as ficolins, bind to non-carbohydrate structures such as acetylated proteins, and that MASP-3 preferentially associates with H-ficolin (Skjoedt et al., *Immunobiol.* 215:921-931, 2010), leaves open the possibility of a significant role for LEA-1 in PNH-associated RBC opsonization as well. Therefore, LEA-1 inhibitors are expected to have additional anti-opsonization effects, and the combination of LEA-1 and

LEA-2 inhibitors is expected to be optimal and mediate the most robust treatment benefit in limiting opsonization and extravascular hemolysis in PNH patients. This concept is further supported by opsonization data shown in **FIGURE 28**: factor D-deficient mouse serum (which lacks the ability to activate the alternative pathway in fluid phase but has a functional classical pathway as well as functional LEA-1 and LEA-2 pathways) shows no deficit in opsonization compared to WT serum. Factor B-deficient serum, which lacks LEA-1, shows reduced opsonization while factor D-deficient serum treated with MASP-2 monoclonal antibody to block LEA-2-mediated complement activation yields a more robust suppression of opsonization (**FIGURE 28**). Importantly, addition of MASP-2 monoclonal antibody to factor B-deficient serum suppressed opsonization more effectively than either MASP-2 blockade or factor D blockade alone. Thus, LEA-2 and LEA-1 act additively or synergistically to promote opsonization, and a crossreactive or bispecific LEA-1/LEA-2 inhibitor is expected to be most effective at blocking opsonization and extravascular hemolysis in PNH.

> v.   Role of MASP-3 inhibitors in PNH

Using an *in vitro* model of PNH, we demonstrated that complement activation and the resulting hemolysis in PNH are indeed initiated by LEA-2 and/or LEA-1 activation, and that it is not an independent function of the alternative pathway. These studies used mannan-sensitized RBCs of various mouse stains, including RBCs from Crry-deficient mice (an important negative regulator of the terminal complement pathway in mice) as well as RBCs from CD55/CD59-deficient mice, which lack the same complement regulators that are absent in PNH patients). When mannan-sensitized Crry-deficient RBCs were exposed to complement-sufficient human serum, the RBCs effectively hemolysed at a serum concentration of 3% (**FIGURE 21** and **22**) while complement-deficient serum (HI: heat-inactivated) was not hemolytic. Remarkably, complement-sufficient serum where LEA-2 was blocked by addition of MASP-2 antibody had reduced hemolytic activity, and 6% serum was needed for effective hemolysis. Similar observations were made when CD55/CD59-deficient RBCs were tested (**FIGURE 24**). Complement-sufficient human serum supplemented with MASP-2 monoclonal antibody (i.e., serum where LEA-2 is suppressed) was about two-fold less effective than untreated serum in supporting hemolysis. Furthermore, higher concentrations of LEA-2-blocked serum (i.e., treated with antiMASP-2 monoclonal antibody) were needed to promote effective hemolysis of untreated WT RBCs compared to untreated serum (**FIGURE 23**).

Even more surprisingly, serum from a 3MC patient homozygous for a dysfunctional MASP-3 protein (and hence lacking LEA-1) was completely unable to hemolyze mannan-sensitized Crry-deficient RBCs (**FIGURE 22** and **FIGURE 23**). A similar outcome was observed when unsensitized normal RBCs were used: As shown in **FIGURE 23**, LEA-1-defective serum isolated from a 3MC patient was completely ineffective at mediating hemolysis. Collectively, these data indicate that whereas LEA-2 contributes significantly to the intravascular hemolysis response, LEA-1 is the predominant complement-initiating pathway leading to hemolysis. Thus, while LEA-2 blocking agents are expected to significantly reduce intravascular hemolysis of RBCs in PNH patients, LEA-1 blocking agents are expected to have a more profound effect and largely eliminate complement-driven hemolysis.

It should be noted that the serum of the LEA-1-deficient 3MC patient used in this study possessed a diminished but functional alternative pathway when tested under conventional alternative pathway assay conditions (**FIGURE 17**). This finding suggests that LEA-1 makes a greater contribution to hemolysis than alternative pathway activity as conventionally defined in this experimental setting of PNH. By inference, it is implied that LEA-1-blocking agents will be at least as effective as agents blocking other aspects of the alternative pathway in preventing or treating intravascular hemolysis in PNH patients.

     vi.   <u>Role of MASP-2 inhibitors in PNH</u>

The data presented herein suggest the following pathogenic mechanisms for anemia in PNH: intravascular hemolysis due to unregulated activation of terminal complement components and lysis of RBC by formation of MAC, which is initiated predominantly, though not exclusively, by LEA-1, and extravascular hemolysis caused by opsonization of RBCs by C3b, which appears to be initiated predominately by LEA-2. While a discernible role for LEA-2 in initiating complement activation and promoting MAC formation and hemolysis is apparent, this process appears substantially less effective than LEA-1-initiated complement activation leading to hemolysis. Thus, LEA-2-blocking agents are expected to significantly reduce intravascular hemolysis in PNH patients, though this therapeutic activity is expected to be only partial. By comparison, a more substantial reduction in intravascular hemolysis in PNH patients is expected for LEA-1-blocking agents.

Extravascular hemolysis, a less dramatic, yet equally important mechanism of RBC destruction that leads to anemia in PNH, is primarily the result of opsonization by C3b, which appears to be predominantly mediated by LEA-2. Thus, LEA-2-blocking agents may be expected to preferentially block RBC opsonization and the ensuing extravascular hemolysis in PNH. This unique therapeutic activity of LEA-2-blocking agents is expected to provide a significant treatment benefit to all PNH patients as no treatment currently exists for those PNH patients who experience this pathogenic process.

      vii.   LEA-2 inhibitors as adjunct treatment to LEA-1 inhibitors or terminal complement blocking agents

The data presented herein detail two pathogenic mechanisms for RBC clearance and anemia in PNH which can be targeted, separately or in combination, by distinct classes of therapeutic agents: the intravascular hemolysis initiated predominantly, though not exclusively, by LEA-1 and thus expected to be effectively prevented by a LEA-1-blocking agent, and extravascular hemolysis due to C3b opsonization driven predominantly by LEA-2, and thus effectively prevented by a LEA-2-blocking agent.

It is well documented that both intravascular and extravascular mechanisms of hemolysis lead to anemia in PNH patients (Risitano et al., *Blood* 113:4094-4100 (2009)). Therefore, it is expected that a LEA-1-blocking agent that prevents intravascular hemolysis in combination with a LEA-2 blocking agent that primarily prevents extravascular hemolysis will be more effective than either agent alone in preventing the anemia that develops in PNH patients. In fact, the combination of LEA-1- and LEA-2-blocking agents is expected to prevent all relevant mechanisms of complement initiation in PNH and thus block all symptoms of anemia in PNH.

It is also known that C5-blocking agents (such as eculizumab) effectively block intravascular hemolysis but do not interfere with opsonization. This leaves some anti-C5-treated PNH patients with substantial residual anemia due to extravascular hemolysis mediated by LEA-2 that remains untreated. Therefore, it is expected that a C5-blocking agent (such as eculizumab) that prevents intravascular hemolysis in combination with a LEA-2 blocking agent that reduces extravascular hemolysis will be more effective than either agent alone in preventing the anemia that develops in PNH patients.

Other agents that block the terminal amplification loop of the complement system leading to C5 activation and MAC deposition (including, but not limited to agents that block properdin, factor B or factor D or enhance the inhibitory activity of factor I, factor

H or other complement inhibitory factors) are also expected to inhibit intravascular hemolysis. However, these agents are not expected to interfere with LEA-2-mediated opsonization in PNH patients. This leaves some PNH patients treated with such agents with substantial residual anemia due to extravascular hemolysis mediated by LEA-2 that remains untreated. Therefore, it is expected that treatment with such agents that prevent intravascular hemolysis in combination with a LEA-2-blocking agent that minimizes extravascular hemolysis will be more effective than either agent alone in preventing the anemia that develops in PNH patients. In fact, the combination of such agents and a LEA-2 blocking agent is expected to prevent all relevant mechanisms of RBC destruction in PNH and thus block all symptoms of anemia in PNH.

        viii.   <u>Use of LEA-1 and LEA-2 multiple, bispecific or pan-specific antibodies to treat PNH</u>

As detailed above, the use of a combination of pharmacologic agents that individually block LEA-1 and LEA-2, and thus in combination block all complement activation events that mediate the intravascular as well as the extravascular hemolysis, is expected to provide the best clinical outcome for PNH patients. This outcome can be achieved for example, by co-administration of an antibody that has LEA-1-blocking activity together with an antibody that has LEA-2-blocking activity. In some embodiments, LEA-1- and LEA-2-blocking activities are combined into a single molecular entity, and that such entity with combined LEA-1- and LEA-2-blocking activity will effectively block intravascular as well as the extravascular hemolysis and prevent anemia in PNH. Such an entity may comprise or consist of a bispecific antibody where one antigen-combining site specifically recognizes MASP-1 and blocks LEA-1 and diminishes LEA-2 and the second antigen-combining site specifically recognizes MASP-2 and further blocks LEA-2. Alternatively, such an entity may consist of a bispecific monoclonal antibody where one antigen-combining site specifically recognizes MASP-3 and thus blocks LEA-1 and the second antigen-combining site specifically recognizes MASP-2 and blocks LEA-2. Such an entity may optimally consist of a bispecific monoclonal antibody where one antigen-combining site specifically recognizes both MASP-1 and MASP-3 and thus blocks LEA-1 and diminishes LEA-2 while the second antigen-combining site specifically recognized MASP-2 and further blocks LEA-2. Based on the similarities in the overall protein sequence and architecture, it can also be envisioned that a conventional antibody with two identical binding sites can be developed

that specifically binds to MASP-1 and to MASP-2 and to MASP-3 in a functional manner, thus achieving functional blockade of LEA-1 and LEA-2. Such an antibody with pan-MASP inhibitory activity is expected to block both the intravascular as well as the extravascular hemolysis and thus effectively treat the anemia in PNH patients.

IV.   MASP INHIBITORY AGENTS

With the recognition that the lectin pathway of complement is composed of two major complement activation arms, LEA-1 and LEA-2, and that there also is a lectin-independent complement activation arm, comes the realization that it would be highly desirable to specifically inhibit one or more of these effector arms that cause a pathology associated with PNH without completely shutting down the immune defense capabilities of complement (i.e., leaving the classical pathway intact). This would leave the C1q-dependent complement activation system intact to handle immune complex processing and to aid in host defense against infection.

i.   Compositions for inhibiting LEA-1-mediated complement activation

As described herein, the inventors have unexpectedly discovered that activation of LEA-1, leading to lysis, is MASP-3-dependent. As further described herein, under physiological conditions, MASP-3-dependent LEA-1 activation also contributes to opsonization, thereby providing an additive effect with LEA-2-mediated complement activation. As demonstrated in Example 7, in the presence of Ca^{++}, factor D is not required, as MASP-3 can drive activation of LEA-1 in factor $D^{-/-}$ sera. MASP-3, MASP-1, and HTRA-1 are able to convert pro-factor D to active factor D. Likewise, MASP-3 activation appears, in many instances, to be dependent on MASP-1, since MASP-3 (in contrast to MASP-1 and MASP-2) is not an auto-activating enzyme and is incapable of converting into its active form without the help of MASP-1 (Zundel, S. et al., *J.Immunol.* 172: 4342-4350 (2004); Megyeri et al., *J. Biol. Chem.* 288:8922–8934 (2013). As MASP-3 does not autoactivate and, in many instances, requires the activity of MASP-1 to be converted into its enzymatically active form, the MASP-3-mediated activation of the alternative pathway C3 convertase C3Bb can either be inhibited by targeting the MASP-3 zymogen or already-activated MASP-3, or by targeting MASP-1-mediated activation of MASP-3, or both, since, in many instances, in the absence of MASP-1 functional activity, MASP-3 remains in its zymogen form and is not capable of driving LEA-1 through direct formation of the alternative pathway C3 convertase (C3bBb).

Therefore, in one aspect of the invention, the preferred protein component to target in the development of therapeutic agents to specifically inhibit LEA-1 is an inhibitor of MASP-3 (including inhibitors of MASP-1-mediated MASP-3 activation (e.g., a MASP-1 inhibitor that inhibits MASP-3 activation)).

In accordance with the foregoing, in one aspect, the invention provides methods of inhibiting the adverse effects of LEA-1 (i.e., hemolysis and opsonization) in a subject suffering from PNH, or at risk for developing PNH, comprising administering to the subject a pharmaceutical composition comprising an amount of a MASP-3 inhibitory agent effective to inhibit MASP-3-dependent complement activation and a pharmaceutically acceptable carrier.

MASP-3 inhibitory agents are administered in an amount effective to inhibit MASP-3-dependent complement activation in a living subject suffering from, or at risk for developing, PNH. In the practice of this aspect of the invention, representative MASP-3 inhibitory agents include: molecules that inhibit the biological activity of MASP-3, including molecules that inhibit at least one or more of the following: lectin MASP-3-dependent activation of factor B, lectin MASP-3-dependent activation of pro-factor D, MASP-3-dependent, lectin-independent activation of factor B, and MASP-3-dependent, lectin-independent activation of pro-factor D (such as small-molecule inhibitors, MASP-3 antibodies and fragments thereof, or blocking peptides which interact with MASP-3 or interfere with a protein-protein interaction), and molecules that decrease the expression of MASP-3 (such as MASP-3 antisense nucleic acid molecules, MASP-3 specific RNAi molecules and MASP-3 ribozymes). A MASP-3 inhibitory agent may effectively block MASP-3 protein-to-protein interactions, interfere with MASP-3 dimerization or assembly, block Ca^{++} binding, interfere with the MASP-3 serine protease active site, or reduce MASP-3 protein expression, thereby preventing MASP-3 from activating LEA-1-mediated, or lectin-independent, complement activation. The MASP-3 inhibitory agents can be used alone as a primary therapy or in combination with other therapeutics as an adjuvant therapy to enhance the therapeutic benefits of other medical treatments, as further described herein.

In one embodiment, the MASP-3 inhibitory agent specifically binds to a portion of MASP-3 (SEQ ID NO:8) with a binding affinity of at least 10 times greater than to other components in the complement system. In another embodiment, a MASP-3 inhibitory agent specifically binds to a portion of MASP-3 (SEQ ID NO:8) with a binding

affinity of at least 100 times greater than to other components in the complement system. In one embodiment, the MASP-3 inhibitory agent specifically binds to the serine protease domain of MASP-3 (aa 450-711 of SEQ ID NO:8) and inhibits MASP-3-dependent complement activation, with the proviso that the inhibitory agent does not bind to the serine protease domain of MASP-1 (SEQ ID NO:10), and it does not bind to the serine protease domain of MASP-2 (SEQ ID NO:5). In one embodiment, the MASP-3 inhibitory agent is a MASP-3 monoclonal antibody, or fragment thereof, that specifically binds to MASP-3.

In another embodiment, the MASP-3 inhibitory agent specifically binds to a portion of MASP-1 (SEQ ID NO:10) with a binding affinity of at least 10 times greater than to other components in the complement system, and inhibits MASP-1-mediated activation of MASP-3. In another embodiment, the MASP-3 inhibitory agent specifically binds to a portion of MASP-1 (SEQ ID NO:10) with a binding affinity of at least 100 times greater than to other components (i.e., polypeptides, or fragments thereof) in the complement system, and inhibits MASP-1-mediated activation of MASP-3. In some embodiments, the MASP-3 inhibitory agent specifically binds to the serine protease domain of MASP-1 (aa 449-694 of SEQ ID NO:10) and inhibits MASP-1-mediated activation of MASP-3, with the proviso that the inhibitory agent does not bind to the serine protease domain of MASP-2 (SEQ ID NO:5), and it does not bind to the serine protease domain of MASP-3 (SEQ ID NO:8). In one embodiment, the MASP-3 inhibitory agent is a MASP-1 monoclonal antibody, or fragment thereof, that specifically binds to MASP-1 and inhibits MASP-1-mediated activation of MASP-3. In some embodiments, the MASP-3 inhibitory agent that binds to MASP-1 inhibits MASP-1-mediated activation of MASP-3 and further inhibits MASP-1-mediated maturation of factor D.

In another embodiment, the MASP-3 inhibitory agent binds to a portion of MASP-3 (SEQ ID ON:8) and also binds to a portion of MASP-1 (SEQ ID NO:10), with the proviso that the inhibitory agent does not bind to MASP-2 (SEQ ID NO:5), or MAp19 (SEQ ID NO:3). In one embodiment, the MASP-3 inhibitory agent binds to a portion of MASP-3 (SEQ ID ON:8) and also binds to a portion of MASP-1 (SEQ ID NO:10), with the proviso that the inhibitory agent does not bind to MASP-2 (SEQ ID NO:5) or MAp19 (SEQ ID NO:3). In one embodiment, the MASP-3 inhibitory agent binds to a portion of MASP-3 (SEQ ID ON:8) and also binds to a portion of MASP-1 (SEQ ID NO:10), with

the proviso that the inhibitory agent does not bind to MASP-2 (SEQ ID NO:5), MAp19 (SEQ ID NO:3), or MAp44 (SEQ ID NO:11), thereby providing allowing for a lower effective dose for inhibiting MASP-3-dependent complement activation due to the lack of binding to MAp44, which is present at a high concentration in human serum.

In one embodiment, the MASP-3 inhibitory agent is a MASP-1/MASP-3 dual inhibitory agent that binds to an epitope within the amino acid region that is conserved between MASP-1 and MASP-3, such as the CUBI-CCP2 domain (aa 25-432 of SEQ ID NO:10), as illustrated in **FIGURES 3-5**. In one embodiment, the MASP-3 inhibitory agent is a MASP-1/MASP-3 dual inhibitory agent that binds to an epitope within the amino acid region that is conserved between MASP-1 and MASP-3, with the proviso that the inhibitory agent does not bind to MAp44, such as the CCP domain (aa 367-432 of SEQ ID NO:10). In another embodiment, the MASP-3 inhibitory agent is a bispecific inhibitory agent, such as a bispecific monoclonal antibody, that specifically binds to an epitope on the MASP-3 protein (SEQ ID NO:8) and an epitope on the MASP-1 protein (SEQ ID NO:10). In some embodiments, the MASP-3 inhibitory agent is a bispecific monoclonal antibody that binds to the serine protease domain of MASP-1 (aa 449-694 of SEQ ID NO:10) and also binds to a domain in the serine protease of MASP-3 (aa 450-711 of SEQ ID NO:8).

The binding affinity of the MASP-3 inhibitory agents can be determined using a suitable binding assay.

The inhibition of MASP-3-dependent complement activation is characterized by at least one of the following changes in a component of the complement system that occurs as a result of administration of a MASP-3 inhibitory agent in accordance with the methods of the invention: the inhibition of LEA-1-mediated complement activation (inhibition of hemolysis and/or opsonization); inhibition of lectin-independent conversion of factor B; inhibition of lectin-independent conversion of factor D, inhibition of MASP-3 serine protease substrate-specific cleavage, the reduction of hemolysis (measured, for example as described in Example 5) or the reduction of C3 cleavage and C3b deposition (measured, for example, as described in Example 4 and Example 11).

In some embodiments, the MASP-3 inhibitory agents selectively inhibit MASP-3-dependent complement activation (i.e., LEA-1-mediated complement activation and/or lectin-independent conversion of factor B and/or lectin-independent conversion of factor D), leaving the C1q-dependent complement activation system functionally intact.

In some embodiments, the MASP-3 inhibitory agents are antibodies, or fragments thereof, including MASP-3 antibodies and MASP-3 binding fragments thereof, MASP-1 antibodies and fragments thereof, natural and synthetic peptides, or small-molecules. In some embodiments, the MASP-3 inhibitory agents are small-molecule protease inhibitors that are selective for MASP-1, or selective for MASP-3, or selective for MASP-1 and MASP-3.

ii.   Compositions for inhibiting activation of LEA-2

As described herein, LEA-2-mediated complement activation is MASP-2-dependent, leading to opsonization and/or lysis. Therefore, the preferred protein component to target in the development of therapeutic agents to specifically inhibit the LEA-2 lectin-dependent complement system is MASP-2. Several proteins have been shown to bind to, or interact with MASP-2 through protein-to-protein interactions. For example, MASP-2 is known to bind to, and form calcium-dependent complexes with, the lectin proteins MBL, H-ficolin and L-ficolin and collectin-11. Ma Y., et al., *J Innate Immun*. Epub Dec 4 (2012). Each MASP-2/lectin complex has been shown to activate complement through the MASP-2-dependent cleavage of proteins C4 and C2 (Ikeda, K., et al., *J. Biol. Chem.* *262*:7451-7454, (1987); Matsushita, M., et al., *J. Exp. Med.* *176*:1497-2284, (2000); Matsushita, M., et al., *J. Immunol.* *168*:3502-3506, (2002)). Studies have shown that the CUB1-EGF domains of MASP-2 are essential for the association of MASP-2 with MBL (Thielens, N.M., et al., *J. Immunol. 166*:5068, (2001)). It has also been shown that the CUB1EGFCUBII domains mediate dimerization of MASP-2, which is required for formation of an active MBL complex (Wallis, R., et al., *J. Biol. Chem. 275*:30962-30969, 2000). Therefore, MASP-2 inhibitory agents can be identified that bind to or interfere with MASP-2 target regions known to be important for MASP-2-dependent complement activation.

In accordance with the foregoing, in one aspect, the invention provides methods of inhibiting the adverse effects of LEA-2-mediated complement activation in a subject suffering from PNH, or at risk for developing PNH, comprising administering to the subject a pharmaceutical composition comprising an amount of a MASP-2 inhibitory agent effective to inhibit MASP-2-dependent complement activation and a pharmaceutically acceptable carrier.

MASP-2 inhibitory agents are administered in an amount effective to inhibit MASP-2-dependent LEA-2 in a living subject suffering from, or at risk for developing

PNH. In the practice of this aspect of the invention, representative MASP-2 inhibitory agents include: molecules that inhibit the biological activity of MASP-2 (such as small-molecule inhibitors, MASP-2 antibodies or blocking peptides that interact with MASP-2 or interfere with a protein-protein interaction), and molecules that decrease the expression of MASP-2 (such as MASP-2 antisense nucleic acid molecules, MASP-2 specific RNAi molecules and MASP-2 ribozymes), thereby preventing MASP-2 from activating LEA-2.

A MASP-2 inhibitory agent may effectively block MASP-2 protein-to-protein interactions, interfere with MASP-2 dimerization or assembly, block Ca^{++} binding, interfere with the MASP-2 serine protease active site, or may reduce MASP-2 protein expression, thereby preventing MASP-2 from activating LEA-2. The MASP-2 inhibitory agents can be used alone as a primary therapy or in combination with other therapeutics as an adjuvant therapy to enhance the therapeutic benefits of other medical treatments, as further described herein.

In one embodiment, the MASP-2 inhibitory agent specifically binds to a portion of MASP-2 (SEQ ID NO:5) with a binding affinity of at least 10 times greater than to other antigens in the complement system. In another embodiment, the MASP-2 inhibitory agent specifically binds to a portion of MASP-2 (SEQ ID NO:5) with a binding affinity of at least 100 times greater than to other antigens in the complement system. In one embodiment, the MASP-2 inhibitory agent specifically binds to at least one of (i) the CCP1-CCP2 domain (aa 300-431 of SEQ ID NO:5) or the serine protease domain of MASP-2 (aa 445-682 of SEQ ID NO:5) and inhibits MASP-2-dependent complement activation, with the proviso that the inhibitory agent does not bind to the serine protease domain of MASP-1 (SEQ ID NO:10), and it does not bind to the serine protease domain of MASP-3 (SEQ ID NO:8). In one embodiment, the MASP-2 inhibitory agent is a MASP-2 monoclonal antibody, or fragment thereof that specifically binds to MASP-2.

The binding affinity of the MASP-2 inhibitory agent can be determined using a suitable binding assay.

The inhibition of MASP-2-dependent complement activation is characterized by at least one of the following changes in a component of the complement system that occurs as a result of administration of a MASP-2 inhibitory agent in accordance with the methods of the invention: the inhibition of the generation or production of MASP-2-dependent complement-activation-system products C4b, C3a, C5a and/or C5b-9 (MAC) (measured, for example, as described in Example 2 of US Patent No. 7,919,094),

the reduction of C4 cleavage and C4b deposition (measured, for example as described in Example 8 or Example 9), or the reduction of C3 cleavage and C3b deposition (measured, for example, as described in Example 11).

In some embodiments, the MASP-2 inhibitory agents selectively inhibit MASP-2 complement activation (i.e., LEA-2), leaving the C1q-dependent complement activation system functionally intact.

In some embodiments, the MASP-2 inhibitory agents are antibodies, or fragments thereof, including MASP-2 antibodies and MASP-2 binding fragments thereof, natural and synthetic peptides, or small-molecules. In some embodiments, the MASP-2 inhibitory agents are small-molecule protease inhibitors that are selective for MASP-2.

iii.   Compositions for inhibiting LEA-1-mediated complement activation and LEA-2-mediated complement activation

In another aspect, the invention provides methods for inhibiting the adverse effects of LEA-1 and inhibiting the adverse effects of LEA-2 in a subject suffering from one or more aspects of PNH, or at risk for developing PNH.

In one embodiment, this aspect of the invention is directed to a method of increasing the survival of red blood cells in a subject suffering from PNH, comprising administering to the subject a composition comprising an amount of at least one of a MASP-1 inhibitory agent and/or a MASP-3 inhibitory agent effective to increase the survival of red blood cells.

In one embodiment, the composition comprises a MASP-1 inhibitory agent. In one embodiment, the MASP-1 inhibitory agent inhibits MASP-3-mediated complement activation and also inhibits MASP-2-mediated complement activation.

In one embodiment, the composition comprises a MASP-3 inhibitory agent. In one embodiment, the MASP-3 inhibitory agent inhibits at least one of: lectin MASP-3-dependent activation of factor B; lectin MASP-3-dependent activation of factor D; MASP-3-dependent, lectin-independent activation of factor B; and/or MASP-3-dependent, lectin-independent, activation of factor D.

In one embodiment, the composition comprises a MASP-1 inhibitory agent and a MASP-3 inhibitory agent.

In some embodiments, the method further comprises administering to the subject a composition comprising a MASP-2 inhibitory agent.

In another embodiment, this aspect of the invention comprises administering to a subject suffering from PNH a pharmaceutical composition comprising an amount of a MASP-2 inhibitory agent effective to inhibit MASP-2-dependent complement activation and an amount of a MASP-3 inhibitory agent effective to inhibit MASP-3-dependent complement activation and a pharmaceutically acceptable carrier.

In some embodiments, the composition comprises a single agent that inhibits both LEA-1 and LEA-2 (i.e., a dual MASP-2/MASP-3 inhibitory agent, a dual MASP-1/MASP-2 inhibitory agent, a bispecific MASP-2/MASP-3 inhibitory agent, a bispecific MASP-1/MASP-2 inhibitory agent, or a pan-MASP-1/2/3 inhibitory agent or a trispecific MASP-1/2/3 inhibitory agent). In some embodiments, the composition comprises a combination of LEA-1 and LEA-2 inhibitory agents, for example, a combination of dual inhibitory agents plus a single inhibitory agent, a combination of bispecific inhibitory agents plus a single inhibitory agent, or a combination of any of the MASP-1, MASP-2 and/or MASP-3 inhibitory agents as described herein that in combination inhibit both LEA-1 and LEA-2, as further described herein.

In one embodiment, the invention provides a pharmaceutical composition for inhibiting both LEA-1 and LEA-2, comprising at least one MASP-3 inhibitory agent and at least one MASP-2 inhibitory agent and a pharmaceutically acceptable carrier. In one embodiment, the pharmaceutical composition comprises a combination of a first molecule that is a MASP-3 inhibitory agent and a second molecule that is a MASP-2 inhibitory agent. In another embodiment, the pharmaceutical composition comprises a single molecular entity that includes activity as a MASP-3 inhibitory agent and activity as a MASP-2 inhibitory agent (i.e., an inhibitory agent that inhibits both MASP-2-mediated LEA-2 activation and MASP-3-mediated LEA-1 activation). In one embodiment, the inhibitory agent is a MASP-2/MASP-3 dual inhibitory agent that binds to an epitope within an amino acid region that is conserved between MASP-2 (SEQ ID NO:5) and MASP-3 (SEQ ID NO:8), such as the serine protease domain, for example the N-terminal region of the beta chain (e.g., the first 150 aa of the N-terminal region of the beta chain of SEQ ID NO5 and SEQ ID NO:8:), as shown in **FIGURES 4, 6 and 7C**. In one embodiment, the inhibitory agent is a bispecific inhibitory agent, such as a bispecific monoclonal antibody, that specifically binds to an epitope on the MASP-2 protein (SEQ ID NO:5) and an epitope on the MASP-3 protein (SEQ ID NO:8). In some embodiments, the inhibitory agent is a bispecific monoclonal antibody that binds to at least one of the

CCP1-CCP2 domain of MASP-2 (aa 300-431 of SEQ ID NO:5) or the serine protease domain of MASP-2 (aa 445-682 of SEQ ID NO:5) and also binds to an epitope in the serine protease of MASP-3 (aa 450-711 of SEQ ID NO:8).

In another embodiment, the invention provides a composition for inhibiting both LEA-1 and LEA-2, comprising an inhibitory agent that inhibits both MASP-2-mediated LEA-2 activation and MASP-1-mediated activation of MASP-3, thereby inhibiting MASP-3-mediated LEA-1 activation (and optionally also inhibiting the MASP-1-mediated maturation of factor D). In one embodiment, the inhibitory agent is a MASP-1/MASP-2 dual inhibitory agent that binds to an epitope within an amino acid region that is conserved between MASP-1 (SEQ ID NO:10) and MASP-2 (SEQ ID NO:5), such as the serine protease domain, as shown in **FIGURES 4, 6** and **7A**. In one embodiment, the inhibitory agent is a bispecific inhibitory agent, such as a bispecific monoclonal antibody, that specifically binds to an epitope on the MASP-1 protein (SEQ ID NO:10) and an epitope on the MASP-2 protein (SEQ ID NO:5). In some embodiments, the inhibitory agent is a bispecific monoclonal antibody that binds to the serine protease domain of MASP-1 (aa 449-694 of SEQ ID NO:10) and also binds to at least one of the CCP1-CCP2 domain of MASP-2 (aa 300-431 of SEQ ID NO:5) or the serine protease domain of MASP-2 (aa 445-682 of SEQ ID NO:5).

In another embodiment, the invention provides a composition for inhibiting both LEA-1 and LEA-2, comprising an inhibitory agent that inhibits MASP-2-mediated LEA-2 activation, MASP-3-mediated LEA-1 activation by directly binding to MASP-3 and also inhibits MASP-1-mediated activation of MASP-3, thereby inhibiting MASP-3-mediated LEA-1 activation (and optionally also inhibiting the MASP-1-mediated maturation of factor D). In one embodiment, the inhibitory agent is a pan-MASP inhibitor that binds to an amino acid region that is conserved between MASP-1 (SEQ ID NO:10), MASP-2 (SEQ ID NO:5) and MASP-3 (SEQ ID NO:8), for example a conserved region in the CUBI-EGF-CUB2 domain, as shown in **FIGURES 4** and **5**. As illustrated in **FIGURES 4** and **5**, there are numerous patches of identity shared between MASP-1, MASP-2 and MASP-3 in the CUBI-EGF-CUBII domains, thereby allowing for the generation of pan-specific MASP antibodies. In some embodiments, the pan-specific MASP antibody can bind to an epitope within the CUB2 domain of MASP-1 (aa 185-296 of SEQ ID NO:10), MASP-2 (aa 184-295 of SEQ ID NO:5) and MASP-3 (aa 185-296 of SEQ ID NO:8). It is noted that a pan-specific MASP inhibitor that binds to CUBI-EGF

of MASP-1, MASP-2 and MASP-3 would also bind to MAp19 and MAp44, therefore the effective therapeutic dosage of such an inhibitor would be adjusted to a higher level to compensate for this binding. It is further noted that a pan-specific MASP inhibitor that binds to the CUBII domain of MASP-1, MASP-2 and MASP-3 would also bind to MAp44, therefore the effective therapeutic dosage of such an inhibitor would be adjusted to a higher level to compensate for this binding.

In one embodiment, the inhibitory agent is a trispecific MASP-1/2/3 inhibitor that binds to an epitope on the MASP-1 protein (SEQ ID NO:10), an epitope on the MASP-2 protein (SEQ ID NO:5) and an epitope on the MASP-3 protein (SEQ ID NO:8). In some embodiments, the inhibitory agent is a trispecific monoclonal antibody that binds to the serine protease domain of MASP-1 (aa 449-694 of SEQ ID NO:10), binds to at least one of the CCP1-CCP2 domain of MASP-2 (aa 300-431 of SEQ ID NO:5) or the serine protease domain of MASP-2 (aa 445-682 of SEQ ID NO:5) and also binds to an epitope in the serine protease of MASP-3 (aa 450-711 of SEQ ID NO:8).

Exemplary inhibitory agents for inhibiting LEA-1, LEA-2 or LEA-1 and LEA-2 are described below in **TABLE 2**.

TABLE 2: MASP Inhibitory Agents

Type of MASP inhibitor	Inhibitor Binding domain(s)	Cross-reactivity*	Assay for inhibitory activity	Therapeutic Utility
MASP-3 specific	MASP-3 serine protease domain (aa 450-711 of SEQ ID NO:8)	Binds to MASP-3; not to MASP-1; MASP-2; MAp44 or MAp19	Inhibition of MASP-3 serine protease substrate-specific cleavage; LEA-1 inhibition, assay for inhibition of factor D activation; inhibition of hemolysis of non-human RBCs by human serum	Inhibit LEA-1-mediated complement activation (inhibit lysis and opsonization)
MASP-2 specific	MASP-2 CCP1-CCP2 domain (aa 300-431 of SEQ ID NO:5); or MASP-2 serine protease domain (aa 445-682 of SEQ ID NO:5)	Binds to MASP-2; not to MASP-1; MASP-3; MAP19 or MAp44	Inhibition of MASP-2-specific protease substrate-specific cleavage, LEA-2 inhibition	Inhibit LEA-2-mediated complement activation (inhibit opsonization and/or lysis)
MASP-1 specific	MASP-1 serine protease domain (aa449-694 of SEQ ID NO:10)	Binds to MASP-1; not to MASP-2, MASP-3, MAp44 or MAp19	Inhibition of MASP-1-specific protease substrate-specific cleavage; LEA-1 and LEA2 inhibition, Assay for inhibition of factor D activation; assay for restoration of AP-1 activity in factor D depleted serum supplemented with pro-factor D	Inhibit LEA-1 and LEA-2mediated complement activation (inhibit lysis and/or opsonization)
MASP-2/MASP-3 dual inhibitor (one antibody binds to conserved region)	Region of serine protease domain conserved between	Binds MASP-2 and MASP-3; not MASP-1, MAp44, or MAp19.	Assay for MASP-2- and MASP-3 protease substrate-specific cleavage, inhibition of	Inhibit LEA-1 and LEA-2-mediated complement activation (inhibit lysis and/or

	MASP-2 and MASP-3, especially the N-terminal region of beta chain (first 150aa)	-3-	LEA-1 and LEA-2	opsonization)
MASP-1/3 dual inhibitor that excludes MAp44	MASP-1/3 CCP2 domain (aa 367-432 of SEQ ID NO:10)	Binds MASP-1 and MASP-3; not MAp44, MASP-2, or MAp19	Assay for MASP-3 and MASP-1 protease substrate-specific cleavage and inhibition of factor D activation, LEA-1 and LEA-2 inhibition	Inhibit LEA-1- and LEA-2- mediated complement activation (inhibit lysis and/or opsonization)
MASP-1/3 dual inhibitor that includes MAp44	MASP-1/3 CUBI-CCP1 domain (aa25-363 of SEQ ID NO:10)	Binds MASP-1, MASP-3, and MAp44; not MASP-2 or MAp19	Assay for MASP-3 and MASP-1 protease substrate-specific cleavage and inhibition of factor D activation, LEA-1 and LEA-2 inhibition	Inhibit LEA-1- and LEA-2- mediated complement activation (inhibit lysis and/or opsonization)
MASP-1/2 dual inhibitor	Region of serine protease domain conserved between MASP-1 and MASP-2	Binds MASP-1 and MASP-2; not MASP-3, MAp19 or MAp44	Assay for inhibition of MASP-1 and MASP-2 serine protease substrate-specific cleavage; LEA-1 and LEA-2 inhibition	Inhibit LEA-1-and LEA-2-mediated complement activation (inhibit lysis and/or opsonization)
MASP-1/2/3 pan inhibitor	Conserved region of CUB1-EGF-CUB2, especially CUB2 domain (common interaction site)	In addition to MASP-1/2/3 would bind to MAp44, and possibly Map19	Assay for MASP-1-, MASP-2- and MASP-3-specific protease substrate-specific cleavage and inhibition of factor D activation; inhibition of LEA-1 and LEA-2	Inhibit LEA-1- and LEA-2- mediated complement activation (inhibit lysis and/or opsonization)

MASP-2/MASP-3 bispecific inhibitor	MASP-2-specific binding to CCP1-CCP2 (aa 300-431 of SEQ ID NO:5); or MASP-2 serine protease domain (aa 445-682 of SEQ ID NO:5) and MASP-3-specific binding to serine protease domain (aa 450-711 of SEQ ID NO:8)	Binds MASP-2 and MASP-3; not MASP-1, MAp44 or MAp19	Assay for MASP-2- and MASP-3-specific protease substrate-specific cleavage, inhibition of LEA-1 and LEA-2	Inhibit LEA-1- and LEA-2-mediated complement activation (inhibit lysis and/or opsonization)
MASP-1/MASP-2 bispecific inhibitor	MASP-1 serine protease domain (aa449-694 of SEQ ID NO:10), and MASP-2-specific binding to CCP1-CCP2 (aa 300-431 of SEQ ID NO:5); or MASP-2 serine protease domain (aa 445-682 of SEQ ID NO:5)	Binds to MASP-1 and to MASP-2; not MASP-3, MAp19 or MAp44	Assay for inhibition of MASP-1- and MASP-2-specific serine protease substrate-specific cleavage; LEA-1 and LEA-2 inhibition	Inhibit LEA-1- and LEA-2-mediated complement activation (inhibit lysis and/or opsonization)
MASP-1/MASP-3 bispecific	MASP-1 serine protease domain (aa449-694 of SEQ ID NO:10) and MASP-3-specific	Binds to MASP-1 and MASP-3; not to MASP-2, MAp44 or MAp19	Assay for MASP-1 and MASP-3 protease substrate-specificcleavage and inhibition of factor D activation, LEA-1 and LEA-2	Inhibit LEA-1- and LEA-2-mediated complement activation (inhibit lysis and/or opsonization)

	binding to serine protease domain (aa 450-711 of SEQ ID NO:8)		inhibition	
MASP-1/MASP-2/MASP-3 trispecific	MASP-1 serine protease domain, MASP-2 serine protease domain or CCP-CCP2 domain and MASP-3 serine protease domain	Binds to MASP-1 and MASP-2 and MASP-3; not MAp19 or MAp44	Assay for MASP-1-, MASP-2- and MASP-3- protease substrate-specific cleavage and inhibition of factor D activation, inhibition of LEA-1 and LEA-2	Inhibit LEA-1- and LEA-2-mediated complement activation (inhibit lysis and/or opsonization)

*With regard to cross-reactivity column as set forth in **TABLE 2**, the designated MASP inhibitor binds to the inhibitor binding domain with a binding affinity of at least 10 times greater (e.g., at least 20 times, at least 50 times or at least 100 times greater) than to the other complement components (*i.e.*, polypeptides or fragments thereof) listed as "not" binding.

In some embodiments, the composition comprises a combination of LEA-1 and LEA-2 inhibitory agents, for example, a combination of single inhibitory agents as described above and shown in **TABLE 2**. For example, in one embodiment, the composition comprises a combination of a MASP-1 antibody and a MASP-2 antibody. In one embodiment, the composition comprises a combination of a MASP-1 antibody and a MASP-3 antibody. In one embodiment, the composition comprises a combination of a MASP-2 antibody and a MASP-3 antibody. In one embodiment, the composition comprises a combination of a MASP-1, and MASP-2 and a MASP-3 antibody. In some embodiments, the methods of the invention comprise administration of a single composition comprising a combination of inhibitory agents. In other embodiments, the methods of the invention comprise co-administering separate compositions.

In some embodiments, the compositions comprise a combination of a dual inhibitory agent plus a single inhibitory agent (i.e., a MASP-2/3 dual inhibitor plus a MASP-1 inhibitor; a MASP-1/3 dual inhibitor plus a MASP-2 inhibitor; or a MASP-1/2

dual inhibitor plus a MASP-3 inhibitor). In other embodiments, the methods of the invention comprise co-administering separate compositions comprising a dual inhibitor and a single inhibitor.

In some embodiments, the compositions comprise a combination of a bispecific inhibitory agent plus a single inhibitory agent (i.e., a MASP-2/3 bispecific inhibitor plus a MASP-1 inhibitor; a MASP-1/3 bispecific inhibitor plus a MASP-2 inhibitor; or a MASP-1/2 bispecific inhibitor plus a MASP-3 inhibitor). In other embodiments, the methods of the invention comprise co-administering separate compositions comprising a bispecific inhibitor and a single inhibitor.

In accordance with various embodiments of the invention, it is noted that MASP-3 inhibitory agents and/or MASP-2 inhibitory agents and/or MASP-1 inhibitory agents would be used to clear the target protein from the plasma as compared to a C5 antibody which must localize to the site of action.

V.   MASP ANTIBODIES

In some embodiments of this aspect of the invention, the MASP inhibitory agent comprises a MASP antibody (e.g., a MASP-1, MASP-2 or MASP-3 antibody) that inhibits at least one of the LEA-1 and/or LEA-2 complement activation pathways. The MASP antibodies useful in this aspect of the invention include polyclonal, monoclonal or recombinant antibodies derived from any antibody producing mammal and may be multispecific (i.e., bispecific or trispecific), chimeric, humanized, fully human, anti-idiotype, and antibody fragments. Antibody fragments include Fab, Fab', $F(ab)_2$, $F(ab')_2$, Fv fragments, scFv fragments and single-chain antibodies as further described herein.

MASP antibodies can be screened for the ability to inhibit the LEA-1 or LEA-2-dependent complement activation system using the assays described herein. Several MASP-1, MASP-2 and MASP-3 antibodies have been described in the literature and some have been newly generated, some of which are listed below in **TABLE 3**. These exemplary MASP antibodies can be screened for the ability to inhibit the LEA-1- and/or LEA-2-dependent complement activation system using the assays described herein. For example, as described in Examples 11-13 herein, anti-rat MASP-2 Fab2 antibodies have been identified that block MASP-2-dependent complement activation. As further described in Example 14, fully human MASP-2 scFv antibodies have been identified that

block MASP-2-dependent complement activation. As further described in Example 15, MASP-3 antibodies have been generated. Once a MASP antibody is identified that functions as an inhibitor of LEA-1 or LEA-2, it can be used in a pharmaceutical composition as descrbed herein, and it can also be used to generate bispecific and trispecific inhibitory agents, as set forth in **TABLE 2** and further described herein (see e.g., Example 8).

TABLE 3: MASP-1, MASP-2 and MASP-3 SPECIFIC ANTIBODIES

TARGET	ANTIGEN	ANTIBODY TYPE	REFERENCE
MASP-2	Recombinant MASP-2	Rat Polyclonal	Peterson, S.V., et al., *Mol. Immunol.* 37:803-811, 2000
MASP-2	Recombinant human CCP1/2-SP fragment (MoAb 8B5)	Rat MoAb (subclass IgG1)	Moller-Kristensen, M., et al., *J. of Immunol. Methods* 282:159-167, 2003
MASP-2	Recombinant human MAp19 (MoAb 6G12) (cross-reacts with MASP-2)	Rat MoAb (subclass IgG1)	Moller-Kristensen, M., et al., *J. of Immunol. Methods* 282:159-167, 2003
MASP-2	hMASP-2	Mouse MoAb (S/P) Mouse MoAb (N-term)	Peterson, S.V., et al., *Mol. Immunol.* 35:409, April 1998
MASP-2	hMASP-2 (CCP1-CCP2-SP domain	rat MoAb: Nimoab101, produced by hybridoma cell line 03050904 (ECACC)	WO 2004/106384

TARGET	ANTIGEN	ANTIBODY TYPE	REFERENCE
MASP-2	hMASP-2 (full-length his-tagged)	murine MoAbs: NimoAb104, produced by hybridoma cell line M0545YM035 (DSMZ) NimoAb108, produced by hybridoma cell line M0545YM029 (DSMZ) NimoAb109 produced by hybridoma cell line M0545YM046 (DSMZ) NimoAb110 produced by hybridoma cell line M0545YM048 (DSMZ)	WO 2004/106384
MASP-2	Rat MASP-2 (full-length)	MASP-2 Fab2 antibody fragments	Examples 11-12
MASP-2	hMASP-2 (full-length)	Fully human scFv clones	Example 14
MASP-1	hMASP-1 (full-length)	Mouse MoAbs: MoaAbs1E2 and 2B11 produced by hybridoma line 1E2 and 2B11 (do not cross-react with MASP-2). Both abs recognize the heavy chain common to both MASP-1 and MASP-3	Terai I. et al., *Clin Exp Immunol* 110:317-323 (1997); MoAb1E2: Commercially available from Hycult Biotech Cat#HM2092 MoAb2B11: commercially available from Hycult Biotech: Cat#HM2093

TARGET	ANTIGEN	ANTIBODY TYPE	REFERENCE
MASP-1	hMASP-1 (full-length)	Mouse MoAb 4C2	Endo M. et al., *Nephrol Dial Transplant* 13:1984-1990 (1998)
MASP-1	hMASP-1 (full-length)	MASP-1 chicken abs	Example 15
MASP-3	hMASP-3 (full-length)	Mouse MoAbs: MoAb-7D8;MoAb-7B7;MoAb-8B3; and MoAb-5H3 MoAb-7D8 and mAb-5H3 are MASP-3-specific, others cross-react with MASP-1	Skjoedt et al., *Immunobiology* 215(11):921-31 (2010)
MASP-3	hMASP-3 (full-length)	Rat MoAb 38:12-3, Does not recognize MASP-1	Moller-Kristensen et al., *Int Immunol* 19:141 (2007); Commercially available from Hycult Biotech: Cat #HM2216
MASP-3	hMASP-3 (full-length)	MASP-3 chicken abs	Example 15

i.   MASP antibodies with reduced effector function

In some embodiments of this aspect of the invention, the MASP antibodies described herein have reduced effector function in order to reduce inflammation that may arise from the activation of the classical complement pathway. The ability of IgG molecules to trigger the classical complement pathway has been shown to reside within the Fc portion of the molecule (Duncan, A.R., et al., *Nature 332*:738-740 (1988)). IgG molecules in which the Fc portion of the molecule has been removed by enzymatic cleavage are devoid of this effector function (see Harlow, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, New York, 1988). Accordingly, antibodies with reduced effector function can be generated as the result of lacking the Fc portion of the molecule by having a genetically engineered Fc sequence that minimizes effector function, or being of either the human IgG_2 or IgG_4 isotype.

Antibodies with reduced effector function can be produced by standard molecular biological manipulation of the Fc portion of the IgG heavy chains as described in Jolliffe et al., *Int'l Rev. Immunol. 10*:241-250, (1993), and Rodrigues et al., *J. Immunol. 151*:6954-6961, (1998). Antibodies with reduced effector function also include human IgG2 and IgG4 isotypes that have a reduced ability to activate complement and/or interact with Fc receptors (Ravetch, J.V., et al., *Annu. Rev. Immunol. 9*:457-492, (1991); Isaacs, J.D., et al., *J. Immunol. 148*:3062-3071, 1992; van de Winkel, J.G., et al., *Immunol. Today 14*:215-221, (1993)). Humanized or fully human antibodies specific to human MASP-1, MASP-2 or MASP-3 (including dual, pan, bispecific or trispecific antibodies) comprised of IgG2 or IgG4 isotypes can be produced by one of several methods known to one of ordinary skilled in the art, as described in Vaughan, T.J., et al., *Nature Biotechnical 16*:535-539, (1998).

ii.   Production of MASP antibodies

MASP-1, MASP-2 or MASP-3 antibodies can be produced using MASP-1, MASP-2 or MASP-3 polypeptides (e.g., full-length MASP-1, MASP-1 or MASP-3) or using antigenic MASP-1, 2 or 3 epitope-bearing peptides (e.g., a portion of the MASP-2 polypeptide). Immunogenic peptides may be as small as five amino acid residues. For example, the MASP-2 polypeptide including the entire amino acid sequence of SEQ ID NO:5 may be used to induce MASP-2 antibodies useful in the method of the invention. Particular MASP domains known to be involved in protein-protein interactions, such as the CUBI, and CUBI-EGF domains, as well as the region encompassing the

serine-protease active site, for example, as set forth in **TABLE 2**, may be expressed as recombinant polypeptides using methods well known in the art and used as antigens. In addition, peptides comprising a portion of at least 6 amino acids of the MASP-1 polypeptide (SEQ ID NO:10), or of the MASP-2 polypeptide (SEQ ID NO:5) or of the MASP-3 polypeptide (SEQ ID NO:8) are also useful to induce MASP-1, MASP-2 or MASP-3 antibodies, respectively. The MASP peptides and polypeptides used to raise antibodies may be isolated as natural polypeptides, or recombinant or synthetic peptides and catalytically inactive recombinant polypeptides. Antigens useful for producing MASP antibodies also include fusion polypeptides, such as fusions of a MASP polypeptide or a portion thereof with an immunoglobulin polypeptide or with maltose-binding protein. The polypeptide immunogen may be a full-length molecule or a portion thereof. If the polypeptide portion is hapten-like, such portion may be advantageously joined or linked to a macromolecular carrier (such as keyhole limpet hemocyanin (KLH), bovine serum albumin (BSA) or tetanus toxoid) for immunization.

iii.   Polyclonal antibodies

Polyclonal antibodies against MASP-1, MASP-2 or MASP-3 can be prepared by immunizing an animal with MASP-1, MASP-2 or MASP-3 polypeptide or an immunogenic portion thereof using methods well known to those of ordinary skill in the art. See, for example, Green et al., "Production of Polyclonal Antisera," in *Immunochemical Protocols* (Manson, ed.). The immunogenicity of a MASP polypeptide can be increased through the use of an adjuvant, including mineral gels, such as aluminum hydroxide or Freund's adjuvant (complete or incomplete), surface active substances such as lysolecithin, pluronic polyols, polyanions, oil emulsions, KLH and dinitrophenol. Polyclonal antibodies are typically raised in animals such as horses, cows, dogs, chicken, rats, mice, rabbits, guinea pigs, goats, or sheep. Alternatively, a MASP antibody useful in the present invention may also be derived from a subhuman primate. General techniques for raising diagnostically and therapeutically useful antibodies in baboons may be found, for example, in Goldenberg et al., International Patent Publication No. WO 91/11465, and in Losman, M.J., et al., *Int. J. Cancer 46*:310, (1990). Sera containing immunologically active antibodies are then produced from the blood of such immunized animals using standard procedures well known in the art.

iv.   Monoclonal antibodies

In some embodiments, the LEA-2 inhibitory agent is a MASP-2 monoclonal antibody and/or the LEA-1 inhibitory agent is a MASP-3 monoclonal antibody or a MASP-1 monoclonal antibody. As described above, in some embodiments, MASP-1, MASP-2 and MASP-3 monoclonal antibodies are highly specific, being directed against a single MASP-1, MASP-2 or MASP-3 epitope. As used herein, the modifier "monoclonal" indicates the character of the antibody as being obtained from a substantially homogenous population of antibodies, and is not to be construed as requiring production of the antibody by any particular method. Monoclonal antibodies can be obtained using any technique that provides for the production of antibody molecules by continuous cell lines in culture, such as the hybridoma method described by Kohler, G., et al., *Nature 256*:495, (1975), or they may be made by recombinant DNA methods (see, e.g., U.S. Patent No. 4,816,567 to Cabilly). Monoclonal antibodies may also be isolated from phage antibody libraries using the techniques described in Clackson, T., et al., *Nature 352*:624-628, (1991), and Marks, J.D., et al., *J. Mol. Biol. 222*:581-597, (1991). Such antibodies can be of any immunoglobulin class including IgG, IgM, IgE, IgA, IgD and any subclass thereof.

For example, monoclonal antibodies can be obtained by injecting a suitable mammal (e.g., a BALB/c mouse) with a composition comprising a MASP-1 polypeptide, a MASP-2 polypeptide or a MASP-3 polypeptide, or portion thereof. After a predetermined period of time, splenocytes are removed from the mouse and suspended in a cell culture medium. The splenocytes are then fused with an immortal cell line to form a hybridoma. The formed hybridomas are grown in cell culture and screened for their ability to produce a monoclonal antibody against MASP-1, MASP-2 or MASP-3. (See also *Current Protocols in Immunology*, Vol. 1., John Wiley & Sons, pages 2.5.1-2.6.7, 1991.)

Human monoclonal antibodies may be obtained through the use of transgenic mice that have been engineered to produce specific human antibodies in response to antigenic challenge. In this technique, elements of the human immunoglobulin heavy and light chain locus are introduced into strains of mice derived from embryonic stem cell lines that contain targeted disruptions of the endogenous immunoglobulin heavy chain and light chain loci. The transgenic mice can synthesize human antibodies specific for human antigens, such as the MASP-2 antigens described herein, and the mice can be used

to produce human MASP-2 antibody-secreting hybridomas by fusing B-cells from such animals to suitable myeloma cell lines using conventional Kohler-Milstein technology. Methods for obtaining human antibodies from transgenic mice are described, for example, by Green, L.L., et al., *Nature Genet. 7*:13, 1994; Lonberg, N., et al., *Nature 368*:856, 1994; and Taylor, L.D., et al., *Int. Immun. 6*:579, 1994.

Monoclonal antibodies can be isolated and purified from hybridoma cultures by a variety of well-established techniques. Such isolation techniques include affinity chromatography with Protein-A Sepharose, size-exclusion chromatography, and ion-exchange chromatography (see, for example, Coligan at pages 2.7.1-2.7.12 and pages 2.9.1-2.9.3; Baines et al., "Purification of Immunoglobulin G (IgG)," in *Methods in Molecular Biology*, The Humana Press, Inc., Vol. 10, pages 79-104, 1992).

Once produced, polyclonal, monoclonal or phage-derived antibodies are first tested for specific MASP-1, MASP-2 or MASP-3 binding or, where desired, dual MASP-1/3, MASP-2/3 or MASP-1/2 binding. Methods for determining whether an antibody binds to a protein antigen and/or the affinity for an antibody to a protein antigen are known in the art. For example, the binding of an antibody to a protein antigen can be detected and/or quantified using a variety of techniques such as, but not limited to, Western blot, dot blot, plasmon surface resonance method (e.g., BIAcore system; Pharmacia Biosensor AB, Uppsala, Sweden and Piscataway, NJ), or enzyme-linked immunosorbent assays (ELISA). See, e.g., Harlow and Lane (1988) "Antibodies: A Laboratory Manual" Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N. Y.; Benny K. C. Lo (2004) "Antibody Engineering: Methods and Protocols," Humana Press (ISBN: 1588290921); Borrebaek (1992) "Antibody Engineering, A Practical Guide," W.H. Freeman and Co., NY; Borrebaek (1995) "Antibody Engineering," 2nd Edition, Oxford University Press, NY, Oxford; Johne et al. (1993), Immunol. Meth. 160:191-198; Jonsson et al. (1993) Ann. Biol. Clin. 51: 19-26; and Jonsson et al. (1991) Biotechniques 11:620-627. See also, U.S. Patent No. 6,355,245.

The affinity of MASP monoclonal antibodies can be readily determined by one of ordinary skill in the art (see, e.g., Scatchard, A., *NY Acad. Sci. 51*:660-672, 1949). In one embodiment, the MASP-1, MASP-2 or MASP-3 monoclonal antibodies useful for the methods of the invention bind to MASP-1, MASP-2, or MASP-3 with a binding affinity of <100 nM, preferably <10 nM and most preferably <2 nM.

Once antibodies are identified that specifically bind to MASP-1, MASP-2 or MASP-3, the MASP-1, MASP-2 or MASP-3 antibodies are tested for the ability to function as a LEA-1 inhibitory agent or a LEA-2 inhibitory agent in one of several functional assays, for example as described in **TABLE 2**. For example, antibodies identified that specifically bind to MASP-2 are tested for the ability to function as a LEA-2 inhibitory agent in one of several assays, such as, for example, as described in **TABLE 2** (e.g., a lectin-specific C4 cleavage assay (such as the assay described in Example 8 or Example 9), or a C3b deposition assay (such as the assay described in Example 4 or Example 11)). As a further example, antibodies identified that specifically bind to MASP-1 or MASP-3 are tested for the ability to function as a LEA-1 inhibitory agent in one of several assays, such as, for example, as described in **TABLE 2** (e.g., the reduction of hemolysis, measured, for example as described in Example 5, or the reduction of C3 cleavage and C3b deposition, measured, for example, as described in Example 4 and Example 11).

v.   Chimeric/humanized antibodies

Monoclonal antibodies useful in the method of the invention include chimeric antibodies in which a portion of the heavy and/or light chain is identical with or homologous to corresponding sequences in antibodies derived from a particular species or belonging to a particular antibody class or subclass, while the remainder of the chain(s) is identical with or homologous to corresponding sequences in antibodies derived from another species or belonging to another antibody class or subclass, as well as fragments of such antibodies (U.S. Patent No. 4,816,567, to Cabilly; and Morrison, S.L., et al., *Proc. Nat'l Acad. Sci. USA 81*:6851-6855, (1984)).

One form of a chimeric antibody useful in the invention is a humanized monoclonal MASP-1, MASP-2 or MASP-3 antibody. Humanized forms of non-human (e.g., murine) antibodies are chimeric antibodies, which contain minimal sequence derived from non-human immunoglobulin. Humanized monoclonal antibodies are produced by transferring the non-human (e.g., mouse) complementarity determining regions (CDR), from the heavy and light variable chains of the mouse immunoglobulin into a human variable domain. Typically, residues of human antibodies are then substituted in the framework regions of the non-human counterparts. Furthermore, humanized antibodies may comprise residues that are not found in the recipient antibody or in the donor antibody. These modifications are made to further refine antibody

performance. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains in which all or substantially all of the hypervariable loops correspond to those of a non-human immunoglobulin and all or substantially all of the Fv framework regions are those of a human immunoglobulin sequence. The humanized antibody optionally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin. For further details, see Jones, P.T., et al., *Nature 321*:522-525, (1986); Reichmann, L., et al., *Nature 332*:323-329, (1988); and Presta, *Curr. Op. Struct. Biol. 2*:593-596, (1992).

The humanized antibodies useful in the invention include human monoclonal antibodies including at least a MASP-1, MASP-2, or MASP-3 binding CDR3 region. In addition, the Fc portions may be replaced so as to produce IgA or IgM as well as human IgG antibodies. Such humanized antibodies will have particular clinical utility because they will specifically recognize human MASP-1, MASP-2 or MASP-3 but will not evoke an immune response in humans against the antibody itself. Consequently, they are better suited for *in vivo* administration in humans, especially when repeated or long-term administration is necessary.

Techniques for producing humanized monoclonal antibodies are also described, for example, by Jones, P.T., et al., *Nature 321*:522, (1986); Carter, P., et al., *Proc. Nat'l. Acad. Sci. USA 89*:4285, (1992); Sandhu, J.S., *Crit. Rev. Biotech. 12*:437, (1992); Singer, I.I., et al., *J. Immun. 150*:2844, (1993); Sudhir (ed.), *Antibody Engineering Protocols,* Humana Press, Inc., (1995); Kelley, "Engineering Therapeutic Antibodies," in *Protein Engineering: Principles and Practice*, Cleland et al. (eds.), John Wiley & Sons, Inc., pages 399-434, (1996); and by U.S. Patent No. 5,693,762, to Queen, 1997. In addition, there are commercial entities that will synthesize humanized antibodies from specific murine antibody regions, such as Protein Design Labs (Mountain View, CA).

    vi.   <u>Recombinant antibodies</u>

MASP-1, MASP-2 or MASP-3 antibodies can also be made using recombinant methods. For example, human antibodies can be made using human immunoglobulin expression libraries (available for example, from Stratagene, Corp., La Jolla, CA) to produce fragments of human antibodies (V_H, V_L, Fv, Factor D, Fab or F(ab')$_2$). These fragments are then used to construct whole human antibodies using techniques similar to those for producing chimeric antibodies.

vii.   Anti-idiotype antibodies

Once MASP-1, MASP-2 or MASP-3 antibodies are identified with the desired inhibitory activity, these antibodies can be used to generate anti-idiotype antibodies that resemble a portion of MASP-1, MASP-2 or MASP-3 using techniques that are well known in the art. See, e.g., Greenspan, N.S., et al., *FASEB J.* 7:437, (1993). For example, antibodies that bind to MASP-2 and competitively inhibit a MASP-2 protein interaction required for complement activation can be used to generate anti-idiotypes that resemble the MBL binding site on MASP-2 protein and therefore bind and neutralize a binding ligand of MASP-2 such as, for example, MBL.

viii.   Immunoglobulin fragments

The MASP-2 and MASP-3 inhibitory agents useful in the method of the invention encompass not only intact immunoglobulin molecules but also the well known fragments including Fab, Fab', F(ab)$_2$, F(ab')$_2$ and Fv fragments, scFv fragments, diabodies, linear antibodies, single-chain antibody molecules and multispecific (e.g., bispecific and trispecific) antibodies formed from antibody fragments.

It is well known in the art that only a small portion of an antibody molecule, the paratope, is involved in the binding of the antibody to its epitope (see, e.g., Clark, W.R., *The Experimental Foundations of Modern Immunology*, Wiley & Sons, Inc., NY, 1986). The pFc' and Fc regions of the antibody are effectors of the classical complement pathway but are not involved in antigen binding. An antibody from which the pFc' region has been enzymatically cleaved, or which has been produced without the pFc' region, is designated an F(ab')$_2$ fragment and retains both of the antigen binding sites of an intact antibody. An isolated F(ab')$_2$ fragment is referred to as a bivalent monoclonal fragment because of its two antigen binding sites. Similarly, an antibody from which the Fc region has been enzymatically cleaved, or which has been produced without the Fc region, is designated a Fab fragment, and retains one of the antigen binding sites of an intact antibody molecule.

Antibody fragments can be obtained by proteolytic hydrolysis, such as by pepsin or papain digestion of whole antibodies by conventional methods. For example, antibody fragments can be produced by enzymatic cleavage of antibodies with pepsin to provide a 5S fragment denoted F(ab')$_2$. This fragment can be further cleaved using a thiol reducing agent to produce 3.5S Fab' monovalent fragments. Optionally, the cleavage reaction can be performed using a blocking group for the sulfhydryl groups that result from cleavage

-88-

of disulfide linkages. As an alternative, an enzymatic cleavage using pepsin produces two monovalent Fab fragments and an Fc fragment directly. These methods are described, for example, U.S. Patent No. 4,331,647 to Goldenberg; Nisonoff, A., et al., *Arch. Biochem. Biophys. 89*:230, (1960); Porter, R.R., *Biochem. J. 73*:119, (1959); Edelman, et al., in *Methods in Enzymology 1*:422, Academic Press, (1967); and by Coligan at pages 2.8.1-2.8.10 and 2.10.-2.10.4.

In some embodiments, the use of antibody fragments lacking the Fc region are preferred to avoid activation of the classical complement pathway which is initiated upon binding Fc to the Fcγ receptor. There are several methods by which one can produce a monoclonal antibody that avoids Fcγ receptor interactions. For example, the Fc region of a monoclonal antibody can be removed chemically using partial digestion by proteolytic enzymes (such as ficin digestion), thereby generating, for example, antigen-binding antibody fragments such as Fab or F(ab)$_2$ fragments (Mariani, M., et al., *Mol. Immunol. 28*:69-71, (1991)). Alternatively, the human γ4 IgG isotype, which does not bind Fcγ receptors, can be used during construction of a humanized antibody as described herein. Antibodies, single chain antibodies and antigen-binding domains that lack the Fc domain can also be engineered using recombinant techniques described herein.

ix.   Single-chain antibody fragments

Alternatively, one can create single peptide chain binding molecules specific for MASP-1, MASP-2 or MASP-3 in which the heavy and light chain Fv regions are connected. The Fv fragments may be connected by a peptide linker to form a single-chain antigen binding protein (scFv). These single-chain antigen binding proteins are prepared by constructing a structural gene comprising DNA sequences encoding the V_H and V_L domains which are connected by an oligonucleotide. The structural gene is inserted into an expression vector, which is subsequently introduced into a host cell, such as *E. coli*. The recombinant host cells synthesize a single polypeptide chain with a linker peptide bridging the two V domains. Methods for producing scFvs are described for example, by Whitlow, et al., "Methods: A Companion to Methods in Enzymology" *2*:97, (1991); Bird, et al., *Science 242*:423, (1988); U.S. Patent No. 4,946,778, to Ladner; Pack, P., et al., *Bio/Technology 11*:1271, (1993).

As an illustrative example, a MASP-3-specific scFv can be obtained by exposing lymphocytes to MASP-3 polypeptide *in vitro* and selecting antibody display libraries in

phage or similar vectors (for example, through the use of immobilized or labeled MASP-3 protein or peptide). Genes encoding polypeptides having potential MASP-3 polypeptide binding domains can be obtained by screening random peptide libraries displayed on phage or on bacteria such as *E. coli*. These random peptide display libraries can be used to screen for peptides which interact with MASP-3. Techniques for creating and screening such random peptide display libraries are well known in the art (U.S. Patent No. 5,223,409, to Lardner; U.S. Patent No. 4,946,778, to Ladner; U.S. Patent No. 5,403,484, to Lardner; U.S. Patent No. 5,571,698, to Lardner; and Kay et al., *Phage Display of Peptides and Proteins* Academic Press, Inc., 1996) and random peptide display libraries and kits for screening such libraries are available commercially, for instance from CLONTECH Laboratories, Inc. (Palo Alto, Calif.), Invitrogen Inc. (San Diego, Calif.), New England Biolabs, Inc. (Beverly, Mass.), and Pharmacia LKB Biotechnology Inc. (Piscataway, N.J.).

Another form of a MASP-3 antibody fragment useful in this aspect of the invention is a peptide coding for a single complementarity-determining region (CDR) that binds to an epitope on a MASP-3 antigen and inhibits MASP-3-dependent complement activation (i.e., LEA-1). Another form of a MASP-1 antibody fragment useful in this aspect of the invention is a peptide coding for a single complementarity-determining region (CDR) that binds to an epitope on a MASP-1 antigen and inhibits MASP-3-dependent complement activation (i.e., LEA-1). Another form of a MASP-2 antibody fragment useful in this aspect of the invention is a peptide coding for a single complementarity-determining region (CDR) that binds to an epitope on a MASP-2 antigen and inhibits MASP-2-dependent complement activation (i.e., LEA-2).

CDR peptides ("minimal recognition units") can be obtained by constructing genes encoding the CDR of an antibody of interest. Such genes are prepared, for example, by using the polymerase chain reaction to synthesize the variable region from RNA of antibody-producing cells (see, for example, Larrick et al., *Methods: A Companion to Methods* in *Enzymology 2*:106, (1991); Courtenay-Luck, "Genetic Manipulation of Monoclonal Antibodies," in *Monoclonal Antibodies: Production, Engineering and Clinical Application*, Ritter et al. (eds.), page 166, Cambridge University Press, (1995); and Ward et al., "Genetic Manipulation and Expression of Antibodies," in *Monoclonal Antibodies: Principles and Applications*, Birch et al. (eds.), page 137, Wiley-Liss, Inc., 1995).

The MASP antibodies described herein are administered to a subject in need thereof to inhibit LEA-1, LEA-2 or a combination of LEA-1 and LEA-2 complement activation. In some embodiments, the MASP inhibitory agent is a high-affinity human or humanized monoclonal MASP-1, MASP-2 or MASP-3 antibody with reduced effector function.

      x.   <u>Bispecific antibodies</u>

The MASP-2 and MASP-3 inhibitory agents useful in the method of the invention encompass multispecific (i.e., bispecific and trispecific) antibodies. Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. As described above and shown in **TABLE 2**, in one embodiment, the method comprises the use of a bispecific antibody comprising a binding specificity for MASP-2 (e.g., binding to at least one of CCP1-CCP2 or serine protease domain of MASP-2) and a binding specificity for MASP-3 (e.g., binding to the serine protease domain of MASP-3). In another embodiment, the method comprises the use of a bispecific antibody comprising a binding specificity for MASP-1 (e.g., binding to the serine protease domain of MASP-1) and a binding specificity for MASP-2 (e.g., binding to at least one of CCP1-CCP2 or serine protease domain of MASP-2). In another embodiment, the method comprises the use of a bispecific antibody comprising a binding specificity for MASP-1 (e.g., binding to the serine protease domain of MASP-1) and a binding specificity for MASP-3 (e.g., binding to the serine protease domain of MASP-3). In another embodiment, the method comprises the use of a trispecific antibody comprising a binding specificity for MASP-1 (e.g., binding to the serine protease domain of MASP-1), a binding specificity for MASP-2 (e.g., binding to at least one of CCP1-CCP2 or serine protease domain of MASP-2) and a binding specificity for MASP-3 (e.g., binding to the serine protease domain of MASP-3).

Methods for making bispecific antibodies are within the purview of those skilled in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities (Milstein and Cuello, *Nature* 305:537-539 (1983)). Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, including at least part of the hinge, C_H2, and C_H3 regions. DNAs encoding the immunoglobulin

heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of illustrative currently known methods for generating bispecific antibodies see, e.g., Suresh et al., *Methods in Enzymology* 121:210 (1986); WO96/27011; Brennan et al., *Science* 229:81 (1985); Shalaby et al., *J. Exp. Med.* 175:217-225 (1992); Kostelny et al., *J. Immunol.* 148(5):1547-1553 (1992); Hollinger et al. *Proc. Natl. Acad. Sci* USA 90:6444-6448 (1993); Gruber et al., *J. Immunol.* 152:5368 (1994); and Tutt et al., *J. Immunol.* 147:60 (1991). Bispecific antibodies also include cross-linked or heteroconjugate antibodies. Heteroconjugate antibodies may be made using any convenient cross -linking methods. Suitable crosslinking agents are well known in the art, and are disclosed in U.S. Pat. No. 4,676,980, along with a number of cross-linking techniques.

Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. (See, e.g., Kostelny et al. *J.Immunol.* 148(5):1547-1553 (1992)). The "diabody" technology described by Hollinger et al. *Proc. Natl. Acad. Sci* USA 90:6444-6448 (1993), has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (VH) connected to a light-chain variable domain (VL) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the VH and VL domains of one fragment are forced to pair with the complementary VL and VH domains of another fragment, thereby forming two antigen-binding sites. Bispecific diabodies, as opposed to bispecific whole antibodies, may also be particularly useful because they can be readily constructed and expressed in E. coli. Diabodies (and many other polypeptides such as antibody fragments) of appropriate binding specificities can be readily selected using phage display (WO94/13804) from libraries. If one arm of the diabody is to be kept constant, for instance, with a specificity directed against antigen X, then a library can be made where the other arm is varied and an antibody of appropriate specificity selected.

Another strategy for making bispecific antibody fragments by the use of single-chain Fv (scFv) dimers has also been reported. (See, e.g., Gruber et al. *J. Immunol.*, 152:5368 (1994)). Alternatively, the antibodies can be "linear antibodies" as described in, e.g., Zapata et al., *Protein Eng.* 8(10):1057-1062 (1995). Briefly described, these

antibodies comprise a pair of tandem Factor D segments (V_H-C_HI-V_H-C_HI) which form a pair of antigen binding regions. Linear antibodies can be bispecific or monospecific. The methods of the invention also embrace the use of variant forms of bispecific antibodies such as the tetravalent dual variable domain immunoglobulin (DVD-Ig) molecules described in Wu et al., *Nat Biotechnol* 25:1290-1297 (2007). The DVD-Ig molecules are designed such that two different light chain variable domains (VL) from two different parent antibodies are linked in tandem directly or via a short linker by recombinant DNA techniques, followed by the light chain constant domain. Methods for generating DVD-Ig molecules from two parent antibodies are further described in, e.g., WO08/024188 and WO07/024715, the disclosures of each of which are incorporated herein by reference in their entirety.

VI.   NON-PEPTIDE INHIBITORS

In some embodiments, the MASP-3 or MASP-2 inhibitory agent is a MASP-3 or a MASP-2 or a MASP-1 inhibitory peptide or a non-peptide inhibitor of MASP-3, or of MASP-2 or of MASP-1. Non-peptide MASP inhibitory agents may be administered to the subject systemically, such as by intra-arterial, intravenous, intramuscular, subcutaneous or other parenteral administration, or by oral administration. The MASP inhibitory agent may be administered periodically over an extended period of time for treatment or control of a chronic condition, or may be by single or repeated administration in the period before, during or following acute trauma or injury.

VII. PHARMACEUTICAL COMPOSITIONS AND DELIVERY METHODS

Dosing

In another aspect, the invention provides compositions for inhibiting the adverse effects of MASP-3-dependent complement activation in a subject suffering from a hemolytic disease, such as PNH, comprising administering to the subject a composition comprising an amount of a MASP-3 inhibitory agent effective to inhibit MASP-3-dependent complement activation and a pharmaceutically acceptable carrier. In some embodiments, the method further comprises administering a composition comprising a MASP-2 inhibitory agent. The MASP-3 and MASP-2 inhibitory agents can be administered to a subject in need thereof, at therapeutically effective doses to treat or ameliorate conditions associated with MASP-3-dependent complement activation (LEA-

1), and optionally also MASP-2-dependent complement activation (LEA-2). A therapeutically effective dose refers to the amount of the MASP-3 inhibitory agent, or a combination of a MASP-3 inhibitory agent and a MASP-2 inhibitory agent sufficient to result in amelioration of symptoms of the condition.

Toxicity and therapeutic efficacy of MASP-3 and MASP-2 inhibitory agents can be determined by standard pharmaceutical procedures employing experimental animal models. Using such animal models, the NOAEL (no observed adverse effect level) and the MED (the minimally effective dose) can be determined using standard methods. The dose ratio between NOAEL and MED effects is the therapeutic ratio, which is expressed as the ratio NOAEL/MED. MASP-3 inhibitory agents and MASP-2 inhibitory agents that exhibit large therapeutic ratios or indices are most preferred. The data obtained from the cell culture assays and animal studies can be used in formulating a range of dosages for use in humans. The dosage of the MASP-3 inhibitory agent and MASP-2 inhibitory agent preferably lies within a range of circulating concentrations that include the MED with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized.

For any compound formulation, the therapeutically effective dose can be estimated using animal models. For example, a dose may be formulated in an animal model to achieve a circulating plasma concentration range that includes the MED. Quantitative levels of the MASP-3 inhibitory agent or MASP-2 inhibitory agent in plasma may also be measured, for example, by high performance liquid chromatography.

In addition to toxicity studies, effective dosage may also be estimated based on the amount of target MASP protein present in a living subject and the binding affinity of the MASP-3 or MASP-2 inhibitory agent.

It has been reported that MASP-1 levels in normal human subjects is present in serum in levels in the range of from 1.48 to 12.83 μg/mL (Terai I. et al, *Clin Exp Immunol* 110:317-323 (1997); Theil et al., *Clin. Exp. Immunol.* 169:38 (2012)). The mean serum MASP-3 concentrations in normal human subjects has been reported to be in the range of about 2.0 to 12.9 μg/mL (Skjoedt M et al., *Immunobiology* 215(11):921-31 (2010); Degn et al., *J. Immunol Methods*, 361-37 (2010); Csuka et al., *Mol. Immunol.* 54:271 (2013). It has been shown that MASP-2 levels in normal human subjects is present in serum in low levels in the range of 500 ng/mL, and MASP-2 levels in a particular subject can be determined using a quantitative assay for MASP-2 described in

Moller-Kristensen M., et al., *J. Immunol. Methods 282*:159-167 (2003) and Csuka et al., *Mol. Immunol.* 54:271 (2013).

Generally, the dosage of administered compositions comprising MASP-3 inhibitory agents or MASP-2 inhibitory agents varies depending on such factors as the subject's age, weight, height, sex, general medical condition, and previous medical history. As an illustration, MASP-3 inhibitory agents or MASP-2 inhibitory agents (such as MASP-3 antibodies, MASP-1 antibodies or MASP-2 antibodies), can be administered in dosage ranges from about 0.010 to 100.0 mg/kg, preferably 0.010 to 10 mg/kg, preferably 0.010 to 1.0 mg/kg, more preferably 0.010 to 0.1 mg/kg of the subject body weight. In some embodiments, MASP-2 inhibitory agents (such as MASP-2 antibodies) are administered in dosage ranges from about preferably 0.010 to 10 mg/kg, preferably 0.010 to 1.0 mg/kg, more preferably 0.010 to 0.1 mg/kg of the subject body weight. In some embodiments, MASP-1 inhibitory agents (such as MASP-1 antibodies) or MASP-3 inhibitory agents (such as MASP-3 antibodies) are administered in dosage ranges from about 0.010 to 100.0 mg/kg, preferably 0.010 to 10 mg/kg, preferably 0.010 to 1.0 mg/kg, more preferably 0.010 to 0.1 mg/kg of the subject body weight.

Therapeutic efficacy of MASP-3 inhibitory compositions, optionally in combination with MASP-2 inhibitory compositions, or of MASP-1 inhibitory compositions, optionally in combination with MASP-2 inhibitory compositions, and methods of the present invention in a given subject, and appropriate dosages, can be determined in accordance with complement assays well known to those of skill in the art. Complement generates numerous specific products. During the last decade, sensitive and specific assays have been developed and are available commercially for most of these activation products, including the small activation fragments C3a, C4a, and C5a and the large activation fragments iC3b, C4d, Bb, and sC5b-9. Most of these assays utilize monoclonal antibodies that react with new antigens (neoantigens) exposed on the fragment, but not on the native proteins from which they are formed, making these assays very simple and specific. Most rely on ELISA technology, although radioimmunoassay is still sometimes used for C3a and C5a. These latter assays measure both the unprocessed fragments and their 'desArg' fragments, which are the major forms found in the circulation. Unprocessed fragments and $C5a_{desArg}$ are rapidly cleared by binding to cell surface receptors and are hence present in very low concentrations, whereas $C3a_{desArg}$ does not bind to cells and accumulates in plasma. Measurement of C3a provides a

sensitive, pathway-independent indicator of complement activation. Alternative pathway activation can be assessed by measuring the Bb fragment and/or measurement of factor D activation. Detection of the fluid-phase product of membrane attack pathway activation, sC5b-9, provides evidence that complement is being activated to completion. Because both the lectin and classical pathways generate the same activation products, C4a and C4d, measurement of these two fragments does not provide any information about which of these two pathways has generated the activation products.

The inhibition of MASP-3-dependent complement activation is characterized by at least one of the following changes in a component of the complement system that occurs as a result of administration of a MASP-3 inhibitory agent in accordance with the methods of the invention: the inhibition of LEA-1-mediated complement activation (inhibition of hemolysis and opsonization); inhibition of MASP-3 serine protease substrate-specific cleavage, the reduction of hemolysis (measured, for example as described in Example 5) or the reduction of C3 cleavage and C3b deposition (measured, for example, as described in Example 4 or Example 11).

The inhibition of MASP-2-dependent complement activation is characterized by at least one of the following changes in a component of the complement system that occurs as a result of administration of a MASP-2 inhibitory agent in accordance with the methods of the invention: the inhibition of the generation or production of MASP-2-dependent complement activation system products C4b, C3a, C5a and/or C5b-9 (MAC) (measured, for example, as described in measured, for example, as described in Example 2 of US Patent No. 7,919,094), the reduction of C4 cleavage and C4b deposition (measured, for example as described in Example 8 or Example 9), or the reduction of C3 cleavage and C3b deposition (measured, for example, as described in Example 11).

i.   Pharmaceutical carriers and delivery vehicles

In general, the MASP-3 inhibitory agent compositions and the MASP-2 inhibitory agent compositions of the present invention, or compositions comprising a combination of MASP-2 and MASP-3 inhibitory agents, may be combined with any other selected therapeutic agents, are suitably contained in a pharmaceutically acceptable carrier. The carrier is non-toxic, biocompatible and is selected so as not to detrimentally affect the biological activity of the MASP-3 inhibitory agent or the MASP-2 inhibitory agent (and any other therapeutic agents combined therewith). Exemplary pharmaceutically acceptable carriers for peptides are described in U.S. Patent No. 5,211,657 to Yamada.

The MASP antibodies useful in the invention, as described herein, may be formulated into preparations in solid, semi-solid, gel, liquid or gaseous forms such as tablets, capsules, powders, granules, ointments, solutions, depositories, inhalants and injections allowing for oral, parenteral or surgical administration. The invention also contemplates local administration of the compositions by coating medical devices and the like.

Suitable carriers for parenteral delivery via injectable, infusion or irrigation and topical delivery include distilled water, physiological phosphate-buffered saline, normal or lactated Ringer's solutions, dextrose solution, Hank's solution, or propanediol. In addition, sterile, fixed oils may be employed as a solvent or suspending medium. For this purpose any biocompatible oil may be employed including synthetic mono- or diglycerides. In addition, fatty acids such as oleic acid find use in the preparation of injectables. The carrier and agent may be compounded as a liquid, suspension, polymerizable or non-polymerizable gel, paste or salve.

The carrier may also comprise a delivery vehicle to sustain (i.e., extend, delay or regulate) the delivery of the agent(s) or to enhance the delivery, uptake, stability or pharmacokinetics of the therapeutic agent(s). Such a delivery vehicle may include, by way of non-limiting example, microparticles, microspheres, nanospheres or nanoparticles composed of proteins, liposomes, carbohydrates, synthetic organic compounds, inorganic compounds, polymeric or copolymeric hydrogels and polymeric micelles. Suitable hydrogel and micelle delivery systems include the PEO:PHB:PEO copolymers and copolymer/cyclodextrin complexes disclosed in WO 2004/009664 A2 and the PEO and PEO/cyclodextrin complexes disclosed in U.S. Patent Application Publication No. 2002/0019369 A1. Such hydrogels may be injected locally at the site of intended action, or subcutaneously or intramuscularly to form a sustained release depot.

Compositions of the present invention may be formulated for delivery subcutaneously, intra-muscularly, intravenously, intra-arterially or as an inhalant.

For intra-articular delivery, the MASP-3 inhibitory agent or the MASP-2 inhibitory agent may be carried in above-described liquid or gel carriers that are injectable, above-described sustained-release delivery vehicles that are injectable, or a hyaluronic acid or hyaluronic acid derivative.

For oral administration of non-peptidergic agents, the MASP-3 inhibitory agent or MASP-2 inhibitory agent may be carried in an inert filler or diluent such as sucrose, cornstarch, or cellulose.

For topical administration, the MASP-3 inhibitory agent or MASP-2 inhibitory agent may be carried in ointment, lotion, cream, gel, drop, suppository, spray, liquid or powder, or in gel or microcapsular delivery systems via a transdermal patch.

Various nasal and pulmonary delivery systems, including aerosols, metered-dose inhalers, dry powder inhalers, and nebulizers, are being developed and may suitably be adapted for delivery of the present invention in an aerosol, inhalant, or nebulized delivery vehicle, respectively.

For intrathecal (IT) or intracerebroventricular (ICV) delivery, appropriately sterile delivery systems (e.g., liquids; gels, suspensions, etc.) can be used to administer the present invention.

The compositions of the present invention may also include biocompatible excipients, such as dispersing or wetting agents, suspending agents, diluents, buffers, penetration enhancers, emulsifiers, binders, thickeners, flavoring agents (for oral administration).

ii.   Pharmaceutical carriers for antibodies and peptides

More specifically with respect to MASP antibodies, as described herein, exemplary formulations can be parenterally administered as injectable dosages of a solution or suspension of the compound in a physiologically acceptable diluent with a pharmaceutical carrier that can be a sterile liquid such as water, oils, saline, glycerol or ethanol. Additionally, auxiliary substances such as wetting or emulsifying agents, surfactants, pH buffering substances and the like can be present in compositions comprising MASP antibodies. Additional components of pharmaceutical compositions include petroleum (such as of animal, vegetable or synthetic origin), for example, soybean oil and mineral oil. In general, glycols such as propylene glycol or polyethylene glycol are preferred liquid carriers for injectable solutions.

The MASP antibodies can also be administered in the form of a depot injection or implant preparation that can be formulated in such a manner as to permit a sustained or pulsatile release of the active agents.

VIII. MODES OF ADMINISTRATION

The pharmaceutical compositions comprising the MASP-3 inhibitory agents or MASP-2 inhibitory agents may be administered in a number of ways depending on whether a local or systemic mode of administration is most appropriate for the condition

being treated. Further, the compositions of the present invention can be delivered by coating or incorporating the compositions on or into an implantable medical device.

  i.   <u>Systemic delivery</u>

  As used herein, the terms "systemic delivery" and "systemic administration" are intended to include but are not limited to oral and parenteral routes including intramuscular (IM), subcutaneous, intravenous (IV), intraarterial, inhalational, sublingual, buccal, topical, transdermal, nasal, rectal, vaginal and other routes of administration that effectively result in dispersement of the delivered agent to a single or multiple sites of intended therapeutic action. Preferred routes of systemic delivery for the present compositions include intravenous, intramuscular, subcutaneous, intraarterial and inhalational. It will be appreciated that the exact systemic administration route for selected agents utilized in particular compositions of the present invention will be determined in part to account for the agent's susceptibility to metabolic transformation pathways associated with a given route of administration. For example, peptidergic agents may be most suitably administered by routes other than oral.

  The MASP inhibitory antibodies, as described herein, can be delivered into a subject in need thereof by any suitable means. Methods of delivery of MASP antibodies and polypeptides include administration by oral, pulmonary, parenteral (e.g., intramuscular, intraperitoneal, intravenous (IV) or subcutaneous injection), inhalation (such as via a fine powder formulation), transdermal, nasal, vaginal, rectal, or sublingual routes of administration, and can be formulated in dosage forms appropriate for each route of administration.

  By way of representative example, MASP inhibitory antibodies and peptides can be introduced into a living body by application to a bodily membrane capable of absorbing the polypeptides, for example the nasal, gastrointestinal and rectal membranes. The polypeptides are typically applied to the absorptive membrane in conjunction with a permeation enhancer. (See, e.g., Lee, V.H.L., *Crit. Rev. Ther. Drug Carrier Sys.* 5:69, (1988); Lee, V.H.L., *J. Controlled Release 13*:213, (1990); Lee, V.H.L., Ed., *Peptide and Protein Drug Delivery,* Marcel Dekker, New York (1991); DeBoer, A.G., et al., *J. Controlled Release 13*:241, (1990). For example, STDHF is a synthetic derivative of fusidic acid, a steroidal surfactant that is similar in structure to the bile salts, and has been used as a permeation enhancer for nasal delivery. (Lee, W.A., *Biopharm. 22*, Nov./Dec. 1990.)

The MASP inhibitory antibodies as described herein may be introduced in association with another molecule, such as a lipid, to protect the polypeptides from enzymatic degradation. For example, the covalent attachment of polymers, especially polyethylene glycol (PEG), has been used to protect certain proteins from enzymatic hydrolysis in the body and thus prolong half-life (Fuertges, F., et al., *J. Controlled Release 11*:139, (1990)). Many polymer systems have been reported for protein delivery (Bae, Y.H., et al., *J. Controlled Release 9*:271, (1989); Hori, R., et al., *Pharm. Res. 6*:813, (1989); Yamakawa, I., et al., *J. Pharm. Sci. 79*:505, (1990); Yoshihiro, I., et al., *J. Controlled Release 10*:195, (1989); Asano, M., et al., *J. Controlled Release 9*:111, (1989); Rosenblatt, J., et al., *J. Controlled Release 9*:195, (1989); Makino, K., *J. Controlled Release 12*:235, (1990); Takakura, Y., et al., *J. Pharm. Sci. 78*:117, (1989); Takakura, Y., et al., *J. Pharm. Sci. 78*:219, (1989)).

Recently, liposomes have been developed with improved serum stability and circulation half-times (see, e.g., U.S. Patent No. 5,741,516, to Webb). Furthermore, various methods of liposome and liposome-like preparations as potential drug carriers have been reviewed (see, e.g., U.S. Patent No. 5,567,434, to Szoka; U.S. Patent No. 5,552,157, to Yagi; U.S. Patent No. 5,565,213, to Nakamori; U.S. Patent No. 5,738,868, to Shinkarenko; and U.S. Patent No. 5,795,587, to Gao).

For transdermal applications, the MASP inhibitory antibodies, as described herein, may be combined with other suitable ingredients, such as carriers and/or adjuvants. There are no limitations on the nature of such other ingredients, except that they must be pharmaceutically acceptable for their intended administration, and cannot degrade the activity of the active ingredients of the composition. Examples of suitable vehicles include ointments, creams, gels, or suspensions, with or without purified collagen. The MASP inhibitory antibodies may also be impregnated into transdermal patches, plasters, and bandages, preferably in liquid or semi-liquid form.

The compositions of the present invention may be systemically administered on a periodic basis at intervals determined to maintain a desired level of therapeutic effect. For example, compositions may be administered, such as by subcutaneous injection, every two to four weeks or at less frequent intervals. The dosage regimen will be determined by the physician considering various factors that may influence the action of the combination of agents. These factors will include the extent of progress of the condition being treated, the patient's age, sex and weight, and other clinical factors. The

dosage for each individual agent will vary as a function of the MASP-3 inhibitory agent or the MASP-2 inhibitory agent that is included in the composition, as well as the presence and nature of any drug delivery vehicle (e.g., a sustained release delivery vehicle). In addition, the dosage quantity may be adjusted to account for variation in the frequency of administration and the pharmacokinetic behavior of the delivered agent(s).

ii.   Local delivery

As used herein, the term "local" encompasses application of a drug in or around a site of intended localized action, and may include for example topical delivery to the skin or other affected tissues, ophthalmic delivery, intrathecal (IT), intracerebroventricular (ICV), intra-articular, intracavity, intracranial or intravesicular administration, placement or irrigation. Local administration may be preferred to enable administration of a lower dose, to avoid systemic side effects, and for more accurate control of the timing of delivery and concentration of the active agents at the site of local delivery. Local administration provides a known concentration at the target site, regardless of interpatient variability in metabolism, blood flow, etc. Improved dosage control is also provided by the direct mode of delivery.

Local delivery of a MASP-3 inhibitory agent or a MASP-2 inhibitory agent may be achieved in the context of surgical methods for treating a disease or condition, such as for example during procedures such as arterial bypass surgery, atherectomy, laser procedures, ultrasonic procedures, balloon angioplasty and stent placement. For example, a MASP-3 inhibitory agent or a MASP-2 inhibitory agent can be administered to a subject in conjunction with a balloon angioplasty procedure. A balloon angioplasty procedure involves inserting a catheter having a deflated balloon into an artery. The deflated balloon is positioned in proximity to the atherosclerotic plaque and is inflated such that the plaque is compressed against the vascular wall. As a result, the balloon surface is in contact with the layer of vascular endothelial cells on the surface of the blood vessel. The MASP-3 inhibitory agent or MASP-2 inhibitory agent may be attached to the balloon angioplasty catheter in a manner that permits release of the agent at the site of the atherosclerotic plaque. The agent may be attached to the balloon catheter in accordance with standard procedures known in the art. For example, the agent may be stored in a compartment of the balloon catheter until the balloon is inflated, at which point it is released into the local environment. Alternatively, the agent may be impregnated on the balloon surface, such that it contacts the cells of the arterial wall as

the balloon is inflated. The agent may also be delivered in a perforated balloon catheter such as those disclosed in Flugelman, M.Y., et al., *Circulation 85*:1110-1117, (1992). See also published PCT Application WO 95/23161 for an exemplary procedure for attaching a therapeutic protein to a balloon angioplasty catheter. Likewise, the MASP-3 inhibitory agent or MASP-2 inhibitory agent may be included in a gel or polymeric coating applied to a stent, or may be incorporated into the material of the stent, such that the stent elutes the MASP-3 inhibitory agent or MASP-2 inhibitory agent after vascular placement.

MASP-3 inhibitory agents or MASP-2 inhibitory agents used in the treatment of arthritides and other musculoskeletal disorders may be locally delivered by intra-articular injection. Such compositions may suitably include a sustained release delivery vehicle. As a further example of instances in which local delivery may be desired, MASP-2 inhibitory compositions used in the treatment of urogenital conditions may be suitably instilled intravesically or within another urogenital structure.

IX.   TREATMENT REGIMENS

In prophylactic applications, the pharmaceutical compositions are administered to a subject susceptible to, or otherwise at risk of, PNH in an amount sufficient to eliminate or reduce the risk of developing symptoms of the condition. In therapeutic applications, the pharmaceutical compositions are administered to a subject suspected of, or already suffering from, PNH in a therapeutically effective amount sufficient to relieve, or at least partially reduce, the symptoms of the condition.

In one embodiment, the subject's red blood cells are opsonized by fragments of C3 in the absence of the composition, and administration of the composition to the subject increases the survival of red blood cells in the subject. In one embodiment, the subject exhibits one or more symptoms in the absence of the composition selected from the group consisting of (i) below normal levels of hemoglobin, (ii) below normal levels of platelets; (iii) above normal levels of reticulocytes, and (iv) above normal levels of bilirubin, and administration of the composition to the subject improves at least one or more of the symptoms, resulting in (i) increased, normal, or nearly normal levels of hemoglobin (ii) increased, normal or nearly normal levels of platelets, (iii) decreased, normal or nearly normal levels of reticulocytes, and/or (iv) decreased, normal or nearly normal levels of bilirubin.

In both prophylactic and therapeutic regimens, compositions comprising MASP-3 inhibitory agents and optionally MASP-2 inhibitory agents may be administered in several dosages until a sufficient therapeutic outcome has been achieved in the subject. In one embodiment of the invention, the MASP-3 and/or MASP-2 inhibitory agent comprises a MASP-1 antibody, a MASP-2 antibody or a MASP-3 antibody, which suitably may be administered to an adult patient (e.g., an average adult weight of 70 kg) in a dosage of from 0.1 mg to 10,000 mg, more suitably from 1.0 mg to 5,000 mg, more suitably 10.0 mg to 2,000 mg, more suitably 10.0 mg to 1,000 mg and still more suitably from 50.0 mg to 500 mg, or 10 to 200 mg. For pediatric patients, dosage can be adjusted in proportion to the patient's weight.

Application of the MASP-3 inhibitory compositions and optional MASP-2 inhibitory compositions of the present invention may be carried out by a single administration of the composition (e.g., a single composition comprising MASP-2 and MASP-3 inhibitory agents, or bispecific or dual inhibitory agents, or co-administration of separate compositions), or a limited sequence of administrations, for treatment of PNH. Alternatively, the composition may be administered at periodic intervals such as daily, biweekly, weekly, every other week, monthly or bimonthly over an extended period of time for treatment of PNH.

In some embodiments, a first composition comprising at least one MASP-3 inhibitory agent and a second composition comprising at least one MASP-2 inhibitory agent are administered to a subject suffering from PNH. In one embodiment, the first composition comprising at least one MASP-3 inhibitory agent and a second composition comprising at least one MASP-2 inhibitory agent are administered simultaneously (i.e., within a time separation of no more than about 15 minutes or less, such as no more than any of 10, 5 or 1 minute). In one embodiment, the first composition comprising at least one MASP-3 inhibitory agent and a second composition comprising at least one MASP-2 inhibitory agent are administered sequentially (i.e., the first composition is administered either prior to or after the administration of the second composition, wherein the time separation of administration is more than 15 minutes). In some embodiments, the first composition comprising at least one MASP-3 inhibitory agent and a second composition comprising at least one MASP-2 inhibitory agent are administered concurrently (i.e., the administration period of the first composition overlaps with the administration of the second composition). For example, in some embodiments, the first composition and/or

the second composition are administered for a period of at least one, two, three or four weeks or longer. In one embodiment, at least one MASP-3 inhibitory agent and at least one MASP-2 inhibitory agent are combined in a unit dosage form. In one embodiment, a first composition comprising at least one MASP-3 inhibitory agent and a second composition comprising at least one MASP-2 inhibitory agent are packaged together in a kit for use in treatment of PNH.

In some embodiments, the subject suffering from PNH has previously undergone, or is currently undergoing treatment with a terminal complement inhibitor that inhibits cleavage of complement protein C5. In some embodiments, the method comprises administering to the subject a composition of the invention comprising a MASP-3 and optionally a MASP-2 inhibitor and further administering to the subject a terminal complement inhibitor that inhibits cleavage of complement protein C5. In some embodiments, the terminal complement inhibitor is a humanized anti-C5 antibody or antigen-binding fragment thereof. In some embodiments, the terminal complement inhibitor is eculizumab.

X.   EXAMPLES

The following examples merely illustrate the best mode now contemplated for practicing the invention, but should not be construed to limit the invention. All literature citations herein are expressly incorporated by reference.

EXAMPLE 1

This Example demonstrates that MASP-2 deficient mice are protected from *Neisseria meningitidis* induced mortality after infection with either *N. meningitidis* serogroup A or *N. meningitidis* serogroup B.

Methods:

MASP-2 knockout mice (MASP-2 KO mice) were generated as described in Example 1 of US 7,919,094, hereby incorporated herein by reference. 10-week-old MASP-2 KO mice (n=10) and wild-type (WT) C57/BL6 mice (n=10) were inoculated by intraperitoneal (i.p.) injection with a dosage of 2.6 x 10^7 CFU of *N. meningitidis* serogroup A Z2491 in a volume of 100 μl. The infective dose was administered to mice in conjunction with iron dextran at a final concentration of 400 mg/kg. Survival of the mice after infection was monitored over a 72-hour time period.

In a separate experiment, 10-week-old MASP-2 KO mice (n=10) and WT C57/BL6 mice (n=10) were inoculated by i.p. injection with a dosage of 6 x 10^6 CFU of

N. meningitidis serogroup B strain MC58 in a volume of 100 μl. The infective dose was administered to mice in conjunction with iron dextran at a final dose of 400 mg/kg. Survival of the mice after infection was monitored over a 72-hour time period. An illness score was also determined for the WT and MASP-2 KO mice during the 72-hour time period after infection, based on the illness scoring parameters described below in **TABLE 4**, which is based on the scheme of Fransen et al. (2010) with slight modifications.

TABLE 4: Illness Scoring associated with clinical signs in infected mice

Signs	Score
Normal	0
Slightly ruffled fur	1
Ruffled fur, slow and sticky eyes	2
Ruffled fur, lethargic and eyes shut	3
Very sick and no movement after stimulation	4
Dead	5

Blood samples were taken from the mice at hourly intervals after infection and analyzed to determine the serum level (log cfu/mL) of *N. meningitidis* in order to verify infection and determine the rate of clearance of the bacteria from the serum.

Results:

FIGURE 8 is a Kaplan-Meyer plot graphically illustrating the percent survival of MASP-2 KO and WT mice after administration of an infective dose of 2.6×10^7 cfu of *N. meningitidis* serogroup A Z2491. As shown in **FIGURE 8**, 100% of the MASP-2 KO mice survived throughout the 72-hour period after infection. In contrast, only 80% of the WT mice ($p=0.012$) were still alive 24 hours after infection, and only 50% of the WT mice were still alive at 72 hours after infection. These results demonstrate that MASP-2-deficient mice are protected from *N. meningitidis* serogroup A Z2491-induced mortality.

FIGURE 9 is a Kaplan-Meyer plot graphically illustrating the percent survival of MASP-2 KO and WT mice after administration of an infective dose of 6×10^6 cfu of *N. meningitidis* serogroup B strain MC58. As shown in **FIGURE 9**, 90% of the MASP-2 KO mice survived throughout the 72-hour period after infection. In contrast, only 20% of

the WT mice (*p*=0.0022) were still alive 24 hours after infection. These results demonstrate that MASP-2-deficient mice are protected from *N. meningitidis* serogroup B strain MC58-induced mortality.

FIGURE 10 graphically illustrates the log cfu/mL of *N. meningitidis* serogroup B strain MC58 recovered at different time points in blood samples taken from the MASP-2 KO and WT mice after i.p. infection with 6×10^6 cfu of *N. meningitidis* serogroup B strain MC58 (n=3 at different time points for both groups of mice). The results are expressed as Means±SEM. As shown in FIGURE 10, in WT mice the level of *N. meningitidis* in the blood reached a peak of about 6.0 log cfu/mL at 24 hours after infection and dropped to about 4.0 log cfu/mL by 36 hours after infection. In contrast, in the MASP-2 KO mice, the level of *N. meningitidis* reached a peak of about 4.0 log cfu/mL at 12 hours after infection and dropped to about 1.0 log cfu/mL by 36 hours after infection (the symbol "*" indicates p<0.05; the symbol "**" indicates p=0.0043). These results demonstrate that although the MASP-2 KO mice were infected with the same dose of *N. meningitidis* serogroup B strain MC58 as the WT mice, the MASP-2 KO mice have enhanced clearance of bacteraemia as compared to WT.

FIGURE 11 graphically illustrates the average illness score of MASP-2 KO and WT mice at 3, 6, 12 and 24 hours after infection with 6×10^6 cfu of *N. meningitidis* serogroup B strain MC58. As shown in FIGURE 11, the MASP-2-deficient mice showed high resistance to the infection, with much lower illness scores at 6 hours (symbol "*" indicates p=0.0411), 12 hours (symbol "**" indicates p=0.0049) and 24 hours (symbol "***" indicates p=0.0049) after infection, as compared to WT mice. The results in FIGURE 11 are expressed as means±SEM.

In summary, the results in this Example demonstrate that MASP-2-deficient mice are protected from *N. meningitides*-induced mortality after infection with either *N. meningitidis* serogroup A or *N. meningitidis* serogroup B.

EXAMPLE 2

This Example demonstrates that the administration of MASP-2 antibody after infection with *N. meningitidis* increases the survival of mice infected with *N. meningitidis*.

Background/Rationale:

As described in Example 24 of US Patent 7,919,094, incorporated herein by reference, rat MASP-2 protein was utilized to pan a Fab phage display library, from

which Fab2 #11 was identified as a functionally active antibody. Full-length antibodies of the rat IgG2c and mouse IgG2a isotypes were generated from Fab2 #11. The full-length MASP-2 antibody of the mouse IgG2a isotype was characterized for pharmacodynamic parameters (as described in Example 38 of US Patent 7,919,094).

In this Example, the mouse MASP-2 full-length antibody derived from Fab2 #11 was analyzed in the mouse model of *N. meningitidis* infection.

Methods:

The mouse IgG2a full-length MASP-2 antibody isotype derived from Fab2 #11, generated as described above, was tested in the mouse model of *N. meningitidis* infection as follows.

1.   Administration of mouse-MASP-2 monoclonal antibodies (MoAb) after infection

9-week-old C57/BL6 Charles River mice were treated with inhibitory mouse MASP-2 antibody (1.0 mg/kg) (n=12) or control isotype antibody (n=10) at 3 hours after i.p. injection with a high dose (4×10^6 cfu) of *N. meningitidis* serogroup B strain MC58.

Results:

FIGURE 12 is a Kaplan-Meyer plot graphically illustrating the percent survival of mice after administration of an infective dose of 4×10^6 cfu of *N. meningitidis* serogroup B strain MC58, followed by administration 3 hours post-infection of either inhibitory MASP-2 antibody (1.0 mg/kg) or control isotype antibody. As shown in **FIGURE 12**, 90% of the mice treated with MASP-2 antibody survived throughout the 72-hour period after infection. In contrast, only 50% of the mice treated with isotype control antibody survived throughout the 72-hour period after infection. The symbol "*" indicates p=0.0301, as determined by comparison of the two survival curves.

These results demonstrate that administration of a MASP-2 antibody is effective to treat and improve survival in subjects infected with N. *meningitidis*.

As demonstrated herein, the use of MASP-2 antibody in the treatment of a subject infected with *N. meningitidis* is effective when administered within 3 hours post-infection, and is expected to be effective within 24 hours to 48 hours after infection. Meningococcal disease (either meningococcemia or meningitis) is a medical emergency, and therapy will typically be initiated immediately if meningococcal disease is suspected (i.e., before *N. meningitidis* is positively identified as the etiological agent).

In view of the results in the MASP-2 KO mouse demonstrated in EXAMPLE 1, it is believed that administration of MASP-2 antibody prior to infection with *N. meningitidis* would also be effective to prevent or ameliorate the severity of infection.

EXAMPLE 3

This Example demonstrates the complement-dependent killing of *N. meningitidis* in human sera is MASP-3-dependent.

<u>**Rationale:**</u>

Patients with decreased serum levels of functional MBL display increased susceptibility to recurrent bacterial and fungal infections (Kilpatrick et al., *Biochim Biophys Acta* 1572:401-413 (2002)). It is known that *N. meningitidis* is recognized by MBL, and it has been shown that MBL-deficient sera do not lyse *N. meningitidis*.

In view of the results described in Examples 1 and 2, a series of experiments were carried out to determine the efficacy of administration of MASP-2 antibody to treat *N. meningitidis* infection in complement-deficient and control human sera. Experiments were carried out in a high concentration of serum (20%) in order to preserve the complement pathway.

<u>**Methods:**</u>

1. Serum bactericidal activity in various complement-deficient human sera and in human sera treated with human MASP-2 antibody

The following complement-deficient human sera and control human sera were used in this experiment:

TABLE 5: Human serum samples tested (as shown in FIGURE 13)

Sample	Serum type
A	Normal human sera (NHS) + human MASP-2 Ab
B	NHS + isotype control Ab
C	MBL -/- human serum
D	NHS
E	Heat-Inactivated (HI) NHS

A recombinant antibody against human MASP-2 was isolated from a combinatorial Antibody Library (Knappik, A., et al., *J. Mol. Biol. 296*:57-86 (2000)), using recombinant human MASP-2A as an antigen (Chen, C.B. and Wallis, *J. Biol. Chem. 276*:25894-25902 (2001)). An anti-human scFv fragment that potently inhibited

lectin pathway-mediated activation of C4 and C3 in human plasma (IC50~20 nM) was identified and converted to a full-length human IgG4 antibody.

N. meningitidis serogroup B-MC58 was incubated with the different sera show in **TABLE 5**, each at a serum concentration of 20%, with or without the addition of inhibitory human MASP-2 antibody (3 µg in 100 µl total volume) at 37°C with shaking. Samples were taken at the following time points: 0-, 30-, 60- and 90-minute intervals, plated out and then viable counts were determined. Heat-inactivated human serum was used as a negative control.

<u>Results</u>:

FIGURE 13 graphically illustrates the log cfu/mL of viable counts of *N. meningitidis* serogroup B-MC58 recovered at different time points in the human sera samples shown in **TABLE 5**. **TABLE 6** provides the Student's t-test results for **FIGURE 13**.

TABLE 6: Student's t-test Results for **FIGURE 13** (time point 60 minutes)

	Mean Diff. (Log)	Significant? P<0.05?	P value summary
A vs B	-0.3678	Yes	***(0.0002)
A vs C	-1.1053	Yes	***(p<0.0001)
A vs D	-0.2111	Yes	**(0.0012)
C vs D	1.9	Yes	***(p<0.0001)

As shown in **FIGURE 13** and **TABLE 6**, complement-dependent killing of *N. meningitidis* in human 20% serum was significantly enhanced by the addition of the human MASP-2 inhibitory antibody.

2. Serum bactericidal activity in various complement-deficient human sera

The following complement-deficient human sera and control human sera were used in this experiment:

TABLE 7: Human serum samples tested (as shown in **FIGURE 14**)

Sample	Serum Type
A	Normal human serum (NHS)
B	Heat-inactivated NHS
C	MBL -/-
D	MASP-3 -/- (MASP-1 +)

Note: The MASP-3 -/- (MASP-1 +) serum in sample D was taken from a subject with 3MC syndrome, which is a unifying term for the overlapping Carnevale, Mingarelli, Malpuech and Michels syndromes. As further described in Example 4, the mutations in exon 12 of the MASP-1/3 gene render the serine protease domain of MASP-3, but not MASP-1 dysfunctional. It is also known that factor D is intact in 3MC serum.

N. meningitidis serogroup B-MC58 was incubated with different complement-deficient human sera, each at a serum concentration of 20%, at 37°C with shaking. Samples were taken at the following time points: 0-, 15-, 30-, 45-, 60-, 90- and 120-minute intervals, plated out and then viable counts were determined. Heat-inactivated human serum was used as a negative control.

Results:

FIGURE 14 graphically illustrates the log cfu/mL of viable counts of *N. meningitidis* serogroup B-MC58 recovered at different time points in the human sera samples shown in **TABLE 7**. As shown in **FIGURE 14**, the WT (NHS) serum has the highest level of bactericidal activity for *N. meningitidis*. In contrast, the MBL -/- and MASP-3 -/- (which is MASP-1-sufficient) human sera do not have any bactericidal activity. These results indicate that complement-dependent killing of *N. meningitidis* in human 20% (v/v) serum is MASP-3- and MBL-dependent. **TABLE 8** provides the Student's t-test results for **FIGURE 14**.

TABLE 8: Student's t-test Results for **FIGURE 14**

Comparison	Time Point (min)	Mean Diff. (Log)	Significant? P<0.05?	P value Summary
A vs B	60	-0.8325	Yes	***(p<0.0001)
A vs B	90	-1.600	Yes	***(p<0.0001)
A vs C	60	-1.1489	Yes	***(p<0.0001)
A vs C	90	-1.822	Yes	***(p<0.0001)
A vs D	60	-1.323	Yes	***(0.0005)
A vs D	90	-2.185	Yes	***(p<0.0001)

In summary, the results shown in **FIGURE 14** and **TABLE 8** demonstrate that complement-dependent killing of *N. meningitidis* in 20% human serum is MASP-3- and MBL-dependent.

3. Complement-dependent killing of *N. meningitidis* in 20% (v/v) mouse sera deficient of MASP-2, MASP-1/3 or MBL A/C.

The following complement-deficient mouse sera and control mouse sera were used in this experiment:

TABLE 9: Mouse serum samples tested (as shown in **FIGURE 15**)

Sample	Serum Type
A	WT
B	MASP-2 -/-
C	MASP-1/3 -/-
D	MBL A/C -/-
E	WT heat-inactivated (HIS)

N. meningitidis serogroup B-MC58 was incubated with different complement-deficient mouse sera, each at a serum concentration of 20%, at 37°C with shaking. Samples were taken at the following time points: 0-, 15-, 30-, 60-, 90- and 120-minute intervals, plated out and then viable counts were determined. Heat-inactivated human serum was used as a negative control.

Results:

FIGURE 15 graphically illustrates the log cfu/mL of viable counts of *N. meningitidis* serogroup B-MC58 recovered at different time points in the mouse serum samples shown in **TABLE 9**. As shown in **FIGURE 15**, the MASP-2 -/- mouse sera have a higher level of bactericidal activity for *N. meningitidis* than WT mouse sera. In contrast, the MASP-1/3 -/- mouse sera do not have any bactericidal activity. The symbol "**" indicates p=0.0058, the symbol "***" indicates p=0.001. **TABLE 10** provides the Student's t-test results for **FIGURE 15**.

TABLE 10: Student's t-test Results for **FIGURE 15**

Comparison	Time point	Mean Diff. (LOG)	Significant? (p<0.05)?	P value summary
A vs. B	60 min.	0.39	yes	** (0.0058)
A vs. B	90 min.	0.6741	yes	*** (0.001)

In summary, the results in this Example demonstrate that MASP-2 -/- serum has a higher level of bactericidal activity for *N. meningitidis* than WT serum and that complement-dependent killing of *N. meningitidis* in 20% serum is MASP-3- and MBL-dependent.

EXAMPLE 4

This Example describes a series of experiments that were carried out to determine the mechanism of the MASP-3-dependent resistance to *N. meningitidis* infection observed in MASP-2 KO mice, as described in Examples 1-3.

Rationale:

In order to determine the mechanism of MASP-3-dependent resistance to *N. meningitidis* infection observed in MASP-2 KO mice (described in Examples 1-3 above), a series of experiments were carried out as follows.

1. MASP-1/3-deficient mice are not deficient of lectin pathway functional activity (also referred to as "LEA-2")

Methods:

In order to determine whether MASP-1/3-deficient mice are deficient of lectin pathway functional activity (also referred to as LEA-2), an assay was carried out to measure the kinetics of C3 convertase activity in plasma from various complement-deficient mouse strains tested under lectin activation pathway-specific assay conditions (1% plasma), as described in Schwaeble W. et al., PNAS vol 108(18):7523-7528 (2011), hereby incorporated herein by reference.

Plasma was tested from WT, C4-/-, MASP-1/3-/-; Factor B-/-, and MASP-2-/- mice as follows.

To measure C3 activation, microtiter plates were coated with mannan (1 μg/well), zymosan (1 μg/well) in coating buffer (15 mM Na_2Co_3, 35 mM $NaHCO_3$), or immune complexes, generated *in situ* by coating with 1% human serum albumin (HSA) in coating buffer then adding sheep anti-HAS serum (2 μg/mL) in TBS (10mM Tris, 140 mM NaCl, pH 7.4) with 0.05% Tween 20 and 5 mM Ca^{++}. Plates were blocked with 0.1% HSA in TBS and washed three times with TBS/Tween20/ Ca^{++}. Plasma samples were diluted in 4 mM barbital, 145 mM NaCl, 2 mM $CaCl_2$, 1 mM $MgCl_2$, pH 7.4, added to the plates and incubated for 1.5 h at 37°C. After washing, bound C3b was detected using rabbit anti-human C3c (Dako), followed by alkaline phosphatase-conjugated goat anti-rabbit IgG and p-nitrophenyl phosphate.

Results:

The kinetics of C3 activation (as measured by C3b deposition on mannan-coated plates with 1% serum) under lectin pathway-specific conditions is shown in **FIGURE 16**. No C3 cleavage was seen in MASP-2-/- plasma. Factor B-/- (Factor B -/-) plasma cleaved C3 at half the rate of WT plasma, likely due to the loss of the amplification loop. A significant delay in the lectin pathway-dependent conversion of C3 to C3b was seen in C4-/- ($T_{1/2}$=33min) as well as in MASP-1/3-/- deficient plasma ($T_{1/2}$=49 min). This delay of C3 activation in MASP-1/3 -/- plasma has been shown to be MASP-1- rather than MASP-3-dependent. (See Takahashi M. et al., J Immunol 180:6132-6138 (2008)). These results demonstrate that MASP-1/3-deficient mice are not deficient of lectin pathway functional activity (also referred to as "LEA-2").

2. Effect of hereditary MASP-3 deficiency on alternative pathway activation.

Rationale:

The effect of hereditary MASP-3 deficiency on alternative pathway activation was determined by testing serum of a MASP-3-deficient patient with 3MC syndrome caused by a frame-shift mutation in the exon encoding the serine protease of MASP-3. The 3MC syndrome is a unifying term for the overlapping Carneavale, Mingarelli, Malpuech and Michels syndromes. These rare autosomal recessive disorders exhibit a spectrum of developmental features, including characteristic facial dysmorphism, cleft lip and/or palate, craniosynostosis, learning disability and genital, limb and vesicorenal abnormalities. Rooryck et al., *Nature Genetics* 43:197-203 (2011) studied 11 families with 3MC syndrome and identified two mutated genes, COLEC11 and MASP-1. The mutations in the MASP-1 gene render the exon encoding the serine protease domain of MASP-3, but not the exons encoding the serine protease of MASP-1, dysfunctional. Therefore, 3MC patients with mutations in the exon encoding the serine protease of MASP-3 are deficient of MASP-3 but sufficient in MASP-1.

Methods:

MASP-3-deficient serum was obtained from a 3MC patient, the mother and father of the 3MC patient (both heterozygous for the allele bearing a mutation that renders the exon encoding the MASP-3 serine protease domain dysfunctional), as well as from a C4-deficient patient (deficient in both human C4 genes) and an MBL-deficient subject. An alternative pathway assay was carried out under traditional AP-specific conditions (BBS/ Mg^{++}/EGTA, without Ca^{++}, wherein BBS = barbital buffered saline containing sucrose), as described in Bitter-Suermann et al., *Eur. J. Immunol* 11:291-295 (1981)), on zymosan-coated microtiter plates at serum concentrations ranging from 0.5 to 25% and C3b deposition was measured over time.

Results:

FIGURE 17 graphically illustrates the level of alternative pathway-driven C3b deposition on zymosan-coated microtiter plates as a function of serum concentration in serum samples obtained from MASP-3-deficient, C4-deficient and MBL-deficient subjects. As shown in FIGURE 17, MASP-3-deficient patient serum has residual alternative pathway (AP) activity at high serum concentrations (25%, 12.5%, 6.25% serum concentrations), but a significantly higher AP_{50} (i.e.. 9.8% of serum needed to achieve 50% of maximum C3 deposition).

FIGURE 18 graphically illustrates the level of alternative pathway-driven C3b deposition on zymosan-coated microtiter plates under "traditional" alternative pathway-specific (AP-specific) conditions (*i.e.,* BBS/EGTA/Mg^{++} without Ca^{++}) as a function of time in 10% human serum samples obtained from MASP-3-deficient, C4-deficient and MBL-deficient human subjects.

TABLE 11 below summarizes the AP$_{50}$ results shown in FIGURE 17 and the half-times for C3b deposition shown in FIGURE 18.

TABLE 11: Summary of Results shown in FIGURES 17 and 18

Serum type	AP$_{50}$ (%)	T$_{1/2}$ (min)
MASP-3-deficient (3MC patient)	9.8	37.4
Mother of 3MC patient (heterozygous)	4.3	17.2
Father of 3MC patient (heterozygous)	4.3	20.9
C4-deficient	4.0	11.6
MBL-deficient	4.8	11.0

Note: In BBS/ Mg^{++}/EGTA buffer, the lectin pathway-mediated effects are deficient due to absence of Ca^{++} in this buffer.

While not wishing to be bound by any particular theory, it is believed that the lower alternative pathway activity observed in the MASP-3-deficient serum is caused because the 3MC patient has active factor D in his serum, and since this patient still expresses MASP-1 and HTRA1, conversion of pro-factor D is still able to occur in the absence of MASP-3, although at a lower level

3.   Measurement of C3b deposition on mannan, zymosan and S. pneumonia D39 in mouse sera deficient of MASP-2 or MASP-1/3.

Methods:

C3b deposition was measured on mannan, zymosan and *S. pneumonia* D39-coated microtiter plates using mouse serum concentrations ranging from 0% to 20% obtained from MASP-2-/-, MASP-1/3-/- and WT mice. The C3b deposition assays were carried

out under either "traditional" alternative pathway-specific conditions (*i.e.* BBS/EGTA/Mg^{++} without Ca^{++}), or under physiological conditions allowing both the lectin pathway and the alternative pathway to function (*i.e.,* BBS/Mg^{++}/Ca^{++}).

Results:

FIGURE 19A graphically illustrates the level of C3b deposition on mannan-coated microtiter plates as a function of serum concentration in serum samples obtained from WT, MASP-2-deficient, and MASP-1/3-deficient mice under traditional alternative pathway-specific conditions (*i.e.,* BBS/EGTA/Mg^{++} without Ca^{++}), or under physiological conditions allowing both the lectin pathway and the alternative pathway to function (BBS/Mg^{++}/Ca^{++}). **FIGURE 19B** graphically illustrates the level of C3b deposition on zymosan-coated microtiter plates as a function of serum concentration in serum samples from WT, MASP-2-deficient, and MASP-1/3-deficient mice under traditional AP-specific conditions (*i.e.,* BBS/EGTA/Mg^{++} without Ca^{++}), or under physiological conditions allowing both the lectin pathway and the alternative pathway to function (BBS/Mg^{++}/Ca^{++}). **FIGURE 19C** graphically illustrates the level of C3b deposition on *S. pneumoniae* D39-coated microtiter plates as a function of serum concentration in serum samples from WT, MASP-2-deficient, and MASP-1/3-deficient mice under traditional AP-specific conditions (*i.e.,* BBS/EGTA/Mg^{++} without Ca^{++}), or under physiological conditions allowing both the lectin pathway and the alternative pathway to function (BBS/Mg^{++}/Ca^{++}).

FIGURE 20A graphically illustrates the results of a C3b deposition assay in highly diluted sera carried out on mannan-coated microtiter plates under traditional AP-specific conditions (*i.e.* BBS/EGTA/Mg^{++} without Ca^{++}) or under physiological conditions allowing both the lectin pathway and the alternative pathway to function (BBS/Mg^{++}/Ca^{++}), using serum concentrations ranging from 0 % up to 1.25%. **FIGURE 20B** graphically illustrates the results of a C3b deposition assay carried out on zymosan-coated microtiter plates under traditional AP-specific conditions (*i.e.* BBS/EGTA/Mg^{++} without Ca^{++}) or under physiological conditions allowing both the lectin pathway and the alternative pathway to function (BBS/EGTA/Mg^{++}/Ca^{++}), using serum concentrations ranging from 0 % up to 1.25%. **FIGURE 20C** graphically illustrates the results of a C3b deposition assay carried out on *S. pneumoniae* D39-coated microtiter plates under traditional AP-specific conditions (*i.e.* BBS/EGTA/Mg^{++} without Ca^{++}) or under physiological conditions allowing both the lectin pathway and the alternative pathway to

function (BBS/EGTA/Mg^{++}/Ca^{++}), using serum concentrations ranging from 0 % up to 1.25%.

As shown in **FIGURES 20A-C**, C3b deposition assays were also carried out under traditional alternative pathway-specific conditions (*i.e.* BBS/EGTA/Mg^{++} without Ca^{++}) or under physiological conditions allowing both the lectin pathway and the alternative pathway to function (BBS/Mg^{++}/Ca^{++}), using higher dilutions ranging from 0 % up to 1.25% serum on mannan-coated plates (**FIGURE 20A**); zymosan-coated plates (**FIGURE 20B**) and *S. pneumoniae* D39-coated plates (**FIGURE 20C**). The alternative pathway tails off under higher serum dilutions, so the activity observed in the MASP-1/3-deficient serum in the presence of Ca^{++} is MASP-2-mediated LP activity, and the activity in MASP-2-deficient serum in the presence of Ca^{++} is MASP-1/3-mediated residual activation of the AP.

Discussion:

The results described in this Example demonstrate that a MASP-2 inhibitor (or MASP-2 KO) provides significant protection from *N. meningitidis* infection by promoting MASP-3-driven alternative pathway activation. The results of the mouse serum bacteriolysis assays and the human serum bacteriolysis assays further show, by monitoring the serum bactericidal activity against *N. meningitidis*, that bactericidal activity against *N. meningitidis* is absent in MBL-deficient (mouse MBL A and MBL C double-deficient and human MBL-deficient sera).

FIGURE 1 illustrates the new understanding of the lectin pathway and alternative pathway based on the results provided herein. **FIGURE 1** delineates the role of LEA-2 in both opsonization and lysis. While MASP-2 is the initiator of "downstream" C3b deposition (and resultant opsonization) in multiple lectin-dependent settings physiologically (**FIGURE 20A, 20B, 20C**), it also plays a role in lysis of serum-sensitive bacteria. As illustrated in **FIGURE 1**, the proposed molecular mechanism responsible for the increased bactericidal activity of MASP-2-deficient or MASP-2-depleted serum/plasma for serum-sensitive pathogens such as *N. meningitidis* is that, for the lysis of bacteria, lectin pathway recognition complexes associated with MASP-1 and MASP-3 have to bind in close proximity to each other on the bacterial surface, thereby allowing MASP-1 to cleave MASP-3. In contrast to MASP-1 and MASP-2, MASP-3 is not an auto-activating enzyme, but, in many instances, requires activation/cleavage by MASP-1 to be converted into its enzymatically active form.

As further shown in **FIGURE 1**, activated MASP-3 can then cleave C3b-bound factor B on the pathogen surface to initiate the alternative pathway activation cascade by formation of the enzymatically active alternative pathway C3 and C5 convertase C3bBb and C3bBb(C3b)n, respectively. MASP-2-bearing lectin-pathway activation complexes have no part in the activation of MASP-3 and, in the absence or after depletion of MASP-2, all-lectin pathway activation complexes will either be loaded with MASP-1 or MASP-3. Therefore, in the absence of MASP-2, the likelihood is markedly increased that on the microbial surface MASP-1 and MASP-3-bearing lectin-pathway activation complexes will come to sit in close proximity to each other, leading to more MASP-3 being activated and thereby leading to a higher rate of MASP-3-mediated cleavage of C3b-bound factor B to form the alternative pathway C3 and C5 convertases C3bBb and C3bBb(C3b)n on the microbial surface. This leads to the activation of the terminal activation cascades C5b-C9 that forms the Membrane Attack Complex, composed of surface-bound C5b associated with C6, C5bC6 associated with C7, C5bC6C7 associated with C8, and C5bC6C7C8, leading to the polymerization of C9 that inserts into the bacterial surface structure and forms a pore in the bacterial wall, which will lead to osmolytic killing of the complement-targeted bacterium.

The core of this novel concept is that the data provided herein clearly show that the lectin-pathway activation complexes drive the following two distinct activation routes, as illustrated in **FIGURE 1**:

EXAMPLE 5

This Example demonstrates the inhibitory effect of MASP-2 deficiency and/or MASP-3 deficiency on lysis of red blood cells from blood samples obtained from a mouse model of paroxysmal nocturnal hemoglobinuria (PNH).

Background/Rationale:

Paroxysmal nocturnal hemoglobinuria (PNH), also referred to as Marchiafava-Micheli syndrome, is an acquired, potentially life-threatening disease of the blood, characterized by complement-induced intravascular hemolytic anemia. The hallmark of PNH is the chronic complement-mediated intravascular hemolysis that is a consequence of unregulated activation of the alternative pathway of complement due to the absence of the complement regulators CD55 and CD59 on PNH erythrocytes, with subsequent hemoglobinuria and anemia. Lindorfer, M.A., et al., *Blood 115*(11) (2010), Risitano,

A.M, *Mini-Reviews in Medicinal Chemistry*, 11:528-535 (2011). Anemia in PNH is due to destruction of red blood cells in the bloodstream. Symptoms of PNH include red urine, due to appearance of hemoglobin in the urine, back pain, fatigue, shortness of breath and thrombosis. PNH may develop on its own, referred to as "primary PNH" or in the context of other bone marrow disorders such as aplastic anemia, referred to as "secondary PNH". Treatment for PNH includes blood transfusion for anemia, anticoagulation for thrombosis and the use of the monoclonal antibody eculizumab (Soliris®), which protects blood cells against immune destruction by inhibiting the complement system (Hillmen P. et al., *N. Engl. J. Med. 350*(6):552-9 (2004)). Eculizumab (Soliris®) is a humanized monoclonal antibody that targets the complement component C5, blocking its cleavage by C5 convertases, thereby preventing the production of C5a and the assembly of MAC. Treatment of PNH patients with eculizumab has resulted in a reduction of intravascular hemolysis, as measured by lactate dehydrogenase (LDH), leading to hemoglobin stabilization and transfusion independence in about half of the patients (Hillmen P, et al., Mini-Reviews in Medicinal Chemistry, vol 11(6) (2011)). While nearly all patients undergoing therapy with eculizumab achieve normal or almost normal LDH levels (due to control of intravascular hemolysis), only about one third of the patients reach a hemoglobin value about 11gr/dL, and the remaining patients on eculizumab continue to exhibit moderate to severe (*i.e.*, transfusion-dependent) anemia, in about equal proportions (Risitano A.M. et al., *Blood* 113:4094-100 (2009)). As described in Risitano et al., Mini-Reviews in *Medicinal Chemistry* 11:528-535 (2011), it was demonstrated that PNH patients on eculizumab contained C3 fragments bound to a substantial portion of their PNH erythrocytes (while untreated patients did not), leading to the conclusion that membrane-bound C3 fragments work as opsonins on PNH erythrocytes, resulting in their entrapment in the reticuloendothelial cells through specific C3 receptors and subsequent extravascular hemolysis. Therefore, therapeutic strategies in addition to the use of eculizumab are needed for those patients developing C3 fragment-mediated extravascular hemolysis because they continue to require red cell transfusions.

This Example describes methods to assess the effect of MASP-2- and MASP-3-deficient serum on lysis of red blood cells from blood samples obtained from a mouse model of PNH and demonstrates the efficacy of MASP-2 inhibition and/or MASP-3 inhibition to treat subjects suffering from PNH, and also supports the use of inhibitors of MASP-2 and/or inhibitors of MASP-3 (including dual or bispecific MASP-2/MASP-3

inhibitors) to ameliorate the effects of C3 fragment-mediated extravascular hemolysis in PNH subjects undergoing therapy with a C5 inhibitor such as eculizumab.

Methods:

PNH animal model:

Blood samples were obtained from gene-targeted mice with deficiencies of Crry and C3 (Crry/C3-/-) and CD55/CD59-deficient mice. These mice are missing the respective surface complement regulators on their erythrocytes and these erythrocytes are, therefore, susceptible to spontaneous complement autolysis as are PNH human blood cells.

In order to sensitize these erythrocytes even more, these cells were used with and without coating by mannan and then tested for hemolysis in WT C56/BL6 plasma, MBL null plasma, MASP-2 -/- plasma, MASP-1/3 -/- plasma, human NHS, human MBL -/- plasma, and NHS treated with human MASP-2 antibody.

1. Hemolysis assay of Crry/C3 and CD55/CD59 double-deficient murine erythrocytes in MASP-2-deficient/depleted sera and controls

Day 1. Preparation of murine RBC (± mannan coating).

Materials included: fresh mouse blood, BBS/Mg$^{++/}$ Ca^{++} (4.4 mM barbituric acid, 1.8 mM sodium barbitone, 145 mM NaCl, pH 7.4, 5mM Mg^{++}, 5mM Ca^{++}), chromium chloride, CrCl$_3$·6H$_2$0 (0.5mg/mL in BBS/Mg^{++}/ Ca^{++}) and mannan, 100 μg/mL in BBS/Mg^{++}/Ca^{++}.

Whole blood (2 mL) was spun down for 1-2 min at 2000xg in a refrigerated centrifuge at 4°C. The plasma and buffy coat were aspirated off. The sample was then washed 3x by re-suspending RBC pellet in 2 mL ice-cold BBS/gelatin/Mg^{++}/Ca^{++} and repeating centrifugation step. After the third wash, the pellet was re-suspended in 4 mL BBS/Mg^{++}/Ca^{++}. A 2 mL aliquot of the RBC was set aside as an uncoated control. To the remaining 2 mL, 2 mL CrCl3 and 2 mL mannan were added and the sample was incubated with gentle mixing at RT for 5min. The reaction was terminated by adding 7.5 mL BBS/gelatin/Mg^{++}/Ca^{++}. The sample was spun down as above, re-suspended in 2 mL BBS/gelatin/Mg^{++}/Ca^{++} and washed a further two times as above, then stored at 4°C.

Day 2. Hemolysis assay

Materials included BBS/gelatin/Mg^{++}/Ca^{++} (as above), test sera, 96-well round-bottomed and flat-bottomed plates and a spectrophotometer that reads 96-well plates at 410-414 nm.

The concentration of the RBC was first determined and the cells were adjusted to 10^9/mL, and stored at this concentration. Before use, the cells were diluted in assay buffer to 10^8/mL, and then 100 ul per well was used. Hemolysis was measured at 410-414 nm (allowing for greater sensitivity than 541nm). Dilutions of test sera were prepared in ice-cold BBS/gelatin/Mg^{++}/Ca^{++}. 100μl of each serum dilution was pipetted into round-bottomed plate. 100 μl of appropriately diluted RBC preparation was added (i.e., 10^8/mL), incubated at 37°C for about 1 hour, and observed for lysis. (The plates may be photographed at this point.) The plate was then spun down at maximum speed for 5 minutes. 100 μl of the fluid phase was aspirated, transferred to flat-bottom plates, and the OD was recorded at 410-414 nm. The RBC pellets were retained (these can be subsequently lysed with water to obtain an inverse result).

Experiment #1

Fresh blood was obtained from CD55/CD59 double-deficient mice and blood of Crry/C3 double-deficient mice and erythrocytes were prepared as described in detail in the above protocol. The cells were split and half of the cells were coated with mannan and the other half were left untreated, adjusting the final concentration to 10^8/mL, of which 100 μl was used in the hemolysis assay, which was carried out as described above.

Results of Experiment #1: The lectin pathway is involved in erythrocyte lysis in the PNH animal model

In an initial experiment, it was determined that non-coated WT mouse erythrocytes were not lysed in any mouse serum. It was further determined that mannan-coated Crry-/- mouse erythrocytes were slowly lysed (more than 3 hours at 37 degrees) in WT mouse serum, but they were not lysed in MBL null serum. (Data not shown).

It was determined that mannan-coated Crry-/- mouse erythrocytes were rapidly lysed in human serum but not in heat-inactivated NHS. Importantly, mannan-coated Crry-/- mouse erythrocytes were lysed in NHS diluted down to 1/640 (i.e., 1/40, 1/80, 1/160, 1/320 and 1/640 dilutions all lysed). (Data not shown). In this dilution, the alternative pathway does not work (AP functional activity is significantly reduced below 8% serum concentration).

Conclusions from Experiment #1

Mannan-coated Crry-/- mouse erythrocytes are very well lysed in highly diluted human serum with MBL but not in that without MBL. The efficient lysis in every serum concentration tested implies that the alternative pathway is not involved or needed for this lysis. The inability of MBL-deficient mouse serum and human serum to lyse the mannan-coated Crry-/- mouse erythrocytes indicates that the classical pathway also has nothing to do with the lysis observed. As lectin pathway recognition molecules are required (i.e., MBL), this lysis is mediated by the lectin pathway.

Experiment #2

Fresh blood was obtained from the Crry/C3 and CD55/CD59 double-deficient mice and mannan-coated Crry-/- mouse erythrocytes were analyzed in the haemolysis assay as described above in the presence of the following human serum: MASP-3 -/-; MBL null; WT; NHS pretreated with human MASP-2 antibody; and heat-inactivated NHS as a control.

Results of Experiment #2: MASP-2 inhibitors and MASP-3 deficiency prevents erythrocyte lysis in PNH animal model

With the mannan-coated Crry-/- mouse erythrocytes, NHS was incubated in the dilutions diluted down to 1/640 (i.e., 1/40, 1/80, 1/160, 1/320 and 1/640), human MBL-/- serum, human MASP-3-deficient serum (from 3MC patient), and NHS pretreated with MASP-2 mAb, and heat-inactivated NHS as a control.

The ELISA microtiter plate was spun down and the non-lysed erythrocytes were collected on the bottom of the round-well plate. The supernatant of each well was collected and the amount of hemoglobin released from the lysed erythrocytes was measured by reading the OD415 nm in an ELISA reader.

It was observed that MASP-3-/- serum did not lyse mannan-coated mouse erythrocytes at all. In the control heat-inactivated NHS (negative control), as expected, no lysis was observed. MBL-/- human serum lysed mannan-coated mouse erythrocytes at 1/8 and 1/16 dilutions. MASP-2-antibody-pretreated NHS lysed mannan-coated mouse erythrocytes at 1/8 and 1/16 dilutions while WT human serum lysed mannan-coated mouse erythrocytes down to dilutions of 1/32.

FIGURE 21 graphically illustrates hemolysis (as measured by hemoglobin release of lysed mouse erythrocytes (Crry/C3-/-) into the supernatant measured by

photometry) of mannan-coated murine erythrocytes by human serum over a range of serum dilutions in serum from MASP-3-/-, heat-inactivated (HI) NHS, MBL-/-, NHS pretreated with MASP-2 antibody, and NHS control.

FIGURE 22 graphically illustrates hemolysis (as measured by hemoglobin release of lysed mouse erythrocytes (Crry/C3-/-) into the supernatant measured by photometry) of mannan-coated murine erythrocytes by human serum over a range of serum concentration in serum from MASP-3-/-, heat-inactivated (HI) NHS, MBL-/-, NHS pretreated with MASP-2 antibody, and NHS control.

From the results shown in **FIGURE 21** and **22**, it is demonstrated that inhibiting MASP-3 will prevent any complement-mediated lysis of sensitized erythrocytes with deficient protection from autologous complement activation. MASP-2 inhibition with MASP-2 antibody significantly shifted the CH_{50} and was protective to some extent, but MASP-3 inhibition was more effective.

Experiment #3

Non-coated Crry-/- mouse erythrocytes obtained from fresh blood from the Crry/C3 and CD55/CD59 double-deficient mice were analyzed in the hemolysis assay as described above in the presence of the following sera: MASP-3-/-; MBL-/-; WT; NHS pretreated with human MASP-2 antibody, and heat-inactivated NHS as a control.

Results:

FIGURE 23 graphically illustrates hemolysis (as measured by hemoglobin release of lysed WT mouse erythrocytes into the supernatant measured by photometry) of non-coated murine erythrocytes over a range of serum concentrations in human sera from a 3MC (MASP-3-/-) patient, heat inactivated (HI) NHS, MBL-/-, NHS pretreated with MASP-2 antibody, and NHS control. As shown in **FIGURE 23** and summarized in **TABLE 12**, it is demonstrated that inhibiting MASP-3 inhibits complement-mediated lysis of non-sensitized WT mouse erythrocytes.

FIGURE 24 graphically illustrates hemolysis (as measured by hemoglobin release of lysed mouse erythrocytes (CD55/59 -/-) into the supernatant measured by photometry) of non-coated murine erythrocytes by human serum over a range of serum concentrations in human sera from heat-inactivated (HI) NHS, MBL-/-, NHS pretreated with MASP-2 antibody, and NHS control. As shown in **FIGURE 24** and summarized in **TABLE 12**, it is demonstrated that inhibiting MASP-2 was protective to a limited extent.

TABLE 12: CH$_{50}$ values expressed as serum concentrations

Serum	WT	CD55/59 -/-
3MC patient	No lysis	No lysis
Heat-inactivated NHS	No lysis	No lysis
MBL AO/XX donor (MBL deficient)	7.2%	2.1%
NHS + MASP-2 antibody	5.4%	1.5%
NHS	3.1%	0.73%

Note: "CH$_{50}$" is the point at which complement-mediated hemolysis reachs 50%.

In summary, the results in this Example demonstrate that inhibiting MASP-3 prevents any complement lysis of sensitized and non-sensitized erythrocytes with deficient protection from autologous complement activation. MASP-2 inhibition also is protective to some extent. Therefore, MASP-2 and MASP-3 inhibitors alone or in combination (*i.e.*, co-administered, administered sequentially) or MASP-2/MASP-3 bispecific or dual inhibitors may be used to treat subjects suffering from PNH, and may also be used to ameliorate (*i.e.*, inhibit, prevent or reduce the severity of) extravascular hemolysis in PNH patients undergoing treatment with a C5 inhibitor such as eculizumab (Soliris®).

EXAMPLE 6

This Example describes a hemolysis assay testing mannan-coated rabbit erythrocytes for lysis in the presence of WT or MASP-1/3-/- mouse sera.

Methods:

1. Hemolysis assay of rabbit RBC (mannan coated) in mouse MASP-1/3-deficient sera and WT control sera

Day 1. Preparation of rabbit RBC.

Materials included: fresh rabbit blood, BBS/ Mg^{++}/Ca^{++} (4.4 mM barbituric acid, 1.8 mM sodium barbitone, 145 mM NaCl, pH 7.4, 5 mM Mg^{++}, 5 mM Ca^{++}), BBS/ Mg^{++}/Ca^{++} with 0.1% gelatin, chromium chloride contained in buffer; i.e., CrCl$_3$.6 H$_2$O (0.5 mg /mL in BBS/ Mg^{++}/Ca^{++}) and mannan, 100 µg/mL in BBS/ Mg^{++}/Ca^{++}.

1.   Rabbit whole blood (2 mL) was split into two 1.5 mL eppendorf tubes and centrifuged for 3 minutes at 8000 rpm (approximately 5.9 rcf) in a refrigerated eppendorf

centrifuge at 4°C. The RBC pellet was washed three times after re-suspending in ice-cold BBS/Mg^{++}/Ca^{++}. After the third wash, the pellet was re-suspended in 4 mL BBS/Mg^{++}/Ca^{++}. Two mL of this aliquot were added to a 15-mL falcon tube to be used as the uncoated control. The remaining 2 mL of the RBCs aliquot were diluted in 2 mL of CrCl$_3$ buffer, 2 mL of the mannan solution were added and the suspension was incubated at room temperature for 5 minutes with gentle mixing. The reaction was terminated by adding 7.5 mL of BBS/0.1% gelatin/Mg^{++}/Ca^{++} to the mixture. The erythrocytes were pelleted and the RBCs were washed twice with BBS/0.1% gelatin/Mg^{++}/Ca^{++} as described above. The RBCs suspension was stored in BBS/0.1% gelatin/ Mg^{++}/Ca^{++} at 4°C.

2.   100 µl of suspended RBCs were diluted with 1.4 mL water and spun down at 8000 rpm (approximately 5.9 rcf) for 3 minutes and the OD of the supernatant was adjusted to 0.7 at 541nm (an OD of 0.7 at 541nm corresponds to approximately 10^9 erythrocytes/mL).

3.   The re-suspended RBCs were diluted with BBS/0.1% gelatin/Mg^{++}/Ca^{++} to a concentration of 10^8 /mL.

4.   Dilutions of the test sera were prepared in ice-cold BBS/gelatin/ Mg^{++}/Ca^{++} and 100 µl of each serum dilution were pipetted into the corresponding well of round-bottom plate. 100 µl of appropriately diluted RBC (108/mL) were added to each well. As a control for complete lysis, purified water (100 µL) was mixed with the diluted RBC (100 µL) to cause 100% lysis, while BBS/0.1% gelatin/ Mg^{++}/Ca^{++} without serum (100 µL) was used as a negative control. The plate was then incubated for 1 hour at 37°C.

5.   The round-bottom plate was centrifuged at 3250 rpm for 5 minutes. The supernatant from each well (100 µL) was transferred into the corresponding wells of a flat-bottom plate and OD was read in an ELISA reader at 415-490nm. Results are reported as the ratio of the OD at 415 nm to that at 49 0nm.

Results:

FIGURE 25 graphically illustrates hemolysis (as measured by hemoglobin release of lysed rabbit erythrocytes into the supernatant measured by photometry) of mannan-coated rabbit erythrocytes by mouse serum over a range of serum concentrations in serum from MASP-1/3-/- and WT control. As shown in **FIGURE 25**, it is demonstrated that inhibiting MASP-3 prevents complement-mediated lysis of mannan-

coated WT rabbit erythrocytes. These results further support the use of MASP-3 inhibitors for the treatment of one or more aspects of PNH as described in Example 5.

EXAMPLE 7

This Example demonstrates that the alternative pathway is activated in factor D-deficient serum in the presence of Ca^{++}.

Experiment #1: C3b deposition assay under alternative pathway specific conditions

Methods:

A C3b deposition assay on a zymosan-coated microtiter plate was carried out under alternative pathway-specific conditions (BBS/EGTA/Mg^{++}, no Ca^{++}) using increasing dilutions of the following mouse sera: factor D-/-; MASP- -/-; and WT.

Results:

FIGURE 26 graphically illustrates the level of C3b deposition (OD 405 nm) as a function of serum concentration in serum samples from factor D-/-, MASP-2 -/-; and WT mice sera in a C3 deposition assay carried out under alternative pathway specific conditions. As shown in **FIGURE 26**, under these conditions, factor D -/- mouse serum does not activate C3 at all and the alternative pathway is not working. MASP-2-/- serum shows alternative pathway activation at a similar rate as WT serum. These results confirm that, in the absence of Ca^{++}, factor D is required for C3b deposition. This is consistent with the evidence that MASP-3 cannot be converted into its enzymatically active form under these conditions because the interactions of MASP-1, the MASP-3 activating enzyme, and MASP-3 with their respective carbohydrate recognition components is Ca^{++}-dependent.

Experiment #2: C3b deposition assay under physiological conditions

Methods:

A C3b deposition assay was carried under physiological conditions (BBS/Ca^{++}/Mg^{++}) (allowing both the LP and AP to function) using increasing dilutions of the following mouse sera: factor D -/-; MASP-2 -/-; and WT.

Results:

FIGURE 27 graphically illustrates the level of C3b deposition (OD 405 nm) as a function of serum concentration using samples of sera from factor D-/-; MASP-2-/-; and WT mice in a C3b deposition assay carried out under physiological conditions (in the presence of Ca^{++}). As shown in **FIGURE 27**, factor D-/- mouse serum activates C3 via both the lectin and the alternative pathway with no difference as compared to WT serum through the serum dilutions indicated. MASP- -/- serum shows the turnover of C3 in lower serum dilutions by the alternative pathway only (i.e., MASP-3-driven alternative pathway activation). These results indicate that in the presence of Ca^{++}, factor D is not required given that MASP-3 can drive alternative pathway activity.

Experiment #3: C3b Deposition Assay Using Mouse Sera deficient in factor B or factor D in the presence or absence of MASP-2 mAb

Methods:

A C3b deposition assay was carried out under physiological conditions (BBS/Ca^{++}/Mg^{++}) on mannan coated microtiter plates as follows:

1. Micro-titer ELISA plates were coated overnight at 4°C with mannan (1 μg/mL) in coating buffer (15 mM Na$_2$CO$_3$, 35 mM NaHCo$_3$, 0.02% sodium azide, pH 9.6).

2. The next day, residual protein binding sites were blocked for 2 hours at room temperature with 250 μl/well with 0.1% HSA in BBS (4 mM barbital, 145 mM NaCl, 2 mM CaCl$_2$, 1 mM MgCl$_2$, pH 7.4).

3. Plates were washed three times with wash buffer (TBS with 0.05% Tween 20 and 5 mM CaCl$_2$).

4. 1:10 diluted serum samples in BBS were added to the wells at the specified time points. Wells receiving only buffer were used as negative controls. The plate was incubated at 37°C for up to 40 minutes.

5. The plates were then washed 3 times with the wash buffer.

6. Then 100 μl of rabbit anti-human C3c (Dako) diluted 1:5000 in washing buffer was added to the wells and plates were incubated for 90 minutes at 37°C.

7. After being washed for three times with washing buffer, 100 μl of alkaline phosphatase-conjugated anti-rabbit diluted 1:5000 in washing buffer was added to the wells followed by incubation for 90 minutes at room temperature.

8. After washing, alkaline phosphatase was detected by adding 100 μl of substrate solution.

9. After incubation for 15 minutes, the optical density was measured at OD 405 nm.

Results:

FIGURE 28 graphically illustrates the level of C3b deposition (OD 405 nm) as a function of serum incubation time (minutes) in mouse serum samples obtained from factor D-/- or factor B-/- mice in the presence or absence of MASP-2 mAb in a C3b deposition assay carried out under physiological conditions (in the presence of Ca^{++}). As shown in **FIGURE 28**, there is no difference in the amount of C3b deposition in WT and factor D-/- serum, providing strong support for the conclusion that MASP-3 can initiate alternative pathway activation, even in the absence of factor D. The observed signal is thought to be due to both lectin pathway and alternative pathway activation. As further shown in **FIGURE 28**, factor D-/- plus MASP-2 mAb shows MASP-3-mediated alternative pathway activation only. The factor B-/- plus MASP-2 mAb was background only (data not shown). Heat-inactivated serum was used as the background control value, which was identical to factor D-/- and factor B-/- with MASP-2 (data not shown).

In summary, the results in this Example demonstrate that factor D is only essential under non-physiological conditions (i.e. when testing for alternative pathway activation in BBS/EGTA/ Mg^{++} in the absence of Ca^{++}). In contrast, when testing for alternative pathway activation under physiological conditions (in the presence of Ca^{++}), which allows the alternative pathway to be activated via MASP-3, factor D-deficient serum is not at all deficient in alternative pathway activity as compared to the WT control. Therefore, under physiological conditions, factor D is redundant, in that the initiation of alternative pathway activation is driven by MASP-3. These results support the conclusion that the lectin pathway directs AP activation through a MASP-3-dependent activation event.

EXAMPLE 8

This example describes exemplary methods for producing murine monoclonal antibodies against human MASP-1, MASP-2 or MASP-3 polypeptides, and for generating dual, bispecific or pan-specific MASP antibodies.

1. *Methods for generating MASP antibodies*

Male A/J mice (Harlan, Houston, Tex.), 8 to 12 weeks of age, are injected subcutaneously with 100 µg human full-length polypeptides: rMASP-1 (SEQ ID NO:10), rMASP-2 (SEQ ID NO:5) or rMASP-3 (SEQ ID NO:8), or antigen fragments thereof, for example as set forth in **TABLE 2**, in complete Freund's adjuvant (Difco Laboratories, Detroit, Mich.) in 200 µl of phosphate buffered saline (PBS) pH 7.4. Two weeks later, the mice are injected subcutaneously with 50 µg of the same human polypeptide in incomplete Freund's adjuvant. At the sixth week, the mice are injected with 50 µg of the same human polypeptide in PBS and are fused 4 days later.

For each fusion, single-cell suspensions are prepared from the spleen of an immunized mouse and used for fusion with Sp2/0 myeloma cells. 5×10^8 of the Sp2/0 and 5×10^8 spleen cells are fused in a medium containing 50% polyethylene glycol (M.W. 1450) (Kodak, Rochester, N.Y.) and 5% dimethylsulfoxide (Sigma Chemical Co., St. Louis, Mo.). The cells are then adjusted to a concentration of 1.5×10^5 spleen cells per 200 µl of the suspension in Iscove medium (Gibco, Grand Island, N.Y.), supplemented with 10% fetal bovine serum, 100 units/mL of penicillin, 100 µg/mL of streptomycin, 0.1 mM hypoxanthine, 0.4 µM aminopterin and 16 µM thymidine. Two hundred microliters of the cell suspension are added to each well contained in roughly twenty 96-well microculture plates. After about ten days, culture supernatants are withdrawn for screening for reactivity with the target purified antigen (MASP-1, MASP-2 or MASP-3, or the antigen fragment from **TABLE 2**) in an ELISA assay.

ELISA Assay (described with reference to MASP-2): Wells of Immulon 2 (Dynatech Laboratories, Chantilly, Va.) microtest plates are coated by adding 50 µl of purified hMASP-2 at 50 ng/mL overnight at room temperature. The low concentration of MASP-2 used for coating enables the selection of high-affinity antibodies. After the coating solution is removed by flicking the plate, 200 µl of BLOTTO (non-fat dry milk) in PBS is added to each well for one hour to block the non-specific sites. An hour later, the wells are then washed with a buffer PBST (PBS containing 0.05% Tween 20). The culture supernatants from each fusion well (50 uL) are mixed with 50 µl of BLOTTO and

then added to individual MASP-2-coated wells of the microtest plates. After one hour of incubation, the wells are washed with PBST and antibody binding to MASP-2 is detected by adding horseradish peroxidase (HRP)-conjugated goat anti-mouse IgG (Fc specific) (Jackson ImmunoResearch Laboratories, West Grove, Pa.). The HRP-conjugated anti-mouse IgG is diluted appropriately in BLOTTO to provide an appropriate signal to noise ratio, and added to each sample-containing well. After washing, the bound HRP-conjugated antibody is detected with the peroxidase substrate solution. Peroxidase substrate solution containing 0.1% 3,3,5,5 tetramethyl benzidine (Sigma, St. Louis, Mo.) and 0.0003% hydrogen peroxide (Sigma) is added to the wells for color development for 30 minutes. The reaction is terminated by addition of 50 μl of 2M H_2SO_4 per well and the optical density at 450 nm of the reaction mixture is measured with a BioTek ELISA Reader (BioTek Instruments, Winooski, Vt.).

Binding Assay (described with reference to MASP-2):

Culture supernatants that test positive in the MASP-2 ELISA assay described above can be tested in a binding assay to determine the binding affinity that the MASP-2 inhibitory agents have for MASP-2. A similar assay can also be used to determine if the inhibitory agents bind to other antigens in the complement system.

Polystyrene microtiter plate wells (96-well medium binding plates, Corning Costar, Cambridge, MA) are coated with MASP-2 (20 ng/100 μl/well, Advanced Research Technology, San Diego, CA) in phosphate-buffered saline (PBS) pH 7.4 overnight at 4°C. After aspirating the MASP-2 solution, wells are blocked with PBS containing 1% bovine serum albumin (BSA; Sigma Chemical) for 2 hours at room temperature. Wells without MASP-2 coating serve as the background controls. Aliquots of hybridoma supernatants or purified MASP-2 MoAbs, at varying concentrations in BSA PBS blocking solution, are added to the wells. Following a two-hour incubation at room temperature, the wells are extensively rinsed with PBS. MASP-2-bound MASP-2 MoAb is detected by the addition of peroxidase-conjugated goat anti-mouse IgG (Sigma Chemical) in blocking solution, which is allowed to incubate for 1hour at room temperature. The plate is rinsed again thoroughly with PBS, and 100 μl of 3,3',5,5'-tetramethyl benzidine (TMB) substrate (Kirkegaard and Perry Laboratories, Gaithersburg, MD) is added. The reaction of TMB is quenched by the addition of 100 μl of 1M phosphoric acid, and the plate is read at 450 nm in a microplate reader (SPECTRA MAX 250, Molecular Devices, Sunnyvale, CA).

The culture supernatants from the positive wells are then tested for the ability to inhibit complement activation in a functional assay such as the C4 cleavage assay as described herein (Example 9). The cells in positive wells are then cloned by limiting dilution. The MoAbs are tested again for reactivity with hMASP-2 in an ELISA assay as described above. The selected hybridomas are grown in spinner flasks and the spent culture supernatant collected for antibody purification by protein A affinity chromatography.

MASP-2 antibodies may be assayed for LEA-2 inhibitory activity in a C4 cleavage assay, for example as described in Example 9.

While the ELISA and Binding Assay above are described with reference to MASP-2, it will be understood by those of skill in the art that the same ELISA and binding assays may be carried out using MASP-1 or MASP-3 polypeptides and antigen fragments thereof (e.g., as described in **TABLE 2**). MASP-3 antibodies may be assayed for inhibition of MASP-3 serine protease cleavage of a MASP-3 substrate and for LEA-1 inhibitory activity in a C3b deposition assay, for example as described in Example 4, in a hemolysis assay as described in Example 5. MASP-1 antibodies may be assayed for inhibition of MASP-1 serine protease cleavage of a MASP-1 substrate, for inhibition of MASP-3 activation, and for LEA-1 inhibitory activity in a C3b deposition assay, for example as described in Example 4, and in a hemolysis assay as described in Example 5.

2. *Methods for Generating Dual-MASP antibodies*

MASP-2/3 dual inhibitory antibodies: As shown in **FIGURES 4, 6** and **7C**, there are regions conserved between MASP-2 and MASP-3 in the serine protease domain, encoded by the beta chain of SEQ ID NO:5 and SEQ ID NO:8. Therefore, a dual MASP-2/3 antibody can be generated using an antigen comprising or consisting of the serine protease domain of MASP-2 (or MASP-3), such as the beta chain of SEQ ID NO:5 (or SEQ ID NO:8) to generate a monoclonal antibody as described above, or alternatively, these antigen(s) may be used to screen a phage library for clones that specifically bind to these antigen(s), followed by screening for dual binding to MASP-3 (or MASP-1). The dual MASP-2/3 antibodies are then screened for inhibitory activity in a functional assay, for example as described in **TABLE 2**.

MASP-1/3 dual inhibitory antibodies: As shown in **FIGURES 3-5**, MASP-1 and MASP-3 share an identical conserved region in the CUBI-CCP2 domain (aa 25-432 of SEQ ID NO:10), which is also shared by MAp44. As shown in **FIGURE 3**, MAp44 does

not contain a CCP2 domain. Therefore, a dual MASP-1/3 antibody inclusive of MAp44 is generated using an antigen comprising or consisting of the CUBI-CCP-2 domain of MASP-1 (or MASP-3) to generate a monoclonal antibody as described above, or alternatively, this antigen is used to screen a phage library for clones that specifically bind to this antigen, followed by screening for dual binding to MASP-3 (or MASP-1). A dual MASP-1/3 antibody exclusive of MAp44 is generated in a similar manner, using an antigen comprising or consisting of the CCP2 domain of MASP-1 (or MASP-3). The dual MASP-1/3 antibodies are then screened for inhibitory activity in a functional assay, for example as described in **TABLE 2**.

MASP-1/2 dual inhibitory antibodies: As shown in **FIGURES 4**, **6** and **7A**, the serine protease domain of MASP-1 and MASP-2 contains regions that are conserved. Therefore, a dual MASP-1/2 antibody is generated using an antigen comprising or consisting of the serine protease domain of MASP-1 (or MASP-2) to generate a monoclonal antibody as described above, or alternatively, this antigen is used to screen a phage library for clones that specifically bind to this antigen, followed by screening for dual binding to MASP-2 (or MASP-1). The dual MASP-1/2 antibodies are then screened for inhibitory activity in a functional assay, for example as described in **TABLE 2**.

3. *Methods for Generating Pan-specific MASP antibodies:*

Alpha Chain: Numerous patches of identity between MASP-2 and MASP-1/3 suggest that it may be possible to generate monoclonal antibodies that bind MASP-1/3 and MASP-2. In particular, most of the identity lies within the CUB1-EGF-CUB2 domains, as shown in **FIGURE 5**. The various domains illustrated in **FIGURE 5** were identified according to Yongqing, et al., *Biochemica et Biophysica Acta* 1824:253-262 (2012); Teillet et al., *J. Biol. Chem.* 283:25715-25724 (2008); and Marchler-Bauer et al., *Nucleic Acids Res.* 39:D225-229 (2011).

Beta Chain: Numerous patches of identity between MASP-2 and MASP-1/3, as shown in **FIGURE 6**, would allow for the generation of a pan-specific MASP-1/2/3 inhibitor.

Methods:

Pan-specific MASP inhibitory antibodies (*i.e.,* antibodies that inhibit MASP-1, 2 and 3 activity) are generated as follows:

1. Screen a library against MASP-1/3 and MASP-2 Alpha-chain CUB1-EGF-CUB2 domains and select clones that cross-react to both MASP-1/3 and MASP-2.

2. Screen the clones for the ability to inhibit functional activity, for example as described in **TABLE 2**.

3. Use the DTLacO affinity/functionality maturation technology (Yabuki et al., *PLoS ONE*, 7(4):e36032 (2012)) to optimize both binding to all three proteins and inhibitory function.

4. As described in **TABLE 2**, pan-MASP inhibitors can be used to inhibit LEA-1- and LEA-2-mediated complement activation.

4. Methods for generating bispecific MASP-2/3 antibodies

Bispecific MASP-2/3 inhibitory antibodies are generated as follows:

1. Exemplary MASP-2 specific inhibitory antibodies that bind to the CCP1 domain and inhibit MASP-2-dependent complement activation have been identified, as described in Examples 11-14.

2. A MASP-3 specific inhibitory antibody is generated by screening a library against the MASP-3 polypeptide and identifying MASP-3 antibodies, as described in Example 15, followed by assaying the antibodies for LEA-1 inhibitory activity in a functional assay, for example as described in **TABLE 2**. Exemplary MASP-3 antibodies are described in Example 15.

3. The antigen binding region specific for MASP-2 and MASP-3 are cloned into a framework to generate a bi-specific antibody. Numerous bispecific antibody formats have been described, including immunoglobulin G-like formats as well as various fusion protein and single chain variable fragment configurations (Holmes, *Nature Reviews, Drug Discovery* 10:798-800 (2011), Müller and Kontermann, *Biodrugs* 24:89-98 (2010)). In one example, bispecific antibodies can be generated by fusing two hybridomas expressing antibodies against two distinct antigens, resulting in various heavy and light chain pairings, a percentage of which comprise a heavy and light chain specific for one antigen paired with a heavy and light chain specific for the other antigen (Milstein and Cuello, *Nature* 305:537-539 (1983)). A similar bispecific antibody may be generated recombinantly, by co-expressing two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) (e.g. MASP-2 antibodies as described in Examples 11-14, MASP-3 antibodies as described in Example 15) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, including at least part of the

hinge, C_H2, and C_H3 regions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism.

In addition to paired immunoglobulin heavy and light chains, linkage of single chain variable fragments specific for two different targets is exemplified in Kipriyanov et al., *J. Mol. Biol.* 293:41 (1999)). In this example, a single polynucleotide expression construct is designed to encode two pairs of heavy and light chain variable regions separated by linker peptides, with each pair imparting specificity for a distinct protein target. Upon expression, the polypeptide assembles in a configuration in which the heavy and light chain pair specific for one target forms one antigen-binding surface of the protein, and the other pair forms a separate antigen-binding surface, creating a molecule termed a single chain diabody. Depending on the length of the linker between the central heavy and light chain variable region pair, the polypeptide can also be forced to dimerize, resulting in the formation of a tandem diabody.

For example, DNA encoding the following immunoglobulin polypeptides may be inserted into one or more vectors and expressed in a suitable host organism to generate the following illustrative, non-limiting examples of a bi-specific antibodies.

MASP-2/3 bispecific antibodies

In one embodiment, a bispecific antibody is provided that binds human MASP-2 and human MASP-3 and comprises:

(I) a MASP-2 specific binding region comprising at least one or more of the following:a) a heavy chain variable region comprising: i) a heavy chain CDR1 comprising the amino acid sequence from 31-35 of SEQ ID NO:21; and ii) a heavy chain CDR2 comprising the amino acid sequence from 50-65 of SEQ ID NO:21; and iii) a heavy chain CDR3 comprising the amino acid sequence from 95-102 of SEQ ID NO:21; and/or at least one or more of the following:b) a light chain variable region comprising: i) a light chain CDR1 comprising the amino acid sequence from 24-34 of either SEQ ID NO:25 or SEQ ID NO:27; and ii) a light chain CDR2 comprising the amino acid sequence from 50-56 of either SEQ ID NO:25 or SEQ ID NO:27; and iii) a light chain CDR3 comprising the amino acid sequence from 89-97 of either SEQ ID NO:25 or SEQ ID NO:27; and

(II) a MASP-3 specific binding region, optionally a MASP-3 specific binding region comprising at least one of a) a heavy chain variable region comprising: i) a heavy

chain CDR1 comprising the amino acid sequence from 31-35 of SEQ ID NO:25 or SEQ ID NO:26; and ii) a heavy chain CDR2 comprising the amino acid sequence from 50-65 of SEQ ID NO:25 or SEQ ID NO:26; and iii) a heavy chain CDR3 comprising the amino acid sequence from 95-102 of SEQ ID NO:25 or SEQ ID NO:26; and

b) a light chain variable region comprising: i) a light chain CDR1 comprising the amino acid sequence from 24-34 of either SEQ ID NO:28 or SEQ ID NO:29; and ii) a light chain CDR2 comprising the amino acid sequence from 50-56 of either SEQ ID NO:28 or SEQ ID NO:29; and iii) a light chain CDR3 comprising the amino acid sequence from 89-97 of either SEQ ID NO:28 or SEQ ID NO:29.

MASP-1/2 bispecific antibodies

In one embodiment, a bispecific antibody is provided that binds human MASP-1 and human MASP-2 and comprises:

(I) a MASP-2 specific binding region comprising at least one or more of the following:a) a heavy-chain variable region comprising: i) a heavy-chain CDR1 comprising the amino acid sequence from 31-35 of SEQ ID NO:21; and ii) a heavy-chain CDR2 comprising the amino acid sequence from 50-65 of SEQ ID NO:21; and iii) a heavy-chain CDR3 comprising the amino acid sequence from 95-102 of SEQ ID NO:21; and/or at least one or more of the following:b) a light-chain variable region comprising: i) a light-chain CDR1 comprising the amino acid sequence from 24-34 of either SEQ ID NO:25 or SEQ ID NO:27; and ii) a light chain CDR2 comprising the amino acid sequence from 50-56 of either SEQ ID NO:25 or SEQ ID NO:27; and iii) a light-chain CDR3 comprising the amino acid sequence from 89-97 of either SEQ ID NO:25 or SEQ ID NO:27; and

(II) a MASP-1 specific binding region.

4. Testing for functional inhibitory activity against MASP-2 and/or MASP-3 is carried out, for example as described in **TABLE 2**, and as further described herein.

EXAMPLE 9

This example describes an *in vitro* C4 cleavage assay used as a functional screen to identify MASP-2 inhibitory agents capable of blocking MASP-2-dependent complement activation via L-ficolin/P35, H-ficolin, M-ficolin or mannan.

<u>C4 Cleavage Assay</u>: A C4 cleavage assay has been described by Petersen, S.V., et al., *J. Immunol. Methods* 257:107, 2001, which measures lectin pathway activation resulting from lipoteichoic acid (LTA) on *S. aureus,* which binds to L-ficolin.

Reagents: Formalin-fixed *S. aureus* (DSM20233) is prepared as follows: bacteria is grown overnight at 37°C in tryptic soy blood medium, washed three times with PBS, then fixed for 1 hour at room temperature in PBS/0.5% formalin, and washed a further three times with PBS, before being resuspended in coating buffer (15 mM Na_2CO_3, 35 mM $NaHCO_3$, pH 9.6).

Assay: The wells of a Nunc MaxiSorb microtiter plate (Nalgene Nunc International, Rochester, NY) are coated with: 100 µl of formalin-fixed *S. aureus* DSM20233 ($OD_{550} = 0.5$) in coating buffer with 1 µg of L-ficolin in coating buffer. After overnight incubation, wells are blocked with 0.1% human serum albumin (HSA) in TBS (10 mM Tris-HCl, 140 mM NaCl, pH 7.4), then are washed with TBS containing 0.05% Tween 20 and 5 mM $CaCl_2$ (wash buffer). Human serum samples are diluted in 20 mM Tris-HCl, 1 M NaCl, 10 mM $CaCl_2$, 0.05% Triton X-100, 0.1% HSA, pH 7.4, which prevents activation of endogenous C4 and dissociates the C1 complex (composed of C1q, C1r and C1s). MASP-2 inhibitory agents, including MASP-2 MoAbs, are added to the serum samples in varying concentrations. The diluted samples are added to the plate and incubated overnight at 4°C. After 24 hours, the plates are washed thoroughly with wash buffer, then 0.1 µg of purified human C4 (obtained as described in Dodds, A.W., *Methods Enzymol.* 223:46, 1993) in 100 µl of 4 mM barbital, 145 mM NaCl, 2 mM $CaCl_2$, 1 mM $MgCl_2$, pH 7.4 is added to each well. After 1.5 hours at 37°C, the plates are washed again and C4b deposition is detected using alkaline phosphatase-conjugated chicken anti-human C4c (obtained from Immunsystem, Uppsala, Sweden) and measured using the colorimetric substrate ρ-nitrophenyl phosphate.

C4 Assay on mannan: The assay described above is adapted to measure lectin pathway activation via MBL by coating the plate with LSP and mannan prior to adding serum mixed with various MASP-2 inhibitory agents.

C4 assay on H-ficolin (Hakata Ag): The assay described above is adapted to measure lectin pathway activation via H-ficolin by coating the plate with LPS and H-ficolin prior to adding serum mixed with various MASP-2 inhibitory agents.

EXAMPLE 10

The following assay is used to test whether a MASP inhibitory agent blocks the classical pathway by analyzing the effect of a MASP inhibitory agent under conditions in which the classical pathway is initiated by immune complexes.

Methods: To test the effect of a MASP inhibitory agent on conditions of complement activation where the classical pathway is initiated by immune complexes, triplicate 50 µl samples containing 90% NHS are incubated at 37°C in the presence of 10 µg/mL immune complex or PBS, and parallel triplicate samples (+/- immune complexes) are also included containing 200 nM anti-properdin monoclonal antibody during the 37°C incubation. After a two-hour incubation at 37°C, 13 mM EDTA is added to all samples to stop further complement activation and the samples are immediately cooled to 5°C. The samples are then stored at -70°C prior to being assayed for complement activation products (C3a and sC5b-9) using ELISA kits (Quidel, Catalog Nos. A015 and A009) following the manufacturer's instructions.

EXAMPLE 11

This example describes the identification of high-affinity MASP-2 Fab2 antibody fragments that block MASP-2 activity.

Background and rationale: MASP-2 is a complex protein with many separate functional domains, including: binding site(s) for MBL and ficolins, a serine protease catalytic site, a binding site for proteolytic substrate C2, a binding site for proteolytic substrate C4, a MASP-2 cleavage site for autoactivation of MASP-2 zymogen, and two Ca^{++} binding sites. Fab2 antibody fragments were identified that bind with high affinity to MASP-2, and the identified Fab2 fragments were tested in a functional assay to determine if they were able to block MASP-2 functional activity.

To block MASP-2 functional activity, an antibody or Fab2 antibody fragment must bind and interfere with a structural epitope on MASP-2 that is required for MASP-2 functional activity. Therefore, many or all of the high-affinity binding MASP-2 Fab2s may not inhibit MASP-2 functional activity unless they bind to structural epitopes on MASP-2 that are directly involved in MASP-2 functional activity.

A functional assay that measures inhibition of lectin pathway C3 convertase formation was used to evaluate the "blocking activity" of MASP-2 Fab2s. It is known that the primary physiological role of MASP-2 in the lectin pathway is to generate the next functional component of the lectin-mediated complement pathway, namely the lectin pathway C3 convertase. The lectin pathway C3 convertase is a critical enzymatic complex (C4bC2a) that proteolytically cleaves C3 into C3a and C3b. MASP-2 is not a structural component of the lectin pathway C3 convertase (C4bC2a); however, MASP-2

functional activity is required in order to generate the two protein components (C4b, C2a) that comprise the lectin pathway C3 convertase. Furthermore, all of the separate functional activities of MASP-2 listed above appear to be required in order for MASP-2 to generate the lectin pathway C3 convertase. For these reasons, a preferred assay to use in evaluating the "blocking activity" of MASP-2 Fab2s is believed to be a functional assay that measures inhibition of lectin pathway C3 convertase formation.

Generation of High Affinity Fab2s: A phage display library of human variable light and heavy chain antibody sequences and automated antibody selection technology for identifying Fab2s that react with selected ligands of interest was used to create high-affinity Fab2s to rat MASP-2 protein (SEQ ID NO:13). A known amount of rat MASP-2 (~1 mg, >85% pure) protein was utilized for antibody screening. Three rounds of amplification were utilized for selection of the antibodies with the best affinity. Approximately 250 different hits expressing antibody fragments were picked for ELISA screening. High affinity hits were subsequently sequenced to determine uniqueness of the different antibodies.

Fifty unique MASP-2 antibodies were purified and 250 μg of each purified Fab2 antibody was used for characterization of MASP-2 binding affinity and complement pathway functional testing, as described in more detail below.

Assays used to Evaluate the Inhibitory (blocking) Activity of MASP-2 Fab2s

1. *Assay to Measure Inhibition of Formation of Lectin Pathway C3 Convertase:*

Background: The lectin pathway C3 convertase is the enzymatic complex (C4bC2a) that proteolytically cleaves C3 into the two potent proinflammatory fragments, anaphylatoxin C3a and opsonic C3b. Formation of C3 convertase appears to be a key step in the lectin pathway in terms of mediating inflammation. MASP-2 is not a structural component of the lectin pathway C3 convertase (C4bC2a); therefore MASP-2 antibodies (or Fab2) will not directly inhibit activity of preexisting C3 convertase. However, MASP-2 serine protease activity is required in order to generate the two protein components (C4b, C2a) that comprise the lectin pathway C3 convertase. Therefore, MASP-2 Fab2, which inhibits MASP-2 functional activity (i.e., blocking MASP-2 Fab2) will inhibit *de novo* formation of lectin pathway C3 convertase. C3 contains an unusual and highly reactive thioester group as part of its structure. Upon cleavage of C3 by C3 convertase in this assay, the thioester group on C3b can form a covalent bond with

hydroxyl or amino groups on macromolecules immobilized on the bottom of the plastic wells via ester or amide linkages, thus facilitating detection of C3b in the ELISA assay.

Yeast mannan is a known activator of the lectin pathway. In the following method to measure formation of C3 convertase, plastic wells coated with mannan were incubated for 30 minutes at 37°C with diluted rat serum to activate the lectin pathway. The wells were then washed and assayed for C3b immobilized onto the wells using standard ELISA methods. The amount of C3b generated in this assay is a direct reflection of the *de novo* formation of lectin pathway C3 convertase. MASP-2 Fab2s at selected concentrations were tested in this assay for their ability to inhibit C3 convertase formation and consequent C3b generation.

Methods:

96-well Costar Medium Binding plates were incubated overnight at 5°C with mannan diluted in 50 mM carbonate buffer, pH 9.5 at 1 μg/50 μl/well. After overnight incubation, each well was washed three times with 200 μl PBS. The wells were then blocked with 100 μl/well of 1% bovine serum albumin in PBS and incubated for one hour at room temperature with gentle mixing. Each well was then washed three times with 200 μl of PBS. The MASP-2 Fab2 samples were diluted to selected concentrations in Ca^{++} and Mg^{++} containing GVB buffer (4.0 mM barbital, 141 mM NaCl, 1.0 mM $MgCl_2$, 2.0 mM $CaCl_2$, 0.1% gelatin, pH 7.4) at 5°C. A 0.5% rat serum was added to the above samples at 5°C and 100 μl was transferred to each well. Plates were covered and incubated for 30 minutes in a 37°C waterbath to allow complement activation. The reaction was stopped by transferring the plates from the 37°C waterbath to a container containing an ice-water mix. Each well was washed five times with 200 μl with PBS-Tween 20 (0.05% Tween 20 in PBS), then washed two times with 200 μl PBS. A 100 μl/well of 1:10,000 dilution of the primary antibody (rabbit anti-human C3c, DAKO A0062) was added in PBS containing 2.0 mg/mL bovine serum albumin and incubated 1 hour at room temperature with gentle mixing. Each well was washed 5 times with 200 μl PBS. 100 μl/well of 1:10,000 dilution of the secondary antibody (peroxidase-conjugated goat anti-rabbit IgG, American Qualex A102PU) was added in PBS containing 2.0 mg/mL bovine serum albumin and incubated for one hour at room temperature on a shaker with gentle mixing. Each well was washed five times with 200 μl with PBS. 100 μl/well of the peroxidase substrate TMB (Kirkegaard & Perry Laboratories) was added

and incubated at room temperature for 10 minutes. The peroxidase reaction was stopped by adding 100 Tl/well of 1.0 M H_3PO_4 and the OD_{450} was measured.

2.   *Assay to Measure Inhibition of MASP-2-dependent C4 Cleavage*

Background: The serine protease activity of MASP-2 is highly specific and only two protein substrates for MASP-2 have been identified; C2 and C4. Cleavage of C4 generates C4a and C4b. MASP-2 Fab2 may bind to structural epitopes on MASP-2 that are directly involved in C4 cleavage (e.g., MASP-2 binding site for C4; MASP-2 serine protease catalytic site) and thereby inhibit the C4 cleavage functional activity of MASP-2.

Yeast mannan is a known activator of the lectin pathway. In the following method to measure the C4 cleavage activity of MASP-2, plastic wells coated with mannan were incubated for 30 minutes at 37°C with diluted rat serum to activate the lectin pathway. Since the primary antibody used in this ELISA assay only recognizes human C4, the diluted rat serum was also supplemented with human C4 (1.0 µg/mL). The wells were then washed and assayed for human C4b immobilized onto the wells using standard ELISA methods. The amount of C4b generated in this assay is a measure of MASP-2-dependent C4 cleavage activity. MASP-2 Fab2 at selected concentrations was tested in this assay for ability to inhibit C4 cleavage.

Methods: 96-well Costar Medium Binding plates were incubated overnight at 5°C with mannan diluted in 50 mM carbonate buffer, pH 9.5 at 1.0 Tg/50 µl/well. Each well was washed 3 times with 200 µl PBS. The wells were then blocked with 100 µl/well of 1% bovine serum albumin in PBS and incubated for one hour at room temperature with gentle mixing. Each well was washed 3 times with 200 µl of PBS. MASP-2 Fab2 samples were diluted to selected concentrations in Ca^{++} and Mg^{++} containing GVB buffer (4.0 mM barbital, 141 mM NaCl, 1.0 mM $MgCl_2$, 2.0 mM $CaCl_2$, 0.1% gelatin, pH 7.4) at 5°C. 1.0 µg/mL human C4 (Quidel) was also included in these samples. 0.5% rat serum was added to the above samples at 5°C and 100 µl was transferred to each well. The plates were covered and incubated for 30 minutes in a 37°C waterbath to allow complement activation. The reaction was stopped by transferring the plates from the 37°C waterbath to a container containing an ice-water mix. Each well was washed 5 times with 200 µl with PBS-Tween 20 (0.05% Tween 20 in PBS), then each well was washed with 2 times with 200 µl PBS. 100 µl/well of 1:700 dilution of biotin-conjugated chicken anti-human C4c (Immunsystem AB, Uppsala, Sweden) was added in PBS

containing 2.0 mg/mL bovine serum albumin (BSA) and incubated one hour at room temperature with gentle mixing. Each well was washed 5 times with 200 μl PBS. 100 μl/well of 0.1 μg/mL of peroxidase-conjugated streptavidin (Pierce Chemical #21126) was added in PBS containing 2.0 mg/mL BSA and incubated for one hour at room temperature on a shaker with gentle mixing. Each well was washed 5 x 200 μl with PBS. 100 μl/well of the peroxidase substrate TMB (Kirkegaard & Perry Laboratories) was added and incubated at room temperature for 16 min. The peroxidase reaction was stopped by adding 100 μl/well of 1.0 M H_3PO_4 and the OD_{450} was measured.

3.   *Binding Assay of anti-rat MASP-2 Fab2 to 'Native' rat MASP-2*

Background: MASP-2 is usually present in plasma as a MASP-2 dimer complex that also includes specific lectin molecules (mannose-binding protein (MBL) and ficolins). Therefore, if one is interested in studying the binding of MASP-2 Fab2 to the physiologically relevant form of MASP-2, it is important to develop a binding assay in which the interaction between the Fab2 and 'native' MASP-2 in plasma, rather than purified recombinant MASP-2, is used. In this binding assay, the 'native' MASP-2-MBL complex from 10% rat serum was first immobilized onto mannan-coated wells. The binding affinity of various MASP-2 Fab2s to the immobilized 'native' MASP-2 was then studied using a standard ELISA methodology.

Methods: 96-well Costar High Binding plates were incubated overnight at 5°C with mannan diluted in 50 mM carbonate buffer, pH 9.5 at 1 μg/50 μl/well. Each well was washed 3 times with 200 μl PBS. The wells were blocked with 100 μl/well of 0.5% nonfat dry milk in PBST (PBS with 0.05% Tween 20) and incubated for one hour at room temperature with gentle mixing. Each well was washed 3 times with 200 μl of TBS/Tween/Ca^{++} Wash Buffer (Tris-buffered saline, 0.05% Tween 20, containing 5.0 mM $CaCl_2$, pH 7.4. 10% rat serum in High Salt Binding Buffer (20 mM Tris, 1.0 M NaCl, 10 mM $CaCl_2$, 0.05% Triton-X100, 0.1% (w/v) bovine serum albumin, pH 7.4) was prepared on ice. 100 μl/well was added and incubated overnight at 5°C. Wells were washed 3 times with 200 μl of TBS/Tween/Ca^{++} Wash Buffer. Wells were then washed 2 times with 200 μl PBS. 100 μl/well of selected concentration of MASP-2 Fab2 diluted in Ca^{++} and Mg^{++} containing GVB Buffer (4.0 mM barbital, 141 mM NaCl, 1.0 mM $MgCl_2$, 2.0 mM $CaCl_2$, 0.1% gelatin, pH 7.4) was added and incubated for one hour at room temperature with gentle mixing. Each well was washed 5 times with 200 μl PBS. 100 μl/well of HRP-conjugated goat anti-Fab2 (Biogenesis Cat No 0500-0099) diluted 1:5000

in 2.0 mg/mL bovine serum albumin in PBS was added and incubated for one hour at room temperature with gentle mixing. Each well was washed 5 times with 200 μl PBS. 100 μl/well of the peroxidase substrate TMB (Kirkegaard & Perry Laboratories) was added and incubated at room temperature for 70 minutes. The peroxidase reaction was stopped by adding 100 μl/well of 1.0 M H_3PO_4 and OD_{450} was measured.

RESULTS:

Approximately 250 different Fab2s that reacted with high affinity to the rat MASP-2 protein were picked for ELISA screening. These high-affinity Fab2s were sequenced to determine the uniqueness of the different antibodies, and 50 unique MASP-2 antibodies were purified for further analysis. 250 ug of each purified Fab2 antibody was used for characterization of MASP-2 binding affinity and complement pathway functional testing. The results of this analysis are shown below in **TABLE 13**.

TABLE 13: MASP-2 FAB2 THAT BLOCK LECTIN PATHWAY COMPLEMENT ACTIVATION

Fab2 antibody #	C3 Convertase (IC_{50} (nM)	K_d (nM)	C4 Cleavage IC_{50} (nM)
88	0.32	4.1	ND
41	0.35	0.30	0.81
11	0.46	0.86	<2 nM
86	0.53	1.4	ND
81	0.54	2.0	ND
66	0.92	4.5	ND
57	0.95	3.6	<2 nM
40	1.1	7.2	0.68
58	1.3	2.6	ND
60	1.6	3.1	ND
52	1.6	5.8	<2 nM
63	2.0	6.6	ND
49	2.8	8.5	<2 nM
89	3.0	2.5	ND
71	3.0	10.5	ND
87	6.0	2.5	ND
67	10.0	7.7	ND

As shown above in **TABLE 13**, of the 50 MASP-2 Fab2s tested, 17 were identified as MASP-2-blocking Fab2s that potently inhibit C3 convertase formation with IC_{50} equal to or less than 10 nM Fab2s (a 34% positive hit rate). Eight of the 17 Fab2s identified have IC_{50}s in the subnanomolar range. Furthermore, all seventeen of the MASP-2 blocking Fab2s shown in **TABLE 13** gave essentially complete inhibition of C3 convertase formation in the lectin pathway C3 convertase assay. This is an important consideration, since it is theoretically possible that a "blocking" Fab2 may only fractionally inhibit MASP-2 function even when each MASP-2 molecule is bound by the Fab2.

Although mannan is a known activator of the lectin pathway, it is theoretically possible that the presence of anti-mannan antibodies in the rat serum might also activate the classical pathway and generate C3b via the classical pathway C3 convertase. However, each of the seventeen blocking MASP-2 Fab2s listed in this example potently inhibits C3b generation (>95 %), thus demonstrating the specificity of this assay for lectin pathway C3 convertase.

Binding assays were also performed with all seventeen of the blocking Fab2s in order to calculate an apparent K_d for each. The results of the binding assays of anti-rat MASP-2 Fab2s to native rat MASP-2 for six of the blocking Fab2s are also shown in **TABLE 13**. Similar binding assays were also carried out for the other Fab2s, the results of which are shown in **TABLE 13**. In general, the apparent K_ds obtained for binding of each of the six Fab2s to 'native' MASP-2 corresponds reasonably well with the IC_{50} for the Fab2 in the C3 convertase functional assay. There is evidence that MASP-2 undergoes a conformational change from an 'inactive' to an 'active' form upon activation of its protease activity (Feinberg et al., *EMBO J 22*:2348-59 (2003); Gal et al., *J. Biol. Chem. 280*:33435-44 (2005)). In the normal rat plasma used in the C3 convertase formation assay, MASP-2 is present primarily in the 'inactive' zymogen conformation. In contrast, in the binding assay, MASP-2 is present as part of a complex with MBL bound to immobilized mannan; therefore, the MASP-2 would be in the 'active' conformation (Petersen et al., *J. Immunol Methods 257*:107-16, 2001). Consequently, one would not necessarily expect an exact correspondence between the IC_{50} and K_d for each of the seventeen blocking Fab2 tested in these two functional assays because, in each assay, the Fab2 would be binding a different conformational form of MASP-2. Nevertheless, with the exception of Fab2 #88, there appears to be a reasonably close correspondence

between the IC_{50} and apparent K_d for each of the other sixteen Fab2 tested in the two assays (see **TABLE 13**).

Several of the blocking Fab2s were evaluated for inhibition of MASP-2-mediated cleavage of C4. As shown in **TABLE 13**, all of the Fab2s tested were found to inhibit C4 cleavage with IC_{50}s similar to those obtained in the C3 convertase assay.

Although mannan is a known activator of the lectin pathway, it is theoretically possible that the presence of anti-mannan antibodies in the rat serum might also activate the classical pathway and thereby generate C4b by C1s-mediated cleavage of C4. However, several MASP-2 Fab2s have been identified that potently inhibit C4b generation (>95 %), thus demonstrating the specificity of this assay for MASP-2-mediated C4 cleavage. C4, like C3, contains an unusual and highly reactive thioester group as part of its structure. Upon cleavage of C4 by MASP-2 in this assay, the thioester group on C4b can form a covalent bond with hydroxyl or amino groups on macromolecules immobilized on the bottom of the plastic wells *via* ester or amide linkages, thus facilitating detection of C4b in the ELISA assay.

These studies clearly demonstrate the creation of high-affinity FAB2s to rat MASP-2 protein that functionally block both C4 and C3 convertase activity, thereby preventing lectin pathway activation.

EXAMPLE 12

This Example describes the epitope mapping for several of the blocking anti-rat MASP-2 Fab2 antibodies that were generated as described in Example 11.

Methods:

The following proteins, all with N-terminal 6X His tags were expressed in CHO cells using the pED4 vector:

rat MASP-2A, a full-length MASP-2 protein, inactivated by altering the serine at the active center to alanine (S613A);

rat MASP-2K, a full-length MASP-2 protein altered to reduce autoactivation (R424K);

CUBI-II, an N-terminal fragment of rat MASP-2 that contains the CUBI, EGF-like and CUBII domains only; and

CUBI/EGF-like, an N-terminal fragment of rat MASP-2 that contains the CUBI and EGF-like domains only.

These proteins were purified from culture supernatants by nickel-affinity chromatography, as previously described (Chen et al., *J. Biol. Chem.* 276:25894-02 (2001)).

A C-terminal polypeptide (CCPII-SP), containing CCPII and the serine protease domain of rat MASP-2, was expressed in *E. coli* as a thioredoxin fusion protein using pTrxFus (Invitrogen). Protein was purified from cell lysates using Thiobond affinity resin. The thioredoxin fusion partner was expressed from empty pTrxFus as a negative control.

All recombinant proteins were dialyzed into TBS buffer and their concentrations determined by measuring the OD at 280 nm.

Dot Blot Analysis:

Serial dilutions of the five recombinant MASP-2 polypeptides described above (and the thioredoxin polypeptide as a negative control for CCPII-serine protease polypeptide) were spotted onto a nitrocellulose membrane. The amount of protein spotted ranged from 100 ng to 6.4 pg, in five-fold steps. In later experiments, the amount of protein spotted ranged from 50 ng down to 16 pg, again in five-fold steps. Membranes were blocked with 5% skimmed milk powder in TBS (blocking buffer) then incubated with 1.0 μg/mL MASP-2 Fab2s in blocking buffer (containing 5.0 mM Ca^{++}). Bound Fab2s were detected using HRP-conjugated anti-human Fab (AbD/Serotec; diluted 1/10,000) and an ECL detection kit (Amersham). One membrane was incubated with polyclonal rabbit-anti human MASP-2 Ab (described in Stover et al., *J Immunol 163*:6848-59 (1999)) as a positive control. In this case, bound Ab was detected using HRP-conjugated goat anti-rabbit IgG (Dako; diluted 1/2,000).

MASP-2 Binding Assay:

ELISA plates were coated with 1.0 μg/well of recombinant MASP-2A or CUBI-II polypeptide in carbonate buffer (pH 9.0) overnight at 4°C. Wells were blocked with 1% BSA in TBS, then serial dilutions of the MASP-2 Fab2s were added in TBS containing 5.0 mM Ca^{++}. The plates were incubated for one hour at RT. After washing three times with TBS/tween/Ca^{++}, HRP-conjugated anti-human Fab (AbD/Serotec) diluted 1/10,000 in TBS/Ca^{++} was added and the plates incubated for a further one hour at room temperature. Bound antibody was detected using a TMB peroxidase substrate kit (Biorad).

Results:

Results of the dot blot analysis demonstrating the reactivity of the Fab2s with various MASP-2 polypeptides are provided below in **TABLE 14**. The numerical values provided in **TABLE 14** indicate the amount of spotted protein required to give approximately half-maximal signal strength. As shown, all of the polypeptides (with the exception of the thioredoxin fusion partner alone) were recognized by the positive control Ab (polyclonal anti-human MASP-2 sera, raised in rabbits).

TABLE 14: REACTIVITY WITH VARIOUS RECOMBINANT RAT MASP-2 POLYPEPTIDES ON DOT BLOTS

Fab2 Antibody #	MASP-2A	CUBI-II	CUBI/EGF-like	CCPII-SP	Thioredoxin
40	0.16 ng	NR	NR	0.8 ng	NR
41	0.16 ng	NR	NR	0.8 ng	NR
11	0.16 ng	NR	NR	0.8 ng	NR
49	0.16 ng	NR	NR	>20 ng	NR
52	0.16 ng	NR	NR	0.8 ng	NR
57	0.032 ng	NR	NR	NR	NR
58	0.4 ng	NR	NR	2.0 ng	NR
60	0.4 ng	0.4 ng	NR	NR	NR
63	0.4 ng	NR	NR	2.0 ng	NR
66	0.4 ng	NR	NR	2.0 ng	NR
67	0.4 ng	NR	NR	2.0 ng	NR
71	0.4 ng	NR	NR	2.0 ng	NR
81	0.4 ng	NR	NR	2.0 ng	NR
86	0.4 ng	NR	NR	10 ng	NR
87	0.4 ng	NR	NR	2.0 ng	NR
Positive Control	<0.032 ng	0.16 ng	0.16 ng	<0.032 ng	NR

NR = No reaction. The positive control antibody is polyclonal anti-human MASP-2 sera, raised in rabbits.

All of the Fab2s reacted with MASP-2A as well as MASP-2K (data not shown). The majority of the Fab2s recognized the CCPII-SP polypeptide but not the N-terminal

fragments.   The two exceptions are Fab2 #60 and Fab2 #57.   Fab2 #60 recognizes MASP-2A and the CUBI-II fragment, but not the CUBI/EGF-like polypeptide or the CCPII-SP polypeptide, suggesting it binds to an epitope in CUBII, or spanning the CUBII and the EGF-like domain.   Fab2 # 57 recognizes MASP-2A but not any of the MASP-2 fragments tested, perhaps indicating that this Fab2 recognizes an epitope in CCP1. Fab2 #40 and #49 bound only to complete MASP-2A. In the ELISA binding assay, Fab2 #60 also bound to the CUBI-II polypeptide, albeit with a slightly lower apparent affinity (data not shown).

These finding demonstrate the identification of unique blocking Fab2s to multiple regions of the MASP-2 protein.

EXAMPLE 13

This Example describes the pharmacodynamic analysis of representative high-affinity MASP-2 Fab2 antibodies that were identified as described in Example 11.

Background/Rationale:

As described in **Example 11**, in order to identify high-affinity antibodies that block the rat lectin pathway, rat MASP-2 protein was utilized to pan a phage display library. This library was designed to provide for high immunological diversity and was constructed using entirely human immunoglobin gene sequences.   As shown in **Example 11**, approximately 250 individual phage clones were identified that bound with high affinity to the rat MASP-2 protein by ELISA screening. Sequencing of these clones identified 50 unique MASP-2 antibody-encoding phage.   Fab2 protein was expressed from these clones, purified and analyzed for MASP-2 binding affinity and lectin complement pathway functional inhibition.

As shown in **TABLE 13** of **Example 11**, 17 MASP-2 Fab2s with functional blocking activity were identified as a result of this analysis (a 34% hit rate for blocking antibodies).   Functional inhibition of the lectin complement pathway by Fab2s was apparent at the level of C4 deposition, which is a direct measure of C4 cleavage by MASP-2.   Importantly, inhibition was equally evident when C3 convertase activity was assessed, demonstrating functional blockade of the lectin complement pathway. The 17 MASP-2 blocking Fab2s identified as described in **Example 11** potently inhibit C3 convertase formation with IC_{50} values equal to or less than 10 nM. Eight of the 17 Fab2s identified have IC_{50} values in the sub-nanomolar range.   Furthermore, all 17 of the MASP-2 blocking Fab2s gave essentially complete inhibition of the C3 convertase

formation in the lectin pathway C3 convertase assay, as summarized in **TABLE 13** of Example 11. Moreover, each of the 17 blocking MASP-2 Fab2s shown in **TABLE 13** potently inhibit C3b generation (>95%), thus demonstrating the specificity of this assay for lectin pathway C3 convertase.

Rat IgG2c and mouse IgG2a full-length antibody isotype variants were derived from Fab2 #11. This Example describes the *in vivo* characterization of these isotypes for pharmacodynamic parameters.

Methods:

As described in **Example 11**, rat MASP-2 protein was utilized to pan a Fab phage display library, from which Fab2 #11 was identified. Rat IgG2c and mouse IgG2a full-length antibody isotype variants were derived from Fab2 #11. Both rat IgG2c and mouse IgG2a full-length antibody isotypes were characterized *in vivo* for pharmacodynamic parameters as follows.

In vivo study in mice:

A pharmacodynamic study was carried out in mice to investigate the effect of MASP-2 antibody dosing on the plasma lectin pathway activity *in vivo*. In this study, C4 deposition was measured *ex vivo* in a lectin pathway assay at various time points following subcutaneous (sc) and intraperitoneal (ip) administration of 0.3 mg/kg or 1.0 mg/kg of the mouse MASP-2 MoAb (mouse IgG2a full-length antibody isotype derived from Fab2#11).

FIGURE 29A graphically illustrates lectin pathway specific C4b deposition on a zymosan-coated microtiter plate, measured *ex vivo* in undiluted serum samples taken from mice (n=3 mice/group) at various time points after subcutaneous dosing of either 0.3 mg/kg or 1.0 mg/kg of the mouse MASP-2 MoAb. Serum samples from mice collected prior to antibody dosing served as negative controls (100% activity), while serum supplemented *in vitro* with 100 nM of the same blocking MASP-2 antibody was used as a positive control (0% activity).

The results shown in **FIGURE 29A** demonstrate a rapid and complete inhibition of C4b deposition following subcutaneous administration of 1.0 mg/kg dose of mouse MASP-2 MoAb. A partial inhibition of C4b deposition was seen following subcutaneous administration of a dose of 0.3 mg/kg of mouse MASP-2 MoAb.

The time course of lectin pathway recovery was followed for three weeks following a single ip administration of mouse MASP-2 MoAb at 0.6 mg/kg in mice. As

shown in **FIGURE 29B**, a precipitous drop in lectin pathway activity occurred after antibody dosing followed by complete lectin pathway inhibition that lasted for about 7 days after i.p. administration. Slow restoration of lectin pathway activity was observed over the second and third weeks, with complete lectin pathway restoration in the mice by 17 days following MASP-2 MoAb administration.

These results demonstrate that the mouse MASP-2 Moab derived from Fab2 #11 inhibits the lectin pathway of mice in a dose-responsive manner when delivered systemically.

EXAMPLE 14

This example describes the identification, using phage display, of fully human scFv antibodies that bind to MASP-2 and inhibit lectin-mediated complement activation (LEA-2) while leaving the classical (C1q-dependent) pathway component of the immune system intact.

Overview:

Fully human, high-affinity MASP-2 antibodies were identified by screening a phage display library. The variable light and heavy chain fragments of the antibodies were isolated in both a scFv format and in a full-length IgG format. The human MASP-2 antibodies are useful for inhibiting cellular injury associated with lectin pathway-mediated alternative complement pathway activation while leaving the classical (C1q-dependent) pathway component of the immune system intact. In some embodiments, the subject MASP-2 inhibitory antibodies have the following characteristics: (a) high affinity for human MASP-2 (e.g., a K_D of 10 nM or less), and (b) inhibit MASP-2-dependent complement activity in 90% human serum with an IC_{50} of 30 nM or less.

Methods:

Expression of full-length catalytically inactive MASP-2:

The full-length cDNA sequence of human MASP-2 (SEQ ID NO: 4), encoding the human MASP-2 polypeptide with leader sequence (SEQ ID NO:5) was subcloned into the mammalian expression vector pCI-Neo (Promega), which drives eukaryotic expression under the control of the CMV enhancer/promoter region (described in Kaufman R.J. et al., *Nucleic Acids Research 19*:4485-90, 1991; Kaufman, *Methods in Enzymology, 185*:537-66 (1991)).

In order to generate catalytically inactive human MASP-2A protein, site-directed mutagenesis was carried out as described in US2007/0172483, hereby incorporated herein by reference. The PCR products were purified after agarose gel electrophoresis and band preparation and single adenosine overlaps were generated using a standard tailing procedure. The adenosine-tailed MASP-2A was then cloned into the pGEM-T easy vector and transformed into *E. coli*. The human MASP-2A was further subcloned into either of the mammalian expression vectors pED or pCI-Neo.

The MASP-2A expression construct described above was transfected into DXB1 cells using the standard calcium phosphate transfection procedure (Maniatis et al., 1989). MASP-2A was produced in serum-free medium to ensure that preparations were not contaminated with other serum proteins. Media was harvested from confluent cells every second day (four times in total). The level of recombinant MASP-2A averaged approximately 1.5 mg/liter of culture medium. The MASP-2A (Ser-Ala mutant described above) was purified by affinity chromatography on MBP-A-agarose columns

MASP-2A ELISA on ScFv Candidate Clones identified by panning/scFv conversion and filter screening

A phage display library of human immunoglobulin light- and heavy-chain variable region sequences was subjected to antigen panning followed by automated antibody screening and selection to identify high-affinity scFv antibodies to human MASP-2 protein. Three rounds of panning the scFv phage library against HIS-tagged or biotin-tagged MASP-2A were carried out. The third round of panning was eluted first with MBL and then with TEA (alkaline). To monitor the specific enrichment of phages displaying scFv fragments against the target MASP-2A, a polyclonal phage ELISA against immobilized MASP-2A was carried out. The scFv genes from panning round 3 were cloned into a pHOG expression vector and run in a small-scale filter screening to look for specific clones against MASP-2A.

Bacterial colonies containing plasmids encoding scFv fragments from the third round of panning were picked, gridded onto nitrocellulose membranes and grown overnight on non-inducing medium to produce master plates. A total of 18,000 colonies were picked and analyzed from the third panning round, half from the competitive elution and half from the subsequent TEA elution. Panning of the scFv phagemid library against MASP-2A followed by scFv conversion and a filter screen yielded 137 positive clones. 108/137 clones were positive in an ELISA assay for MASP-2 binding (data not shown),

of which 45 clones were further analyzed for the ability to block MASP-2 activity in normal human serum.

Assay to Measure Inhibition of Formation of Lectin Pathway C3 Convertase

A functional assay that measures inhibition of lectin pathway C3 convertase formation was used to evaluate the "blocking activity" of the MASP-2 scFv candidate clones. MASP-2 serine protease activity is required in order to generate the two protein components (C4b, C2a) that comprise the lectin pathway C3 convertase. Therefore, a MASP-2 scFv that inhibits MASP-2 functional activity (i.e., a blocking MASP-2 scFv), will inhibit *de novo* formation of lectin pathway C3 convertase. C3 contains an unusual and highly reactive thioester group as part of its structure. Upon cleavage of C3 by C3 convertase in this assay, the thioester group on C3b can form a covalent bond with hydroxyl or amino groups on macromolecules immobilized on the bottom of the plastic wells via ester or amide linkages, thus facilitating detection of C3b in the ELISA assay.

Yeast mannan is a known activator of the lectin pathway. In the following method to measure formation of C3 convertase, plastic wells coated with mannan were incubated with diluted human serum to activate the lectin pathway. The wells were then washed and assayed for C3b immobilized onto the wells using standard ELISA methods. The amount of C3b generated in this assay is a direct reflection of the *de novo* formation of lectin pathway C3 convertase. MASP-2 scFv clones at selected concentrations were tested in this assay for their ability to inhibit C3 convertase formation and consequent C3b generation.

Methods:

The 45 candidate clones identified as described above were expressed, purified and diluted to the same stock concentration, which was again diluted in Ca^{++} and Mg^{++} containing GVB buffer (4.0 mM barbital, 141 mM NaCl, 1.0 mM $MgCl_2$, 2.0 mM $CaCl_2$, 0.1% gelatin, pH 7.4) to assure that all clones had the same amount of buffer. The scFv clones were each tested in triplicate at the concentration of 2 μg/mL. The positive control was OMS100 Fab2 and was tested at 0.4 μg/mL. C3c formation was monitored in the presence and absence of the scFv/IgG clones.

Mannan was diluted to a concentration of 20 μg/mL (1 μg/well) in 50mM carbonate buffer (15mM Na_2CO_3 + 35mM $NaHCO_3$ + 1.5 mM NaN_3), pH 9.5 and coated on an ELISA plate overnight at 4°C. The next day, the mannan-coated plates were

washed 3 times with 200 μl PBS. 100 μl of 1% HSA blocking solution was then added to the wells and incubated for 1 hour at room temperature. The plates were washed 3 times with 200 μl PBS, and stored on ice with 200 μl PBS until addition of the samples.

Normal human serum was diluted to 0.5% in CaMgGVB buffer, and scFv clones or the OMS100 Fab2 positive control were added in triplicates at 0.01 μg/mL; 1 μg/mL (only OMS100 control) and 10 μg/mL to this buffer and preincubated 45 minutes on ice before addition to the blocked ELISA plate. The reaction was initiated by incubation for one hour at 37°C and was stopped by transferring the plates to an ice bath. C3b deposition was detected with a Rabbit α-Mouse C3c antibody followed by Goat α-Rabbit HRP. The negative control was buffer without antibody (no antibody = maximum C3b deposition), and the positive control was buffer with EDTA (no C3b deposition). The background was determined by carrying out the same assay except that the wells were mannan-free. The background signal against plates without mannan was subtracted from the signals in the mannan-containing wells. A cut-off criterion was set at half of the activity of an irrelevant scFv clone (VZV) and buffer alone.

Results: Based on the cut-off criterion, a total of 13 clones were found to block the activity of MASP-2. All 13 clones producing > 50% pathway suppression were selected and sequenced, yielding 10 unique clones. All ten clones were found to have the same light chain subclass, λ3, but three different heavy chain subclasses: VH2, VH3 and VH6. In the functional assay, five out of the ten candidate scFv clones gave IC_{50} nM values less than the 25 nM target criteria using 0.5% human serum.

To identify antibodies with improved potency, the three mother scFv clones, identified as described above, were subjected to light-chain shuffling. This process involved the generation of a combinatorial library consisting of the VH of each of the mother clones paired up with a library of naïve, human lambda light chains (VL) derived from six healthy donors. This library was then screened for scFv clones with improved binding affinity and/or functionality.

TABLE 15: Comparison of functional potency in IC_{50} (nM) of the lead daughter clones and their respective mother clones (all in scFv format)

scFv clone	1% human serum C3 assay (IC_{50} nM)	90% human serum C3 assay (IC_{50} nM)	90% human serum C4 assay (IC_{50} nM)
17D20mc	38	nd	nd
17D20m_d3521N11	26	>1000	140
17N16mc	68	nd	nd
17N16m_d17N9	48	15	230

Presented below are the heavy-chain variable region (VH) sequences for the mother clones and daughter clones shown above in **TABLE 15**, and listed below in **TABLES 16A-F**.

The Kabat CDRs (31-35 (H1), 50-65 (H2) and 95-102 (H3)) are bolded; and the Chothia CDRs (26-32 (H1), 52-56 (H2) and 95-101 (H3)) are underlined.

17D20_35VH-21N11VL heavy chain variable region (VH) (SEQ ID NO:15, encoded by SEQ ID NO:14)

QVTLKESGPVLVKPTETLTLTCTVS**GFSLS****RGKMG**VSWIRQPPGKALEW**LA****HIFSS**DEKSYRTSLKSRLTISKDTSKNQVVLTMTNMDPVDTAT**YYCARIRR**G GIDYWGQGTLVTVSS

d17N9 heavy chain variable region (VH) (SEQ ID NO:16)

QVQLQQSGPGLVKPSQTLSLTCAIS**GDSVSST****SAA**WNWIRQSPSRGLEW**L****GRTY****YR**SKWYNDYAVSVKSRITINPDTSKNQFSLQLNSVTPEDT**AVYYCARD**PFGVPF DIWGQGTMVTVSS

Heavy Chain Variable Region

TABLE 16A: Heavy chain (aa 1-20)

Heavy chain																				
aa	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**	**14**	**15**	**16**	**17**	**18**	**19**	**20**
d3521N11 (SEQ:15)	Q	V	T	L	K	E	S	G	P	V	L	V	K	P	T	E	T	L	T	L
d17N9 (SEQ:16)	Q	V	Q	L	Q	Q	S	G	P	G	L	V	K	P	S	Q	T	L	S	L

TABLE 16B: Heavy chain (aa 21-40)

Heavy chain						CDR-H1														
aa	**21**	**22**	**23**	**24**	**25**	**26**	**27**	**28**	**29**	**30**	**31**	**32**	**33**	**34**	**35**	**36**	**37**	**38**	**39**	**40**
d3521N11 (SEQ:15)	T	C	T	V	S	G	F	S	L	S	R	G	K	M	G	V	S	W	I	R
d17N9 (SEQ:16)	T	C	A	I	S	G	D	S	V	S	S	T	S	A	A	W	N	W	I	R

TABLE 16C: Heavy chain (aa 41-60)

Heavy chain									CDR-H2											
aa	**41**	**42**	**43**	**44**	**45**	**46**	**47**	**48**	**49**	**50**	**51**	**52**	**53**	**54**	**55**	**56**	**57**	**58**	**59**	**60**
d3521N11 (SEQ:15)	Q	P	P	G	K	A	L	E	W	L	A	H	I	F	S	S	D	E	K	S
d17N9 (SEQ:16)	Q	S	P	S	R	G	L	E	W	L	G	R	T	Y	Y	R	S	K	W	Y

TABLE 16D: Heavy chain (aa 61-80)

Heavy chain	CDR-H2 (cont'd)																			
aa	**61**	**62**	**63**	**64**	**65**	**66**	**67**	**68**	**69**	**70**	**71**	**72**	**73**	**74**	**75**	**76**	**77**	**78**	**79**	**80**
d3521N11 (SEQ:15)	Y	R	T	S	L	K	S	R	L	T	I	S	K	D	T	S	K	N	Q	V
d17N9 (SEQ:16)	N	D	Y	A	V	S	V	K	S	R	I	T	I	N	P	D	T	S	K	N

TABLE 16E: Heavy chain (aa 81-100)

Heavy chain														CDR-H3					
aa	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
d3521N11 (SEQ:15)	V	L	T	M	T	N	M	D	P	V	D	T	A	T	**Y**	**Y**	**C**	**A**	**R**	**I**
d17N9 (SEQ:16)	Q	F	S	L	Q	L	N	S	V	T	P	E	D	T	**A**	**V**	**Y**	**Y**	**C**	**A**

TABLE 16F: heavy chain (aa 101-118)

Heavy chain	CDR-H3 (cont'd)																			
aa	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120
d3521N11 (SEQ:15)	**R**	R	G	G	I	D	Y	W	G	Q	G	T	L	V	T	V	S	S		
d17N9 (SEQ:16)	**R**	D	P	F	G	V	P	F	D	I	W	G	Q	G	T	M	V	T	V	S

Presented below are the light-chain variable region (VL) sequences for the mother clones and daughter clones listed below in **TABLES 17A-F**.

The Kabat CDRs (24-34 (L1); 50-56 (L2); and 89-97 (L3) are bolded; and the Chothia CDRs (24-34 (L1); 50-56 (L2) and 89-97 (L3) are underlined. These regions are the same whether numbered by the Kabat or Chothia system.

<u>17D20m_d3521N11 light chain variable region (VL) (SEQ ID NO:17)</u>

QPVLTQPPSLSVSPGQTASITCS**<u>GEKLGDKYAYW</u>**YQQKPGQSPVLVMYQ**<u>DKQRPSG</u>**IPERFSGSNSGNTATLTISGTQAMDEADYYCQ**<u>AWDSSTAVF</u>**GGGTKLTVL

<u>17N16m_d17N9 light chain variable region (VL) (SEQ ID NO:19, encoded by SEQ ID NO:18)</u>

SYELIQPPSVSVAPGQTATITCA**<u>GDNLGKKRVHW</u>**YQQRPGQAPVLVIYD**<u>DSDRPSG</u>**IPDRFSASNSGNTATLTITRGEAGDEADYYCQ**<u>VWDIATDHV</u>**VFGGGTKLTVLAAAGSEQKLISE

TABLE 17A: Light chain (aa 1-20)

Light chain																				
aa	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
d3521N11 (SEQ:17)	Q	P	V	L	T	Q	P	P	S	**L**	S	V	S	P	G	Q	T	A	S	I
d17N9 (SEQ:19)	S	Y	**E**	L	**I**	Q	P	P	S	V	S	V	A	P	G	Q	T	A	**T**	I

TABLE 17B: Light chain (aa 21-40)

Light chain			CDR-L1																	
aa	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
d3521N11 (SEQ:17)	T	C	S	<u>G</u>	<u>E</u>	<u>K</u>	<u>L</u>	<u>G</u>	<u>D</u>	<u>K</u>	<u>**Y**</u>	<u>A</u>	<u>Y</u>	<u>W</u>	Y	Q	Q	K	P	G
d17N9 (SEQ:19)	T	C	**A**	<u>G</u>	<u>**D**</u>	<u>N</u>	<u>L</u>	<u>G</u>	<u>**K**</u>	<u>K</u>	<u>**R**</u>	<u>V</u>	<u>H</u>	<u>W</u>	Y	Q	Q	**R**	P	G

TABLE 17C: Light chain (aa 41-60)

Light chain									CDR-L2										
aa	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
d3521N11 (SEQ:17)	**Q**	S	P	V	L	V	**M**	Y	Q	<u>D</u>	<u>**K**</u>	<u>**Q**</u>	<u>R</u>	<u>P</u>	<u>S</u>	<u>G</u>	I	P	**E**	R
d17N9 (SEQ:19)	Q	A	P	V	L	V	**I**	Y	D	<u>D</u>	<u>S</u>	<u>D</u>	<u>R</u>	<u>P</u>	<u>S</u>	<u>G</u>	I	P	**D**	R

TABLE 17D: Light chain (aa 61-80)

Light chain	CDR-L2 (cont'd)																			
aa	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
d3521N11 (SEQ:17)	F	S	G	S	N	S	G	N	T	A	T	L	T	I	S	G	T	Q	A	M
d17N9 (SEQ:19)	F	S	**A**	S	N	S	G	N	T	A	T	L	T	**I**	**T**	R	**G**	E	A	G

TABLE 17E: Light chain (aa 81-100)

Light chain									CDR-L3											
aa	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
d3521N11 (SEQ:17)	D	**X**	A	D	Y	Y	C	Q	<u>A</u>	<u>W</u>	<u>D</u>	<u>S</u>	<u>S</u>	<u>T</u>	<u>A</u>	<u>V</u>	<u>F</u>	G	**G**	G
d17N9 (SEQ:19)	D	E	A	D	Y	Y	C	Q	<u>V</u>	<u>W</u>	<u>D</u>	<u>I</u>	<u>A</u>	<u>T</u>	<u>D</u>	<u>H</u>	<u>V</u>	V	F	G

TABLE 17F: Light chain (aa 101-120)

Light chain	CDR-L3 (cont'd)																			
aa	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120
d3521N11 (SEQ:17)	T	K	L	T	V	L	A	A	A	G	S	E	Q	K	L	I	S	E	E	D
d17N9 (SEQ:19)	G	G	T	K	L	T	V	L	A	A	A	G	S	E	Q	K	L	I	S	E

The MASP-2 antibodies OMS100 and MoAb_d3521N11VL, which have both been demonstrated to bind to human MASP-2 with high affinity and have the ability to block functional complement activity, were analyzed with regard to epitope binding by dot blot analysis. The results show that d3521N11 and OMS100 antibodies are highly specific for MASP-2 and do not bind to MASP-1/3. Neither antibody bound to MAp19 nor to MASP-2 fragments that did not contain the CCP1 domain of MASP-2, leading to the conclusion that the binding sites encompass CCP1.

Accordingly, in one embodiment, a MASP-2 inhibitory agent for use in the compositions and methods of the claimed invention comprises a human antibody that binds a polypeptide consisting of human MASP-2 (SEQ ID NO:3), wherein the antibody comprises:

I) a) a heavy chain variable region comprising: i) a heavy chain CDR1 comprising the amino acid sequence from 31-35 of SEQ ID NO:21; and ii) a heavy chain CDR2 comprising the amino acid sequence from 50-65 of SEQ ID NO:21; and iii) a heavy chain CDR3 comprising the amino acid sequence from 95-102 of SEQ ID NO:21; and

b) a light chain variable region comprising: i) a light chain CDR1 comprising the amino acid sequence from 24-34 of either SEQ ID NO:25 or SEQ ID NO:27; and ii) a light chain CDR2 comprising the amino acid sequence from 50-56 of either SEQ ID NO:25 or SEQ ID NO:27; and iii) a light chain CDR3 comprising the amino acid sequence from 89-97 of either SEQ ID NO:25 or SEQ ID NO:27; or II) a variant thereof that is otherwise identical to said variable domains, except for up to a combined total of 6 amino acid substitutions within said CDR regions of said heavy-chain variable region and up to a combined total of 6 amino acid substitutions within said CDR regions of said light-chain variable region, wherein the antibody or variant thereof inhibits MASP-2-dependent complement activation.

EXAMPLE 15

This Example describes the generation of MASP-1 and MASP-3 monoclonal antibodies using an *in vitro* system comprising a modified DT40 cell line, DTLacO.

Background/Rationale:

Antibodies against human MASP-1 and MASP-3 were generated using an *in vitro* system comprising a modified DT40 cell line, DTLacO, that permits reversible induction of diversification of a particular polypeptide, as further described in WO2009029315 and US2010093033. DT40 is a chicken B cell line that is known to constitutively mutate its heavy and light chain immunoglobulin (Ig) genes in culture. Like other B cells, this constitutive mutagenesis targets mutations to the V region of Ig genes, and thus, the CDRs of the expressed antibody molecules. Constitutive mutagenesis in DT40 cells takes place by gene conversion using as donor sequences an array of non-functional V gene segments (pseudo-V genes; ψV) situated upstream of each functional V region. Deletion of the ψV region was previously shown to cause a switch in the mechanism of diversification from gene conversion to somatic hypermutation, the mechanism commonly observed in human B cells. The DT40 chicken B cell lymphoma line has been shown to be a promising starting point for antibody evolution *ex vivo* (Cumbers, S.J. *et al. Nat Biotechnol* 20, 1129-1134 (2002); Seo, H. *et al. Nat Biotechnol* 23, 731-735 (2005)). DT40 cells proliferate robustly in culture, with an 8-10 hour doubling time (compared to 20-24 hr for human B cell lines), and they support very efficient homologous gene targeting (Buerstedde, J.M. *et al. Embo J* 9, 921-927 (1990)). DT40 cells command enormous potential V region sequence diversity given that they can access two distinct physiological pathways for diversification, gene conversion and somatic hypermutation,

which create templated and nontemplated mutations, respectively (Maizels, N. *Annu Rev Genet* 39, 23-46 (2005)). Diversified heavy and light chain immunoglobulins (Igs) are expressed in the form of a cell-surface displayed IgM. Surface IgM has a bivalent form, structurally similar to an IgG molecule. Cells that display IgM with specificity for a particular antigen can be isolated by binding either immobilized soluble or membrane displayed versions of the antigen. However, utility of DT40 cells for antibody evolution has been limited in practice because — as in other transformed B cell lines — diversification occurs at less than 1% the physiological rate.

In the system used in this example, as described in WO2009029315 and US2010093033, the DT40 cells were engineered to accelerate the rate of Ig gene diversification without sacrificing the capacity for further genetic modification or the potential for both gene conversion and somatic hypermutation to contribute to mutagenesis. Two key modifications to DT40 were made to increase the rate of diversification and, consequently, the complexity of binding specificities in our library of cells. First, Ig gene diversification was put under the control of the potent *E. coli* lactose operator/repressor regulatory network. Multimers consisting of approximately 100 polymerized repeats of the potent *E. coli* lactose operator (PolyLacO) were inserted upstream of the rearranged and expressed Igλ and IgH genes by homologous gene targeting. Regulatory factors fused to lactose repressor protein (LacI) can then be tethered to the LacO regulatory elements to regulate diversification, taking advantage of the high affinity ($k_D=10^{-14}$ M) of lactose repressor for operator DNA. DT40 PolyLacO-λR cells, in which PolyLacO was integrated only at Igλ, exhibited a 5-fold increase in Ig gene diversification rate relative to the parental DT40 cells prior to any engineering (Cummings, W.J. *et al. PLoS Biol* 5, e246 (2007)). Diversification was further elevated in cells engineered to carry PolyLacO targeted to both the Igλ and the IgH genes ("DTLacO"). DTLacO cells were demonstrated to have diversification rates 2.5- to 9.2-fold elevated relative to the 2.8% characteristic of the parental DT40 PolyLacO-λR LacI-HP1 line. Thus, targeting PolyLacO elements to both the heavy and light chain genes accelerated diversification 21.7-fold relative to the DT40 parental cell line. Tethering regulatory factors to the Ig loci not only alters the frequency of mutagenesis, but also can change the pathway of mutagenesis creating a larger collection of unique sequence changes (Cummings et al. 2007; Cummings et al. 2008). Second, a diverse collection of sequence starting points for the tethered factor-accelerated Ig gene diversification was

generated. These diverse sequence starting points were added to DTLacO by targeting rearranged Ig heavy-chain variable regions, isolated from a two month old chick, to the heavy chain locus. The addition of these heavy chain variable regions created a repertoire of 10^7 new starting points for antibody diversification. Building these new starting points into the DTLacO cell line permits the identification of clones that bind a particular target, and then rapid affinity maturation by the tethered factors. Following affinity maturation, a full-length, recombinant chimeric IgG is made by cloning the matured, rearranged heavy- and light-chain variable sequences (VH and Vλ; consisting of chicken framework regions and the complementarity determining regions or CDRs) into expression vectors containing human IgG1 and lambda constant regions. These recombinant mAbs are suitable for *in vitro* and *in vivo* applications, and they serve as the starting point for humanization.

Methods:

Selection for MASP-1 and MASP-3 antigen binding.

Initial selections were performed by binding DTLacO populations diversified by gene targeting to beads complexed with human MASP-1 (SEQ ID NO:10) and MASP-3 antigen (SEQ ID NO:8); and subsequent selections by FACS, using fluorescence-labeled soluble antigen (Cumbers, S.J. *et al. Nat Biotechnol* **20**, 1129-1134 (2002); Seo, H. *et al. Nat Biotechnol* **23**, 731-735 (2005). Because of the conserved amino acid sequence in the alpha chain that is shared between MASP-1 and MASP-3 (shown in **FIGURE 5**), and the distinct beta chain sequences (shown in **FIGURE 6**), separate, parallel screens for binders to MASP-1 and MASP-3 were carried out to identify MASP-1 specific mAbs, MASP-3 specific mAbs and also mAbs capable of binding to both MASP-1 and MASP-3 (dual-specific). Two forms of antigen were used to select and screen for binders. First, recombinant MASP-1 or MASP-3, either full-length or a fragment, fused to an Fc domain were bound to Dynal magnetic Protein G beads or used in FACS-based selections using a PECy5-labeled anti-human IgG(Fc) secondary antibody. Alternatively, recombinant versions of MASP-1 or MASP-3 proteins were directly labeled with Dylight flours and used for selections and screening.

Binding and affinity.

Recombinant antibodies were generated by cloning PCR-amplified V regions into a vector that supported expression of human IgG1 in 293F cells (Yabuki et al., *PLoS ONE*, 7(4):e36032 (2012)). Saturation binding kinetics were determined by staining

DTLacO cells expressing antibody binding MASP-1 or MASP-3 with various concentrations of fluorescent-labeled soluble antigen. Functional assays for MASP-3 specific activityincluding MASP-3-dependent C3b deposition and MASP-3-dependent factor D cleavage were carried out as described in Examples 17 and 18, respectively. A functional assay for MASP-1-specific activity, namely the inhibition of MASP-1-dependent C3b deposition was carried out as described below.

Results:

Numerous MASP-1 and MASP-3 binding antibodies were generated using the methods described above. Binding, as demonstrated by FACS analysis, is described for the representative clones M3J5 and M3M1, which were isolated in screens for MASP-3 binders.

FIGURE 30A is a FACS histogram of MASP-3 antigen/antibody binding for DTLacO clone M3J5. **FIGURE 30B** is a FACS histogram of MASP-3 antigen/antibody binding for DTLacO clone M3M1. In **FIGURES 30A** and **30B** the gray filled curves are IgG1-stained negative control, and thick black curves are MASP-3-staining.

FIGURE 31 graphically illustrates a saturation binding curve of clone M3J5 (Clone 5) for the MASP-3 antigen. As shown in **FIGURE 31**, the apparent binding affinity of the M3J5 antibody for MASP-3 is about 31 nM.

Sequence analysis of identified clones was performed using standard methods. All clones were compared to the common (DT40) VH and VL sequences and to each other. Sequences for the two aforementioned clones, M3J5 and M3M1 are provided in an alignment with two additional representative clones, D14 and 1E10, which were identified in screens for CCP1-CCP2-SP fragments of MASP-1 and MASP-3, respectively. D14 and 1E10 bind regions common to both MASP-1 and MASP-3.

FIGURE 32A is an amino acid sequence alignment of the VH regions of M3J5, M3M1, D14 and 1E10 to the chicken DT40 VH sequence.

FIGURE 32B is an amino acid sequence alignment of the VL regions of M3J5, M3M1, D14 and 1E10 to the chicken DT40 VL sequence.

The VH and VL amino acid sequence of each clone is provided below.

Heavy Chain Variable Region (VH) sequences

FIGURE 32A shows an amino acid alignment of the heavy-Chain Variable Region (VH) sequences for the parent DTLacO (SEQ ID NO: 24), the MASP-3-binding

clones M3J5 (SEQ ID NO: 25), and M3M1 (SEQ ID NO: 26), and the MASP-1/MASP-3 dual binding clones D14 (SEQ ID NO:30), and 1E10.

The Kabat CDRs in the VH sequences below are located at the following amino acid positions::H1:aa 31-35; H2:aa 50-62; and H3:aa 95-102.

The Chothia CDRs in the VH sequences below are located at the following amino acid positions: H1:aa 26-32; H2: aa 52-56; and H3: aa 95-101.

Parent DTLacO VH (SEQ ID NO:24)

AVTLDESGGGLQTPGGALSLVCKASGFTFSSNAMGWVRQAPGKGLEWVAGIDD
DGSGTRYAPAVKGRATISRDNGQSTLRLQLNNLRAEDTGTYYCTKCAYSSGCDY
EGGYIDAWGHGTEVIVSS

Clone M3J5 VH: (SEQ ID NO:25)

AVTLDESGGGLQTPGGGLSLVCKASGFTFSSYAMGWMRQAPGKGLEYVAGIRS
DGSFTLYATAVKGRATISRDNGQSTVRLQLNNLRAEDTATYFCTRSGNVGDIDA
WGHGTEVIVSS

Clone M3M1 VH: (SEQ ID NO:26)

AVTLDESGGGLQTPGGGLSLVCKASGFDFSSYQMNWIRQAPGKGLEFVAAINRF
GNSTGHGAAVKGRVTISRDDGQSTVRLQLSNLRAEDTATYYCAKGVYGYCGSY
SCCGVDTIDAWGHGTEVIVSS

Clone D14 VH: (SEQ ID NO:30)

AVTLDESGGGLQTPGGALSLVCKASGFTFSSYAMHWVRQAPGKGLEWVAGIYK
SGAGTNYAPAVKGRATISRDNGQSTVRLQLNNLRAEDTGTYYCAKTTGSGCSSG
YRAEYIDAWGHGTEVIVSS

Clone 1E10 VH: (SEQ ID NO:32)

AVTLDESGGGLQTPGGALSLVCKASGFTFSSYDMVWVRQAPGKGLEFVAGISRN
DGRYTEYGSAVKGRATISRDNGQSTVRLQLNNLRAEDTATYYCARDAGGSAYW
FDAGQIDAWGHGTEVIVSS

Light Chain Variable Region (VL) sequences

FIGURE 32B shows an amino acid alignment of the light-Chain Variable Region (VL) sequences for the parent DTLacO (SEQ ID NO:27) and the MASP-3-binding clones M3J5 (SEQ ID NO:28), and M3M1 (SEQ ID NO:29), and the MASP-1/MASP-3 dual binding clones D14 (SEQ ID NO:31) and 1E10 (SEQ ID NO: 33).

Parent DTLacO VL (SEQ ID NO:27):

ALTQPASVSANLGGTVKITCSGGGSYAGSYYYGWYQQKSPGSAPVTVIYDNDKR
PSDIPSRFSGSLSGSTNTLTITGVRADDEAVYFCGSADNSGAAFGAGTTLTVL

Clone M3J5 VL (SEQ ID NO:28):

ALTQPASVSANPGETVKITCSGGYSGYAGSYYYGWYQQKAPGSAPVTLIYYNNK
RPSDIPSRFSGSLSGSTNTLTITGVRADDEAVYFCGSADNSGAAFGAGTTLTVL

Clone M3M1 VL (SEQ ID NO:29):

ALTQPASVSANPGETVKITCSGGGSYAGSYYYGWYQQKAPGSAPVTLIYYNNKR
PSDIPSRFSGSLSGSTNTLTITGVRADDEAVYFCGSADNSGAAFGAGTTLTVL

Clone D14 VL: (SEQ ID NO:31)

ALTQPASVSANPGETVKITCSGGGSYAGSYYYGWYQQKAPGSAPVTLIYYNNKR
PSDIPSRFSGSLSGSTNTLTITGVRADDEAVYFCGSADNSGAAFGAGTTLTVL

Clone 1E10 VL: (SEQ ID NO:33)

ALTQPASVSANPGETVKITCSGGGSYAGSYYYGWYQQKAPGSAPVTLIYYNNKR
PSDIPSRFSGSLSGSTNTLTITGVRADDEAVYFCGSADNSGAAFGAGTTLTVL

LEA-2 (MASP-2-dependent) Functional Assay

MASP-1 contributes to LEA-2 via its ability to activate MASP-2 (see **FIGURE 1**). The Wieslab® Complement System Screen MBL assay (Euro Diagnostica, Malmö, Sweden) measures C5b-C9 deposition under conditions that isolate LEA-2-dependent activation (i.e., traditional lectin pathway activity). The assay was carried out according to the manufacturer's instructions with representative clone 1E10 tested as a final concentration of 400 nM.

FIGURE 33 is a bar graph showing the inhibitory activity of the mAb 1E10 in comparison to the positive serum provided with the assay kit, as well as an isotype control antibody. As shown in **FIGURE 33**, mAb 1E10 demonstrates partial inhibition of LEA-2-dependent activation (via inhibition of MASP-1-dependent activation of MASP-2), whereas the isotype control antibody does not. Stronger inhibition should be achieved by continued affinity maturation of this antibody for MASP-1 binding using the tethered factors in the DTLacO system.

LEA-1 (MASP-3-dependent) Function Assays for representative mAbs are described below in Examples 17 and 18.

<u>Summary of Results:</u>

The above results showed that the DTLacO platform permitted rapid *ex vivo* discovery of MASP-1 and MASP-3 monoclonal antibodies with inhibitory properties on LEA-1 (as shown below in Examples 17 and 18) and on LEA-2 (as shown in this Example).

EXAMPLE 16

This Example describes the generation of polypeptide inhibitors of MASP-1 and MASP-2.

<u>Rationale:</u>

The generation of specific inhibitors of MASP-1 and MASP-2, termed SGMI-1 and SGMI-2, respectively, is described in Heja et al., *J Biol Chem* 287:20290 (2012) and Heja et al., *PNAS* 109:10498 (2012), each of which is hereby incorporated herein by reference. SGMI-1 and SGMI-2 are each 36 amino acid peptides which were selected from a phage library of variants of the *Schistocerca gregaria* protease inhibitor 2 in which six of the eight positions of the protease binding loop were fully randomized. Subsequent *in vitro* evolution yielded mono-specific inhibitors with single digit nM K_I values (Heja et al., *J. Biol. Chem.* 287:20290, 2012). Structural studies revealed that the optimized protease binding loop forms the primary binding site that defines the specificity of the two inhibitors. The amino acid sequences of the extended secondary and internal binding regions are common to the two inhibitors and contribute to the contact interface (Heja et al., 2012. *J. Biol. Chem.* 287:20290). Mechanistically, both SGMI-1 and SGMI-2 block the lectin pathway of complement activation without affecting the classical or alternative pathways (Heja et al., 2012. *Proc. Natl. Acad. Sci.* 109:10498).

The amino acid sequences of the SGMI-1 and SGMI-2 inhibitors are set forth below:

SGMI-1-full-length: LEVTCEPGTTFKDKCNTCRCGSDGKSA<u>FCTRKLCYQ</u> (SEQ ID NO:34)

SGMI-2-full-length: LEVTCEPGTTFKDKCNTCRCGSDGKSA<u>VCTKLWCNQ</u> (SEQ ID NO:35)

SGMI-1 and SGMI-2 are highly specific inhibitors of MASP-1 and MASP-2, respectively. However, as peptides they have limited potential for use in biological studies. To address these limitations, we engrafted these bioactive peptide amino acid sequences onto the amino terminus of human IgG1 Fc region to create an Fc-fusion protein,

Methods:

To express the SGMI-IgG1 Fc fusion proteins, polynucleotides encoding the SGMI-1 (SEQ ID NO:34) and SGMI-2 (SEQ ID NO:35) peptides were synthesized (DNA 2.0) and inserted into the expression vector pFUSE-hIgG1-Fc2 (InvivoGen) between nucleotide sequences encoding the IL-2 signal sequence and the human IgG1 Fc region (SEQ ID NO:36). A flexible polypeptide linker (e.g., SEQ ID NO:37 or SEQ ID NO:38) was included between the SGMI peptide and the IgG1 Fc region.

Flexible Polypeptide Linker Sequences:

GTGGGSGSSSRS (SEQ ID NO:37)

GTGGGSGSSS (SEQ ID NO:38)

The resulting constructs are described as follows:

A polynucleotide encoding the polypeptide fusion comprising the human IL-2 signal sequence, SGMI-1, linker and human IgG1-Fc (pFUSE-SGMI-1Fc), is set forth as SEQ ID NO:39, which encodes the mature polypeptide fusion comprising SGMI-1 (underlined), linker region (italicized) and human IgG1-Fc (together referred to as "SGMI-1Fc"), which is set forth as SEQ ID NO:40.

SEQ ID NO:40

LEVTCEPGTTFKDKCNTCRCGSDGKSAFCTRKLCYQ*GTGGGSGSSSRS*DK
THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP
APIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN
GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT
QKSLSLSPGK

A polynucleotide encoding the polypeptide fusion comprising the human IL-2
signal sequence, SGMI-2, linker and human IgG1-Fc (pFUSE-SGMI-2Fc), is set forth as
SEQ ID NO:41, which encodes the mature polypeptide fusion comprising SGMI-2
(underlined), linker region (italicized) and human IgG1-Fc (together referred to as
"SGMI-2Fc"), which is set forth as SEQ ID NO:42:

SEQ ID NO:42

LEVTCEPGTTFKDKCNTCRCGSDGKSAVCTKLWCNQ*GTGGGSGSSSRS*DK
THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP
APIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN
GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT
QKSLSLSPGK

Production of Recombinant proteins:

Freestyle 293-F or Expi293F cells (Invitrogen) were transiently transfected
according to the supplier's protocol with one of the two expression plasmids (pFUSE-
SGMI-1Fc (SEQ ID NO:39) and pFUSE-SGMI-2Fc (SEQ ID NO:41). After four days of
incubation at 37°C, the culture media were harvested. The Fc-fusion proteins were
purified by Protein A affinity chromatography.

Assays measuring activation of the lectin pathway.

The SGMI-1Fc and SGMI-2Fc fusion proteins were tested for the ability to inhibit
deposition of C3b from 1% serum on a mannan-coated 96-well plate, which is a measure
of lectin pathway activity. SGMI-1Fc and SGMI-2Fc were pre-incubated with 1%
normal human serum for one hour on ice before addition to wells coated with mannan (2

μg/well). C3b deposition was measured by ELISA as described in Schwaeble et al. *PNAS* 108:7523, 2011.

FIGURE 34 graphically illustrates the level of C3b deposition for 1% normal human serum plus isotype control, SGMI-1Fc or SGMI-2Fc over a concentration range of 0.15 to 1000 nM. As shown in **FIGURE 34**, both SGMI-1Fc and SGMI-2Fc inhibited C3b deposition from normal serum in mannan-coated ELISA wells, with IC_{50} values of approximately 27nM and 300nM, respectively.

These results demonstrate that the MASP-1 and MASP-2 inhibitory functions of the SGMI peptides are retained in the SGMI-1Fc and SGMI-2Fc fusion proteins.

EXAMPLE 17

Analysis of the complement pathway in 3MC serum with *S. aureus*

Background/Rationale:

It was determined that MASP-3 is not activated through exposure to non-immobilized fluid-phase mannan, zymosan A or N-acetyl cysteine either in the presence or absence of normal human serum. However it was determined that recombinant and native MASP-3 are activated on the surface of heat-inactivated *S. aureus* in the presence and absence of normal human serum (NHS) or heat-inactivated human serum (HIS) (data not shown). It was also determined that C3b deposition occurs on the surface of *S. aureus* in the presence of normal human serum, and that the deposition can be monitored using a flow cytometer. Therefore, the alternative pathway (AP) response to *S. aureus* was measured as described in this Example as a means of assessing the contribution of MASP-3 to LEA-1.

Methods:

Recombinant MASP-3: polynucleotide sequences encoding full length recombinant human MASP-3, a truncated serine protease (SP) active version of MASP-3 (CCP1-CCP2-SP), and a SP-inactivated form of MASP-3 (S679A) were cloned into the pTriEx7 mammalian expression vector (Invivogen). The resulting expression constructs encode the full length MASP-3 or the CCP1-CCP2-SP fragment with an amino-terminal Streptag and a carboxy-terminal His_6 tag. The expression constructs were transfected into Freestyle 293-F or Expi293F cells (Invitrogen) according to the protocols provided by the manufacturer. After three to four days of culture in 5% CO_2 at 37°C, recombinant proteins were purified utilizing Streptactin affinity chromatography.

Recombinant MASP-1: the full length or truncated CCP1-CCP2-SP forms of recombinant MASP-1 with or without the stabilizing R504Q (Dobo et al., *J. Immunol* 183:1207, 2009) or SP inactivating (S646A) mutations and bearing an amino-terminal Steptag and a carboxy-terminal His6 tag were generated as described for recombinant MASP-3 above.

1. C3b deposition and factor B cleavage on S. aureus in 3MC (human) serum

An initial experiment was carried out to demonstrate that the flow cytometry assay is able to detect the presence or absence of AP-driven C3b deposition (AP-C3b) as follows. Five percent of the following sera: normal human serum, factor B (Factor B)- depleted human serum, factor D-depleted human serum and properdin-depleted human serum (obtained from Complement Technology, Tyler, Texas, USA) were mixed with test antibody in either Mg^{++}/EGTA buffer or EDTA at 4°C overnight. Heat-killed *S. aureus* (10^8/reaction) was added to each mixture to a total volume of 100 μL and rotated at 37°C for 40 minutes. Bacteria were washed in washing buffer, the bacterial pellet was re-suspended in washing buffer and a 80 μL aliquot of each sample was analyzed for C3b deposition on the bacterial surface, which was detected with anti-human C3c (Dako, UK) using flow cytometry.

The results of the flow cytometry detection of C3b are shown in **FIGURE 35A**. As shown in **FIGURE 35A**, panel 1, normal human serum in the presence of EDTA, which is known to inactivate the AP, no C3b deposition was observed (negative control). In normal human serum treated with Mg^{++}/EGTA, only lectin-independent complement pathways can function. In panel 2, Mg^{++}/EGTA buffer is used, therefore the AP is active, and AP-driven C3b deposition is observed (positive control). As shown in panel 3, 4 and 5, in factor B-depleted, factor D-depleted and properdin-depleted serum, respectively, no alternative pathway driven C3b deposition is observed, as expected. These results demonstrate that the assay is capable of detecting AP-dependent C3b deposition.

A C3b deposition on *S. aureus* assay was carried out as described above to assess the ability of recombinant MASP-3 to reconstitute the AP (LEA-1) in human 3MC serum, which is deficient in MASP-3 (Rooryck C, et al., Nat Genet. 43(3):197-203 (2011)). The following combinations of reagents were tested.

    1. 5% normal human serum +EDTA

    2. 5% normal human serum +Mg/EGTA

    3. 5% human 3MC (MASP-3$^{-/-}$) serum + Mg^{++}/EGTA

4. 5% human 3MC (MASP-3$^{-/-}$) serum + Mg^{++}/EGTA plus active full-length rMASP-3

5. 5% human 3MC (MASP-3$^{-/-}$) serum + Mg^{++}/EGTA plus truncated active rMASP-3 (CCP1/CCP2/SP)

6. 5% human 3MC (MASP-3$^{-/-}$) serum + Mg^{++}/EGTA plus inactive rMASP-3 (S679A)

7. 5% human 3MC (MASP-3$^{-/-}$) serum + Mg^{++}/EGTA plus active full length rMASP-1

The various mixtures of 5% serum and recombinant proteins (5 µg of each) as shown above were incubated in the specified buffer conditions (either Mg^{++}/EGTA buffer or EDTA) at 4°C overnight. After the incubation overnight, 10^8 heat-killed *S. aureus* were added to each mixture in a total volume of 100 µL and rotated at 37°C for 40 minutes. Bacteria were washed and re-suspended in washing buffer and an 80 µl aliquot of each sample was analyzed for C3b deposition by FACS. The remaining 20 µL aliquot of each sample was used to measure factor B cleavage by Western blot using anti-factor B antibody as described below.

The results of the flow cytometery detection of C3b are shown in **FIGURE 35B**. Panel numbers correspond to the numbers designated for each of the reagent combination outlined above. The negative control (panel 1) and positive control (panel 2) show the absence and presence of C3b deposition, as expected. Panel 3 shows that AP-driven C3b deposition is absent in 3MC serum. Panels 4 and 5 show that active full length rMASP-3 (panel 4) and active rMASP-3 (CCP1-CCP2-SP) (panel 5) both restore AP-driven C3b deposition in 3MC serum. Panel 6 shows that inactive rMASP-3 (S679A) does not restore AP-driven C3b deposition in 3MC serum. Panel 7 shows that rMASP-1 does not restore AP-driven C3b deposition in 3MC serum.

Taken together, these results demonstrate that MASP-3 is required for AP-driven C3b deposition on *S. aureus* in human serum.

2. *MASP-3-dependent Activation of Factor B*

In order to analyze MASP-3-dependent activation of Factor B, the various mixtures of 5% serum (either normal human serum or 3MC patient serum) and recombinant proteins as shown above were assayed as described above. From each reaction mixture, 20 µL were removed and added to protein sample loading buffer. The samples were heated at 70°C for 10 minutes and loaded onto an SDS-PAGE gel. Western

blot analysis was performed using a Factor B polyclonal antibody (R&D Systems). Activation of Factor B was apparent by the formation of two lower molecular weight cleavage products (Bb and Ba) derived from the higher molecular weight pro-Factor B protein.

FIGURE 36 shows the results of a Western blot analysis to determine factor B cleavage in response to *S. aureus* in 3MC serum in the presence or absence of rMASP-3. As shown in lane 1, the normal human serum in the presence of EDTA (negative control) demonstrates very little Factor B cleavage relative to normal human serum in the presence of Mg^{++}/EGTA, shown in lane 2 (positive control). As shown in lane 3, 3MC serum demonstrates very little Factor B cleavage in the presence of Mg^{++}/EGTA. However, as shown in lane 4, Factor B cleavage is restored by the addition and pre-incubation of full-length, recombinant MASP-3 protein (5 μg) to the 3MC serum.

3. *Assay to determine the effect of rMASP-3 on pro-factor D in factor B/C3(H2O) Cleavage*

The following assay was carried out to determine the minimal requirement for MASP-3-dependent activation/cleavage of factor B.

C3(H₂O) (200ng), purified plasm factor B (20 μg), recombinant pro-factor D (200 ng) and recombinant human MASP-3 (200 ng) were mixed together in various combinations (as shown in **FIGURE 37**), in a total volume of 100 μL in BBS/Ca^{++}/ Mg^{++} and incubated at 30°C for 30 minutes. The reaction was stopped by adding 25 uL of SDS loading dye containing 5% 2-mercaptoethanol. After boiling at 95°C for 10 minutes under shaking (300 rpm), the mixture was spun down at 1400 rpm for 5 minutes and 20 uL of the supernatant was loaded and separated on a 10% SDS gel. The gel was stained with Coomassie brilliant blue.

Results:

FIGURE 37 shows a Comassie-stained SDS-PAGE gel in which factor B cleavage is analyzed. As shown in lane 1, factor B cleavage is most optimal in the presence of C3, MASP-3 and pro-factor D. As shown in lane 2, C3 is absolutely required; however, as shown in lanes 4 and 5, either MASP-3 or pro-factor D are able to mediate factor B cleavage, as long as C3 is present.

4. Analysis of the ability of MASP-3 mAbs to inhibit MASP-3-dependent AP-driven C3b deposition

As described in this Example it was demonstrated that MASP-3 is required for AP-driven C3b deposition on *S. aureus* in human serum. Therefore, the following assay was carried out to determine if a representative MASP-3 mAb identified as described in Example 15, could inhibit activity of MASP-3. Active, recombinant MASP-3 (CCP1-CCP2-SP) fragment protein (250 ng) was pre-incubated with an isotype control mAb, mAb1A5 (control obtained from the DTLacO platform that does not bind MASP-3 or MASP-1), or mAbD14 (binds MASP-3) at three different concentrations (0.5, 2 and 4 µM) for 1 hour on ice. The enzyme-mAb mixture was exposed to 5% 3MC serum (MASP-3 deficient) and 5×10^7 heat-killed *S. aureus* in a final reaction volume of 50 µL. The reactions were incubated at 37°C for 30 minutes, and then stained for the detection of C3b deposition. The stained bacterial cells were analyzed by a flow cytometer.

FIGURE 38 graphically illustrates the mean fluorescent intensities (MFI) of C3b staining obtained from the three antibodies plotted as a function of mAb concentration in 3MC serum with the presence of rMASP-3. As shown in **FIGURE 38**, mAbD14 demonstrates inhibition of C3b deposition in a concentration-dependent manner. In contrast, neither of the control mAbs inhibited C3b deposition. These results demonstrate that mAbD14 is able to inhibit MASP-3-dependent C3b deposition. Improved inhibitory activity for mAbD14 is expected following continued affinity maturation of this antibody for MASP-3 binding using the tethered factors in the DTLacO system.

Summary of Results:

In summary, the results in this Example demonstrate a clear defect of the AP in serum deficient for MASP-3. Thus, MASP-3 has been demonstrated to make a critical contribution to the AP, using factor B activation and C3b deposition as functional end-points. Furthermore, addition of functional, recombinant MASP-3, including the catalytically-active C-terminal portion of MASP-3 corrects the defect in factor B activation and C3b deposition in the serum from the 3MC patient. Conversely, as further demonstrated in this Example, addition of a MASP-3 antibody (e.g.,mAbD14) in 3MC serum with rMASP-3 inhibits AP-driven C3b deposition. A direct role of MASP-3 in Factor B activation, and therefore the AP, is demonstrated by the observation that recombinant MASP-3, along with C3, is sufficient to activate recombinant factor B.

EXAMPLE 18

This Example demonstrates that MASP-1 and MASP-3 activate factor D.

Methods:

Recombinant MASP-1 and MASP-3 were tested for their ability to cleave two different recombinant versions of pro-factor D. The first version (pro-factor D-His) lacks an N-terminal tag, but has a C-terminal His tag. Thus, this version of pro-factor D contains the 5 amino acid pro-peptide that is removed by cleavage during activation. The second version (ST-pro-factor D-His) has a Strep-TagII sequence on the N-terminus, thus increasing the cleaved N-terminal fragment to 15 amino acids. ST-pro-factor D also contains a His_6 tag at the C-terminus. The increased length of the propeptide of ST-pro-factor D-His improves the resolution between the cleaved and uncleaved forms by SDS-PAGE compared to the resolution possible with the pro-factor D-HIS form.

Recombinant MASP-1 or MASP-3 proteins (2 μg) was added to either pro-factor D-His or ST-pro-factor D-His substrates (100 ng) and incubated for 1 hour at 37°C. The reactions were electrophoresed on a 12% Bis-Tris gel to resolve pro-factor D and the active factor D cleavage product. The resolved proteins were transferred to a PVDF membrane and analyzed by Western blot by detection with a biotinylated factor D antibody (R&D Systems).

Results:

FIGURE 39 shows the Western blot analysis of pro-factor D substrate cleavage. As shown in **FIGURE 39**, only full length MASP-3 (lane 2) and the MASP-1 CCP1-CCP2-SP) fragment (lane 5) cleaved ST-pro-factor D-His_6. The catalytically-inactive full length MASP-3 (S679A; lane 3) and MASP-1 (S646A; lane 3) failed to cleave either substrate. Identical results were obtained with the pro-factor D-His_6 polypeptide (not shown). The comparison of a molar excess of MASP-1 (CCP1-CCP2-SP) relative to MASP-3 suggests that MASP-3 is a more effective catalyst of pro-factor D cleavage than is MASP-1, as least under the condtions described herein.

Conclusions: Both MASP-1 and MASP-3 are capable of cleaving and activating factor D. This activity directly connects LEA-1 with the activation of the AP. More specifically, activation of factor D by MASP-1 or MASP-3 will lead to factor B activation, C3b deposition, and likely opsonization and/or lysis.

1. *Assay for Inhibition of MASP-3-dependent Cleavage of pro-factor D with MASP-3 antibodies*

An assay was carried out to determine the inhibitory effect of representative MASP-3 and MASP-1 mAbs, identified as described in Example 15, on MASP-3-dependent

factor D cleavage as follows. Active, recombinant MASP-3 protein (80 ng) was pre-incubated with 1 μg of representative mAbs D14, M3M1 and a control antibody (which binds specifically to MASP-1, but not to MASP-3) at room temperature for 15 minutes. Pro-factor D with an N-terminal Strep-tag (ST-pro-factor D-His, 70 ng) was added and the mixture was incubated at 37°C for 75 minutes. The reactions were then electrophoresed, blotted and stained with anti-factor D as described above.

FIGURE 40 is a Western blot showing the partial inhibitory activity of the mAbs D14 and M3M1 in comparison to a control reaction containing only MASP-3 and ST-pro-factor D-His (no mAb; lane 1), as well as a control reaction containing a mAb obtained from the DTLacO library that binds MASP-1, but not MASP-3 (lane 4). As shown in **FIGURE 40**, in the absence of an inhibitory antibody, MASP-3 cleaves approximately 50% of pro-factor D into factor D (lane 1). The control MASP-1 specific antibody (lane 4) does not change the ratio of pro-factor D to factor D. In contrast, as shown in lanes 2 and 3, both mAb D14 and mAb M3M1 inhibit MASP-3-dependent cleavage of pro-factor D to factor D, resulting in a reduction in factor D generated.

Conclusions: These results demonstrate that MASP-3 mAbs D14 and M3M1 are able to inhibit MASP-3-dependent factor D cleavage. Improved inhibitory activity for mAbD14 and mAb M3M1 is expected following continued affinity maturation of these antibodies for MASP-3 binding using the tethered factors in the DTLacO system.

EXAMPLE 19

This Example demonstrates that MASP-3 deficiency prevents complement-mediated lysis of mannan-coated WT rabbit erythrocytes.

Background/Rationale:

As described in Examples 5 and 6 herein, the effect of MASP-2- and MASP-3-deficient serum on lysis of red blood cells from blood samples obtained from a mouse model of PNH demonstrated the efficacy of MASP-2 inhibition and/or MASP-3 inhibition to treat subjects suffering from PNH, and also supported the use of inhibitors of MASP-2 and/or inhibitors of MASP-3 (including dual or bi-specific MASP-2/MASP-3

inhibitors) to ameliorate the effects of C3 fragment-mediated extravascular hemolysis in PNH subjects undergoing therapy with a C5 inhibitor such as eculizumab.

As described in this Example, C3b deposition experiments and hemolysis experiments were carried out in MASP-3 deficient serum from additional 3MC patients, confirming the results obtained in Examples 5 and 6. In addition, experiments were carried out which demonstrated that addition of rMASP-3 to 3MC serum was able to reconstitute C3b deposition and hemolytic activity.

Methods:

MASP-3-deficient serum was obtained from three different 3MC patients as follows:

3MC Patient 1: contains an allele bearing a mutation that renders the exon encoding the MASP-3 serine protease domain dysfunctional, supplied along with the mother and father of the 3MC patient (both heterozygous for the allele bearing a mutation that renders the exon encoding the MASP-3 serine protease domain dysfunctional),

3MC Patient 2: Has C1489T (H497Y) mutation in exon 12 of MASP-1, the exon that encodes the serine protease domain of MASP-3, resulting in nonfunctional MASP-3, but functional MASP-1 proteins.

3MC Patient 3: Has a confirmed defect in the MASP-1 gene, resulting in nonfunctional MASP-3 but functional MASP-1 proteins.

Experiment #1: C3b Deposition Assay

An AP assay was carried out under traditional AP-specific conditions (BBS/ Mg^{++}/EGTA, without Ca^{++}, wherein BBS= barbital buffered saline containing sucrose), as described in Bitter-Suermann et al., *Eur. J. Immunol* 11:291-295 (1981)), on zymosan-coated microtiter plates at serum concentrations ranging from 0.5 to 25% and C3b deposition was measured over time.

Results:

FIGURE 41 graphically illustrates the level of AP-driven C3b deposition on zymosan-coated microtiter plates as a function of serum concentration in serum samples obtained from MASP-3-deficient (3MC), C4-deficient and MBL-deficient subjects. As shown in **FIGURE 41**, and summarized below in **TABLE 18**, MASP-3-deficient patient sera from Patient 2 and Patient 3 have residual AP activity at high concentrations (25%, 12.5%, 6.25% serum concentrations), but a significantly higher AP_{50} (i.e., 8.2% and 12.3% of serum needed to achieve 50% of maximum C3 deposition).

FIGURE 42 graphically illustrates the level of AP-driven C3b deposition on zymosan-coated microtiter plates under "traditional" AP-specific conditions (i.e., BBS/EGTA/Mg^{++} without Ca^{++}) as a function of time in 10% human serum samples obtained from MASP-3 deficient, C4-deficient and MBL-deficient human subjects.

TABLE 18 below summarizes the AP$_{50}$ results shown in **FIGURE 41** and the half-times for C3b deposition shown in **FIGURE 42**.

TABLE 18: Summary of Results shown in **FIGURES 41** and **42**

Serum type	AP$_{50}$ (%)	T$_{1/2}$ (min)
Normal	4.5	26.3
MBL-deficient (MBL-/-)	5.7	27.5
C4-deficient (C4-/-)	5.1	28.6
3MC (Patient 3)	8.2	58.2
3MC (Patient 2)	12.3	72.4

Note: In BBS/Mg^{++}/EGTA buffer, the lectin pathway-mediated effects are deficient due to absence of Ca^{++} in this buffer.

Experiment #2: Hemolysis assay testing mannan-coated rabbit erythrocytes for lysis in the presence of human normal or 3MC serum (in the absence of Ca^{++})

Methods:

Preparation of rabbit RBC in the absence of Ca^{++} (i.e., by using EGTA)

Rabbit whole blood (2 mL) was split into two 1.5 mL eppendorf tubes and centrifuged for 3 minutes at 8000 rpm (approximately 5.9 rcf) in a refrigerated eppendorf centrifuge at 4°C. The RBC pellet was washed three times after re-suspending in ice-cold BBS/ Mg^{++}/Ca^{++} (4.4 mM barbituric acid, 1.8 mM sodium barbitone, 145 mM NaCl, pH 7.4, 5 mM Mg^{++}, 5 mM Ca^{++}). After the third wash, the pellet was re-suspended in 4 mL BBS/ Mg^{++}/Ca^{++}. The erythrocytes were pelleted and the RBCs were washed with BBS/0.1% gelatin/Mg^{++}/Ca^{++} as described above. The RBCs suspension was stored in BBS/0.1% gelatin/ Mg^{++}/Ca^{++} at 4°C. Then, 100 μL of suspended RBCs were diluted with 1.4 mL water and spun down at 8000 rpm (approximately 5.9 rcf) for 3 minutes and the OD of the supernatant was adjusted to 0.7 at 541nm (an OD of 0.7 at 541nm corresponds to approximately 10^9 erythrocytes/ml). After that, 1 mL of the resuspended

RBCs at OD 0.7 were added to 9 ml of $BBS/Mg^{++}/EGTA$ in order to achieve a concentration of 10^8 erythrocytes/ml. Dilutions of the test sera or plasma were prepared in ice-cold BBS, Mg^{++}, EGTA and 100 μL of each serum or plasma dilution was pipetted into the corresponding well of round-bottom plate. 100 μL of appropriately diluted RBC (10^8 erythrocytes/ml) were added to each well. Nano-water was used to produce the positive control (100% lysis), while a dilution with $BBS/Mg^{++}/EGTA$ without serum or plasma was used as a negative control. The plate was then incubated for 1 hour at 37°C. The round bottom plate was spun down at 3750 rpm for 5 minutes. Then, 100 μL of the supernatant from each well was transferred into the corresponding wells of a flat-bottom plate and OD was read at 415-490 nm.

Results:

FIGURE 43 graphically illustrates the percent hemolysis (as measured by hemoglobin release of lysed rabbit erythrocytes into the supernatant measured by photometry) of mannan-coated rabbit erythrocytes over a range of serum concentrations in serum from normal subjects and from two 3MC patients (Patient 2 and Patient 3), measured in the absence of Ca^{++}. As shown in **FIGURE 43**, it is demonstrated that MASP-3 deficiency reduces the percentage of complement-mediated lysis of mannan-coated erythrocytes as compared to normal human serum. The differences between the two curves from the normal human serum and the two curves from the 3MC patients is significant ($p=0.013$, Friedman test).

TABLE 19 below summarizes the AP_{50} results shown in **FIGURE 43**.

TABLE 19: Summary of Results shown in **FIGURE 43**

Serum type	AP_{50} (%)
Normal human serum #1	7.1
Normal human serum #2	8.6
3MC Patient #2	11.9
3MC Patient #3	14.3

It is noted that when the serum samples shown in **TABLE 19** were pooled, the AP_{50} value for normal human serum = 7.9 and the AP_{50} value for 3MC serum = 12.8 ($p=0.031$, Wilcox matched-pairs signed rank test).

Experiment #3: Reconstitution of human 3MC serum by recombinant MASP-3 restores AP-driven C3b deposition on zymosan coated plates

Methods:

An AP assay was carried out under traditional AP-specific conditions (BBS/Mg^{++}/EGTA, without Ca^{++}, wherein BBS=barbital buffered saline containing sucrose), as described in Bitter-Suermann et al., *Eur. J. Immunol* 11:291-295 (1981)), on zymosan-coated microtiter plates in the following serum samples (1) 5% human serum from 3MC Patient #2 with full length active rMASP-3 added in at a range of 0 to 20 μg/ml; (2) 10% human serum from 3MC Patient #2 with full length active rMASP-3 added in at a range of 0 to 20 μg/ml; and (3) 5% human serum from 3MC Patient #2 with inactive rMASP-3A (S679A) added in at a range of 0 to 20 μg/ml.

Results:

FIGURE 44 graphically illustrates the level of AP-driven C3b deposition on zymosan-coated microtiter plates as a function of the concentration of rMASP-3 protein added to serum samples obtained from human 3MC Patient #2 (MASP-3-deficient). As shown in **FIGURE 44**, active recombinant MASP-3 protein reconstitutes AP-driven C3b deposition on zymosan-coated plates in a concentration-dependent manner. As further shown in **FIGURE 44**, no C3b deposition was observed in the 3MC serum containing inactive rMASP-3 (S679A).

Experiment #4: Reconstitution of human 3MC serum by recombinant MASP-3 restores hemolytic activity in 3MC patient serum

Methods:

A hemolytic assay was carried out using rabbit RBC using the methods described above in Experiment #2 with the following test sera at a range of 0 to 12% serum: (1) normal human serum; (2) 3MC patient serum; (3) 3MC patient serum plus active full length rMASP-3 (20 μg/ml); and (4) heat-inactivated human serum.

Results:

FIGURE 45 graphically illustrates the percent hemolysis (as measured by hemoglobin release of lysed rabbit erythrocytes into the supernatant measured by photometry) of mannan-coated rabbit erythrocytes over a range of serum concentrations in (1) normal human serum; (2) 3MC patient serum; (3) 3MC patient serum plus active full length rMASP-3 (20 μg/ml); and (4) heat-inactivated human serum, measured in the absence of Ca^{++}. As shown in **FIGURE 45**, the percent lysis of rabbit RBC is

significantly increased in 3MC serum including rMASP-3 as compared to the percent lysis in 3MC serum without rMASP-3 (p=0.0006).

FIGURE 46 graphically illustrates the percentage of rabbit erythrocyte lysis in 7% human serum from 3MC Patient 2 and from 3MC Patient 3 containing active rMASP-3 at a concentration range of 0 to 110 μg/ml in BBS/Mg^{++}/EGTA. As shown in FIGURE 46, the percentage of rabbit RBC lysis is restored with the amount of rMASP-3 in a concentration-dependent manner up to 100% activity.

Experiment #5: Serum of MASP-3 deficient (CMC) patient has functional MASP-2 if MBL is present

Methods:

A C3b deposition assay was carried out using Mannan-coated ELISA plates under to examine whether 3MC serum is deficient in LEA-2. Citrate plasma was diluted in BBS buffer in serial dilutions (starting at 1:80, 1:160, 1: 320, 1:640, 1:1280, 1:2560) and plated on Mannan-coated plates. Deposited C3b was detected using a chicken anti-human C3b assay. LEA-2 driven C3b deposition (the plasma dilutions are to high for the AP and LEA-1 to work) on Mannan-coated ELISA plates was evaluated as a function of human serum concentration in serum from a normal human subject (NHS), from two 3MC patients (Patient 2 and Patient 3), from the parents of Patient 3 and from a MBL-deficient subject.

Results:

FIGURE 47 graphically illustrates the level of LEA-2-driven (i.e., MASP-2-driven) C3b deposition on Mannan-coated ELISA plates as a function of the concentration of human serum diluted in BBS buffer, for serum from a normal human subject (NHS), from two 3MC patients (Patient 2 and Patient 3), from the parents of Patient 3 and from a MBL-deficient subject. These data indicate that Patient 2 is MBL sufficient. However, Patient 3 and the mother of Patient 3 are MBL deficient, and therefore their serum does not deposit C3b on Mannan via LEA-2. Replacement of MBL in these sera restores LEA-2 mediated C3b deposition in the serum of Patient 3 (who is homozygous for the SNP leading to MASP-3 deficiency) and his mother (who is heterozygous for the mutant MASP-3 allele) (data not shown). This finding demonstrates that 3MC serum is not deficient in LEA-2, but rather appears to have functional MASP-2 and functional MASP-1.

Overall summary and Conclusions:

These results demonstrate that MASP-3 deficiency in human serum results in loss of AP activity, as manifested in reduced C3b deposition on zymosan-coated wells and reduced rabbit erythrocyte lysis. The AP can be restored in both assays by supplementing the sera with functional, recombinant human MASP-3.

While the preferred embodiment of the invention has been illustrated and described, it will be appreciated that various changes can be made therein without departing from the spirit and scope of the invention.

CLAIMS

The embodiments of the invention in which an exclusive property or privilege is claimed are defined as follows:

1.   A method of inhibiting MASP-3-dependent complement activation in a subject suffering from paroxysmal nocturnal hemoglobinuria (PNH), comprising administering to the subject a composition comprising an amount of a MASP-3 inhibitory agent effective to inhibit MASP-3-dependent complement activation.

2.   The method of Claim 1, wherein the MASP-3 inhibitory agent is a MASP-3 monoclonal antibody, or fragment thereof that specifically binds to a portion of SEQ ID NO:8.

3.   The method of Claim 1, further comprising administering to the subject a composition comprising a MASP-1 inhibitory agent.

4.   The method of Claim 3, wherein the MASP-1 inhibitory agent is a MASP-1 monoclonal antibody, or fragment thereof, that specifically binds to a portion of SEQ ID NO:10.

5.   The method of Claim 1, further comprising administering to the subject a composition comprising a MASP-2 inhibitory agent.

6.   The method of Claim 5, wherein the MASP-2 inhibitory agent is a MASP-2 monoclonal antibody, or fragment thereof that specifically binds to a portion of SEQ ID NO:5.

7.   The method of Claim 1, further comprising administering to the subject a composition comprising a MASP-1 inhibitory agent and a MASP-2 inhibitory agent.

8.   The method of any one of Claims 1-7, wherein the composition increases the survival of red blood cells in the subject.

9.   The method of Claim 8, wherein the subject exhibits one or more symptoms selected from the group consisting of (i) below normal levels of hemoglobin, (ii) below normal levels of platelets; (iii) above normal levels of reticulocytes, and (iv) above normal levels of bilirubin.

10. The method of Claim 1, wherein the subject has previously undergone, or is currently undergoing treatment with a terminal complement inhibitor that inhibits cleavage of complement protein C5.

11. The method of Claim 1, wherein the method further comprises administering to the subject a terminal complement inhibitor that inhibits cleavage of complement protein C5.

12. The method of Claim 11, wherein the terminal complement inhibitor is a humanized anti-C5 antibody or antigen-binding fragment thereof.

13. The method of Claim 12, wherein the terminal complement inhibitor is eculizumab.

14. The method of Claim 1, wherein the MASP-3 inhibitory agent inhibits alternative-pathway driven C3b deposition.

15. The method of Claim 1, wherein the MASP-3 inhibitory agent inhibits factor D maturation.

16. The method of Claim 3, wherein the MASP-1 inhibitory agent specifically binds to a portion of MASP-1 with an affinity of at least 10 times greater than it binds to MASP-3 (SEQ ID NO:8).

17. The method of Claim 3, wherein the MASP-1 inhibitory agent specifically binds to the serine protease domain of MASP-1 (aa 449-694 of SEQ ID NO:10).

18. The method of Claim 1, wherein the MASP-3 inhibitory agent also binds to a portion of MASP-1 (SEQ ID NO:10).

19. The method of Claim 18, wherein the MASP-3 inhibitory agent is a dual MASP-1/MASP-3 inhibitor that binds to a consensus region within the CUBI-CCP2 domains.

20. The method of Claim 18, wherein the MASP-3 inhibitory agent is a dual MASP-1/MASP-3 inhibitor that binds to a consensus region within the CCP2 domain.

21.   The method of Claim 18, wherein the MASP-3 inhibitory agent is a bi-specific monoclonal antibody that binds to the serine protease domain of MASP-1 (aa 449-694 of SEQ ID NO:10) and also binds to the serine protease domain of MASP-3 (aa 450-711 of SEQ ID NO:8).

22.   The method of Claim 1, wherein the MASP-3 inhibitory agent also binds to a portion of MASP-2 (SEQ ID NO:5).

23.   The method of Claim 22, wherein the MASP-3 inhibitory agent is a dual MASP-3/MASP-2 inhibitor that binds to a conserved region within the serine protease domains of MASP-3 and MASP-2.

24.   The method of Claim 22, wherein the MASP-3 inhibitory agent is a bispecific monoclonal antibody that binds to the serine protease domain of MASP-3 (aa450-711 of SEQ ID NO:8) and also binds to at least one of the serine protease domain of MASP-2 (aa 445-682 of SEQ ID NO:5) or the CCP-1-CCP2 domain of MASP-2 (aa300-431 of SEQ ID NO:5).

25.   The method of Claim 1, wherein the MASP-3 inhibitory agent binds to a portion of MASP-3 (SEQ ID NO:8) and does not inhibit MASP-1 or MASP-2.

26.   The method of Claim 1, wherein the MASP-3 inhibitory agent specifically binds to a portion of MASP-3 with an affinity of at least 10 times greater than it binds to MASP-1 (SEQ ID NO:10).

27.   The method of Claim 1, wherein the MASP-3 inhibitory agent specifically binds to the serine protease domain of MASP-3 (aa 450-711 of SEQ ID NO:8).

28.   The method of Claim 1, wherein the MASP-3 inhibitory agent is a pan inhibitor of MASP-1, MASP-2 and MASP-3 and binds to a conserved region in the CUB1-EGF-CUB2 domains.

29.   The method of Claim 1, wherein the MASP-3 inhibitory agent is a trispecific inhibitor of MASP-1, MASP-2 and MASP-3.

30.   The method of Claim 2, wherein the composition further comprises a MASP-2 antibody.

31.   The method of Claim 2, wherein the composition further comprises a MASP-1 antibody.

32.   The method of Claim 7, wherein the composition comprises a MASP-1 antibody, and MASP-2 antibody and a MASP-3 antibody.

33.   The method of Claim 7, wherein the method comprises co-administration of a composition comprising at least one of a MASP-2 antibody, a MASP-1 antibody, or a MASP-3 antibody.

34.   The method of Claim 18, wherein the composition further comprises a MASP-2 antibody.

35.   The method of Claim 22, wherein the composition further comprises a MASP-1 antibody.

36.   The method of Claim 1, wherein the antibody or fragment thereof is selected from the group consisting of a recombinant antibody, an antibody having reduced effector function, a chimeric, and a humanized or human antibody.

37.   The method of Claim 1, wherein the composition is administered systemically.

38.   The method of Claim 37, wherein the composition is administered subcutaneously, intra-muscularly, intravenously, intra-arterially or as an inhalant.

39.   A method of increasing the survival of red blood cells in a subject suffering from paroxysmal nocturnal hemoglobinuria (PNH), comprising administering to the subject a composition comprising an amount of at least one of a MASP-1 inhibitory agent and/or a MASP-3 inhibitory agent effective to increase the survival of red blood cells.

40.   The method of claim 39, wherein the composition comprises a MASP-1 inhibitory agent.

41.   The method of claim 39, wherein the composition comprises a MASP-3 inhibitory agent.

42.   The method of claim 39, wherein the composition comprises a MASP-1 inhibitory agent and a MASP-3 inhibitory agent.

43.   The method of claim 39, further comprising administering to the subject a composition comprising a MASP-2 inhibitory agent.

44.   The method of claim 40, wherein the MASP-1 inhibitory agent is a MASP-1 monoclonal antibody.

45.   The method of claim 41, wherein the MASP-3 inhibitory agent is a MASP-3 monoclonal antibody.

46.   The method of claim 43, wherein the MASP-2 inhibitory agent is a MASP-2 monoclonal antibody.

47.   A pharmaceutical composition comprising at least one complement pathway inhibitory agent, wherein the at least one inhibitory agent comprises a MASP-2 inhibitory agent and at least one of a MASP-3 inhibitory agent and/or a MASP-1 inhibitory agent and a pharmaceutically acceptable carrier.

48.   The pharmaceutical composition of Claim 47, wherein the at least one inhibitory agent comprises a combination of a first molecule that is a MASP-3 inhibitory agent and a second molecule that is a MASP-2 inhibitory agent.

49.   The pharmaceutical composition of Claim 47, wherein the at least one inhibitory agent comprises a single molecular entity that includes activity as a MASP-3 inhibitory agent and activity as a MASP-2 inhibitory agent.

50.   The pharmaceutical composition of Claim 47, wherein the MASP-3 inhibitory agent is a MASP-3 monoclonal antibody, or fragment thereof.

51.   The pharmaceutical composition of Claim 47, wherein the MASP-2 inhibitory agent is a MASP-2 antibody, or fragment thereof.

52.   The pharmaceutical composition of Claim 47, wherein the MASP-3 inhibitory agent inhibits MASP-3-mediated cleavage of factor B.

53.   The pharmaceutical composition of Claim 47, wherein the MASP-3 inhibitory agent inhibits factor D maturation.

54.   The pharmaceutical composition of Claim 47, wherein the MASP-1 inhibitory agent is a MASP-1 antibody, or fragment thereof.

55.   The pharmaceutical composition of Claim 47, wherein the MASP-1 inhibitory agent specifically binds to a portion of MASP-1 with an affinity of at least 10 times greater than it binds to MASP-3 (SEQ ID NO:8).

56.   The pharmaceutical composition of Claim 47, wherein the MASP-1 inhibitory agent specifically binds to the serine protease domain of MASP-1 (aa 449-694 of SEQ ID NO:10).

57.   The pharmaceutical composition of Claim 47, wherein the MASP-1 inhibitory agent also binds to a portion of MASP-3 (SEQ ID NO:8). 58.   The pharmaceutical composition of Claim 57, wherein the MASP-3 inhibitory agent is a dual MASP-1/MASP-3 inhibitor that binds to a consensus region within the CUBI-CCP2 domains.

59.   The pharmaceutical composition of Claim 57, wherein the MASP-3 inhibitory agent is a dual MASP-1/MASP-3 inhibitor that binds to a consensus region within the CCP2 domain.

60.   The pharmaceutical composition of Claim 57, wherein the MASP-3 inhibitory agent is a bispecific monoclonal antibody that binds to the serine protease domain of MASP-1 (aa 449-694 of SEQ ID NO:10) and also binds to the serine protease domain of MASP-3 (aa 450-711 of SEQ ID NO:8).

61.   The pharmaceutical composition of Claim 47, wherein the MASP-1 inhibitory agent also binds to a portion of MASP-2 (SEQ ID NO:5).

62.   The pharmaceutical composition of Claim 61, wherein the MASP-1 inhibitory agent is a dual MASP-1/MASP-2 inhibitor that binds to a conserved region within the serine protease domains of MASP-1 and MASP-2.

63.   The pharmaceutical composition of Claim 61, wherein the MASP-1 inhibitory agent is a bispecific monoclonal antibody that binds to the serine protease domain of MASP-1 (aa449-694 of SEQ ID NO:10) and also binds to at least one of the serine protease domain of MASP-2 (aa 445-682 of SEQ ID NO:5) or the CCP-1-CCP2 domain of MASP-2 (aa300-431 of SEQ ID NO:5).

64.   The pharmaceutical composition of Claim 47, wherein the MASP-3 inhibitory agent specifically binds to a portion of MASP-3 (SEQ ID NO:8: full-length).

65.   The pharmaceutical composition of Claim 47, wherein the MASP-3 inhibitory agent specifically binds to a portion of MASP-3 with an affinity of at least 10 times greater than it binds to MASP-1 (SEQ ID NO:10).

66.   The pharmaceutical composition of Claim 64, wherein the MASP-3 inhibitory agent specifically binds to the serine protease domain of MASP-3 (aa 450-711 of SEQ ID NO:8).

67.   The pharmaceutical composition of Claim 47, wherein the MASP-3 inhibitory agent also binds to a portion of MASP-2 (SEQ ID NO:5).

68.   The pharmaceutical composition of Claim 67, wherein the MASP-3 inhibitory agent is a dual MASP-2/MASP-3 inhibitor that binds to a conserved region within the serine protease domains of MASP-2 and MASP-3.

69.   The pharmaceutical composition of Claim 67, wherein the MASP-3 inhibitory agent is a bispecific monoclonal antibody that binds to the serine protease domain of MASP-3 (aa450-711 of SEQ ID NO:8) and also binds to at least one of the serine protease domain of MASP-2 (aa 445-682 of SEQ ID NO:5) or the CCP-1-CCP2 domain of MASP-2 (aa300-431 of SEQ ID NO:5).

70.   The pharmaceutical composition of Claim 47, wherein the MASP-3 inhibitory agent is a pan inhibitor of MASP-1, MASP-2 and MASP-3 and binds to a conserved region in the CUB1-EGF-CUB2 domains of the three proteins.

71.   The pharmaceutical composition of Claim 47, wherein the MASP-3 inhibitory agent is a trispecific inhibitor of MASP-1, MASP-2 and MASP-3.

72.   The pharmaceutical composition of Claim 47, wherein the MASP-3 inhibitory agent is a MASP-3 antibody, and wherein the composition further comprises a MASP-2 antibody.

73.   The pharmaceutical composition of Claim 47, wherein the MASP-3 inhibitory agent is a MASP-3 antibody, and wherein the composition further comprises a MASP-1 antibody.

74.   The pharmaceutical composition of Claim 47, wherein the MASP-3 inhibitory agent is a MASP-3 antibody, and wherein the composition further comprises a MASP-2 antibody.

75.   The pharmaceutical composition of Claim 47, wherein the composition comprises a MASP-1 antibody, and MASP-2 antibody and a MASP-3 antibody.

76.   The pharmaceutical composition of Claim 57, wherein the composition further comprises a MASP-2 antibody.

77.   The pharmaceutical composition of Claim 61, wherein the composition further comprises a MASP-3 antibody.

78.   The pharmaceutical composition of Claim 67, wherein the composition further comprises a MASP-1 antibody.

79.   The pharmaceutical composition of Claim 47, wherein the antibody or fragment thereof is selected from the group consisting of a recombinant antibody, an antibody having reduced effector function, a chimeric, and a humanized or human antibody.

80.   The pharmaceutical composition of Claim 47, wherein the MASP-1 inhibitory agent inhibits factor D maturation81.   The pharmaceutical composition of Claim 47, wherein the composition is formulated for systemic delivery.

82.   The pharmaceutical composition of Claim 81, wherein the composition is formulated for delivery subcutaneously, intra-muscularly, intravenously, intra-arterially or as an inhalant.

83.   A pharmaceutical composition comprising a MASP-3 inhibitory agent that binds to a portion of MASP-1 (SEQ ID NO: 10: full-length) and that also binds to a portion of MASP-3 (SEQ ID NO:8) and a pharmaceutical carrier.

84.   The composition of Claim 83, wherein the MASP-3 inhibitory agent is a dual MASP-1/MASP-3 inhibitor.

85.   The composition of Claim 83, wherein the MASP-3 inhibitory agent is a bispecific antibody.

86.   The composition of Claim 85, wherein the MASP-3 inhibitory agent is a bispecific monoclonal antibody that binds to the serine protease domain of MASP-1 (aa 449-694 of SEQ ID NO:10) and also binds to the serine protease domain of MASP-3 (aa 450-711 of SEQ ID NO:8).

87.   A pharmaceutical composition comprising a MASP-3 inhibitory agent that binds to a portion of MASP-2 (SEQ ID NO: 5: full-length) and that also binds to a portion of MASP-3 (SEQ ID NO:8) and a pharmaceutical carrier.

88.   The composition of Claim 87, wherein the MASP-3 inhibitory agent is a dual MASP-2/MASP-3 inhibitor.

89.   The composition of Claim 87, wherein the MASP-3 inhibitory agent is a bispecific MASP-2/MASP-3 antibody.

90.   A pharmaceutical composition comprising a MASP-3 inhibitory agent that binds to a portion of MASP-1 (SEQ ID NO: 10 full length), that binds to a portion of MASP-2 (SEQ ID NO: 5: full-length) and that also binds to a portion of MASP-3 (SEQ ID NO:8) and a pharmaceutical carrier.

91.   The composition of Claim 90, wherein the inhibitory agent is a pan-MASP inhibitor.

92.   The composition of Claim 90, wherein the inhibitory agent is a trispecific MASP-1, MASP-2 and MASP-3 antibody.

1/37

FIG. 1

FIG. 2

FIG. 3

CUB/EGF/CCP domain (A-Chain)

serine protease domain (B-chain)

CUB1 and CUB2 domains
EGF domain
CCP1 and CCP2 domains
catalytic triad residues

MASP1
MASP3
MASP2

FIG. 4
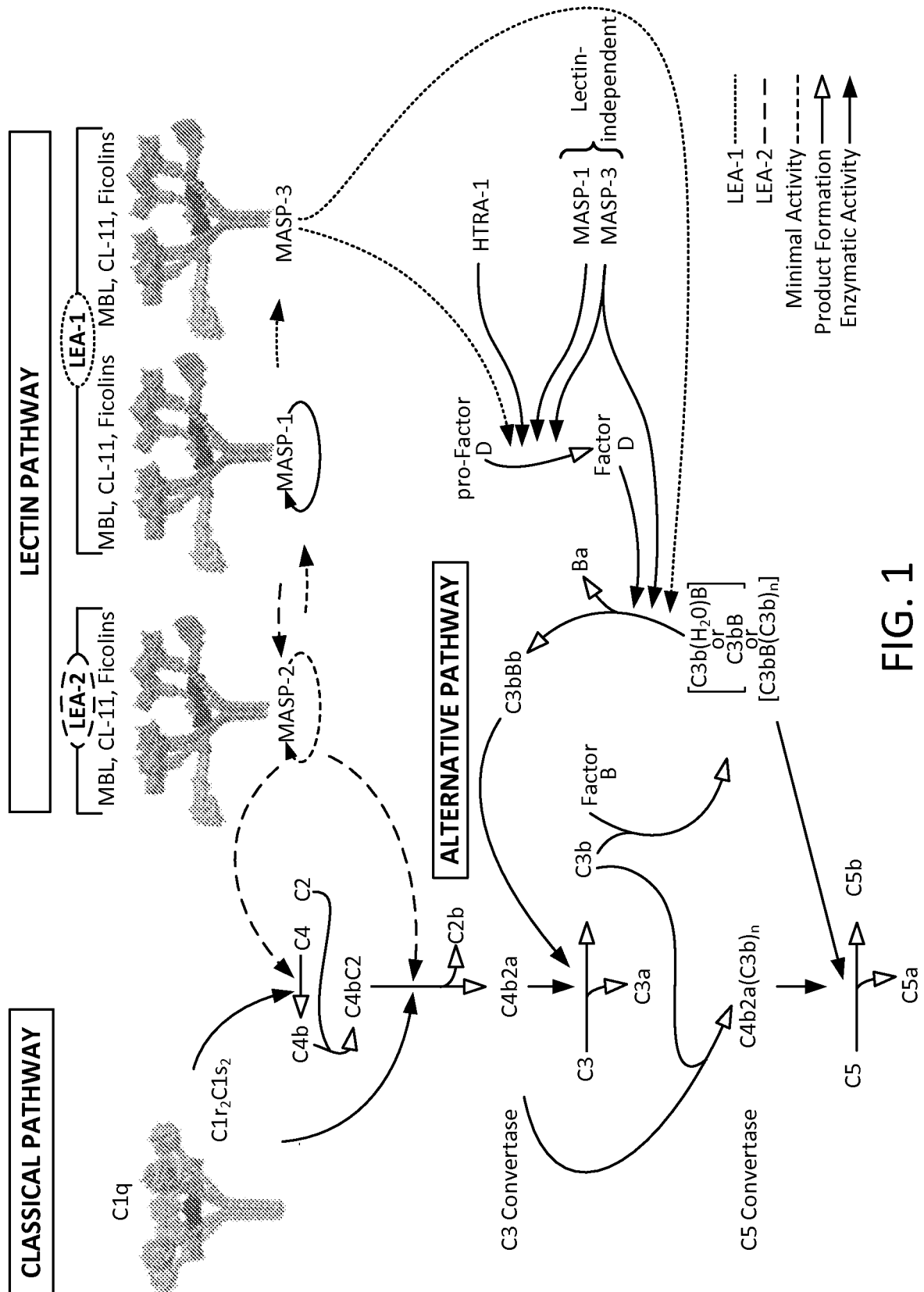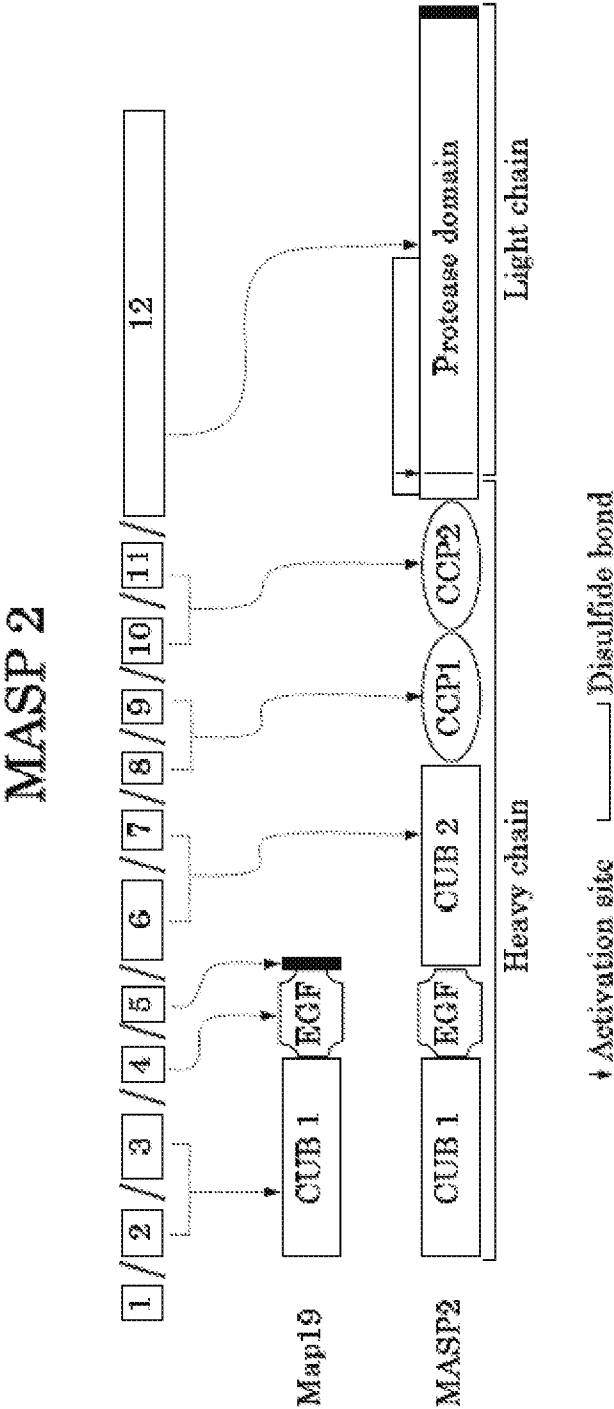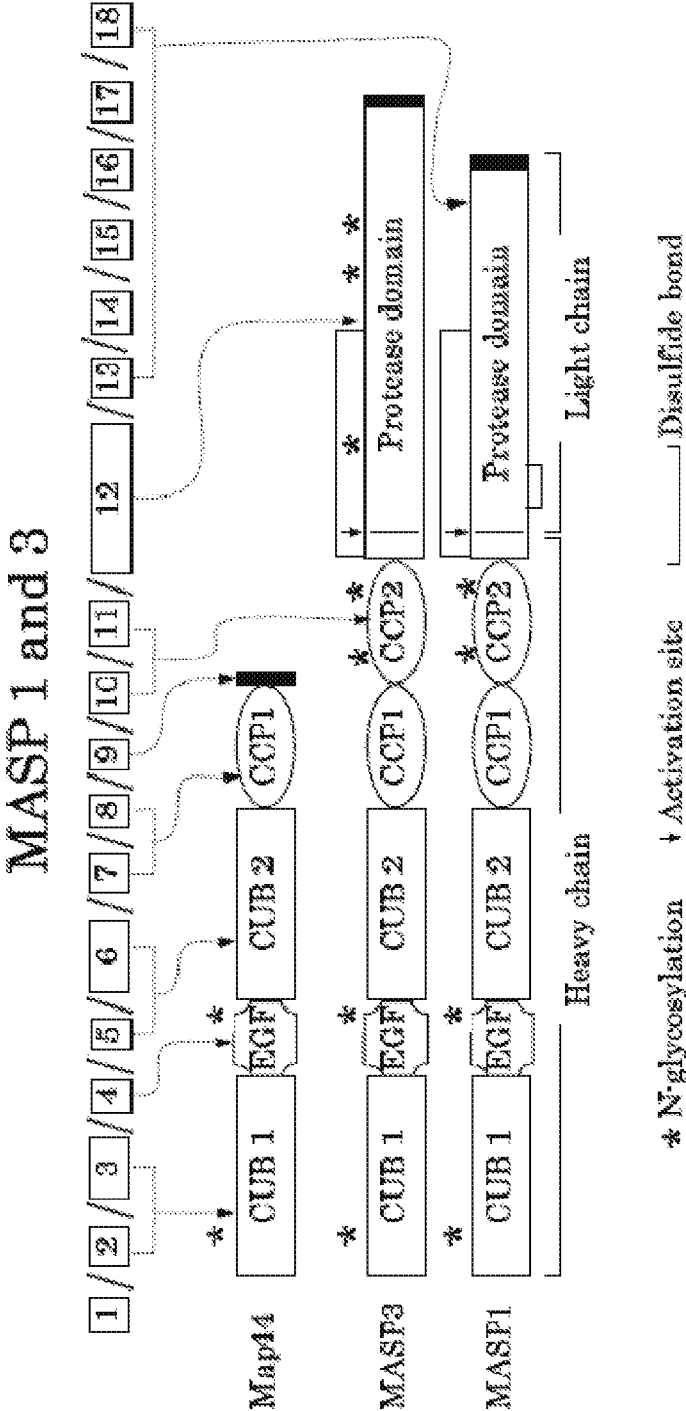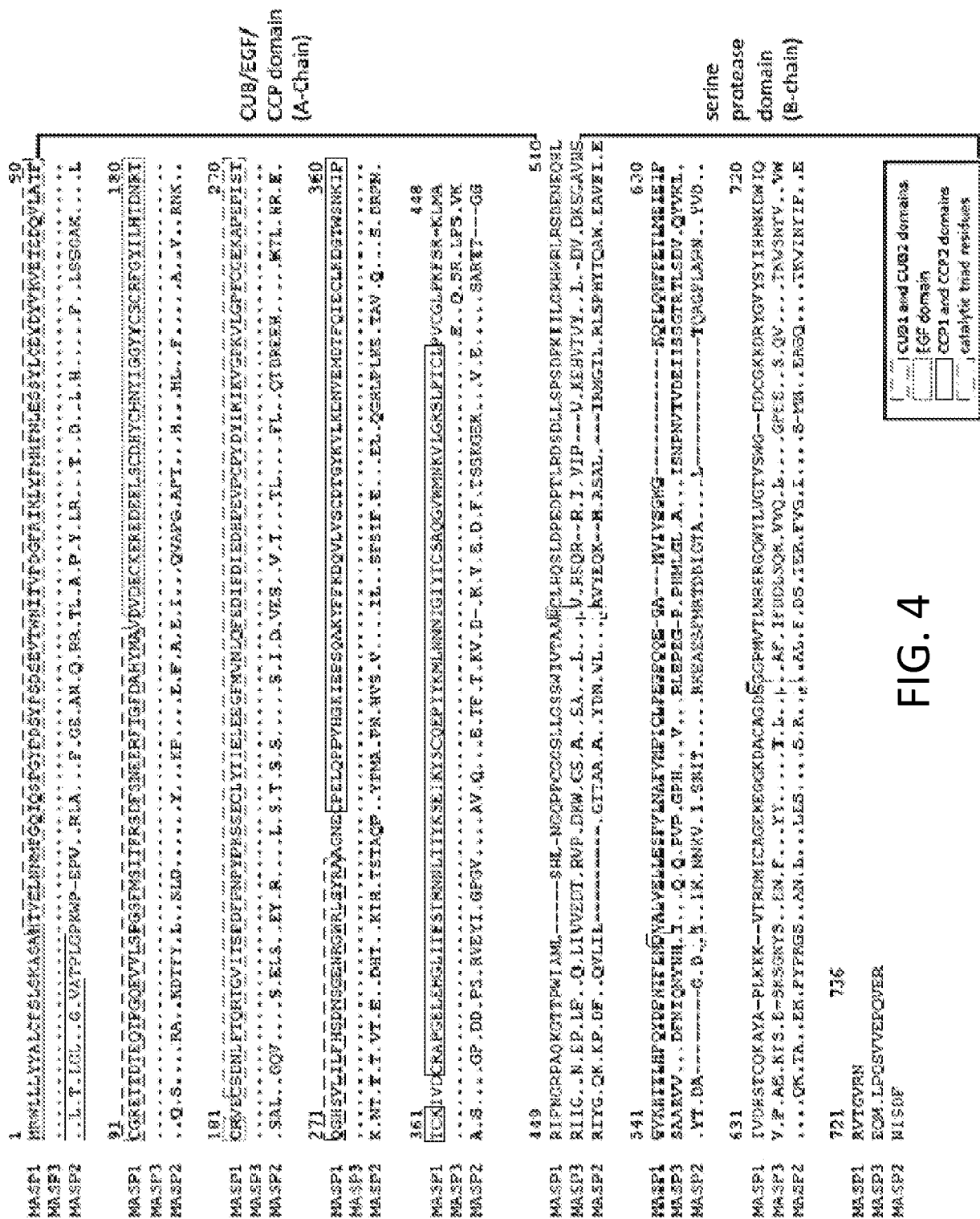
Alignment of MASP A-Chains

FIG. 5

FIG. 6

7/37

Pairwise Alignment of MASP Serine Protease Domains (B-Chains)

FIG. 7A

8/37

FIG. 7B

Pairwise Alignment of MASP Serine Protease Domains (B-Chains)

```
                  1                                                        90
MASP2_Bchain   RIYGGQKAKPGDFPWQVLILGGTTA----------ACALLYDNWVLTAAHAVYEQKHDASALDI-RMGTLKRLSPHPTQAWSEAV----------
MASP3_Bchain   ..IL.RN.E.JL...EL.YVEG.SRVPMDKMTGS....SAS.I.....VIRS.RR.ITYIPVSKEHYTY.GL.DVRDK.G..NSSAAR

                  91                                                       180
MASP2_Bchain   FIHEGYTHDAGFDNDIALIKLKNKVVINSHITPICLPRKEAESFMRTDDIGTASGWGLQRGF----------LARNLMYVDIPIVDH
MASP3_Bchain   VYVHPDFNIQNYNH....VY.QEE.EGKHYE.V.....L.t.G-FAFRHL.LVA...LNEHVTVDELLSGGIKT.SUV.Q...EL.V.P.

                  181                                                      270
MASP2_Bchain   QKCTTAYEKPPYPRGSVTANMLCAGLESGGKDSCRGDSGGALVFLDSETERWFVGGIVSWGSMN-CGEAGQYGVYTKVINYIPWIEMLSD
MASP3_Bchain   AE.KES..SPS-GMY...........T.LG......F.IF.DLSQ..V.Q.L...SRUE...SKUV.........S..VD.VHEGWG

                  271    282
MASP2_Bchain   F
MASP3_Bchain   LPQSWEPQVER
```

FIG. 7C

Survival after N. *meningitidis* Serogroup A Z2491 infection
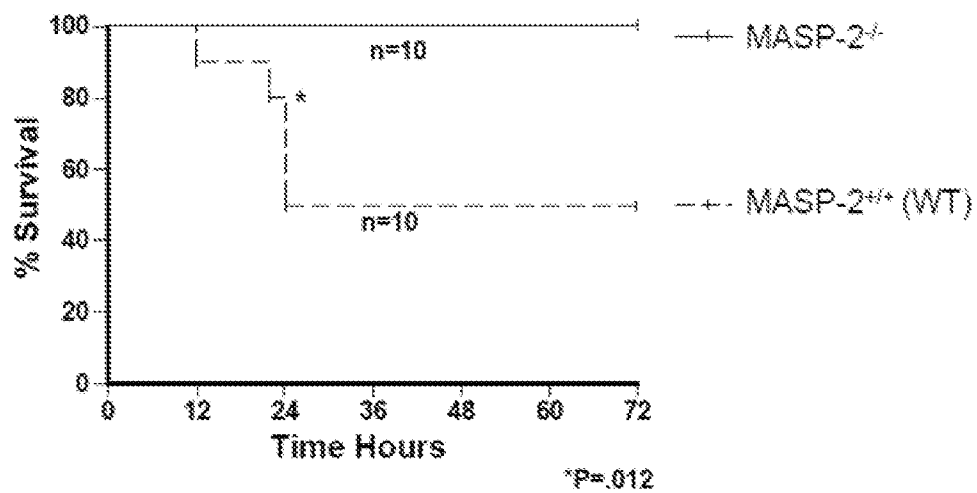
FIG. 8
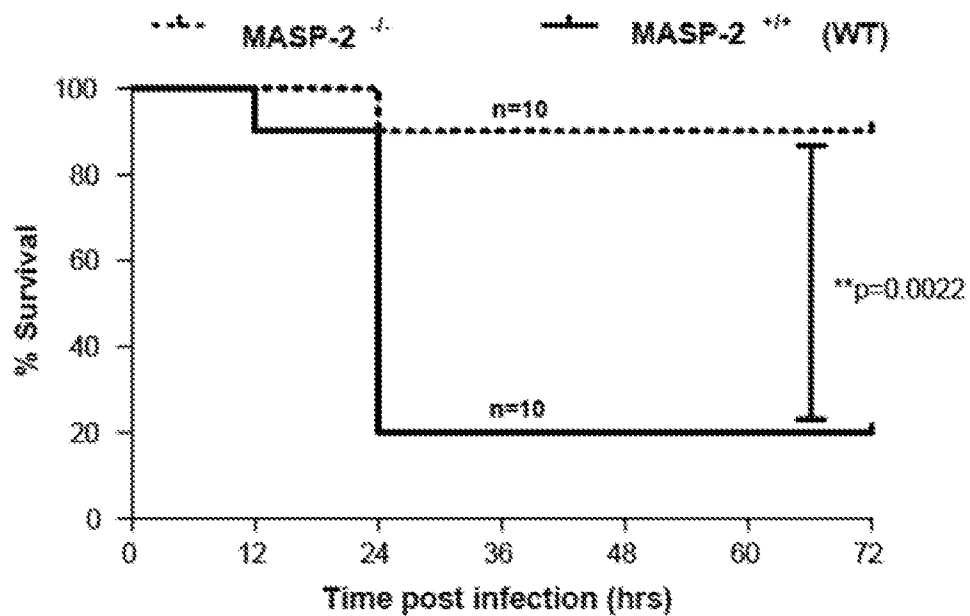
FIG. 9
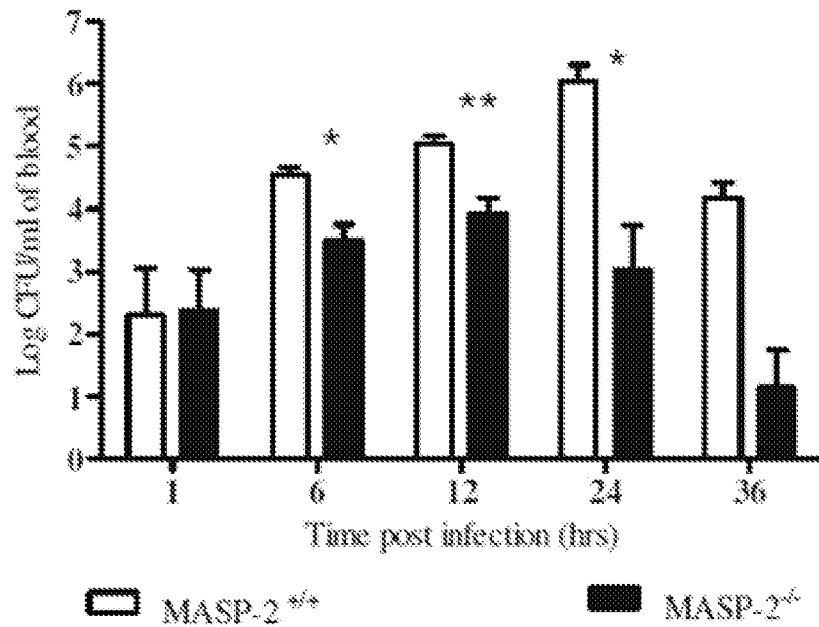
FIG. 10
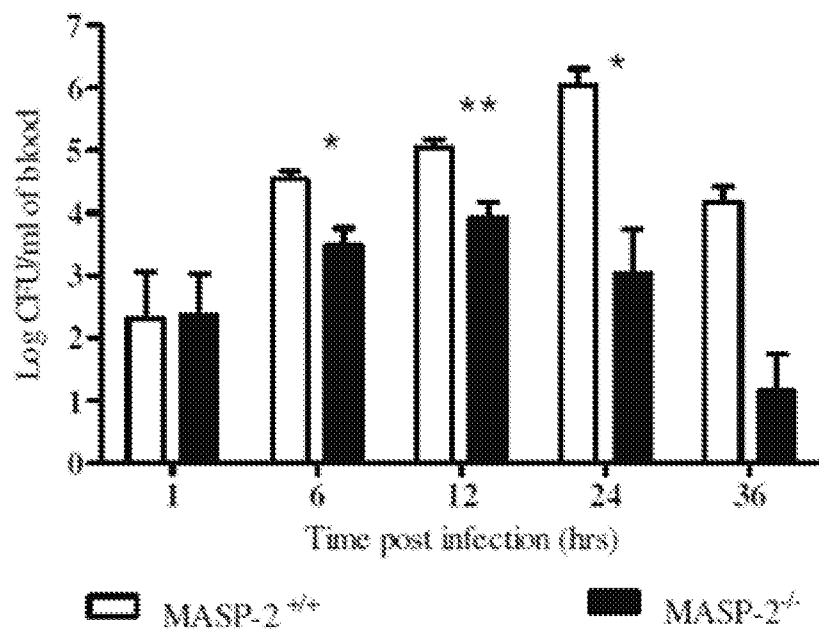
FIG. 11
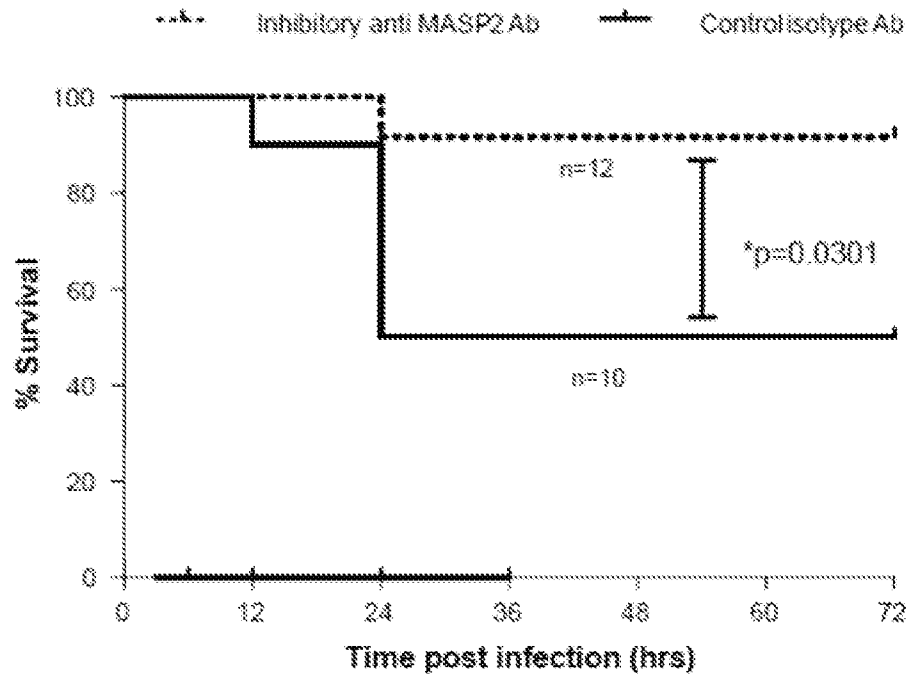
FIG. 12
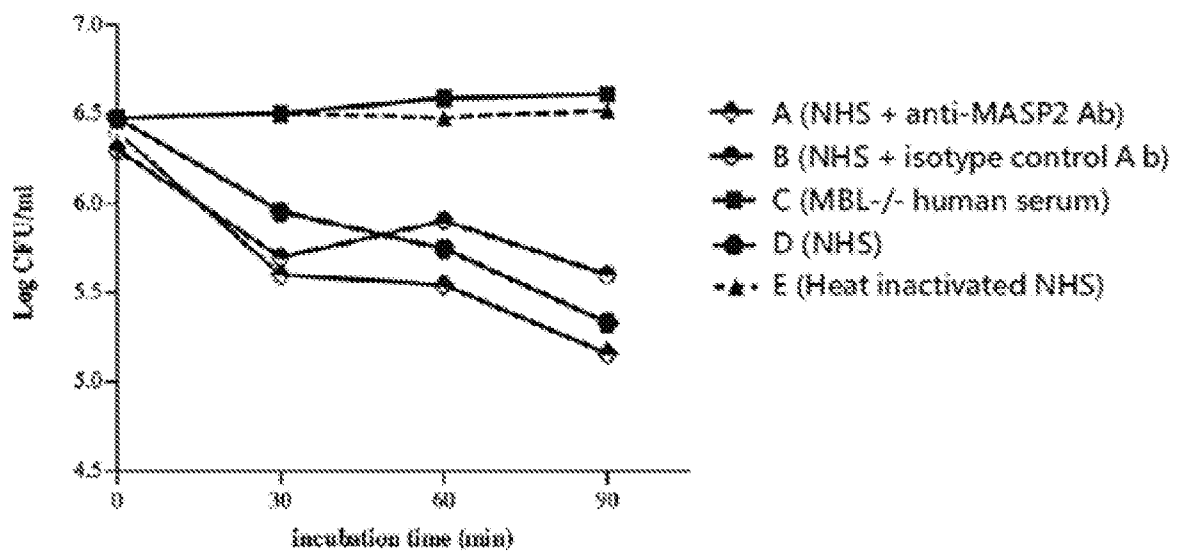
FIG. 13

Complement dependent killing of *Neisseria meningitidis* in human 20% v/v serum

A (NHS)
B (Heat Inactivated NHS)
C (MBL -/-)
D (MASP-3 -/-)
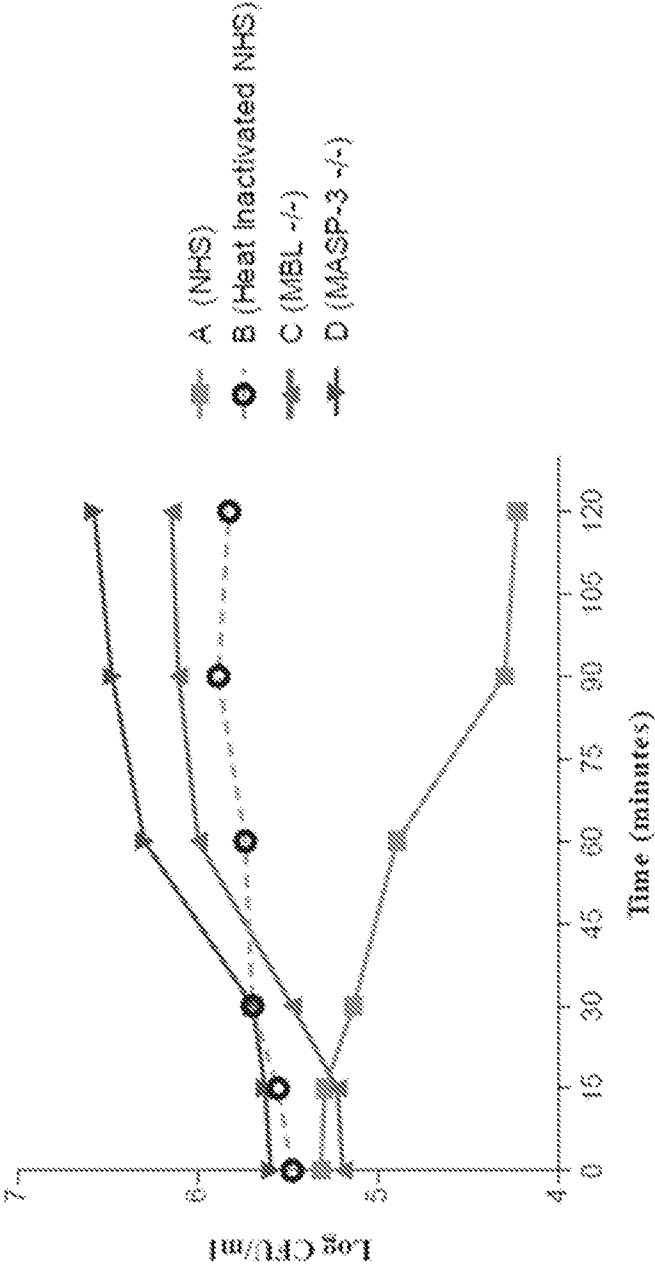
FIG. 14
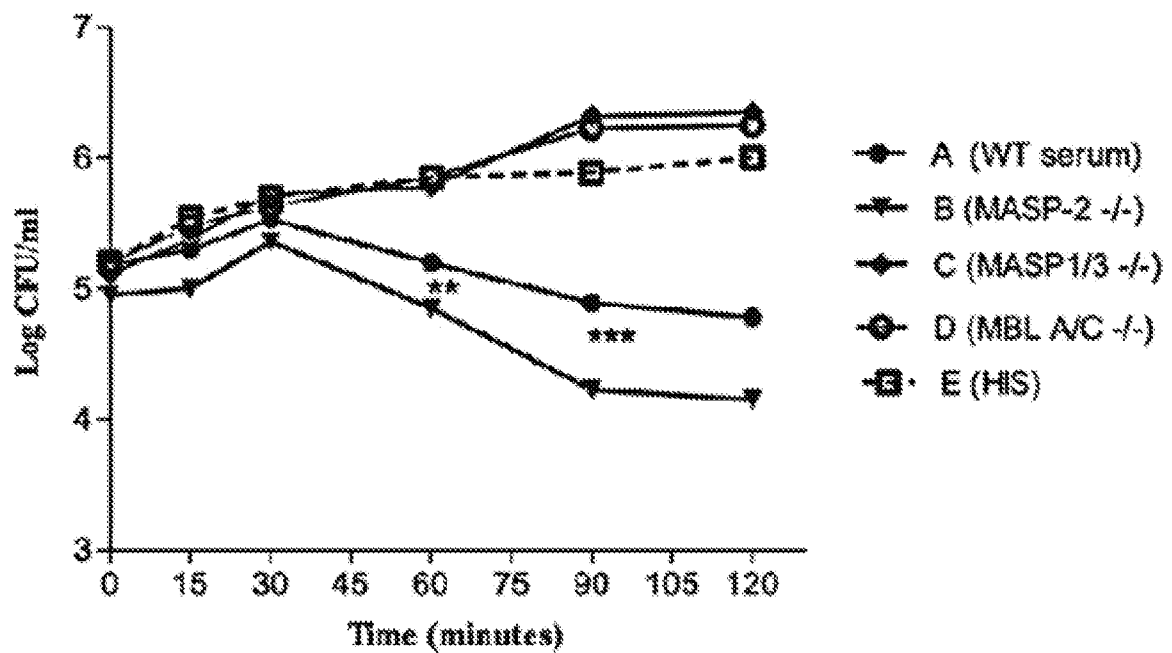
FIG. 15

MASP-1/3 deficient mice are not deficient of LP functional activity
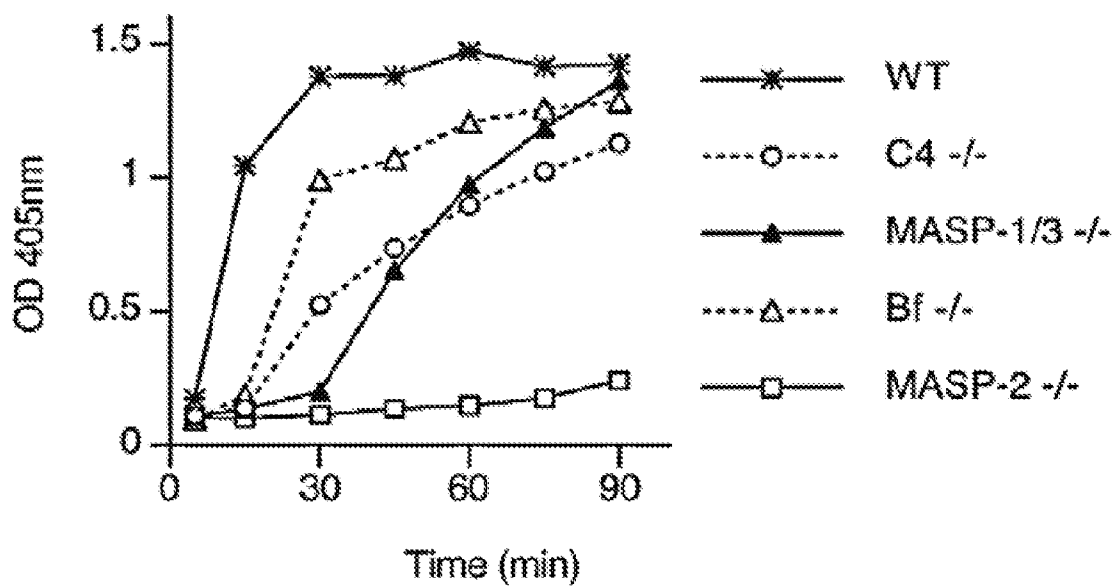
FIG. 16

15/37
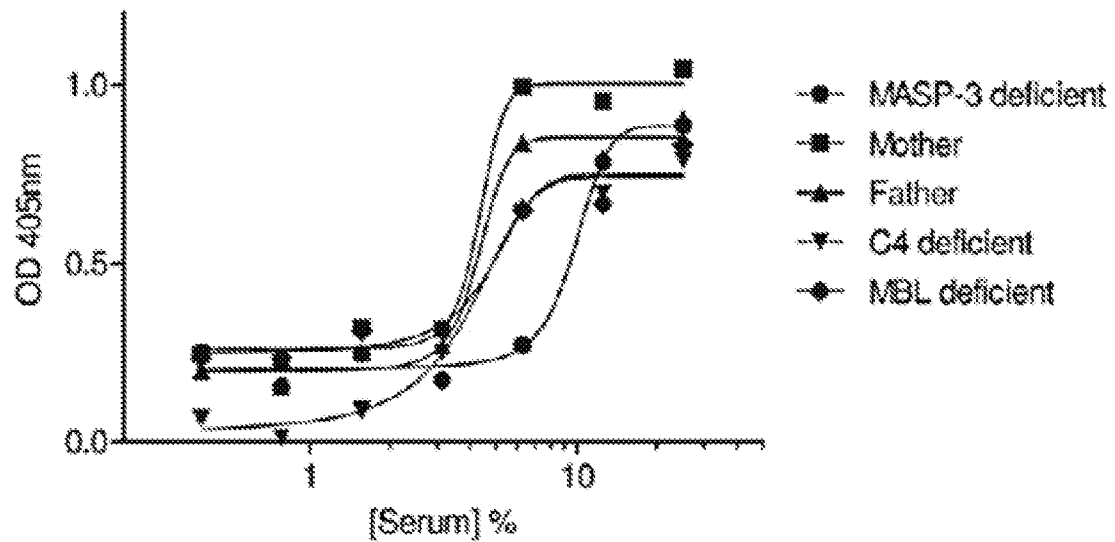
FIG. 17
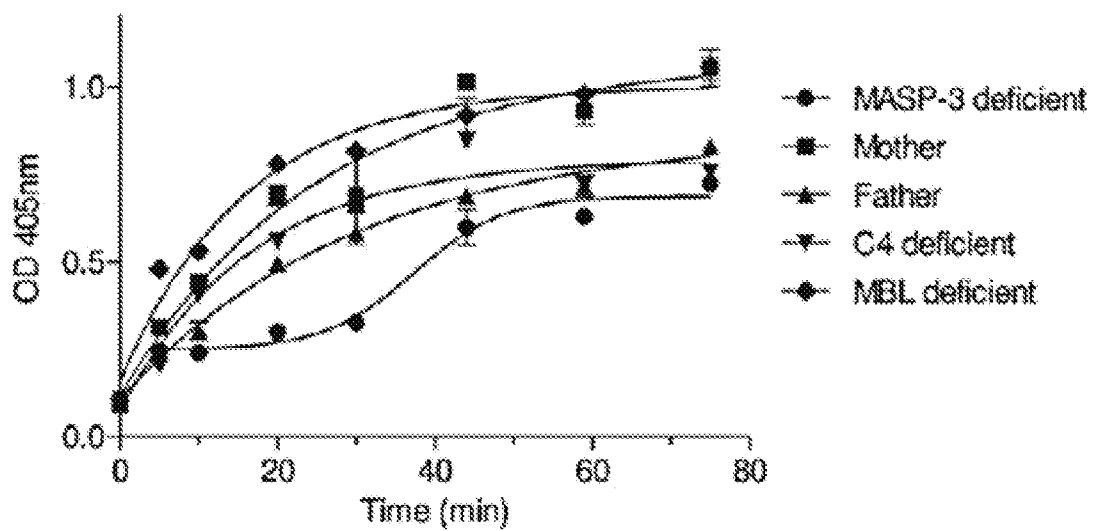
FIG. 18
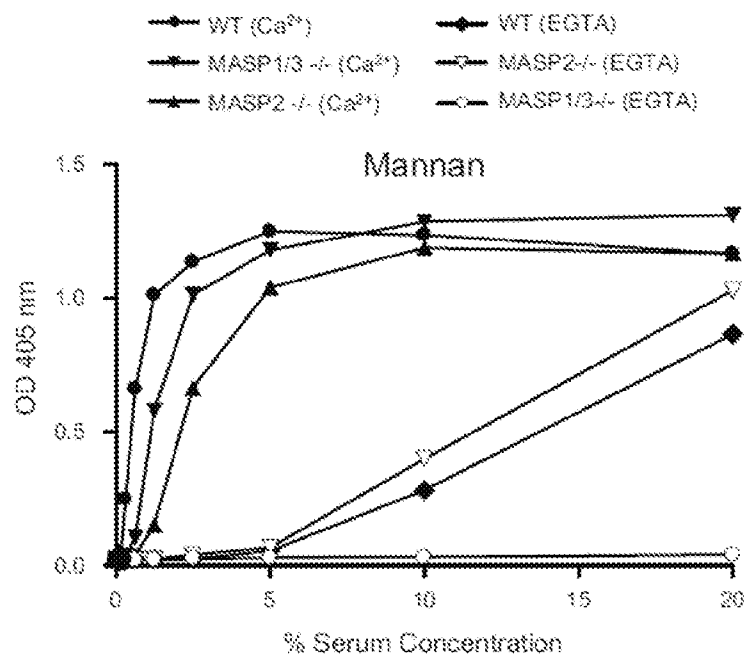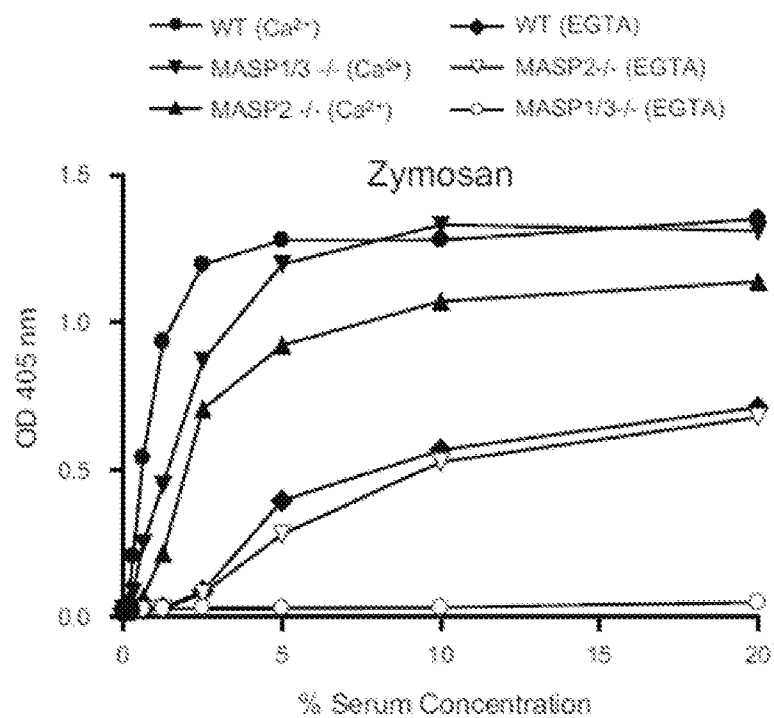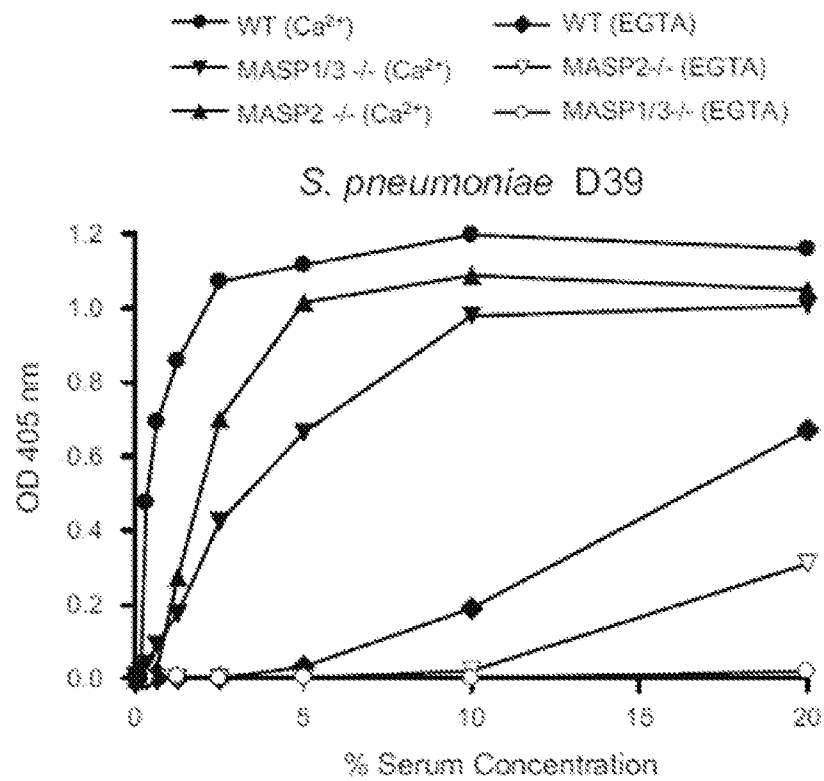
FIG. 19A

FIG. 19B

FIG. 19C
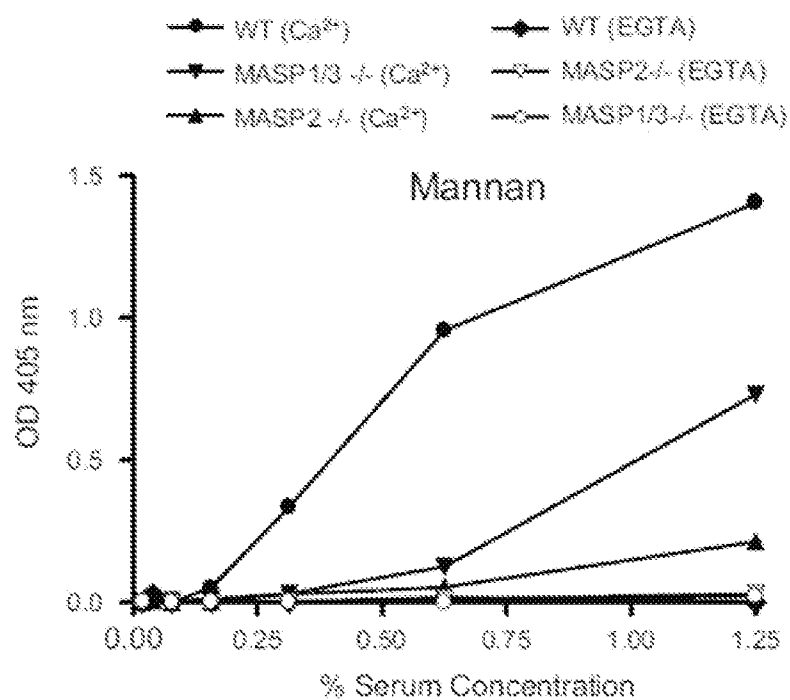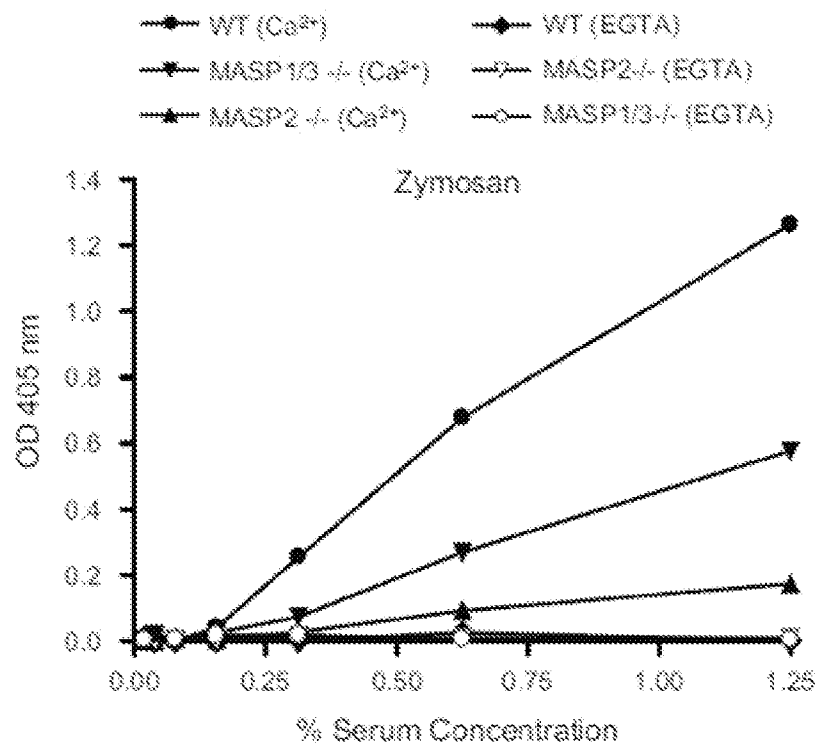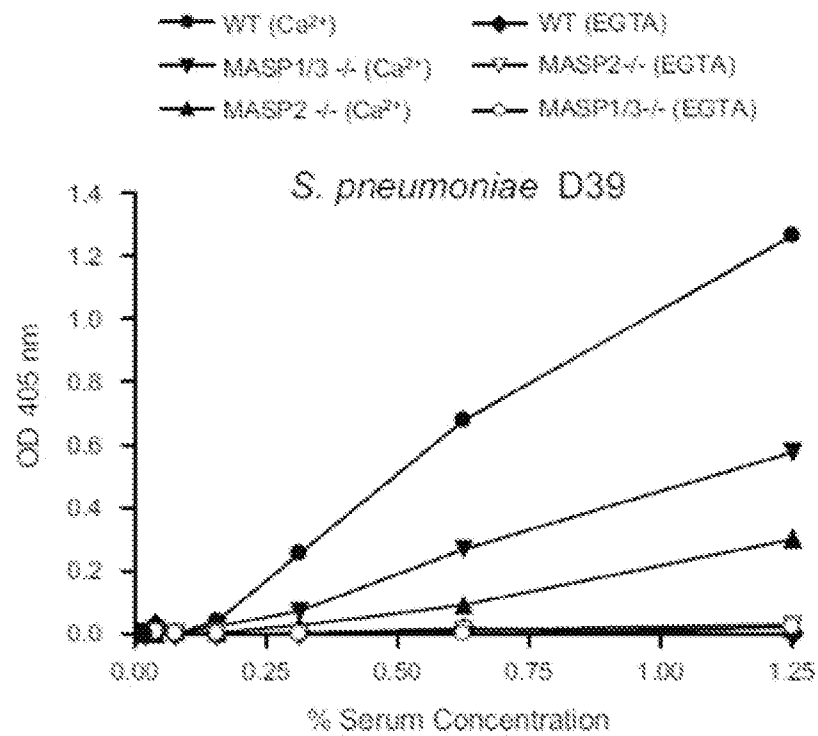
FIG. 20A

FIG. 20B

FIG. 20C

Haemolysis of mannan-coated Murine RBC by human serum
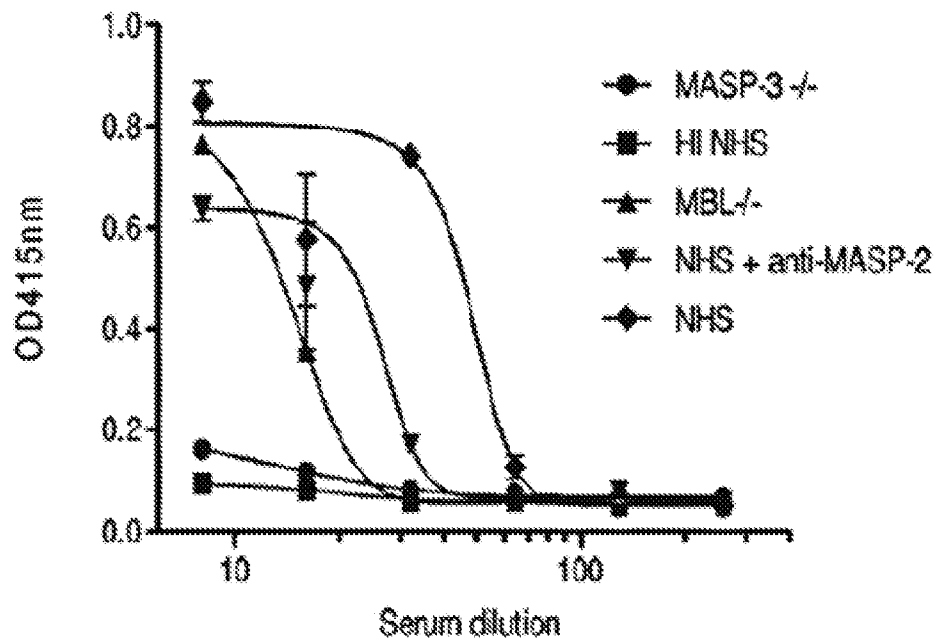
FIG. 21

Haemolysis of mannan-coated Murine RBC by human serum
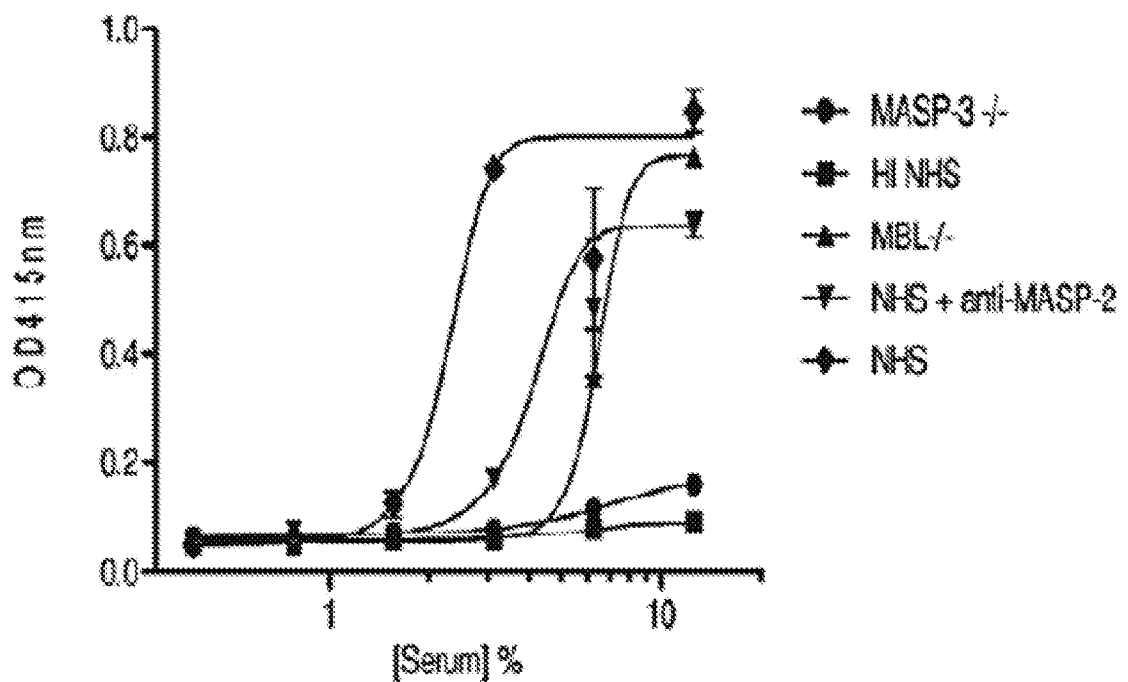
FIG. 22
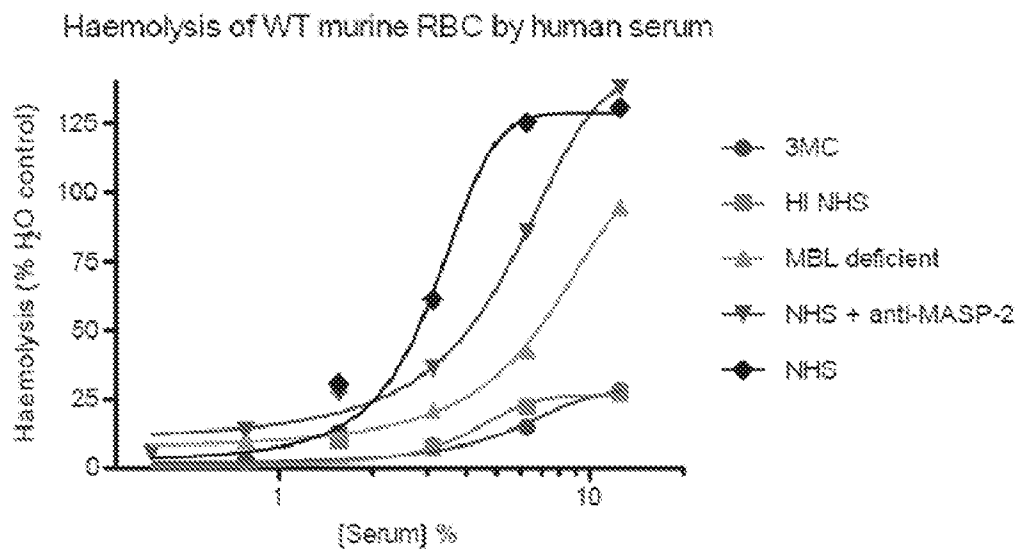
FIG. 23
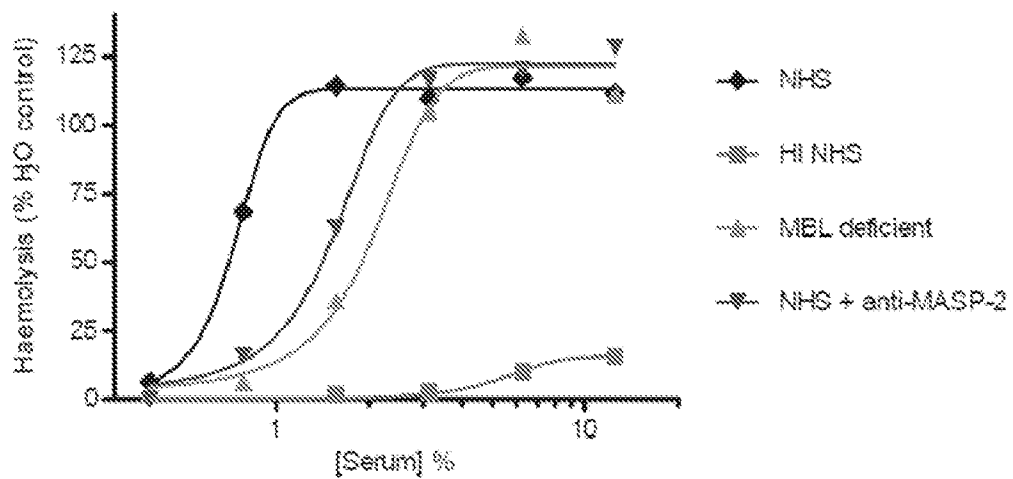
FIG. 24

Haemolytic assay using Rabbit RBCs with WT and MASP-1/3 $^{-/-}$ mouse sera.

FIG. 25

FIG. 26

FIG. 27

FIG. 28

FIG. 29A

FIG. 29B

FIG. 30A

FIG. 30B

FIG. 31

FIG. 32A

```
                 1                                                           65
         VH    AVTLDESGGGLQTPGGALSLVCKASGFTFSSNAMGWVRQAPGKGLEWVAGID-DDGSGTRYAPAV
         M3J5  . . . . . . . . . . . . . . . . . . . . . . . . . . . Y . . . M . . . . . . . Y . . . . . R-S . . . F . L . . T .
         M3M1  . . . . . . . . G . . . . . . . . . . . . . . . G . . . D . . YQ . N . . I . . . . . . . F . A . N-RF . NS . GHGA .
         D14   . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . Y . H . . . . . . . . . . . . . . . . . . Y-KS . A . . N . . . .
         1E10  . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . YD . V . . . . . . . . . . F . . . . . SRN . RY . E . GS .

                66                                                          129
         VH    KGRATISRDNGQSTLRLQLNNLRAEDTGTYYCTKCAYSS-GCDYEGG--YIDAWGHGTEVIVSS
         M3J5  . . . . . . . . . . . . . . . . . . . . . . . . . . . V . . . . . A . F . . RSG----NV--D . . . . . . . . . . . . . .
         M3M1  . V . . . . . . . . . . . . . . . . . . . . . D . . V . . . . . A . . . . GV . GYC . SYSCC . VDT . . . . . . . . . .
         D14   . . . . . . . . . . . . . . . . . . . . . . . . V . . . . . . . . . . . . A . . . TTG . GCSSG . RAE-- . . . . . . . . . . . .
         1E10  . . . . . . . . . . . . . . . . . . . . . . . . V . . . . . A . . . . . ARD . GG . - AYWFDA . - . . Q . . . . . . . . . . . .
```

FIG. 32B

```
                 1                                                           54
         VL    ALTQPASVSANLGGTVKITCSGGGS-YAGSYYYGWQQKSPGSAPVTVIYDNDK
         M3J5  . . . . . . . . . . . . . . . . . . . . . . . . Y . G . . . . . . . . . . . A . . . . . . . . . . . . . L . . Y . N . .
         M3M1  . . . . . . . . . . . . . . . . . . . . . P . E . . . . . . - . . . . . . . A . . . . . . . . . . . . . L . . Y . N . .
         D14   . . . . . . . . . . . . . . . . . . . . . P . E . . . . . . - . . . . . . . A . . . . . . . . . . . . . L . . Y . N . .
         1E10  . . . . . . . . . . . . . . . . . . . . . P . E . . . . . . - . . . . . . . A . . . . . . . . . . . . . L . . Y . N . .

                55                                                          108
         VL    RPSDIPSRFSGSLSGSTNTLTITGVRADDEAVYFCGSADNSGAAFGAGTTLTVL
         M3J5  . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . .
         M3M1  . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . .
         D14   . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . .
         1E10  . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . .
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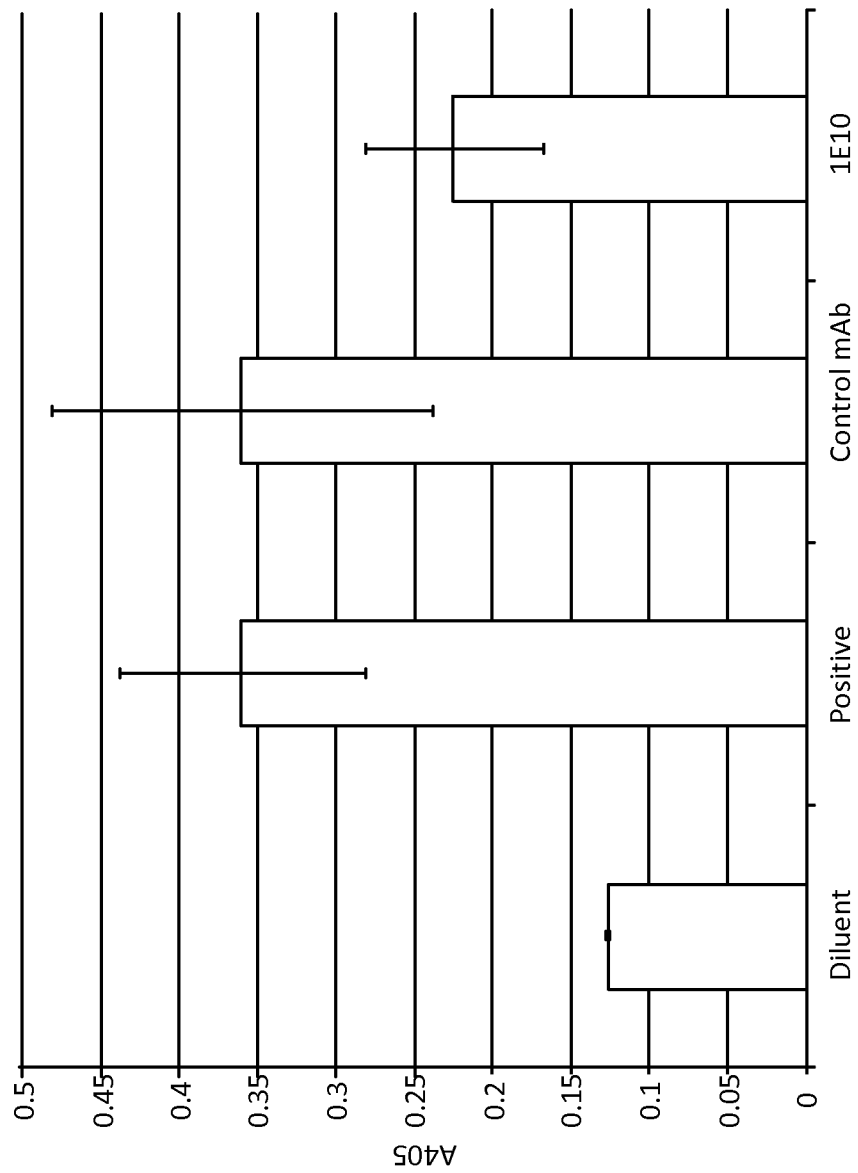
FIG. 33
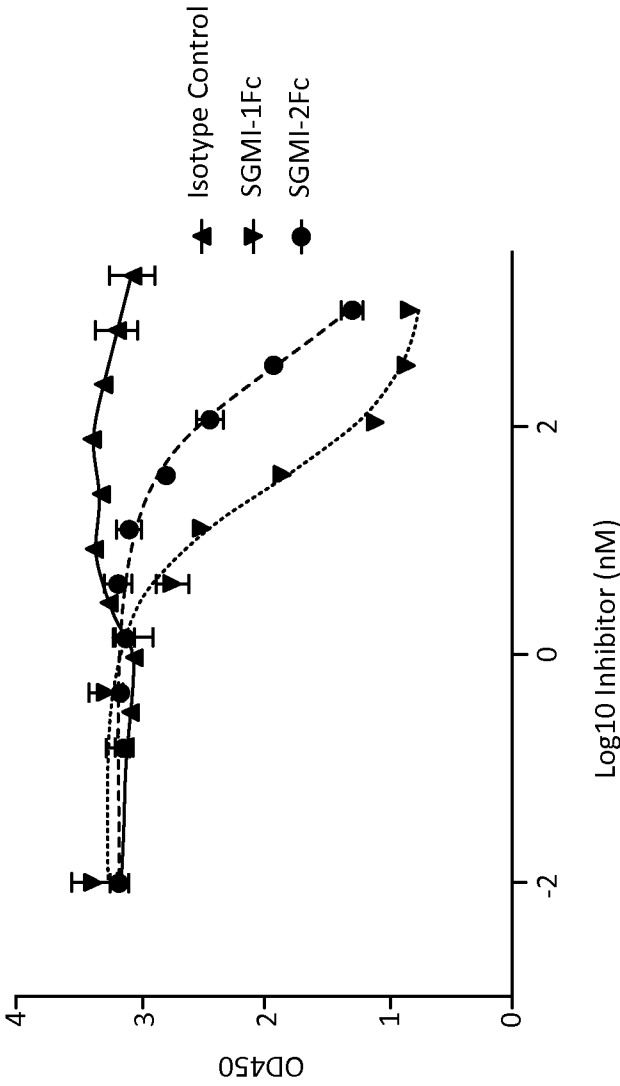
FIG. 34

C3b Deposition on *S. Aureus*
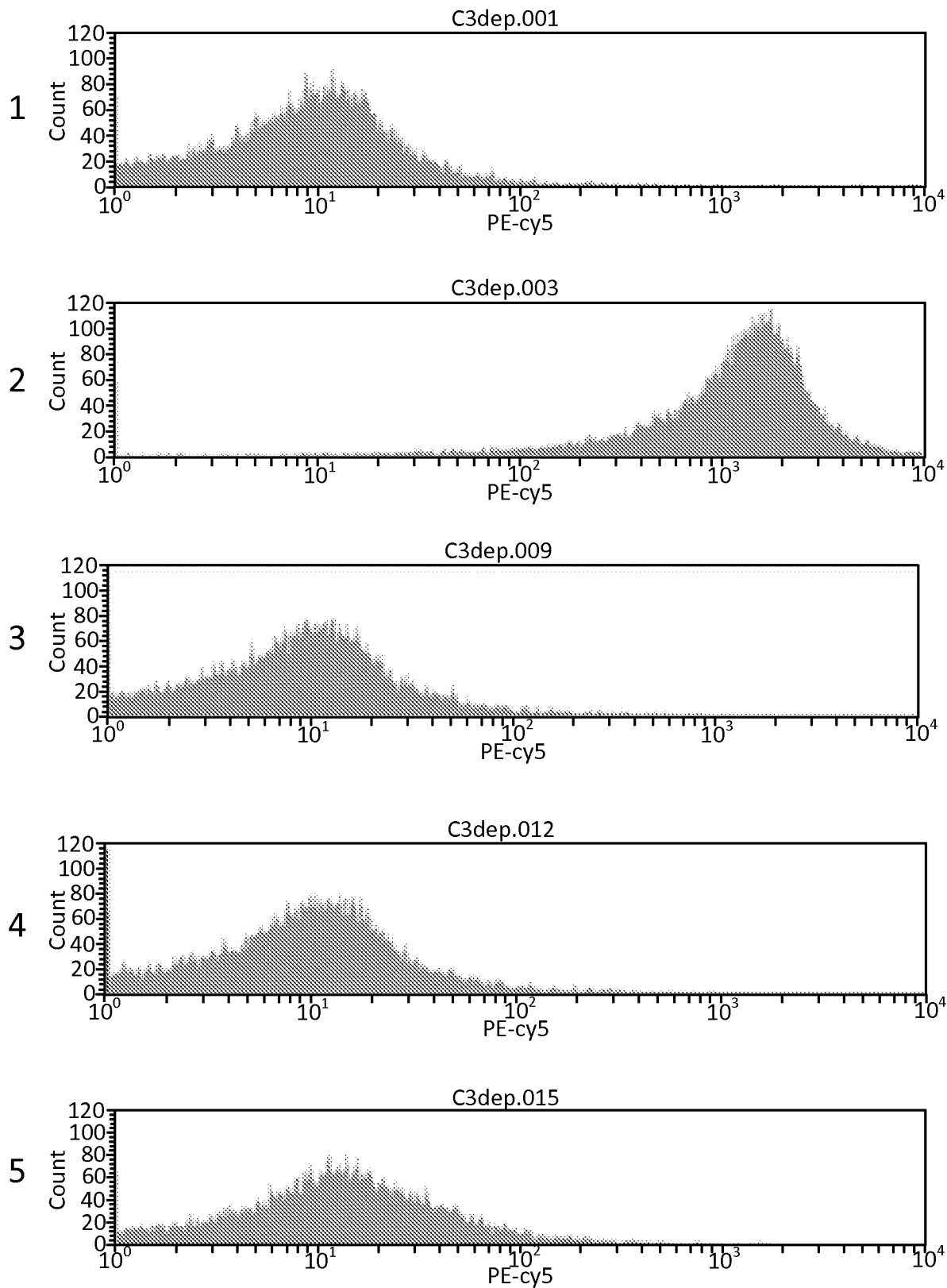
FIG. 35A

C3b Deposition on *S. Aureus*
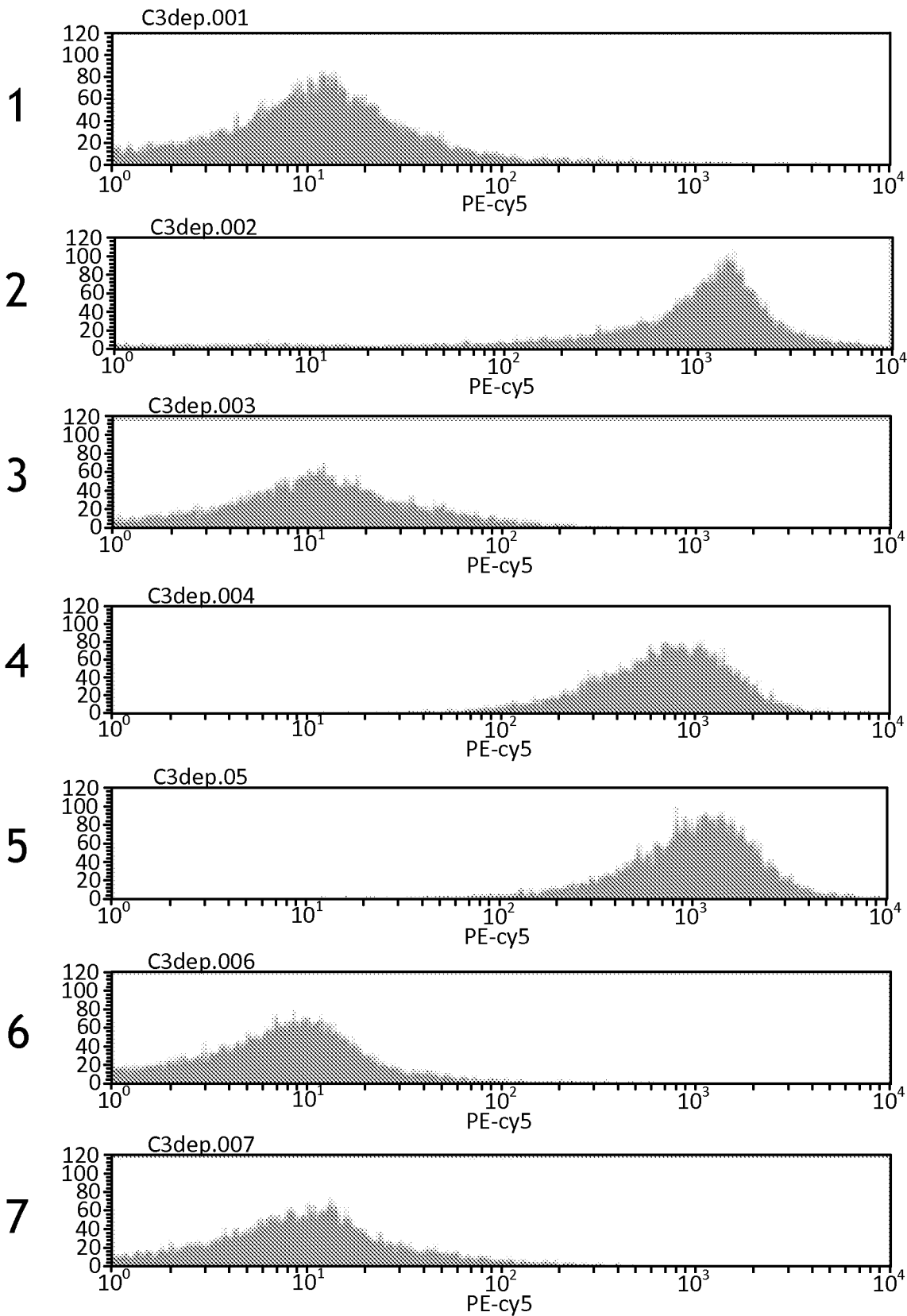
FIG. 35B

31/37

Factor B cleavage in response to *S. aureus*
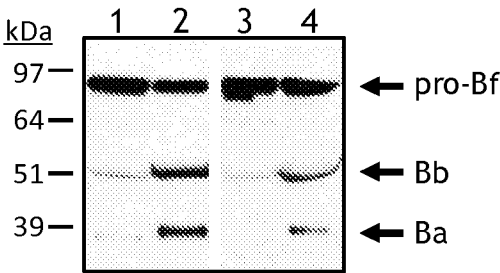
Complementation of 3MC serum with recombinant
MASP-3 does increase Factor B cleavage.

FIG. 36

MASP-3 directly cleaves pro-Bf

	1	2	3	4	5	6	7
C3	+	-	+	+	+	+	-
pro-Bf	+	+	-	+	+	-	+
MASP-3	+	+	+	+	-	-	-
pro-Df	+	+	+	-	+	-	-

FIG. 37

32/37

FIG. 38

MASP-1 and MASP-3 activate pro-Df
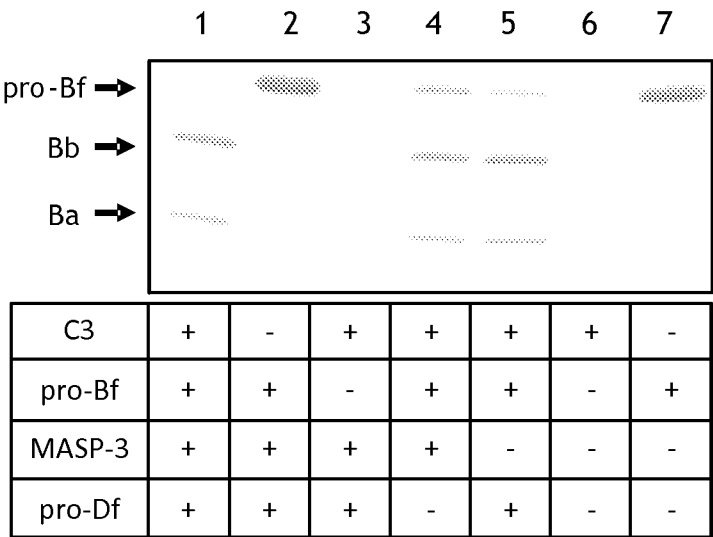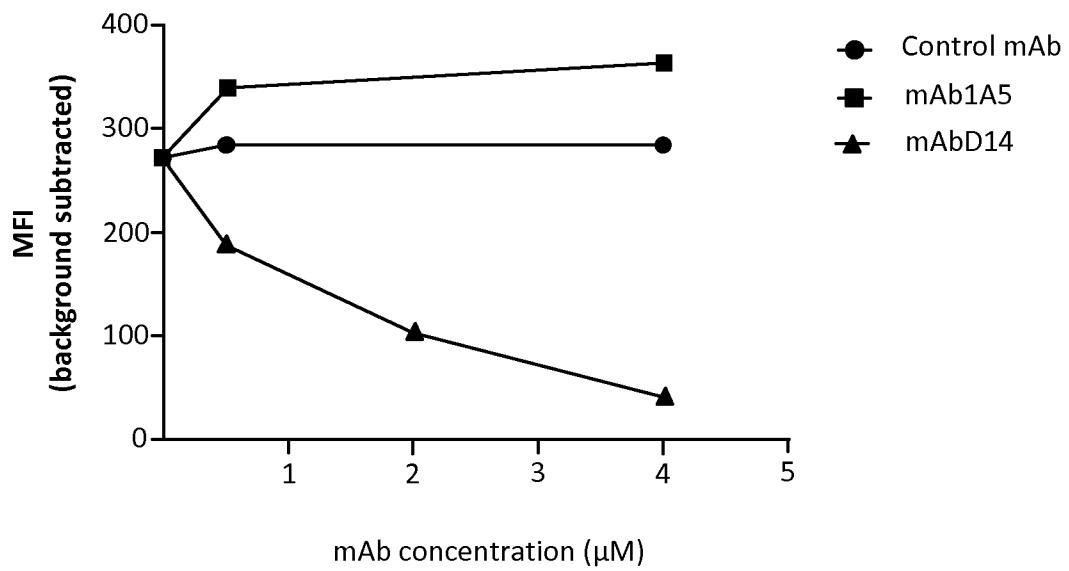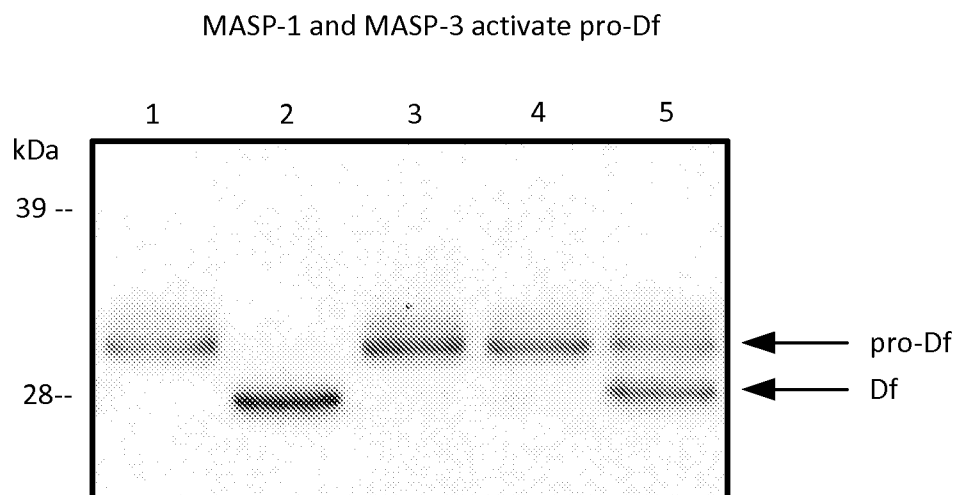
FIG. 39

Partial inhibition of MASP-3 dependent
Cleavage of Pro-Df with MASP-3 antibodies
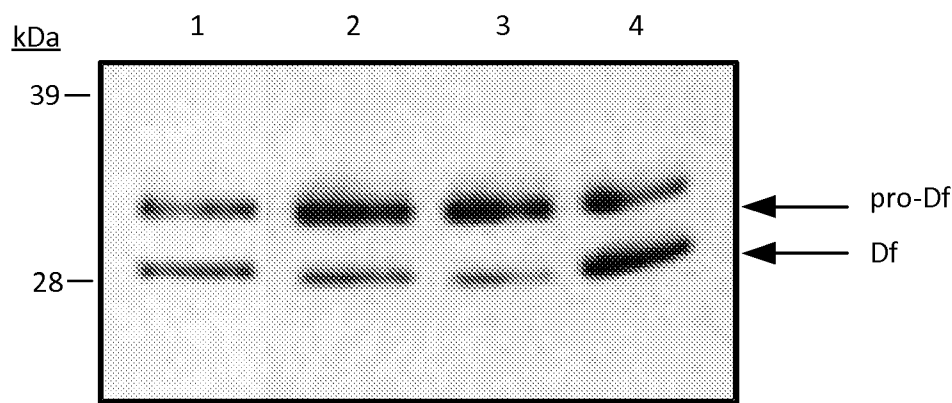
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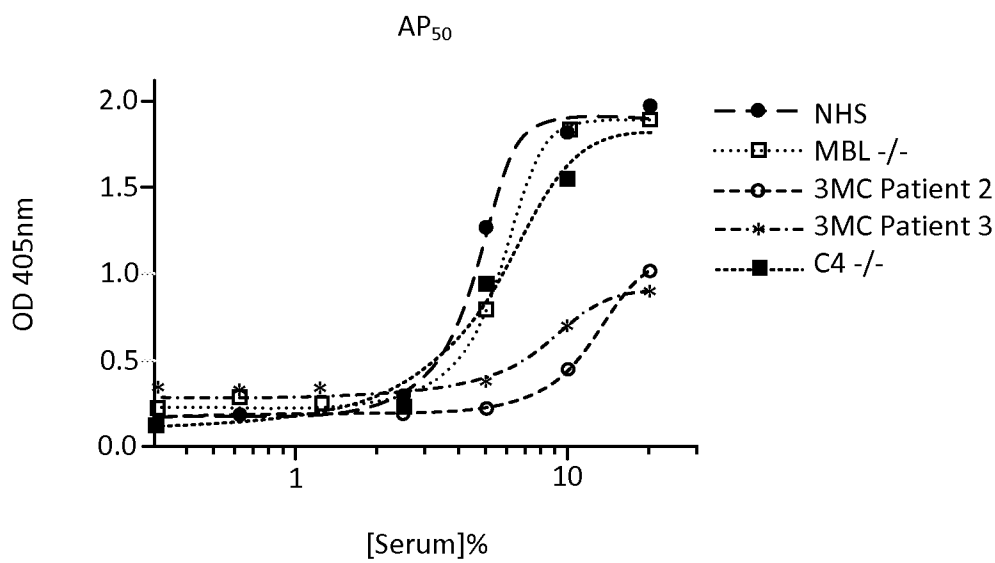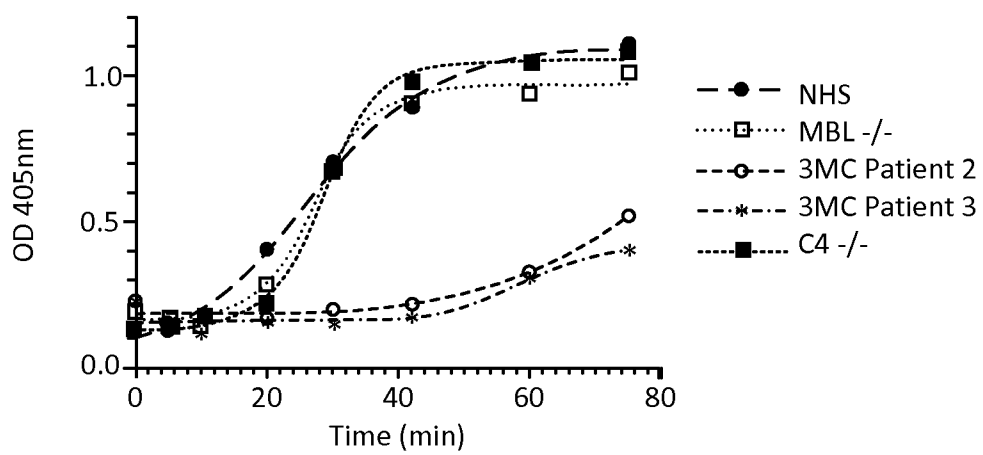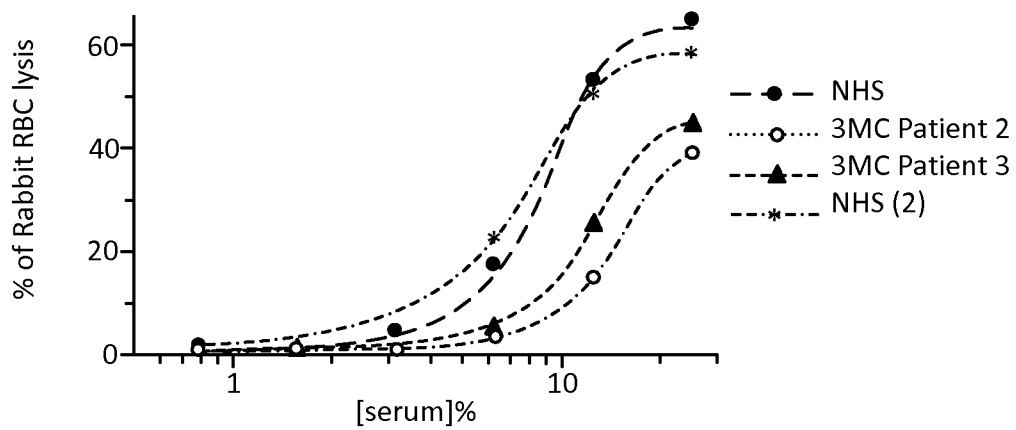
AP_{50}

FIG. 41

34/37

FIG. 42

FIG. 43
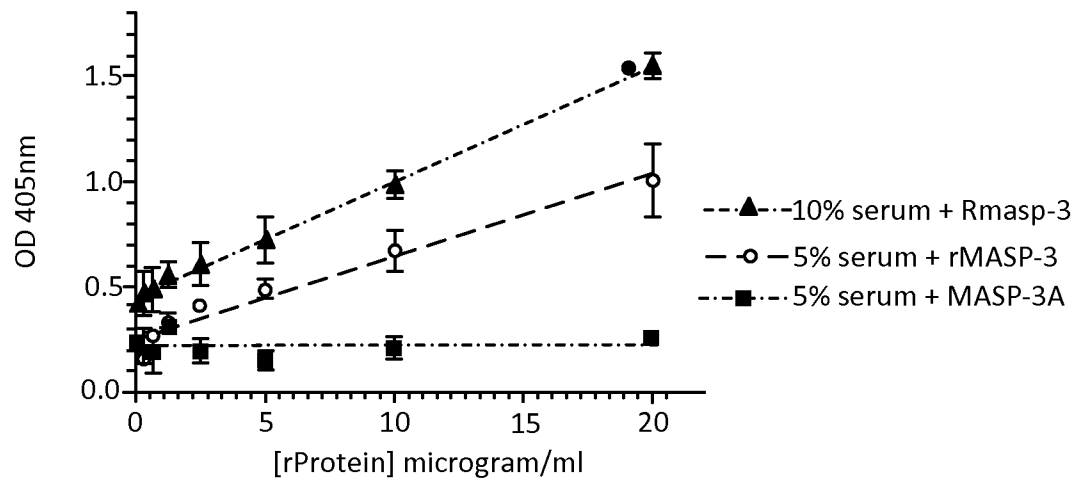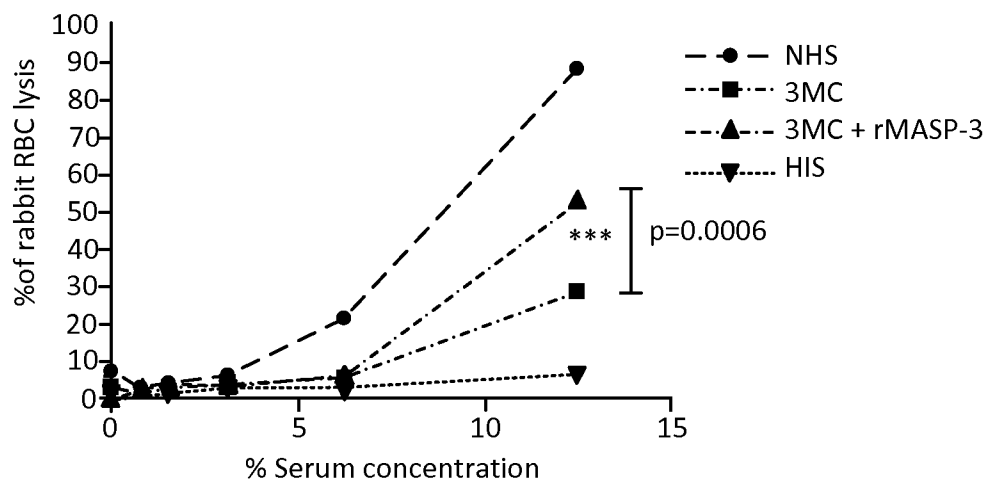
FIG. 44

FIG. 45
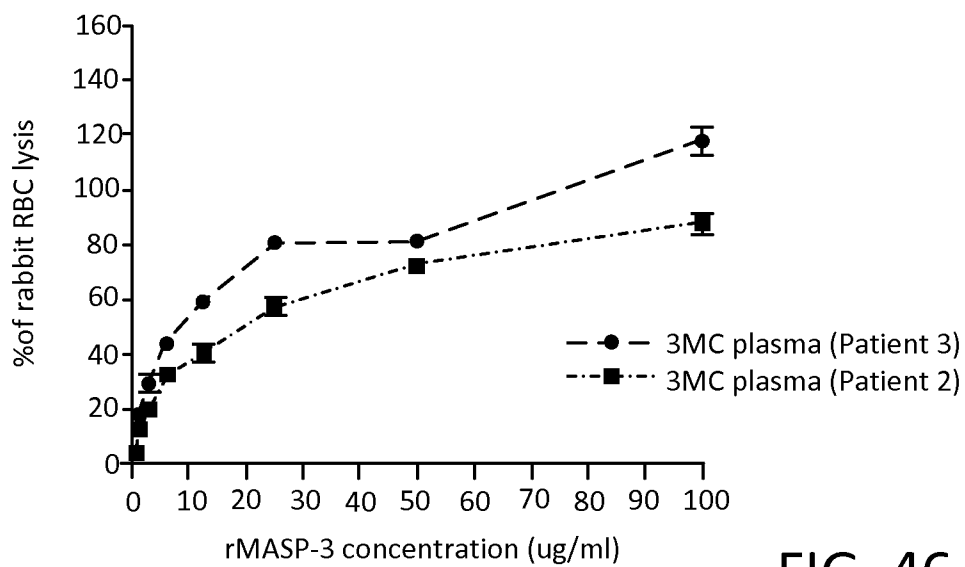
FIG. 46
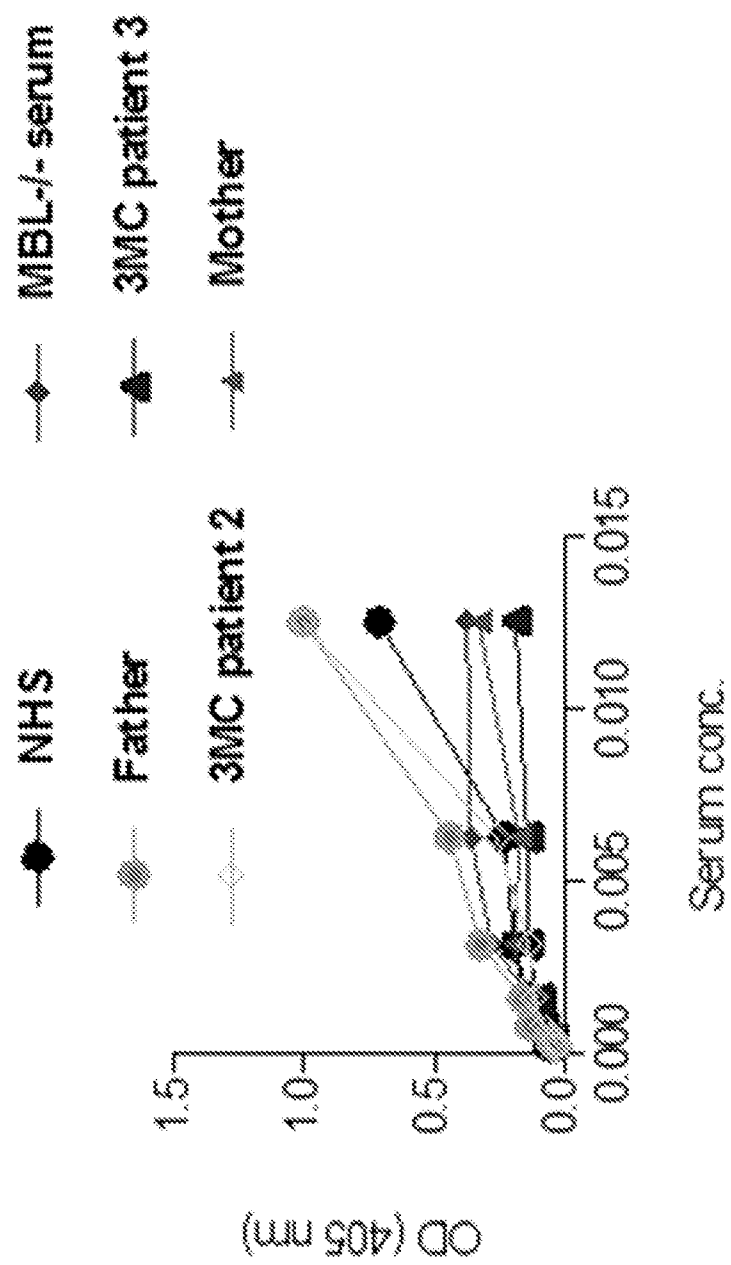
FIG. 47

<110> Omeros Corporation
       University of Leicester

<120> Compositions and Methods of Inhibiting MASP-1 and/or MASP-2
       and/or MASP-3 for the Treatment of Paroxysmal Nocturnal
       Hemoglobinuria

<130> MP.1.0146.PCT

<150> US 61/621,461
<151> 2012-04-06

<160> 42

<170> PatentIn version 3.5

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cccccggctt tccaggggag tatgccaatg accaggagcg cgctggacc ctgactgcac   180

cccccggcta ccgcctgcgc ctctacttca cccacttcga cctggagctc tcccacctct   240

gcgagtacga cttcgtcaag ctgagctcgg gggccaaggt gctggccacg ctgtgcgggc   300

aggagagcac agacacggag cgggcccctg gcaaggacac tttctactcg ctgggctcca   360

gcctggacat taccttccgc tccgactact ccaacgagaa gccgttcacg gggttcgagg   420

ccttctatgc agccgaggac attgacgagt gccaggtggc cccgggagag gcgcccacct   480

gcgaccacca ctgccacaac cacctgggcg gtttctactg ctcctgccgc gcaggctacg   540

tcctgcaccg taacaagcgc acctgctcag agcagagcct agcctccc ctggagctcc   600

ggcctgccca gcaggtcaga agccagagcc agcctgctgg cctcagctcc gggttgggct   660

gagatggctg tgccccaact cccattcacc caccatggac ccaataataa acctggcccc   720

acccc   725

<210> 2
<211> 185
<212> PRT
<213> homo sapiens

<400> 2

Met Arg Leu Leu Thr Leu Leu Gly Leu Leu Cys Gly Ser Val Ala Thr
1   5   10   15

Pro Leu Gly Pro Lys Trp Pro Glu Pro Val Phe Gly Arg Leu Ala Ser
            20   25   30

Pro Gly Phe Pro Gly Glu Tyr Ala Asn Asp Gln Glu Arg Arg Trp Thr
        35   40   45

```
Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His Phe
    50              55                  60

Asp Leu Glu Leu Ser His Leu Cys Glu Tyr Asp Phe Val Lys Leu Ser
65              70                  75                  80

Ser Gly Ala Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser Thr Asp
                85                  90                  95

Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe Tyr Ser Leu Gly Ser Ser
            100             105                 110

Leu Asp Ile Thr Phe Arg Ser Asp Tyr Ser Asn Glu Lys Pro Phe Thr
            115             120                 125

Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Ile Asp Glu Cys Gln Val
    130             135                 140

Ala Pro Gly Glu Ala Pro Thr Cys Asp His His Cys His Asn His Leu
145             150                 155                 160

Gly Gly Phe Tyr Cys Ser Cys Arg Ala Gly Tyr Val Leu His Arg Asn
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Lys Arg Thr Cys Ser Glu Gln Ser Leu
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<213>   homo sapiens

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Ser Pro Gly Phe Pro Gly Glu Tyr Ala Asn Asp Gln Glu Arg Arg Trp
                20                  25                  30

Thr Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His
            35                  40                  45

Phe Asp Leu Glu Leu Ser His Leu Cys Glu Tyr Asp Phe Val Lys Leu
    50                  55                  60

Ser Ser Gly Ala Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser Thr
65                  70                  75                  80

Asp Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe Tyr Ser Leu Gly Ser
                85                  90                  95
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Ser Leu Asp Ile Thr Phe Arg Ser Asp Tyr Ser Asn Glu Lys Pro Phe
           100   105   110

Thr Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Ile Asp Glu Cys Gln
           115   120   125

Val Ala Pro Gly Glu Ala Pro Thr Cys Asp His His Cys His Asn His
    130   135   140

Leu Gly Gly Phe Tyr Cys Ser Cys Arg Ala Gly Tyr Val Leu His Arg
145   150   155   160

Asn Lys Arg Thr Cys Ser Glu Gln Ser Leu
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Pro Gly Phe Pro Gly Glu Tyr Ala Asn Asp Gln Glu Arg Arg Trp Thr
        35   40   45

Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His Phe
    50   55   60

Asp Leu Glu Leu Ser His Leu Cys Glu Tyr Asp Phe Val Lys Leu Ser
65   70   75   80

Ser Gly Ala Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser Thr Asp
                    85   90   95

Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe Tyr Ser Leu Gly Ser Ser
            100   105   110

Leu Asp Ile Thr Phe Arg Ser Asp Tyr Ser Asn Glu Lys Pro Phe Thr
        115   120   125

Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Ile Asp Glu Cys Gln Val
    130   135   140

Ala Pro Gly Glu Ala Pro Thr Cys Asp His His Cys His Asn His Leu
145   150   155   160

Gly Gly Phe Tyr Cys Ser Cys Arg Ala Gly Tyr Val Leu His Arg Asn
                165   170   175

Lys Arg Thr Cys Ser Ala Leu Cys Ser Gly Gln Val Phe Thr Gln Arg
            180   185   190

Ser Gly Glu Leu Ser Ser Pro Glu Tyr Pro Arg Pro Tyr Pro Lys Leu
        195   200   205

Ser Ser Cys Thr Tyr Ser Ile Ser Leu Glu Glu Gly Phe Ser Val Ile
210   215   220

Leu Asp Phe Val Glu Ser Phe Asp Val Glu Thr His Pro Glu Thr Leu
225   230   235   240

Cys Pro Tyr Asp Phe Leu Lys Ile Gln Thr Asp Arg Glu Glu His Gly
            245   250   255

Pro Phe Cys Gly Lys Thr Leu Pro His Arg Ile Glu Thr Lys Ser Asn
            260   265   270

Thr Val Thr Ile Thr Phe Val Thr Asp Glu Ser Gly Asp His Thr Gly
        275   280   285

Trp Lys Ile His Tyr Thr Ser Thr Ala Gln Pro Cys Pro Tyr Pro Met
    290   295   300

Ala Pro Pro Asn Gly His Val Ser Pro Val Gln Ala Lys Tyr Ile Leu
305   310   315   320

Lys Asp Ser Phe Ser Ile Phe Cys Glu Thr Gly Tyr Glu Leu Leu Gln
                325   330   335

Gly His Leu Pro Leu Lys Ser Phe Thr Ala Val Cys Gln Lys Asp Gly
            340   345   350

Ser Trp Asp Arg Pro Met Pro Ala Cys Ser Ile Val Asp Cys Gly Pro
      355   360   365

Pro Asp Asp Leu Pro Ser Gly Arg Val Glu Tyr Ile Thr Gly Pro Gly
370   375   380

Val Thr Thr Tyr Lys Ala Val Ile Gln Tyr Ser Cys Glu Glu Thr Phe
385   390   395   400

Tyr Thr Met Lys Val Asn Asp Gly Lys Tyr Val Cys Glu Ala Asp Gly
            405   410   415

Phe Trp Thr Ser Ser Lys Gly Glu Lys Ser Leu Pro Val Cys Glu Pro
        420   425   430

Val Cys Gly Leu Ser Ala Arg Thr Thr Gly Gly Arg Ile Tyr Gly Gly
      435   440   445

Gln Lys Ala Lys Pro Gly Asp Phe Pro Trp Gln Val Leu Ile Leu Gly
    450   455   460

Gly Thr Thr Ala Ala Gly Ala Leu Leu Tyr Asp Asn Trp Val Leu Thr
465   470   475   480

Ala Ala His Ala Val Tyr Glu Gln Lys His Asp Ala Ser Ala Leu Asp
            485   490   495

Ile Arg Met Gly Thr Leu Lys Arg Leu Ser Pro His Tyr Thr Gln Ala
        500   505   510

Trp Ser Glu Ala Val Phe Ile His Glu Gly Tyr Thr His Asp Ala Gly
      515   520   525

Phe Asp Asn Asp Ile Ala Leu Ile Lys Leu Asn Asn Lys Val Val Ile
    530   535   540

Asn Ser Asn Ile Thr Pro Ile Cys Leu Pro Arg Lys Glu Ala Glu Ser
545   550   555   560

Phe Met Arg Thr Asp Asp Ile Gly Thr Ala Ser Gly Trp Gly Leu Thr
          565   570   575

Gln Arg Gly Phe Leu Ala Arg Asn Leu Met Tyr Val Asp Ile Pro Ile
        580   585   590

Val Asp His Gln Lys Cys Thr Ala Ala Tyr Glu Lys Pro Pro Tyr Pro
      595   600   605

Arg Gly Ser Val Thr Ala Asn Met Leu Cys Ala Gly Leu Glu Ser Gly
    610   615   620

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Gly Lys Asp Ser Cys Arg Gly Asp Ser Gly Gly Ala Leu Val Phe Leu
625             630             635                 640

Asp Ser Glu Thr Glu Arg Trp Phe Val Gly Gly Ile Val Ser Trp Gly
                645             650                 655

Ser Met Asn Cys Gly Glu Ala Gly Gln Tyr Gly Val Tyr Thr Lys Val
                660             665             670

Ile Asn Tyr Ile Pro Trp Ile Glu Asn Ile Ile Ser Asp Phe
            675             680             685
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                20              25              30

Thr Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His
        35              40              45

Phe Asp Leu Glu Leu Ser His Leu Cys Glu Tyr Asp Phe Val Lys Leu
    50              55              60

Ser Ser Gly Ala Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser Thr
65              70              75                  80

Asp Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe Tyr Ser Leu Gly Ser
                85              90              95

Ser Leu Asp Ile Thr Phe Arg Ser Asp Tyr Ser Asn Glu Lys Pro Phe
            100             105             110

Thr Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Ile Asp Glu Cys Gln
        115             120             125

Val Ala Pro Gly Glu Ala Pro Thr Cys Asp His His Cys His Asn His
    130             135             140

Leu Gly Gly Phe Tyr Cys Ser Cys Arg Ala Gly Tyr Val Leu His Arg
145             150             155             160

Asn Lys Arg Thr Cys Ser Ala Leu Cys Ser Gly Gln Val Phe Thr Gln
            165             170             175
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Arg Ser Gly Glu Leu Ser Ser Pro Glu Tyr Pro Arg Pro Tyr Pro Lys
          180   185   190

Leu Ser Ser Cys Thr Tyr Ser Ile Ser Leu Glu Glu Gly Phe Ser Val
          195   200   205

Ile Leu Asp Phe Val Glu Ser Phe Asp Val Glu Thr His Pro Glu Thr
    210   215   220

Leu Cys Pro Tyr Asp Phe Leu Lys Ile Gln Thr Asp Arg Glu Glu His
225   230   235   240

Gly Pro Phe Cys Gly Lys Thr Leu Pro His Arg Ile Glu Thr Lys Ser
          245   250   255

Asn Thr Val Thr Ile Thr Phe Val Thr Asp Glu Ser Gly Asp His Thr
          260   265   270

Gly Trp Lys Ile His Tyr Thr Ser Thr Ala Gln Pro Cys Pro Tyr Pro
          275   280   285

Met Ala Pro Pro Asn Gly His Val Ser Pro Val Gln Ala Lys Tyr Ile
    290   295   300

Leu Lys Asp Ser Phe Ser Ile Phe Cys Glu Thr Gly Tyr Glu Leu Leu
305   310   315   320

Gln Gly His Leu Pro Leu Lys Ser Phe Thr Ala Val Cys Gln Lys Asp
          325   330   335

Gly Ser Trp Asp Arg Pro Met Pro Ala Cys Ser Ile Val Asp Cys Gly
          340   345   350

Pro Pro Asp Asp Leu Pro Ser Gly Arg Val Glu Tyr Ile Thr Gly Pro
          355   360   365

Gly Val Thr Thr Tyr Lys Ala Val Ile Gln Tyr Ser Cys Glu Glu Thr
    370   375   380

Phe Tyr Thr Met Lys Val Asn Asp Gly Lys Tyr Val Cys Glu Ala Asp
385   390   395   400

Gly Phe Trp Thr Ser Ser Lys Gly Glu Lys Ser Leu Pro Val Cys Glu
          405   410   415

Pro Val Cys Gly Leu Ser Ala Arg Thr Thr Gly Gly Arg Ile Tyr Gly
          420   425   430

Gly Gln Lys Ala Lys Pro Gly Asp Phe Pro Trp Gln Val Leu Ile Leu
          435   440   445

Gly Gly Thr Thr Ala Ala Gly Ala Leu Leu Tyr Asp Asn Trp Val Leu
    450   455   460

Thr Ala Ala His Ala Val Tyr Glu Gln Lys His Asp Ala Ser Ala Leu
465   470   475   480

Asp Ile Arg Met Gly Thr Leu Lys Arg Leu Ser Pro His Tyr Thr Gln
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Ala Trp Ser Glu Ala Val Phe Ile His Glu Gly Tyr Thr His Asp Ala
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Gly Phe Asp Asn Asp Ile Ala Leu Ile Lys Leu Asn Asn Lys Val Val
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Ile Asn Ser Asn Ile Thr Pro Ile Cys Leu Pro Arg Lys Glu Ala Glu
    530   535   540

Ser Phe Met Arg Thr Asp Asp Ile Gly Thr Ala Ser Gly Trp Gly Leu
545   550   555   560

Thr Gln Arg Gly Phe Leu Ala Arg Asn Leu Met Tyr Val Asp Ile Pro
            565   570   575

Ile Val Asp His Gln Lys Cys Thr Ala Ala Tyr Glu Lys Pro Pro Tyr
            580   585   590

Pro Arg Gly Ser Val Thr Ala Asn Met Leu Cys Ala Gly Leu Glu Ser
        595   600   605

Gly Gly Lys Asp Ser Cys Arg Gly Asp Ser Gly Gly Ala Leu Val Phe
    610   615   620

Leu Asp Ser Glu Thr Glu Arg Trp Phe Val Gly Gly Ile Val Ser Trp
625   630   635   640

Gly Ser Met Asn Cys Gly Glu Ala Gly Gln Tyr Gly Val Tyr Thr Lys
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Val Ile Asn Tyr Ile Pro Trp Ile Glu Asn Ile Ile Ser Asp Phe
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            20              25                  30

Ser Pro Gly Tyr Pro Asp Ser Tyr Pro Ser Asp Ser Glu Val Thr Trp
        35              40                  45

Asn Ile Thr Val Pro Asp Gly Phe Arg Ile Lys Leu Tyr Phe Met His
    50              55                  60

Phe Asn Leu Glu Ser Ser Tyr Leu Cys Glu Tyr Asp Tyr Val Lys Val
65              70              75                  80

Glu Thr Glu Asp Gln Val Leu Ala Thr Phe Cys Gly Arg Glu Thr Thr
            85              90                  95

Asp Thr Glu Gln Thr Pro Gly Gln Glu Val Val Leu Ser Pro Gly Ser
            100             105                 110

Phe Met Ser Ile Thr Phe Arg Ser Asp Phe Ser Asn Glu Glu Arg Phe
        115                 120             125

Thr Gly Phe Asp Ala His Tyr Met Ala Val Asp Val Asp Glu Cys Lys
    130             135                 140

Glu Arg Glu Asp Glu Glu Leu Ser Cys Asp His Tyr Cys His Asn Tyr
145             150                 155                 160

Ile Gly Gly Tyr Tyr Cys Ser Cys Arg Phe Gly Tyr Ile Leu His Thr
            165                 170                 175

Asp Asn Arg Thr Cys Arg Val Glu Cys Ser Asp Asn Leu Phe Thr Gln
            180                 185                 190

Arg Thr Gly Val Ile Thr Ser Pro Asp Phe Pro Asn Pro Tyr Pro Lys
        195                 200             205

Ser Ser Glu Cys Leu Tyr Thr Ile Glu Leu Glu Glu Gly Phe Met Val
    210                 215             220

Asn Leu Gln Phe Glu Asp Ile Phe Asp Ile Glu Asp His Pro Glu Val
225                 230                 235                 240

Pro Cys Pro Tyr Asp Tyr Ile Lys Ile Lys Val Gly Pro Lys Val Leu
            245                 250                 255

Gly Pro Phe Cys Gly Glu Lys Ala Pro Glu Pro Ile Ser Thr Gln Ser
            260             265                 270

His Ser Val Leu Ile Leu Phe His Ser Asp Asn Ser Gly Glu Asn Arg
        275             280                 285
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Page 12

Gly Trp Arg Leu Ser Tyr Arg Ala Ala Gly Asn Glu Cys Pro Glu Leu
    290   295   300

Gln Pro Pro Val His Gly Lys Ile Glu Pro Ser Gln Ala Lys Tyr Phe
305   310   315   320

Phe Lys Asp Gln Val Leu Val Ser Cys Asp Thr Gly Tyr Lys Val Leu
            325   330   335

Lys Asp Asn Val Glu Met Asp Thr Phe Gln Ile Glu Cys Leu Lys Asp
            340   345   350

Gly Thr Trp Ser Asn Lys Ile Pro Thr Cys Lys Ile Val Asp Cys Arg
        355   360   365

Ala Pro Gly Glu Leu Glu His Gly Leu Ile Thr Phe Ser Thr Arg Asn
    370   375   380

Asn Leu Thr Thr Tyr Lys Ser Glu Ile Lys Tyr Ser Cys Gln Glu Pro
385   390   395   400

Tyr Tyr Lys Met Leu Asn Asn Asn Thr Gly Ile Tyr Thr Cys Ser Ala
            405   410   415

Gln Gly Val Trp Met Asn Lys Val Leu Gly Arg Ser Leu Pro Thr Cys
            420   425   430

Leu Pro Glu Cys Gly Gln Pro Ser Arg Ser Leu Pro Ser Leu Val Lys
        435   440   445

Arg Ile Ile Gly Gly Arg Asn Ala Glu Pro Gly Leu Phe Pro Trp Gln
    450   455   460

Ala Leu Ile Val Val Glu Asp Thr Ser Arg Val Pro Asn Asp Lys Trp
465   470   475   480

Phe Gly Ser Gly Ala Leu Leu Ser Ala Ser Trp Ile Leu Thr Ala Ala
            485   490   495

His Val Leu Arg Ser Gln Arg Arg Asp Thr Thr Val Ile Pro Val Ser
        500   505   510

Lys Glu His Val Thr Val Tyr Leu Gly Leu His Asp Val Arg Asp Lys
        515   520   525

Ser Gly Ala Val Asn Ser Ser Ala Ala Arg Val Val Leu His Pro Asp
    530   535   540

Phe Asn Ile Gln Asn Tyr Asn His Asp Ile Ala Leu Val Gln Leu Gln
545   550   555   560

Page 13

Glu Pro Val Pro Leu Gly Pro His Val Met Pro Val Cys Leu Pro Arg
                565   570   575

Leu Glu Pro Glu Gly Pro Ala Pro His Met Leu Gly Leu Val Ala Gly
            580   585   590

Trp Gly Ile Ser Asn Pro Asn Val Thr Val Asp Glu Ile Ile Ser Ser
            595   600   605

Gly Thr Arg Thr Leu Ser Asp Val Leu Gln Tyr Val Lys Leu Pro Val
    610   615   620

Val Pro His Ala Glu Cys Lys Thr Ser Tyr Glu Ser Arg Ser Gly Asn
625   630   635   640

Tyr Ser Val Thr Glu Asn Met Phe Cys Ala Gly Tyr Tyr Glu Gly Gly
            645   650   655

Lys Asp Thr Cys Leu Gly Asp Ser Gly Gly Ala Phe Val Ile Phe Asp
            660   665   670

Asp Leu Ser Gln Arg Trp Val Val Gln Gly Leu Val Ser Trp Gly Gly
            675   680   685

Pro Glu Glu Cys Gly Ser Lys Gln Val Tyr Gly Val Tyr Thr Lys Val
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Ser Asn Tyr Val Asp Trp Val Trp Glu Gln Met Gly Leu Pro Gln Ser
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Val Val Glu Pro Gln Val Glu Arg
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cttcgaactt cagtttcttc ataagatgga aa   2852

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Ala Ser Ala His Thr Val Glu Leu Asn Asn Met Phe Gly Gln Ile Gln
                20   25   30

Ser Pro Gly Tyr Pro Asp Ser Tyr Pro Ser Asp Ser Glu Val Thr Trp
            35   40   45

Asn Ile Thr Val Pro Asp Gly Phe Arg Ile Lys Leu Tyr Phe Met His
        50   55   60

Phe Asn Leu Glu Ser Ser Tyr Leu Cys Glu Tyr Asp Tyr Val Lys Val
65   70   75   80

Glu Thr Glu Asp Gln Val Leu Ala Thr Phe Cys Gly Arg Glu Thr Thr
                85   90   95

Asp Thr Glu Gln Thr Pro Gly Gln Glu Val Val Leu Ser Pro Gly Ser
                100   105   110

Phe Met Ser Ile Thr Phe Arg Ser Asp Phe Ser Asn Glu Glu Arg Phe
                115   120   125

Thr Gly Phe Asp Ala His Tyr Met Ala Val Asp Val Asp Glu Cys Lys
        130   135   140

Glu Arg Glu Asp Glu Glu Leu Ser Cys Asp His Tyr Cys His Asn Tyr
145   150   155   160

Ile Gly Gly Tyr Tyr Cys Ser Cys Arg Phe Gly Tyr Ile Leu His Thr
                165   170   175

Asp Asn Arg Thr Cys Arg Val Glu Cys Ser Asp Asn Leu Phe Thr Gln
                180   185   190

Arg Thr Gly Val Ile Thr Ser Pro Asp Phe Pro Asn Pro Tyr Pro Lys
            195   200   205

Page 16

Ser Ser Glu Cys Leu Tyr Thr Ile Glu Leu Glu Glu Gly Phe Met Val
210   215   220

Asn Leu Gln Phe Glu Asp Ile Phe Asp Ile Glu Asp His Pro Glu Val
225   230   235   240

Pro Cys Pro Tyr Asp Tyr Ile Lys Ile Lys Val Gly Pro Lys Val Leu
              245   250   255

Gly Pro Phe Cys Gly Glu Lys Ala Pro Glu Pro Ile Ser Thr Gln Ser
          260   265   270

His Ser Val Leu Ile Leu Phe His Ser Asp Asn Ser Gly Glu Asn Arg
        275   280   285

Gly Trp Arg Leu Ser Tyr Arg Ala Ala Gly Asn Glu Cys Pro Glu Leu
    290   295   300

Gln Pro Pro Val His Gly Lys Ile Glu Pro Ser Gln Ala Lys Tyr Phe
305   310   315   320

Phe Lys Asp Gln Val Leu Val Ser Cys Asp Thr Gly Tyr Lys Val Leu
              325   330   335

Lys Asp Asn Val Glu Met Asp Thr Phe Gln Ile Glu Cys Leu Lys Asp
              340   345   350

Gly Thr Trp Ser Asn Lys Ile Pro Thr Cys Lys Ile Val Asp Cys Arg
        355   360   365

Ala Pro Gly Glu Leu Glu His Gly Leu Ile Thr Phe Ser Thr Arg Asn
    370   375   380

Asn Leu Thr Thr Tyr Lys Ser Glu Ile Lys Tyr Ser Cys Gln Glu Pro
385   390   395   400

Tyr Tyr Lys Met Leu Asn Asn Asn Thr Gly Ile Tyr Thr Cys Ser Ala
          405   410   415

Gln Gly Val Trp Met Asn Lys Val Leu Gly Arg Ser Leu Pro Thr Cys
          420   425   430

Leu Pro Val Cys Gly Leu Pro Lys Phe Ser Arg Lys Leu Met Ala Arg
        435   440   445

Ile Phe Asn Gly Arg Pro Ala Gln Lys Gly Thr Thr Pro Trp Ile Ala
    450   455   460

Met Leu Ser His Leu Asn Gly Gln Pro Phe Cys Gly Gly Ser Leu Leu
465   470   475   480

Page 17

Gly Ser Ser Trp Ile Val Thr Ala Ala His Cys Leu His Gln Ser Leu
                485   490   495

Asp Pro Lys Asp Pro Thr Leu Arg Asp Ser Asp Leu Leu Ser Pro Ser
            500   505   510

Asp Phe Lys Ile Ile Leu Gly Lys His Trp Arg Leu Arg Ser Asp Glu
            515   520   525

Asn Glu Gln His Leu Gly Val Lys His Thr Thr Leu His Pro Lys Tyr
    530   535   540

Asp Pro Asn Thr Phe Glu Asn Asp Val Ala Leu Val Glu Leu Leu Glu
545   550   555   560

Ser Pro Val Leu Asn Ala Phe Val Met Pro Ile Cys Leu Pro Glu Gly
                565   570   575

Pro Gln Gln Glu Gly Ala Met Val Ile Val Ser Gly Trp Gly Lys Gln
            580   585   590

Phe Leu Gln Arg Phe Pro Glu Thr Leu Met Glu Ile Glu Ile Pro Ile
    595   600   605

Val Asp His Ser Thr Cys Gln Lys Ala Tyr Ala Pro Leu Lys Lys Lys
    610   615   620

Val Thr Arg Asp Met Ile Cys Ala Gly Glu Lys Glu Gly Gly Lys Asp
625   630   635   640

Ala Cys Ser Gly Asp Ser Gly Gly Pro Met Val Thr Leu Asn Arg Glu
            645   650   655

Arg Gly Gln Trp Tyr Leu Val Gly Thr Val Ser Trp Gly Asp Asp Cys
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Gly Lys Lys Asp Arg Tyr Gly Val Tyr Ser Tyr Ile His His Asn Lys
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Asp Trp Ile Gln Arg Val Thr Gly Val Arg Asn
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<213>   homo sapiens

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1   5   10   15

Ala Ser Ala His Thr Val Glu Leu Asn Asn Met Phe Gly Gln Ile Gln
            20   25   30

Ser Pro Gly Tyr Pro Asp Ser Tyr Pro Ser Asp Ser Glu Val Thr Trp
        35   40   45

Asn Ile Thr Val Pro Asp Gly Phe Arg Ile Lys Leu Tyr Phe Met His
    50   55   60

Phe Asn Leu Glu Ser Ser Tyr Leu Cys Glu Tyr Asp Tyr Val Lys Val
65   70   75   80

Glu Thr Glu Asp Gln Val Leu Ala Thr Phe Cys Gly Arg Glu Thr Thr
            85   90   95

Asp Thr Glu Gln Thr Pro Gly Gln Glu Val Val Leu Ser Pro Gly Ser
            100   105   110

Phe Met Ser Ile Thr Phe Arg Ser Asp Phe Ser Asn Glu Glu Arg Phe
        115   120   125

Thr Gly Phe Asp Ala His Tyr Met Ala Val Asp Val Asp Glu Cys Lys
    130   135   140

Glu Arg Glu Asp Glu Glu Leu Ser Cys Asp His Tyr Cys His Asn Tyr
145   150   155   160

Ile Gly Gly Tyr Tyr Cys Ser Cys Arg Phe Gly Tyr Ile Leu His Thr
            165   170   175

Asp Asn Arg Thr Cys Arg Val Glu Cys Ser Asp Asn Leu Phe Thr Gln
            180   185   190

Arg Thr Gly Val Ile Thr Ser Pro Asp Phe Pro Asn Pro Tyr Pro Lys
        195   200   205

Ser Ser Glu Cys Leu Tyr Thr Ile Glu Leu Glu Glu Gly Phe Met Val
210   215   220

Asn Leu Gln Phe Glu Asp Ile Phe Asp Ile Glu Asp His Pro Glu Val
225   230   235   240

Pro Cys Pro Tyr Asp Tyr Ile Lys Ile Lys Val Gly Pro Lys Val Leu
            245   250   255

Gly Pro Phe Cys Gly Glu Lys Ala Pro Glu Pro Ile Ser Thr Gln Ser
            260   265   270

His Ser Val Leu Ile Leu Phe His Ser Asp Asn Ser Gly Glu Asn Arg
        275   280   285

Gly Trp Arg Leu Ser Tyr Arg Ala Ala Gly Asn Glu Cys Pro Glu Leu
    290   295   300

Gln Pro Pro Val His Gly Lys Ile Glu Pro Ser Gln Ala Lys Tyr Phe
305   310   315   320

Phe Lys Asp Gln Val Leu Val Ser Cys Asp Thr Gly Tyr Lys Val Leu
          325   330   335

Lys Asp Asn Val Glu Met Asp Thr Phe Gln Ile Glu Cys Leu Lys Asp
          340   345   350

Gly Thr Trp Ser Asn Lys Ile Pro Thr Cys Lys Lys Asn Glu Ile Asp
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Leu Ala Phe Pro Glu Lys Tyr Gly Asn His Gln Asp Arg Ser Trp Thr
        35                  40                  45


Leu Thr Ala Pro Pro Gly Phe Arg Leu Arg Leu Tyr Phe Thr His Phe
    50                  55                  60


Asn Leu Glu Leu Ser Tyr Arg Cys Glu Tyr Asp Phe Val Lys Leu Thr
65                  70                  75                  80


Ser Gly Thr Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser Thr Asp
                85                  90                  95


Thr Glu Arg Ala Pro Gly Asn Asp Thr Phe Tyr Ser Leu Gly Pro Ser
            100                 105                 110
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Leu Lys Val Thr Phe His Ser Asp Tyr Ser Asn Glu Lys Pro Phe Thr
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Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Val Asp Glu Cys Arg Thr
    130   135   140

Ser Leu Gly Asp Ser Val Pro Cys Asp His Tyr Cys His Asn Tyr Leu
145   150   155   160

Gly Gly Tyr Tyr Cys Ser Cys Arg Val Gly Tyr Ile Leu His Gln Asn
            165   170   175

Lys His Thr Cys Ser Ala Leu Cys Ser Gly Gln Val Phe Thr Gly Arg
            180   185   190

Ser Gly Phe Leu Ser Ser Pro Glu Tyr Pro Gln Pro Tyr Pro Lys Leu
        195   200   205

Ser Ser Cys Ala Tyr Asn Ile Arg Leu Glu Glu Gly Phe Ser Ile Thr
    210   215   220

Leu Asp Phe Val Glu Ser Phe Asp Val Glu Met His Pro Glu Ala Gln
225   230   235   240

Cys Pro Tyr Asp Ser Leu Lys Ile Gln Thr Asp Lys Arg Glu Tyr Gly
            245   250   255

Pro Phe Cys Gly Lys Thr Leu Pro Pro Arg Ile Glu Thr Asp Ser Asn
            260   265   270

Lys Val Thr Ile Thr Phe Thr Thr Asp Glu Ser Gly Asn His Thr Gly
        275   280   285

Trp Lys Ile His Tyr Thr Ser Thr Ala Gln Pro Cys Pro Asp Pro Thr
    290   295   300

Ala Pro Pro Asn Gly His Ile Ser Pro Val Gln Ala Thr Tyr Val Leu
305   310   315   320

Lys Asp Ser Phe Ser Val Phe Cys Lys Thr Gly Phe Glu Leu Leu Gln
            325   330   335

Gly Ser Val Pro Leu Lys Ser Phe Thr Ala Val Cys Gln Lys Asp Gly
            340   345   350

Ser Trp Asp Arg Pro Ile Pro Glu Cys Ser Ile Ile Asp Cys Gly Pro
        355   360   365

Pro Asp Asp Leu Pro Asn Gly His Val Asp Tyr Ile Thr Gly Pro Glu
370   375   380

Val	Thr	Thr	Tyr	Lys	Ala	Val	Ile	Gln	Tyr	Ser	Cys	Glu	Glu	Thr	Phe
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Trp	Thr	Ser	Ser	Lys	Gly	Glu	Lys	Ser	Leu	Pro	Val	Cys	Lys	Pro	Val
			420					425					430		

Cys	Gly	Leu	Ser	Thr	His	Thr	Ser	Gly	Gly	Arg	Ile	Ile	Gly	Gly	Gln
		435					440					445			

Pro	Ala	Lys	Pro	Gly	Asp	Phe	Pro	Trp	Gln	Val	Leu	Leu	Leu	Gly	Glu
	450					455					460				

Thr	Thr	Ala	Ala	Gly	Ala	Leu	Ile	His	Asp	Asp	Trp	Val	Leu	Thr	Ala
465					470				475						480

Ala	His	Ala	Val	Tyr	Gly	Lys	Thr	Glu	Ala	Met	Ser	Ser	Leu	Asp	Ile
				485				490					495		

Arg	Met	Gly	Ile	Leu	Lys	Arg	Leu	Ser	Leu	Ile	Tyr	Thr	Gln	Ala	Trp
			500					505					510		

Pro	Glu	Ala	Val	Phe	Ile	His	Glu	Gly	Tyr	Thr	His	Gly	Ala	Gly	Phe
		515					520					525			

Asp	Asn	Asp	Ile	Ala	Leu	Ile	Lys	Leu	Lys	Asn	Lys	Val	Thr	Ile	Asn
	530					535					540				

Arg	Asn	Ile	Met	Pro	Ile	Cys	Leu	Pro	Arg	Lys	Glu	Ala	Ala	Ser	Leu
545				550					555						560

Met	Lys	Thr	Asp	Phe	Val	Gly	Thr	Val	Ala	Gly	Trp	Gly	Leu	Thr	Gln
				565				570					575		

Lys	Gly	Phe	Leu	Ala	Arg	Asn	Leu	Met	Phe	Val	Asp	Ile	Pro	Ile	Val
			580					585					590		

Asp	His	Gln	Lys	Cys	Ala	Thr	Ala	Tyr	Thr	Lys	Gln	Pro	Tyr	Pro	Gly
		595					600					605			

Ala	Lys	Val	Thr	Val	Asn	Met	Leu	Cys	Ala	Gly	Leu	Asp	Arg	Gly	Gly
	610					615					620				

Lys	Asp	Ser	Cys	Arg	Gly	Asp	Ser	Gly	Gly	Ala	Leu	Val	Phe	Leu	Asp
625					630					635					640

Asn	Glu	Thr	Gln	Arg	Trp	Phe	Val	Gly	Gly	Ile	Val	Ser	Trp	Gly	Ser
				645				650					655		

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Ile Asn Cys Gly Gly Ser Glu Gln Tyr Gly Val Tyr Thr Lys Val Thr
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Asn Tyr Ile Pro Trp Ile Glu Asn Ile Ile Asn Asn Phe
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gtccttacaa tgaccaacat ggaccctgtg gacacagcca cgtattactg tgcacggata     300

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            20                  25                  30

Lys Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
            35                  40                  45

Trp Leu Ala His Ile Phe Ser Ser Asp Glu Lys Ser Tyr Arg Thr Ser
    50                  55                  60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65                  70                  75                  80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
                85                  90                  95

Cys Ala Arg Ile Arg Arg Gly Gly Ile Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110
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<210>   16
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Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Thr
            20   25   30

Ser Ala Ala Trp Asn Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu
        35   40   45

Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
    50   55   60

Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
65   70   75   80

Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
            85   90   95

Tyr Tyr Cys Ala Arg Asp Pro Phe Gly Val Pro Phe Asp Ile Trp Gly
            100   105   110

Gln Gly Thr Met Val Thr Val Ser Ser
            115   120

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<211>   106
<212>   PRT
<213>   artificial sequence

<220>
<223>   Synthetic

<400>   17

Gln Pro Val Leu Thr Gln Pro Pro Ser Leu Ser Val Ser Pro Gly Gln
1   5   10   15

Thr Ala Ser Ile Thr Cys Ser Gly Glu Lys Leu Gly Asp Lys Tyr Ala
            20   25   30

Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Val Leu Val Met Tyr
        35   40   45

Gln Asp Lys Gln Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
        50   55   60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Met
65   70   75   80

Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Ser Ser Thr Ala Val
                85   90   95

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100   105

<210> 18
<211> 324
<212> DNA
<213> artificial sequence

<220>
<223> Synthetic

<400> 18
tcctatgagc tgatacagcc accctcggtg tcagtggccc caggacagac ggccaccatt   60

acctgtgcgg gagacaacct tgggaagaaa cgtgtgcact ggtaccagca gaggccaggc   120

caggcccctg tgttggtcat ctatgatgat agcgaccggc cctcagggat ccctgaccga   180

ttctctgcct ccaactctgg gaacacggcc accctgacca tcactagggg cgaagccggg   240

gatgaggccg actattattg tcaggtgtgg gacattgcta ctgatcatgt ggtcttcggc   300

ggagggacca agctcaccgt ccta   324

<210> 19
<211> 120
<212> PRT
<213> artificial sequence

<220>
<223> Synthetic

<400> 19

Ser Tyr Glu Leu Ile Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
1   5   10   15

Thr Ala Thr Ile Thr Cys Ala Gly Asp Asn Leu Gly Lys Lys Arg Val
                20   25   30

His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
            35   40   45

Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Ala Ser
        50   55   60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Thr Arg Gly Glu Ala Gly
65   70   75   80

Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ile Ala Thr Asp His
                    85   90   95

Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ala Ala Ala Gly
            100   105   110

Ser Glu Gln Lys Leu Ile Ser Glu
        115   120

<210>   20
<211>   262
<212>   PRT
<213>   artificial sequence

<220>
<223>   Synthetic

<400>   20

Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1   5   10   15

Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Thr
            20   25   30

Ser Ala Ala Trp Asn Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu
        35   40   45

Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
    50   55   60

Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
65   70   75   80

Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
            85   90   95

Tyr Tyr Cys Ala Arg Asp Pro Phe Gly Val Pro Phe Asp Ile Trp Gly
            100   105   110

Gln Gly Thr Met Val Thr Val Ser Ser Lys Leu Ser Gly Ser Ala Ser
            115   120   125

Ala Pro Lys Leu Glu Glu Gly Glu Phe Ser Glu Ala Arg Val Ser Tyr
        130   135   140

Glu Leu Ile Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln Thr Ala
145   150   155   160

Thr Ile Thr Cys Ala Gly Asp Asn Leu Gly Lys Lys Arg Val His Trp
                165   170   175

Tyr Gln Gln Arg Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Asp Asp

```
                 180                         185                        190
```

Ser Asp Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Ala Ser Asn Ser
       195   200   205

Gly Asn Thr Ala Thr Leu Thr Ile Thr Arg Gly Glu Ala Gly Asp Glu
    210   215   220

Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ile Ala Thr Asp His Val Val
225   230   235   240

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ala Ala Ala Gly Ser Glu
            245   250   255

Gln Lys Leu Ile Ser Glu
        260

```
<210>  21
<211>  245
<212>  PRT
<213>  artificial sequence

<220>
<223>  Synthetic

<400>  21
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Gln Val Thr Leu Lys Glu Ser Gly Pro Val Leu Val Lys Pro Thr Glu
1   5   10   15

Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Arg Gly
       20   25   30

Lys Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
       35   40   45

Trp Leu Ala His Ile Phe Ser Ser Asp Glu Lys Ser Tyr Arg Thr Ser
    50   55   60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65   70   75   80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
            85   90   95

Cys Ala Arg Ile Arg Arg Gly Gly Ile Asp Tyr Trp Gly Gln Gly Thr
            100   105   110

Leu Val Thr Val Ser Ser Lys Leu Ser Gly Ser Ala Ser Ala Pro Lys
       115   120   125

Leu Glu Glu Gly Glu Phe Ser Glu Ala Arg Val Gln Pro Val Leu Thr
    130   135   140

```
Gln Pro Pro Ser Leu Ser Val Ser Pro Gly Gln Thr Ala Ser Ile Thr
145               150               155               160

Cys Ser Gly Glu Lys Leu Gly Asp Lys Tyr Ala Tyr Trp Tyr Gln Gln
                165               170               175

Lys Pro Gly Gln Ser Pro Val Leu Val Met Tyr Gln Asp Lys Gln Arg
                180               185               190

Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser Asn Ser Gly Asn Thr
            195               200               205

Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Met Asp Glu Ala Asp Tyr
    210               215               220

Tyr Cys Gln Ala Trp Asp Ser Ser Thr Ala Val Phe Gly Gly Gly Thr
225               230               235               240

Lys Leu Thr Val Leu
                245
```

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<210>  22
<211>  750
<212>  DNA
<213>  artificial sequence

<220>
<223>  Synthetic

<400>  22
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acctgtgcca tctccgggga cagtgtctct agcaccagtg ctgcttggaa ctggatcagg       120

cagtccccat cgagaggcct tgagtggctg ggaaggacat actacaggtc caagtggtat       180

aatgattatg cagtatctgt gaaaagtcga ataaccatca cccagacaca tccaagaac       240

cagttctccc tgcagctgaa ctctgtgact cccgaggaca cggctgtgta ttactgtgca       300

agagatcctt tcggggtacc ttttgatatc tggggccaag gacaatggt  caccgtctct       360

tcaaagcttt cagggagtgc atccgcccca aaacttgaag aaggtgaatt ttcagaagca       420

cgcgtatcct atgagctgat acagccaccc tcggtgtcag tggccccagg acagacggcc       480

accattacct gtgcgggaga caaccttggg aagaaacgtg tgcactggta ccagcagagg       540

ccaggccagg cccctgtgtt ggtcatctat gatgatagcg accggccctc agggatcct       600

gaccgattct ctgcctccaa ctctgggaac acggccaccc tgaccatcac taggggcgaa       660

gccgggggatg aggccgacta ttattgtcag gtgtgggaca ttgctactga tcatgtggtc       720

ttcggcggag ggaccaagct caccgtccta                                       750
```

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<210>  23
<211>  735
<212>  DNA
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<210> artificial sequence

<220>
<223> Synthetic

<220>
<221> misc_feature
<222> (663)..(663)
<223> n is a, c, g, or t

<400> 23

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caggtcacct tgaaggagtc tggtcctgtg ctggtgaaac ccacagagac cctcacgctg       60

acctgcaccg tctctgggtt ctcactcagc aggggtaaaa tgggtgtgag ctggatccgt      120

cagcccccag ggaaggccct ggagtggctt gcacacattt tttcgagtga cgaaaaatcc      180

tacaggacat cgctgaagag caggctcacc atctccaagg acacctccaa aaaccaggtg      240

gtccttacaa tgaccaacat ggaccctgtg gacacagcca cgtattactg tgcacggata      300

cgacgtggag gaattgacta ctggggccag ggaaccctgg tcactgtctc ctcaaagctt      360

tcagggagtg catccgcccc aaaacttgaa gaaggtgaat tttcagaagc acgcgtacag      420

ccagtgctga ctcagccccc ctcactgtcc gtgtccccag acagacagc cagcatcacc      480

tgctctggag agaaattggg ggataaatat gcttactggt atcagcagaa gccaggccag      540

tcccctgtgt tggtcatgta tcaagataaa cagcggccct cagggatccc tgagcgattc      600

tctggctcca actctgggaa cacagccact ctgaccatca gcgggaccca ggctatggat      660

gangctgact attactgtca ggcgtgggac agcagcactg cggtattcgg cggagggacc      720

aagctgaccg tccta                                                       735
```

<210> 24
<211> 125
<212> PRT
<213> artificial sequence

<220>
<223> Synthetic

<400> 24

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Ala Val Thr Leu Asp Glu Ser Gly Gly Gly Leu Gln Thr Pro Gly Gly
1               5                   10                  15


Ala Leu Ser Leu Val Cys Lys Ala Ser Gly Phe Thr Phe Ser Ser Asn
            20                  25                  30


Ala Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ala Gly Ile Asp Asp Asp Gly Ser Gly Thr Arg Tyr Ala Pro Ala Val
    50                  55                  60


Lys Gly Arg Ala Thr Ile Ser Arg Asp Asn Gly Gln Ser Thr Leu Arg
65                  70                  75                  80
```

Leu Gln Leu Asn Asn Leu Arg Ala Glu Asp Thr Gly Thr Tyr Tyr Cys
                85   90   95

Thr Lys Cys Ala Tyr Ser Ser Gly Cys Asp Tyr Glu Gly Gly Tyr Ile
            100   105   110

Asp Ala Trp Gly His Gly Thr Glu Val Ile Val Ser Ser
            115   120   125

<210>   25
<211>   118
<212>   PRT
<213>   artificial sequence

<220>
<223>   Synthetic

<400>   25

Ala Val Thr Leu Asp Glu Ser Gly Gly Gly Leu Gln Thr Pro Gly Gly
1   5   10   15

Gly Leu Ser Leu Val Cys Lys Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20   25   30

Ala Met Gly Trp Met Arg Gln Ala Pro Gly Lys Gly Leu Glu Tyr Val
        35   40   45

Ala Gly Ile Arg Ser Asp Gly Ser Phe Thr Leu Tyr Ala Thr Ala Val
        50   55   60

Lys Gly Arg Ala Thr Ile Ser Arg Asp Asn Gly Gln Ser Thr Val Arg
65   70   75   80

Leu Gln Leu Asn Asn Leu Arg Ala Glu Asp Thr Ala Thr Tyr Phe Cys
                85   90   95

Thr Arg Ser Gly Asn Val Gly Asp Ile Asp Ala Trp Gly His Gly Thr
            100   105   110

Glu Val Ile Val Ser Ser
            115

<210>   26
<211>   128
<212>   PRT
<213>   artificial sequence

<220>
<223>   Synthetic

<400>   26

Ala Val Thr Leu Asp Glu Ser Gly Gly Gly Leu Gln Thr Pro Gly Gly
1   5   10   15

Gly Leu Ser Leu Val Cys Lys Ala Ser Gly Phe Asp Phe Ser Ser Tyr
20   25   30

Gln Met Asn Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Phe Val
35   40   45

Ala Ala Ile Asn Arg Phe Gly Asn Ser Thr Gly His Gly Ala Ala Val
50   55   60

Lys Gly Arg Val Thr Ile Ser Arg Asp Asp Gly Gln Ser Thr Val Arg
65   70   75   80

Leu Gln Leu Ser Asn Leu Arg Ala Glu Asp Thr Ala Thr Tyr Tyr Cys
85   90   95

Ala Lys Gly Val Tyr Gly Tyr Cys Gly Ser Tyr Ser Cys Cys Gly Val
100   105   110

Asp Thr Ile Asp Ala Trp Gly His Gly Thr Glu Val Ile Val Ser Ser
115   120   125

<210>   27
<211>   107
<212>   PRT
<213>   artificial sequence

<220>
<223>   Synthetic

<400>   27

Ala Leu Thr Gln Pro Ala Ser Val Ser Ala Asn Leu Gly Gly Thr Val
1   5   10   15

Lys Ile Thr Cys Ser Gly Gly Gly Ser Tyr Ala Gly Ser Tyr Tyr Tyr
20   25   30

Gly Trp Tyr Gln Gln Lys Ser Pro Gly Ser Ala Pro Val Thr Val Ile
35   40   45

Tyr Asp Asn Asp Lys Arg Pro Ser Asp Ile Pro Ser Arg Phe Ser Gly
50   55   60

Ser Leu Ser Gly Ser Thr Asn Thr Leu Thr Ile Thr Gly Val Arg Ala
65   70   75   80

Asp Asp Glu Ala Val Tyr Phe Cys Gly Ser Ala Asp Asn Ser Gly Ala
85   90   95

Ala Phe Gly Ala Gly Thr Thr Leu Thr Val Leu
100   105

<210>   28

<211> 108
<212> PRT
<213> artificial sequence

<220>
<223> Synthetic

<400> 28

```
Ala Leu Thr Gln Pro Ala Ser Val Ser Ala Asn Pro Gly Glu Thr Val
1               5                   10                  15

Lys Ile Thr Cys Ser Gly Gly Tyr Ser Gly Tyr Ala Gly Ser Tyr Tyr
                20                  25                  30

Tyr Gly Trp Tyr Gln Gln Lys Ala Pro Gly Ser Ala Pro Val Thr Leu
            35                  40                  45

Ile Tyr Tyr Asn Asn Lys Arg Pro Ser Asp Ile Pro Ser Arg Phe Ser
    50                  55                  60

Gly Ser Leu Ser Gly Ser Thr Asn Thr Leu Thr Ile Thr Gly Val Arg
65                  70                  75                  80

Ala Asp Asp Glu Ala Val Tyr Phe Cys Gly Ser Ala Asp Asn Ser Gly
                85                  90                  95

Ala Ala Phe Gly Ala Gly Thr Thr Leu Thr Val Leu
                100                 105
```

<210> 29
<211> 107
<212> PRT
<213> artificial sequence

<220>
<223> Synthetic

<400> 29

```
Ala Leu Thr Gln Pro Ala Ser Val Ser Ala Asn Pro Gly Glu Thr Val
1               5                   10                  15

Lys Ile Thr Cys Ser Gly Gly Gly Ser Tyr Ala Gly Ser Tyr Tyr Tyr
                20                  25                  30

Gly Trp Tyr Gln Gln Lys Ala Pro Gly Ser Ala Pro Val Thr Leu Ile
            35                  40                  45

Tyr Tyr Asn Asn Lys Arg Pro Ser Asp Ile Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Leu Ser Gly Ser Thr Asn Thr Leu Thr Ile Thr Gly Val Arg Ala
65                  70                  75                  80

Asp Asp Glu Ala Val Tyr Phe Cys Gly Ser Ala Asp Asn Ser Gly Ala
```

                             85   90   95

Ala Phe Gly Ala Gly Thr Thr Leu Thr Val Leu
            100   105

<210>   30
<211>   126
<212>   PRT
<213>   artificial sequence

<220>
<223>   Synthetic

<400>   30

Ala Val Thr Leu Asp Glu Ser Gly Gly Gly Leu Gln Thr Pro Gly Gly
1   5   10   15

Ala Leu Ser Leu Val Cys Lys Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20   25   30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ala Gly Ile Tyr Lys Ser Gly Ala Gly Thr Asn Tyr Ala Pro Ala Val
    50   55   60

Lys Gly Arg Ala Thr Ile Ser Arg Asp Asn Gly Gln Ser Thr Val Arg
65   70   75   80

Leu Gln Leu Asn Asn Leu Arg Ala Glu Asp Thr Gly Thr Tyr Tyr Cys
                85   90   95

Ala Lys Thr Thr Gly Ser Gly Cys Ser Ser Gly Tyr Arg Ala Glu Tyr
            100   105   110

Ile Asp Ala Trp Gly His Gly Thr Glu Val Ile Val Ser Ser
            115   120   125

<210>   31
<211>   107
<212>   PRT
<213>   artificial sequence

<220>
<223>   Synthetic

<400>   31

Ala Leu Thr Gln Pro Ala Ser Val Ser Ala Asn Pro Gly Glu Thr Val
1   5   10   15

Lys Ile Thr Cys Ser Gly Gly Gly Ser Tyr Ala Gly Ser Tyr Tyr Tyr
            20   25   30

Gly Trp Tyr Gln Gln Lys Ala Pro Gly Ser Ala Pro Val Thr Leu Ile

Page 34

Tyr Tyr Asn Asn Lys Arg Pro Ser Asp Ile Pro Ser Arg Phe Ser Gly
    50   55   60

Ser Leu Ser Gly Ser Thr Asn Thr Leu Thr Ile Thr Gly Val Arg Ala
65   70   75   80

Asp Asp Glu Ala Val Tyr Phe Cys Gly Ser Ala Asp Asn Ser Gly Ala
                85   90   95

Ala Phe Gly Ala Gly Thr Thr Leu Thr Val Leu
            100   105

<210> 32
<211> 126
<212> PRT
<213> artificial sequence

<220>
<223> Synthetic

<400> 32

Ala Val Thr Leu Asp Glu Ser Gly Gly Gly Leu Gln Thr Pro Gly Gly
1   5   10   15

Ala Leu Ser Leu Val Cys Lys Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20   25   30

Asp Met Val Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Phe Val
            35   40   45

Ala Gly Ile Ser Arg Asn Asp Gly Arg Tyr Thr Glu Tyr Gly Ser Ala
    50   55   60

Val Lys Gly Arg Ala Thr Ile Ser Arg Asp Asn Gly Gln Ser Thr Val
65   70   75   80

Arg Leu Gln Leu Asn Asn Leu Arg Ala Glu Asp Thr Ala Thr Tyr Tyr
            85   90   95

Cys Ala Arg Asp Ala Gly Gly Ser Ala Tyr Trp Phe Asp Ala Gly Gln
            100   105   110

Ile Asp Ala Trp Gly His Gly Thr Glu Val Ile Val Ser Ser
            115   120   125

<210> 33
<211> 107
<212> PRT
<213> artificial sequence

<220>
<223> Synthetic

<400> 33

Ala	Leu	Thr	Gln	Pro	Ala	Ser	Val	Ser	Ala	Asn	Pro	Gly	Glu	Thr	Val
1				5					10					15	

Lys	Ile	Thr	Cys	Ser	Gly	Gly	Gly	Ser	Tyr	Ala	Gly	Ser	Tyr	Tyr	Tyr
			20					25					30		

Gly	Trp	Tyr	Gln	Gln	Lys	Ala	Pro	Gly	Ser	Ala	Pro	Val	Thr	Leu	Ile
		35					40					45			

Tyr	Tyr	Asn	Asn	Lys	Arg	Pro	Ser	Asp	Ile	Pro	Ser	Arg	Phe	Ser	Gly
	50				55					60					

Ser	Leu	Ser	Gly	Ser	Thr	Asn	Thr	Leu	Thr	Ile	Thr	Gly	Val	Arg	Ala
65					70					75					80

Asp	Asp	Glu	Ala	Val	Tyr	Phe	Cys	Gly	Ser	Ala	Asp	Asn	Ser	Gly	Ala
				85					90					95	

Ala	Phe	Gly	Ala	Gly	Thr	Thr	Leu	Thr	Val	Leu
			100					105		

<210> 34
<211> 36
<212> PRT
<213> artificial sequence

<220>
<223> Synthetic

<400> 34

Leu	Glu	Val	Thr	Cys	Glu	Pro	Gly	Thr	Thr	Phe	Lys	Asp	Lys	Cys	Asn
1				5					10					15	

Thr	Cys	Arg	Cys	Gly	Ser	Asp	Gly	Lys	Ser	Ala	Phe	Cys	Thr	Arg	Lys
			20					25					30		

Leu	Cys	Tyr	Gln
			35

<210> 35
<211> 36
<212> PRT
<213> artificial sequence

<220>
<223> Synthetic

<400> 35

Leu	Glu	Val	Thr	Cys	Glu	Pro	Gly	Thr	Thr	Phe	Lys	Asp	Lys	Cys	Asn
1				5					10					15	

Thr	Cys	Arg	Cys	Gly	Ser	Asp	Gly	Lys	Ser	Ala	Val	Cys	Thr	Lys	Leu

20   25   30

Trp Cys Asn Gln
         35

<210>   36
<211>   227
<212>   PRT
<213>   homo sapiens

<400>   36

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1   5   10   15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20   25   30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            35   40   45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        50   55   60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65   70   75   80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85   90   95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100   105   110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
            115   120   125

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
    130   135   140

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145   150   155   160

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165   170   175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180   185   190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            195   200   205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210   215   220

Pro Gly Lys
225

<210> 37
<211> 12
<212> PRT
<213> artificial sequence

<220>
<223> Synthetic

<400> 37

Gly Thr Gly Gly Gly Ser Gly Ser Ser Ser Arg Ser
1   5   10

<210> 38
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> Synthetic

<400> 38

Gly Thr Gly Gly Gly Ser Gly Ser Ser Ser
1   5   10

<210> 39
<211> 888
<212> DNA
<213> artificial sequence

<220>
<223> Synthetic

<400> 39
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ctcgaggtga catgtgaacc cggtacgacg tttaaggata agtgcaacac atgtaggtgc   120

ggtagcgacg gcaaatcagc gttctgtacc cggaaattgt gctaccaggg aactggagga   180

gggtcggggt cctcgtcaag atctgacaaa actcacacat gcccaccgtg cccagcacct   240

gaactcctgg ggggaccgtc agtcttcctc ttccccccaa aacccaagga caccctcatg   300

atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag   360

gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg   420

gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac   480

tggctgaatg gcaaggagta caagtgcaag gtctccaaca aagccctccc agcccccatc   540

gagaaaacca tctccaaagc caaagggcag ccccgagaac acaggtgta caccctgccc   600

ccatcccggg aggagatgac caagaaccag gtcagcctga cctgcctggt caaaggcttc   660

tatcccagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag   720

accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctacagcaa gctcaccgtg   780

gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca cgaggctctg   840

cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtaaatga   888

<210> 40
<211> 275
<212> PRT
<213> artificial sequence

<220>
<223> Synthetic

<400> 40

Leu Glu Val Thr Cys Glu Pro Gly Thr Thr Phe Lys Asp Lys Cys Asn
1   5   10   15

Thr Cys Arg Cys Gly Ser Asp Gly Lys Ser Ala Phe Cys Thr Arg Lys
                20   25   30

Leu Cys Tyr Gln Gly Thr Gly Gly Gly Ser Gly Ser Ser Ser Arg Ser
            35   40   45

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
        50   55   60

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
65   70   75   80

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
                85   90   95

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
                100   105   110

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
            115   120   125

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
        130   135   140

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
145   150   155   160

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
                165   170   175

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
            180   185   190

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
            195   200   205

```
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
    210             215             220

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
225             230             235             240

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            245             250             255

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
        260             265             270

Pro Gly Lys
        275
```

```
<210>  41
<211>  888
<212>  DNA
<213>  artificial sequence

<220>
<223>  Synthetic

<400>  41
atgtacagga tgcaactcct gtcttgcatt gcactaagtc ttgcacttgt cacgaattcg      60

ttggaagtga cgtgtgagcc cggaacgaca ttcaaagaca agtgcaatac ttgtcggtgc     120

ggttcagatg ggaaatcggc ggtctgcaca aagctctggt gtaaccaggg caccggtgga     180

gggtcgggat ccagctcaag atctgacaaa actcacacat gcccaccgtg cccagcacct     240

gaactcctgg ggggaccgtc agtcttcctc ttccccccaa aacccaagga caccctcatg     300

atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag     360

gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg     420

gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac     480

tggctgaatg gcaaggagta caagtgcaag gtctccaaca aagccctccc agcccccatc     540

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gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca cgaggctctg     840

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<213>  artificial sequence

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Thr Cys Arg Cys Gly Ser Asp Gly Lys Ser Ala Val Cys Thr Lys Leu
            20   25   30

Trp Cys Asn Gln Gly Thr Gly Gly Gly Ser Gly Ser Ser Ser Arg Ser
            35   40   45

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
    50   55   60

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
65   70   75   80

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            85   90   95

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
            100   105   110

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
    115   120   125

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
    130   135   140

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
145   150   155   160

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
            165   170   175

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
            180   185   190

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
        195   200   205

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
    210   215   220

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
225   230   235   240

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            245   250   255

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    260   265   270

Pro Gly Lys
            275