ANTI-C5 ANTIBODY COMBINATIONS AND USES THEREOF

This application claims the benefit of U.S. Provisional Patent Application No. 62/598,023 filed December 13, 2017, which is herein incorporated by reference in its entirety.

FIELD

[001] The present invention is related to combinations including antibodies and antigen-binding fragments of antibodies that specifically bind to complement factor C5, and methods of use thereof.

BACKGROUND

[002] The complement system is a group of plasma proteins that when activated lead to target cell lysis and facilitate phagocytosis through opsonization. Complement is activated through a series of proteolytic steps by three major pathways: the classical pathway, which is typically activated by immune-complexes, the alternative pathway that can be induced by unprotected cell surfaces, and the mannose binding lectin pathway. All three pathways of complement cascade converge on proteolytic cleavage of complement component 5 (C5) protein. Cleavage of complement component 5 (C5) results in the production of fragments C5a and C5b, a process that is critical during the activation of the complement cascade. C5a can generate pleiotropic physiological responses through binding to its receptors (Monk *et al.* 2007, Br. J. Pharmacol. 152: 429-448). C5a is a potent pro-inflammatory mediator that induces chemotactic migration, enhances cell adhesion, stimulates the oxidative burst, and induces the release of various inflammatory mediators such as histamine or cytokines. C5b mediates the formation of the membrane-attack complex (MAC, or C5b-9) leading to cell lysis in the late phases of the complement dependent cytotoxicity (CDC). Further, in nucleated cells that are resistant to cytolysis by C5b-9, sublytic quantities of C5b-9 can cause cellular activation which results in cell proliferation, generation of proinflammatory mediators and production of extracellular matrix.

[003] Monoclonal antibodies to C5 are known in the art and have been described, for example, in US Patent/Publication Nos. 9206251, 9107861, 9079949, 9051365, 8999340, 8883158, 8241628, 7999081, 7432356, 7361339, 7279158, 6534058, 6355245, 6074642, 20150299305, 20160051673, 20160031975, 20150158936, 20140056888, 20130022615,

20120308559, and in WO2017218515, WO2015198243, WO2015134894, WO2015120130, EP2563813B1, EP2328616B1, and EP2061810B1.

[004] Anti-C5 antibodies with high affinity and biological activity are known; however, an improvement in biological activity may lead to more potent therapies for subjects suffering from C5-associated diseases and disorders.

SUMMARY

[005] Particular combinations of anti-C5 antibodies and antigen-binding fragments exhibiting surprising and unexpected levels of biological activity (*e.g.*, reduction of red blood cell (RBC) lysis) have been identified. Combinations of anti-C5 antibodies and fragments which do not compete with one another for C5-binding lead to a reduction in RBC lysis beyond reduction associated with a single anti-C5 antibody or fragment. Compositions and therapeutic methods relating to such anti-C5 combinations are provided herein.

[006] The present invention provides a combination (*e.g.*, a kit) comprising a first antigen-binding protein (*e.g.*, antibody or antigen-binding fragment thereof) that binds specifically to C5 (*e.g.*, human C5); and one or more further antigen-binding proteins (*e.g.*, polypeptides (*e.g.*, coversin) or antibodies (*e.g.*, eculizumab) or antigen-binding fragments thereof) that (i) specifically bind to C5 at an epitope which is different from that of the antigen-binding protein; and/or (ii) do not compete with the first antigen-binding protein for binding to C5. The first antigen-binding protein and the further antigen-binding protein can be co-formulated into a single pharmaceutical formulation (*e.g.*, with a pharmaceutically acceptable carrier) or formulated into separate formulations (*e.g.*, each with a pharmaceutically acceptable carrier). In an embodiment of the invention, the first antigen-binding protein and/or the one or more further antigen-binding protein thereof are in a pre-filled injection device (*e.g.*, pre-filled syringe or pre-filled autoinjector) or vessel. For example, in an embodiment of the invention, the first antigen-binding protein (*e.g.*, antibody) comprises CDR-H1, CDR-H2 and CDR-H3 of a heavy chain variable region that comprise the amino acid sequence set forth in SEQ ID NO: 19, and CDR-L1, CDR-L2 and CDR-L3 of a light chain variable region that comprise the amino acid sequence set forth in SEQ ID NO: 27. In an embodiment of the invention, the further antigen-binding protein (*e.g.*, antibody or antigen-binding fragment) comprises (i) CDR-H1, CDR-H2 and CDR-H3 of a heavy chain variable region that comprise the amino acid sequence set forth in SEQ ID NO: 3, and CDR-L1, CDR-L2 and CDR-L3 of a light chain variable region that comprise the amino acid

sequence set forth in SEQ ID NO: 11; (ii) CDR-H1, CDR-H2 and CDR-H3 of a heavy chain variable region that comprise the amino acid sequence set forth in SEQ ID NO: 35, CDR-L1, CDR-L2 and CDR-L3 of a light chain variable region that comprise the amino acid sequence set forth in SEQ ID NO: 43; (iii) CDR-H1, CDR-H2 and CDR-H3 of a heavy chain variable region that comprise the amino acid sequence set forth in SEQ ID NO: 51, CDR-L1, CDR-L2 and CDR-L3 of a light chain variable region that comprise the amino acid sequence set forth in SEQ ID NO: 59; (iv) CDR-H1, CDR-H2 and CDR-H3 of a heavy chain variable region that comprise the amino acid sequence set forth in SEQ ID NO: 67, and CDR-L1, CDR-L2 and CDR-L3 of a light chain variable region that comprise the amino acid sequence set forth in SEQ ID NO: 75; (v) CDR-H1, CDR-H2 and CDR-H3 of a heavy chain variable region that comprise the amino acid sequence set forth in SEQ ID NO: 87, and CDR-L1, CDR-L2 and CDR-L3 of a light chain variable region that comprise the amino acid sequence set forth in SEQ ID NO: 95; and/or (vi) CDR-H1, CDR-H2 and CDR-H3 of a heavy chain variable region that comprise the amino acid sequence set forth in SEQ ID NO: 103, and CDR-L1, CDR-L2 and CDR-L3 of a light chain variable region that comprise the amino acid sequence set forth in SEQ ID NO: 95. In an embodiment of the invention, the first antigen-binding protein (*e.g.*, antibody or fragment) comprises a heavy chain variable region that comprises: a CDR-H1 that comprises the amino acid sequence set forth in SEQ ID NO: 21, a CDR-H2 that comprises the amino acid sequence set forth in SEQ ID NO: 23, and a CDR-H3 that comprises the amino acid sequence set forth in SEQ ID NO: 25, and a light chain variable region that comprises a CDR-L1 that comprises the amino acid sequence set forth in SEQ ID NO: 29), a CDR-L2 that comprises the amino acid sequence set forth in SEQ ID NO: 31, and a CDR-L3 that comprises the amino acid sequence set forth in SEQ ID NO: 33. In an embodiment of the invention, the further antigen-binding protein (*e.g.*, antibody or fragment) comprises a heavy chain variable region that comprises (i) a CDR-H1 that comprises the amino acid sequence set forth in SEQ ID NO: 5, a CDR-H2 that comprises the amino acid sequence set forth in SEQ ID NO: 7; and a CDR-H3 that comprises the amino acid sequence set forth in SEQ ID NO: 9; and a light chain variable region that comprises a CDR-L1 that comprises the amino acid sequence set forth in SEQ ID NO: 13, a CDR-L2 that comprises the amino acid sequence set forth in SEQ ID NO: 15, and a CDR-L3 that comprises the amino acid sequence set forth in SEQ ID NO: 17; (ii) a heavy chain variable region that comprises a CDR-H1 that comprises the amino acid sequence set forth in SEQ ID NO: 37, a CDR-H2 that comprises the amino acid sequence

set forth in SEQ ID NO: 39, and a CDR-H3 that comprises the amino acid sequence set forth in SEQ ID NO: 41; and a light chain variable region that comprises a CDR-L1 that comprises the amino acid sequence set forth in SEQ ID NO: 45, a CDR-L2 that comprises the amino acid sequence set forth in SEQ ID NO: 47, and a CDR-L3 that comprises the amino acid sequence set forth in SEQ ID NO: 49; (iii) a heavy chain variable region that comprises a CDR-H1 that comprises the amino acid sequence set forth in SEQ ID NO: 53, a CDR-H2 that comprises the amino acid sequence set forth in SEQ ID NO: 55, a CDR-H3 that comprises the amino acid sequence set forth in SEQ ID NO: 57; and a light chain variable region that comprises a CDR-L1 that comprises the amino acid sequence set forth in SEQ ID NO: 61, a CDR-L2 that comprises the amino acid sequence set forth in SEQ ID NO: 63, and a CDR-L3 that comprises the amino acid sequence set forth in SEQ ID NO: 65; (iv) a heavy chain variable region that comprises a CDR-H1 that comprises the amino acid sequence set forth in SEQ ID NO: 69, a CDR-H2 that comprises the amino acid sequence set forth in SEQ ID NO: 71, and a CDR-H3 that comprises the amino acid sequence set forth in SEQ ID NO: 73; and a light chain variable region that comprises a CDR-L1 that comprises the amino acid sequence set forth in SEQ ID NO: 77, a CDR-L2 that comprises the amino acid sequence set forth in SEQ ID NO: 79, and a CDR-L3 that comprises the amino acid sequence set forth in SEQ ID NO: 81; (v) a CDR-H1 that comprises the amino acid sequence set forth in SEQ ID NO: 89, a CDR-H2 that comprises the amino acid sequence set forth in SEQ ID NO: 91, a CDR-H3 that comprises the amino acid sequence set forth in SEQ ID NO: 93, a CDR-L1 that comprises the amino acid sequence set forth in SEQ ID NO: 97, a CDR-L2 that comprises the amino acid sequence set forth in SEQ ID NO: 99, a CDR-L3 L2 that comprises the amino acid sequence set forth in SEQ ID NO: 101; or (vi) a CDR-H1 that comprises the amino acid sequence set forth in SEQ ID NO: 105, a CDR-H2 that comprises the amino acid sequence set forth in SEQ ID NO: 107, a CDR-H3 that comprises the amino acid sequence set forth in SEQ ID NO: 109; a CDR-L1 that comprises the amino acid sequence set forth in SEQ ID NO: 97, a CDR-L2 that comprises the amino acid sequence set forth in SEQ ID NO: 99, and a CDR-L3 that comprises the amino acid sequence set forth in SEQ ID NO: 101. In an embodiment of the invention, the combination includes an optional further therapeutic agent. For example, the further therapeutic agent is, in an embodiment of the invention, one or more anti-C5 antibodies such as H2M11683N; H2M11686N; H4H12159P; H4H12163P; H4H12164P; H4H12166P2; H4H12166P3; H4H12166P4; H4H12166P5; H4H12166P6; H4H12166P7; H4H12166P8;

H4H12166P9; H4H12166P10; H4H12167P; H4H12168P; H4H12169P; H4H12176P2; H4H12177P2; H4H12183P2; H2M11682N; H2M11684N; H2M11694N; or H2M11695N or an antibody or antigen-binding fragment comprising the V_H and/or V_L; and/or CDR-Hs and/or CDR-Ls thereof (See International Patent Application No. PCT/US2017/037226, filed June 13, 2017); or an antigen-binding fragment of any of the foregoing (which is not a first or second/further antibody or antigen-binding fragment in the combination). In an embodiment of the invention, the further therapeutic agent is an eculizumab or coversin (if not already a component of the combination), iron, antithymocyte globulin, a growth factor, anti-coagulant, a thrombin inhibitor, an anti-inflammatory drug, an antihypertensive, an immunosuppressive agent, a fibrinolytic agent, a lipid-lowering agent, an inhibitor of hydroxymethylglutaryl CoA reductase, an anti-CD20 agent, an anti-TNFα agent, an anti-seizure agent, a C3 inhibitor, an anti-thrombotic agent, warfarin, aspirin, heparin, phenindione, fondaparinux, idraparinux, argatroban, lepirudin, bivalirudin, or dabigatran, corticosteroids, and non-steroidal anti-inflammatory drugs, vincristine, cyclosporine A, methotrexate, ancrod, ε-aminocaproic acid, antiplasmin-a1, prostacyclin, defibrotide, rituximab and/or magnesium sulfate.

[007] The present invention provides a bispecific or biparatopic antigen-binding protein (*e.g.*, antibody or antigen-binding fragment thereof (*e.g.*, an IgG)) comprising a first antigen-binding domain that binds to C5 (*e.g.*, human C5) at a first epitope (*e.g.*, one antigen-binding domain from the H4H12166P antibody) and a second antigen-binding domain that (i) specifically binds to C5 at a second epitope which is different from that of the first antigen-binding domain and/or (ii) does not compete with the first antigen-binding domain for binding to C5 (*e.g.*, one antigen-binding domain from the eculizumab, H4H12161P, H4H12170P, H4H12171P, H4H12175P, H4H12176P2 or H4H12177P2 antibody, for example, H4H12176P2xH4H12177P2) or a pharmaceutically composition thereof comprising a pharmaceutically acceptable carrier. The present invention also provides a method for treating or preventing a C5-associated disease or disorder in a subject (*e.g.*, a mammal such as a human) in need of such treatment or prevention or for inhibiting both the classical and alternative complement pathway (CP and AP, respectively) in a subject comprising administering (*e.g.*, subcutaneously, intravenously, intradermally, intraperitoneally, orally, intramuscularly or intracranially) an effective amount of a combination of the present invention (and, optionally, one or more further therapeutic

agents, *e.g.*, as discussed herein) to the subject. Such a disease or disorder can be, for example, acute respiratory distress syndrome; adult respiratory distress syndrome; age-related macular degeneration; allergy; Alport's syndrome; Alzheimer's disease; asthma; asthma; atherosclerosis; atypical hemolytic uremic syndrome; autoimmune diseases; complement activation caused by balloon angioplasty; bronchoconstriction; bullous pemphigoid; burns; C3 glomerulopathy; capillary leak syndrome; chemical injury; chronic obstructive pulmonary disease; Crohn's disease; diabetes; diabetic macular edema; diabetic nephropathy; diabetic retinopathy; dyspnea; emphysema; epilepsy; fibrogenic dust diseases; frostbite; geographic atrophy; glomerulopathy; Goodpasture's Syndrome; Guillain-Barre Syndrome; complement activation caused by hemodialysis; hemodialysis complications; hemolytic anemia; hemoptysis; hereditary angioedema; hyperacute allograft rejection; hypersensitivity pneumonitis; immune complex disorders; immune complex-associated inflammation; inflammation of autoimmune diseases; inflammatory disorders; inherited CD59 deficiency; injury due to inert dusts and/or minerals; interleukin-2 induced toxicity during IL-2 therapy; lupus nephritis; membraneproliferative glomerulonephritis; membranoproliferative nephritis; mesenteric artery reperfusion after aortic reconstruction; mesenteric artery reperfusion after infectious disease; mesenteric artery reperfusion after sepsis; multiple sclerosis; myasthenia gravis; myocardial infarction; neuromyelitis optica; neuromyelitis optica; obesity; ocular angiogenesis; organic dust diseases; parasitic diseases; Parkinson's disease; paroxysmal nocturnal hemoglobinuria; pneumonia; post-ischemic reperfusion conditions; post-pump syndrome in cardiopulmonary bypass or renal bypass; progressive kidney failure; proteinuric kidney diseases; psoriasis; pulmonary embolisms and infarcts; pulmonary fibrosis; pulmonary vasculitis; renal ischemia; renal ischemia-reperfusion injury; renal transplant; rheumatoid arthritis; schizophrenia; smoke injury; stroke; stroke; systemic lupus erythematosus; systemic lupus erythematosus nephritis; thermal injury; thermal injury; traumatic brain injury; uveitis; vasculitis; and xenograft rejection. For example, in an embodiment of the invention, the method comprises administering to the subject a first antigen-binding protein that specifically binds C5 and a second antigen-binding protein that specifically binds C5; wherein the first and second antigen-binding proteins: (a) bind to distinct, non-overlapping epitopes on C5; and/or (b) do not compete with one another for binding to C5, *e.g.*, under conditions which are discussed herein.

[008] Kits of the present invention can also be produced by a method comprising the steps of co-packaging the first anti-C5 antigen-binding protein (*e.g.*, antibody or fragment); and one or more of said further anti-C5 antigen-binding proteins (*e.g.*, polypeptides, antibodies or fragments); and, optionally, one or more further therapeutic agents. A kit which is the product of such a method is also part of the present invention.

[009] Co-formulations of the present invention can be produced by a method comprising co-formulating (*e.g.*, mixing) said first antigen-binding protein (*e.g.*, antibody or fragment); and one or more of said further antigen-binding proteins (*e.g.*, polypeptides, antibodies or fragments); and, optionally, one or more further therapeutic agents; and a pharmaceutically acceptable carrier into a single pharmaceutical formulation. A co-formulation which is the product of such a method is also part of the present invention.

BRIEF DESCRIPTION OF THE FIGURES

[0010] **Figure 1A** is a graph showing hemolysis of red blood cells in the presence of serum and an anti-C5 antibody H4H12166P, H4H12170P, H4H12161P, H4H12171P, H4H12175P, H4H12176P2 or H4H12177P2. **Figure 1B** is a graph showing hemolysis of red blood cells in the presence of serum and a combination of H4H12166P + H4H12170P; H4H12166P + H4H12161P; H4H12166P + H4H12171P; H4H12166P + H4H12175P; H4H12166P + H4H12176P2; or H4H12166P + H4H12177P2.

[0011] **Figure 2A** is a graph showing hemolysis of red blood cells in the presence of 25% serum and H4H12166P, H4H12161P or H4H12166P + H4H12161P incubated for 30 or 120 minutes. **Figure 2B** is a graph showing hemolysis of red blood cells and H4H12166P, H4H12161P or H4H12166P + H4H12161P incubated for 120 minutes in the presence of 25% or 48% serum.

[0012] **Figure 3**. Hemolysis of red blood cells in the presence of serum and H4H12166P; H4H12170P Fab or H4H12166P + H4H12170P Fab incubated for 30 or 120 minutes.

[0013] **Figure 4**. Hemolysis of red blood cells in the presence of serum and H4H12176P2; H4H12177P2; or H4H12176P2 + H4H12177P2 incubated for 30 minutes.

[0014] **Figure 5A** is a graph showing hemolysis of red blood cells in the presence of serum and H4H12170P, H4H12159P; or H4H12170P + H4H12159P, incubated for 30 minutes; **Figure 5B** is a graph showing hemolysis of red blood cells in the presence of serum and H4H12175P, H4H12177P2; or H4H12175P + H4H12177P2, incubated for 30 minutes; **Figure 5C** is a graph showing hemolysis of red blood cells in the presence of serum and

H4H12176P2, H4H12164P2; or H4H12176P2 + H4H12164P2, incubated for 30 minutes; **Figure 5D** is a graph showing hemolysis of red blood cells in the presence of serum and H4H12167P, H4H12163P; or H4H12167P + H4H12163P, incubated for 30 minutes.

[0015] **Figure 6**. Hemolysis of red blood cells in the presence of H4H12166P, H4H12161P alone or in combination with C3 protein.

[0016] **Figure 7**. Generation of C5a in the presence of H4H12166P; H4H12161P or H4H12166P + H4H12161P.

[0017] **Figure 8**. Hemolysis assay; alternative complement pathway with 25% normal human serum incubated for 30 minutes.

[0018] **Figure 9**. Hemolysis assay; alternative complement pathway with 25% C5-deficient normal human serum; 145 nM C5 add-back and various ratios of antibody to C5.

[0019] **Figure 10A** and **Figure 10B** are graphs showing hemolysis assay; alternative complement pathway with 25% C5-deficient normal human serum; 125 nM C5 add-back and various ratios of bispecific anti-C5 antibody to C5.

[0020] **Figure 11**. A4F-MALLS analysis of H4H12166P:C5 complexes (mAb:C5::1 μm: 1 μm ratio) in the absence of a secondary antibody.

[0021] **Figure 12**. A4F-MALLS analysis of H4H12166P:C5 complexes with secondary antibodies (mAb2), H4H12175P or H4H12177P2 (mAb1:mAb2:C5::0.5 μm:0.5 μm:1μm ratio).

[0022] **Figure 13**. A4F-MALLS analysis of H4H12166P: H4H12161P:hC5; H4H12166P: H4H12176P2:hC5; and H4H12176P2: H4H12177P2:hC5 complexes (mAb1:mAb2:C5::0.5 μm:0.5 μm:1μm ratio).

[0023] **Figure 14**. A4F-MALLS analysis of H4H12166P:C5 complexes with secondary antibody, H4H12170P (mAb1:mAb2:C5::0.5 μm:0.5 μm:1μm ratio).

[0024] **Figure 15**. A4F-MALLS analysis of H4H12166P:C5 complexes with secondary antibody, H4H12171P (mAb1:mAb2:C5::0.5 μm:0.5 μm:1μm ratio).

[0025] **Figure 16**. A4F-MALLS analysis of H4H12176P2xH4H12177P2:C5 complexes at various ratios (mAb:C5::3:1, 1:1 or 1:3).

DETAILED DESCRIPTION

[0026] Before the present methods are described, it is to be understood that this invention is not limited to particular methods, and experimental conditions described,

as such methods and conditions may vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to be limiting, since the scope of the present invention will be limited only by the appended claims.

[0027] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although any methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, preferred methods and materials are now described. All patents, applications and publications mentioned herein are incorporated herein by reference in their entirety.

Definitions

[0028] The term "surface plasmon resonance", as used herein, refers to an optical phenomenon that allows for the analysis of real-time biomolecular interactions by detection of alterations in protein concentrations within a biosensor matrix, for example using the BIACORE™ system (Pharmacia Biosensor AB, Uppsala, Sweden and Piscataway, N.J.).

[0029] The term "K_D ", as used herein, is intended to refer to the equilibrium dissociation constant of a particular antibody-antigen interaction.

[0030] Sequence identity refers to the degree to which the amino acids of two polypeptides are the same at equivalent positions when the two sequences are optimally aligned. Sequence similarity includes identical residues and nonidentical, biochemically related amino acids. Examples of groups of amino acids that have side chains with similar chemical properties include 1) aliphatic side chains: glycine, alanine, valine, leucine and isoleucine; 2) aliphatichydroxyl side chains: serine and threonine; 3) amide-containing side chains: asparagine and glutamine; 4) aromatic side chains: phenylalanine, tyrosine, and tryptophan; 5) basic side chains: lysine, arginine, and histidine; 6) acidic side chains: aspartate and glutamate, and 7) sulfur-containing side chains: cysteine and methionine. Preferred conservative amino acids substitution groups are: valine-leucine-isoleucine, phenylalanine-tyrosine, lysine-arginine, alanine-valine, glutamate-aspartate, and asparagine-glutamine. Alternatively, a conservative replacement is any change having a positive value in the PAM250 log-likelihood matrix disclosed in Gonnet *et al.* (1992) Science 256: 1443 45, herein incorporated by reference. A "moderately conservative" replacement is any change having a nonnegative value in the PAM250 log-likelihood matrix.

[0031] A “variant” of a polypeptide, such as an immunoglobulin chain or CDR, refers to a polypeptide comprising an amino acid sequence that is at least about 70-99.9% (*e.g.*, 70, 72, 74, 75, 76, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 99.5, 99.9%) identical or similar to a referenced amino acid sequence that is set forth herein; when the comparison is performed by a BLAST algorithm wherein the parameters of the algorithm are selected to give the largest match between the respective sequences over the entire length of the respective reference sequences (*e.g.*, expect threshold: 10; word size: 3; max matches in a query range: 0; BLOSUM 62 matrix; gap costs: existence 11, extension 1; conditional compositional score matrix adjustment).

[0032] A "variant" of a polynucleotide refers to a polynucleotide comprising a nucleotide sequence that is at least about 70-99.9% (*e.g.*, 70, 72, 74, 75, 76, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 99.5, 99.9%) identical to a referenced nucleotide sequence that is set forth herein; when the comparison is performed by a BLAST algorithm wherein the parameters of the algorithm are selected to give the largest match between the respective sequences over the entire length of the respective reference sequences (*e.g.*, expect threshold: 10; word size: 28; max matches in a query range: 0; match/mismatch scores: 1, -2; gap costs: linear).

[0033] The following references relate to BLAST algorithms often used for sequence analysis: BLAST ALGORITHMS: Altschul *et al.* (2005) FEBS J. 272(20): 5101-5109; Altschul, S. F., *et al.*, (1990) J. Mol. Biol. 215:403-410; Gish, W., *et al.*, (1993) Nature Genet. 3:266-272; Madden, T. L., *et al.*, (1996) Meth. Enzymol. 266:131-141; Altschul, S. F., *et al.*, (1997) Nucleic Acids Res. 25:3389-3402; Zhang, J., *et al.*, (1997) Genome Res. 7:649-656; Wootton, J. C., *et al.*, (1993) Comput. Chem. 17:149-163; Hancock, J. M. *et al.*, (1994) Comput. Appl. Biosci. 10:67-70; ALIGNMENT SCORING SYSTEMS: Dayhoff, M. O., *et al.*, "A model of evolutionary change in proteins." in Atlas of Protein Sequence and Structure, (1978) vol. 5, suppl. 3. M. O. Dayhoff (ed.), pp. 345-352, Natl. Biomed. Res. Found., Washington, D.C.; Schwartz, R. M., *et al.*, "Matrices for detecting distant relationships." in Atlas of Protein Sequence and Structure, (1978) vol. 5, suppl. 3." M. O. Dayhoff (ed.), pp. 353-358, Natl. Biomed. Res. Found., Washington, D.C.; Altschul, S. F., (1991) J. Mol. Biol. 219:555-565; States, D. J., *et al.*, (1991) Methods 3:66-70; Henikoff, S., *et al.*, (1992) Proc. Natl. Acad. Sci. USA 89:10915-10919; Altschul, S. F., *et al.*, (1993) J. Mol. Evol. 36:290-300; ALIGNMENT STATISTICS: Karlin, S., *et al.*, (1990) Proc. Natl. Acad. Sci. USA 87:2264-2268; Karlin, S., *et al.*, (1993) Proc. Natl. Acad. Sci. USA 90:5873-

5877; Dembo, A., *et al.*, (1994) Ann. Prob. 22:2022-2039; and Altschul, S. F. "Evaluating the statistical significance of multiple distinct local alignments." in Theoretical and Computational Methods in Genome Research (S. Suhai, ed.), (1997) pp. 1-14, Plenum, NY.

[0034] As used herein, the term "subject" refers to an animal, preferably a mammal, more preferably a human, for example, in need of amelioration, prevention and/or treatment of a C5-associated disease or disorder such as atypical hemolytic uremic syndrome (aHUS) or paroxysmal nocturnal hemoglobinuria (PNH). The term includes human subjects who have or are at risk of having such a disease or disorder.

[0035] As used herein a "combination" refers to a collocation of a first component with is an anti-C5 antigen-binding protein (*e.g.*, antibody or antigen-binding fragment) and one or more further components which is an anti-C5 antigen-binding protein (*e.g.*, antibody, antigen-binding fragment or polypeptide) (*e.g.*, H4H12166P and one of H4H12161P, H4H12170P, H4H12171P, H4H12175P, H4H12176P2 or H4H12177P2). Such a collocation may be in a single liquid (*e.g.*, aqueous) or dry (*e.g.*, lyophilized) composition, *e.g.*, a pharmaceutical composition, that includes both components. A collocation may be a kit comprising each component in two or more separate vessels or devices. With regard to combinations used in connection with methods of treatment or prevention that are discussed herein, each component, in the combination, can be administered to a subject at a different time than when the other component is administered; for example, each administration may be given non-simultaneously (*e.g.*, separately or sequentially) at intervals over a given period of time. Moreover, the separate components may be administered to a subject by the same or by a different route, *e.g.*, wherein an anti-C5 antibody is administered subcutaneously and the other anti-C5 antibody is administered intravenously. In an embodiment of the invention, the components of a combination are located in a common molecule, *e.g.*, a multispecific molecule (e.g. bispecific) that binds to C5 at multiple epitopes. For example, a combination of two anti-C5 antibodies or antigen-binding fragments includes a bispecific or biparatopic antibody or fragment having a first antigen-binding domain that binds to a first epitope on C5 and a second antigen-binding domain that binds to a second, different epitope on C5 and/or which does not compete for binding to C5 with the first antigen-binding domain (*e.g.*, as discussed further herein).

C5

[0036] The present invention relates to combinations including antigen-binding proteins (*e.g.*, antibodies and antigen-binding fragments) that bind to C5 ("complement component 5" or "complement factor 5"), for example, human C5 (*e.g.*, H4H12166P and one of H4H12161P, H4H12170P, H4H12171P, H4H12175P, H4H12176P2 or H4H12177P2).

[0037] The *C5* gene encodes a component of the complement system, a part of the innate immune system that plays an important role in inflammation, host homeostasis, and host defense against pathogens. The *C5* gene product is proteolytically processed to generate multiple protein products, including the C5 alpha chain, C5 beta chain, C5a anaphylatoxin and C5b. The C5 protein includes the C5 alpha and beta chains which are linked by a disulfide bridge.

[0038] The amino acid sequence of full-length C5 protein is exemplified by the amino acid sequence provided in GenBank as accession number NP_001726.2 (SEQ ID NO: 1). The term "C5" includes recombinant C5 protein or a fragment thereof (*e.g.* a mature fragment lacking the N-terminal signal peptide). The term also encompasses C5 protein or a fragment thereof coupled to, for example, histidine tag, mouse or human Fc, or a signal sequence such as ROR1. The term also includes protein variants that comprise a histidine tag at the C-terminal, coupled to amino acid residues 19 – 1676 of full-length C5 protein with a R885H change or a R885C change. In an embodiment of the invention, human C5 comprises the amino acid sequence set forth in SEQ ID NO: 1.

Anti-C5 Antibodies, Fragments and Polypeptides

[0039] The present invention provides combinations comprising a first antigen-binding protein (*e.g.*, an antibody or antigen-binding fragment thereof) that binds specifically to C5 and one or more further antigen-binding proteins (*e.g.*, polypeptides or antibodies or antigen-binding fragments thereof) that (i) specifically bind to C5 at an epitope which is different from that of the first antigen-binding protein; and/or (ii) do not compete with the first antigen-binding protein for binding to C5 (*e.g.*, H4H12166P and one of H4H12161P, H4H12170P, H4H12171P, H4H12175P, H4H12176P2 or H4H12177P2).

[0040] An anti-C5 "antigen-binding protein" is a polypeptide or complex of more than one polypeptide (*e.g.*, a tetrameric IgG antibody) that binds specifically to C5 polypeptide, for example, an anti-C5 antibody or antigen-binding fragment.

[0041] For example, the present invention includes combinations comprising antibody H4H12166P (or an antigen-binding fragment thereof) and any one or more antibodies (or antigen-binding fragments thereof)) selected from H4H12161P, H4H12170P, H4H12171P, H4H12171P, H4H12175P, H4H12176P2 and H4H12177P2; or Eculizumab (sold as "Soliris"); or the polypeptide *Ornithodoros moubata* OmCI (or a variant thereof) or EV576 (coversin). See International patent application publication no. WO2004106369 or U.S. patent application publication no. US20170065677 or WO2007028968.

[0042] The term "antibody", as used herein, refers to antigen-binding proteins which are immunoglobulin molecules comprising four polypeptide chains, two heavy (H) chains and two light (L) chains inter-connected by disulfide bonds (*i.e.*, "full antibody molecules"), as well as multimers thereof (*e.g.*, IgM) or antigen-binding fragments thereof. Each heavy chain includes a heavy chain variable region ("HCVR" or "V_H") and a heavy chain constant region (comprising domains C_{H1}, C_{H2} and C_{H3}). Each light chain includes a light chain variable region ("LCVR" or "V_L") and a light chain constant region (C_L). The V_H and V_L regions can be further subdivided into regions of hypervariability, termed "complementarity determining regions" (CDR), interspersed with regions that are more conserved, termed framework regions (FR). Each V_H and V_L is composed of three CDRs and four FRs, arranged, from amino-terminus to carboxy-terminus, in the following order: FR1, CDR1, FR2, CDR2, FR3, CDR3, FR4. In certain embodiments of the invention, the FRs of the antibody (or antigen binding fragment thereof) may be identical to the human germline sequences, or may be naturally or artificially modified.

[0043] The present invention includes combinations which are multispecific (*e.g.*, bispecific) antigen-binding proteins (*e.g.*, antibodies and antigen-binding fragments thereof) which comprise a first antigen-binding domain that binds to C5 at a first epitope and a second antigen-binding domain that (i) specifically binds to C5 at a second epitope which is different from that of the first antigen-binding domain; and/or (ii) do not compete with the first antigen-binding domain for binding to C5 (or would not compete if the first antigen-binding domain and second antigen-binding domain were in separate monospecific (*e.g.*, bivalent IgG) proteins (*e.g.*, antibodies) that were tested for competition). A bispecific antigen-binding protein (*e.g.*, antibody) may also be called biparatopic insofar as the molecule binds to two epitopes within the same antigen (C5). For example, in an embodiment of the invention, the first antigen-binding domain comprises the heavy and light chain CDRs (CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2 and CDR-L3) or the V_H and V_L or heavy

and light chain of H4H12166P; and the second antigen-binding domain comprises the heavy and light chain CDRs (CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2 and CDR-L3) or the V_H and V_L or heavy and light chain of H4H12161P, H4H12170P, H4H12171P, H4H12175P, H4H12176P2 or H4H12177P2. For example, in an embodiment of the invention, the biparatopic antigen-binding protein (*e.g.*, antibody or antigen-binding fragment) is in a bispecific IgG format (*e.g.*, IgG1, IgG2, IgG3 or IgG4 (*e.g.*, having a Ser228Pro mutation)) that it a tetramer comprising two heavy chain/light chain pairs. In an embodiment of the invention, the otherwise biparatopic antigen-binding protein (*e.g.*, antibody or fragment) is appended with one or more additional antigen-binding immunoglobulins (*e.g.*, an additional C5-binding immunoglobulin) or an additional polypeptide (*e.g.*, coversin). The present invention also provides an anti-C5 antigen-binding protein (*e.g.*, antibody or antigen-binding fragment thereof) that is linked with a polypeptide (*e.g.*, coversin) that binds to C5 at a different epitope than that of the antigen-binding protein (*e.g.*, antibody or fragment) and/or which does not compete with the antigen-binding protein (*e.g.*, antibody or fragment) for binding to C5. In an embodiment of the invention, the bispecific antigen-binding protein is a $F(ab')_2$ of a full bispecific antibody (*e.g.*, IgG antibody), *e.g.*, the product of a pepsin cleavage of a bispecific IgG antibody. In an embodiment of the invention, the bispecific antigen-binding protein is a bivalent/bispecific scFv that comprises a V_L and V_H that binds to a first C5 epitope linked, *e.g.*, via linker (*e.g.*, peptide linker), to a second V_H and V_L that binds to a second C5 epitope.

[0044] Antibodies and antigen-binding fragments discussed herein may be assigned to different classes depending on the amino acid sequences of the constant domain of their heavy chains. There are at least five major classes of immunoglobulins: IgA, IgD, IgE, IgG and IgM, and several of these may be further divided into subclasses (isotypes), *e.g.* IgG1, IgG2, IgG3 and IgG4; IgA1 and IgA2. A human heavy chain constant region can be gamma-4 (IgG4) with a Ser228Pro mutation (Schuurman, J *et al.*, Mol. Immunol. 38: 1-8, 2001). An antibody or antigen-binding fragment can comprises a light chain constant region such as a human light chain constant region (*e.g.*, lambda or kappa human light chain region). The anti-C5 antibody and antigen-binding fragment V_H chains discussed herein may be linked to any of the heavy constant chains discussed herein. The anti-C5 antibody and antigen-binding fragment V_L chains discussed herein may be linked to any of the light constant chains discussed herein.

[0045] Antibodies and antigen-binding fragments discussed herein may comprise a V_H and/or V_L set forth herein and a modified Fc. Non-limiting examples of such Fc modifications include, *e.g.*, a modification at position 250 (*e.g.*, E or Q); 250 and 428 (*e.g.*, L or F); 252 (*e.g.*, L/Y/F/W or T), 254 (*e.g.*, S or T), and 256 (*e.g.*, S/R/Q/E/D or T); or a modification at position 428 and/or 433 (*e.g.*, H/L/R/S/P/Q or K) and/or 434 (*e.g.*, A, W, H, F or Y [N434A, N434W, N434H, N434F or N434Y]); or a modification at position 250 and/or 428; or a modification at position 307 or 308 (*e.g.*, 308F, V308F), and 434. In one embodiment, the modification comprises a 428L (*e.g.*, M428L) and 434S (*e.g.*, N434S) modification; a 428L, 259I (*e.g.*, V259I), and 308F (*e.g.*, V308F) modification; a 433K (*e.g.*, H433K) and a 434 (*e.g.*, 434Y) modification; a 252, 254, and 256 (*e.g.*, 252Y, 254T, and 256E) modification; a 250Q and 428L modification (*e.g.*, T250Q and M428L); and a 307 and/or 308 modification (*e.g.*, 308F or 308P). In yet another embodiment, the modification comprises a 265A (*e.g.*, D265A) and/or a 297A (*e.g.*, N297A) modification. In an embodiment of the invention, a combination comprises one or more anti-C5 antibodies or antigen-binding fragments comprising an Fc domain comprising one or more pairs or groups of mutations selected from the group consisting of: 250Q and 248L (*e.g.*, T250Q and M248L); 252Y, 254T and 256E (*e.g.*, M252Y, S254T and T256E); 428L and 434S (*e.g.*, M428L and N434S); 257I and 311I (*e.g.*, P257I and Q311I); 257I and 434H (*e.g.*, P257I and N434H); 376V and 434H (*e.g.*, D376V and N434H); 307A, 380A and 434A (*e.g.*, T307A, E380A and N434A); and 433K and 434F (*e.g.*, H433K and N434F). All possible combinations of the foregoing Fc domain mutations and other mutations within the antibody variable domains disclosed herein, are contemplated within the scope of the present invention.

[0046] The identification of CDRs within an immunoglobulin chain is well known in the art. The assignment of amino acids to each domain is, in an embodiment of the invention, in accordance with the definitions of Sequences of Proteins of Immunological Interest, Kabat, *et al.*; National Institutes of Health, Bethesda, Md.; 5th ed.; NIH Publ. No. 91-3242 (1991); Kabat (1978) Adv. Prot. Chem. 32:1-75; Kabat, *et al.*, (1977) J. Biol. Chem. 252:6609-6616; Chothia, *et al.*, (1987) J Mol. Biol. 196:901-917 or Chothia, *et al.*, (1989) Nature 342:878-883. Thus, when referring to CDRs in a given immunoglobulin chain, said CDRs may, in an embodiment of the invention, be identified using any of the conventions and methods cited above.

[0047] The present invention relates to anti-C5 antibodies and antigen-binding fragments and polypeptides comprising sequences that are specifically set forth herein as well as variants thereof. A variant of an anti-C5 antibody or fragment disclosed herein may comprise one or more (*e.g.*, 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10) amino acid substitutions, insertions and/or deletions in the framework and/or CDR regions of the heavy and/or light chain variable domains (*e.g.*, in any one or more of CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2 and/or CDR-L3) as compared to the corresponding specific sequences set forth herein. In an embodiment of the invention, a variant of an anti-C5 antibody or fragment has one or more conservative substitutions; for example, having HCVR, LCVR, and/or CDR amino acid sequences with, *e.g.*, 10 or fewer, 8 or fewer, 6 or fewer, 4 or fewer, *etc.* conservative amino acid substitutions relative to any of the HCVR, LCVR, and/or CDR amino acid sequences specifically disclosed herein. In an embodiment of the invention, an anti-C5 antibody, fragment or polypeptide is a variant comprising a polypeptide (*e.g.*, an immunoglobulin heavy and/or light chain variable region) amino acid sequence that is at least about 70-99.9% (*e.g.*, 70, 72, 74, 75, 76, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 99.5, 99.9%) identical or similar to a referenced amino acid sequence that is set forth herein; when the comparison is performed by a BLAST algorithm wherein the parameters of the algorithm are selected to give the largest match between the respective sequences over the entire length of the respective reference sequences (*e.g.*, expect threshold: 10; word size: 3; max matches in a query range: 0; BLOSUM 62 matrix; gap costs: existence 11, extension 1; conditional compositional score matrix adjustment). In an embodiment of the invention, such a variant retains the ability to bind to C5.

[0048] In an embodiment of the invention, the anti-C5 antibody or antigen-binding fragment comprises a heavy chain comprising an amino acid that is at least 70% identical to the amino acid sequence set forth in SEQ ID NO: 3, 19, 35, 51, 67, 82, 84, 87 or 103 and/or a light chain comprising an amino acid that is at least 70% identical to the amino acid sequence set forth in SEQ ID NO: 11, 27, 43, 59, 75, 83, 85 or 95. For example, in an embodiment of the invention, while the overall sequence identity of an immunoglobulin chain is less than 100% relative to that of a reference immunoglobulin chain amino acid sequence, the immunoglobulin chain comprises CDR1, CDR2 and CDR3 which are 100% identical to that of the CDRs in the reference immunoglobulin chain.

[0049] The present invention also relates to combinations including human anti-C5 antigen-binding proteins (*e.g.*, antibodies and antigen-binding fragments thereof). The term "human antibody", as used herein, includes antibodies having variable and constant regions derived from human germline immunoglobulin sequences. The human mAbs of the invention may include amino acid residues not encoded by human germline immunoglobulin sequences (*e.g.*, mutations introduced by random or site-specific mutagenesis *in vitro* or by somatic mutation *in vivo*), for example in the CDRs and in particular CDR3. However, the term "human antibody", as used herein, is not intended to include mAbs in which CDR sequences derived from the germline of another mammalian species (*e.g.*, mouse), have been grafted onto human FR sequences. The term includes antibodies recombinantly produced in a nonhuman mammal, or in cells of a non-human mammal. The term is not intended to include antibodies isolated from or generated in a human subject. Methods for generating human antibodies in transgenic mice are known in the art. Any such known methods can be used in the context of the present invention to make human antibodies that specifically bind to C5 protein. Using VELOCIMMUNE® technology (see, for example, US 6,596,541, Regeneron Pharmaceuticals, VELOCIMMUNE®) or any other known method for generating monoclonal antibodies, high affinity chimeric antibodies to C5 can be initially isolated having a human variable region and a mouse constant region. The VELOCIMMUNE® technology involves generation of a transgenic mouse having a genome comprising human heavy and light chain variable regions operably linked to endogenous mouse constant region loci such that the mouse produces an antibody comprising a human variable region and a mouse constant region in response to antigenic stimulation. The DNA encoding the variable regions of the heavy and light chains of the antibody can be isolated and operably linked to DNA encoding the human heavy and light chain constant regions. The DNA can then be expressed in a cell capable of expressing the fully human antibody. Generally, a VELOCIMMUNE® mouse is challenged with the antigen of interest, and lymphatic cells (such as B-cells) are recovered from the mice that express antibodies. The lymphatic cells may be fused with a myeloma cell line to prepare immortal hybridoma cell lines, and such hybridoma cell lines are screened and selected to identify hybridoma cell lines that produce antibodies specific to the antigen of interest. DNA encoding the variable regions of the heavy chain and light chain may be isolated and linked to desirable isotypic constant regions of the heavy chain and light chain. Such an antibody protein may be produced in a cell, such as a CHO cell. Alternatively, DNA encoding the antigen-specific

chimeric antibodies or the variable domains of the light and heavy chains may be isolated directly from antigen-specific lymphocytes.

[0050] The present invention also relates to combinations including recombinant anti-C5 antigen-binding proteins (*e.g.*, antibodies and antigen-binding fragments thereof). The term "recombinant", as used herein, refers to antibodies or antigen-binding fragments thereof of the invention created, expressed, isolated or obtained by technologies or methods known in the art as recombinant DNA technology which include, *e.g.*, DNA splicing and transgenic expression. The term refers to antigen-binding proteins, such as antibodies, expressed in a non-human mammal (including transgenic non-human mammals, *e.g.*, transgenic mice), or a cell (*e.g.*, CHO cells) expression system or isolated from a recombinant combinatorial human antibody library. See *e.g.*, U.S. patent nos. 4816567; 6331415 and 7923221.

[0051] The present invention also relates to combinations including blocking or neutralizing anti-C5 antigen-binding proteins (*e.g.*, antibodies and antigen-binding fragments thereof and polypeptides). A "blocking" or "neutralizing" antigen-binding protein, *e.g.*, antibody, fragment or polypeptide, as used herein (or an antibody, fragment or polypeptide that "neutralizes C5 activity" or an "antagonist" antibody, fragment or polypeptide), is intended to refer to a protein whose binding to C5 results in inhibition of at least one biological activity of C5. For example, an antibody of the invention may prevent or block complement-mediated hemolysis (*e.g.*, of a red blood cell), *e.g.*, by the classical pathway or the alternative pathway.

[0052] The present invention also relates to combinations including anti-C5 antigen-binding proteins which are antigen-binding fragments of an antibody. The terms "antigen-binding portion" of an antibody, "antigen-binding fragment" of an antibody, and the like, as used herein, include a naturally occurring, enzymatically obtainable, synthetic, or genetically engineered polypeptide or glycoprotein, other than a full antibody, that specifically binds an antigen to form a complex. The terms "antigen-binding fragment" of an antibody, or "antibody fragment", as used herein, refers to one or more fragments of an antibody that retain the ability to bind to C5 protein. Antigen-binding fragments include (i) Fab fragments; (ii) $F(ab')_2$ fragments; (iii) Fd fragments; (iv) Fv fragments; (v) single chain Fv (scFv) molecules; (vi) dAb fragments; and (vii) minimal recognition units including the amino acid residues that mimic the hypervariable region of an antibody (*e.g.*, an isolated complementarity determining region (CDR) such as a CDR3 peptide), or a constrained FR3-CDR3-FR4 peptide. Other engineered molecules, such as domain-specific antibodies,

single domain antibodies, domain-deleted antibodies, chimeric antibodies, CDR-grafted antibodies, diabodies, triabodies, tetrabodies, minibodies, nanobodies (*e.g.*, monovalent nanobodies, bivalent nanobodies, *etc.*), small modular immunopharmaceuticals (SMIPs), and shark variable IgNAR domains, are also encompassed within the expression "antigen-binding fragment," as used herein. In certain embodiments, the term "antigen-binding fragment" refers to a polypeptide fragment of a multi-specific antigen-binding molecule. Antigen-binding fragments of an antibody may be derived, *e.g.*, from full antibody molecules using any suitable standard techniques such as proteolytic digestion or recombinant genetic engineering techniques involving the manipulation and expression of DNA encoding antibody variable and (optionally) constant domains. Such DNA is known and/or is readily available from, *e.g.*, commercial sources, DNA libraries (including, *e.g.*, phage-antibody libraries), or can be synthesized. The DNA may be sequenced and manipulated chemically or by using molecular biology techniques, for example, to arrange one or more variable and/or constant domains into a suitable configuration, or to introduce codons, create cysteine residues, modify, add or delete amino acids, *etc.*

[0053] In an embodiment of the invention, an antigen-binding fragment of an antibody comprises at least one variable domain. The variable domain may be of any size or amino acid composition and will generally comprise at least one CDR, which is adjacent to or in frame with one or more framework sequences. In antigen-binding fragments having a V_H domain associated with a V_L domain, the V_H and V_L domains may be situated relative to one another in any suitable arrangement. For example, the variable region may be dimeric and contain V_H - V_H, V_H - V_L or V_L - V_L dimers. Alternatively, the antigen-binding fragment of an antibody may contain a monomeric V_H or V_L domain.

[0054] In certain embodiments, an antigen-binding fragment of an antibody includes at least one variable domain covalently linked to at least one constant domain. Non-limiting, exemplary configurations of variable and constant domains that may be found within an antigen-binding fragment of an antibody of the present invention include:

(i) V_H -C_{H1};

(ii) V_H -C_{H2};

(iii) V_H -C_{H3};

(iv) V_H -C_{H1}-C_{H2};

(v) V_H -C_{H1}-C_{H2}- C_{H3};

(vi) V_H -C_{H2}-C_{H3};

(vii) V_H -C_L;

(viii) V_L -C_{H1};

(ix) V_L -C_{H2};

(x) V_L -C_{H3};

(xi) V_L -C_{H1}-C_{H2};

(xii) V_L -C_{H1}-C_{H2}-C_{H3};

(xiii) V_L -C_{H2}-C_{H3}; and

(xiv) V_L -C_L.

In any configuration of variable and constant domains, including any of the exemplary configurations listed above, the variable and constant domains may be either directly linked to one another or may be linked by a full or partial hinge or linker region. A hinge region may consist of at least 2 (*e.g.*, 5, 10, 15, 20, 40, 60 or more) amino acids, which result in a flexible or semi-flexible linkage between adjacent variable and/or constant domains in a single polypeptide molecule. Moreover, an antigen-binding fragment of an antibody of the present invention may comprise a homo-dimer or hetero-dimer (or other multimer) of any of the variable and constant domain configurations listed above in non-covalent association with one another and/or with one or more monomeric V_H or V_L domain (*e.g.*, by disulfide bond(s)).

[0055] The present invention also relates to combinations including multispecific (*e.g.*, bispecific) antigen-binding proteins (*e.g.*, antibodies, antigen-binding fragments or polypeptides). The term multispecific includes the term multiparatopic (and biparatopic). Multiparatopic molecules bind to multiple epitopes within the same antigen. A multispecific antigen-binding fragment of an antibody will typically comprise at least two different variable domains, wherein each variable domain is capable of specifically binding to a different antigen or to a different epitope on the same antigen (*e.g.*, biparatopic). A biparatopic IgG antibody comprises two different heavy/light chain pairs that bind to two different epitopes within C5.

[0056] "Isolated" antigen-binding proteins, *e.g.*, antibodies or antigen-binding fragments thereof, polypeptides, polynucleotides and vectors, are at least partially free of other biological molecules from the cells or cell culture from which they are produced. Such biological molecules include nucleic acids, proteins, other antibodies or antigen-binding fragments, lipids, carbohydrates, or other material such as cellular debris and growth medium. Isolated antibodies or antigen-binding fragments thereof, polypeptides,

polynucleotides and vectors may further be at least partially free of expression system components such as biological molecules from a host cell or of the growth medium thereof. Generally, the term "isolated" is not intended to refer to a complete absence of such biological molecules or to an absence of water, buffers, or salts or to components of a pharmaceutical formulation that includes the antibodies or antigen-binding fragments thereof, polypeptides, polynucleotides and/or vectors.

[0057] The term "specifically binds," or "binds specifically to", or the like, means that an antigen-binding protein, *e.g.*, antibody or antigen-binding fragment thereof, forms a complex with an antigen that is relatively stable under physiologic conditions. Specific binding can be characterized by an equilibrium dissociation constant of at least about $1x10^{-8}$ M or a lower number (*e.g.*, a smaller K_D denotes a tighter binding), for example, at least 10^{-9} M or 10^{-10} M, or at least 1.29 X 10^{-10} M for binding to C5 at 25°C as measured by SPR or at least 2.62 X 10^{-10} M for binding to C5 at 37°C as measured by SPR.

[0058] The term "anti-C5" refers to an antigen-binding protein, *e.g.*, an antibody, antigen-binding fragment, polypeptide or other molecule, that specifically binds to C5 polypeptide or an immunogenic fragment thereof.

[0059] Methods for determining whether two molecules specifically bind are well known in the art and include, for example, equilibrium dialysis, surface plasmon resonance, and the like. As described herein, antibodies have been identified by surface plasmon resonance, *e.g.*, BIACORE™, which bind specifically to C5.

[0060] In an embodiment of the invention, antigen-binding proteins, *e.g.*, an antibody or antibody fragment of the invention, may be conjugated to a moiety such a ligand or a therapeutic moiety ("immunoconjugate"), a second anti-C5 antibody, or any other therapeutic moiety useful for treating a C5-associated disease or disorder. In an embodiment of the invention, an anti-C5 antigen-binding protein, *e.g.*, antibody or antigen-binding fragment thereof as set forth herein, is conjugated to coversin polypeptide.

[0061] A selection of anti-C5 antibodies and antigen-binding fragments, wherein each of which do not compete with H4H12166P for C5 binding, includes H4H12161P, H4H12170P, H4H12171P, H4H12175P, H4H12176P2 and H4H12177P2. The present invention includes combinations including any two or more of these antibodies or antigen-binding fragments thereof. As discussed above, a combination may be a multispecific (e.g., bispecific) antibody comprising a heavy and light chain of one such antibody and the heavy and light chain of another such antibody. For example, the scope of the present invention includes a

bispecific antibody or antigen-binding fragment thereof comprising a combination of heavy chain immunoglobulin and light chain immunoglobulin taken from any of H4H12161P, H4H12166P, H4H12170P, H4H12171P, H4H12175P, H4H12176P2 and H4H12177P2 to form an antigen-binding domain and a combination of a different heavy chain immunoglobulin and a different light chain immunoglobulin taken from any of H4H12161P, H4H12166P, H4H12170P, H4H12171P, H4H12175P, H4H12176P2 and H4H12177P2 to form a different antigen-binding domain. A summary of light and heavy chain combinations making up some bispecific antibodies and antigen-binding fragments of the present invention is set forth below in Table A. An "X" indicates a bispecific antibody including an antigen-binding domain from the antibody on the horizontal axis and an antigen-binding domain from an antibody on the vertical axis (*e.g.*, a H4H12176P2xH4H12177P2 bispecific antibody). As used herein bispecific antibodies may be referred to as "AxB" wherein A is the antigen-binding domain of a first antibody and B is the antigen-binding domain from a second, different antibody.

Table A. Exemplary bispecific antibody chain combinations*

	H4H12161P	H4H12166P	H4H12170P	H4H12171P	H4H12175P	H4H12176P2	H4H12177P2
H4H12161P							
H4H12166P	x						
H4H12170P	x	x					
H4H12171P	x	x	x				
H4H12175P	x	x	x	x			
H4H12176P2	x	x	x	x	x		
H4H12177P2	x	x	x	x		x	

*Combinations comprising the two individual antigen-binding proteins indicated in Table A with an "x" are also part of the present invention.

[0062] "H4H12161P", "H4H12166P", "H4H12170P", "H4H12171P", "H4H12175P", "H4H12176P2" and "H4H12177P2", for example, refer to antibodies and antigen-binding fragments thereof (or, in the context of a bispecific antibody or antigen-binding fragment, to an antigen-binding domain thereof) that comprise the heavy chain or V_H (or a variant thereof) and light chain or V_L (or a variant thereof) as set forth below; or that comprise a V_H that comprises the CDRs thereof (CDR-H1 (or a variant thereof), CDR-H2 (or a variant thereof) and CDR-H3 (or a variant thereof)) and a V_L that comprises the CDRs thereof (CDR-L1 (or a variant thereof), CDR-L2 (or a variant thereof) and CDR-L3 (or a variant thereof)), *e.g.*, wherein the immunoglobulin chains, variable regions and/or CDRs comprise the specific amino acid sequences described below. Such nomenclature may be used

herein to refer to other antibodies and antigen binding fragments and antigen-binding domains thereof disclosed in WO2017/218515.

[0063] The present invention, thus, includes, but is not limited to, multispecific (*e.g.*, bispecific or biparatopic) antibodies and antigen-binding fragments thereof including "H4H12161PxH4H12177P2"; "H4H12166PxH4H12177P2"; "H4H12170PxH4H12177P2"; "H4H12171PxH4H12177P2"; "H4H12176P2xH4H12177P2"; "H4H12176P2xH4H12161P"; "H4H12176P2xH4H12166P"; "H4H12176P2xH4H12170P"; "H4H12176P2xH4H12171P"; "H4H12176P2xH4H12175P"; "H4H12175PxH4H12161P"; "H4H12175PxH4H12166P"; "H4H12175PxH4H12170P"; "H4H12175PxH4H12171P"; "H4H12171PxH4H12161P"; "H4H12171PxH4H12166P"; "H4H12171PxH4H12170P"; "H4H12170PxH4H12161P"; "H4H12170PxH4H12166P"; and "H4H12166PxH4H12161P".

[0064] For example, the multispecific (*e.g.*, bispecific or biparatopic) antibody or antigen-binding fragment, H4H12176P2xH4H12177P2, comprises:

a first antigen binding domain comprising:

(1)

a heavy chain immunoglobulin or variable region thereof that comprises CDR-H1, CDR-H2 and CDR-H3 of a heavy chain immunoglobulin or variable region thereof that comprises the amino acid sequence set forth in SEQ ID NO: 87; or a variant thereof; and

a light chain immunoglobulin or variable region thereof that comprises CDR-L1, CDR-L2 and CDR-L3 of a light chain immunoglobulin or variable region thereof that comprises the amino acid sequence set forth in SEQ ID NO: 95 or a variant thereof; and

a second antigen binding domain comprising

a heavy chain immunoglobulin or variable region thereof that comprises CDR-H1, CDR-H2 and CDR-H3 of a heavy chain immunoglobulin or variable region thereof that comprises the amino acid sequence set forth in SEQ ID NO: 103; or a variant thereof; and

a light chain immunoglobulin or variable region thereof that comprises CDR-L1, CDR-L2 and CDR-L3 of a light chain immunoglobulin or variable region thereof that comprises the amino acid sequence set forth in SEQ ID NO: 95 or a variant thereof;

or

(2)

a first antigen binding domain comprising:

a heavy chain variable region comprising

a CDR-H1 comprising the amino acid sequence set forth in SEQ ID NO: 89;

a CDR-H2 comprising the amino acid sequence set forth in SEQ ID NO: 91; and
a CDR-H3 comprising the amino acid sequence set forth in SEQ ID NO: 93;
and a light chain variable region comprising
a CDR-L1 comprising the amino acid sequence set forth in SEQ ID NO: 97;
a CDR-L2 comprising the amino acid sequence set forth in SEQ ID NO: 99; and
a CDR-L3 comprising the amino acid sequence set forth in SEQ ID NO: 101;
and a second antigen binding domain comprising:
a heavy chain variable region comprising
a CDR-H1 comprising the amino acid sequence set forth in SEQ ID NO: 105;
a CDR-H2 comprising the amino acid sequence set forth in SEQ ID NO: 107; and
a CDR-H3 comprising the amino acid sequence set forth in SEQ ID NO: 109;
and a light chain variable region comprising
a CDR-L1 comprising the amino acid sequence set forth in SEQ ID NO: 97;
a CDR-L2 comprising the amino acid sequence set forth in SEQ ID NO: 99; and
a CDR-L3 comprising the amino acid sequence set forth in SEQ ID NO: 101;
or
(3)
a first antigen binding domain comprising:
(a) a heavy chain immunoglobulin or variable region thereof comprising the CDR-H1, CDR-H2 and CDR-H3 of a heavy chain immunoglobulin or variable region thereof comprising an amino acid sequence set forth in SEQ ID NO: 87 and at least 90% amino acid sequence identity to the amino acid sequence set forth in SEQ ID NO: 87; and/or
(b) an light chain immunoglobulin or variable region thereof comprising the CDR-L1, CDR-L2 and CDR-L3 of a light chain immunoglobulin or variable region thereof comprising an amino acid sequence set forth in SEQ ID NO: 95 and at least 90% amino acid sequence identity to the amino acid sequence set forth in SEQ ID NO: 95.
a second antigen binding domain comprising:
(a) a heavy chain immunoglobulin or variable region thereof comprising the CDR-H1, CDR-H2 and CDR-H3 of a heavy chain immunoglobulin or variable region thereof comprising an amino acid sequence set forth in SEQ ID NO: 103 and at least 90% amino acid sequence identity to the amino acid sequence set forth in SEQ ID NO: 103; and/or
(b) an light chain immunoglobulin or variable region thereof comprising the CDR-L1, CDR-L2 and CDR-L3 of a light chain immunoglobulin or variable region thereof comprising an

amino acid sequence set forth in SEQ ID NO: 95 and at least 90% amino acid sequence identity to the amino acid sequence set forth in SEQ ID NO: 95;

or

(4)

a first antigen binding domain comprising:

a heavy chain immunoglobulin or variable region thereof comprising an amino acid sequence having at least 90% (*e.g.*, 100%) amino acid sequence identity to the amino acid sequence set forth in SEQ ID NO: 87; and/or

a light chain immunoglobulin or variable region thereof comprising an amino acid sequence having at least 90% (*e.g.*, 100%)amino acid sequence identity to the amino acid sequence set forth in SEQ ID NO: 95; and

a second antigen binding domain comprising:

a heavy chain immunoglobulin or variable region thereof comprising an amino acid sequence having at least 90% (*e.g.*, 100%)amino acid sequence identity to the amino acid sequence set forth in SEQ ID NO: 103; and/or

a light chain immunoglobulin or variable region thereof comprising an amino acid sequence having at least 90% (*e.g.*, 100%)amino acid sequence identity to the amino acid sequence set forth in SEQ ID NO: 95.

*Analogous multispecific antigen-binding protein embodiments comprising other combinations of immunoglobulin chains which are set forth herein are also part of the present invention.

[0065] Multispecific (*e.g.*, bispecific) antigen-binding proteins of the present invention include two or more different antigen-binding domain which are selected from any of the anti-C5 antibodies set forth in WO2017/218515, *e.g.*, H2M11683N; H2M11686N; H4H12159P; H4H12161P; H4H12163P; H4H12164P; H4H12166P; H4H12166P2; H4H12166P3; H4H12166P4; H4H12166P5; H4H12166P6; H4H12166P7; H4H12166P8; H4H12166P9; H4H12166P10; H4H12167P; H4H12168P; H4H12169P; H4H12170P; H4H12171P; H4H12175P; H4H12176P2; H4H12177P2; H4H12183P2; H2M11682N; H2M11684N; H2M11694N or H2M11695N-in an embodiment of the invention, the antigen binding domains are taken from non-competing antibodies in this list; in an embodiment of the invention, the antigen binding domains are taken from competing antibodies in this list. See Table 1 herein. WO2017/218515 is herein incorporated by reference in its entirety. In

an embodiment of the invention, an antigen-binding domain is taken from eculizumab or ALXN1210 (Ravulizumab).

H4H12161P

V_H domain (DNA):

GAGGTGCAGCTGGTGGAGTCTGGGGGAGACTTGGTCCAGCCTGGAGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGG
ATTCACCTTCAGTGACCACTATATGGACTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGACTGGATTGGCCGTATTA
GAAACAAAGCTAACGCTTATAACACAGAATACGCCGCGTCTGTGAGAGGCAGATTCACCATCTCAAGAGATGATTCA
CAGAATTTACTGTATCTGCAAATGAACAGCCTGAAAACCGATGACACGGCCGTATATTATTGTGTTAGAGTCTGGAA
CTACGCCTACTTCGCTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA

(SEQ ID NO: 2)

V_H domain (Polypeptide):

EVQLVESGGDLVQPGGSLRLSCAASGFTFSDHYMDWVRQAPGKGLDWIGRIRNKANAYNTEYAASVRGRFTISRDDS
QNLLYLQMNSLKTDDTAVYYCVRVWNYAYFAMDVWGQGTTVTVSS

(SEQ ID NO: 3)

CDR-H1 (DNA):

GGA TTC ACC TTC AGT GAC CAC TAT

(SEQ ID NO: 4)

CDR-H1 (Polypeptide):

G F T F S D H Y

(SEQ ID NO: 5 (or a variant thereof having 1, 2, 3 or 4 point mutations and/or point deletions))

CDR-H2 (DNA):

ATT AGA AAC AAA GCT AAC GCT TAT AAC ACA

(SEQ ID NO: 6)

CDR-H2 (Polypeptide):

I R N K A N A Y N T

(SEQ ID NO: 7 (or a variant thereof having 1, 2, 3 or 4 point mutations and/or point deletions))

CDR-H3 (DNA):

GTT AGA GTC TGG AAC TAC GCC TAC TTC GCT ATG GAC GTC

(SEQ ID NO: 8)

CDR-H3 (Polypeptide):

V R V W N Y A Y F A M D V

(SEQ ID NO: 9 (or a variant thereof having 1, 2, 3 or 4 point mutations and/or point deletions))

V_L domain (DNA):

GACATCCAGATGACCCAGTCTCCATCCTCCCTATCTGCATCTGTGGGAGACAGAGTCACCATCACTTGCCGGTCAAG
TCAGAACATTGGAATCTTTTTAAACTGGTATCAACAAAAACCAGGGGAAGCCCCTAACCTCCTGATCTCCGCTGCAT
CCAGTTTACACAGTGGGGTCCCTTCAAGGTTCAGTGGCAGTGGGTCTGGGACAGATTTCACTCTCACCATCGGCAGT
CTGCAGCCTGAAGATTTTGCGACTTACTACTGTCAACAGACGTACAATACCATATTCACTTTCGGCCCTGGGACCAA
AGTGGATATCAAA

(SEQ ID NO: 10)

V_L domain (Polypeptide):

DIQMTQSPSSLSASVGDRVTITCRSSQNIGIFLNWYQQKPGEAPNLLISAASSLHSGVPSRFSGSGSGTDFTLTIGS
LQPEDFATYYCQQTYNTIFTFGPGTKVDIK

(SEQ ID NO: 11)

CDR-L1 (DNA):

CAG AAC ATT GGA ATC TTT

(SEQ ID NO: 12)

CDR-L1 (Polypeptide):

Q N I G I F

(SEQ ID NO: 13 (or a variant thereof having 1, 2, 3 or 4 point mutations and/or point deletions))

CDR-L2 (DNA):

GCT GCA TCC

(SEQ ID NO: 14)

CDR-L2 (Polypeptide):

A A S

(SEQ ID NO: 15 (or a variant thereof having a point mutation or point deletion))

CDR-L3 (DNA):

CAA CAG ACG TAC AAT ACC ATA TTC ACT

(SEQ ID NO: 16)

CDR-L3 (Polypeptide):

Q Q T Y N T I F T

(SEQ ID NO: 17 (or a variant thereof having 1, 2, 3 or 4 point mutations and/or point deletions))

H4H12166P

V_H domain (DNA):

CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCACTGTCTCTGG
TGACTCCGTCAGTAGTTCCTACTGGACCTGGATCCGGCAGCCCCCAGGGAAGGGACTGGAGTGGATTGGCTATATCT
ATTACAGTGGGAGTTCCAACTACAACCCCTCCCTCAAGAGTCGAGCCACCATTTCAGTAGACACGTCCAAGAACCAG
TTCTCCCTGAAGCTGAGTTCTGTGACCGCTGCGGACACGGCCGTATATTACTGTGCGAGAGAAGGGAACGTGGATAC
AACTATGATATTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA

(SEQ ID NO: 18)

V_H domain (Polypeptide):

QVQLQESGPGLVKPSETLSLTCTVSGDSVSSSYWTWIRQPPGKGLEWIGYIYYSGSSNYNPSLKSRATISVDTSKNQ
FSLKLSSVTAADTAVYYCAREGNVDTTMIFDYWGQGTLVTVSS

(SEQ ID NO: 19)

Heavy immunoglobulin chain hIgG4 (M428L N434S)

QVQLQESGPGLVKPSETLSLTCTVSGDSVSSSYWTWIRQPPGKGLEWIGYIYYSGSSNYNPSLKSRATISVDTSKNQ
FSLKLSSVTAADTAVYYCAREGNVDTTMIFDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFP
EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPA
PEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTV

LHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVLHEALHSHYTQKSLSLSLGK

(SEQ ID NO: 82)

CDR-H1 (DNA):

GGT GAC TCC GTC AGT AGT TCC TAC

(SEQ ID NO: 20)

CDR-H1 (Polypeptide):

G D S V S S S Y

(SEQ ID NO: 21 (or a variant thereof having 1, 2, 3 or 4 point mutations and/or point deletions))

CDR-H2 (DNA):

ATC TAT TAC AGT GGG AGT TCC

(SEQ ID NO: 22)

CDR-H2 (Polypeptide):

I Y Y S G S S

(SEQ ID NO: 23 (or a variant thereof having 1, 2, 3 or 4 point mutations and/or point deletions))

CDR-H3 (DNA):

GCG AGA GAA GGG AAC GTG GAT ACA ACT ATG ATA TTT GAC TAC

(SEQ ID NO: 24)

CDR-H3 (Polypeptide):

A R E G N V D T T M I F D Y

(SEQ ID NO: 25 (or a variant thereof having 1, 2, 3 or 4 point mutations and/or point deletions))

V_L domain (DNA):

GCCATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCGGGCAAG
TCAGGGCATTAGAAATGATTTAGGCTGGTATCAACAGAAACCAGGGAAAGCCCCTAAACTCCTGATCTATGCTGCAT

CCAGTTTACAAAGTGGGGTCCCATCGAGGTTCGCCGGCCGTGGATCTGGCACAGATTTCACTCTCACCATCAGCAGC
CTGCAGCCTGAAGATTTTGCAACTTATTACTGTCTACAAGATTTCAATTACCCGTGGACGTTCGGCCAAGGGACCAA
GGTGGAAATCAAA

(SEQ ID NO: 26)

V_L domain (Polypeptide):

AIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKLLIYAASSLQSGVPSRFAGRGSGTDFTLTISS
LQPEDFATYYCLQDFNYPWTFGQGTKVEIK

(SEQ ID NO: 27)

Light immunoglobulin chain (kappa)

AIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKLLIYAASSLQSGVPSRFAGRGSGTDFTLTISS
LQPEDFATYYCLQDFNYPWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

(SEQ ID NO: 83)

CDR-L1 (DNA):

CAG GGC ATT AGA AAT GAT

(SEQ ID NO: 28)

CDR-L1 (Polypeptide):

Q G I R N D

(SEQ ID NO: 29 (or a variant thereof having 1, 2, 3 or 4 point mutations and/or point deletions))

CDR-L2 (DNA):

GCT GCA TCC

(SEQ ID NO: 30)

CDR-L2 (Polypeptide):

A A S

(SEQ ID NO: 31 (or a variant thereof having a point mutation or point deletion))

CDR-L3 (DNA):

CTA CAA GAT TTC AAT TAC CCG TGG ACG

(SEQ ID NO: 32)

CDR-L3 (Polypeptide):

L Q D F N Y P W T

(SEQ ID NO: 33 (or a variant thereof having 1, 2, 3 or 4 point mutations and/or point deletions))

H4H12170P

V_H domain (DNA):

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGG
ATTCACCTTCAGTGGTTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCACTTATAT
GGCTTGATGGAAGTAATGACTACTATGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAAC
ACGTTATATCTGCAAATGAACAGACTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATGGCCCGGTTGC
TGCTATACCCGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA

(SEQ ID NO: 34)

V_H domain (Polypeptide):

QVQLVESGGGVVQPGRSLRLSCAASGFTFSGYGMHWVRQAPGKGLEWVALIWLDGSNDYYADSVKGRFTISRDNSKN
TLYLQMNRLRAEDTAVYYCARDGPVAAIPDYWGQGTLVTVSS

(SEQ ID NO: 35)

Heavy immunoglobulin chain (IgG4):

QVQLVESGGGVVQPGRSLRLSCAASGFTFSGYGMHWVRQAPGKGLEWVALIWLDGSNDYYADSVKGRFTISRDNSKN
TLYLQMNRLRAEDTAVYYCARDGPVAAIPDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPE
PVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPP

(SEQ ID NO: 84)

CDR-H1 (DNA):

GGA TTC ACC TTC AGT GGT TAT GGC

(SEQ ID NO: 36)

CDR-H1 (Polypeptide):

G F T F S G Y G

(SEQ ID NO: 37 (or a variant thereof having 1, 2, 3 or 4 point mutations and/or point deletions))

CDR-H2 (DNA):

ATA TGG CTT GAT GGA AGT AAT GAC

(SEQ ID NO: 38)

CDR-H2 (Polypeptide):

I W L D G S N D

(SEQ ID NO: 39 (or a variant thereof having 1, 2, 3 or 4 point mutations and/or point deletions))

CDR-H3 (DNA):

GCG AGA GAT GGC CCG GTT GCT GCT ATA CCC GAC TAC

(SEQ ID NO: 40)

CDR-H3 (Polypeptide):

A R D G P V A A I P D Y

(SEQ ID NO: 41 (or a variant thereof having 1, 2, 3 or 4 point mutations and/or point deletions))

V_L domain (DNA):

GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCGGGCCAG
TCAGAGTATTAGTAGGTGGTTGGCCTGGTATCAGCTGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATAAGGCGT
CTAGTTTAGAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGACTTCACTCTCACCATCAGCAGC
CTGCAACCTGATGATTTTGCAACTTATTACTGCCAACAGTATAATACTTATTCGTACACTTTTGGCCAGGGGACCAA
GCTGGAGATCAAA

(SEQ ID NO: 42)

V_L domain (Polypeptide):

DIQMTQSPSTLSASVGDRVTITCRASQSISRWLAWYQLKPGKAPKLLIYKASSLESGVPSRFSGSGSGTDFTLTISS
LQPDDFATYYCQQYNTYSYTFGQGTKLEIK

(SEQ ID NO: 43)

Light immunoglobulin chain (kappa)

DIQMTQSPSTLSASVGDRVTITCRASQSISRWLAWYQLKPGKAPKLLIYKASSLESGVPSRFSGSGSGTDFTLTISS
LQPDDFATYYCQQYNTYSYTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

(SEQ ID NO: 85)

CDR-L1 (DNA):

CAG AGT ATT AGT AGG TGG

(SEQ ID NO: 44)

CDR-L1 (Polypeptide):

Q S I S R W

(SEQ ID NO: 45 (or a variant thereof having 1, 2, 3 or 4 point mutations and/or point deletions))

CDR-L2 (DNA):

AAG GCG TCT

(SEQ ID NO: 46)

CDR-L2 (Polypeptide):

K A S

(SEQ ID NO: 47 (or a variant thereof having a point mutation or point deletion))

CDR-L3 (DNA):

CAA CAG TAT AAT ACT TAT TCG TAC ACT

(SEQ ID NO: 48)

CDR-L3 (Polypeptide):

Q Q Y N T Y S Y T

(SEQ ID NO: 49 (or a variant thereof having 1, 2, 3 or 4 point mutations and/or point deletions))

<u>H4H12171P</u>

V_H domain (DNA):

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGTGTGGTACGGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGG
ATTCACCTTTGATGAATATGGCATGACTTGGGTCCGCCAAGTTCCAGGGAAGGGGCTGGAGTGGGTCTCTGGTATTA
CTTGGAATGGTGGTTTCACAGATTATACAGACTCTGTGAAGGGCCGATTCACCAGCTCCAGAGACAACGCCAAGAAC
TCCCTGTATCTGCAAATGAACAGTCTGAGAGCCGAGGACACGGCCTTGTATTACTGTGCGAGAGATGGATATAGCAG
CTCGTGGGGGGCTTATGATATATGGGGCCAAGGGACAATGGTCACCGTCTCTTCA

(SEQ ID NO: 50)

V_H domain (Polypeptide):

EVQLVESGGGVVRPGGSLRLSCAASGFTFDEYGMTWVRQVPGKGLEWVSGITWNGGFTDYTDSVKGRFTSSRDNAKN
SLYLQMNSLRAEDTALYYCARDGYSSSWGAYDIWGQGTMVTVSS

(SEQ ID NO: 51)

CDR-H1 (DNA):

GGA TTC ACC TTT GAT GAA TAT GGC

(SEQ ID NO: 52)

CDR-H1 (Polypeptide):

G F T F D E Y G

(SEQ ID NO: 53 (or a variant thereof having 1, 2, 3 or 4 point mutations and/or point deletions))

CDR-H2 (DNA):

ATT ACT TGG AAT GGT GGT TTC ACA

(SEQ ID NO: 54)

CDR-H2 (Polypeptide):

I T W N G G F T

(SEQ ID NO: 55 (or a variant thereof having 1, 2, 3 or 4 point mutations and/or point deletions))

CDR-H3 (DNA):

GCG AGA GAT GGA TAT AGC AGC TCG TGG GGG GCT TAT GAT ATA

(SEQ ID NO: 56)

CDR-H3 (Polypeptide):

A R D G Y S S S W G A Y D I

(SEQ ID NO: 57 (or a variant thereof having 1, 2, 3 or 4 point mutations and/or point deletions))

V_L domain (DNA):

GACATCCAGATGACCCAGTCTCCATCATCCCTGTCTGCATCTGTGGGAGACAGAGTCACCATCACTTGCCGGGCAAG
TCAGAGCATTAGCACCTATTTAAATTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGCTGCAT
CCAGTTTGCAAAGTGGGGTCCCATTAAGGTTCAGTGGCAGTGGATCTGGGACTGATTTCACTCTCACCATCAGCAGT
CTGCAACCTGAAGATTTTGCAAGTTATTTCTGTCAACAGAGTTACAGTACCCCGTACACTTTTGGCCAGGGGACCAA
GCTGGAGATCAAA

(SEQ ID NO: 58)

V_L domain (Polypeptide):

DIQMTQSPSSLSASVGDRVTITCRASQSISTYLNWYQQKPGKAPKLLIYAASSLQSGVPLRFSGSGSGTDFTLTISS
LQPEDFASYFCQQSYSTPYTFGQGTKLEIK

(SEQ ID NO: 59)

CDR-L1 (DNA):

CAG AGC ATT AGC ACC TAT

(SEQ ID NO: 60)

CDR-L1 (Polypeptide):

Q S I S T Y

(SEQ ID NO: 61 (or a variant thereof having 1, 2, 3 or 4 point mutations and/or point deletions))

CDR-L2 (DNA):

GCT GCA TCC

(SEQ ID NO: 62)

CDR-L2 (Polypeptide):

A A S

(SEQ ID NO: 63 (or a variant thereof having a point mutation or point deletion))

CDR-L3 (DNA):

CAA CAG AGT TAC AGT ACC CCG TAC ACT

(SEQ ID NO: 64)

CDR-L3 (Polypeptide):

Q Q S Y S T P Y T

(SEQ ID NO: 65 (or a variant thereof having 1, 2, 3 or 4 point mutations and/or point deletions))

H4H12175P

V_H domain (DNA):

GAAGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGG
ATTCACCTTTAATGATTATGCCATGCACTGGGTCCGTCAAGCTCCAGGGAAGGGTCTGGAGTGGGTCTCTCTTATTA
GTGGAGATGGTGGTAACACATACTATGCAGACTCTGTGAAGGGCCGACTCACCATCTCCAGAGACAACAGCAAAAAC
TCCCTGTATCTGCAAATGAACAGTCTGAGAACAGAGGACACCGCCTTATATTACTGTGCAAAAGATAAGGGCTGGAA
CTTCGGTTACTTCGATCTCTGGGGCCGTGGCACCCTGGTCACTGTCTCCTCA

(SEQ ID NO: 66)

V_H domain (Polypeptide):

EVQLVESGGGVVQPGGSLRLSCAASGFTFNDYAMHWVRQAPGKGLEWVSLISGDGGNTYYADSVKGRLTISRDNSKN
SLYLQMNSLRTEDTALYYCAKDKGWNFGYFDLWGRGTLVTVSS

(SEQ ID NO: 67)

CDR-H1 (DNA):

GGA TTC ACC TTT AAT GAT TAT GCC

(SEQ ID NO: 68)

CDR-H1 (Polypeptide):

G F T F N D Y A

(SEQ ID NO: 69 (or a variant thereof having 1, 2, 3 or 4 point mutations and/or point deletions))

CDR-H2 (DNA):

ATT AGT GGA GAT GGT GGT AAC ACA

(SEQ ID NO: 70)

CDR-H2 (Polypeptide):

I S G D G G N T

(SEQ ID NO: 71 (or a variant thereof having 1, 2, 3 or 4 point mutations and/or point deletions))

CDR-H3 (DNA)

GCA AAA GAT AAG GGC TGG AAC TTC GGT TAC TTC GAT CTC

(SEQ ID NO: 72)

CDR-H3 (Polypeptide):

A K D K G W N F G Y F D L

(SEQ ID NO: 73 (or a variant thereof having 1, 2, 3 or 4 point mutations and/or point deletions))

V_L domain (DNA):

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTACATCTGTGGGAGACAGAGTCACCATCACTTGCCGGGCAAG
TCAGAACATTGACACCTATTTAAATTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAACTCCTGATCTATGATGCAT
CCAGTTTACAAAGTGGGGTCCCATCACGGTTCAGTGGCAGCGGATCTGGGACAGATTTCACTCTCACCATCACCAGT
CTGCAACCTGAAGATTTTGCCACTTACTACTGTCAACAGAATGACAATATTCTTCACCCTCTCACTTTCGGCGGAGG
GACCAAGGTGGAGATCAAA

(SEQ ID NO: 74)

V_L domain (Polypeptide):

DIQMTQSPSSLSTSVGDRVTITCRASQNIDTYLNWYQQKPGKAPKLLIYDASSLQSGVPSRFSGSGSGTDFTLTITS
LQPEDFATYYCQQNDNILHPLTFGGGTKVEIK

(SEQ ID NO: 75)

CDR-L1 (DNA):

CAG AAC ATT GAC ACC TAT

(SEQ ID NO: 76)

CDR-L1 (Polypeptide):

Q N I D T Y

(SEQ ID NO: 77 (or a variant thereof having 1, 2, 3 or 4 point mutations and/or point deletions))

CDR-L2 (DNA):

GAT GCA TCC

(SEQ ID NO: 78)

CDR-L2 (Polypeptide):

D A S

(SEQ ID NO: 79 (or a variant thereof having a point mutation or point deletion))

CDR-L3 (DNA):

CAA CAG AAT GAC AAT ATT CTT CAC CCT CTC ACT

(SEQ ID NO: 80)

CDR-L3 (Polypeptide):

Q Q N D N I L H P L T

(SEQ ID NO: 81 (or a variant thereof having 1, 2, 3 or 4 point mutations and/or point deletions))

H4H12176P2

V_H domain (DNA):

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAACCGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGG
ATTCCACTCTAATAGATATTGGATGGACTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTGGCCAACATAA
AGCAAGATGGAAGTGAGGAAAACTATGTGGACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAAC
TCACTTTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATCGAAGCACCTC
GTGGGTCCCTTACTGGTTCTTCGATCTCTGGGGCCGTGGCACCCTGGTCACTGTCTCCTCA

(SEQ ID NO: 86)

V_H domain (Polypeptide):

EVQLVESGGGLVQPGGSLRLSCAASGFHSNRYWMDWVRQAPGKGLEWVANIKQDGSEENYVDSVKGRFTISRDNAKN
SLYLQMNSLRAEDTAVYYCARDRSTSWVPYWFFDLWGRGTLVTVSS

(SEQ ID NO: 87)

CDR-H1 (DNA):

GGA TTC CAC TCT AAT AGA TAT TGG

(SEQ ID NO: 88)

CDR-H1 (Polypeptide):

G F H S N R Y W

(SEQ ID NO: 89)

CDR-H2 (DNA):

ATA AAG CAA GAT GGA AGT GAG GAA

(SEQ ID NO: 90)

CDR-H2 (Polypeptide):

I K Q D G S E E

(SEQ ID NO: 91)

CDR-H3 (DNA):

GCG AGA GAT CGA AGC ACC TCG TGG GTC CCT TAC TGG TTC TTC GAT CTC

(SEQ ID NO: 92)

CDR-H3 (Polypeptide):

A R D R S T S W V P Y W F F D L

(SEQ ID NO: 93)

V_L domain (DNA):

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCGGGCAAG
TCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGCTGCAT
CCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGT
CTGCAACCTGAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTCCGATCACCTTCGGCCAAGGGAC
ACGACTGGAGATTAAA

(SEQ ID NO: 94)

V_L domain (Polypeptide):

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPPITFGQGTRLEIK

(SEQ ID NO: 95)

CDR-L1 (DNA):

CAG AGC ATT AGC AGC TAT

(SEQ ID NO: 96)

CDR-L1 (Polypeptide):

Q S I S S Y

(SEQ ID NO: 97)

CDR-L2 (DNA):

GCT GCA TCC

(SEQ ID NO: 98)

CDR-L2 (Polypeptide):

A A S

(SEQ ID NO: 99)

CDR-L3 (DNA):

CAA CAG AGT TAC AGT ACC CCT CCG ATC ACC

(SEQ ID NO: 100)

CDR-L3 (Polypeptide):

Q Q S Y S T P P I T

(SEQ ID NO: 101)

H4H12177P2

V_H domain (DNA):

GAAGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTACAGCGGGGGGAGTCCCTGAGACTCTCCTGTTCAGCCTCTGA
CTTCATCTTTAAAGATTATGCCATGTACTGGGTCCGTCAAATTCCAGGGAAGGGTCTAGAGTGGATCTCTCTTATTA
GTGGTGATGGTGACACTACATGGTATGGAGACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACAACGAAAAC

TCCCTCTTTCTGCAAATGAACGATCTGAGAACTGAGGACACCGCCATGTACTACTGTGCAAGAGATATGGGGTGGAA
CTTCTTTCAGTTGCAATACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA

(SEQ ID NO: 102)

V_H domain (Polypeptide):

EVQLVESGGGVVQRGESLRLSCSASDFIFKDYAMYWVRQIPGKGLEWISLISGDGDTTWYGDSVKGRFTISRDNNEN
SLFLQMNDLRTEDTAMYYCARDMGWNFFQLQYWGQGTLVTVSS

(SEQ ID NO: 103)

CDR-H1 (DNA):

GAC TTC ATC TTT AAA GAT TAT GCC

(SEQ ID NO: 104)

CDR-H1 (Polypeptide):

D F I F K D Y A

(SEQ ID NO: 105)

CDR-H2 (DNA):

ATT AGT GGT GAT GGT GAC ACT ACA

(SEQ ID NO: 106)

CDR-H2 (Polypeptide):

I S G D G D T T

(SEQ ID NO: 107)

CDR-H3 (DNA):

GCA AGA GAT ATG GGG TGG AAC TTC TTT CAG TTG CAA TAC

(SEQ ID NO: 108)

CDR-H3 (Polypeptide):

A R D M G W N F F Q L Q Y

(SEQ ID NO: 109)

V_L domain (DNA):

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCGGGCAAG
TCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGCTGCAT
CCAGTTTGCAAAGTGGGGTCCCGTCAAGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGT
CTGCAACCTGAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTCCGATCACCTTCGGCCAAGGGAC
ACGACTGGAGATTAAA

(SEQ ID NO: 94)

V_L domain (Polypeptide):

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPPITFGQGTRLEIK

(SEQ ID NO: 95)

CDR-L1 (DNA):

CAG AGC ATT AGC AGC TAT

(SEQ ID NO: 96)

CDR-L1 (Polypeptide):

Q S I S S Y

(SEQ ID NO: 97)

CDR-L2 (DNA):

GCT GCA TCC

(SEQ ID NO: 98)

CDR-L2 (Polypeptide):

A A S

(SEQ ID NO: 99)

CDR-L3 (DNA):

CAA CAG AGT TAC AGT ACC CCT CCG ATC ACC

(SEQ ID NO: 100)

CDR-L3 (Polypeptide):

Q Q S Y S T P P I T

(SEQ ID NO: 101)

[0065] See WO2017/218515.

[0066] The present invention further includes a complex comprising a C5 polypeptide or an antigenic fragment thereof bound to one or more anti-C5 antigen-binding proteins. For example, in an embodiment of the invention, the complex comprises one or more C5 polypeptides or antigenic fragments thereof bound to one or more first anti-C5 antigen-binding proteins and one or more further anti-C5 antigen-binding proteins that do not compete for binding to the C5. Complexes can form with various ratios of first antigen-binding protein to second antigen-binding protein to C5. For example, the scope of the present invention includes a complex comprising:
(i) a 1:1:2, 2:2:4 or 3:3:6 ratio of first monospecific anti-C5 antigen-binding protein (*e.g.*, H4H12166P)-to-second monospecific anti-C5 antigen-binding protein-to-C5 polypeptide or fragment
(ii) a 1:1, 1:2, 2:1 or 2:2 ratio of bispecific anti-C5 antigen-binding protein-to-C5 polypeptide or fragment;
(iii) a 1:1:1; 1:1:2 or 1:2:2 ratio of monospecific anti-C5 antigen-binding protein-to-bispecific anti-C5 antigen-binding protein-to-C5 polypeptide or fragment; or
(iv) a 1:2 ratio or monospecific anti-C5 antigen-binding protein-to-C5 polypeptide or fragment.
[0067] In an embodiment of the invention, the monospecific anti-C5 antigen-binding protein is eculizumab, H4H12166P, H4H12177P2 or H4H12176P2. In an embodiment of the invention, the bispecific anti-C5 antigen-binding protein is H4H12176P2xH4H12177P2.
[0068] Some complexes were surmised based upon the calculated molar mass of material eluting after asymmetric flow field-flow fractionation (A4F-MALLS) and the average calculated masses of the individual antibodies and C5 polypeptide in the mixtures analyzed. These data are set forth in Figures 11-16 herein.

Epitope Mapping and Competition

[0069] As discussed herein, the present invention provides combinations including a first antigen-binding protein (*e.g.*, antibody or antigen-binding fragment thereof) that binds specifically to C5 and one or more further antigen-binding proteins (*e.g.*, antibodies or

antigen-binding fragments thereof or polypeptides) (*e.g.*, coversin) that (i) specifically bind to C5 at an epitope which is different from that of the first antigen-binding protein and/or (ii) do not compete with the first antigen-binding protein for binding to C5.

[0070] Bispecific antigen-binding proteins (*e.g.*, antibodies and antigen-binding fragments thereof) having two antigen-binding domains (a first and a second) wherein the first specifically binds to an epitope of C5 and the second (i) specifically bind to C5 at an epitope which is different from that of the first antigen-binding domain and/or (ii) do not compete with the first antigen-binding domain for binding to C5. Such antigen-binding domains, in an embodiment of the invention, are taken from the antibodies or antigen-binding fragments which are set forth in WO2017/218515.

[0071] Two antigen-binding proteins, *e.g.*, antibodies, have a common epitope if there are common amino acids in the C5 antigen to which the antigen-binding proteins exhibit significant binding.

[0072] Methods for determining the epitope of an antigen-binding protein, *e.g.*, antibody or fragment or polypeptide, include alanine scanning mutational analysis, peptide blot analysis (Reineke (2004) Methods Mol. Biol. 248: 443-63), peptide cleavage analysis, crystallographic studies and NMR analysis. In addition, methods such as epitope excision, epitope extraction and chemical modification of antigens can be employed (Tomer (2000) Prot. Sci. 9: 487-496). Another method that can be used to identify the amino acids within a polypeptide with which an antigen-binding protein (*e.g.*, antibody or fragment or polypeptide) (*e.g.*, coversin) interacts is hydrogen/deuterium exchange detected by mass spectrometry. In general terms, the hydrogen/deuterium exchange method involves deuterium-labeling the protein of interest, followed by binding the antigen-binding protein, *e.g.*, antibody or fragment or polypeptide, to the deuterium-labeled protein. Next, the C5 protein/ antigen-binding protein complex is transferred to water and exchangeable protons within amino acids that are protected by the antibody complex undergo deuterium-to-hydrogen back-exchange at a slower rate than exchangeable protons within amino acids that are not part of the interface. As a result, amino acids that form part of the protein/ antigen-binding protein interface may retain deuterium and therefore exhibit relatively higher mass compared to amino acids not included in the interface. After dissociation of the antigen-binding protein (*e.g.*, antibody or fragment or polypeptide), the target protein is subjected to protease cleavage and mass spectrometry analysis, thereby revealing the deuterium-labeled residues which correspond to the specific amino acids with which the

antigen-binding protein interacts. See, *e.g.*, Ehring (1999) Analytical Biochemistry 267: 252-259; Engen and Smith (2001) Anal. Chem. 73: 256A-265A.

[0073] The term "epitope" refers to an antigenic determinant (*e.g.*, on C5) that interacts with a specific antigen-binding site in an antigen-binding protein, *e.g.*, variable region of an antibody molecule, known as a paratope. A single antigen may have more than one epitope. Thus, different antigen-binding proteins, *e.g.*, antibodies, may bind to different areas on an antigen and may have different biological effects. Epitopes, composed of non-contiguous amino acids, may be referred to as "conformational". A linear epitope contains only contiguous amino acids. In certain embodiments, epitopes may include determinants that are chemically active surface groupings of molecules such as amino acids, sugar side chains, phosphoryl groups, or sulfonyl groups, and, in certain embodiments, may have specific three-dimensional structural characteristics, and/or specific charge characteristics.

[0074] For example, the epitope to which antibody H4H12166P bins is defined by: (i) the amino acid sequence NMATGMDSW which corresponds to amino acids 591 to 599 in the beta chain included in SEQ ID NO: 1; and (ii) the amino acid sequence WEVHLVPRRKQLQFALPDSL, which corresponds to amino acids 775 to 794 comprised in the alpha chain included in SEQ ID NO: 1. See for example, PCT International Application No. PCT/US2017/037226. The C5 epitope of Eculizumab is disclosed in Brachet *et al.*, Eculizumab epitope on complement C5: Progress towards a better understanding of the mechanism of action. Mol Immunol. 2016 Sep; 77: 126-131.

[0075] The term "competes" as used herein, refers to an antigen-binding protein (*e.g.*, antibody or antigen-binding fragment thereof) that binds to an antigen and inhibits or blocks the binding of another antigen-binding protein (*e.g.*, antibody or antigen-binding fragment thereof) to the antigen. The term also includes competition between two antigen-binding protein *e.g.*, antibodies, in both orientations, *i.e.*, a first antibody that binds and blocks binding of second antibody and *vice versa*. In certain embodiments, the first antigen-binding protein (*e.g.*, antibody) and second antigen-binding protein (*e.g.*, antibody) may bind to the same epitope. Alternatively, the first and second antigen-binding proteins (*e.g.*, antibodies) may bind to different, but, for example, overlapping epitopes, wherein binding of one inhibits or blocks the binding of the second antibody, *e.g.*, via steric hindrance. Cross-competition between antigen-binding proteins (*e.g.*, antibodies) may be measured by methods known in the art, for example, by a real-time, label-free bio-layer interferometry assay. In an

embodiment of the invention, competition between a first and second anti-C5 antigen-binding protein (*e.g.*, antibody) is determined by measuring the ability of an immobilized first anti-C5 antigen-binding protein (*e.g.*, antibody) (not initially complexed with C5 protein) to bind to soluble C5 protein complexed with a second anti-C5 antigen-binding protein (*e.g.*, antibody). A reduction in the ability of the first anti-C5 antigen-binding protein (*e.g.*, antibody) to bind to the complexed C5 protein, relative to uncomplexed C5 protein, indicates that the first and second anti-C5 antigen-binding proteins (*e.g.*, antibodies) compete. The degree of competition can be expressed as a percentage of the reduction in binding. Such competition can be measured using a real time, label-free bio-layer interferometry assay, *e.g.*, on an Octet RED384 biosensor (Pall ForteBio Corp.), ELISA (enzyme-linked immunosorbent assays) or SPR (surface plasmon resonance).

[0076] Binding competition between anti-C5 antigen-binding proteins (*e.g.*, monoclonal antibodies (mAbs)) can be determined using a real time, label-free bio-layer interferometry assay on an Octet RED384 biosensor (Pall ForteBio Corp.). For example, to determine competition between two anti-human C5 monoclonal antibodies, the anti-C5 mAb can be first captured onto anti-hFc antibody coated Octet biosensor tips (Pall ForteBio Corp., # 18-5060) by submerging the tips into a solution of anti-human C5 mAb (subsequently referred to as "mAb1"). As a positive-control for blocking, the antibody captured biosensor tips can then be saturated with a known blocking isotype control mAb (subsequently referred to as "blocking mAb") by dipping into a solution of blocking mAb. To determine if mAb2 competes with mAb1, the biosensor tips can then be subsequently dipped into a co-complexed solution of human C5 polypeptide and a second anti-human C5 mAb (subsequently referred to as "mAb2"), that had been pre-incubated for a period of time and binding of mAb1 to the C5 polypeptide can be determined. The biosensor tips can be washed in buffer in between every step of the experiment. The real-time binding response can be monitored during the course of the experiment and the binding response at the end of every step can be recorded. mAb2-dependent inhibition of mAb1/C5 binding indicates competition between mAb1 and mAb2 for C5 binding. See *e.g.*, International Patent Application No. PCT/US2017/037226, filed June 13, 2017, *e.g.*, Example 5 therein.

[0077] In an embodiment of the invention, competition between antigen-binding proteins, such as antibodies, is determined under the conditions set forth in Example 5. For example, in an embodiment of the invention, the assay is conducted at 25°C and pH about 7.4, *e.g.*, in the presence of buffer (*e.g.*, HEPES), salt (*e.g.*, NaCl), surfactant (*e.g.*, Tween-20) and a

protein (*e.g.*, bovine serum albumin), *e.g.*, 0.01 M HEPES pH7.4, 0.15M NaCl, 0.05% v/v Surfactant Tween-20, 0.1mg/mL BSA (Octet HBS-P buffer) with the plate shaking at the speed of 1000 rpm.

[0078] Competition between anti-C5 antibodies set forth in International Patent Application No. PCT/US2017/037226 (WO2017/218515), filed June 13, 2017 is summarized below in Table 1. Accordingly, the present invention includes combinations comprising two anti-C5 antibodies or antigen-binding fragments thereof selected from Table 1 wherein the antibodies or fragments do not compete for C5 binding (*e.g.*, H4H12166P and H4H12168P; or H4H12166P and H4H12161P; or H4H12166P and H4H11686N).

Table 1. Competition between pairs of selected anti-C5 antibodies.

First mAb (mAb1) Captured using AHC Octet	mAb2 Antibodies Shown to Compete with mAb1
H4H12183P2	H4H12167P; H4H12166P; H4H12163P
H4H12167P	H4H12183P2; H4H12166P; H4H12163P
H4H12166P	H4H12183P2; H4H12167P; H4H12163P
H4H12163P	H4H12183P2; H4H12167P; H4H12166P
H4H12159P	H4H12169P; H4H11683N; H4H12170P
H4H12169P	H4H12159P; H4H11683N; H4H12170P
H4H11683N	H4H12159P; H4H12169P; H4H12170P
H4H12170P	H4H12159P; H4H12169P; H4H11683N
H4H12175P	H4H12177P2
H4H12177P2	H4H12175P

H4H12176P2	H4H12164P
H4H12164P	H4H12176P2
H4H12168P	none
H4H12161P	none
H4H11686N	none
H4H12171P	none

See WO2017/218515, Table 15.

Pharmaceutical Compositions and Administration

[0079] Combinations of the present invention (*e.g.*, H4H12166P and one of H4H12161P, H4H12170P, H4H12171P, H4H12175P, H4H12176P2 or H4H12177P2) include components that may be formulated into a single, common composition or into multiple/separate compositions. Moreover, separate compositions may be formulated with different varieties of carriers. For example, a first antigen-binding protein (*e.g.*, antibody or antigen-binding fragment thereof) that binds specifically to C5, which is part of a combination of the present invention, can be co-formulated into a single composition (*e.g.*, with a pharmaceutically acceptable carrier) with one or more further antigen-binding proteins (*e.g.*, antibodies or antigen-binding fragments thereof or polypeptides)(*e.g.*, coversin) that (i) specifically bind to C5 at an epitope which is different from that of the first antigen-binding protein (*e.g.*, antibody or fragment) and/or (ii) do not compete with the first antigen-binding protein (*e.g.*, antibody or fragment) for binding to C5. In embodiment of the invention, the first antigen-binding protein (*e.g.*, antibody or fragment) and the second antigen-binding protein (*e.g.*, antibody or fragment or polypeptide) are formulated into separate compositions (*e.g.*, with pharmaceutically acceptable carriers). A further therapeutic agent, in a combination of the present invention, may be formulated into yet another composition. A further therapeutic agent may be included in a combination of the present invention separately from the first antibody or fragment and the second antibody or fragment or polypeptide. In another embodiment of the invention, the further therapeutic agent is formulated into either the first antibody or fragment or the second antibody or fragment or polypeptide (or both).

[0080] To prepare pharmaceutical or sterile compositions comprising the components of the combinations of the present invention, the component(s) may be is admixed with a pharmaceutically acceptable carrier or excipient. See, *e.g.*, Remington's Pharmaceutical

Sciences and U.S. Pharmacopeia: National Formulary, Mack Publishing Company, Easton, Pa. (1984). Combinations including such compositions are part of the present invention.

[0081] The scope of the present invention includes combinations including one or more components in desiccated form, *e.g.*, freeze-dried, substantially lacking water.

[0082] Formulations may be prepared by mixing with acceptable carriers, excipients, or stabilizers in the form of, *e.g.*, lyophilized powders, slurries, aqueous solutions or suspensions (see, *e.g.*, Hardman, *et al.* (2001) Goodman and Gilman's The Pharmacological Basis of Therapeutics, McGraw-Hill, New York, NY; Gennaro (2000) Remington: The Science and Practice of Pharmacy, Lippincott, Williams, and Wilkins, New York, NY; Avis, *et al.* (eds.) (1993) Pharmaceutical Dosage Forms: Parenteral Medications, Marcel Dekker, NY; Lieberman, *et al.* (eds.) (1990) Pharmaceutical Dosage Forms: Tablets, Marcel Dekker, NY; Lieberman, *et al.* (eds.) (1990) Pharmaceutical Dosage Forms: Disperse Systems, Marcel Dekker, NY; Weiner and Kotkoskie (2000) Excipient Toxicity and Safety, Marcel Dekker, Inc., New York, NY).

[0083] If a combination of the present invention includes a further therapeutic agent that is administered to a subject, the further therapeutic agent may be is administered to the subject in accordance with the Physicians' Desk Reference (PDR), *e.g.*, Physicians' Desk Reference 2003 (Thomson Healthcare; 57th edition (Nov. 1, 2002)) and/or may formulated as described in the PDR.

[0084] The mode of administration of a combination or any of the components of a combination can vary. Routes of administration include oral, rectal, transmucosal, intestinal, parenteral; intramuscular, subcutaneous, intradermal, intramedullary, intrathecal, direct intraventricular, intravenous, intraperitoneal, intranasal, intraocular, inhalation, insufflation, topical, cutaneous, transdermal, or intra-arterial.

[0085] The present invention provides methods for administering a combination or component thereof comprising introducing the substance into the body of a subject. For example, the method comprises piercing the body of the subject with a needle of a syringe and injecting the combination or a component thereof into the body of the subject, *e.g.*, into the vein, artery, tumor, muscular tissue or subcutis of the subject.

[0086] The present invention provides a vessel (*e.g.*, a plastic or glass vial, *e.g.*, with a cap or a chromatography column, hollow bore needle or a syringe cylinder) comprising a combination of the present invention or one or more components thereof.

[0087] The present invention also provides an injection device comprising a one or more antigen-binding proteins (*e.g.,* antibody, antigen-binding fragment or polypeptide) from a combination of the present invention or a pharmaceutical composition thereof. For example, one antigen-binding protein (from a combination) may be in a first injection device and another antigen-binding protein (from the combination) may be in a second injection device; or both antigen-binding proteins (from the combination) may be in a common injection device. The injection device(s) may be (co-)packaged into a kit. An injection device is a device that introduces a substance into the body of a subject via a parenteral route, *e.g.*, intramuscular, subcutaneous or intravenous. For example, an injection device may be a syringe (*e.g.*, pre-filled with the pharmaceutical composition, such as an auto-injector) which, for example, includes a cylinder or barrel for holding fluid to be injected (*e.g.*, comprising the antibody or fragment or a pharmaceutical composition thereof), a needle for piecing skin and/or blood vessels for injection of the fluid; and a plunger for pushing the fluid out of the cylinder and through the needle bore. In an embodiment of the invention, an injection device that comprises an antigen-binding protein, *e.g.*, an antibody or antigen-binding fragment thereof, from a combination of the present invention, or a pharmaceutical composition thereof is an intravenous (IV) injection device. Such a device can include the antigen-binding protein or a pharmaceutical composition thereof in a cannula or trocar/needle which may be attached to a tube which may be attached to a bag or reservoir for holding fluid (*e.g.*, saline) introduced into the body of the subject through the cannula or trocar/needle. The antibody or fragment or a pharmaceutical composition thereof may, in an embodiment of the invention, be introduced into the device once the trocar and cannula are inserted into the vein of a subject and the trocar is removed from the inserted cannula. The IV device may, for example, be inserted into a peripheral vein (*e.g.*, in the hand or arm); the superior *vena cava* or inferior *vena cava*, or within the right atrium of the heart (*e.g.*, a central IV); or into a subclavian, internal jugular, or a femoral vein and, for example, advanced toward the heart until it reaches the superior vena cava or right atrium (*e.g.*, a central venous line). In an embodiment of the invention, an injection device is an autoinjector; a jet injector or an external infusion pump. A jet injector uses a high-pressure narrow jet of liquid which penetrate the epidermis to introduce the antibody or fragment or a pharmaceutical composition thereof to a subject's body. External infusion pumps are medical devices that deliver the antibody or fragment or a pharmaceutical composition thereof into a subject's body in controlled amounts. External infusion pumps may be

powered electrically or mechanically. Different pumps operate in different ways, for example, a syringe pump holds fluid in the reservoir of a syringe, and a moveable piston controls fluid delivery, an elastomeric pump holds fluid in a stretchable balloon reservoir, and pressure from the elastic walls of the balloon drives fluid delivery. In a peristaltic pump, a set of rollers pinches down on a length of flexible tubing, pushing fluid forward. In a multi-channel pump, fluids can be delivered from multiple reservoirs at multiple rates.

[0088] The present invention includes methods for treating a C5-associated disease or disorder (*e.g.*, PNH or aHUS) in a subject (*e.g.*, a human) in need thereof by administering (*e.g.*, parenterally), to the subject, a therapeutically effective amount of a combination comprising:

(1) a first antigen-binding protein (*e.g.*, antibody or antigen-binding fragment thereof) that binds specifically to C5 and one or more further antigen-binding proteins (*e.g.*, polypeptides (*e.g.*, coversin) or antibodies or antigen-binding fragments thereof) that (i) specifically bind to C5 at an epitope which is different from that of the first antigen-binding protein (*e.g.*, antibody or fragment) and/or (ii) does not compete with the first antigen-binding protein (*e.g.*, antibody or fragment) for binding to C5; or

(2) a multispecific antigen-binding protein (*e.g.*, antibody or antigen-binding fragment thereof) (*e.g.*, biparatopic anti-C5 IgG antibody) comprising two or more binding domains (*e.g.*, first and second binding domain) that bind to different epitopes of C5 wherein the first binding domain (i) specifically binds to C5 at an epitope which is different from that of the second binding domain and/or (ii) does not compete with the second binding domain for binding to C5;

optionally in association with a further therapeutic agent (*e.g.*, a corticosteroid) and/or procedure (*e.g.*, blood transfusion, *e.g.*, in a human subject suffering from PNH).

[0089] "Treat" or "treating" means to administer a combination of the present invention, to a subject having one or more symptoms of a C5-associated disease or disorder for which the combination is effective, *e.g.*, in the treatment of a subject having paroxysmal nocturnal hemoglobinuria (PNH) or atypical hemolytic uremic syndrome (aHUS), or being suspected of having PNH or aHUS. Typically, the combination is administered in an effective or therapeutically amount or dose (as discussed herein).

[0090] Guidance in selecting appropriate doses of combination of the present or a component thereof is available (see, *e.g.*, Wawrzynczak (1996) Antibody Therapy, Bios Scientific Pub. Ltd, Oxfordshire, UK; Kresina (ed.) (1991) Monoclonal Antibodies, Cytokines

and Arthritis, Marcel Dekker, New York, N.Y.; Bach (ed.) (1993) Monoclonal Antibodies and Peptide Therapy in Autoimmune Diseases, Marcel Dekker, New York, N.Y.; Baert *et al.* (2003) New Engl. J. Med. 348:601-608; Milgrom *et al.* (1999) New Engl. J. Med. 341:1966-1973; Slamon *et al.* (2001) New Engl. J. Med. 344:783-792; Beniaminovitz *et al.* (2000) New Engl. J. Med. 342:613-619; Ghosh *et al.* (2003) New Engl. J. Med. 348:24-32; Lipsky *et al.* (2000) New Engl. J. Med. 343:1594-1602).

[0091] An effective or therapeutically effective dose of anti-C5 antigen-binding protein (*e.g.*, antibody or antigen-binding fragment or polypeptide) in a combination of the invention for treating a C5-associated disease or disorder refers to the amount of the combination sufficient to alleviate one or more signs and/or symptoms of the disease or disorder (*e.g.*, an underlying cause such as complement activation) in the treated subject or population, whether by inducing the regression or elimination of such signs and/or symptoms or by inhibiting the progression of such signs and/or symptoms. The dose amount may vary depending upon the age and the size of a subject to be administered, target disease, conditions, route of administration, and the like. In an embodiment of the invention, an effective or therapeutically effective dose of antigen-binding protein (*e.g.*, antibody or antigen-binding fragment thereof) of a combination of the present invention, for treating or preventing a C5-associated disease or disorder, *e.g.*, in an adult human subject, is a single dose of about 0.1 to about 100 mg/kg body weight, *e.g.*, about 5 to about 80, *e.g.*, about 10 to about 70, or about 20 to about 50 mg/kg body weight. Depending on the severity of the condition, the frequency and the duration of the treatment can be adjusted. In certain embodiments, the antigen-binding protein (*e.g.*, antibody or antigen-binding fragment thereof) in a combination of the present invention can be administered as an initial dose of at least about 0.1 mg to about 800 mg, about 1 to about 600 mg, about 5 to about 500 mg, or about 10 to about 400 mg. In certain embodiments, the initial dose may be followed by administration of a second or a plurality of subsequent doses of the antigen-binding protein (*e.g.*, antibody or antigen-binding fragment thereof) in an amount that can be approximately the same or less than that of the initial dose, wherein the subsequent doses are separated by at least 1 day to 3 days; at least one week, at least 2 weeks; at least 3 weeks; at least 4 weeks; at least 5 weeks; at least 6 weeks; at least 7 weeks; at least 8 weeks; at least 9 weeks; at least 10 weeks; at least 12 weeks; or at least 14 weeks.

[0092] In an embodiment of the invention, coversin, in a combination of the present invention, is administered, for a first dose, at 0.57 mg/kg, followed by daily repeat maintenance doses wherein initial repeat dose is 25% of the ablating dose.

[0093] A "C5-associated" disease or disorder refers to a disease or disorder which is caused (directly or indirectly) by inflammation, cell injury and/or cell killing that is mediated by C5a and/or C5b.

[0094] A C5-associated disease or disorder includes atypical hemolytic uremic syndrome (aHUS). The present invention provides a method for treating or preventing aHUS or for inducing the regression or elimination or inhibiting the progression of at least one sign or symptom of aHUS such as:

- platelet activation;
- hemolysis;
- systemic thrombotic microangiopathy (formation of blood clots in small blood vessels throughout the body), *e.g.*, leading to stroke;
- heart attack;
- kidney failure (*e.g.*, leading to death);
- end-stage renal disease;
- permanent renal damage;
- abdominal pain;
- confusion;
- edema;
- fatigue;
- nausea/vomiting;
- diarrhea; and/or
- microangiopathic anemia,

in a subject in need thereof (*e.g.*, in a subject suffering from aHUS and suffering from one or more of such signs or symptoms) by administering a therapeutically effective amount of the combination to the subject.

[0095] A C5-associated disease or disorder includes paroxysmal nocturnal hemoglobinuria (PNH). The present invention provides a method for treating or preventing PNH or for inducing the regression or elimination or inhibiting the progression of at least one sign or symptom of PNH such as:

- destruction of red blood cells;
- thrombosis (*e.g.*, deep vein thrombosis and/or pulmonary embolism);
- intravascular hemolytic anemia;
- red discoloration of urine;
- anemia;
- tiredness;
- shortness of breath;
- heart palpitations;
- abdominal pain; and/or
- difficulty swallowing,

in a subject in need thereof (*e.g.*, in a subject suffering from aHUS and suffering from one or more of such signs or symptoms) by administering a therapeutically effective amount of the combination to the subject.

[0096] A C5-associated disease or disorder includes neurological disorders, renal disorders, multiple sclerosis, stroke, Guillain Barre Syndrome, traumatic brain injury, Parkinson's disease, disorders of inappropriate or undesirable complement activation, hemodialysis complications, hyperacute allograft rejection, xenograft rejection, interleukin-2 induced toxicity during IL-2 therapy, inflammatory disorders, inflammation of autoimmune diseases, Crohn's disease, adult respiratory distress syndrome, thermal injury including burns or frostbite, post-ischemic reperfusion conditions, myocardial infarction, capillary leak syndrome, obesity, diabetes, Alzheimer's disease, schizophrenia, stroke, epilepsy, atherosclerosis, vasculitis, bullous pemphigoid, C3 glomerulopathy, membraneproliferative glomerulonephritis, complement activation caused by balloon angioplasty, post-pump syndrome in cardiopulmonary bypass or renal bypass, complement activation caused by hemodialysis, renal ischemia, mesenteric artery reperfusion after aortic reconstruction, infectious disease or sepsis, immune complex disorders and autoimmune diseases, diabetic nephropathy, Alport's syndrome, progressive kidney failure, proteinuric kidney diseases, renal ischemia-reperfusion injury, lupus nephritis, glomerulopathy, rheumatoid arthritis, systemic lupus erythematosus (SLE), SLE nephritis, membranoproliferative nephritis, hemolytic anemia, neuromyelitis optica, renal transplant, inherited CD59 deficiency, psoriasis, and myasthenia gravis. The present invention includes methods for treating or preventing any of the foregoing C5-related diseases or disorders, in a subject, by

administering a therapeutically effective amount of a combination of the present invention to the subject in need thereof.

[0097] In certain other embodiments, the combinations of the present invention are useful for treating or preventing at least one symptom or indication of a C5-associated disease or disorder selected from the group consisting of lung disease and disorders such as dyspnea, hemoptysis, ARDS, asthma, chronic obstructive pulmonary disease (COPD), emphysema, pulmonary embolisms and infarcts, pneumonia, fibrogenic dust diseases, injury due to inert dusts and minerals (*e.g.*, silicon, coal dust, beryllium, and asbestos), pulmonary fibrosis, organic dust diseases, chemical injury (due to irritant gasses and chemicals, *e.g.*, chlorine, phosgene, sulfur dioxide, hydrogen sulfide, nitrogen dioxide, ammonia, and hydrochloric acid), smoke injury, thermal injury (*e.g.*, burn, freeze), asthma, allergy, bronchoconstriction, hypersensitivity pneumonitis, parasitic diseases, Goodpasture's Syndrome, pulmonary vasculitis, hereditary angioedema, and immune complex-associated inflammation. The present invention includes methods for treating or preventing any of the foregoing C5-related diseases or disorders, in a subject, by administering a therapeutically effective amount of a combination of the present invention to the subject in need thereof.

[0098] An ocular disease which is a C5-related disease or disorder includes, for example, age-related macular degeneration (AMD), diabetic macular edema (DME), diabetic retinopathy, ocular angiogenesis (ocular neovascularization affecting choroidal, corneal or retinal tissue), geographic atrophy (GA), uveitis and neuromyelitis optica. The present invention provides a method for treating or preventing an ocular disease or for inducing the regression or elimination or inhibiting the progression of at least one sign or symptom of an ocular disease such as:

- increased rate of loss of vision;
- drusen in the eye (*e.g.*, of a subject with dry AMD);
- loss of vision;
- gradual loss of central vision (*e.g.*, in subjects with non-exudative macular degeneration);
- visual distortion;
- difficulty adapting to low light levels;
- crooked central vision;
- haziness of central and/or overall vision;

- eye pigmentary changes;
- distorted vision (*e.g.*, metamorphopsia in which a grid of straight lines appears wavy and parts of the grid may appear blank);
- exudative changes (*e.g.*, hemorrhages in the eye, hard exudates, subretinal/sub-RPE/intraretinal fluid);
- slow recovery of visual function after exposure to bright light (*e.g.*, as determined in a photostress test);
- incipient and/or geographic atrophy;
- drastically decreasing visual acuity (*e.g.*, two levels or more, *e.g.*, 20/20 to 20/80);
- preferential hyperacuity perimetry changes (*e.g.*, in a subject with wet AMD);
- blurred vision;
- rapid onset of vision loss (*e.g.*, caused by leakage and bleeding of abnormal blood vessels in subjects with exudative macular degeneration);
- central scotomas (shadows or missing areas of vision);
- trouble discerning colors (*e.g.*, specifically dark colors from other dark colors and/or light colors from other light colors);
- loss in contrast sensitivity; and/or
- straight lines appear curved in an Amsler grid,

in a subject in need thereof (*e.g.*, in a subject suffering from an ocular disease and suffering from one or more of such signs or symptoms) by administering a therapeutically effective amount of the combination to the subject.

[0099] It is also contemplated herein to administer a therapeutically effective amount of a combination of the present invention prophylactically to subjects at risk for developing a C5-associated disease or disorder, *e.g.*, aHUS, PNH or macular degeneration, such as subjects over the age of 50, subjects with a family history of macular degeneration, smokers, and subjects with obesity, high cholesterol, cardiovascular disease, and/or unhealthy diet.

Combination Therapies

[00100] The present invention provides combinations comprising a first antigen-binding protein (*e.g.*, antibody or antigen-binding fragment thereof) that binds specifically to C5 and one or more further antigen-binding proteins (*e.g.*, polypeptides or antibodies or

antigen-binding fragments thereof) that (i) specifically bind to C5 at an epitope which is different from that of the first antigen-binding protein (*e.g.*, antibody or fragment) and/or (ii) does not compete with the first antigen-binding protein (*e.g.*, antibody or fragment) for binding to C5 (*e.g.*, H4H12166P and one of H4H12161P, H4H12170P, H4H12171P, H4H12175P, H4H12176P2 or H4H12177P2). Such combinations may further include one or more further therapeutic agents and/or one or more therapeutic methods. For example, the further therapeutic agent may be formulated into a single composition with one or more components of a combination of the present invention or formulated separately from one or both of the components. The present invention provides a method for treating or preventing a C5-associated disease or disorder or for treating or ameliorating at least one symptom or indication of such a disease or disorder in a subject in need thereof by administering a therapeutically effective amount of the combination to the subject, optionally in association with one or more further therapeutic agents.

[00101] In an embodiment of the invention, the further therapeutic agent is another anti-C5 antibody or antigen-binding fragment thereof which is not, itself a first or second/further antibody or fragment in the combination, such as for example, one or more antibodies or antigen-binding fragments thereof selected from H2M11683N; H2M11686N; H4H12159P; H4H12163P; H4H12164P; H4H12166P2; H4H12166P3; H4H12166P4; H4H12166P5; H4H12166P6; H4H12166P7; H4H12166P8; H4H12166P9; H4H12166P10; H4H12167P; H4H12168P; H4H12169P; H4H12176P2; H4H12177P2; H4H12183P2; H2M11682N; H2M11684N; H2M11694N; and H2M11695N- as set forth in International PCT patent application no. PCT/US2017/037226 (or a variant thereof; or an antigen-binding protein such as an antibody or antigen-binding fragment that comprises a heavy chain immunoglobulin including CDR-H1, CDR-H2 and CDR-H3; and a light chain immunoglobulin including CDR-L1, CDR-L2 and CDR-L3 of any of the foregoing antibodies) (which is not a first or second/further antibody or antigen-binding fragment in the combination).

[00102] Such a further therapeutic agent includes, for example, iron, antithymocyte globulin, a growth factor, an anti-coagulant (*e.g.*, warfarin, aspirin, heparin, phenindione, fondaparinux, idraparinux, and thrombin inhibitors such as argatroban, lepirudin, bivalirudin, or dabigatran) an anti-inflammatory drug (*e.g.*, corticosteroids, and non-steroidal anti-inflammatory drugs), an antihypertensive (*e.g.*, an angiotensin converting enzyme inhibitor), an immunosuppressive agent (*e.g.*, vincristine, cyclosporine A, or methotrexate), a

fibrinolytic agent (*e.g.*, ancrod, ε-aminocaproic acid, antiplasmin-a1, prostacyclin, and defibrotide), a lipid-lowering agent such as an inhibitor of hydroxymethylglutaryl CoA reductase (*e.g.*, atorvastatin), an anti-CD20 agent such as rituximab, an anti-TNFα agent such as infliximab, an anti-seizure agent (*e.g.*, magnesium sulfate), a C3 inhibitor, an anti-thrombotic agent, avacopan (CCX168; CAS#: 1346623-17-3), ravulizumab or zimura (avacincaptad pegol; CAS # 1491144-00-3).

[00103] In an embodiment of the invention, the further therapeutic agent is an agent that inhibits an activity of C5; or C5 cleavage into C5a and C5b; or C5 expression. In an embodiment of the invention, the further therapeutic agent is C5 RNAi molecule or a polypeptide that binds to C5, *e.g.*, a monoclonal antibody or peptide (*e.g.*, cyclic peptide).

[00104] A further therapeutic agent that is administered to a subject in association with anti-C5 antibodies or antigen-binding fragments or polypeptides are, in an embodiment of the invention, administered to the subject in accordance with the Physicians' Desk Reference, *e.g.*, Physicians' Desk Reference 2003 (Thomson Healthcare; 57th edition (Nov. 1, 2002)).

[00105] The further therapeutic agent may be administered to a subject sequentially or simultaneously with administration of the components of the combinations of the invention. “Simultaneous” administration refers to the administration (*e.g.*, injection) of two or more substances in a single, common formulation or in separate formulations which are administered during the same treatment session. “Sequential” administration refers to administration of two or more substances during separate treatment sessions (substantially separated by time). For example, a first component may be deemed to be administered, in an sequential administration regimen, "prior to" a second component *e.g.*, wherein the first component is administered 1 week before, 72 hours before, 60 hours before, 48 hours before, 36 hours before, 24 hours before, 12 hours before, 6 hours before, 5 hours before, 4 hours before, 3 hours before, 2 hours before, 1 hour before, or 30 minutes before administration of the second component. In other embodiments, the additional therapeutically active component(s) may be administered to a subject after administration of an anti-C5 antibody of the present invention.

[00106] In an embodiment of the invention, the subject is further administered a therapeutic procedure, *e.g.*, directed to the treatment of a C5-associated disease or

disorder such as PNS or aHUS, *e.g.*, dialysis, a blood or plasma transfusion or exchange and/or a bone marrow/stem cell transplant (BMT/SCT).

[00107] The present invention includes multispecific or multiparatopic antigen-binding proteins, as discussed herein, in association with a further therapeutic agent, e.g., as discussed herein (*e.g.*, pharmaceutical compositions or kits thereof) as well as methods of using such proteins to treat or prevent a C5-associated disease or disorder, e.g., as discussed herein.

Kits

[00108] The present invention provides kits comprising one or more components of a combination of the present invention, optionally, in association with one or more further therapeutic agents, *e.g.*, as discussed herein (*e.g.*, H4H12166P and one of H4H12161P, H4H12170P, H4H12171P, H4H12175P, H4H12176P2 or H4H12177P2). In one embodiment of the invention, the kit includes an anti-C5 antigen-binding protein (*e.g.*, antibody or antigen-binding fragment thereof) of the invention or a pharmaceutical composition thereof in one device (*e.g.*, pre-filled syringe) or container (*e.g.*, in a sterile glass or plastic vial) and another anti-C5 antigen-binding protein (*e.g.*, antibody or antigen-binding fragment) of the invention or a pharmaceutical composition thereof in another device (*e.g.*, pre-filled syringe) or container (*e.g.*, in a sterile glass or plastic vial).

[00109] In another embodiment, the kit comprises a combination of the invention, including two or more anti-C5 antigen-binding proteins (*e.g.*, antibodies or antigen-binding fragments) or a pharmaceutical composition thereof in a single, common container or device.

[00110] If the kit includes a pharmaceutical composition for parenteral administration to a subject, the kit can include a device for performing such administration. For example, the kit can include one or more hypodermic needles or other injection devices as discussed above. Thus, the present invention includes a kit comprising an injection device and one or more anti-C5 antigen-binding protein (*e.g.*, antibodies or antigen-binding fragments thereof) of the present invention, *e.g.*, wherein the injection device includes the antibody or fragment or wherein the antibody or fragment is in a separate vessel.

[00111] The kit can include a package insert including information concerning the pharmaceutical compositions and dosage forms in the kit. Generally, such information aids patients/ subjects and physicians in using the enclosed pharmaceutical compositions and

dosage forms effectively and safely. For example, the following information regarding a combination of the invention may be supplied in the insert: pharmacokinetics, pharmacodynamics, clinical studies, efficacy parameters, indications and usage, contraindications, warnings, precautions, adverse reactions, overdosage, proper dosage and administration, how supplied, proper storage conditions, references, manufacturer/distributor information and patent information.

[00112] The present invention includes methods for making a kit comprising a combination of the present invention. Such a method includes the steps of co-packaging the first anti-C5 antigen-binding protein (*e.g.*, antibody or antigen-binding fragment); with the one or more of said further antigen-binding proteins (*e.g.*, polypeptides, antibodies or antigen-binding fragments) into a kit. The method optionally includes the step of including one or more further therapeutic agents and/or other materials (*e.g.*, as discussed herein) in the kit.

EXAMPLES

[00113] The following examples are put forth so as to provide those of ordinary skill in the art with a complete disclosure and description of how to make and use the methods and compositions of the invention, and are not intended to limit the scope of what the inventors regard as their invention. Efforts have been made to ensure accuracy with respect to numbers used (*e.g.*, amounts, temperature, *etc.*) but some experimental errors and deviations should be accounted for. Unless indicated otherwise, parts are parts by weight, molecular weight is average molecular weight, temperature is in degrees Centigrade, room temperature is about 25°C, and pressure is at or near atmospheric. Any antibody combination or multispecific antibody set forth herein forms part of the present invention.

[00114] Example 1: Dual, but not single, anti C5 mAb treatment achieves complete inhibition of alternative complement pathway activation.

[00115] The ability of various anti-C5 antibodies, individually or in combination with other agents and under various conditions, to inhibit hemolysis was investigated.

Materials and Methods

[00116] ***Alternative pathway hemolysis assay***. Alternative pathway hemolysis assay was used as the measure of complement activation to evaluate the ability of anti-C5 mAbs to block the lysis of rabbit red blood cells (RbRBCs). Lysis of rabbit red blood cells by membrane attack complex is the basis of the assay by which complement activation is experimentally measured.

[00117] A desired number of RbRBCs are washed in GVB-Mg^{2+}/EGTA buffer and re-suspended at 2x10^8 cells/ml. To test the efficacy of either single anti-C5 mAb or a combination of anti-C5 mAbs, normal human serum was diluted to 50-96% in GVB-Mg^{2+}/EGTA buffer to achieve a final concentration of 25-48% when added to RBC. Round bottom 96 well plates were used to measure hemolysis activity. A total of 100ul RbRBCs (2x10^8 cells/ml) were plated into 96-well plate at 37°C followed by addition of 100ul of diluted serum. Cells were gently mixed and incubated at 37°C for 30-120 minutes. After incubation time, the cells were spun down by centrifugation at 1250 x g at 4°C. A total of 100uL of the supernatant was transferred to a fresh 96 flat bottom plate and read at 412nm on a Spectramax microplate reader. The calculation of percent of hemolysis was done as described below.

[00118] The percentage of hemolysis was calculated with the absorbance values by using the following equation:

$$\%Hemolysis = 100 \times \frac{(Experimental\ Cell\ Lysis - Background\ Cell\ Lysis)}{(Maximum\ Cell\ Lysis - Background\ Cell\ Lysis)}$$

[00119] In this equation "background cell lysis" was the OD at A412nm from the cells incubated in GVB-Mg^{2+}/EGTA buffer only containing no serum. The "maximum cell lysis" was the OD at A412nm from the cells treated with water. Maximum inhibition of lysis was calculated as a difference between bottom and top values in the curve expressed as a percentage of top value. Data was represented as mean ± Standard error of mean.

[00120] ***Anti-C5 monoclonal antibodies tested***. A panel of 12 anti-C5 mAbs were tested, which included H4H12166P, H4H12170P, H4H12171P, H4H12175P, H4H12177P2, H4H12176P2, H4H12161P, H4H12183P2, H4H12159P, H4H12164P, H4H12167P, and H4H12163P. A Fab version of H4H12170P was also evaluated in the assay.

Results

[00121] ***H4H12166P in combination with other anti-C5 mAbs completely block hemolysis of RbRBCs via alternative pathway activation.*** As shown in Figure 1A and Table 2A, under standard assay conditions of 25% NHS (normal human serum) and 30 min incubation time, all single mAb treatments plateaued at around 80% inhibition (or less) of AP hemolysis. When used in a 1:1 molar ratio with H4H12166P, however, all combos blocked AP hemolysis down to essentially zero (Figure 2B and Table 2B).

Table 2A. Red blood cell lysis in the presence of single antibodies.

Antibody	% Max Inh. of Lysis
H4H12166P	81.25
H4H12170P	88.66
H4H12161P	59.24
H4H12171P	36.63
H4H12175P	77.83
H4H12176P2	62.80
H4H12177P2	76.21

Table 2B. Red blood cell lysis in the presence of antibody combinations.

Antibody Combinations	% Max Inh. of Lysis
H4H12166P + H4H12170P	97.59
H4H12166P + H4H12161P	98.11
H4H12166P + H4H12171P	98.16
H4H12166P + H4H12175P	98.10

H4H12166P + H4H12176P2	97.29
H4H12166P + H4H12177P2	98.14

[00122] ***Inhibition with combination anti-C5 mAbs persists at high serum concentrations or longer incubation times.*** Increasing incubation time from 30 min to 120 min (Figure 2A and Table 3A) or serum concentration from 25% to 48% (120 minute incubation) (Figure 2B and Table 3B) both significantly decreased the efficacy of inhibition by single mAbs. However, H4H12166P, in combination with H4H12161P, was still able to fully block AP hemolysis despite higher serum concentrations or longer incubation times, demonstrating that blockade was robust and complete.

Table 3A. Red blood cell lysis in the presence of antibodies incubated for 30 or 120 minutes.

Antibodies	% Max Inh. of Lysis	
	30 min	120 min
H4H12166P	82.79	57.21
H4H12161P	59.24	43.55
H4H12166P + H4H12161P	98.11	98.05

Table 3B. Red blood cell lysis in the presence of antibodies and 25 or 48% serum.

Antibodies	% Max Inh. of Lysis	
	25% NHS 120 min	48% NHS 120 min
H4H12166P	57.21	30.00

H4H12161P	**43.55**	**17.37**
H4H12166P + H4H12161P	**98.05**	**96.26**

[00123] ***Combo effect is also observed with a Fab not just mAbs, also is not dependent on H4H12166P, but requires the combination mAbs from different epitope bins.*** A Fab version of H4H12170P when used in a 2:1 molar ratio with H4H12166P, also achieved complete blockade at both 30 min and 120 min incubation times (Figure 3 and Table 4). Next, whether H4H12166P was required for the observed combination effect was tested. As shown in Figure 4 and Table 5, a different combination of antibodies, H4H12176P2 and H4H12177P2, also offered complete blockade of RbRBC hemolysis *via* alternative pathway showing the combination effect was independent of H4H12166P. However, as shown in Figure 5, the maximal inhibition of hemolysis was not observed when testing combination mAbs from the same epitope bins (H4H12170P + H4H12159P, H4H12175P + H4H12177P2, H4H12176P2 + H4H12164P, H4H12167P + H4H12163P) demonstrating that different binding sites were required for this observed effect.

Table 4. Red blood cell lysis in the presence of a Fab version of H4H12170P when used in a 2:1 molar ratio with H4H12166P.

Antibodies	% Max Inh. of Lysis	
	30 min	120 min
H4H12166P	**65.88**	**42.31**
H4H12170P	**76.42**	**36.19**
H4H12166P 8 + H4H12170P	**98.14**	**98.10**

Table 5. Red blood cell lysis in the presence of H4H12176P2 and/or H4H12177P2

Antibodies	% Max Inh. of Lysis
H4H12176P2	61.88
H4H12177P2	75.12
H4H12176P2 + H4H12177P2	98.05

[00124] ***Addition of C3 led to decreased blockade effect of single anti-C5, but not, combination mAbs.*** At 1 μM concentration with H4H12166P or H4H12161P mAbs, the addition of surplus human C3 protein resulted in partial recovery of AP activity in the single but not combination mAb condition, suggesting that addition of C3 overcame the effect of single, but not, combination of anti-C5 mAbs (Figure 6).

[00125] ***Inhibition with combination anti-C5 mAbs does not cause more suppression of C5a generation compared to single anti-C5 mAb.*** As shown in Figure 7, the blockade effects on C5a generation does not appear to be different between single (H4H12166P or H4H12161P) and combination anti-C5 mAbs (H4H12166P + H4H12161P).

Example 2: A C5 bispecific antibody achieves complete inhibition of alternative complement pathway activation similar to combination of anti-C5 mAbs

Alternative pathway hemolysis assay was used as the measure of complement activation to evaluate the ability of anti-C5 mAbs to block the lysis of rabbit red blood cells (RbRBCs). Lysis of rabbit red blood cells by membrane attack complex is the basis of the assay by which complement activation is experimentally measured.

A desired number of RbRBCs were washed in GVB-Mg^{2+}/EGTA buffer and resuspended at $2x10^8$ cells/ml. To test the efficacy of either single anti-C5 mAb or a combination of anti-C5 mAbs, normal human serum was diluted to 50-96% in GVB-Mg^{2+}/EGTA buffer to achieve a final concentration of 25-48% when added to RBC. Round bottom 96 well plates were used to measure hemolysis activity. A total of 100 ul RbRBCs ($2x10^8$ cells/ml) were plated into 96-well plate at 37°C followed by addition of 100 ul of diluted serum. Cells were gently mixed and incubated at 37°C for 30-120 minutes. After incubation time, the cells were spun down by centrifugation at 1250xg at 4°C. A total of 100

uL of the supernatant was transferred to a fresh 96 flat bottom plate and read at 412 nm on a Spectramax microplate reader. The calculation of percent of hemolysis was done as described below.

The percentage of hemolysis was calculated with the absorbance values by using the following equation:

$$\%Hemolysis = 100 \times \frac{(Experimental\ Cell\ Lysis - Background\ Cell\ Lysis)}{(Maximum\ Cell\ Lysis - Background\ Cell\ Lysis)}$$

In this equation, "background cell lysis" was the OD at A_{412nm} from the cells incubated in GVB-Mg^{2+}/EGTA buffer only containing no serum. The "maximum cell lysis" was the OD at A_{412nm} from the cells treated with water. Maximum inhibition of lysis was calculated as a difference between bottom and top values in the curve expressed as a percentage of top value. Data are represented as mean $\pm$ Standard error of mean.

For the experiments to examine the molar ratio of mAb/C5, a fixed concentration of 125 or 145 nM of C5 (purchased from CompTech Inc.) was added to the C5-deficient normal human serum (purchased from CompTech Inc.) and titrated against various concentration of antibodies before testing in alternative pathway hemolysis assay.

Anti-C5 monoclonal antibodies tested:

- H412176P2
- H412177P2
- A bispecific antibody made from H412176P2 and H412177P2 ("H412176P2xH412177P2")

H412176P2xH412177P2, *a C5 bispecific antibody, completely blocked hemolysis of RbRBCs via alternative pathway activation.* As shown in Figure 8 and Table 6, under standard assay conditions of 25% NHS and 30 min incubation times, a single mAb treatment of H412176P2 or H412177P2 led to partial inhibition of AP hemolysis. When used in a 1:1 molar ratio, a combination of H412176P2 + H412177P2, however, blocked AP hemolysis down to essentially zero. H412176P2xH412177P2, a bispecific antibody made from the heavy and light Ig chains of H412176P2 and H412177P2, also showed complete suppression of AP hemolysis similar to the combination of mAbs.

Table 6. Percentage of lysis inhibition

ABPID	% Max Inh. of Lysis
H4H12176P2	27.45
H4H12177P2	42.65
H4H12176P2 + H4H12177P2	98.10
H412176P2xH412177P2	98.06

Near molar equivalent of combination of antibodies or C5-bispecific is enough to completely block hemolysis of RbRBCs via alternative pathway activation. As shown in Figure 9, a mAb/C5 ratio of about 1.29 of either combination mAbs (H412176P2 + H412177P2) or C5 bispecific (H412176P2xH412177P2) blocked hemolysis to close to zero. Individual mAbs at this ratio, or even above, offered only partial inhibition. Further experiments with H412176P2xH412177P2 showed a mAb/C5 ratio between 1.0-1.5 completely blocked alternative pathway hemolysis assay (Figure 10A and 10B).

Example 3: Size analysis of *in vitro* complexes formed between hC5 and anti-hC5 monoclonal antibodies (mAbs) by asymmetrical flow field-flow fractionation coupled to multi-angle laser light scattering (A4F-MALLS)

The A4F-MALLS system is composed of an Eclipse™ 3+ A4F Separation System coupled to an Agilent 1200 Series HPLC system equipped with a ultraviolet (UV) diode array detector, Wyatt Technology Dawn HELEOS® II laser light scattering instrument (LS), and an Optilab® T-rEX differential refractometer (RI) detector. The detectors were connected in series in the following order: UV-LS-RI. LS and RI detectors were calibrated according to instructions provided by Wyatt Technology.

Defined amounts of anti-hC5 mAbs were each combined with human complement C5 (hC5; EMD Millipore) and diluted in 1X DPBS, pH 7.4 to yield the final molar ratios listed in Table 7. All samples were incubated at ambient temperature for 2 hours and maintained unfiltered at 4°C prior to injection into an Eclipse™ short channel fitted with a W350 spacer foil (350 µm spacer thickness, 2.2 cm spacer width) and using a 10 kDa MWCO Nadir regenerated cellulose membrane. The channel was pre-equilibrated with the mobile phase

buffer (10 mM sodium phosphate, 500 mM sodium chloride, pH 7.0 ± 0.1), prior to the injection of each sample. Bovine serum albumin (BSA; 2 mg/mL; 10 µg sample load) was injected separately and included as a system suitability control.

The fractionation method consisted of four steps: injection, focusing, elution, and a channel "wash-out" step. The A4F-MALLS mobile phase buffer (10 mM sodium phosphate, 500 mM sodium chloride, pH 7.0 ± 0.1) was used throughout the fractionation method. Each sample (7 µg total protein load) was injected at a flow rate of 0.2 mL/min for 1 min and subsequently focused for 2 min with a focus flow rate of 1.5 mL/min. The sample was eluted with a channel flow rate of 1.0 mL/min and a linear gradient cross flow from 3.0 mL/min to 0 mL/min over 45 min. Finally, the cross flow was held at 0 mL/min for an additional 5 min to wash out the channel. BSA was fractionated using the same parameter settings.

Table 7. Concentrations of Each Component for Sample Preparation

Sample	mAb1:mAb2:hC5 Molar Ratio (µM: µM: µM)	Figure	Table
H4H12166P:hC5	1:1	11	9
H4H12166P: H4H12175P:hC5	0.5:0.5:1	12	10
H4H12166P: H4H12177P2:hC5	0.5:0.5:1	12	10
H4H12166P: H4H12161P:hC5	0.5:0.5:1	13	10
H4H12166P: H4H12176P2:hC5	0.5:0.5:1	13	10
H4H12176P2: H4H12177P2:hC5	0.5:0.5:1	13	10
H4H12166P: H4H12170P:hC5	0.5:0.5:1	14	10
H4H12166P: H4H12171P:hC5	0.5:0.5:1	15	10
H4H12176P2xH4H12177P2 bispecific Ab:hC5	3:1	16	11
H4H12176P2xH4H12177P2 bispecific Ab:hC5	1:1	16	11
H4H12176P2xH4H12177P2 bispecific Ab:hC5	1:3	16	11

A4F-MALLS Data Analysis. Data were analyzed using ASTRA V software (version 5.3.4.14, Wyatt Technology). The data were fit to the equation that relates the excess scattered light to the solute concentration and weight-average molar mass, Mw, (Kendrick BS, Kerwin BA, Chang BS, Philo JS. (2001). Anal Biochem. 299(2), 136- 46, "Online Size-Exclusion High-

Performance Liquid Chromatography Light Scattering and Differential Refractometry Methods to Determine Degree of Polymer Conjugation to Proteins and Protein-Protein or Protein-Ligand Association States"; Wyatt, PJ. (1993) Anal. Chim. Acta 272(1), 1-40, "Light Scattering and the Absolute Characterization of Macromolecules"):

Equation 1: $$\frac{K^* c}{R(\theta,c)} = \frac{1}{MwP(\theta)} + 2A_2 c$$

where c is the solute concentration, R(θ,c) is the excess Raleigh ratio from the solute as a function of scattering angle and concentration, Mw is the molar mass, P(θ) describes the angular dependence of scattered light (~1 for particles with radius of gyration < 50 nm), A_2 is the second virial coefficient in the expansion of osmotic pressure (which can be neglected since measurements are performed on dilute solutions) and K* is defined by Equation 2:

Equation 2: $$K^* = \frac{4\pi^2 n_0^2}{N_A \lambda_0^4}\left(\frac{dn}{dc}\right)^2$$

where n_o represents the solvent refractive index, N_A is Avogadro's number, λ_0 is the wavelength of the incident light in a vacuum, and dn/dc represents the specific refractive index increment for the solute.

The normalization coefficients for the light scattering detectors, inter-detector delay volume and band broadening terms were calculated from the BSA chromatograms collected for the A4F-MALLS condition employed. These values were applied to the data files collected for all other samples to correct for these terms.

The dn/dc value and the extinction coefficient at 215 nm (corrected for glycosylation) were experimentally determined using the protein conjugate analysis provided in the Astra software. The corrected extinction coefficient and dn/dc value was used to analyze all protein-protein complex samples. The molar mass of BSA monomer served to evaluate the calibration constants of the light scattering and differential refractive index detectors during data collection (system suitability check). The relative standard deviation of the average molar mass of BSA determined from the UV and RI detectors was ≤ 5.0%.

A4F-MALLS was used to assess the relative size distribution of complexes formed between anti-hC5 antibodies and hC5. The theoretical molar mass of potential mAb:hC5 complexes along with their predicted stoichiometry is provided in Table 8.

Initial screening of anti-hC5 mAb combinations highlight differences in size distribution of complexes formed with hC5. In the absence of secondary mAbs, H4H12166P formed canonical 1:1 and 1:2 complexes with hC5 when mixed in equimolar amounts (Figure 11, Table 9).

Overall, all mAb combinations examined exhibited the ability to form heteromeric complexes with hC5, with most combinations favoring a smaller, discrete species consistent with a 2:2 mAb:hC5 heteromeric complex under the conditions tested (Peak 1, Figures 12 and 13; Table 10). Although minor amounts of larger, discrete complexes could also be detected in these samples (Peak 2), formation of very large, heterogeneous, extended antibody-antigen lattices (≥ ~1500 kDa; Peaks 3-4) – a process termed "paper-dolling" – was limited. In contrast, combinations of H4H12166P with H4H12170P favored larger, more heterogeneous complexes with hC5 indicative of a higher degree of "paper-dolling" compared to other combinations tested (Figure 14; Table 10). Finally, combinations of H4H12166P and H4H12171P displayed a reduced tendency to form heteromeric complexes with hC5 as evidenced by the presence of free mAb and 1:1 mAb:hC5 homomeric complex (*) detected in this sample (Figure 15; Table 10). This may suggest that the binding of one mAb influences the affinity (and/or off-rate) of the other for hC5 in this combination. Alternatively, this may indicate a reduced stability of the heteromeric complexes in this sample during the fractionation process compared to the other combinations tested.

Analysis of complexes formed between H412176P2xH412177P2 *(bispecific anti-hC5 mAb) and hC5 revealed a stable 1:1* H412176P2xH412177P2*:hC5 complex was favored under all conditions.* When mixed at various molar ratios, H412176P2xH412177P2 bispecific antibody predominantly forms a stable 1:1 complex with hC5 suggesting that both arms of the H412176P2xH412177P2 prefer to engage a single molecule of hC5 – termed a monogamous, bivalent interaction (Figure 16; Table 11). While minor amounts of additional discrete complexes consistent with 1:2, 2:1, and 2:2 mAb:hC5 could be detected under various conditions, no additional higher order complexes were observed indicating that H412176P2xH412177P2 does not promote "paper-dolling" with hC5.

Table 8. Theoretical Molar Mass of mAb:hC5 Complexes

mAb:hC5 Complex	Theoretical Molar Mass (kDa)
1:0	150
0:1	195
1:1	345
2:1	495
1:2	540
2:2	690
3:2	840
2:3	885
3:4	1230
4:4	1380
5:5	1725
6:5	1875
5:6	1920
6:6	2070

Table 9.Summary Table of Approximate Molar Mass and Retention Time of hC5 Complexes with H4H12166P Alone

Sample	Molar Ratio (µM: µM)	Peak 1		Peak 2	
		$[mAb]_1$: $[hC5]_1$ Complex		$[mAb]_1$: $[hC5]_2$ Complex	
		R_t, min	M_w, kDa	R_t, min	M_w, kDa
H4H12166P:hC5	1:1	13.7	341.1	15.3	498.7

R_t: Retention Time; M_w: weight average molar mass; min:minutes; kDa: kiloDaltons;

Table 10. Summary Table of Approximate Molar Mass and Retention Time of hC5 Complexes with Anti-hC5 mAb Combinations

Sample	Molar Ratio (μM: μM:μM)	Peak 1		Peak 2		Peak 3		Peak 4	
		$[mAb]_{1-2}$: $hC5]_2$ Complex		$[mAb]_{3-4}$: $[hC5]_4$ Complex		$[mAb]_{5-6}$: $[hC5]_{5-6}$ Complex		Higher Order Heteromeric Complexes ($[mAb]_{\geq 7}$: $[hC5]_{\geq 7}$)	
		R_t, min	M_w, kDa	R_t, min	M_w, kDa	R_t, min	M_w, kDa	R_t, min	M_w, kDa
H4H12166P:H4H12175P: hC5	0.5:0.5:1	16.0	684.4	18.5	1342.4	20.1	1876.0	21.5	~2250-3560
H4H12166P:H4H12177P2: hC5	0.5:0.5:1	16.1	687.7	18.5	1327.4	20.1	1865.6	21.5	~2380-4250
H4H12166P:H4H12161P: hC5	0.5:0.5:1	16.4	684.7	18.4	1261.8	NA	NA	20.2	~1700-2700
H4H12166P:H4H12176P2: hC5	0.5:0.5:1	15.7	685.9	17.7	1319.8	19.4	1849.8	20.6	~2300-3800
H4H12176P2:H4H12177P2: hC5	0.5:0.5:1	15.8	687.7	17.8	1333.8	19.3	1871.6	20.6	~2300-3600
H4H12166P:H4H12170P: hC5	0.5:0.5:1	15.5	664.8	19.2	1304.3	21.9	1901.1	23.6	~2300-4100
H4H12166P:H4H12171P: hC5	0.5:0.5:1	15.9	649.6	19.1	1288.2	ND	ND	20.6	~1700-2300

R_t: Retention Time; M_w: weight average molar mass; min:minutes; kDa: kiloDaltons; ND: not detected

Table 11. Summary Table of Approximate Molar Mass and Retention Time of hC5 Complexes with H412176P2xH412177P2 (Anti-hC5 Bispecific mAb)

Sample	Molar Ratio (μM: μM)	Peak 1		Peak 2		Peak 3		Peak 4	
		$[mAb]_1$: $[hC5]_1$ Complex		$[mAb]_2$: $[hC5]_1$ Complex		$[mAb]_1$: $[hC5]_2$ Complex		$[mAb]_2$: $[hC5]_2$ Complex	
		R_t, min	M_w, kDa	R_t, min	M_w, kDa	R_t, min	M_w, kDa	R_t, min	M_w, kDa
H412176P2xH412177P2: hC5	3:1	11.2	359.3	11.9	506.5	N/A	N/A	N/A	N/A
H412176P2xH412177P2: hC5	1:1	11.2	347.2	ND	ND	N/A	N/A	12.3	681.3
H412176P2xH412177P2: hC5	1:3	11.1	350.9	N/A	N/A	12.2	559.5	ND	ND

R_t: Retention Time; M_w: weight average molar mass; min:minutes; kDa: kiloDaltons; ND: not detected

CLAIMS

1. A combination comprising a first antibody or antigen-binding fragment thereof that binds specifically to C5, and a second antibody or antigen-binding fragment thereof that binds specifically to C5, wherein:

(i) the first antibody or antigen-binding fragment thereof binds specifically to C5 at a first epitope, and the second antibody or antigen-binding fragment thereof binds specifically to C5 at a second epitope which is different from the first epitope and/or

(ii) the first antibody or antigen-binding fragment thereof and the second antibody or antigen-binding fragment thereof do not compete for binding to C5;

wherein the first antibody or antigen-binding fragment thereof comprises a heavy chain variable region (V_H) comprising three heavy chain complementarity determining regions (CDRs) (CDR-H1, CDR-H2, and CDR-H3) of a heavy chain variable region V_H that comprises the amino acid sequence set forth in SEQ ID NO: 87, and a light chain variable region (V_L) comprising three light chain CDRs (CDR-L1, CDR-L2, and CDR-L3) of a V_L that comprises the amino acid sequence set forth in SEQ ID NO: 95; and

the second antibody or antigen-binding fragment thereof comprises a V_H comprising CDR-H1, CDR-H2, and CDR-H3 of a V_H that comprises the amino acid sequence set forth in SEQ ID NO: 103, and a V_L comprising CDR-L1, CDR-L2, and CDR-L3 of a V_L that comprises the amino acid sequence set forth in SEQ ID NO: 95.

2. The combination of claim 1, wherein:

(i) the first antibody or antigen-binding fragment thereof comprises:

a V_H comprising CDR-H1 comprising the amino acid sequence set forth in SEQ ID NO: 89, CDR-H2 comprising the amino acid sequence set forth in SEQ ID NO: 91, and CDR-H3 comprising the amino acid sequence set forth in SEQ ID NO: 93; and

a V_L comprising CDR-L1 comprising the amino acid sequence set forth in SEQ ID NO: 97, CDR-L2 comprising the amino acid sequence set forth in SEQ ID NO: 99, and CDR-L3 comprising the amino acid sequence set forth in SEQ ID NO: 101; and

(ii) the second antibody or antigen-binding fragment thereof comprises:

a V_H comprising CDR-H1 comprising the amino acid sequence set forth in SEQ ID NO: 105, CDR-H2 comprising the amino acid sequence set forth in SEQ ID NO: 107, and CDR-H3 comprising the amino acid sequence set forth in SEQ ID NO: 109; and

a V_L comprising CDR-L1 comprising the amino acid sequence set forth in SEQ ID NO: 97, CDR-L2 comprising the amino acid sequence set forth in SEQ ID NO: 99, and CDR-L3 comprising the amino acid sequence set forth in SEQ ID NO: 101.

3. The combination of claim 1 or 2, wherein:

the first antibody or antigen-binding fragment thereof comprises a V_H that comprises the amino acid sequence set forth in SEQ ID NO: 87, and a V_L that comprises the amino acid sequence set forth in SEQ ID NO: 95; and

the second antibody or antigen-binding fragment thereof comprises a V_H that comprises the amino acid sequence set forth in SEQ ID NO: 103, and a V_L that comprises the amino acid sequence set forth in SEQ ID NO: 95.

4. The combination of any one of claims 1-3, wherein the first antibody or antigen-binding fragment thereof is an IgG4 (S228P) antibody, and the second antibody or antigen-binding fragment thereof is an IgG4 (S228P) antibody.

5. The combination of any one of claims 1-4, wherein the first antibody or antigen-binding fragment thereof and the second antibody or antigen-binding fragment thereof are formulated in a single composition.

6. The combination of any one of claims 1-5, comprising a further therapeutic agent.

7. The combination of claim 6, wherein the further therapeutic agent is an antibody or antigen-binding fragment that specifically binds to C5.

8. The combination of claim 6, wherein the further therapeutic agent is an antibody that specifically binds to C5, an anti-coagulant, a thrombin inhibitor, an anti-inflammatory drug, an antihypertensive, an immunosuppressive agent, a fibrinolytic agent, a lipid-lowering agent, an

inhibitor of hydroxymethylglutaryl CoA reductase, an anti-CD20 agent, an anti-TNFα agent, an anti-seizure agent, a C3 inhibitor, or an anti-thrombotic agent.

9. The combination of claim 6, wherein the further therapeutic agent is selected from: warfarin, aspirin, heparin, phenindione, fondaparinux, idraparinux, argatroban, lepirudin, bivalirudin, or dabigatran, corticosteroids, and non-steroidal anti-inflammatory drugs, vincristine, cyclosporine A, methotrexate, ancrod, ε-aminocaproic acid, antiplasmin-a1, prostacyclin, defibrotide, rituximab, and magnesium sulfate.

10. A biparatopic antibody or antigen-binding fragment thereof comprising a first antigen-binding domain that binds specifically to C5 and a second antigen-binding domain that binds specifically to C5, wherein:

(i) the first antigen-binding domain binds specifically to C5 at a first epitope, and the second antigen-binding domain binds specifically to C5 at a second epitope which is different from the first epitope and/or

(ii) the first antigen-binding domain and the second antigen-binding domain do not compete for binding to C5;

wherein the first antigen-binding domain comprises a heavy chain variable region (V_H) comprising three heavy chain complementarity determining regions (CDRs) (CDR-H1, CDR-H2, and CDR-H3) of a heavy chain variable region V_H that comprises the amino acid sequence set forth in SEQ ID NO: 87, and a light chain variable region (V_L) comprising three light chain CDRs (CDR-L1, CDR-L2, and CDR-L3) of a V_L that comprises the amino acid sequence set forth in SEQ ID NO: 95; and

the second antigen-binding domain comprises a V_H comprising CDR-H1, CDR-H2, and CDR-H3 of a V_H that comprises the amino acid sequence set forth in SEQ ID NO: 103, and a V_L comprising CDR-L1, CDR-L2, and CDR-L3 of a V_L that comprises the amino acid sequence set forth in SEQ ID NO: 95.

11. The biparatopic antibody or antigen-binding fragment thereof of claim 10, wherein:

(i) the first antigen-binding domain comprises:

a V_H comprising CDR-H1 comprising the amino acid sequence set forth in SEQ ID NO: 89, CDR-H2 comprising the amino acid sequence set forth in SEQ ID NO: 91, and CDR-H3 comprising the amino acid sequence set forth in SEQ ID NO: 93; and

a V_L comprising CDR-L1 comprising the amino acid sequence set forth in SEQ ID NO: 97, CDR-L2 comprising the amino acid sequence set forth in SEQ ID NO: 99, and CDR-L3 comprising the amino acid sequence set forth in SEQ ID NO: 101; and

(ii) the second antigen-binding domain comprises:

a V_H comprising CDR-H1 comprising the amino acid sequence set forth in SEQ ID NO: 105, CDR-H2 comprising the amino acid sequence set forth in SEQ ID NO: 107, and CDR-H3 comprising the amino acid sequence set forth in SEQ ID NO: 109; and

a V_L comprising CDR-L1 comprising the amino acid sequence set forth in SEQ ID NO: 97, CDR-L2 comprising the amino acid sequence set forth in SEQ ID NO: 99, and CDR-L3 comprising the amino acid sequence set forth in SEQ ID NO: 101.

12. The biparatopic antibody or antigen-binding fragment thereof of claim 10 or 11, wherein:

the first antigen-binding domain comprises a V_H that comprises the amino acid sequence set forth in SEQ ID NO: 87, and a V_L that comprises the amino acid sequence set forth in SEQ ID NO: 95; and

the second antigen-binding domain comprises a V_H that comprises the amino acid sequence set forth in SEQ ID NO: 103, and a V_L that comprises the amino acid sequence set forth in SEQ ID NO: 95.

13. A complex comprising: one or more C5 polypeptides or antigenic fragments thereof bound to a first antibody or antigen-binding fragment thereof that binds specifically to C5, and a second antibody or antigen-binding fragment thereof that binds specifically to C5, wherein the first antibody or antigen-binding fragment thereof and the second antibody or antigen-binding fragment thereof do not compete for binding to C5, and wherein:

the first antibody or antigen-binding fragment thereof comprises a heavy chain variable region (V_H) comprising three heavy chain complementarity determining regions (CDRs) (CDR-H1, CDR-H2, and CDR-H3) of a heavy chain variable region V_H that comprises the amino acid sequence set forth in SEQ ID NO: 87, and a light chain variable region (V_L) comprising three

light chain CDRs (CDR-L1, CDR-L2, and CDR-L3) of a V_L that comprises the amino acid sequence set forth in SEQ ID NO: 95; and

the second antibody or antigen-binding fragment thereof comprises a V_H comprising CDR-H1, CDR-H2, and CDR-H3 of a V_H that comprises the amino acid sequence set forth in SEQ ID NO: 103, and a V_L comprising CDR-L1, CDR-L2, and CDR-L3 of a V_L that comprises the amino acid sequence set forth in SEQ ID NO: 95.

14. A complex comprising:

(i) a 1:1:2, 2:2:4 or 3:3:6 ratio of first monospecific anti-C5 antibody or antigen-binding fragment thereof-to-second monospecific anti-C5 antibody or antigen-binding fragment thereof-to-C5 polypeptide or antigenic fragment thereof;

(ii) a 1:1, 1:2, 2:1 or 2:2 ratio of biparatopic anti-C5 antibody or antigen-binding fragment thereof-to-C5 polypeptide or antigenic fragment thereof; or

(iii) a 1:1:1; 1:1:2 or 1:2:2 ratio of monospecific anti-C5 antibody or antigen-binding fragment thereof-to-biparatopic anti-C5 antibody or antigen-binding fragment thereof-to-C5 polypeptide or antigenic fragment thereof;

wherein:

(i) the first monospecific anti-C5 antibody or antigen-binding fragment thereof comprises a heavy chain variable region (V_H) comprising three heavy chain complementarity determining regions (CDRs) (CDR-H1, CDR-H2, and CDR-H3) of a V_H that comprises the amino acid sequence set forth in SEQ ID NO: 87, and a light chain variable region (V_L) comprising three light chain CDRs (CDR-L1, CDR-L2, and CDR-L3) of a V_L that comprises the amino acid sequence set forth in SEQ ID NO: 95; and

the second monospecific anti-C5 antibody or antigen-binding fragment thereof comprises a V_H comprising CDR-H1, CDR-H2, and CDR-H3 of a V_H that comprises the amino acid sequence set forth in SEQ ID NO: 103, and a V_L comprising CDR-L1, CDR-L2, and CDR-L3 of a V_L that comprises the amino acid sequence set forth in SEQ ID NO: 95;

and/or

(ii) the biparatopic anti-C5 antibody or antigen-binding fragment thereof comprises a first antigen-binding domain comprising a V_H comprising CDR-H1, CDR-H2, and CDR-H3 of a V_H that comprises the amino acid sequence set forth in SEQ ID NO: 87, and a V_L comprising CDR-

L1, CDR-L2, and CDR-L3 of a V_L that comprises the amino acid sequence set forth in SEQ ID NO: 95; and

the biparatopic anti-C5 antibody or antigen-binding fragment thereof comprises a second antigen-binding domain comprising a V_H comprising CDR-H1, CDR-H2, and CDR-H3 of a V_H that comprises the amino acid sequence set forth in SEQ ID NO 103, and a V_L comprising CDR-L1, CDR-L2, and CDR-L3 of a V_L that comprises the amino acid sequence set forth in SEQ ID NO: 95.

15. The combination of any one of claims 1-9, the biparatopic antibody or antigen-binding fragment thereof of any one of claims 10-12, or the complex of claim 13 for use in a method of treating a C5-associated disease and/or inhibiting both the classical complement pathway and the alternative complement pathway in a subject in need thereof

16. The combination, biparatopic antibody or antigen-binding fragment thereof, or complex of claim 15, wherein the C5-associated disease or disorder is selected from: acute respiratory distress syndrome; adult respiratory distress syndrome; age-related macular degeneration; allergy; Alport's syndrome; Alzheimer's disease; asthma; atherosclerosis; atypical hemolytic uremic syndrome; an autoimmune disease; complement activation caused by balloon angioplasty; bronchoconstriction; bullous pemphigoid; a burn; C3 glomerulopathy; capillary leak syndrome; chemical injury; chronic obstructive pulmonary disease; Crohn's disease; diabetes; diabetic macular edema; diabetic nephropathy; diabetic retinopathy; dyspnea; emphysema; epilepsy; a fibrogenic dust disease; frostbite; geographic atrophy; glomerulopathy; Goodpasture's Syndrome; Guillain-Barre Syndrome; complement activation caused by hemodialysis; a hemodialysis complication; hemolytic anemia; hemoptysis; hereditary angioedema; hyperacute allograft rejection; hypersensitivity pneumonitis; an immune complex disorder; immune complex-associated inflammation; inflammation of an autoimmune disease; an inflammatory disorder; inherited CD59 deficiency; injury due to inert dusts and/or minerals; interleukin-2 induced toxicity during IL-2 therapy; lupus nephritis; membranoproliferative glomerulonephritis; membranoproliferative nephritis; mesenteric artery reperfusion after aortic reconstruction; mesenteric artery reperfusion after infectious disease; mesenteric artery reperfusion after sepsis; multiple sclerosis; myasthenia gravis; myocardial infarction; neuromyelitis optica; obesity;

ocular angiogenesis; an organic dust disease; a parasitic disease; Parkinson's disease; paroxysmal nocturnal hemoglobinuria; pneumonia; a post-ischemic reperfusion condition; post-pump syndrome in cardiopulmonary bypass or renal bypass; progressive kidney failure; a proteinuric kidney disease; psoriasis; a pulmonary embolism; a pulmonary infarct; pulmonary fibrosis; pulmonary vasculitis; renal ischemia; renal ischemia-reperfusion injury; renal transplant; rheumatoid arthritis; schizophrenia; smoke injury; stroke; systemic lupus erythematosus; systemic lupus erythematosus nephritis; thermal injury; traumatic brain injury; uveitis; vasculitis; and xenograft rejection.

17. The combination, biparatopic antibody or antigen-binding fragment thereof, or complex of claim 15 or 16, wherein the method further comprises administering to the subject one or more further therapeutic agents and/or one or more therapeutic procedures.

18. The combination, biparatopic antibody or antigen-binding fragment thereof, or complex of claim of 17, wherein the one or more further therapeutic agents is an antibody that specifically binds to C5, an anti-coagulant, a thrombin inhibitor, an anti-inflammatory drug, an antihypertensive, an immunosuppressive agent, a fibrinolytic agent, a lipid-lowering agent, an inhibitor of hydroxymethylglutaryl CoA reductase, an anti-CD20 agent, an anti-TNFα agent, an anti-seizure agent, a C3 inhibitor, or an anti-thrombotic agent;

and/or wherein the one or more therapeutic procedures is dialysis, a blood or plasma transfusion or exchange and/or a bone marrow/stem cell transplant (BMT/SCT).

19. The combination, biparatopic antibody or antigen-binding fragment thereof, or complex of claim of 17, wherein the one or more further therapeutic agents is selected from: eculizumab, coversin, iron, antithymocyte globulin, a growth factor, warfarin, aspirin, heparin, phenindione, fondaparinux, idraparinux, argatroban, lepirudin, bivalirudin, or dabigatran, corticosteroids, and non-steroidal anti-inflammatory drugs, vincristine, cyclosporine A, methotrexate, ancrod, ε-aminocaproic acid, antiplasmin-a1, prostacyclin, defibrotide, rituximab, magnesium sulfate, avacopan, ravulizumab, and avacincaptad pegol.

20. The combination of any one of claims 15-19, wherein one or more of the components of the combination are administered to the subject subcutaneously or intravenously.

21. The combination, biparatopic antibody or antigen-binding fragment thereof, or complex of any one of claims 15-20, wherein the subject is human.

22. A method for making the combination of any one of claims 1-9, comprising co-packaging:

the first antibody or antigen-binding fragment thereof;

the second antibody or antigen-binding fragment thereof; and

optionally, one or more further therapeutic agents,

into a kit.

23. A method for making the combination of any one of claims 1-9, comprising co-formulating:

the first antibody or antigen-binding fragment thereof;

the second antibody or antigen-binding fragment thereof;

optionally, one or more further therapeutic agents; and

a pharmaceutically acceptable carrier,

into a single pharmaceutical formulation and, optionally, incorporating the formulation into a device or vessel.

24. A combination which is the product of the method of claim 22 or 23.