(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
16 August 2012 (16.08.2012)

WIPO | PCT

(10) International Publication Number
WO 2012/109530 A1

(51) International Patent Classification:
C07K 16/40 (2006.01)

(21) International Application Number:
PCT/US2012/024633

(22) International Filing Date:
10 February 2012 (10.02.2012)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
61/442,126 11 February 2011 (11.02.2011) US

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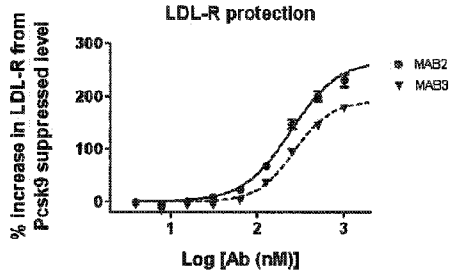
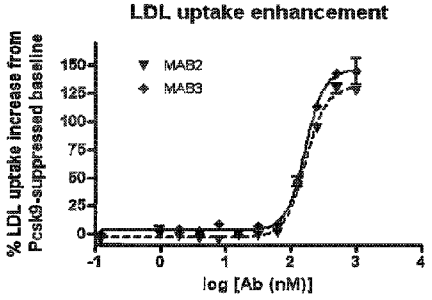
(54) Title: PCSK9 ANTAGONISTS

(57) Abstract: The present invention provides antibody antagonists against proprotein convertase subtilisin/kexin type 9a ("PCSK9") and methods of using such antibodies.

Figure 8

Antibody	LDL-R protection EC50 (nM)	LDL uptake EC50 (nM)
MAB1	309	194
MAB2	324	210
MAB3	300	168





WO 2012/109530 A1

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(81) **Designated States** *(unless otherwise indicated, for every kind of national protection available)*: AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IS, JP, KE, KG, KM, KN, KP, KR, KZ, LA, LC, LK, LR, LS, LT, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

(84) **Designated States** *(unless otherwise indicated, for every kind of regional protection available)*: ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Declarations under Rule 4.17:

— *as to applicant's entitlement to apply for and be granted a patent (Rule 4.17(ii))*

— *of inventorship (Rule 4.17(iv))*

Published:

— *with international search report (Art. 21(3))*

— *before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments (Rule 48.2(h))*

— *with sequence listing part of description (Rule 5.2(a))*

PCSK9 ANTAGONISTS

CROSS-REFERENCE TO RELATED PATENT APPLICATIONS

[0001] The present application claims benefit of priority to US Provisional Patent Application No. 61/442,126, filed February 11, 2011, which is incorporated by reference for all purposes.

FIELD OF THE INVENTION

[0002] The present invention relates to antibody antagonists against PCSK9.

BACKGROUND OF THE INVENTION

[0003] The low-density lipoprotein receptor (LDL-R) prevents atherosclerosis and hypercholesterolemia through the clearance of the low-density lipoproteins (LDL) in the bloodstream. LDL-R is regulated at the posttranslational level by proprotein convertase subtilisin/kexin type 9a ("PCSK9"). Recently, the knockout of PCSK9 was reported in mice. These mice showed an approximate 50% reduction in the plasma cholesterol levels and showed enhanced sensitivity to statins in reducing plasma cholesterol (Rashid S, *et al* (2005) *Proc Natl Acad Sci* 102:5374-5379. Human genetic data also support the role of PCSK9 in LDL homeostasis. Two mutations were recently identified that are presumably "loss-of-function" mutations in PCSK9. The individuals with these mutations have an approximately 40% reduction in the plasma levels of LDL-C which translates into an approximate 50-90% decrease in coronary heart disease. Taken together, these studies indicate that an inhibitor of PCSK9 would be beneficial for lowering plasma concentrations of LDL-C and other disease conditions mediated by PCSK9 and could be co-administered, *e.g.*, with a second agent useful for lowering cholesterol for increased efficacy.

BRIEF SUMMARY OF THE INVENTION

[0004] The present invention provides antibodies that bind to and antagonize the function of proprotein convertase subtilisin/kexin type 9 (PCSK9) (*e.g.,* SEQ ID NO:43), and methods for using such antibodies, *e.g.*, to treat disease conditions mediated by PCSK9.

[0005] In one aspect, the invention provides antibodies and antigen binding molecules that bind to proprotein convertase subtilisin/kexin type 9 (PCSK9). In some embodiments, the antibody blocks the interaction of PCSK9 with low density lipoprotein receptor (LDLR) and inhibits PCSK9-mediated degradation of LDLR, wherein the antibody comprises:

a) a heavy chain variable region comprising a human heavy chain V-segment, a heavy chain complementary determining region 3 (CDR3), and a heavy chain framework region 4 (FR4); and

b) a light chain variable region comprising a human light chain V-segment, a light chain CDR3, and a light chain FR4, wherein

i) the heavy chain CDR3 variable region comprises the amino acid sequence ITTEGGFAY (SEQ ID NO:17); and

ii) the light chain CDR3 variable region comprises the amino acid sequence QQSNYWPLT (SEQ ID NO:24).

[0006] In some embodiments, the antibody or antigen binding molecule binds to human PCSK9 with an equilibrium dissociation constant (KD) of about 500 pM or less. For example, in some embodiments, the antibody or antigen binding molecule binds to human PCSK9 with an equilibrium dissociation constant (KD) of about 400 pM, 300 pM, 250 pM, 200 pM, 190 pM, 180 pM, 170 pM, 160 pM, 150 pM, 140 pM, or less.

[0007] In some embodiments, the heavy chain V-segment has at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity to SEQ ID NO:27, and the light chain V segment has at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity to SEQ ID NO:28.

[0008] In some embodiments, the heavy chain V-segment has at least 85%,86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity to the amino acid sequence selected from the group consisting of SEQ ID NO:25 and SEQ ID NO:26, and the

light chain V-segment has at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity to SEQ ID NO:28.

[0009] In some embodiments, the heavy chain FR4 is a human germline FR4. In some embodiments, the heavy chain FR4 is SEQ ID NO:35.

[0010] In some embodiments, the light chain FR4 is a human germline FR4. In some embodiments, the light chain FR4 is SEQ ID NO:39.

[0011] In some embodiments, the heavy chain V-segment and the light chain V-segment each comprise a complementary determining region 1 (CDR1) and a complementary determining region 2 (CDR2); wherein:

i) the CDR1 of the heavy chain V-segment comprises the amino acid sequence of SEQ ID NO:15;

ii) the CDR2 of the heavy chain V-segment comprises the amino acid sequence of SEQ ID NO:16;

iii) the CDR1 of the light chain V-segment comprises the amino acid sequence of SEQ ID NO:20; and

iv) the CDR2 of the light chain V-segment comprises the amino acid sequence of SEQ ID NO:23.

[0012] In some embodiments,

i) the CDR1 of the heavy chain V-segment comprises SEQ ID NO:14;

ii) the CDR2 of the heavy chain V-segment comprises SEQ ID NO:16;

iii) the heavy chain CDR3 comprises SEQ ID NO:17;

iv) the CDR1 of the light chain V-segment comprises SEQ ID NO:19;

v) the CDR2 of the light chain V-segment comprises SEQ ID NO:22; and

vi) the light chain CDR3 comprises SEQ ID NO:24.

[0013] In some embodiments, the heavy chain variable region has at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% amino acid sequence identity to the variable region of SEQ ID NO:40 and the light chain variable region has at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% amino acid sequence identity to the variable region of SEQ ID NO:41.

[0014] In some embodiments, the antibody comprises a heavy chain comprising SEQ ID NO:40 and a light chain comprising SEQ ID NO:41.

[0015] In some embodiments, the heavy chain variable region has at least 85%,86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% amino acid sequence identity to the variable region selected from the group consisting of SEQ ID NO:5 and SEQ ID NO:9 and the light chain variable region has at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% amino acid sequence identity to the variable region selected from the group consisting of SEQ ID NO:7 and SEQ ID NO:11.

[0016] In some embodiments, the heavy chain variable region comprises the amino acid sequence selected from the group consisting of SEQ ID NO:5 and SEQ ID NO:9 and the light chain variable region comprises the amino acid sequence selected from the group consisting of SEQ ID NO:7 and SEQ ID NO:11.

[0017] In some embodiments, the antibody is an IgG. In some embodiments, the antibody is an IgG1.

[0018] In some embodiments, the antibody is a FAb' fragment. In some embodiments, the antibody is a single chain antibody (scFv). In some embodiments, the antibody comprises human constant regions. In some embodiments, the antibody comprises a human IgG1 constant region. In some embodiments, the human IgG1 constant region is mutated to have reduced binding affinity for an effector ligand such as Fc receptor (FcR), *e.g.*, Fc gamma R1, on a cell or the C1 component of complement. *See*, *e.g.*, U.S. Patent No. 5,624,821. In some embodiments, amino acid residues L234 and L235 of the IgG1 constant region are substituted to Ala234 and Ala235. The numbering of the residues in the heavy chain constant region is that of the EU index (*see*, Kabat, et al., (1983) "Sequences of Proteins of Immunological Interest," U.S. Dept. Health and Human Services).

[0019] In some embodiments, the antibody is linked to a carrier protein, for example, albumin.

[0020] In some embodiments, the antibody is PEGylated.

[0021] In a further aspect, the invention provides compositions comprising an antibody or antigen binding molecule as described herein and a physiologically compatible excipient.

[0022] In some embodiments, the composition further comprises a second agent that reduces low density lipoprotein cholesterol (LDL-C) levels in an individual.

[0023] In some embodiments, the second agent is a statin. For example, the statin can be selected from the group consisting of atorvastatin, cerivastatin, fluvastatin, lovastatin, mevastatin, pitavastatin, pravastatin, rosuvastatin, and simvastatin.

[0024] In some embodiments, the second agent is selected from the group consisting of fibrates, niacin and analogs thereof, a cholesterol absorption inhibitor, a bile acid sequestrant, a thyroid hormone mimetic, a microsomal triglyceride transfer protein (MTP) inhibitor, a diacylglycerol acyltransferase (DGAT) inhibitor, an inhibitory nucleic acid targeting PCSK9 and an inhibitory nucleic acid targeting apoB100.

[0025] In a further aspect, the invention provides methods of reducing LDL-C, non-HDL-C and/or total cholesterol in an individual in need thereof, the method comprising administering a therapeutically effective amount to the individual an antibody or antigen binding molecule as described herein.

[0026] In some embodiments, the individual is hyporesponsive or resistant to statin therapy. In some embodiments, the individual is intolerant to statin therapy. In some embodiments, the individual has a baseline LDL-C level of at least about 100 mg/dL, for example, at least about 110, 120, 130, 140, 150, 160, 170, 180, 190 mg/dL, or higher. In some embodiments, the individual has familial hypercholesterolemia. In some embodiments, the individual has triglyceridemia. In some embodiments, the individual has a gain-of-function PCSK9 gene mutation. In some embodiments, the individual has drug-induced dyslipidemia.

[0027] In some embodiments, total cholesterol is reduced with LDL-C.

[0028] In some embodiments, the methods further comprise administering a therapeutically effective amount of a second agent effective in reducing LDL-C to the individual.

[0029] In some embodiments, the second agent is a statin. For example, the statin can be selected from the group consisting of atorvastatin, cerivastatin, fluvastatin, lovastatin, mevastatin, pitavastatin, pravastatin, rosuvastatin, and simvastatin.

[0030] In some embodiments, the second agent is selected from the group consisting of fibrates, niacin and analogs thereof, cholesterol absorption inhibitors, bile acid sequestrants,

thyroid hormone mimetics, a microsomal triglyceride transfer protein (MTP) inhibitor, a diacylglycerol acyltransferase (DGAT) inhibitor, an inhibitory nucleic acid targeting PCSK9 and an inhibitory nucleic acid targeting apoB100.

[0031] In some embodiments, the antibody or antigen binding molecule and the second agent are co-administered as a mixture.

[0032] In some embodiments, the antibody or antigen binding molecule and the second agent are co-administered separately.

[0033] In some embodiments the antibody is administered intravenously. In some embodiments, the antibody is administered subcutaneously.

DEFINITIONS

[0034] An "antibody" refers to a polypeptide of the immunoglobulin family or a polypeptide comprising fragments of an immunoglobulin that is capable of noncovalently, reversibly, and in a specific manner binding a corresponding antigen. An exemplary antibody structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kD) and one "heavy" chain (about 50-70 kD), connected through a disulfide bond. The recognized immunoglobulin genes include the κ, λ, α, γ, δ, ε, and μ constant region genes, as well as the myriad immunoglobulin variable region genes. Light chains are classified as either κ or λ. Heavy chains are classified as γ, μ, α, δ, or ε, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD, and IgE, respectively. The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The terms variable light chain (V_L) and variable heavy chain (V_H) refer to these regions of light and heavy chains respectively. As used in this application, an "antibody" encompasses all variations of antibody and fragments thereof that possess a particular binding specifically, *e.g.*, for PCSK9. Thus, within the scope of this concept are full length antibodies, chimeric antibodies, humanized antibodies, single chain antibodies (ScFv), Fab, Fab', and multimeric versions of these fragments (*e.g.*, $F(ab')_2$) with the same binding specificity.

[0035] "Complementarity-determining domains" or "complementary-determining regions ("CDRs") interchangeably refer to the hypervariable regions of V_L and V_H. The CDRs are the target protein-binding site of the antibody chains that harbors specificity for such target protein.

There are three CDRs (CDR1-3, numbered sequentially from the N-terminus) in each human V_L or V_H, constituting about 15-20% of the variable domains. The CDRs are structurally complementary to the epitope of the target protein and are thus directly responsible for the binding specificity. The remaining stretches of the V_L or V_H, the so-called framework regions, exhibit less variation in amino acid sequence (Kuby, Immunology, 4th ed., Chapter 4. W.H. Freeman & Co., New York, 2000).

[0036] The positions of the CDRs and framework regions are determined using various well known definitions in the art, *e.g.*, Kabat, Chothia, international ImMunoGeneTics database (IMGT) (on the worldwide web at imgt.cines.fr/), and AbM (see, *e.g.*, Johnson *et al.*, Nucleic Acids Res., 29:205-206 (2001); Chothia and Lesk, J. Mol. Biol., 196:901-917 (1987); Chothia *et al.*, Nature, 342:877-883 (1989); Chothia *et al.*, J. Mol. Biol., 227:799-817 (1992); Al-Lazikani *et al.*, J.Mol.Biol., 273:927-748 (1997)). Definitions of antigen combining sites are also described in the following: Ruiz *et al.*, Nucleic Acids Res., 28:219–221 (2000); and Lefranc, M.P., Nucleic Acids Res., 29:207-209 (2001); MacCallum *et al.*, J. Mol. Biol., 262:732-745 (1996); and Martin *et al.*, Proc. Natl. Acad. Sci. USA, 86:9268–9272 (1989); Martin *et al.*, Methods Enzymol., 203:121–153 (1991); and Rees *et al.*, In Sternberg M.J.E. (ed.), Protein Structure Prediction, Oxford University Press, Oxford, 141–172 (1996).

[0037] The term "binding specificity determinant" or "BSD" interchangeably refer to the minimum contiguous or non-contiguous amino acid sequence within a complementary determining region necessary for determining the binding specificity of an antibody. A minimum binding specificity determinant can be within one or more CDR sequences. In some embodiments, the minimum binding specificity determinants reside within (*i.e.*, are determined solely by) a portion or the full-length of the CDR3 sequences of the heavy and light chains of the antibody.

[0038] An "antibody light chain" or an "antibody heavy chain" as used herein refers to a polypeptide comprising the V_L or V_H, respectively. The endogenous V_L is encoded by the gene segments V (variable) and J (junctional), and the endogenous V_H by V, D (diversity), and J. Each of V_L or V_H includes the CDRs as well as the framework regions. In this application, antibody light chains and/or antibody heavy chains may, from time to time, be collectively referred to as "antibody chains." These terms encompass antibody chains containing mutations that do not disrupt the basic structure of V_L or V_H, as one skilled in the art will readily recognize.

[0039] Antibodies exist as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. Thus, for example, pepsin digests an antibody below the disulfide linkages in the hinge region to produce $F(ab)'_2$, a dimer of Fab' which itself is a light chain joined to V_H-C_H1 by a disulfide bond. The $F(ab)'_2$ may be reduced under mild conditions to break the disulfide linkage in the hinge region, thereby converting the $F(ab)'_2$ dimer into an Fab' monomer. The Fab' monomer is essentially Fab with part of the hinge region. Paul, *Fundamental Immunology* 3d ed. (1993). While various antibody fragments are defined in terms of the digestion of an intact antibody, one of skill will appreciate that such fragments may be synthesized de novo either chemically or by using recombinant DNA methodology. Thus, the term "antibody," as used herein, also includes antibody fragments either produced by the modification of whole antibodies, or those synthesized *de novo* using recombinant DNA methodologies (*e.g.*, single chain Fv) or those identified using phage display libraries (see, *e.g.*, McCafferty *et al.*, *Nature* 348:552-554 (1990)).

[0040] For preparation of monoclonal or polyclonal antibodies, any technique known in the art can be used (see, *e.g.*, Kohler & Milstein, *Nature* 256:495-497 (1975); Kozbor *et al.*, *Immunology Today* 4:72 (1983); Cole *et al.*, Monoclonal Antibodies and Cancer Therapy, pp. 77-96. Alan R. Liss, Inc. 1985). Techniques for the production of single chain antibodies (U.S. Patent No. 4,946,778) can be adapted to produce antibodies to polypeptides of this invention. Also, transgenic mice, or other organisms such as other mammals, may be used to express humanized antibodies. Alternatively, phage display technology can be used to identify antibodies and heteromeric Fab fragments that specifically bind to selected antigens (see, *e.g.*, McCafferty *et al.*, *supra*; Marks *et al.*, *Biotechnology*, 10:779-783, (1992)).

[0041] Methods for humanizing or primatizing non-human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source which is non-human. These non-human amino acid residues are often referred to as import residues, which are typically taken from an import variable domain. Humanization can be essentially performed following the method of Winter and co-workers (*see, e.g.*, Jones *et al.*, *Nature* 321:522-525 (1986); Riechmann *et al.*, *Nature* 332:323-327 (1988); Verhoeyen *et al.*, *Science* 239:1534-1536 (1988) and Presta, *Curr. Op. Struct. Biol.* 2:593-596 (1992)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted

by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some complementary determining region ("CDR") residues and possibly some framework ("FR") residues are substituted by residues from analogous sites in rodent antibodies.

[0042] Antibodies or antigen-binding molecules of the invention further includes one or more immunoglobulin chains that are chemically conjugated to, or expressed as, fusion proteins with other proteins. It also includes bispecific antibody. A bispecific or bifunctional antibody is an artificial hybrid antibody having two different heavy/light chain pairs and two different binding sites. Other antigen-binding fragments or antibody portions of the invention include bivalent scFv (diabody), bispecific scFv antibodies where the antibody molecule recognizes two different epitopes, single binding domains (dAbs), and minibodies.

[0043] The various antibodies or antigen-binding fragments described herein can be produced by enzymatic or chemical modification of the intact antibodies, or synthesized de novo using recombinant DNA methodologies (e.g., single chain Fv), or identified using phage display libraries (see, e.g., McCafferty et al., Nature 348:552-554, 1990). For example, minibodies can be generated using methods described in the art, e.g., Vaughan and Sollazzo, Comb Chem High Throughput Screen. 4:417-30 2001. Bispecific antibodies can be produced by a variety of methods including fusion of hybridomas or linking of Fab' fragments. See, e.g., Songsivilai & Lachmann, Clin. Exp. Immunol. 79:315-321 (1990); Kostelny et al., J. Immunol. 148, 1547-1553 (1992). Single chain antibodies can be identified using phage display libraries or ribosome display libraries, gene shuffled libraries. Such libraries can be constructed from synthetic, semi-synthetic or native and immunocompetent sources.

[0044] A "chimeric antibody" is an antibody molecule in which (a) the constant region, or a portion thereof, is altered, replaced or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, e.g., an enzyme, toxin, hormone, growth factor, drug, etc.; or (b) the variable region, or a portion thereof, is altered, replaced or exchanged with a variable region having a different or altered antigen specificity. For example, as shown in the Examples below, a mouse anti-PCSK9 antibody can be modified by replacing its constant region with the constant region from a human immunoglobulin. Due to the replacement with a human constant region, the chimeric antibody

can retain its specificity in recognizing human PCSK9 while having reduced antigenicity in human as compared to the original mouse antibody.

[0045] The term "antibody binding molecule" or "non-antibody ligand" refers to antibody mimics that use non-immunoglobulin protein scaffolds, including adnectins, avimers, single chain polypeptide binding molecules, and antibody-like binding peptidomimetics.

[0046] The term "variable region" or "V-region" interchangeably refer to a heavy or light chain comprising FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4. *See*, Figure 1. An endogenous variable region is encoded by immunoglobulin heavy chain V-D-J genes or light chain V-J genes. A V-region can be naturally occurring, recombinant or synthetic.

[0047] As used herein, the term "variable segment" or "V-segment" interchangeably refer to a subsequence of the variable region including FR1-CDR1-FR2-CDR2-FR3. *See*, Figure 1. An endogenous V-segment is encoded by an immunoglobulin V-gene. A V-segment can be naturally occurring, recombinant or synthetic.

[0048] As used herein, the term "J-segment" refers to a subsequence of the variable region encoded comprising a C-terminal portion of a CDR3 and the FR4. An endogenous J-segment is encoded by an immunoglobulin J-gene. *See*, Figure 1. A J-segment can be naturally occurring, recombinant or synthetic.

[0049] A "humanized" antibody is an antibody that retains the reactivity of a non-human antibody while being less immunogenic in humans. This can be achieved, for instance, by retaining the non-human CDR regions and replacing the remaining parts of the antibody with their human counterparts. *See*, *e.g.*, Morrison *et al.*, *Proc. Natl. Acad. Sci. USA*, 81:6851-6855 (1984); Morrison and Oi, *Adv. Immunol.*, 44:65-92 (1988); Verhoeyen *et al.*, *Science*, 239:1534-1536 (1988); Padlan, *Molec. Immun.*, 28:489-498 (1991); Padlan, *Molec. Immun.*, 31(3):169-217 (1994).

[0050] The term "corresponding human germline sequence" refers to the nucleic acid sequence encoding a human variable region amino acid sequence or subsequence that shares the highest determined amino acid sequence identity with a reference variable region amino acid sequence or subsequence in comparison to all other all other known variable region amino acid sequences encoded by human germline immunoglobulin variable region sequences. The corresponding human germline sequence can also refer to the human variable region amino acid sequence or

subsequence with the highest amino acid sequence identity with a reference variable region amino acid sequence or subsequence in comparison to all other evaluated variable region amino acid sequences. The corresponding human germline sequence can be framework regions only, complementary determining regions only, framework and complementary determining regions, a variable segment (as defined above), or other combinations of sequences or subsequences that comprise a variable region. Sequence identity can be determined using the methods described herein, for example, aligning two sequences using BLAST, ALIGN, or another alignment algorithm known in the art. The corresponding human germline nucleic acid or amino acid sequence can have at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity with the reference variable region nucleic acid or amino acid sequence. Corresponding human germline sequences can be determined, for example, through the publicly available international ImMunoGeneTics database (IMGT) (on the worldwide web at imgt.cines.fr/) and V-base (on the worldwide web at vbase.mrc-cpe.cam.ac.uk).

[0051] The phrase "specifically (or selectively) bind," when used in the context of describing the interaction between an antigen, *e.g.*, a protein, to an antibody or antibody-derived binding agent, refers to a binding reaction that is determinative of the presence of the antigen in a heterogeneous population of proteins and other biologics, *e.g.*, in a biological sample, *e.g.*, a blood, serum, plasma or tissue sample. Thus, under designated immunoassay conditions, the antibodies or binding agents with a particular binding specificity bind to a particular antigen at least two times the background and do not substantially bind in a significant amount to other antigens present in the sample. Specific binding to an antibody or binding agent under such conditions may require the antibody or agent to have been selected for its specificity for a particular protein. As desired or appropriate, this selection may be achieved by subtracting out antibodies that cross-react with, *e.g.*, PCSK9 molecules from other species (*e.g.*, mouse) or other PCSK subtypes. A variety of immunoassay formats may be used to select antibodies specifically immunoreactive with a particular protein. For example, solid-phase ELISA immunoassays are routinely used to select antibodies specifically immunoreactive with a protein (see, *e.g.*, Harlow & Lane, Using Antibodies, A Laboratory Manual (1998), for a description of immunoassay formats and conditions that can be used to determine specific immunoreactivity). Typically a specific or selective binding reaction will produce a signal at least twice over the background signal and more typically at least 10 to 100 times over the background.

[0052] The term "equilibrium dissociation constant (K_D, M)" refers to the dissociation rate constant (k_d, $time^{-1}$) divided by the association rate constant (k_a, $time^{-1}$, M^{-1}). Equilibrium dissociation constants can be measured using any known method in the art. The antibodies of the present invention generally will have an equilibrium dissociation constant of less than about 10^{-7} or 10^{-8} M.

[0053] As used herein, the term "antigen-binding region" refers to a domain of the PCSK9-binding molecule of this invention that is responsible for the specific binding between the molecule and PCSK9. An antigen-binding region includes at least one antibody heavy chain variable region and at least one antibody light chain variable region. There is at least one such antigen-binding region present in each PCSK9-binding molecule of this invention, and each of the antigen-binding regions may be identical or different from the others. In some embodiments, at least one of the antigen-binding regions of a PCSK9-binding molecule of this invention acts as an antagonist of PCSK9.

[0054] The term "antagonist," as used herein, refers to an agent that is capable of specifically binding and inhibiting the activity of the target molecule. For example, an antagonist of PCSK9 specifically binds to PCSK9 and fully or partially inhibits PCSK9-mediated degradation of the LDLR. As used herein, inhibiting PCSK9-mediated degradation of the LDLR interferes with PCSK9 binding to the LDLR. In some cases, a PCSK9 antagonist can be identified by its ability to bind to PCSK9 and inhibit binding of PCSK9 to the LDLR. Inhibition occurs when PCSK9-mediated degradation of the LDLR, when exposed to an antagonist of the invention, is at least about 10% less, for example, at least about 25%, 50%, 75% less, or totally inhibited, in comparison to PCSK9-mediated degradation in the presence of a control or in the absence of the antagonist. A control can be exposed to no antibody or antigen binding molecule, an antibody or antigen binding molecule that specifically binds to another antigen, or an anti-PCSK9 antibody or antigen binding molecule known not to function as an antagonist. An "antibody antagonist" refers to the situation where the antagonist is an inhibiting antibody.

[0055] The term "PCSK9" or "proprotein convertase subtilisin/kexin type 9a" interchangeably refer to a naturally-occurring human proprotein convertase belonging to the proteinase K subfamily of the secretory subtilase family. PCSK9 is synthesized as a soluble zymogen that undergoes autocatalytic intramolecular processing in the endoplasmic reticulum, and is thought to function as a proprotein convertase. PCSK9 plays a role in cholesterol homeostasis and may

have a role in the differentiation of cortical neurons. Mutations in this the PCSK9 gene have been associated with a form of autosomal dominant familial hypercholesterolemia. *See*, *e.g.*, Burnett and Hooper, *Clin Biochem Rev* (2008) 29(1):11-26. The nucleic acid and amino acid sequences of PCSK9 are known, and have been published in GenBank Accession Nos. NM_174936.2 and NP_777596.2, respectively. As used herein, a PCSK9 polypeptide functionally binds to LDLR and promotes the degradation of LDLR. Structurally, a PCSK9 amino acid sequence has at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity with the amino acid sequence of GenBank Accession No. NP_777596.2. Structurally, a PCSK9 nucleic acid sequence has at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity with the nucleic acid sequence of GenBank accession no. NM_174936.2.

[0056] The phrase "PCSK9 gain-of-function mutation" refers to natural mutations occurring in PCSK9 genes that are associated with and/or causative of the familial hypercholesterolemia phenotype, accelerated atherosclerosis and premature coronary heart disease, *e.g.*, due to enhanced LDLR degradation and a reduction of LDLR levels. The allele frequency of PCSK9 gain-of-function mutations is rare. *See*, Burnett and Hooper, *Clin Biochem Rev.* (2008) 29(1):11-26. Exemplary PCSK9 gain-of-function mutations include D129N, D374H, N425S and R496W. *See*, Fasano, *et al.*, *Atherosclerosis* (2009) 203(1):166-71. PCSK9 gain-of-function mutations are reviewed, *e.g.*, in Burnett and Hooper, *supra*; Fasano, *et al*, *supra*; Abifadel, *et al.*, *J Med Genet* (2008) 45(12):780-6; Abifadel, *et al.*, *Hum Mutat* (2009) 30(4):520-9; and Li, *et al.*, *Recent Pat DNA Gene Seq* (2009) Nov. 1 (PMID 19601924).

[0057] "Activity" of a polypeptide of the invention refers to structural, regulatory, or biochemical functions of a polypeptide in its native cell or tissue. Examples of activity of a polypeptide include both direct activities and indirect activities. Exemplary direct activities of PCSK9 are the result of direct interaction with the polypeptide, including binding to LDLR and PCSK9-mediated degradation of LDLR. Exemplary indirect activities in the context of PCSK9 are observed as a change in phenotype or response in a cell, tissue, organ or subject to a polypeptide's directed activity, e.g., reducing increased liver LDLR, reduced plasma HDL-C, decreased plasma cholesterol, enhances sensitivity to statins.

[0058] The term "isolated," when applied to a nucleic acid or protein, denotes that the nucleic acid or protein is essentially free of other cellular components with which it is associated in the

natural state. It is preferably in a homogeneous state. It can be in either a dry or aqueous solution. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A protein that is the predominant species present in a preparation is substantially purified. In particular, an isolated gene is separated from open reading frames that flank the gene and encode a protein other than the gene of interest. The term "purified" denotes that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Particularly, it means that the nucleic acid or protein is at least 85% pure, more preferably at least 95% pure, and most preferably at least 99% pure.

[0059] The term "nucleic acid" or "polynucleotide" refers to deoxyribonucleic acids (DNA) or ribonucleic acids (RNA) and polymers thereof in either single- or double-stranded form. Unless specifically limited, the term encompasses nucleic acids containing known analogues of natural nucleotides that have similar binding properties as the reference nucleic acid and are metabolized in a manner similar to naturally occurring nucleotides. Unless otherwise indicated, a particular nucleic acid sequence also implicitly encompasses conservatively modified variants thereof (*e.g.*, degenerate codon substitutions), alleles, orthologs, SNPs, and complementary sequences as well as the sequence explicitly indicated. Specifically, degenerate codon substitutions may be achieved by generating sequences in which the third position of one or more selected (or all) codons is substituted with mixed-base and/or deoxyinosine residues (Batzer *et al.*, *Nucleic Acid Res.* **19**:5081 (1991); Ohtsuka *et al.*, *J. Biol. Chem.* **260**:2605-2608 (1985); and Rossolini *et al.*, *Mol. Cell. Probes* **8**:91-98 (1994)).

[0060] The terms "polypeptide," "peptide," and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers and non-naturally occurring amino acid polymer.

[0061] The term "amino acid" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function in a manner similar to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as those amino acids that are later modified, *e.g.*, hydroxyproline, γ-carboxyglutamate, and O-phosphoserine. Amino acid analogs refer to compounds that have the same basic

chemical structure as a naturally occurring amino acid, *i.e.*, an α-carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, *e.g.*, homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs have modified R groups (*e.g.*, norleucine) or modified peptide backbones, but retain the same basic chemical structure as a naturally occurring amino acid. Amino acid mimetics refers to chemical compounds that have a structure that is different from the general chemical structure of an amino acid, but that functions in a manner similar to a naturally occurring amino acid.

[0062] "Conservatively modified variants" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode any given protein. For instance, the codons GCA, GCC, GCG and GCU all encode the amino acid alanine. Thus, at every position where an alanine is specified by a codon, the codon can be altered to any of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations," which are one species of conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes every possible silent variation of the nucleic acid. One of skill will recognize that each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally identical molecule. Accordingly, each silent variation of a nucleic acid that encodes a polypeptide is implicit in each described sequence.

[0063] As to amino acid sequences, one of skill will recognize that individual substitutions, deletions or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known in the art. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention.

[0064] The following eight groups each contain amino acids that are conservative substitutions for one another:

1) Alanine (A), Glycine (G);

2) Aspartic acid (D), Glutamic acid (E);

3) Asparagine (N), Glutamine (Q);

4) Arginine (R), Lysine (K);

5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V);

6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W);

7) Serine (S), Threonine (T); and

8) Cysteine (C), Methionine (M) (*see*, *e.g.*, Creighton, *Proteins* (1984)).

[0065] "Percentage of sequence identity" is determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (*i.e.*, gaps) as compared to the reference sequence (*e.g.*, a polypeptide of the invention), which does not comprise additions or deletions, for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the percentage of sequence identity.

[0066] The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same sequences. Two sequences are "substantially identical" if two sequences have a specified percentage of amino acid residues or nucleotides that are the same (*i.e.*, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity over a specified region, or, when not specified, over the entire sequence of a reference sequence), when compared and aligned for maximum correspondence over a comparison window, or designated region as measured using one of the following sequence comparison algorithms or by manual alignment and visual inspection. The invention provides polypeptides or polynucleotides that are substantially identical to the polypeptides or polynucleotides, respectively, exemplified herein (*e.g.*, the variable regions exemplified in any one of SEQ ID NOS:1, 3, 5, 7, 9, 11, and 40-41; the variable segments exemplified in any one of SEQ ID NOS:25-29; the CDRs exemplified in any one of SEQ ID NOS:13-24; the FRs exemplified in any one of SEQ ID NOS:30-39; and the

nucleic acid sequences exemplified in any one of SEQ ID NOS:2, 4, 6, 8, 10, 12, and 46-49). Optionally, the identity exists over a region that is at least about 15, 25 or 50 nucleotides in length, or more preferably over a region that is 100 to 500 or 1000 or more nucleotides in length, or over the full length of the reference sequence. With respect to amino acid sequences, identity or substantial identity can exist over a region that is at least 5, 10, 15 or 20 amino acids in length, optionally at least about 25, 30, 35, 40, 50, 75 or 100 amino acids in length, optionally at least about 150, 200 or 250 amino acids in length, or over the full length of the reference sequence. With respect to shorter amino acid sequences, *e.g.*, amino acid sequences of 20 or fewer amino acids, substantial identity exists when one or two amino acid residues are conservatively substituted, according to the conservative substitutions defined herein.

[0067] For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

[0068] A "comparison window", as used herein, includes reference to a segment of any one of the number of contiguous positions selected from the group consisting of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well known in the art. Optimal alignment of sequences for comparison can be conducted, *e.g.*, by the local homology algorithm of Smith and Waterman (1970) *Adv. Appl. Math.* 2:482c, by the homology alignment algorithm of Needleman and Wunsch (1970) *J. Mol. Biol.* 48:443, by the search for similarity method of Pearson and Lipman (1988) *Proc. Nat'l. Acad. Sci. USA* 85:2444, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (*see, e.g.,* Ausubel *et al.*, *Current Protocols in Molecular Biology* (1995 supplement)).

[0069] Two examples of algorithms that are suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul *et al.* (1977) *Nuc. Acids Res.* 25:3389-3402, and Altschul *et al.* (1990) *J. Mol. Biol.* 215:403-410, respectively. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information. This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al.*, *supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) or 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (*see* Henikoff and Henikoff (1989) *Proc. Natl. Acad. Sci. USA* 89:10915) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

[0070] The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (*see, e.g.*, Karlin and Altschul (1993) *Proc. Natl. Acad. Sci. USA* 90:5873-5787). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01, and most preferably less than about 0.001.

[0071] An indication that two nucleic acid sequences or polypeptides are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid, as described below. Thus, a polypeptide is typically substantially identical to a second polypeptide, for example, where the two peptides differ only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules or their complements hybridize to each other under stringent conditions, as described below. Yet another indication that two nucleic acid sequences are substantially identical is that the same primers can be used to amplify the sequence.

[0072] The term "link," when used in the context of describing how the antigen-binding regions are connected within a PCSK9-binding molecule of this invention, encompasses all possible means for physically joining the regions. The multitude of antigen-binding regions are frequently joined by chemical bonds such as a covalent bond (*e.g.*, a peptide bond or a disulfide bond) or a non-covalent bond, which can be either a direct bond (*i.e.*, without a linker between two antigen-binding regions) or indirect bond (*i.e.*, with the aid of at least one linker molecule between two or more antigen-binding regions).

[0073] The terms "subject," "patient," and "individual" interchangeably refer to a mammal, for example, a human or a non-human primate mammal. The mammal can also be a laboratory mammal, *e.g.*, mouse, rat, rabbit, hamster. In some embodiments, the mammal can be an agricultural mammal (e.g., equine, ovine, bovine, porcine, camelid) or domestic mammal (e.g., canine, feline).

[0074] The term "therapeutically acceptable amount" or "therapeutically effective dose" interchangeably refer to an amount sufficient to effect the desired result (*i.e.*, a reduction in plasma non-HDL-C, hypercholesterolemia, atherosclerosis, coronary heart disease). In some embodiments, a therapeutically acceptable amount does not induce or cause undesirable side effects. A therapeutically acceptable amount can be determined by first administering a low dose, and then incrementally increasing that dose until the desired effect is achieved. A "prophylactically effective dosage," and a "therapeutically effective dosage," of a PCSK9 antagonizing antibody of the invention can prevent the onset of, or result in a decrease in severity of, respectively, disease symptoms associated with the presence of PCSK9 (*e.g.*, hypercholesterolemia). Said terms can also promote or increase, respectively, frequency and

duration of periods free from disease symptoms. A "prophylactically effective dosage," and a "therapeutically effective dosage," can also prevent or ameliorate, respectively, impairment or disability due to the disorders and diseases resulting from activity of PCSK9.

[0075] The term "co-administer" refers to the simultaneous presence of two active agents in the blood of an individual. Active agents that are co-administered can be concurrently or sequentially delivered.

[0076] The term "statin" refers to a class of pharmacological agents that are competitive inhibitors of 3-hydroxy-3-methylglutaryl coenzyme A (HMG-CoA) reductase.

BRIEF DESCRIPTION OF THE DRAWINGS

[0077] **Figure 1** illustrates the heavy (SEQ ID NO:1) and light (SEQ ID NO:3) chain amino acid sequences of parent mouse monoclonal antibody MAB1. The sequences of CDR1, CDR2 and CDR3 are underlined and in bold.

[0078] **Figure 2** illustrates the heavy (SEQ ID NO:5) and light (SEQ ID NO:7) chain amino acid sequences of Humaneered™ antibody MAB2. The sequences of CDR1, CDR2 and CDR3 are underlined and in bold.

[0079] **Figure 3** illustrates the heavy (SEQ ID NO:9) and light (SEQ ID NO:11) chain amino acid sequences of Humaneered™ antibody MAB3. The sequences of CDR1, CDR2 and CDR3 are underlined and in bold.

[0080] **Figures 4A-B** illustrate ELISA assay testing of binding of (A) MAB2 and (B) MAB3 in comparison to MAB1 to several different human and mouse antigens.

[0081] **Figures 5A-C** illustrate binding of MAB2 and MAB3 to (A) human Pcsk9 and (B) cyno Pcsk9. (C) Data were fitted to the model described in Piehler, *et al.*, (1997) *J Immunol Methods* 201:189-206 and K_d values were calculated from the fit. Graphs are representative of at least 2 independent experiments.

[0082] **Figure 6** illustrates that the parent mouse monoclonal antibody, MAB1, likely binds to an epitope within the amino acid residues 159-182 (ERITPPRYRADEYQPPDGGSLVE; SEQ ID NO:42) based on deuterium exchange mass spectrometry. Automated hydrogen/deuterium exchange mass spectrometry experiments were performed with a similar setup and similar

fashion as described in Chalmers *et al., Anal Chem* **2006**, *78*, 1005-1014. Briefly, a LEAP Technologies Pal HTS liquid-handler (LEAP Technologies, Carrboro, NC) was used for all liquid handling operations. The liquid-handler was controlled by automation scripts written in LEAP Shell and was housed in a refrigerated enclosure maintained at 2°C. A 6-port injection valve and a wash station were mounted on the liquid-handler rail and facilitated sample injection into the chromatographic system and syringe washing. For on-line digestion, an enzyme column (ABI immobilized pepsin) was placed in line between the injection valve and the trapping column. The chromatographic system, consisting of two additional valves (15kPSI Valco, Houston, TX), a 4µL EXP Halo C18 reversed-phase trap cartridge (Optimize Technologies Inc., Oregon City, OR), and an analytical column (300µm ID, Halo 2.7µm C18, Michrom Bioresources Inc.), was housed in a separate cooled enclosure that was mounted in front of the source of the LTQ-Orbitrap mass spectrometer (ThermoElectron Corp.). The temperature of the enclosure housing the chromatographic system was maintained at 0°C by peltier coolers mounted to the top of the enclosure. For the analyses of PCSK9, four 96-well plates containing the sample, diluent, reductant, and quench, were loaded into the liquid-handler before the start of each experimental sequence. Prior to each injection, 25µL of protein solution (~2mg/mL) was mixed with either 25µL of 50mM TEA buffer (pH 7.4) or 25µL 50mM TEA buffer (pH 7.4) containing ~21µg 13C10-FAB and allowed to mix for 30 min. To initiate the exchange reaction, 150 µL of D_2O buffer (D_20, 150mM NaCl) or H_20 buffer (150mM NaCl) was added and allowed to exchange for 1 min. Then 200uL of redux buffer (1M TCEP, 8M Urea, pH 4.0) was added and the mixture was allowed to react for ~1min. The mixture was then quenched with 300uL of quench buffer (5% TFA) to reduce the mixture to pH 2.5. 500uL of sample was then injected and online digested and the resulting peptides were trapped, and analyzed by LC-MS as described below. The chromatography system used two separate HPLC pumps to perform in-line digestion, trap the digested peptides onto a C18 trap column, and elute trapped peptides through an analytical column. A "loading" pump, operated at a flow rate of 125µL/min (0.05% TFA), transferred samples from the PAL injection valve sample loop (500µL), through a pepsin column, and to the reversed-phase trap cartridge. After a 6 min. loading step, the 1st 15kPSI valve was switched to allow fluid from a "gradient" pump to flow through the trap for a 3min desalting period (25µL/min). After the desalting step, the 2nd 15kPSI valve was switched to facilitate elution of peptides from the trap and into the analytical column and ion source of the mass spectrometer. The gradient pump (Waters Nano Acquity) delivered a gradient of 0 to 40% mobile phase B at 5µL/min, and then delivered a second gradient from 40 to 75% mobile phase

B. The total time for the gradient was 75 min. The gradient pump buffer compositions were A: 99.75:0.25 %v/v (H_20: formic acid) and B: 99.75:0.25 %v/v (acetonitrile:formic acid).

[0083] For mass spectrometry, LC-ESI-MS was performed on a LTQ-Orbitrap (ThermoElectron, San Jose, CA). Data-dependent MS/MS experiments were performed to collect tandem mass spectra for the purpose of identifying the sequences of the peptides generated by proteolysis. For these acquisitions, MS/MS were acquired in the LTQ and MS scans were acquired in the Orbitrap. Acquisitions performed for the purpose of deuteration level determination were acquired at a resolution of 60,000 in the Orbitrap (over m/z 400-2000). The instrument parameters used for all experiments included a spray voltage of 3.5kV, a maximum injection time of 1000 ms, LTQ AGC target for MS of 50,000 ions and an FTMS AGC target for MS of 1,000,000 ions. The Orbitrap .RAW files were converted into .mzXML files using an in-house program (RawXtract). Subsequently, .mzXML files were converted into .mzBIN files and tandem MS acquisitions were searched using SEQUEST (ThermoElectron). Using the peptide sequence identifications, an in-house written program (Deutoronomy) was used to automatically extract chromatograms for each identified sequence and generate average spectra. Average spectra were then smoothed and centroided to determine the level of deuterium uptake. After the initial automated processing, the quality and centroiding of each average spectrum was manually validated or corrected using an interactive data viewer built into Deutoronomy. Humaneered™ antibodies MAB2 and MAB3 were found to compete for the same epitope as MAB1 using a bio-layer interferometry-based epitope competition assay.

[0084] **Figure 7** illustrates that MAB2 and MAB3 can block the interaction of PCSK9 and LDL-R, as determined in a time-resolved fluorescence resonance energy transfer (TR-FRET) biochemical assay. Binding of Pcsk9 antagonist antibodies to Pcsk9 may disrupt the ability of Pcsk9 to form a complex with LDLr, thus protecting LDLr from downregulation / degradation, and enhancing LDL-uptake. To test this, human PCSK9 labeled with a fluorophore (hPCSK9-AF) was incubated with MAB2 or MAB3 in assay buffer (20 mM HEPES, pH 7.2, 150 mM NaCl, 1 mM $CaCl_2$, 0.1% v/v Tween 20, and 0.1% w/v BSA) for 30 minutes at room temperature. This was followed by addition of europium-labeled LDL-R (hLDL-R-Eu), and further incubation at room temperature for 90 minutes, such that final concentrations were 8 nM hPcsk9-AF and 1 nM hLDL-R-Eu. TR-FRET signal (330 nm excitation and 665 nm emission) was measured with a plate reader (EnVision 2100, Perkin Elmer) and % inhibition in the presence of the Pcsk9 antibodies calculated. IC_{50} values were calculated by plotting percent

inhibition values in Prism (GraphPad). Each data point represents mean ± SD (n = 4 replicates per point). Data are representative of at least two independent experiments. The Humaneered™ antibodies MAB2 and MAB3 were able to disrupt the complex with IC_{50} values of 20 nM and 28 nM, resepectively, which is comparable to the IC_{50} of 77 nM found for the parent antibody MAB1 (data not shown).

[0085] **Figure 8** illustrates that the Humaneered™ antibodies MAB2 and MAB3 are equivalent to mouse antibody MAB1 at leading to increased LDL-R levels and LDL-uptake by HepG2 cells. For LDL-R measurement, cells were incubated with PCSK9-binding antibodies and labeled with anti-LDL-R antibodies. For LDL uptake, cells were incubated with PCSK9-binding antibodies, PCSK9, and DiI-LDL. LDL-R antibodies and DiI- LDL fluorescence were measured by flow cytometry. Mean + SEM for replicate measurements are shown for the graphs of MAB2 and MAB3. Results are representative of 2 independent experiments.

[0086] For LDL-uptake assays, PCSK9-binding antibodies were incubated for 30 min at room temperature in DMEM containing 10% fetal bovine lipoprotein-deficient serum (Intracel) and 200 nM human PCSK9 (Hampton *et al.* PNAS (2007)104:14604-14609), and the antibody/PCSK9/media solutions were added to cells in 96-well plates and incubated overnight. The following day, 1,1'-dioctadecyl-3,3,3',3'-tetramethyl-indocarbocyanine perchlorate-labeled LDL (DiI-LDL, Biomedical Technologies) was added for an additional 2 h. Medium was then aspirated, cells washed three times with PBS, and cells dissociated with 0.25% trypsin-EDTA. Cells were then transferred into FACS buffer (PBS containing 5% fetal bovine serum, 2mM EDTA and 0.2% sodium azide), centrifuged at 1000 x g for 10 min, aspirated, and fixed in 1% paraformaldehyde. LDL uptake was measured by cellular DiI fluorescence (excitation at 488nm and emission at 575nm) using flow cytometry (Becton Dickinson LSR II). For surface LDL-R assays, cells were incubated with serum-free media containing antibodies, washed with PBS, and harvested in Versine (Biowhittaker, 17-771E) and FACS buffer. The cells were transferred to new plates, centrifuged at 1200 rpm for 5 m, and blocked with normal rabbit IgG (MP biomedicals). Cells were labeled with rabbit-anti-hLDL-R-Alexa 647 IgG (5 μg/ml) labeled antibodies in FACS buffer, centrifuged, washed, and fixed in 1% paraformaldehyde. Surface LDL-R was measured by flow cytometry (excitation of 488 nm and emission of 633 nm). EC50s were calculated using Prism (GraphPad).

[0087] **Figure 9** provides a schematic of the study design for the human PCSK9 infusion mouse model to determine the cholesterol lowering effect of the present antibodies. MAB2 and MAB3 are Humaneered™ anti-PCSK9 antibodies that bind with high affinity to hPCSK9 with no detectable binding to murine PCSK9. To test whether the antibodies could both inhibit hPCSK9-mediated elevation of non-HDL cholesterol and prevent PCSK9-mediated degradation of hepatic LDL-R, the antibodies were each injected into mice 3 h before osmotic mini-pump implantation containing hPCSK9 (for continuous infusion). Plasma and liver tissue harvest were performed 24 h after hPCSK9 injection.

[0088] **Figure 10** shows that treatment with antibodies MAB2 and MAB3 resulted in accumulation of human PCSK9 ("hPCSK9") in the infusion mouse model. Both plasma IgG and hPCSK9 levels were quantified by Meso Scale Discovery (MSD) assay. For the IgG MSD assay, MSD Standard 96 plates (L11XA-3) were used. Briefly, plates were coated with 25 to 28 µl capture antigen, PCSK9-His, 1 µg/ml in PBS (25-28 ng/well) overnight at 4°C. The coating solution was dumped and the plates were blocked with 150 µl/well of 5% MSD Blocker A (R93AA-2) shaking for 1 h at room temperature. After washing the plate with PBS + 0.05% Tween-20 300 µl x 3 times, 25 µl of IgG calibrator dilutions (10 series dilutions with MSD blocker A from 10,000 to 0.0003 ng/ml), unknown plasma sample dilutions (10,000X with MSD blocker A), or quality control samples were added and incubated with shaking for 1 h at room temperature. After washing, 25 µl/well of 1 µg/ml detection antibody (MSD goat anti-mouse SULFO-TAG Labeled detection antibody, R32AC-5, diluted with 1% BSA / PBS / 0.05% Tween 20) (MSD goat anti-human SULFO-TAG Labeled detection antibody, R32AJ-5) was added and incubated with shaking for 1 h at room temperature. After wash and addition of 150 µl/well 1X read buffer T, plate was read immediately on MSD SECTOR Imager 6000. A plot of the standard curve and unknown samples were calculated using MSD data analysis software.

[0089] Plasma IgG levels were quantified by Meso Scale Discovery (MSD) assay. Free antibody was measured using hPCSK9 for capture. This assay measured "free" antibody and possibly measures 1:1 Ab:PCSK9 complexes. For IgG MSD assay, MSD Standard 96 plates (L11XA-3) were used. Briefly, plates were coated with 25 to 28 µl capture antigen, PCSK9-His, 1 µg/ml in PBS (25-28 ng/well) overnight at 4°C. The coating solution was removed and the plates were blocked with 150 µl/well of 5% MSD Blocker A (R93AA-2) shaking for 1 h at room temperature. After washing the plate with PBS + 0.05% Tween-20 300 µl x 3 times, 25 µl of IgG calibrator dilutions (10 series dilutions with MSD blocker A from 10,000 to 0.0003 ng/ml),

unknown plasma sample dilutions (10,000X with MSD blocker A), or quality control samples were added and incubated with shaking for 1 h at room temperature. After washing, 25 µl/well of 1 µg/ml detection antibody (MSD goat anti-mouse SULFO-TAG Labeled detection antibody, R32AC-5, diluted with 1% BSA / PBS / 0.05% Tween 20) was added and incubated with shaking for 1 h at room temperature. After wash and addition of 150 µl/well 1X read buffer T, plate was read immediately on MSD SECTOR Imager 6000. A plot of the standard curve and unknown samples were calculated using MSD data analysis software.

[0090] The MSD hPCSK9 assay is similar to IgG assay, but with the following exceptions. The plates were coated with 25-28 µl capture antibody (7D16.C3: 2.95 mg/ml) at 1 µg/ml. After blocking the plates, 25 µl of hPCSK9 calibrator dilutions (10 points from 10,000 to 0.0003 ng/ml) and plasma sample dilutions (2,000X with MSD blocker A) were incubated with shaking for 1 h at room temperature followed by incubation with primary detection antibody (rabbit anti-PCSK9 polyclonal antibody, Ab4, in-house Rabbit ID #RB11835). An additional incubation step with secondary detection antibody (MSD goat anti-rabbit SULFO-TAG Labeled detection antibody, R32AB-5) was added before read with MSD SECTOR Imager 6000.

[0091] **Figure 11** illustrates that antibodies MAB2 and MAB3 lead to reduction in plasma non-HDL-cholesterol in the hPCSK9 infusion mouse model. Pre-injection of MAB2 antibody resulted in a 52% protection from hPCSK9-mediated elevation in non-HDL cholesterol. Pre-injection of MAB3 resulted in equivalent protection from hPCSK9-mediated elevation in non-HDL cholesterol. C57BL/6 mice were treated with vehicle alone, PCSK9 alone, PCSK9 + 20 mg/kg MAB2, or PCSK9 + 20 mg/kg MAB3. Individual values are shown with mean value demarcated as a horizontal bar. To quantify plasma total cholesterol level, Olympus clinical analyzer (Olympus America Inc.: Olympus AU400) was used. Plasma samples were diluted 1:3 in ddH2O and 40 µl of diluted plasma samples were quantified for total cholesterol level according to the manufacturer's directions. To quantify plasma HDL and non-HDL, lipoprotein cholesterol fractions were obtained using Spife 3000 from Helena Laboratories. All procedures, including sample preparation, gel preparation, sample application, gel electrophoresis, staining, washing, and drying were following the instructions provided in the operator's manual. The gel was then scanned in the Quick Scan 2000 using Slit 5 and the relative percentage of the lipoprotein cholesterol fractions was calculated using Helena densitometer. Finally, the absolute values of HDL and non-HDL were calculated by multiplication of the percentage of each fraction and total cholesterol levels.

[0092] **Figure 12** illustrates rat pharmacokinetic (PK) profiles for antibodies MAB2 and MAB3 (human IgG1-silent) in comparison with a "typical" IgG1 (PK) profile. There was no evidence of target mediated disposition (TMD), indicating that the antibodies are not cross-reactive with rodent PCSK9). For each test antibody, 3 male Lewis rats were injected at 10 mgs/kg. At time = 0, 1, 6, 24 h, 2, 4, 8 and 16 days, 250 µl of blood was sampled, and the cleared plasma diluted and evaluated in a capture ELISA (goat anti-human IgG) to measure total human antibody recovered. A standard curve was also generated for each test antibody. The quantity of the recovered IgG was graphed versus the expected recovery of a typical human IgG in a rat.

DETAILED DESCRIPTION

I. Introduction

[0093] The antibodies and antigen-binding molecules of the present invention specifically bind to proprotein convertase subtilisin/kexin type 9a ("PCSK9"). The present anti-PCSK9 antibodies and antigen-binding molecules bind to the catalytic domain of PCSK9 and disrupt the PCSK9/ low density lipoprotein receptor (LDL-R) complex, thereby preventing PCSK9-mediated downregulation of cellular LDL-R and LDL update. In particular, the anti-PCSK9 antibodies and antigen binding molecules bind to an epitope within residues 159-182 of PCSK9, for example, an epitope within the amino acid sequence ERITPPRYRADEYQPPDGGSLVE (SEQ ID NO:42), located in the catalytic domain of PCSK9. The anti-PCSK9 antibodies and antigen binding molecules of the invention are antagonists of PCSK9 in that they prevent, reduce and/or inhibit the interaction of PCSK9 with the low density lipid receptor (LDLR) and prevent, reduce and/or inhibit PCSK9-mediated degradation of the LDL-R, thereby facilitating increased uptake of low density lipoprotein cholesterol (LDL-C). The anti-PCSK9 antibodies and antigen binding molecules find use in treating subjects suffering from, *e.g.*, dyslipidemia, hypercholesterolemia, triglyceridemia and other PCSK9-mediated disease conditions.

II. Improved Anti-PCSK9 Antibodies Generally

[0094] Anti-PCSK9 antibody fragments can be produced by any means known in the art, including but not limited to, recombinant expression, chemical synthesis, and enzymatic digestion of antibody tetramers, whereas full-length monoclonal antibodies can be obtained by, *e.g.*, hybridoma or recombinant production. Recombinant expression can be from any

appropriate host cells known in the art, for example, mammalian host cells, bacterial host cells, yeast host cells, insect host cells, etc. When present, the constant regions of the anti-PCSK9 antibodies can be any type or subtype, as appropriate, and can be selected to be from the species of the subject to be treated by the present methods (*e.g.*, human, non-human primate or other mammal, for example, agricultural mammal (*e.g.*, equine, ovine, bovine, porcine, camelid), domestic mammal (*e.g.*, canine, feline) or rodent (*e.g.*, rat, mouse, hamster, rabbit). In some embodiments the anti-PCSK9 antibodies are humanized or Humaneered™. In some embodiments, the constant region isotype is IgG, for example, IgG1. In some embodiments, the human IgG1 constant region is mutated to have reduced binding affinity for an effector ligand such as Fc receptor (FcR), *e.g.*, Fc gamma R1, on a cell or the C1 component of complement. *See*, *e.g.*, U.S. Patent No. 5,624,821. Antibodies containing such mutations mediate reduced or no antibody-dependent cellular cytotoxicity (ADCC) or complement-dependent cytotoxicity (CDC). In some embodiments, amino acid residues L234 and L235 of the IgG1 constant region are substituted to Ala234 and Ala235. The numbering of the residues in the heavy chain constant region is that of the EU index (*see*, Kabat, et al., (1983) "Sequences of Proteins of Immunological Interest," U.S. Dept. Health and Human Services). *See also*, *e.g.*, Woodle, *et al*, *Transplantation* (1999) 68(5):608-616; Xu, *et al.*, *Cell Immunol* (2000) 200(1):16-26; and Hezareh, *et al.*, *J Virol* 75(24):12161-8.

[0095] Anti-PCSK9 antibodies or antigen-binding molecules of the invention also include single domain antigen-binding units which have a camelid scaffold. Animals in the camelid family include camels, llamas, and alpacas. Camelids produce functional antibodies devoid of light chains. The heavy chain variable (VH) domain folds autonomously and functions independently as an antigen-binding unit. Its binding surface involves only three CDRs as compared to the six CDRs in classical antigen-binding molecules (Fabs) or single chain variable fragments (scFvs). Camelid antibodies are capable of attaining binding affinities comparable to those of conventional antibodies. Camelid scaffold-based anti-PCSK9 molecules with binding specificities of the anti-PCSK9 antibodies exemplified herein can be produced using methods well known in the art, e.g., Dumoulin et al., Nature Struct. Biol. 11:500–515, 2002; Ghahroudi et al., FEBS Letters 414:521–526, 1997; and Bond et al., J Mol Biol. 332:643-55, 2003.

[0096] The improved anti-PCSK9 antibodies of the invention are engineered human antibodies with V-region sequences having substantial amino acid sequence identity to human germline V-region sequences while retaining the specificity and affinity of a reference antibody. *See*,

U.S. Patent Publication No. 2005/0255552 and U.S. Patent Publication No. 2006/0134098, both of which are hereby incorporated herein by reference. The process of improvement identifies minimal sequence information required to determine antigen-binding specificity from the variable region of a reference antibody, and transfers that information to a library of human partial V-region gene sequences to generate an epitope-focused library of human antibody V-regions. A microbial-based secretion system can be used to express members of the library as antibody Fab fragments and the library is screened for antigen-binding Fabs, for example, using a colony-lift binding assay. *See, e.g.*, U.S. Patent Publication No. 2007/0020685. Positive clones can be further characterized to identify those with the highest affinity. The resultant engineered human Fabs retain the binding specificity of the parent, reference anti-PCSK9 antibody, typically have equivalent or higher affinity for antigen in comparison to the parent antibody, and have V-regions with a high degree of sequence identity compared with human germ-line antibody V-regions.

[0097] The minimum binding specificity determinant (BSD) required to generate the epitope-focused library is typically represented by a sequence within the heavy chain CDR3 ("CDRH3") and a sequence within the light chain of CDR3 ("CDRL3"). The BSD can comprise a portion or the entire length of a CDR3. The BSD can be comprised of contiguous or non-contiguous amino acid residues. In some cases, the epitope-focused library is constructed from human V-segment sequences linked to the unique CDR3-FR4 region from the reference antibody containing the BSD and human germ-line J-segment sequences (*see*, U.S. Patent Publication No. 2005/0255552). Alternatively, the human V-segment libraries can be generated by sequential cassette replacement in which only part of the reference antibody V-segment is initially replaced by a library of human sequences. The identified human "cassettes" supporting binding in the context of residual reference antibody amino acid sequences are then recombined in a second library screen to generate completely human V-segments (*see*, U.S. Patent Publication No. 2006/0134098).

[0098] In each case, paired heavy and light chain CDR3 segments, CDR3-FR4 segments, or J-segments, containing specificity determinants from the reference antibody, are used to constrain the binding specificity so that antigen-binders obtained from the library retain the epitope-specificity of the reference antibody. Additional maturational changes can be introduced in the CDR3 regions of each chain during the library construction in order to identify antibodies with optimal binding kinetics. The resulting engineered human antibodies have V-segment sequences

derived from the human germ-line libraries, retain the short BSD sequence from within the CDR3 regions and have human germ-line framework 4 (FR4) regions.

[0099] Accordingly, in some embodiments, the anti-PCSK9 antibodies contain a minimum binding sequence determinant (BSD) within the CDR3 of the heavy and light chains derived from the originating or reference monoclonal antibody. The remaining sequences of the heavy chain and light chain variable regions (CDR and FR), *e.g.*, V-segment and J-segment, are from corresponding human germline and affinity matured amino acid sequences. The V-segments can be selected from a human V-segment library. Further sequence refinement can be accomplished by affinity maturation.

[0100] In another embodiment, the heavy and light chains of the anti-PCSK9 antibodies contain a human V-segment from the corresponding human germline sequence (FR1-CDR1-FR2-CDR2-FR3), *e.g.*, selected from a human V-segment library, and a CDR3-FR4 sequence segment from the originating monoclonal antibody. The CDR3-FR4 sequence segment can be further refined by replacing sequence segments with corresponding human germline sequences and/or by affinity maturation. For example, the FR4 and/or the CDR3 sequence surrounding the BSD can be replaced with the corresponding human germline sequence, while the BSD from the CDR3 of the originating monoclonal antibody is retained.

[0101] In some embodiments, the corresponding human germline sequence for the heavy chain V-segment is VH2 2-05. In some embodiments, the corresponding human germline sequence for the heavy chain J-segment is JH1, JH4, or JH5. The variable region genes are referenced in accordance with the standard nomenclature for immunoglobulin variable region genes. Current immunoglobulin gene information is available through the worldwide web, for example, on the ImMunoGeneTics (IMGT), V-base and PubMed databases. *See also*, Lefranc, *Exp Clin Immunogenet.* 2001;18(2):100-16; Lefranc, *Exp Clin Immunogenet.* 2001;18(3):161-74; *Exp Clin Immunogenet.* 2001;18(4):242-54; and Giudicelli, *et al.*, *Nucleic Acids Res.* 2005 Jan 1;33(Database issue):D256-61.

[0102] In some embodiments, the corresponding human germline sequence for the light chain V-segment is VK1 O2 or VK1 O12. In some embodiments, the corresponding human germline sequence for the light chain J-segment is JK2.

[0103] In some embodiments, the heavy chain V-segment has at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to the

amino acid sequence Q(I/V)TLKESGPVLVKPT(E/Q)TLTLTCTVSGFSLSTSG(M/V)GVGWIRQPPGKALEWLADIWWDDNKYYNPSLKSRLTISKDTSKNQVVLTMTNMDPVDTATYYCAR (SEQ ID NO:27). In some embodiments, the heavy chain V-segment has at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to the amino acid sequence QITLKESGPVLVKPTETLTLTCTVSGFSLSTSGVGVGWIRQPPGKALEWLADIWWDDNKYYNPSLKSRLTISKDTSKNQVVLTMTNMDPVDTATYYCAR (SEQ ID NO:25). In some embodiments, the heavy chain V-segment has at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to the amino acid sequence QVTLKESGPTLVKPTQTLTLTCTVSGFSLSTSGVGVGWIRQSPGKALEWLADIWWDDNKYYNPSLKSRLTISKDTSKNQVVLTMTNMDPVDTATYYCAR sequence (SEQ ID NO:26).

[0104] In some embodiments, the light chain V-segment has at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 85%, 89%, 90%, 93%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to the amino acid sequence DIQMTQSPSSLSASVGDRVTITCRA(G/S)Q(R/S)I(N/S)(H/N)NLHWYQQKPDESPRLLINFASRLISGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC (SEQ ID NO:29). In some embodiments, the heavy chain V-segment has at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 85%, 89%, 90%, 93%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to the amino acid sequence DIQMTQSPSSLSASVGDRVTITCRAGQRISHNLHWYQQKPDESPRLLINFASRLISGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC (SEQ ID NO:28).

[0105] In some embodiments:

i) the heavy chain CDR3 comprises the amino acid sequence ITTEGGFAY (SEQ ID NO:17); and

ii) the light chain CDR3 variable region comprises the amino acid sequence QQSNYWPLT (SEQ ID NO:24).

[0106] In some embodiments, the antibodies of the invention comprise a heavy chain variable region comprising a CDR1 comprising an amino acid sequence TSG(M/V)GVG (SEQ ID

NO:15); a CDR2 comprising an amino acid sequence DIWWDDNKYYNPSLKS (SEQ ID NO:16); and a CDR3 comprising an amino acid sequence of ITTEGGFAY(SEQ ID NO:17).

[0107] In some embodiments, the antibodies of the invention comprise a light chain variable region comprising a CDR1 comprising an amino acid sequence RA(G/S)Q(R/S)I(N/S)(H/N)NLH (SEQ ID NO:20); a CDR2 comprising an amino acid sequence FASR(L/S)IS (SEQ ID NO:23); and a CDR3 comprising an amino acid sequence of QQSNYWPLT (SEQ ID NO:24).

[0108] In some embodiments, the heavy chain variable region comprises a FR1 comprising the amino acid sequence of SEQ ID NO:32; a FR2 comprising the amino acid sequence of SEQ ID NO:33; a FR3 comprising the amino acid sequence of SEQ ID NO:34; and a FR4 comprising the amino acid sequence of SEQ ID NO:35. The identified amino acid sequences may have one or more substituted amino acids (*e.g.*, from affinity maturation) or one or two conservatively substituted amino acids.

[0109] In some embodiments, the light chain variable region comprises a FR1 comprising an amino acid sequence of SEQ ID NO:36; a FR2 comprising the amino acid sequence of SEQ ID NO:37; a FR3 comprising the amino acid sequence of SEQ ID NO:38; and a FR4 comprising the amino acid sequence of SEQ ID NO:39. The identified amino acid sequences may have one or more substituted amino acids (*e.g.*, from affinity maturation) or one or two conservatively substituted amino acids.

[0110] Over their full length, the variable regions of the anti-PCSK9 antibodies of the present invention generally will have an overall variable region (*e.g.*, FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4) amino acid sequence identity of at least about 85%, for example, at least about 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% to the corresponding human germline variable region amino acid sequence. For example, the heavy chain of the anti-PCSK9 antibodies can have at least about 85%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the human germline variable region Vh2 2-05. The light chain of the anti-PCSK9 antibodies can have at least about 85%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the human germline variable region Vk1 O2. In some embodiments, only amino acids within the framework regions are added, deleted or substituted. In some embodiments, the sequence identity comparison excludes the CD3.

[0111] In some embodiments, the anti-PCSK9 antibodies of the invention comprise a heavy chain variable region having at least 85%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to a heavy chain variable region of SEQ ID NO:40 and comprise a light chain variable region having at least 85%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to a light chain variable region of SEQ ID NO:41 (*i.e.*, consensus sequences).

[0112] In some embodiments, the anti-PCSK9 antibodies of the invention comprise a heavy chain variable region having at least 85%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to a heavy chain variable region of SEQ ID NO:1 and comprise a light chain variable region having at least 85%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to a light chain variable region of SEQ ID NO:3 (*i.e.*, mouse MAB1).

[0113] In some embodiments, the anti-PCSK9 antibodies of the invention comprise a heavy chain variable region having at least 85%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to a heavy chain variable region of SEQ ID NO:5 and comprise a light chain variable region having at least 85%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to a light chain variable region of SEQ ID NO:7 (*i.e.*, MAB2).

[0114] In some embodiments, the anti-PCSK9 antibodies of the invention comprise a heavy chain variable region having at least 85%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to a heavy chain variable region of SEQ ID NO:9 and comprise a light chain variable region having at least 85%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to a light chain variable region of SEQ ID NO:11 (*i.e.*, MAB3).

[0115] For identified amino acid sequences less than 20 amino acids in length, one or two conservative amino acid residue substitutions can be tolerated while still retaining the desired specific binding and/or antagonist activity.

[0116] The anti-PCSK9 antibodies of the present invention generally will bind PCSK9 with an equilibrium dissociation constant (K_D) of less than about 10^{-8} M or 10^{-9} M, for example, less than about 10^{-10} M or 10^{-11} M, in some embodiments less than about 10^{-12} M or 10^{-13} M.

[0117] The anti-PCSK9 antibodies optionally can be multimerized and used according to the methods of this invention. The anti- PCSK9 antibodies can be a full-length tetrameric antibody (*i.e.*, having two light chains and two heavy chains), a single chain antibody (*e.g.*, a scFv), or a molecule comprising antibody fragments that form one or more antigen-binding sites and confer PCSK9-binding specificity, *e.g.*, comprising heavy and light chain variable regions (for instance, Fab' or other similar fragments).

[0118] The invention further provides polynucleotides encoding the antibodies described herein, *e.g.*, polynucleotides encoding heavy or light chain variable regions or segments comprising the complementary determining regions as described herein. In some embodiments, the polynucleotide sequence is optimized for expression, e.g., optimized for mammalian expression or optimized for expression in a particular cell type. In some embodiments, the polynucleotide encoding the heavy chain has at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% nucleic acid sequence identity with a polynucleotide selected from the group consisting of SEQ ID NO:2, SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:46, and SEQ ID NO:48. In some embodiments, the polynucleotide encoding the light chain has at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% nucleic acid sequence identity with a polynucleotide selected from the group consisting of SEQ ID NO:4, SEQ ID NO:8, SEQ ID NO:12, SEQ ID NO:47, and SEQ ID NO:49.

[0119] In some embodiments, the polynucleotide encoding the heavy chain has at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% nucleic acid sequence identity with a polynucleotide of SEQ ID NO:2. In some embodiments, the polynucleotide encoding the light chain has at least 85%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% nucleic acid sequence identity with a polynucleotide of SEQ ID NO:4 (*i.e.*, MAB1).

[0120] In some embodiments, the polynucleotide encoding the heavy chain has at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% nucleic acid sequence identity with a polynucleotide selected from the group consisting of SEQ ID NO:6 and SEQ ID NO:46. In some embodiments, the polynucleotide encoding the light chain has at least 85%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% nucleic acid

sequence identity with a polynucleotide selected from the group consisting of SEQ ID NO:8 and SEQ ID NO: 47 (*i.e.*, MAB2).

[0121] In some embodiments, the polynucleotide encoding the heavy chain has at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% nucleic acid sequence identity with a polynucleotide selected from the group consisting of SEQ ID NO:10 and SEQ ID NO:48. In some embodiments, the polynucleotide encoding the light chain has at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% nucleic acid sequence identity with a polynucleotide selected from the group consisting of SEQ ID NO:12 and SEQ ID NO:49 (*i.e.*, MAB3).

III. Assays for Identifying Anti-PCSK9 Antibodies

[0122] Antagonist antibodies can be identified by generating anti-PCSK9 antibodies and then testing each antibody for the ability to reduce or inhibit PCSK9 mediated events, *e.g.*, binding to the LDLR, promoting the degradation of the LDLR. The assays can be carried out *in vitro* or *in vivo*. Exemplary antibodies bind to PCSK9, disrupt PCSK9 from forming a complex with LDLR, and reduce or inhibit PCSK9-mediated degradation of LDLR.

[0123] The binding of the antibodies or antigen binding molecules to PCSK9 can be determined using any method known in the art, including without limitation, ELISA, Biacore and Western Blot.

[0124] PCSK9-mediated degradation of LDLR also can be measured using any method known in the art. In one embodiment, the ability of the anti-PCSK9 antibody or antigen binding molecule to inhibit LDLR degradation is determined using an infusion mouse model. Anti-PCSK9 antibodies or antigen binding molecules are infused intravenously (*e.g.*, 3 µg/hour) into a mouse and the levels of LDLR in liver membrane preparations is determined in comparison to the levels of LDLR in liver membrane preparations from a mouse that has received intravenous infusions of a control antibody (*e.g.*, that binds to an unrelated antigen). Mice that have received antagonist anti-PCSK9 antibodies will have detectably higher levels of LDLR, *e.g.*, at least 10%, 20%, 50%, 80%, 100% higher, in comparison to mice that have received the control antibody.

[0125] Anti-PCSK9 antagonist antibodies also can be tested for their therapeutic efficacy in reducing plasma levels of LCL-C, non-HDL-C and/or total cholesterol. Anti-PCSK9 antibodies or antigen binding molecules are infused intravenously (*e.g.*, 3 µg/hour) into a mammal (*e.g.*,

mouse, rat, non-human primate, human) and the plasma levels of LCL-C, non-HDL-C and/or total cholesterol is determined in comparison to the plasma levels of LCL-C, non-HDL-C and/or total cholesterol from the same mammal before treatment or from a mammal that has received intravenous infusions of a control antibody (*e.g.*, that binds to an unrelated antigen). The mammal that has received antagonist anti-PCSK9 antibodies will have detectably lower plasma levels of LCL-C, non-HDL-C and/or total cholesterol, *e.g.*, at least 10%, 20%, 50%, 80%, 100% lower, in comparison to the mammal before treatment or the mammal that has received the control antibody.

IV. Compositions Comprising Anti-PCSK9 Antibodies

[0126] The invention provides pharmaceutical compositions comprising the present anti-PCSK9 antibodies or antigen-binding molecules formulated together with a pharmaceutically acceptable carrier. The compositions can additionally contain other therapeutic agents that are suitable for treating or preventing a given disorder. Pharmaceutically carriers enhance or stabilize the composition, or to facilitate preparation of the composition. Pharmaceutically acceptable carriers include solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like that are physiologically compatible.

[0127] A pharmaceutical composition of the present invention can be administered by a variety of methods known in the art. The route and/or mode of administration vary depending upon the desired results. It is preferred that administration be intravenous, intramuscular, intraperitoneal, or subcutaneous, or administered proximal to the site of the target. The pharmaceutically acceptable carrier should be suitable for intravenous, intramuscular, subcutaneous, parenteral, intranasal, inhalational, spinal or epidermal administration (e.g., by injection or infusion). Depending on the route of administration, the active compound, i.e., antibody, bispecific and multispecific molecule, may be coated in a material to protect the compound from the action of acids and other natural conditions that may inactivate the compound.

[0128] The antibodies, alone or in combination with other suitable components, can be made into aerosol formulations (i.e., they can be "nebulized") to be administered via inhalation. Aerosol formulations can be placed into pressurized acceptable propellants, such as dichlorodifluoromethane, propane, nitrogen, and the like.

[0129] In some embodiments, the composition is sterile and fluid. Proper fluidity can be maintained, for example, by use of coating such as lecithin, by maintenance of required particle size in the case of dispersion and by use of surfactants. In many cases, it is preferable to include isotonic agents, for example, sugars, polyalcohols such as mannitol or sorbitol, and sodium chloride in the composition. Long-term absorption of the injectable compositions can be brought about by including in the composition an agent which delays absorption, for example, aluminum monostearate or gelatin.

[0130] Pharmaceutical compositions of the invention can be prepared in accordance with methods well known and routinely practiced in the art. Pharmaceutically acceptable carriers are determined in part by the particular composition being administered, as well as by the particular method used to administer the composition. Accordingly, there is a wide variety of suitable formulations of pharmaceutical compositions of the present invention. Applicable methods for formulating the antibodies and determining appropriate dosing and scheduling can be found, for example, in *Remington: The Science and Practice of Pharmacy*, 21st Ed., University of the Sciences in Philadelphia, Eds., Lippincott Williams & Wilkins (2005); and in *Martindale: The Complete Drug Reference*, Sweetman, 2005, London: Pharmaceutical Press., and in Martindale, *Martindale: The Extra Pharmacopoeia*, 31st Edition., 1996, Amer Pharmaceutical Assn, and Sustained and Controlled Release Drug Delivery Systems, J.R. Robinson, ed., Marcel Dekker, Inc., New York, 1978, each of which are hereby incorporated herein by reference. Pharmaceutical compositions are preferably manufactured under GMP conditions. Typically, a therapeutically effective dose or efficacious dose of the anti-PCSK9 antibody is employed in the pharmaceutical compositions of the invention. The anti-PCSK9 antibodies are formulated into pharmaceutically acceptable dosage forms by conventional methods known to those of skill in the art. Dosage regimens are adjusted to provide the desired response (e.g., a therapeutic response). In determining a therapeutically or prophylactically effective dose, a low dose can be administered and then incrementally increased until a desired response is achieved with minimal or no undesired side effects. For example, a single bolus may be administered, several divided doses may be administered over time or the dose may be proportionally reduced or increased as indicated by the exigencies of the therapeutic situation. It is especially advantageous to formulate parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units suited as unitary dosages for the subjects to be treated; each unit contains a predetermined quantity of active

compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier.

[0131] Actual dosage levels of the active ingredients in the pharmaceutical compositions of the present invention can be varied so as to obtain an amount of the active ingredient which is effective to achieve the desired therapeutic response for a particular patient, composition, and mode of administration, without being toxic to the patient. The selected dosage level depends upon a variety of pharmacokinetic factors including the activity of the particular compositions of the present invention employed, or the ester, salt or amide thereof, the route of administration, the time of administration, the rate of excretion of the particular compound being employed, the duration of the treatment, other drugs, compounds and/or materials used in combination with the particular compositions employed, the age, sex, weight, condition, general health and prior medical history of the patient being treated, and like factors.

[0132] In some embodiments, the pharmacological compositions comprise a mixture of the anti-PCSK9 antibody or antigen binding molecule and a second pharmacological agent. For example, the compositions may comprise a anti-PCSK9 antibody or antigen-binding molecule of the invention and an agent known to be beneficial for reducing cholesterol, including LDL-C, non-HDL-C and total cholesterol and/or raising HDL-C.

[0133] Exemplary second agents for inclusion in mixtures with the present anti-PCSK9 antagonist antibody or antigen binding molecule include without limitation an HMG-CoA reductase inhibitor (*i.e.*, a statin), fibrates (*e.g.*, clofibrate, gemfibrozil, fenofibrate, ciprofibrate, bezafibrate), niacin and analogs thereof, cholesterol absorption inhibitors, bile acid sequestrants (*e.g.*, cholestyramine, colestipol, colesvelam), an ileal bile acid transport (IBAT) inhibitor, a thyroid hormone mimetic (*e.g.*, compound KB2115), a microsomal triglyceride transfer protein (MTP) inhibitor, a dual peroxisome proliferator-activated receptor (PPAR) alpha and gamma agonist, an acyl CoA:diacylglycerol acyltransferase (DGAT) inhibitor, an acyl CoA:cholesterol acyltransferase (ACAT) inhibitor, a Niemann Pick C1-like 1 (NPC1-L1) inhibitor (*e.g.*, ezetimibe), an agonist of ATP Binding Cassette (ABC) proteins G5 or G8, a cholesterol ester transfer protein (CETP) inhibitor, an inhibitory nucleic acid targeting PCSK9 and an inhibitory nucleic acid targeting apoB100. Lipid-lowering agents are known in the art, and described, *e.g.*, in *Goodman and Gilman's The Pharmacological Basis of Therapeutics*, 11th Ed., Brunton, Lazo

and Parker, Eds., McGraw-Hill (2006); *2009 Physicians' Desk Reference (PDR)*, for example, in the 63rd (2008) Eds., Thomson PDR.

[0134] Additional lipid lowering agents of use in the present compositions are described and/or reviewed in, *e.g.*, Chang, *et al.*, *Curr Opin Drug Disco Devel* (2002) 5(4):562-70; Sudhop, *et al.*, *Drugs* (2002) 62(16):2333-47; Bays and Stein, *Expert Opin Pharmacother* (2003) 4(11):1901-38; Kastelein, *Int J Clin Pract Suppl* (2003) Mar(134):45-50; Tomoda and Omura, *Pharmacol Ther* (2007) 115(3):375-89; Tenenbaum, *et al.*, *Adv Cardiol* (2008) 45:127-53; Tomkin, *Diabetes Care* (2008) 31(2):S241-S248; Lee, *et al.*, *J Microbiol Biotechnol* (2008) 18(11):1785-8; Oh, *et al.*, *Arch Pharm Res* (2009) 32(1): 43-7; Birch, *et al*, *J Med Chem* (2009) 52(6):1558-68; and Baxter and Webb, *Nature Reviews Drug Discovery* (2009) 8:308-320.

[0135] In some embodiments, the anti-PCSK9 antibodies or antigen binding molecules of the invention are provided as a mixture with a statin. Exemplary statins include without limitation, atorvastatin, cerivastatin, fluvastatin, lovastatin, mevastatin, pitavastatin, pravastatin, rosuvastatin, and simvastatin.

[0136] In some embodiments, the anti-PCSK9 antibodies or antigen binding molecules of the invention are provided as a mixture with a pharmacological agent that induces hypercholesterolemia or triglyceridemia. For example, the second pharmacological agent may be a protease inhibitor, for example, Saquinavir, Ritonavir, Indinavir, Nelfinavir, Amprenavir, Lopinavir, Atazanavir, Fosamprenavir, Tipranavir, Darunavir, abacavir-lamivudine-zidovudine (Trizivir). In some embodiments, the second pharmacological agent is Tacrolimus.

V. Methods of Using Anti-PCSK9 Antibodies

A. Conditions Subject to Treatment with Anti-PCSK9 Antibodies

[0137] The anti-PCSK9 antagonist antibodies and antigen binding molecules of the invention find use in treating any disease condition mediated by the activity or over-activity of PCSK9.

[0138] For example, individuals who have or who are at risk of developing dyslipidemia or hypercholesterolemia for any number of reasons or etiologies may benefit from administration of the present anti-PCSK9 antagonist antibodies and antigen binding molecules. For example, the individual may have familial or genetically transmitted homozygous or heterozygous hypercholesterolemia in which a functional LDL-R is present. Genetic mutations associated

with and/or causative of familial or genetically inherited hypercholesterolemia are summarized, *e.g.*, in Burnett and Hooper, *Clin Biochem Rev* (2008) 29(1):11-26. The individual may also have other disease conditions or engage in behaviors that contribute to or increase the risk of developing dyslipidemia or hypercholesterolemia. For example, the individual may be obese, or suffer from diabetes or metabolic syndrome. The individual may be a smoker, lead a sedentary lifestyle, or have a diet high in cholesterol.

[0139] Targeting PCSK9 is useful for the reduction, reversal, inhibition or prevention of dyslipidemia, hypercholesterolemia and postprandial triglyceridemia. *See*, *e.g.*, Le May, *et al.*, *Arterioscler Thromb Vasc Biol* (2009) 29(5):684-90; Seidah, *Expert Opin Ther Targets* (2009) 13(1):19-28; and Poirier, *et al.*, *J Biol Chem* (2009) PMID 19635789. Accordingly, administration of the present anti-PCSK9 antagonist antibodies and antigen binding molecules finds use in reducing, reversing, inhibiting and preventing, dyslipidemia, hypercholesterolemia and postprandial triglyceridemia in an individual in need thereof.

[0140] The present anti-PCSK9 antagonist antibodies and antigen binding molecules find use in reducing or lowering low density lipoprotein cholesterol (LDL-C) in an individual in need thereof. The individual may have persistently elevated levels of LDL-C. In some embodiments, the individual has LDL-C plasma levels consistently above 80 mg/dL, for example above 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190 mg/dL, or higher. The present anti-PCSK9 antagonist antibodies and antigen binding molecules also find use in reducing or lowering non-high density lipoprotein cholesterol (non-HDL-C) or total cholesterol in an individual in need thereof.

[0141] The individual may already be taking another pharmacological agent to lower cholesterol, and be resistant or intolerant to this agent. For example, the individual may already be under a therapeutic regimen of a statin, which may have proven inefficacious in this individual in lowering LDL-C, non-HDL-C or total cholesterol to acceptable levels. The individual may also be intolerant to the administration of a statin. Combined administration of the present anti-PCSK9 antagonist antibodies and antigen binding molecules with a second agent useful in lowering LDL-C or non-HDL-C and/or raising HDL-C will improve the efficaciousness and tolerance of the second agent, for example, by allowing lower doses of the second agent to be administered.

[0142] In some embodiments, the individual has a gain-of-function mutation in the PCSK9 gene, for example, that results in an aberrant increase in the degradation of the LDLR.

[0143] In some embodiments, the individual is receiving a pharmacological agent the induces dyslipidemia or hypercholesterolemia, *i.e.*, the individual has drug-induced dyslipidemia or hypercholesterolemia. For example, the individual may be receiving a therapeutic regime of protease inhibitors, *e.g.*, for the treatment of an HIV infection. Another pharmacological agent known to cause elevated levels of plasma triglycerides is Tacrolimus, an immunosuppressive drug administered to transplantation patients. Cyclosporin has been shown to increase LDL significantly. *See*, *e.g.*, Ballantyne, *et al.* (1996) 78(5):532-5. Second-generation antipsychotics (*e.g.*, aripiprazole, clozapine, olanzapine, quetiapine, risperidone, and ziprasidone) have also been associated with dyslipidemia. *See*, *e.g.*, Henderson, *J Clin Psychiatry* (2008) 69(2):e04 and Brooks, *et al.*, *Curr Psychiatry Rep* (2009) 11(1):33-40.

B. Administration of Anti-PCSK9 Antibodies

[0144] A physician or veterinarian can start doses of the antibodies of the invention employed in the pharmaceutical composition at levels lower than that required to achieve the desired therapeutic effect and gradually increase the dosage until the desired effect is achieved. In general, effective doses of the compositions of the present invention vary depending upon many different factors, including the specific disease or condition to be treated, means of administration, target site, physiological state of the patient, whether the patient is human or an animal, other medications administered, and whether treatment is prophylactic or therapeutic. Treatment dosages need to be titrated to optimize safety and efficacy. For administration with an antibody, the dosage ranges from about 0.0001 to 100 mg/kg, and more usually 0.01 to 5 mg/kg, of the host body weight. For example dosages can be 1 mg/kg body weight or 10 mg/kg body weight or within the range of 1-10 mg/kg. Dosing can be daily, weekly, bi-weekly, monthly, or more or less often, as needed or desired. An exemplary treatment regime entails administration once weekly, once per every two weeks or once a month or once every 3 to 6 months.

[0145] In some embodiments, an polynucleotide encoding an anti-PCSK9 antibody or antigen binding molecule of the invention is administered. In embodiments where the agent is a nucleic acid, typical dosages can range from about 0.1 mg/kg body weight up to and including about 100 mg/kg body weight, *e.g.*, between about 1 mg/kg body weight to about 50 mg/kg body weight. In some embodiments, about 1, 2, 3, 4, 5, 10, 15, 20, 30, 40 or 50 mg/kg body weight.

[0146] The antibody can be administered in single or divided doses. Antibody is usually administered on multiple occasions. Intervals between single dosages can be weekly, bi-weekly, monthly or yearly, as needed or desired. Intervals can also be irregular as indicated by measuring blood levels of anti-PCSK9 antibody in the patient. In some methods, dosage is adjusted to achieve a plasma antibody concentration of 1–1000 μg/ml and in some methods 25-300 μg/ml. Alternatively, antibody can be administered as a sustained release formulation, in which case less frequent administration is required. Dosage and frequency vary depending on the half-life of the antibody in the patient. In general, humanized antibodies show longer half life than that of chimeric antibodies and nonhuman antibodies. The dosage and frequency of administration can vary depending on whether the treatment is prophylactic or therapeutic. In prophylactic applications, a relatively low dosage is administered at relatively infrequent intervals over a long period of time. Some patients continue to receive treatment for the rest of their lives. In therapeutic applications, a relatively high dosage at relatively short intervals is sometimes required until progression of the disease is reduced or terminated, and preferably until the patient shows partial or complete amelioration of symptoms of disease. Thereafter, the patient can be administered a prophylactic regime. In some embodiments, the anti-PCSK9 antibody or antigen binding agent is administered when plasma LDL-C levels in the patient rise above a predetermined threshold level, for example, at least about 80 mg/dL, for example, at least about 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190 mg/dL, or higher.

C. Co-Administration with a Second Agent

[0147] The PCSK9 antibody antagonist can be used in combination with agents known to be beneficial for reducing cholesterol, including LDL-C, non-HDL-C and total cholesterol and/or raising HDL-C.

[0148] Active agents can be administered together in a mixture with the anti-PCSK9 antagonist antibody or each agent can be administered separately. The antibody agent and the other active agent can, but need not, be administered concurrently.

[0149] Exemplary second agents for use in co-administration with the present anti-PCSK9 antagonist antibody or antigen binding molecule include without limitation an HMG-CoA reductase inhibitor (*i.e.*, a statin), fibrates (*e.g.*, clofibrate, gemfibrozil, fenofibrate, ciprofibrate, bezafibrate), niacin and analogs thereof, cholesterol absorption inhibitors, bile acid sequestrants (*e.g.*, cholestyramine, colestipol, colesvelam), an ileal bile acid transport (IBAT) inhibitor, a

thyroid hormone mimetic (*e.g.*, compound KB2115), a microsomal triglyceride transfer protein (MTP) inhibitor, a dual peroxisome proliferator-activated receptor (PPAR) alpha and gamma agonist, an acyl CoA:diacylglycerol acyltransferase (DGAT) inhibitor, an acyl CoA:cholesterol acyltransferase (ACAT) inhibitor, a Niemann Pick C1-like 1 (NPC1-L1) inhibitor (*e.g.*, ezetimibe), an agonist of ATP Binding Cassette (ABC) proteins G5 or G8, a cholesterol ester transfer protein (CETP) inhibitor, an inhibitory nucleic acid targeting PCSK9 and an inhibitory nucleic acid targeting apoB100.

[0150] Additional lipid lowering agents of use are described and/or reviewed in, *e.g.*, Chang, *et al.*, *Curr Opin Drug Disco Devel* (2002) 5(4):562-70; Sudhop, *et al.*, *Drugs* (2002) 62(16):2333-47; Bays and Stein, *Expert Opin Pharmacother* (2003) 4(11):1901-38; Kastelein, *Int J Clin Pract Suppl* (2003) Mar(134):45-50; Tomoda and Omura, *Pharmacol Ther* (2007) 115(3):375-89; Tenenbaum, *et al.*, *Adv Cardiol* (2008) 45:127-53; Tomkin, *Diabetes Care* (2008) 31(2):S241-S248; Lee, *et al.*, *J Microbiol Biotechnol* (2008) 18(11):1785-8; Oh, *et al.*, *Arch Pharm Res* (2009) 32(1): 43-7; Birch, *et al*, *J Med Chem* (2009) 52(6):1558-68; and Baxter and Webb, *Nature Reviews Drug Discovery* (2009) 8:308-320.

[0151] In some embodiments, the anti-PCSK9 antibodies or antigen binding molecules of the invention are co-administered with a statin. Exemplary statins include without limitation, atorvastatin, cerivastatin, fluvastatin, lovastatin, mevastatin, pitavastatin, pravastatin, rosuvastatin, and simvastatin.

[0152] In some embodiments, the anti-PCSK9 antibodies or antigen binding molecules of the invention are co-administered with a pharmacological agent that induces hypercholesterolemia or triglyceridemia. For example, the second pharmacological agent may be a protease inhibitor, for example, Saquinavir, Ritonavir, Indinavir, Nelfinavir, Amprenavir, Lopinavir, Atazanavir, Fosamprenavir, Tipranavir, Darunavir, abacavir-lamivudine-zidovudine (Trizivir). In some embodiments, the second pharmacological agent is Tacrolimus.

[0153] In some embodiments, the anti-PCSK9 antibodies or antigen binding molecules of the invention are co-administered with an inhibitory nucleic acid (*e.g.*, an siRNA, an miRNA, an antisense sequence, a ribozyme) that specifically targets PCSK9 or apoB100.

VI. Kits

[0154] The pharmaceutical compositions of the present invention can be provided in a kit. In certain embodiments, a kit of the present invention comprises an anti-PCSK9 antagonist antibody or antigen binding molecule of the invention, as described herein. The anti-PCSK9 antibodies or antigen binding molecules can be provided in uniform or varying dosages.

[0155] In some embodiments, the kits comprise one or more second pharmacological agents, as described herein. The second pharmacological agent can be provided in the same formulation or in separate formulations from the anti-PCSK9 antibodies or antigen binding molecules. The dosages of the first and second agents can be independently uniform or varying.

[0156] In some embodiments, the kits comprise the PCSK9 antibody antagonist and one or more agents known to be beneficial for reducing cholesterol, including LDL-C, non-HDL-C and total cholesterol and/or raising HDL-C.

[0157] Exemplary second agents for inclusion in the kits with the present anti-PCSK9 antagonist antibody or antigen binding molecule include without limitation an HMG-CoA reductase inhibitor (*i.e.*, a statin), fibrates (*e.g.*, clofibrate, gemfibrozil, fenofibrate, ciprofibrate, bezafibrate), niacin and analogs thereof, cholesterol absorption inhibitors, bile acid sequestrants (*e.g.*, cholestyramine, colestipol, colesvelam), an ileal bile acid transport (IBAT) inhibitor, a thyroid hormone mimetic (*e.g.*, compound KB2115), a microsomal triglyceride transfer protein (MTP) inhibitor, a dual peroxisome proliferator-activated receptor (PPAR) alpha and gamma agonist, an acyl CoA:diacylglycerol acyltransferase (DGAT) inhibitor, an acyl CoA:cholesterol acyltransferase (ACAT) inhibitor, a Niemann Pick C1-like 1 (NPC1-L1) inhibitor (*e.g.*, ezetimibe), an agonist of ATP Binding Cassette (ABC) proteins G5 or G8, a cholesterol ester transfer protein (CETP) inhibitor, an inhibitory nucleic acid targeting PCSK9 and an inhibitory nucleic acid targeting apoB100.

[0158] Additional lipid lowering agents of use in the kits are described and/or reviewed in, *e.g.*, Chang, *et al.*, *Curr Opin Drug Disco Devel* (2002) 5(4):562-70; Sudhop, *et al.*, *Drugs* (2002) 62(16):2333-47; Bays and Stein, *Expert Opin Pharmacother* (2003) 4(11):1901-38; Kastelein, *Int J Clin Pract Suppl* (2003) Mar(134):45-50; Tomoda and Omura, *Pharmacol Ther* (2007) 115(3):375-89; Tenenbaum, *et al.*, *Adv Cardiol* (2008) 45:127-53; Tomkin, *Diabetes Care* (2008) 31(2):S241-S248; Lee, *et al.*, *J Microbiol Biotechnol* (2008) 18(11):1785-8; Oh, *et*

al., *Arch Pharm Res* (2009) 32(1): 43-7; Birch, *et al*, *J Med Chem* (2009) 52(6):1558-68; and Baxter and Webb, *Nature Reviews Drug Discovery* (2009) 8:308-320.

[0159] In some embodiments, the anti-PCSK9 antibodies or antigen binding molecules of the invention are provided in kits with a statin. Exemplary statins include without limitation, atorvastatin, cerivastatin, fluvastatin, lovastatin, mevastatin, pitavastatin, pravastatin, rosuvastatin, and simvastatin.

[0160] In some embodiments, the anti-PCSK9 antibodies or antigen binding molecules of the invention are provided in kits with a pharmacological agent that induces hypercholesterolemia or triglyceridemia. For example, the second pharmacological agent may be a protease inhibitor, for example, Saquinavir, Ritonavir, Indinavir, Nelfinavir, Amprenavir, Lopinavir, Atazanavir, Fosamprenavir, Tipranavir, Darunavir, abacavir-lamivudine-zidovudine (Trizivir). In some embodiments, the second pharmacological agent is Tacrolimus.

EXAMPLES

[0161] The following examples are offered to illustrate, but not to limit the claimed invention.

Example 1: Generation and Identification of the PCSK9 Antagonist MAB1

Summary

[0162] Studies were performed to generate a functional antibody antagonist against Pcsk9. Multiple hybridomas were identified that secreted an antibody capable of binding to a His-tagged version of the protein. Antibodies from hybridomas were evaluated for functional antagonist activity as measured by their ability to inhibit Pcsk9-mediated degradation of the LDL receptor on HepG2 cells resulting in an increased ability of these cells to take up LDL cholesterol. A potent functional murine anti-human Pcsk9 IgG1-kappa monoclonal antibody was identified and designated as MAB1.

Methods

Antigen and other proteins

[0163] A stable expression cell line secreting human Pcsk9 protein was generated by transfection of HEK293 Freestyle™ cells (Invitrogen, Carlsbad, Ca). Briefly, the cells cultivated in Freestyle™ medium (Invitrogen) plus 10 % fetal calf serum in adherent mode on BioCoat flasks (Becton Dickinson) were transfected using Lipofectamine 2000™ transfection reagent and a recombinant plasmid featuring the mellittin signal sequence, the mature Pcsk9 cDNA (aa 31-692) and a his_6 tag at the C-terminus of the sequence (cloned by E.Hampton, GNF, NPL 010051). 48 hours post transfection selection of positive transfectants was started by adding 100 µg/mL Zeocin into the cultivation medium. Four weeks later four stable cell pools of Pcsk9-producing cells had emerged. Pool 4, being the highest producer, was adapted to serum-free suspension conditions in Freestyle™ medium and was subsequently scaled up for large scale production using the Wave™ bioreactor at a scale of 10-20 L production volume.

[0164] Several runs were performed over time yielding recombinant protein produced at rates between 12 and 30 mg/L. The cell supernatants were harvested and concentrated by crossflow filtration. The resulting concentrate was applied to a 25 mL NiNTA His-Bind Superflow column (equilibrated with 50 mM Tris/300 mM NaCl/1 mM $CaCl_2$/2 mM β- Mercaptoethanol, pH 7.4) at 0.5 mL/min. After baseline washing with 50 mM Tris/300 mM NaCl/20 mM Imidazole, pH 7.4, bound material was eluted with 50 mM Tris/300 mM NaCl/250 mM Imidazole, pH 7.4. The resulting eluate was dialyzed against PBS, pH 7.3, sterile filtered and aliquotted. A sample was analyzed by analytical size-exclusion chromatography for determination of oligomerization. The HPLC chromatogram obtained of the purified protein shows two peaks, the major one

accounting for 85%. HPLC-ESI MS analysis of full length protein reveals a mass of 58176.0 Da which is according the expected mass from mellitin-hsPcsk9 aa31-692-His with all Cysteine residues oxidized. Part of sample is additionally N-glycosylated. The contaminating protein of approx 13 kD mass resembles, most likely, the free pro-domain of the protein. The corresponding homologues of Pcsk9 from mouse, rat, and cynomolgus monkey were produced in large-scale transient expression approaches using again HEK293 Freestyle cells cultivated in serum-free suspension in Freestyle medium. The recombinant plasmids, mouse/rat Pcsk9 cDNA featuring a natural leader sequence and a his_6-tag at the C-terminus, and cyno Pcsk9 featuring a CD33 leader sequence and a C-terminal his_6 tag were transfected into Freestyle cells using Polyethylenimine as carrier of plasmid DNA at a ratio of 1:3 (μg/mL:μg/mL DNA:PEI). Production runs were carried out at the 10 liter scale in Wave™ bioreactors; protein purification and characterization was done analogously to the protocols described above for the human Pcsk9 protein.

Screening of hybridomas secreting functional antibodies to PCSK9

[0165] Hybridomas were generated, and ten days after fusion, hybridoma plates were screened for the presence of Pcsk9 specific antibodies. For the ELISA screen, Maxisorp 384-well plates (Nunc #464718) were coated with 50 μL of Pcsk9 (diluted to 15 ng/well in PBS) and incubated overnight at 4 °C. The remaining protein was aspirated and wells were blocked with 1 % BSA in PBS. After 30 min incubation at room temperature, the wells were washed four times with PBS + 0.05 % Tween (PBST). 15 μL of hybridoma supernatant was transferred to the ELISA plates. 15 μL of mouse serum, taken at the time of PLN removal, was diluted 1:1000 in PBS and added as a positive control. PBST. 50 μL of secondary antibody (goat anti mouse IgG – HRP (Jackson Immuno Research #115-035-071), diluted 1:5000 in PBS) was added to all wells on the ELISA plates. After incubation at room temperature for 1 h, the plates were washed eight times with PBST. 25 μL of TMB (KPL #50-76-05) was added and after 30 min incubation at room temperature; the plates were read at an absorbance of 605 nm.Cells from positive wells were expanded into 24- well plates in HT media (DMEM + 20 % FBS, Pen/Strep/Glu, 1x NEAA, 1x HT, 0.5x HFCS).

Antibody purification

[0166] Supernatant containing MAB1 was purified using protein G (Upstate # 16-266 (Billerica, MA)). Prior to loading the supernatant, the resin was equilibrated with 10 column volumes of PBS. Following binding of the sample, the column was washed with 10 column

volumes of PBS, and the antibody was then eluted with 5 column volumes of 0.1 M Glycine, pH 2.0. Column fractions were immediately neutralized with 1/10th volume of Tris HCl, pH 9.0. The OD280 of the fractions was measured, and positive fractions were pooled and dialyzed overnight against PBS, pH 7.2.

Affinity determination by solution equilibrium titration

[0167] Serial dilutions of Pcsk9 were prepared, and antibodies were added to each antigen concentration to reach a constant antibody concentration of 100 pM. 100 µL/well of each dilution mix was distributed in duplicate to a 96-well polypropylene microtiter plate (Greiner). The plate was sealed and incubated over night at room temperature. A 96-well Standard Bind microtiter plate (Meso Scale Discovery) was coated with 25µL of 1µg/mL Pcsk9 diluted in PBS. This plate was sealed and incubated over night at 4°C. After the incubation the antigen-coated Standard Bind micro titer plate was washed three times with 200 µL per well PBS/0.05 % (w/v) Tween 20. Subsequently, the plate was blocked with 150 µL/well PBS/5 % (w/v) BSA and incubated for one hour at room temperature with shaking. The washing steps were repeated and 25µL/well of the antibody-antigen preparation from the polypropylene microtiter plate was transferred into the antigen-coated Standard Bind plate. The Standard Bind plate was incubated for 60 min at room temperature with shaking. After three additional washing steps, 25µL of 1µg/mL Sulfo-Tag-labeled goat anti-mouse detection antibody (R32AC-5, Meso Scale Discovery) diluted in PBS/1% (w/v) BSA/0.05% (w/v) Tween20, buffer were added to each well and incubated one hour at room temperature with shaking. After washing the plate three times, 150 µL of 2X Read Buffer (R92TC-1, Meso Scale Discovery) was transferred into each well. Electrochemiluminescence signals were generated and detected by a Sector Imager 6000 (Meso Scale Discovery). The electrochemiluminescence data were exported and processed using prism software and the following equation:

$$y = \frac{[B_0]}{2} - \frac{\left[\frac{[B_0] + [A_0] + \frac{1}{K_d}}{2} - \sqrt{\frac{([B_0] + [A_0] + \frac{1}{K_d})^2}{4} - [B_0][A_0]}\right]^2}{2[B_0]}$$

TR-FRET assay

[0168] The TR-FRET assay was performed in 384-well white, shallow plates (Perkin Elmer, 6008280). hPcsk9-AF (10.7 nM) was incubated with serial dilutions of unlabeled hPcsk9 protein

and MAB1, MAB2, or MAB3 antibodies for 30 minutes at room temperature in 15 µL of assay buffer (20 mM HEPES, pH 7.2, 150 mM NaCl, 1 mM $CaCl_2$, 0.1% v/v Tween 20, and 0.1% w/v BSA). This was followed by addition of 5 µL of hLDL-R-Eu (4 nM) in assay buffer to the hPcsk9 and antibody preincubated complex, and incubation at room temperature for 90 minutes. The final concentrations of these labeled proteins were 8 nM of hPcsk9-AF and 1 nM of hLDL-R-Eu. The TR-FRET signal was measured with EnVision 2100 multilabel reader (Perkin Elmer) at 330 nm excitation and 665 nm emission. Data was converted to normalized values using the following formula: [(665 nm value x 10,000)/(615 nm value)]. The percentage inhibition was calculated with the following formula: 100 - [(normalized value of treated sample/averaged normalized value of untreated samples) x 100]. The percentage inhibition dose response curves were plotted using Prism version 5 with the formula, Y = Bottom + (Top - Bottom)/(1+10^((LogIC$_{50}$- X)*HillSlope)) (GraphPad Prism Software).

LDL-R turnover assay

[0169] HepG2 cells were trypsinized and seeded at 6 x 10_4 cells per well in 100 µL of culture medium in flat bottomed 96-well plates (Corning, 3595) which were pre-coated with 1% v/v collagen), then incubated at 37°C in 5% CO_2 for 24 hours. Generally, cells were treated with 100 µL of serum-free medium containing either hPcsk9 protein and MAB1, MAB2, or MAB3 antibody. After treatment, the medium was discarded, and the cells were washed with 100 µL of PBS. To harvest the cells, 100 µL of Versine (Biowhittaker, 17-771E) was added and incubated for one hour at 37°C in 5% CO_2, followed by addition of 100 µL of FACS buffer. The cells were transferred to V-bottom 96-well plates (Corning, 3894) and centrifuged at 1200 rpm for 5 minutes to pellet the cells. To block non-specific binding sites on the cells, 50 µL of 100 µg/mL normal rabbit IgG (MP biomedicals, 55944) and mouse IgG (Sigma, I5381) in FACS buffer were added to each well and incubated for 30 minutes in ice. Cells were centrifuged at 1200 rpm for 5 min, and the buffer was removed by flicking the plate. To label the cells, 10 µL of rabbit anti-hLDL-R-Alexa 647 IgG (5 µg/mL) and 10 µL of mouse anti-transferrin-R-phycoerythrin (PE) IgG (2 µg/mL) (CD71, Becton Dickinson Biosciences, 624048) labeled antibodies in FACS buffer were added to each well and incubated for 60 minutes in ice. Cells were centrifuged at 1200 rpm for 5 min, and the buffer was removed by flicking the plate. Unbound antibodies were removed by washing the cells twice with 200 µL per well of FACS buffer. Cells were fixed in 1% paraformaldehyde in PBS, and viable cells were gated (5000) and analyzed using a BD LSR II flow cytometer and FACSDIVA software (Becton Dickinson). The median value of PE

fluorescence was measured at excitation of 488 nm and emission of 575 nm. The median value of Alexa 647 fluorescence was measured at excitation of 488 nm and emission of 633 nm. A custom made rabbit anti-hLDL-R polyclonal IgG 583 was custom produced by Covance (Denver, PA, USA) for the FACS detection of surface hLDL-R on HepG2 cells. The rabbit anti-hLDL-R IgG 583 exhibited approximately a 7-fold window for detection of hLDL-R on the surface of HepG2 cells as compared to normal rabbit IgG. To determine the specificity of the anti-hLDL-R IgG 583 for LDL-R on the surface of HepG2 cells, an experiment was performed using hLDL-R protein as a competitor for binding of this IgG. A dose-dependent decrease in the average medium fluorescence for the anti-hLDL-R IgG 583 towards HepG2 cells was observed with increasing concentrations of hLDL-R protein. This demonstrated the anti-hLDL-R IgG 583 specifically recognizes the LDL-R on the surface of HepG2 cells as measured by FACS. Future work used directly labeled anti-hLDL-R-583-Alexa 647 IgG for the FACS quantification of LDL-R on the surface of HepG2 cells.

LDL-C uptake

[0170] HepG2 cells were trypsinized and seeded at 6 x 10^4 cells per well in 100 µL of culture medium in flat bottomed 96-well plates (Corning, 3595, which were pre-coated with 1% v/v collagen), then incubated at 37°C in 5% CO_2 for 24 hours. Unless otherwise stated, cells were treated with 100 µL of serum-free medium containing hPcsk9 protein and MAB1, MAB2, or MAB3 antibodies. After treatment, each well received 20 µL of 30 µg/mL 3,3'-dioctadecylindocarbocyanine-labeled low-density lipoprotein (DiI-LDL) (Intracell, RP-077-175) in serum-free medium and incubated at 37°C in 5% CO_2 for 2 hours. The medium was removed by flicking the plates, and the cells were washed with 100 µL of phosphate buffered saline (PBS without calcium or magnesium, Invitrogen, 14190-144). The PBS was removed by flicking the plates, and 100 µL of 0.25% trypsin-EDTA was added to each well and incubated for 5 minutes at 37°C in 5% CO_2. One hundred µL of FACS buffer (PBS containing 5% FBS, 2 mM EDTA, and 0.2% sodium azide) was added to each well, and the cells were pelleted by centrifugation at 1200 rpm for 5 minutes. The medium was discarded by flicking the plate, and the cells were fixed by addition of 50 µL of 1% paraformaldehyde (Electron Microscopy Sciences, 15710) in PBS per well. Viable cells were gated and analyzed using a BD LSR II flow cytometer and FACSDIVA software (Becton Dickinson). The median value of DiI-LDL fluorescence was measured at excitation 488 nm and emission 575 nm, and 5000 cells were analyzed. Bar graphs were generated using Microsoft Excel 2002 (Microsoft Corporation). Percentage of activation

was calculated as follows, % Activation = [1 - (X ÷ A)] x 100, where X = medium fluorescence reading from sample well and A = medium fluorescence reading from well with only hPcsk9 treatment.

[0171] Percentage of activation was plotted versus treatment to determine EC_{50}'s from dose response curves generated using the equation Y = Bottom + (Top-Bottom)/(1+10^((LogEC_{50}-X) x HillSlope)) and GraphPad Prism 5 (GraphPad Software).

Results

Generation of an anti-human Pcsk9 monoclonal antibody

[0172] B-cells were harvested from the primary lymph nodes of animals immunized with Pcsk9 protein. Hybridomas were generated using standard PEG-mediated fusion. The resulting fusion was assayed by ELISA, and positive binders to human Pcsk9 were identified and expanded to generate supernatants. A potent functional murine anti-human Pcsk9 IgG1-kappa monoclonal antibody was identified and designated as MAB1.

Screning of MAB1 for binding specifically to Pcsk9

[0173] MAB1 specificity was examined by evaluating binding in ELISA to a series of other proteins. The binding of MAB1 to six other proteins was compared to binding to Pcsk9-HIS. This demonstrated that the binding to Pcsk9 is specific and that the antibody was not binding to the HIS tag.

Evaluation of MAB1 for binding to the cynomolgus Pcsk9

[0174] The binding of MAB1 to the cynomolgus homolog of Pcsk9 was determined. For this assay, the supernatants from cells expressing the cynomolgus HIS-tagged Pcsk9 were utilized along with a Ni capture plate, avoiding the need to purify the material. Human Pcsk9 was dilute and also captured via its HIS-tag. MAB1 was able to bind to both human and cynomolgus Pcsk9.

Binding kinetics of MAB1

[0175] The mouse antibody MAB1, that recognizes the human Pcsk9 protein, was analyzed for its binding affinity by using solution equilibrium titration (SET). MAB1 was found to bind with high affinity to recombinant human Pcsk9 with sub-nanomolar affinity (K_d = 270 pM).

Screening of MAB1 for blocking Pcsk9 LDL-R interaction

[0176] TR-FRET assay was used for determining if the anti-hPcsk9 antibody MAB1 could disrupt the interaction between hPcsk9-AF and hLDL-R-Eu labeled proteins. Unlabeled hPcsk9 protein or EGF-A peptide were evaluated to demonstrate the assay could detect the disruption of the TR-FRET signal generated by interaction of hLDL-R-Eu and hPcsk9-AF labeled proteins. Increasing concentrations of unlabeled hPcsk9 competed with hPcsk9-AF for binding to hLDL-R-Eu, which resulted in a decrease of the TR-FRET signal. The EGF-A peptide disrupted the interaction between hLDL-R-Eu and hPcsk9-AF with an IC_{50} of 2.5 μM. MAB1 disrupted the TR-FRET signal between hPcsk9-Eu and hLDL-R-AF with an IC_{50} = 77 nM.

Screening of MAB1 for inhibiting Pcsk9-mediated degradation of the LDL-R

[0177] Pcsk9 binding to the LDL-R has been shown to lead to LDL-R degradation, and this was confirmed using HepG2 cells and recombinant human Pcsk9. The ability of MAB1 to bind Pcsk9 and block this effect was determined. MAB1 inhibited this effect in exogenous hPcsk9 treated HepG2 cells and led to increased cell-surface LDL-R.

Screening of MAB1 for inhibiting Pcsk9 and restoring LDL uptake.

[0178] The inhibition of Pcsk9 degradation of the LDL-R should restore the ability of HepG2 cells to internalize LDL-C. MAB1 prevented Pcsk9-mediated LDL-R degradation on HepG2 cells treated with exogenous hPcsk9 and led to increased DiI-LDL-uptake with an EC_{50} of 194 nM.

Example 2: Creation of PCSK9 Antagonist Antibodies MAB2 and MAB3

Summary

[0179] This example the generation of human antibodies MAB2 and MAB3 by engineering the murine monoclonal PCSK9 antagonist antibody MAB1 to have greater sequence homology to a human germline antibody. MAB2 and MAB3 retain the epitope specificity, affinity, and cynomolgus macaque PCSK9 cross-reactivity of the parent murine antibody. MAB2 and and MAB3 have much higher homology to the human germline sequence than the original murine antibody and should therefore be better tolerated by the human immune system.

[0180] Mouse monoclonal antibody MAB1 was Humaneered™ to bring its protein sequence closer to a human germline sequence and decrease its immunogenicity. Humaneering™ technology is available through KaloBios of South San Francisco (on the worldwide web at

kalobios.com). Antibody Humaneering™ generates engineered human antibodies with V-region sequences that have high homology to a human germline sequence while still retaining the specificity and affinity of the parent or reference antibody (U.S. Patent Publ. 2005/0255552 and 2006/0134098). The process first identifies the minimum antigen binding specificity determinants (BSDs) in the heavy and light chain variable regions of a reference Fab (typically sequences within the heavy chain CDR3 and the light chain CDR3). As these heavy and light chain BSDs are maintained in all libraries constructed during the Humaneering™ process, each library is epitope-focused, and the final, fully Humaneered™ antibodies retain the epitope specificity of the original mouse antibody.

[0181] Next, full-chain libraries (in which an entire light or heavy chain variable region is replaced with a library of human sequences) and/or cassette libraries (in which a portion of the heavy or light chain variable region of the mouse Fab is replaced with a library of human sequences) are generated. A bacterial secretion system is used to express members of the library as antibody Fab fragments, and the library is screened for Fabs that bind antigen using a colony-lift binding assay (CLBA). Positive clones are further characterized to identify those with the highest affinity. Identified human cassettes supporting binding in the context of residual murine sequences are then combined in a final library screen to generate completely human V-regions.

[0182] The resulting Humaneered™ Fabs have V-segment sequences derived from human libraries, retain the short BSD sequences identified within the CDR3 regions, and have human germline Framework 4 regions. These Fabs are converted to full IgGs by cloning the variable regions of the heavy and light chains into IgG expression vectors. Fully Humaneered™ antibodies generated in this process retain the binding specificity of the parent, murine antibody, typically have equivalent or higher affinity for antigen than the parent antibody, and have V-regions with a high degree of sequence identity compared with human germline antibody genes at the protein level.

Methods

Cloning of murine V-regions

[0183] The V-region DNA from murine monoclonal MAB1 was amplified by RT-PCR from RNA isolated from the hybridoma cell line using standard methods. Primers successfully used for PCR amplification of the heavy chain variable region from hybridoma cDNA were V_H8 (5'-GTCCCTGCATATGTCYT-3'; SEQ ID NO:50) (Chardes T, et al 1999) and HCconstant (5'-

GCGTCTAGAAYCTCCACACACAGGRRCCAGTGGATAGAC-3'; SEQ ID NO:51). Primers successfully used for PCR amplification of the light (kappa) chain variable region from hybridoma cDNA were Vκ23 (5'-CTGGAYTYCAGCCTCCAGA-3'; SEQ ID NO:52) (Chardes T, et al 1999) and LCconstant (5'-GCGTCTAGAACTGGATGGTGGGAAGATGG-3'; SEQ ID NO:53). The amplified heavy and light chain variable regions were sequenced. PCR was then used to amplify the V-genes and to incorporate restriction enzyme sites for cloning into KaloBios vectors: Vh into KB1292-His (modified version of KB1292 that encodes a C-terminal flexible linker and 6-His (SEQ ID NO:45) tag of amino acid sequence AAGASHHHHHH (SEQ ID NO:54) on CH1) at *Nco*I (5') and *Nhe*I (3'); Vk into KB1296 at *Nco*I (5') and *Bsi*WI (3'). These separate heavy and light chain vectors were then combined into a single bicistronic KaloBios Fab expression vector by restriction digest with *Bss*HII and *Cla*I and ligation. Fab fragments were expressed in *E. coli* from this vector. This Fab was tested for PCSK9-antigen binding and is referred to as reference Fab SR101-B1.

Fab purification

[0184] Fab fragments were expressed by secretion from *E. coli* using KaloBios expression vectors. Cells were grown in 2xYT medium to an OD_{600} of ~0.6. Expression was induced by adding IPTG to 100 μM and shaking for 4 hours at 33°C. Assembled Fab was obtained from periplasmic fractions by osmotic lysis and purification by affinity chromatography using Ni-NTA columns (HisTrap HP columns; GE Healthcare catalog #17-5247-01) according to standard methods. Fabs were eluted in buffer containing 500 mM imidazole and thoroughly dialyzed against PBS pH 7.4 without calcium and magnesium.

Library construction

[0185] Libraries were constructed by joining KaloBios human library sequences, parent murine sequences and the unique CDR3-FR4 regions containing the BSD. The BSD contained human germline J-segment sequences and CDR3 from the optimized reference Fab EJS005 and were attached to the human V-segment libraries using overlapping PCR. KaloBios human cassette libraries were based on the human germline sequence closest to the original murine Vh and Vk's in the CDR regions. The original murine MAB1 Vh is closest to human germline sequence Vh2-70, so the KaloBios library that contains Vh2 subgroup members (KB1412) was used in making Vh cassette libraries. Likewise, as the MAB1 Vk is closest to the Vk1 O2 human germline sequence, a mixture of the two KaloBios human V-segment libraries containing Vk1 subgroup members (KB1419 and KB1420) was used inmaking Vk cassette libraries. These

cassette libraries were joined by overlapping PCR to sequence from the parent murine variable region to complete a V-segment. Two types of cassettes were constructed by bridge PCR: front-end cassettes containing human sequences in FR1, CDR1, and the first part of FR2 were amplified from the mixture of Vh2 library (KB1412) or the mixture of Vk1 libraries (KB1419 and KB1420) described above as a template. Middle cassettes containing human sequences in the last part of FR2, CDR2, and FR3 were amplified using the full human Vh- or Vk-region libraries described above as templates. Vh cassettes had overlapping common sequences in FR2 at amino acid positions 45-49 (Kabat numbering); Vk cassettes had overlapping common sequences in FR2 at amino acid residues 42-47 (Kabat numbering). In this way, front-end and middle human cassette libraries were constructed by PCR for human V-heavy 2 and V-kappa 1 isotypes. Each Vh cassette library was cloned into vector KB1292-His at *Nco*I (5') and *Kpn*I (3'); each Vk cassette library was cloned into vector KB1296-B (modified version of KaloBios vector KB1296 which has a silent *Hind*III site added in FR4) at *Nco*I (5') and *Hind*III (3'). Resultant Vh or Vk plasmid libraries were then combined with the complementary chain from the reference Fab JG024 (*e.g.*, the Vh front-end library was combined with the optimized reference Vk vector) by digestion with *Bss*HII and *Cla*I and subsequent ligation to create libraries of dicistronic vectors expressing full Fabs.

General ELISA

[0186] Recombinant human or cynomolgus macaque PCSK9-His6 antigen was used for all ELISA assays. Typically, PCSK9-His6 antigen diluted in PBS pH 7.4 was bound to a 96-well microtiter plate at 300 ng/well by overnight incubation at 4°C. The plate was blocked with a solution of 3% BSA in PBS for one hour at 37°C, and then rinsed once with PBST. Fab-containing induced cell medium or diluted, purified Fab (50 µL) was then added to each well. After a one-hour incubation at 37°C, the plate was rinsed three times with PBST. Anti-human-kappa chain HRP conjugate (Sigma #A7164) diluted 1:5000 in PBS (50 µL) was added to each well, and the plate was incubated for 45 min at room temperature. The plate was washed three times with PBST, then 100 µL of SureBlue TMB substrate (KPL #52-00-03) was added to each well and the plate was incubated for ~10 min at room temperature. The plate was read at 650 nm in a spectrophotometer.

[0187] For specificity ELISAs on purified human and mouse IgGs, a 384-well plate was coated with a panel of purified human or mouse antigens at 88 ng per well and incubated overnight at 4°C. The plate was blocked and washed as described above, then 22 µL of purified

mouse or human anti-PCSK9 antibody diluted to 2 μg/mL in PBS was added to each well. The plate was incubated for 1 hr at 37°C then washed with PBST. Anti-mouse Fc antibody (Jackson ImmunoResearch Labs #115-035-071) or anti-human kappa antibody (Sigma #A7164) conjugated to HRP was diluted 1:5000 in PBS (25 μL) and added to each well. The plate was incubated for 1 hr at room temperature, then washed and developed as described above.

Colony lift binding assay (CLBA)

[0188] Screening of humaneered libraries of Fab fragments was carried out essentially as described in (U.S. Patent Publ. 2005/0255552 and 2006/0134098) using nitrocellulose filters coated with PCSK9-His_6 at 1 μg/mL. Fabs bound to the antigen-coated filter were detected using an alkaline phosphatase-conjugated anti-human kappa light chain antibody (Sigma #A3813) diluted 1:5000 in PBST, and blots were developed with DuoLux chemiluminescent substrate for alkaline phosphatase (Vector Laboratories #SK-6605).

Generation of biotinylated recombinant PCSK9 and affinity measurements

[0189] PCSK9 with C-terminal Avi- (for site-directed biotinylation) and His6-tags (PCSK9-Avi-His6) was generated by inserting an EcoRI restriction site between the gene encoding PCSK9 and the His6 tag in the pRS5a/PCSK9 plasmid; expresses amino acids 31-692 of PCSK9 Uniprot Accession Q8NBP7 with a C-terminal His6 (SEQ ID NO:45) tag). Oligonucleotides encoding the Avi tag (amino acid sequence: GGGLNDIFEAQKIEWHE; SEQ ID NO:55) and flanked with EcoRI overhangs were phosphorylated with T4 polynucleotide kinase (Invitrogen), annealed, and subsequently ligated into pRS5a/PCSK9 using the newly inserted EcoRI site. Clones containing the Avi tag were verified by sequence analysis. Expression of PCSK9-Avi-His6 was performed in the 293 Freestyle Expression System (Invitrogen), and secreted recombinant protein was purified using Ni-NTA resin (QIAGEN). Following purification, PCSK9-Avi-His6 protein was dialyzed against 10 mM Tris pH 8.0, 50 mM NaCl. The protein was biotinylated in vitro with biotin-protein ligase (Avidity) according to the manufacturer's protocol. Upon completion, the reaction was dialyzed against PBS pH 7.2, and biotinylation was verified by Western blot, probing with HRP-conjugated streptavidin.

[0190] The binding kinetics of IgGs and Fab fragments produced during the Humaneering™ process were analyzed using a ForteBio Octet QK system according to the manufacturer's instructions. Biotinylated PCSK9-Avi-His_6 antigen was coupled to Streptavidin High Binding Biosensors (ForteBio #18-0006). Fab binding to antigen was monitored in real time using bio-

layer interferometry analysis and software provided by the manufacturer. Affinities were calculated from the determined association and dissociation constants. The binding kinetics of the final selected candidates were analyzed using a Solution Equilibrium Titration ("SET") assay. Briefly, serial dilutions of human, cyno, mouse, or rat Pcsk9 were prepared, and anti-Pcsk9 Ab was added to each antigen concentration to reach a constant antibody concentration of 100 pM. 100 µL/well of each dilution mix was distributed in duplicate to a 96-well polypropylene microtiter plate (Greiner). The plate was sealed and incubated over night at room temperature. A 96-well Standard Bind microtiter plate (Meso Scale Discovery) was coated with 25 µL of 1 µg/mL Pcsk9 diluted in PBS. This plate was sealed and incubated overnight at 4°C. After the incubation the antigen-coated Standard Bind micro titer plate was washed three times with 200 µL per well PBS/0.05 % (w/v) Tween 20. Subsequently, the plate was blocked with 150µL/well PBS/5% (w/v) BSA and incubated for one hour at room temperature with shaking. The washing steps were repeated and 25 µL/well of the antibody-antigen preparation from the polypropylene microtiter plate was transferred into the antigen-coated Standard Bind plate. The Standard Bind plate was incubated for 60 min at room temperature with shaking. After three additional washing steps, 25 µL of 1 µg/mL Sulfo-Tag-labeled goat anti-human-detection antibody (R32AJ-5, Meso Scale Discovery) diluted in PBS/1 % (w/v) BSA/0.05 % (w/v) Tween 20, buffer were added to each well and incubated one hour at room temperature with shaking. After washing the plate three times, 150 µL of 2X Read Buffer (R92TC-1, Meso Scale Discovery) was transferred into each well. Electrochemiluminescence signals were generated and detected by a Sector Imager 6000 (Meso Scale Discovery). Data were processed with the excel add-in XLfit 4.3.2 (ID Business Solutions) using the fitting model applicable for antibodies described in Piehler, *et al.*, (1997) *J Immunol Methods* 201:189-206. High affinity binding was observed between human and cyno PCSK9 and the antibodies MAB2 and MAB3 in solution.

Antibody production and purification

[0191] Fully Humaneered™ MAB2 and MAB3 antibodies (silent IgG1 kappa) were produced by co-transfection of vectors pJG04 (heavy chain) and pJG10 (light chain) into 293 Freestyle cells using 293fectin transfection reagent (Invitrogen #51-0031) according to the manufacturer's protocol. Antibody was purified from 293 Freestyle cell supernatants using a 5-mL HiTrap Protein A HP column (GE Healthcare #17-0403-03). Antibody was eluted using IgG Elution Buffer (Pierce #21004), and buffer exchanged into PBS by dialysis. Protein A affinity

chromatography was performed on an AKTAFPLC liquid chromatography system (GE Healthcare).

Epitope competition assay

[0192] Competition between the original mouse antibody MAB1 and its Humaneered™ derivatives MAB2 and MAB3 for epitope binding on PCSK9 was assayed using the ForteBio Octet QK system and Streptavidin High Binding Biosensors coated with biotinylated PCSK9-Avi-His6. Four different antibodies were then bound to separate PCSK9-coated sensors to saturation: mouse MAB1, fully human MAB2, fully human MAB3, or the humaneered anti-PCSK-9 antibody NVP-LGT209 (known to have a separate epitope from that of MAB1). Next, all sensors were dipped into wells containing MAB1 mouse antibody to determine whether the first antibody could block MAB1 binding.

Results

Murine and reference V-region amino acid sequences

[0193] RT-PCR products from hybridoma cells that express MAB1 were sequenced, and this sequence was largely (95% or greater) verified at the protein level using a ThermoElectron LTQ-Orbitrap Mass Spectrometer. The heavy and light chain variable regions of MAB1 were then cloned into KaloBios vectors in order to create the reference Fab SR101-B1. In addition to the reference Fab (SR101-B1), an optimized reference Fab, JG024, was constructed. Several framework amino acid residues in SR101-B1 were changed to human germline in JG024.

Reference and optimized reference Fab affinity analysis

[0194] The human germline residues incorporated into the optimized reference Fab J EJS005 in FR1 and FR3 are those specified by the PCR primers used to amplify the human V-segment repertoire and thus are present in all members of the humaneered V-region libraries. The optimized reference Fab was constructed to assess whether or not any of the changes to human germline alter the properties of Fab binding. By dilution ELISA using purified Fabs, the affinities of SR101B-1 and EJS005 for recombinant PCSK9 antigen appear to be within experimental noise, indicating that the amino acid changes in EJS005 are tolerated.

Library construction and selection of fully Humaneered™ Fabs

[0195] Heavy and light chain front-end and middle cassette libraries subgroup-restricted to Vh2 or Vk1 were generated and screened by CLBA. For Vh, front-end cassettes which supported binding to PCSK9 antigen were identified by colony-lift binding assay, but Vh middle

cassettes were not. In Vk as well, only front-end cassettes were identified by colony lift. Many binders from each front-end library reconfirmed in an ELISA assay on Fab-containing cell supernatants, and were further rank-ordered by concentration normalized affinity ELISA.

[0196] Since no V-heavy middle cassettes that supported PCSK9 binding were identified, an Fr-3 library was constructed using the cassettes identified in the front-end screen joined to CDR-2 that was amplified from the optimized reference Fab and a Fr-3 library amplified from KaloBios Vh2 libraries. Thus, a Fr-3 human cassette library was built in the context of antigen binding front end cassettes, screened, and antigen-binding clones identified.

[0197] The middle of Vk followed a different path. In Vk middle, mutagenic libraries were constructed that stretched from Fr-2 to CDR-2 and which encoded either the parental murine residue or the closest human germline residue. This was joined to a Vk1 Fr-3 library. The resulting library had antigen binding Fe cassettes joined to a Fr-2 and Cdr-2 mutatgenic library joined to an Fr-3 library.

[0198] From the libraries described above, front-end and middle human cassettes that supported binding to PCSK9 antigen were successfully identified for both the heavy and light chains by CLBA. These libraries were screened in context so that CLBA positive clones would contain completely Humaneered™ Fabs. The CLBA positive clones were all confirmed and rank-ordered by normalized affinity ELISA. The six Fabs that had the highest affinity and whose sequence showed the highest germline identity were purified and more accurate affinity measurements were made using the ForteBio Octet system.

Testing the affinity of fully Humaneered™ Fabs for PCSK9 antigen using ForteBio Octet analysis

[0199] The binding kinetics of six human Fabs were then compared to the kinetics of the reference Fab JG024 using the ForteBio Octet system (numerical data summarized in Table 1).

Table 1. Affinity of fully Humaneered™ Fabs for PCSK9

Fab	k_a	k_d	K_D
Clone #44	8.48E3	1.89E-4	2.23E-8
Clone #45	2.67E4	1.00E-4	3.75E-9
Clone #46	2.03E4	1.21E-3	5.93E-8

Fab	k_a	k_d	K_D
Clone #56	1.38E4	1.08E-4	7.79E-9
Clone #57	1.43E4	6.37E-5	4.46E-9
Clone #58	3.63E4	9.92E-4	2.73E-8
RefFab (JG024)	7.70E3	2.08E-4	2.70E-8

[0200] Protein concentration determination for these Fabs was difficult; as such, the off-rate (k_d) data are much more reliable than the on-rate (k_a) and K_D data (only off-rates are concentration-independent). All but one of the Humaneered™ Fabs tested appeared to have off-rates that were about as good (*i.e.,* slower) than that of the reference Fab. Although less reliable, the K_a measurements for all six Fabs were similar or better (faster) to the reference Fab.

[0201] From this selection of antigen binding Humaneered™ Fabs, the most human chains with the highest affinity were selected to be made into full IgG antibodies. Thus, the variable region of MAB2 contains the heavy chain from Clone 44 and the light chain from Clone 45. The variable region of MAB3 contains the heavy chain of Clone 37 from the Vh2 Fr3 library screen and the light chain of Clone 45 from the full light chain library. Since this combination of heavy and light chains was not identified from the same screen, they were cloned into an expression vector, expressed, and affinity was measured by ForteBio Octet. Following confirmation that the candidate Fab's affinity met or exceeded the affinity of the reference Fab, it was cloned into full IgG vectors.

Analysis of binding kinetics of MAB2 and MAB3 using the Solution Equilibrium Titration (SET) system

[0202] Using the SET assay, the binding affinities of the MAB2 and MAB3 antibodies to human PCSK9 were determined to be 260 and 300 pM, respectively, as indicated in Table 2. This suggests high affinity interaction between the antibodies and PCSK9 in solution.

Table 2. Binding kinetics of MAB2 and MAB3

Antibody	k_D [pM]
MAB2	260 ± 50
MAB3	300 ± 20

Analysis of antigen specificity of MAB2 and MAB3 by ELISA

[0203] In order to test whether the antigen specificity of the parental mouse antibody MAB1 was retained in the final Humaneered™ IgGs, MAB2 and MAB3, binding of the antibodies to a panel of human and mouse antigens (as well as human PCSK9) was tested in an ELISA assay. The results of this assay (Figures 4A-B) show that MAB2 and MAB3 retain high specificity for PCSK9, similar to the murine antibody MAB1.

Antibody binding to human and cynomolgus macaque Pcsk9 protein in ELISA

[0204] MAB2 and MAB3 were evaluated for specific binding to human and cynomolgus macaque (cyno) Pcsk9. This ELISA assay shows that, like the parental mouse antibody MAB1, the Humaneered™ antibodies MAB2 and MAB3 are able to bind both human and cyno Pcsk9 in a similar manner (Figures 5A-C).

Bio-layer interferometry-based epitope competition assay

[0205] In order to test whether the epitope specificity of the parent murine antibody MAB1 was retained in the final Humaneered™ antibodies MAB2 and MAB3, a competition assay using the ForteBio Octet system was developed. The Humaneered™ antibodies MAB2 and MAB3 block binding of the parental mouse antibody MAB1, indicating that the Humaneered™ antibodies retain the epitope specificity of the original murine antibody. Similar results were obtained when the order of loading of antibodies was switched, *i.e.,* MAB1 bound first, followed by the Humaneered™ antibody.

Amino acid sequence of Humaneered™ antibodies MAB2 and MAB3 and percent identity to human germline sequence

[0206] The variable region amino acid sequences of final Humaneered™ IgG MAB2 and MAB3 are shown in Figures 2 and 3, respectively; CDRs are underlined and in bold. Nucleotide sequences are included in the sequence listing.

[0207] The percent identity to human germline sequences for MAB2 and MAB3 was determined by aligning the Vh and Vk amino acid sequences against a single human germline sequence (Vh2 2-05 and Vk1 O2, respectively; Table 3). Residues in CDRH3 and CDRL3 were omitted from the calculation for each chain.

Table 3. Percent identity of MAB2 and MAB3 to human germline sequences

Vh versus Vh2 2-05	Vk versus Vk1 O2
90.0%	86.7%

[0208] Additional information regarding the functional characterization of the humaneered antibodies is discussed in the figure legends of Figures 7-12.

[0209] It is understood that the examples and embodiments described herein are for illustrative purposes only and that various modifications or changes in light thereof will be suggested to persons skilled in the art and are to be included within the spirit and purview of this application and scope of the appended claims. All publications, patents, patent applications, and sequence accession entries cited herein are hereby incorporated by reference in their entirety for all purposes.

WHAT IS CLAIMED IS:

1. An antibody that binds to proprotein convertase subtilisin/kexin type 9 (PCSK9), wherein the antibody blocks the interaction of PCSK9 with low density lipoprotein receptor (LDLR) and inhibits PCSK9-mediated degradation of LDLR, wherein the antibody comprises:

a) a heavy chain variable region comprising a human heavy chain V-segment, a heavy chain complementary determining region 3 (CDR3), and a heavy chain framework region 4 (FR4); and

b) a light chain variable region comprising a human light chain V-segment, a light chain CDR3, and a light chain FR4, wherein

i) the heavy chain CDR3 variable region comprises the amino acid sequence ITTEGGFAY (SEQ ID NO:17); and

ii) the light chain CDR3 variable region comprises the amino acid sequence QQSNYWPLT (SEQ ID NO:24).

2. The antibody of claim 1, wherein the antibody binds to human PCSK9 with an equilibrium dissociation constant (K_D) of about 500 pM or less.

3. The antibody of claim 1, wherein the heavy chain V-segment has at least 85% sequence identity to SEQ ID NO:27, and wherein the light chain V-segment has at least 85% sequence identity to SEQ ID NO:28.

4. The antibody of claim 1, wherein the heavy chain V-segment has at least 85% sequence identity to the amino acid sequence selected from the group consisting of SEQ ID NO:25 and SEQ ID NO:26, and wherein the light chain V-segment has at least 85% sequence identity to SEQ ID NO:28.

5. The antibody of claim 1, wherein the heavy chain FR4 is a human germline FR4.

6. The antibody of claim 5, wherein the heavy chain FR4 is SEQ ID NO:35.

7. The antibody of claim 1, wherein the light chain FR4 is a human germline FR4.

8. The antibody of claim 7, wherein the light chain FR4 is SEQ ID NO:39.

9. The antibody of claim 1, wherein the heavy chain V-segment and the light chain V-segment each comprise a complementary determining region 1 (CDR1) and a complementary determining region 2 (CDR2); wherein:

i) the CDR1 of the heavy chain V-segment comprises the amino acid sequence of SEQ ID NO:15;

ii) the CDR2 of the heavy chain V-segment comprises the amino acid sequence of SEQ ID NO:16;

iii) the CDR1 of the light chain V-segment comprises the amino acid sequence of SEQ ID NO:20; and

iv) the CDR2 of the light chain V-segment comprises the amino acid sequence of SEQ ID NO:23.

10. The antibody of claim 9, wherein

i) the CDR1 of the heavy chain V-segment comprises SEQ ID NO:14;

ii) the CDR2 of the heavy chain V-segment comprises SEQ ID NO:16;

iii) the heavy chain CDR3 comprises the amino acid sequence of SEQ ID NO:17;

iv) the CDR1 of the light chain V-segment comprises SEQ ID NO:19;

v) the CDR2 of the light chain V-segment comprises SEQ ID NO:22; and

vi) the light chain CDR3 comprises SEQ ID NO:24.

11. The antibody of claim 1, wherein the heavy chain variable region has at least 90% amino acid sequence identity to the variable region of SEQ ID NO:40 and the light chain variable region has at least 90% amino acid sequence identity to the variable region of SEQ ID NO:41.

12. The antibody of claim 1, wherein the heavy chain variable region has at least 95% amino acid sequence identity to the variable region of SEQ ID NO:40 and the light chain variable region has at least 95% amino acid sequence identity to the variable region of SEQ ID NO:41.

13. The antibody of claim 1, wherein the antibody comprises a heavy chain comprising SEQ ID NO:40 and a light chain comprising SEQ ID NO:41.

14. The antibody of claim 1, wherein the heavy chain variable region has at least 90% amino acid sequence identity to the variable region selected from the group consisting of SEQ ID NO:5 and SEQ ID NO:9 and the light chain variable region has at least 90% amino acid sequence identity to the variable region selected from the group consisting of SEQ ID NO:7 and SEQ ID NO:11.

15. The antibody of claim 1, wherein the heavy chain variable region has at least 95% amino acid sequence identity to the variable region selected from the group consisting of SEQ ID NO:5 and SEQ ID NO:9 and the light chain variable region has at least 95% amino acid sequence identity to the variable region selected from the group consisting of SEQ ID NO:7 and SEQ ID NO:11.

16. The antibody of claim 1, wherein the heavy chain variable region comprises the amino acid sequence selected from the group consisting of SEQ ID NO:5 and SEQ ID NO:9 and the light chain variable region comprises the amino acid sequence selected from the group consisting of SEQ ID NO:7 and SEQ ID NO:11.

17. The antibody of claim 1, wherein the antibody is a FAb' fragment.

18. The antibody of claim 1, wherein the antibody is an IgG.

19. The antibody of claim 1, wherein the antibody is a single chain antibody (scFv).

20. The antibody of claim 1, wherein the antibody comprises human constant regions.

21. The antibody of claim 1, wherein the antibody is linked to a carrier protein.

22. The antibody of claim 1, wherein the antibody is PEGylated.

23. A composition comprising an antibody of any of claims 1-22 and a physiologically compatible excipient.

24. The composition of claim 23, wherein the composition further comprises a second agent that reduces low density lipoprotein cholesterol (LDL-C) levels in an individual.

25. The composition of claim 24, wherein the second agent is a statin.

26. The composition of claim 25, wherein the statin is selected from the group consisting of atorvastatin, cerivastatin, fluvastatin, lovastatin, mevastatin, pitavastatin, pravastatin, rosuvastatin, and simvastatin.

27. The composition of claim 24, wherein the second agent is selected from the group consisting of fibrates, niacin and analogs thereof, cholesterol absorption inhibitors, bile acid sequestrants, thyroid hormone mimetics, a microsomal triglyceride transfer protein (MTP) inhibitor, a diacylglycerol acyltransferase (DGAT) inhibitor, an inhibitory nucleic acid targeting PCSK9 and an inhibitory nucleic acid targeting apoB100.

28. A method of reducing LDL-C in an individual in need thereof, the method comprising administering a therapeutically effective amount of the antibody of claim 1 to the individual, thereby reducing LDL-C in the individual.

29. The method of claim 28, wherein the individual is hyporesponsive or resistant to statin therapy.

30. The method of claim 28, wherein the individual is intolerant to statin therapy.

31. The method of claim 28, wherein the individual has a baseline LDL-C level of at least about 100 mg/dL.

32. The method of claim 28, wherein the individual has familial hypercholesterolemia.

33. The method of claim 28, wherein total cholesterol is reduced with LDL-C.

34. The method of claim 28, wherein the individual has triglyceridemia.

35. The method of claim 28, wherein the individual has a gain-of-function PCSK9 gene mutation.

36. The method of claim 28, wherein the individual has drug-induced dyslipidemia.

37. The method of claim 28, further comprising administering a therapeutically effective amount of a second agent effective in reducing LDL-C to the individual.

38. The method of claim 37, wherein the second agent is a statin.

39. The method of claim 38, wherein the statin is selected from the group consisting of atorvastatin, cerivastatin, fluvastatin, lovastatin, mevastatin, pitavastatin, pravastatin, rosuvastatin, and simvastatin.

40. The method of claim 37, wherein the second agent is selected from the group consisting of fibrates, niacin and analogs thereof, cholesterol absorption inhibitors, bile acid sequestrants, thyroid hormone mimetics, a microsomal triglyceride transfer protein (MTP) inhibitor, a diacylglycerol acyltransferase (DGAT) inhibitor, an inhibitory nucleic acid targeting PCSK9 and an inhibitory nucleic acid targeting apoB100.

41. The method of claim 37, wherein the antibody and the second agent are co-administered as a mixture.

42. The method of claim 37, wherein the antibody and the second agent are co-administered separately.

43. The method of claim 28, wherein the antibody is administered intravenously.

44. The method of claim 28, wherein the antibody is administered subcutaneously.

Figure 1

Variable region sequences of parent mouse mAb MAB1

MAB1 Heavy Chain Variable Region

QVTLKESGPGILQPSQTLSLTCSFSGFSLS**TSGMGVG**WIRQPSGEGLEWLA**DIWWDDN**
KYYNPSLKSRLTVSKDTSSNQVFLKITSVDTADTATYYCAL**ITTEGGFAY**WGQGTLVT
VSA

MAB1 Light (kappa) Chain Variable Region

DIVLTQSPATLSVTPGDSVSLSC**RASQSINNNLH**WYQQKSHESPRLLIK**FASRSIS**GIPSK
FSGSGSGTDFTLSINSVETEDFGMYFC**QQSNYWPLT**FGAGTNLELI

Figure 2

Variable region sequences of Ab MAB2

MAB2 Heavy Chain Variable Region

QITLKESGPVLVKPTETLTLTCTVSGFSLS**TSGVGVG**WIRQPPGKALEWLA**DIWWDDN KYYNPSLKS**RLTISKDTSKNQVVLTMTNMDPVDTATYYCAR**ITTEGGFAY**WGQGTLV TVSS

MAB2 Light (kappa) Chain Variable Region

DIQMTQSPSSLSASVGDRVTITC**RAGQRISHNLH**WYQQKPDESPRLLIN**FASRLIS**GVPS RFSGSGSGTDFTLTISSLQPEDFATYYC**QQSNYWPLT**FGQGTKLEIK

Figure 3

Variable region sequences of Ab MAB3

MAB3 Heavy Chain Variable Region

QVTLKESGPTLVKPTQTLTLTCTVSGFSLS**TSGVGVG**WIRQSPGKALEWLA**DIWWDDN**
KYYNPSLKSRLTISKDTSKNQVVLTMTNMDPVDTATYYCAR**ITTEGGFAY**WGQGTLV
TVSS

MAB3 Light (kappa) Chain Variable Region

DIQMTQSPSSLSASVGDRVTITC**RAGQRISHNLH**WYQQKPDESPRLLIN**FASRLIS**GVPS
RFSGSGSGTDFTLTISSLQPEDFATYYC**QQSNYWPLT**FGQGTKLEIK

Figure 4A

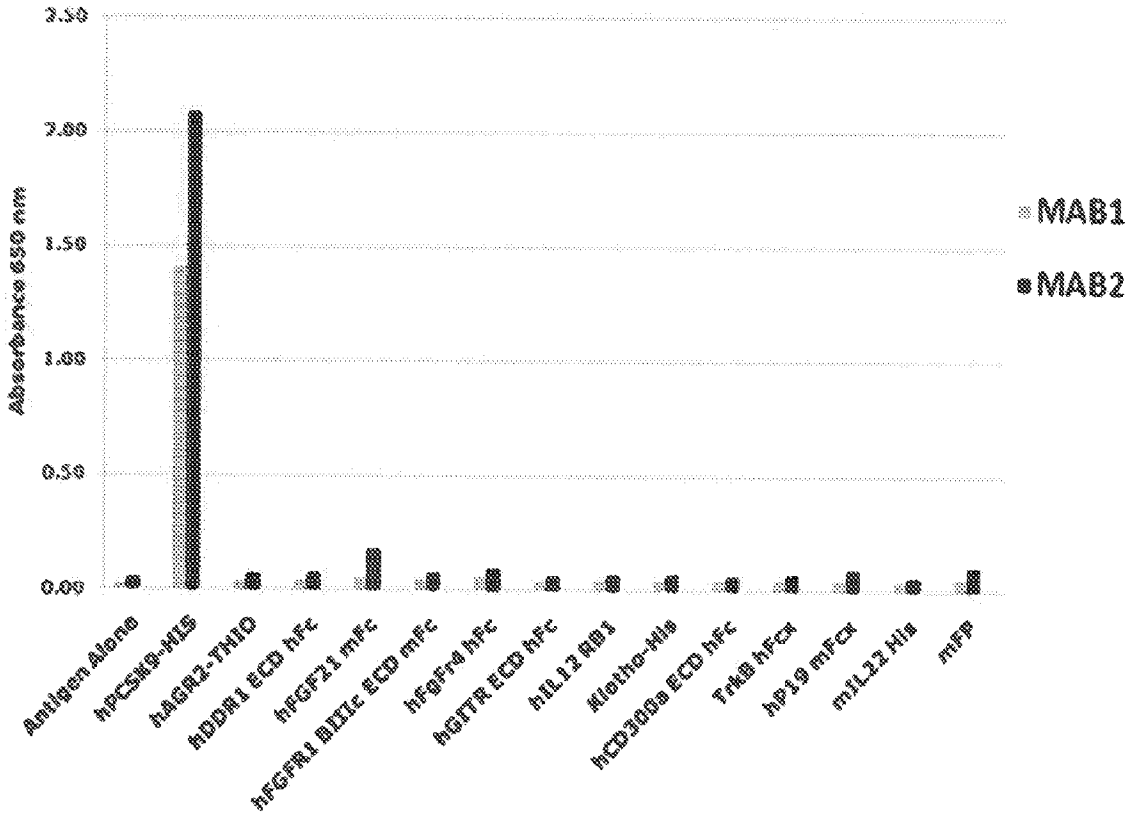

3.50
3.00
2.50
2.00
1.50
1.00
0.50
0.00
Absorbance 650 nm
MAB1
MAB2
Antigen Alone
hPCSK9-HIS
hAGRP-THIO
hDDR1 ECD hFc
hFGF21 mFc
hFGFR1 IIIC ECD mFc
hFgFr4 hFc
hGFTR ECD hFc
hIL13 RB1
Klotho-His
hCD300a ECD hFc
Tr4B hFcx
hP19 mFcx
mIL22 His
mFP

Figure 4B

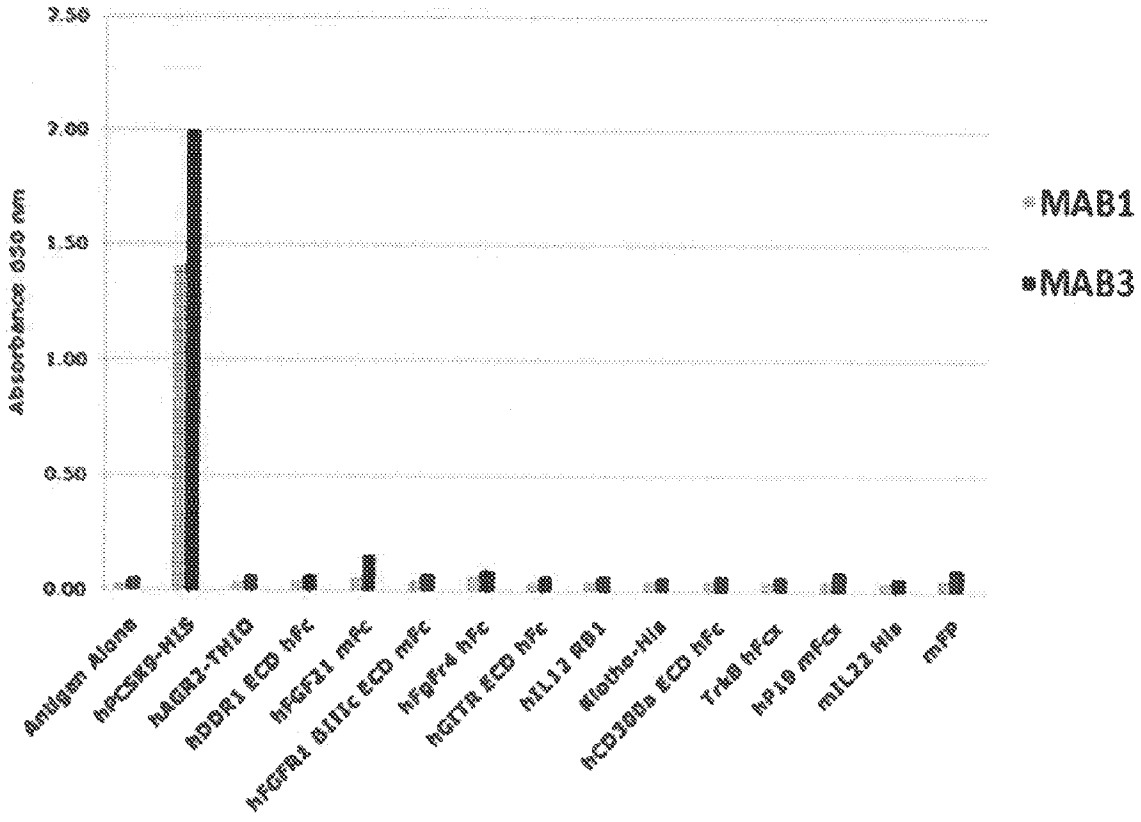

2.50
2.00
1.50
1.00
0.50
0.00
Absorbance 630 nm
MAB1
MAB3
Antigen Alone
hPCSK9-HIS
hAGR2-TM10
hDDR1 ECD hFc
hPGFR1 mFc
hFGFR4 B111c ECD mFc
hFgFr4 hFc
hGITR ECD hFc
hIL13 RB1
Klotho-His
hCD300a ECD hFc
Trk8 hFcx
hP19 mFcx
mIL23 His
mFP

Figure 5A

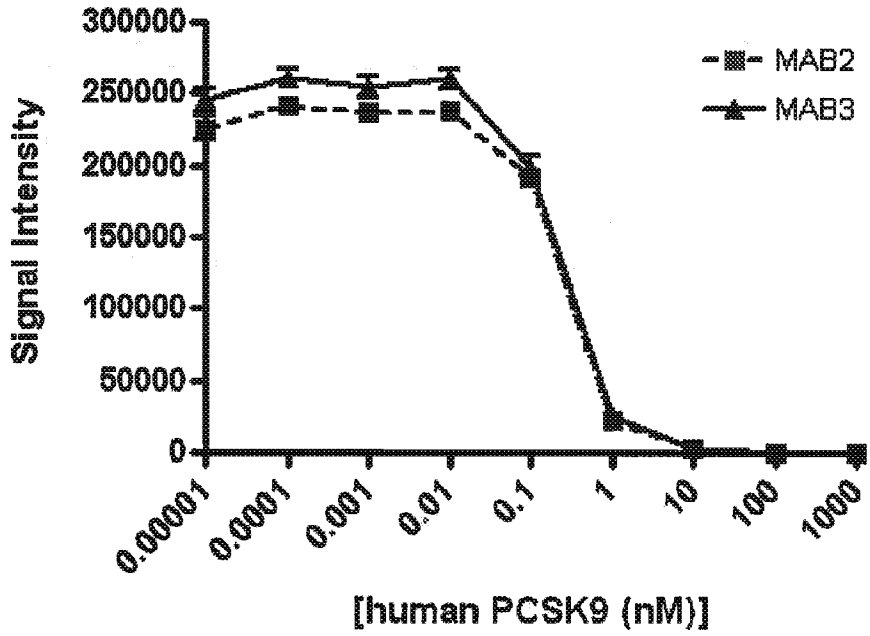

300000
250000
200000
150000
100000
50000
0
Signal Intensity
MAB2
MAB3
0.00001
0.0001
0.001
0.01
0.1
1
10
100
1000
[human PCSK9 (nM)]

Figure 5B

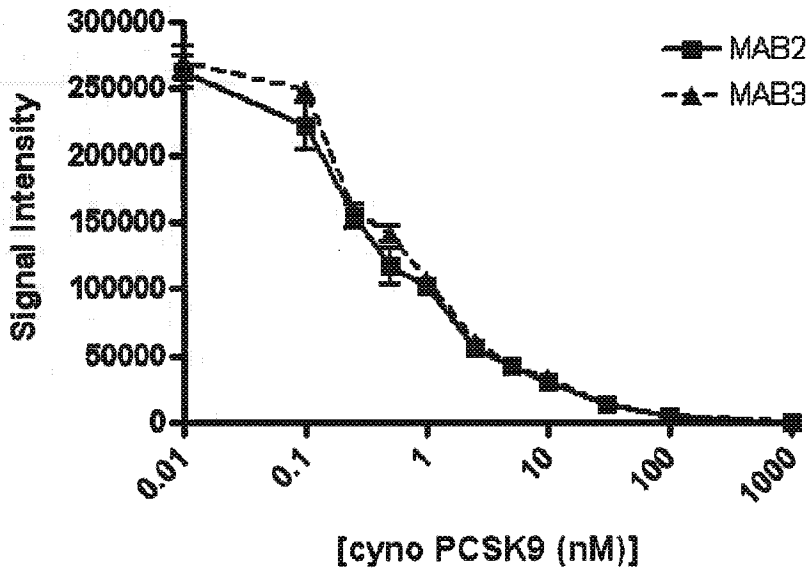

300000
250000
200000
150000
100000
50000
0
Signal Intensity
0.01
0.1
1
10
100
1000
[cyno PCSK9 (nM)]
MAB2
MAB3

Figure 5C

Antibody	Pcsk9 homolog	K_d (nM)	SEM (nM)
MAB2	Human	0.26	0.05
	Cyno	0.40	0.10
	Mouse	>10,000	-
	Rat	>10,000	-
MAB3	Human	0.30	0.02
	Cyno	0.40	0.21
	Mouse	>10,000	-
	Rat	>10,000	-
MAB1	Human	0.27	-
	Cyno	0.23	-
	Mouse	> 10,000	-

Figure 6

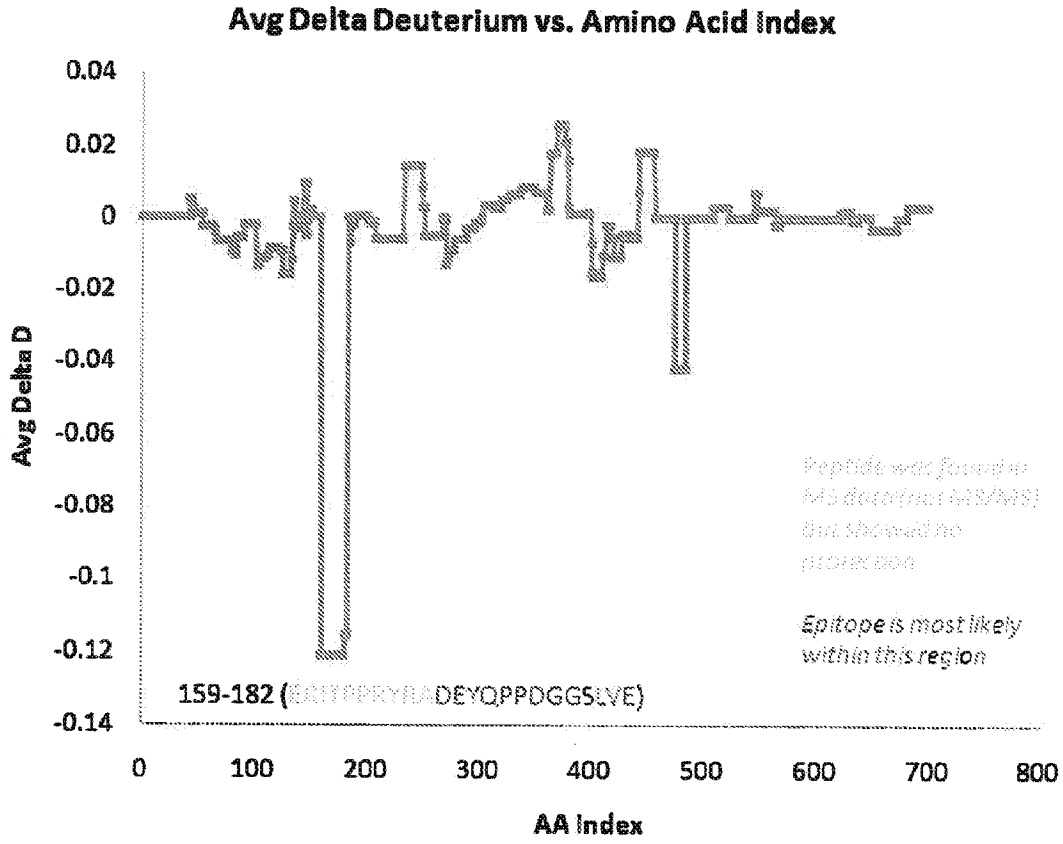

Avg Delta Deuterium vs. Amino Acid Index
Avg Delta D
0.04
0.02
0
-0.02
-0.04
-0.06
-0.08
-0.1
-0.12
-0.14
0
100
200
300
400
500
600
700
800
AA Index
Peptide was found in MS data (not MS/MS) but showed no protection
Epitope is most likely within this region
159-182 (DEYQPPDGGSLVE)

Figure 7

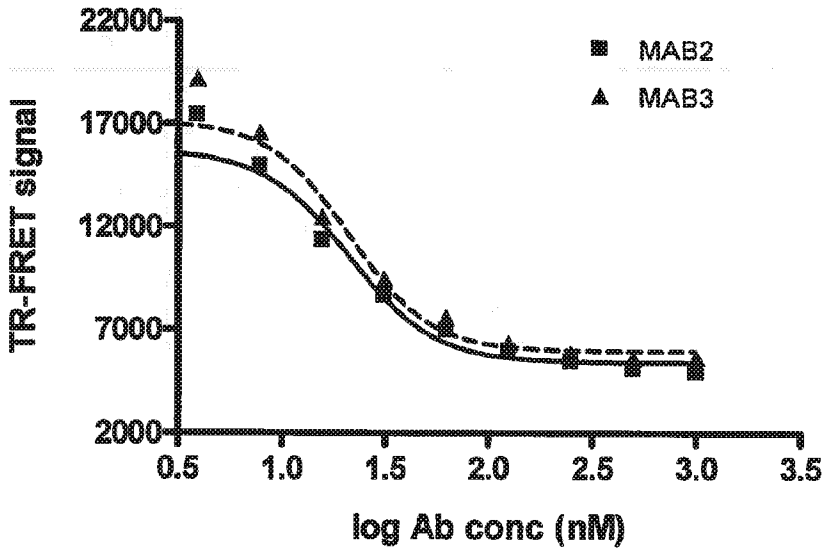
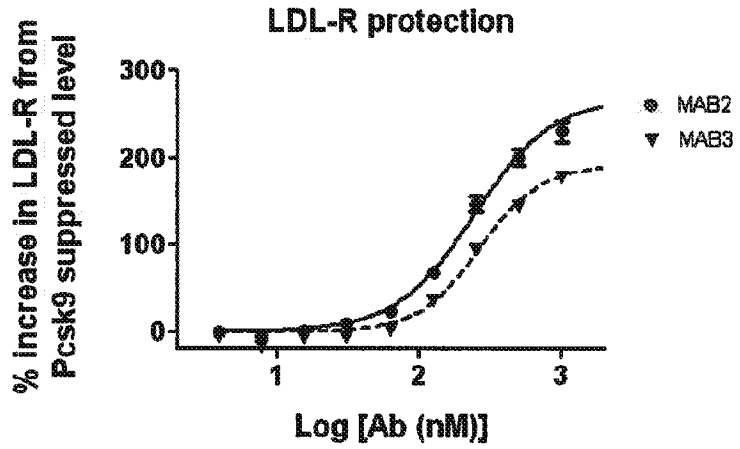

22000
17000
12000
7000
2000
TR-FRET signal
0.5
1.0
1.5
2.0
2.5
3.0
3.5
log Ab conc (nM)
MAB2
MAB3

Figure 8

Antibody	LDL-R protection EC50 (nM)	LDL uptake EC50 (nM)
MAB1	309	194
MAB2	324	210
MAB3	300	168



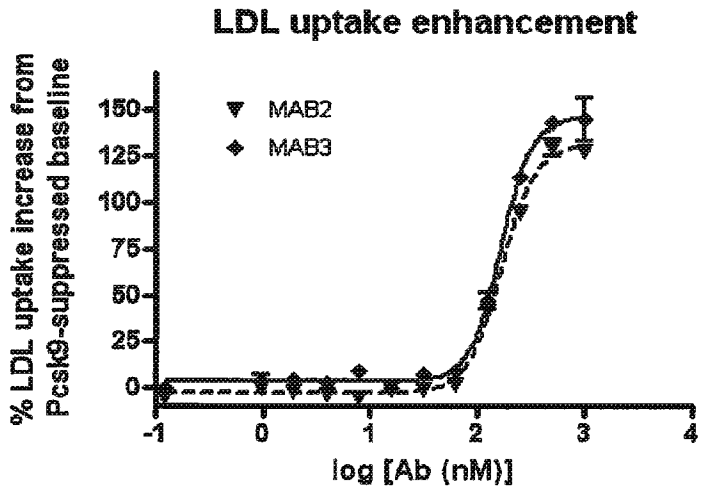


Figure 9

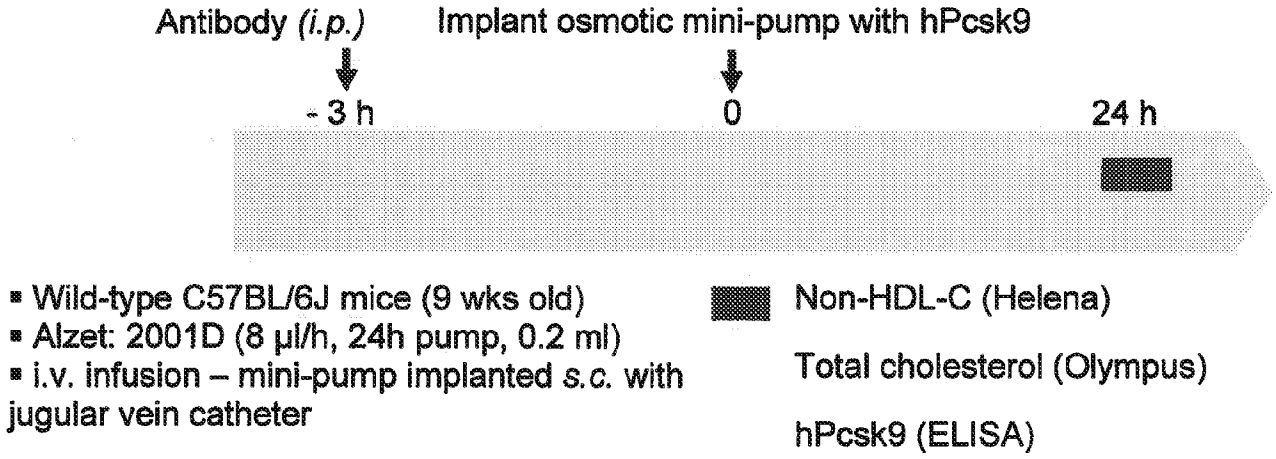

Antibody (i.p.)
Implant osmotic mini-pump with hPcsk9
- 3 h
0
24 h
▪ Wild-type C57BL/6J mice (9 wks old)
▪ Alzet: 2001D (8 µl/h, 24h pump, 0.2 ml)
▪ i.v. infusion – mini-pump implanted s.c. with jugular vein catheter
Non-HDL-C (Helena)
Total cholesterol (Olympus)
hPcsk9 (ELISA)

Figure 10

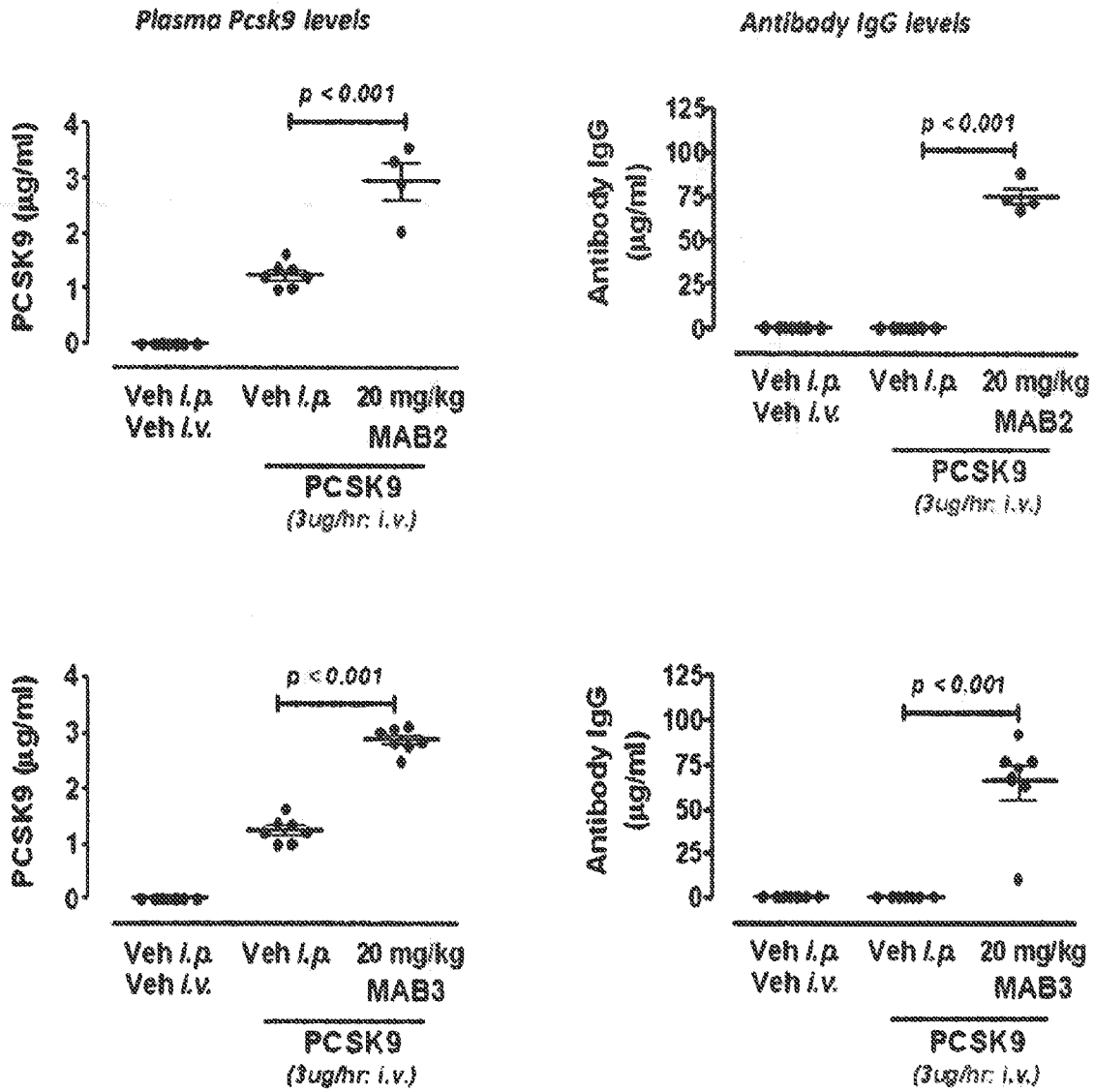

Plasma Pcsk9 levels
Antibody IgG levels
PCSK9 (µg/ml)
Antibody IgG (µg/ml)
p < 0.001
Veh i.p.
Veh i.v.
Veh i.p.
20 mg/kg MAB2
PCSK9 (3ug/hr; i.v.)
20 mg/kg MAB3

Figure 11

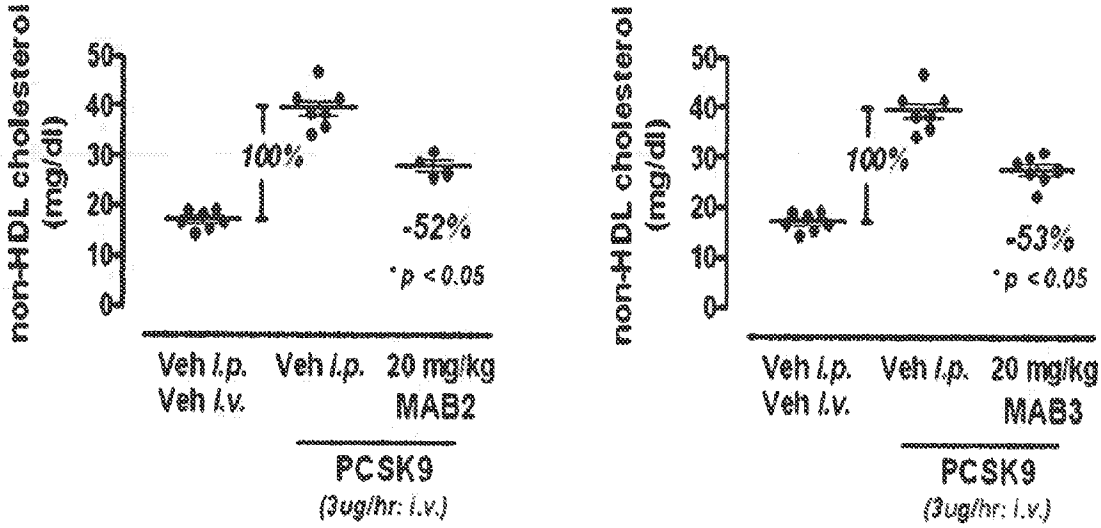
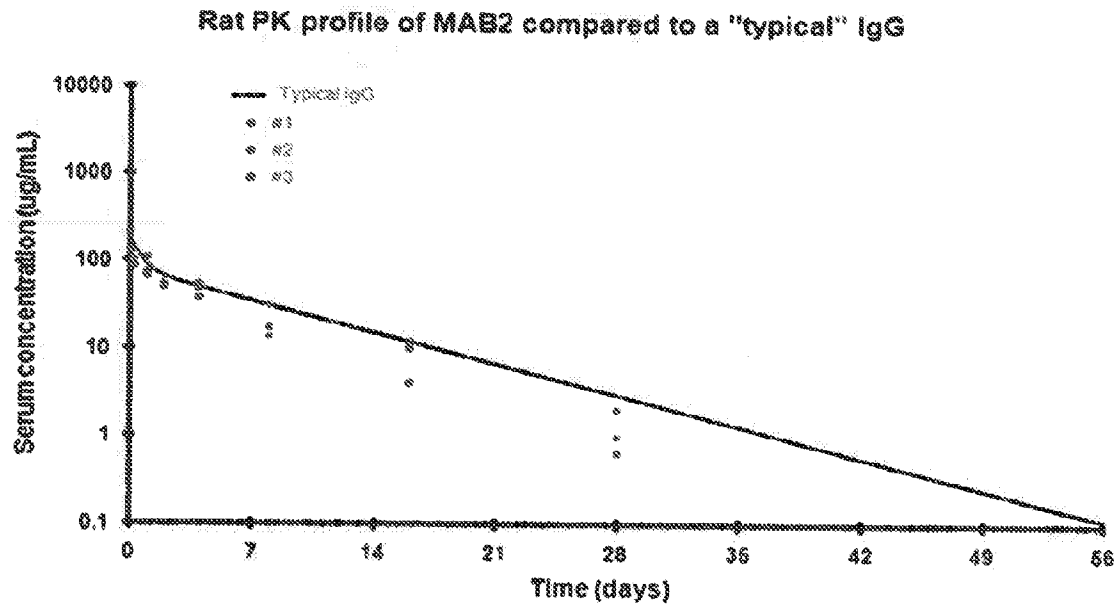
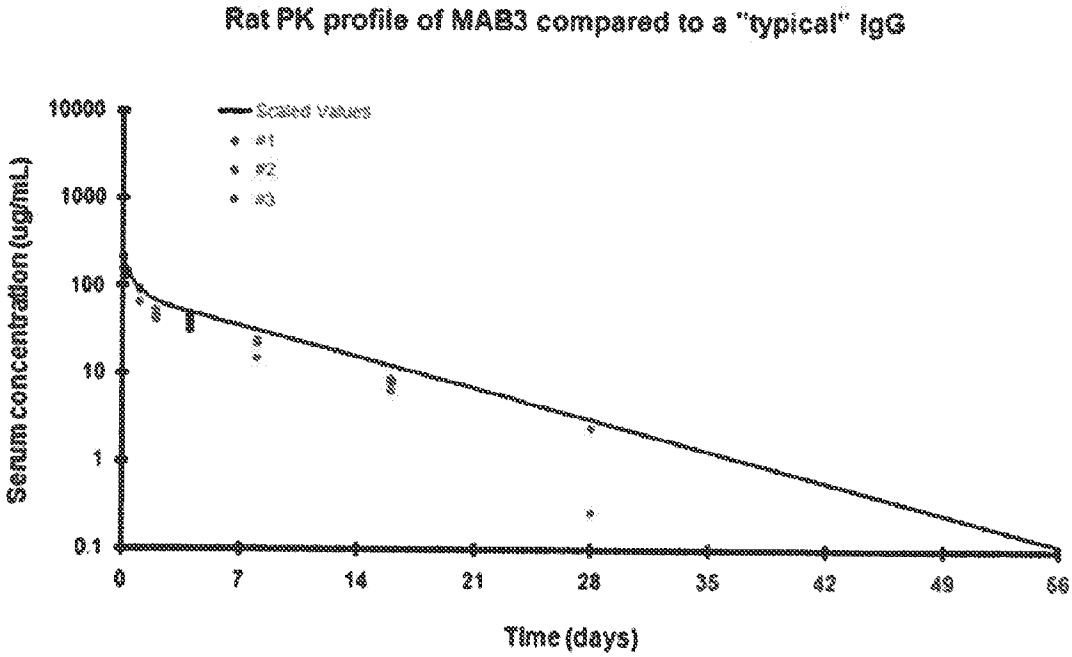

non-HDL cholesterol (mg/dl)
50
40
30
20
10
0
100%
-52%
*p < 0.05
Veh i.p.
Veh i.v.
Veh i.p.
20 mg/kg MAB2
PCSK9
(3ug/hr: i.v.)
non-HDL cholesterol (mg/dl)
50
40
30
20
10
0
100%
-53%
*p < 0.05
Veh i.p.
Veh i.v.
Veh i.p.
20 mg/kg MAB3
PCSK9
(3ug/hr: i.v.)

Figure 12


Rat PK profile of MAB2 compared to a "typical" IgG
Typical IgG
#1
#2
#3
Serum concentration (ug/mL)
10000
1000
100
10
1
0.1
0
7
14
21
28
35
42
49
56
Time (days)


Rat PK profile of MAB3 compared to a "typical" IgG
Scaled Values
#1
#2
#3
Serum concentration (ug/mL)
10000
1000
100
10
1
0.1
0
7
14
21
28
35
42
49
56
Time (days)

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2012/024633

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fees, this Authority did not invite payment of additional fees.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-13, 17-44(all partially)

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.

☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.

☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No
PCT/US2012/024633

A. CLASSIFICATION OF SUBJECT MATTER
INV. C07K16/40
ADD.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
EPO-Internal, WPI Data, BIOSIS, CHEM ABS Data, EMBASE

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 2009/100297 A1 (MERCK & CO INC [US]; ANGELETTI P IST RICHERCHE BIO [IT]; CONDRA JON H) 13 August 2009 (2009-08-13) figures 2,4a,4b; examples 8,10,11	1-13, 17-44

-/--

[X] Further documents are listed in the continuation of Box C.

[X] See patent family annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
13 April 2012	26/07/2012

Name and mailing address of the ISA/	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Fax: (+31-70) 340-3016	Vadot, Pierre

INTERNATIONAL SEARCH REPORT

International application No
PCT/US2012/024633

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	JOYCE C Y CHAN ET AL: "A proprotein convertase subtilisin/kexin type 9 neutralizing antibody reduces serum cholesterol in mice and nonhuman primates", PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA, NATIONAL ACADEMY OF SCIENCE, WASHINGTON, DC; US, vol. 106, no. 24, 16 June 2009 (2009-06-16), pages 9820-9825, XP002657619, ISSN: 0027-8424, DOI: 10.1073/PNAS.0903849106 [retrieved on 2009-05-14] see mAb1 sterically hinders the binding of PCSK9 to LDLR	1-13, 17-44
X	WO 2009/026558 A1 (AMGEN INC [US]; JACKSON SIMON MARK [US]; WALKER NIGEL PELHAM CLINTON [] 26 February 2009 (2009-02-26) paragraph [0557]; example 40	1-13, 17-44
X	DUFF CHRISTOPHER J ET AL: "Antibody-mediated disruption of the interaction between PCSK9 and the low-density lipoprotein receptor", BIOCHEMICAL JOURNAL, THE BIOCHEMICAL SOCIETY, LONDON, GB, vol. 419, no. 3, 1 May 2009 (2009-05-01), pages 577-584, XP002619050, ISSN: 0264-6021 see Blocking the PCSK9-LDLR interaction inhibits PCSK9 function and restores cellular LDL uptake ; Figure 4 ; first of the Discussion	1-13, 17-44

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No
PCT/US2012/024633

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 2009100297 A1	13-08-2009	AR 070316 A1	31-03-2010
		AU 2009212262 A1	13-08-2009
		CA 2711794 A1	13-08-2009
		CN 102066420 A	18-05-2011
		EP 2245071 A1	03-11-2010
		JP 2011511637 A	14-04-2011
		PA 8815301 A1	17-09-2009
		TW 200938552 A	16-09-2009
		US 2009246192 A1	01-10-2009
		WO 2009100297 A1	13-08-2009
WO 2009026558 A1	26-02-2009	AR 068011 A1	28-10-2009
		AU 2008288791 A1	26-02-2009
		CA 2696252 A1	26-02-2009
		CN 101932607 A	29-12-2010
		CO 6230997 A2	20-12-2010
		CR 11328 A	12-07-2010
		EA 201000356 A1	30-08-2010
		EP 2215124 A1	11-08-2010
		JP 2010536384 A	02-12-2010
		KR 20100057070 A	28-05-2010
		PE 10062009 A1	14-08-2009
		TW 200916481 A	16-04-2009
		US 2009142352 A1	04-06-2009
		US 2009326202 A1	31-12-2009
		US 2011027287 A1	03-02-2011
		US 2012020975 A1	26-01-2012
		US 2012020976 A1	26-01-2012
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FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. claims: 1-13, 17-44(all partially)

   An antibody internally called MAB1 and defined by the SEQ ID N0: 1 and 3; a composition comprising thereof ; a method of reducing LDL-C using the antibody thereof.

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2. claims: 1-44(partially)

   An antibody internally called MAB2 and defined by the SEQ ID N0: 5 and 7; a composition comprising thereof ; a method of reducing LDL-C using the antibody thereof.

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3. claims: 1-44

   An antibody internally called MAB3 and defined by the SEQ ID N0: 9 and 11; a composition comprising thereof ; a method of reducing LDL-C using the antibody thereof.
