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

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
18 September 2014 (18.09.2014)

WIPO | PCT

(10) International Publication Number
WO 2014/140210 A1

(51) International Patent Classification:
A61K 39/00 (2006.01) *C07K 14/47* (2006.01)
C07K 14/435 (2006.01)

(21) International Application Number:
PCT/EP2014/055013

(22) International Filing Date:
13 March 2014 (13.03.2014)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
61/781,511 14 March 2013 (14.03.2013) US
13175023.4 4 July 2013 (04.07.2013) EP

(71) Applicants: **PIERIS AG** [DE/DE]; Lise-Meitner-Strasse 30, 85354 Freising-Weihenstephan (DE). **DAIICHI SANKYO CO., LTD** [JP/JP]; 3-5-1, Nihonbashi-honcho, Chuo-ku, Tokyo, 103-8426 (JP).

(72) Inventors: **MATSCHINER, Gabriele**; Gabelsbergerstr. 70, 80333 Muenchen (DE). **ROTHE, Christine**; Heinrich-Nikolaus-Strasse 26, 85221 Dachau (DE). **HOHLBAUM, Andreas**; Schuetzenstrasse 4, 85276 Pfaffenhofen (DE). **BEL AIBA, Rachida Siham**; Erhardtstrasse 15, 80469 Munich (DE). **HINNER, Marlon**; Eugen-Papst-Strasse 9, 81247 Munich (DE). **ALLERSDORFER, Andrea**; Hochstrasse 8a, 85301 Geisenhausen (DE). **LUNDE, Bradley**; General von Nagel Strasse 4C, 85354 Freising (DE). **WIEDENMANN, Alexander**; Bluetenweg 19, 85375 Neufahrn bei Freising (DE). **YAMAGUCHI, Shinji**; DAIICHI SANKYO COMPANY, LIMITED, 1-2-58, Hiromachi, Shinagawa-ku, Tokyo, 140-8710 (JP). **ABURATANI, Takahide**; DAIICHI SANKYO COMPANY, LIMITED, 1-2-58, Hiromachi, Shinagawa-ku, Tokyo, 140-8710 (JP). **HASHIMOTO, Ryuji**; DAIICHI SANKYO COMPANY, LIMITED, 1-2-58, Hiromachi, Shinagawa-ku, Tokyo, 140-8710 (JP). **TAKAHASHI, Tohru**; DAIICHI SANKYO COMPANY, LIMITED, 1-2-58, Hiromachi, Shinagawa-ku, Tokyo, 140-8710 (JP). **NAGASAKI, Chikako**; DAIICHI SANKYO COMPANY, LIMITED, 1-2-58, Hiromachi, Shinagawa-ku, Tokyo, 140-8710 (JP). **NARA, Futoshi**; DAIICHI SANKYO COMPANY, LIMITED, 1-2-58, Hiromachi, Shinagawa-ku, Tokyo, 140-8710 (JP). **NISHIZAWA, Tomohiro**; DAIICHI SANKYO COMPANY, LIMITED, 1-2-58, Hiromachi, Shinagawa-ku, Tokyo, 140-8710 (JP).

(74) Agents: **WEINZIERL, Gerhard** et al.; Schiweck Weinzierl Koch, Landsberger Str. 98, 80339 Munich (DE).

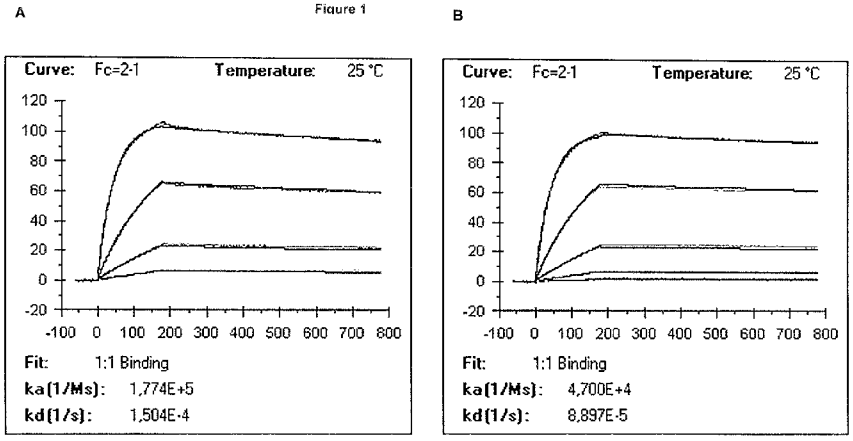
(81) Designated States *(unless otherwise indicated, for every kind of national protection available)*: AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IR, IS, JP, KE, KG, 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, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SA, 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, 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,

[Continued on next page]

(54) Title: NOVEL BINDING PROTEINS FOR PCSK9

Figure 1



(57) Abstract: The present disclosure relates to novel lipocalin muteins which bind to PCSK9. The disclosure also provides corresponding nucleic acid molecules encoding lipocalin muteins and methods for producing lipocalin muteins as well as their encoding nucleic acid molecules.

WO 2014/140210 A1

TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, KM, ML, MR, NE, SN, TD, TG).

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))*

NOVEL BINDING PROTEINS FOR PCSK9

I. BACKGROUND

[0001] Human proprotein convertase subtilisin/kexin type 9 (PCSK9) is a secreted protein expressed primarily in the kidneys, liver and intestines. It has three domains: an inhibitory pro-domain (amino acids 1-152; including a signal sequence at amino acids 1-30), a serine protease domain (or catalytic domain; at amino acids 153-448), and a C-terminal domain (or cysteine/histidine-rich domain) of 210 residues in length (at amino acids 449-692), which is rich in cysteine residues. PCSK9 is synthesized as a zymogen that undergoes autocatalytic cleavage between the pro-domain and catalytic domain in the endoplasmic reticulum. The pro-domain remains bound to the mature protein after cleavage, and the complex is secreted. The cysteine-rich domain may play a role analogous to the P-(processing) domains of other Furin/Kexin/Subtilisin-like serine proteases, which appear to be essential for folding and regulation of the activated protease.

[0002] PCSK9 is a member of the proteinase K secretory subtilisin-like subfamily of serine proteases (Naureckiene et al., 2003 *Arc. Biochem. Biophys.* 420:55-67) and functions as a strong negative regulator of hepatic low density lipoprotein receptors (LDL-R). PCSK9 plays a critical role in cholesterol metabolism by controlling the levels of low density lipoprotein (LDL) particles that circulate in the bloodstream. Elevated levels of PCSK9 have been shown to reduce LDL-R levels in the liver, resulting in high levels of low density lipoprotein cholesterol (LDL-c) in the plasma and increased susceptibility to coronary artery disease. (Peterson et a.l, *J Lipid Res.* 49(7): 1595-9 (2008)).

[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 PCSK9. PCSK9 knockout mice showed an approximate 50% reduction in the plasma LDL-c levels and showed enhanced sensitivity to statins in reducing plasma LDL-c (Rashid S, et al (2005) Proc Natl Acad Sci 102:5374-5379. Human genetic data also support the role of PCSK9 in homeostasis. Mutations in PCSK9 are associated with abnormal levels of LDL-c in the blood plasma

(Horton et al., 2006 *Trends. Biochem. Sci.* 32(2):71-77). 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.

[0004] Therefore, it would be highly advantageous to produce an inhibitor of PCSK9 that antagonizes the activity of PCSK9 and blocks or reduces the corresponding role PCSK9 plays in various pathologic conditions.

II. DEFINITIONS

[0005] The following list defines terms, phrases, and abbreviations used throughout the instant specification. All terms listed and defined herein are intended to encompass all grammatical forms.

[0006] As used herein, the term “lipocalin” refers to a polypeptide defined by its supersecondary structure, namely cylindrical β-pleated sheet supersecondary structural region comprising eight β-strands connected pair-wise by four loops at one end to define thereby a binding pocket. Lipocalins (Pervaiz and Brew, *FASEB J. 1* (1987), 209-214) are a family of small, often monomeric secretory proteins which have been isolated from various organisms (Flower, *Biochem. J.* 318 (1996), 1-12). The lipocalins bear relatively little mutual sequence similarity and their belonging to the same protein structural family was first eluicidated by X-ray structure analysis (Sawyer et al., *Nature* 327 (1987), 659).

[0007] In this regard, a “lipocalin mutein”, as used in the present discussed, refers to a mutein derieved from a lipocalin and having a cylindrical β-pleated sheet supersecondary structural region comprising eight β-strands connected pair-wise by four loops at one end to define thereby a binding pocket, wherein at least one amino acid of each of at least three of said four loops has been mutated (see, for example, PCT publication WO 1999/16873). In some particular embodiments, said lipocalin mutein may be derived from human tear lipocalin. In some other particular embodiments, however, said lipocalin mutein may be derived from a lipocalin other than human tear lipocalin.

[0008] As used herein, the term "subject" includes any vertebrates e.g., mammals. Mammals include, but are not limited to, domesticated animals (e.g., cows, sheep, cats, dogs, and horses), primates (e.g., humans and non-human primates such as monkeys), rabbits, and rodents (e.g., mice and rats). In certain embodiments, the individual or subject is a human.

[0009] The term "proprotein convertase subtilisin kexin type 9" ("PCSK9," interchangeable with "NARC-1") as used herein, refers to any native PCSK9 from any vertebrate source, including mammals such as primates (e.g. humans) and rodents (e.g., mice and rats), unless otherwise indicated. The term encompasses "full-length," unprocessed PCSK9 as well as any form of PCSK9 that results from processing in the cell or any fragment thereof. The term also encompasses naturally occurring variants of PCSK9, e.g., splice variants or allelic variants.

[0010] The term "vector," as used herein, refers to a nucleic acid molecule capable of propagating another nucleic acid to which it is linked. The term includes the vector as a self-replicating nucleic acid structure as well as the vector incorporated into the genome of a host cell into which it has been introduced. Certain vectors are capable of directing the expression of nucleic acid sequences to which they are operatively linked. Such vectors are referred to herein as "expression vectors."

III. DESCRIPTIONS OF FIGURES

[0011] **Figure 1:** provides typical measurements of on-rate and off-rate by Surface Plasmon Resonance for the lipocalin muteins SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 6 and SEQ ID NO: 11. The resulting dissociation constants (K_D) to human PCSK9 ("hPCSK9") (SEQ ID NO: 34), the association rates (k_{on}), and the dissociation rates (k_{off}) are summarized in **Table 1** of **Example 6**.

[0012] **Figure 2**: demonstrates that the lipocalin muteins SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 7 and SEQ ID NO: 8 were capable of blocking the interaction between PCSK9 and its receptor LDL-R. Either biotinylated hPCSK9 (**Fig. 2A**) or biotinylated hPCSK9_D374Y mutant (**Fig. 2B**) were pre-incubated with variable concentrations of said muteins and non-neutralized PCSK9 was quantified on an ELISA plate with immobilized soluble LDL-R. Negative control SEQ ID NO: 2 had no competitive effect. Data were fitted with a single-site binding model. Resulting IC50 values are summarized in **Table 2** of **Example 7**.

[0013] **Figure 3**: shows the crossreactivity profile of the lipocalin muteins of SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8 and SEQ ID NO: 9 as measured in an ELISA format. Full crossreactivity of the lipocalin muteins to hPCSK9_D374Y mutant and to cynomolgus monkey PCSK9 is evident from nearly identical K_D values (see **Table 3**). Within the concentration range tested, there is also

crossreactivity to mouse PCSK9 but with lower affinities. No binding was detected of the negative control (SEQ ID NO: 2). Data were fitted with a single-site binding model.

[0014] **Figure 4:** illustrates that the lipocalin muteins of SEQ NO: 3, SEQ NO: 4, SEQ NO: 6, SEQ NO: 7, and SEQ NO: 8 are effective in blocking hPCSK9 binding to its receptor LDL-R in a cell-based assay. The assay is based on PCSK9-induced internalization of LDL-R on HepG2 cells leading to reduced intracellular uptake of fluorescence-labeled Dil-LDL. Cells are incubated with a fixed concentration of hPCSK9 (100 nM) and titrated with the lipocalin muteins. Plotted is the normalized fluorescence signal of intracellular Dil-LDL measured at 485/535 nm using a BMG PheraStar reader, against the concentration of lipocalin muteins. The resulting IC50 values for the lipocalin muteins of SEQ NO: 3, SEQ NO: 4, SEQ NO: 6, SEQ NO: 7 and SEQ NO: 8 are given in **Table 4**. Binding of lipocalin muteins to PCSK9 restored PCSK9-mediated reduction of Dil-LDL uptake into cells whereas the negative control of SEQ ID NO: 2 had no effect. The curves were fitted by GraphPad Prism 4 using nonlinear regression "sigmoidal dose – response, variable slope" model (5PL fit). Data were normalized by the value of PCSK9 stimulated and non-stimulated cells.

[0015] **Figure 5:** provides typical measurements of on-rate and off-rate for binding and unbinding of lipocalin muteins of SEQ ID NO: 13 (**Fig. 5C**), SEQ ID NO: 20 (**Fig. 5A**) and SEQ ID NO: 21 (**Fig. 5B**) to hPCSK9 as measured by Surface Plasmon Resonance. The resulting K_Ds are summarized in **Table 5** (see **Example 10**).

[0016] **Figure 6:** provides typical measurements of on-rate and off-rate for binding and unbinding of lipocalin mutein (SEQ ID NO: 20) to various PCSK9 species as measured by Surface Plasmon Resonance. The resulting K_D for lipocalin mutein SEQ ID NO: 20 and for other muteins are summarized in **Table 6** (see **Example 11**).

[0017] **Figure 7:** demonstrates that the PEGylated versions of lipocalin muteins of SEQ ID NO: 30, SEQ ID NO: 31 and SEQ ID NO: 32 are capable of binding to hPCSK9 with an IC50 of 0.19, 0.53, and 0.37 nM, respectively, similar to the unmodified lipocalin mutein of SEQ ID NO: 13, which displayed an IC50 of 0.16 nM. Biotinylated hPCSK9 was pre-incubated with variable concentrations of the lipocalin muteins and non-neutralized hPCSK9 was quantified on an ELISA plate immobilized with a benchmark antibody (its light chain is represented by SEQ ID NO: 29 while its heavy chain is represented by SEQ ID NO: 33), which was used as a positive control to compete with the lipocalin muteins for binding to hPCSK9. Data were fitted with a single-site binding model.

[0018] **Figure 8:** demonstrates that the lipocalin muteins of SEQ ID NO: 22, SEQ ID NO: 13 and SEQ ID NO: 20 and their respective PEGylated variants of SEQ ID NO: 30, SEQ ID NO: 31 and SEQ ID NO: 32 are capable of blocking biological activity of hPCSK9 in a cell-based LDL-R depletion assay. Dilution series of the tested lipocalin muteins and negative control of SEQ ID NO: 2 are incubated with a constant concentration of hPCSK9 on LDL starved HepG2 cells. Levels of LDL-R on the HepG2 surface were assessed by using a specific goat anti-hLDL-R antibody (R&D Cat. No. AF2148). PCSK9-induced maximal LDL-R internalization was set up at 100%. Addition of lipocalin muteins blocked PCSK9's activity in a dose-dependent manner. In this regard, IC50 values for lipocalin muteins of SEQ ID NO: 22, SEQ ID NO: 13 and SEQ ID NO: 20 were 76 nM, 103 nM and 91 nM, respectively. Thus, PEGylation did not affect lipocalin muteins' blocking ability since IC50 measured for the PEGylated lipocalin muteins (comprising SEQ ID NOs: 30-32, respectively, which represent amino acid sequences of variants of three lipocalin muteins of the disclosure but do not include sequence of the polyethylene glycol (PEG) molecule) did not differ from their respective unPEGylated forms (SEQ ID NOs: 13, 20 and 22, respectively). Negative control of SEQ ID NO: 2 had no effect on PCSK9's activity. In summary, the lipocalin muteins inhibited biological activity of PCSK9 and therefore restore LDL-R on the cell surface. The data was fitted with a sigmoidal dose-response model.

[0019] **Figure 9:** shows the expression vector pTLPC26 (also called pTlc26) which encodes a fusion protein comprising the OmpA signal sequence (OmpA) and a human tear lipocalin mutein followed by the Strep-tag II. Both the *Bst*XI-restriction sites used for the cloning of the mutated gene cassette and the restriction sites flanking the structural gene are labeled. Gene expression is under the control of the tetracycline promoter/operator ($tet^{p/o}$). Transcription is terminated at the lipoprotein transcription terminator (t_{lpp}). The vector further comprises an origin of replication (ori), the intergenic region of the filamentous phage f1 (f1-IG), the ampicillin resistance gene (amp) and the tetracycline repressor gene (tetR). A relevant segment of the nucleic acid sequence of pTLPC26 is given in the sequence listing as SEQ ID NO: 35. The segment begins with the *Xba*I restriction site and ends with the *Hin*dIII restriction site. The vector elements outside this region are identical with the vector pASK75, the complete nucleotide sequence of which is given in the German patent publication DE 44 17 598 Al.

[0020] **Figure 10:** depicts an alignment of amino acid sequences of certain human tear lipocalin based muteins (listed as SEQ ID NOs: 2-28) in comparison with the polypeptide sequence of mature human tear lipocalin (SEQ ID NO: 1).

[0021] **Figure 11: Fig. 11 A** provides the expected distribution of amino acids encoded for **Example 3**. Note that for clarity, all amino acids having a frequency of less than 1% are omitted; the amber stop codon (TAG) is taken as encoding glutamine because a codon suppresor bacterial strain, TG1 F, is used in the phage display process. In addition, experimental data obtained from the sequencing of maturation libraries (**Fig. 11 B** and **Fig. 11 C**) shows that there is a good match between the expected and the experimental distribution, albeit with the frequency of serine being higher than desired, reflecting either biases in oligo synthesis or oligo assembly by PCR. In line with this finding, the experimentally obtained frequency of mutation distributions for two libraries (**Fig. 11 E** and **Fig. 11 F**) are close to the theoretically expected distribution (**Fig. 11 D**), but shifted to a lower frequency.

[0022] **Figure 12:** depicts a thermogram, obtained from a nano Differential Scanning Calorimeter ("nanoDSC") measurement using a capillary nanoDSC instrument (Q2000, TA Instruments), representing overlays of melting curves of lipocalin muteins (SEQ ID NO: 13 and SEQ ID NOs: 63-65). Melting curves of thermo-stabilized derivatives (SEQ ID NOs: 63-65) are significantly shifted compared to SEQ ID NO: 13.

[0023] **Figure 13:** provides typical measurements of on-rate and off-rate by Surface Plasmon Resonance for the lipocalin muteins (SEQ ID NOs: 62-71). **Fig.13A-Fig.13J** corresponds to SEQ ID NOs: 62-71 respectively. The resulting dissociation constants (KD), the association rates (kon) and the dissociation rates (koff) to human PCSK9 ("hPCSK9") (SEQ ID NO: 34) are summarized in **Table 10** of **Example 17**.

[0024] **Figure 14:** depicts an alignment of amino acid sequences of certain human tear lipocalin based muteins (listed as SEQ ID NOs: 13, 22, 62-71) in comparison with the polypeptide sequence of mature human tear lipocalin (SEQ ID NO: 1).

IV. DETAILED DESCRIPTION OF THE DISCLOSURE

[0025] In one aspect, the present disclosure provides muteins of human tear lipocalin that bind to proprotein convertase subtilisin/kexin type 9 or PCSK9. In some embodiments, the lipocalin muteins have a high affinity for PCSK9. PCSK9 as a target of a mutein of the present disclosure is typically a mammalian protein, for example, a non-human primate

protein or a human protein. Full-length human PCSK9 has the amino acid sequence shown in SEQ ID NO: 34.

[0026] A lipocalin mutein of the disclosure may also be able to bind an immunogenic fragment of PCSK9. An immunogenic fragment of PCSK9 is a fragment that has one or more epitopes, mimotopes or other antigenic determinants, and is thus capable of inducing an immune response or against which an antibody can be raised. The immunogenic fragment may include a single epitope or may have a plurality of epitopes. Since an antigen-presenting system, e.g. a carrier protein, may be used to provide the size required for recognition by an immune system, no particular size limitation applies to the immunogenic fragment. Hence, the immunogenic fragment may also be a "hapten", i.e. a fragment that need not be antigenic per se or may have low immunogenicity, in particular due to its small molecular weight and accordingly size. Typically an immunogenic fragment can, alone or when presented on a carrier, be bound by an immunoglobulin. An immunogenic fragment of PCSK9 is typically capable of interacting with LDL-R and thereby modulating low density lipoprotein (LDL) particles that circulate in the bloodstream. In some embodiments, an immunogenic fragment of PCSK9 retains the capability of the full length ligand to be recognized and/or bound by a lipocalin mutein according to the disclosure. For example, the immunogenic fragment may be an N-terminally and/or C-terminally shortened protein or peptide.

[0027] In various embodiments, the lipocalin muteins of the disclosure are able to bind PCSK9 of a non-human primate PCSK9 (e.g., cynomolgus monkey PCSK9 or chimpanzee PCSK9) or an immunogenic fragment thereof with detectable affinity, i.e. with a K_D of at least 200 nM. In some embodiments a lipocalin mutein of the disclosure may bind a non-human primate PCSK9 or an immunogenic fragment thereof with a K_D equal to or less than about 10 nM, about 1 nM or about 0.3 nM. In various embodiments, antigen binding portion binds to mouse PCSK9 or an immunogenic fragment thereof with a K_D equal to or less than about 10 nM, about 1 nM or about 0.5 nM.

[0028] In various embodiments, one or more lipocalin muteins of the disclosure are able to bind human PCSK9 or an immunogenic fragment thereof with detectable affinity, i.e. with a K_D of at least 200 nM. In some embodiments a lipocalin mutein of the disclosure may bind human PCSK9 or an immunogenic fragment thereof with a K_D equal to or less than about 10 nM, about 1 nM, about 0.1 nM, about 0.5 nM, about0.25 nM, about 10 pM or even less.

[0029] In some further embodiments, binding affinities of one or more lipocalin muteins to human PCSK9 or an immunogenic fragment thereof have been found to be of a K_D below 0.1 nM and in some embodiments be of a K_D equal to or less than about 1 picomolar (pM) (see **Figure 7**).

[0030] The binding affinity of a lipocalin mutein to a selected target, in the present case PCSK9, can be measured and thereby K_D values of a mutein-ligand complex be determine by a multitude of methods known to those skilled in the art. Such methods include, but are not limited to, fluorescence titration, competition ELISA, calorimetric methods, such as isothermal titration calorimetry (ITC), and surface plasmon resonance (BIAcore). Examples for such methods are detailed below (See e.g. **Example 7**).

[0031] In one embodiment, a lipocalin mutein of the disclosure may act as an antagonist of PCSK9. The term "antagonist of PCSK9," as used herein, refers to an agent that is capable of interfere with the binding between PCSK9 and LDL-R. In some cases, a PCSK9 antagonist can be identified by its ability to fully or partically inhibit the binding between PCSK9 and LDL-R.

[0032] Futhermore, a lipocalin mutein of the disclosure may be competitive for binding of LDL-R to PCSK9 (see **Example 7**).

[0033] In addition, a lipocalin mutein of the disclosure may be competitive for binding of a monoclonal antibody comprising SEQ ID NO: 29 and SEQ ID NO: 33 to PCSK9 (see **Example 12**).

[0034] In a further embodiment, a lipocalin mutein of the disclosure may be able to fully or partially inhibit PCSK9-mediated downregulation of LDL-R. Inhibition occurs, for example, where PCSK9-mediated downregulation of LDL-R, when exposed to a lipocalin mutein of the disclosure, is at least about 10% less, e.g. at least about 25%, 50%, 75% less, or totally inhibited, in comparison to PCSK9-mediated downregulation of LDL-R in the presence of a control or in the absence of the lipocalin mutein. In some still further embodiments, a lipocalin mutein of the disclosure may be able to inhibit PCSK9-mediated downregulation of LDL-R in a dose-dependent manner. In some still further embodiments, the inhibition of PCSK9-mediated downregulation of LDL-R can be demonstrated in a HEPG2-cell-based assay as essentially described in **Example 13**.

[0035] In yet another embodiment, a lipocalin mutein of the disclosure may be able to restore LDL uptake in the presence of PCSK9. In some further embodiments, the restorage of LDL updtake in the presence of PCSK9 can be demonstrated in a HEPG2-cell-based assay as essentially described in **Example 11**. In some still furtherembodiments, to set up the assay, HEPG2 cells may be incubated with a fixed concentration of hPCSK9 (e.g. 100 nM) and then may be titrated with one or more lipocalin muteins.

[0036] PCSK9 can be taken to define a non-natural ligand of human tear lipocalin. The term "non-natural ligand" refers to a compound, which does not bind to mature human tear lipocalin under physiological conditions. The term "human tear lipocalin" as used herein refers to the mature human tear lipocalin corresponding to the protein of the SWISS-PROT Data Bank Accession Number P31025, while the mature human tear lipocalin (SEQ ID NO: 1) does not include the N-terminal signal peptide that is included in the sequence of SWISS-PROT Accession Number P31025.

[0037] The amino acid sequence of a mutein of the disclosure has a high sequence identity to mature human tear lipocalin (SEQ ID NO: 1). In this context, the amino acid sequence of a mutein of the disclosure may be substantially similar to the amino acid sequence of mature human tear lipocalin. A respective sequence of a lipocalin mutein of the disclosure, being substantially similar to the sequences of mature human tear lipocalin, may have in various embodiments at least 70%, at least 75%, at least 80%, at least 82%, at least 85%, at least 87% or at least 90% identity, including at least 95% identity, to the sequence of mature human tear lipocalin (see, for example, **Figure 10** and **Figure 14**), with the proviso that the altered position or sequence is retained.

[0038] By "identity" is meant a property of sequences that measures their similarity or relationship. Identity is measured by dividing the number of identical residues by the total number of residues and multiplying the product by 100. As two illustrative examples, the mutein of the SEQ ID NO: 3 has a sequence identity of 82.28% with the amino acid sequence of mature human tear lipocalin, and the mutein of the SEQ ID NO: 7 has an amino acid sequence identity of 83.54% with mature human tear lipocalin.

[0039] "Gaps" are spaces in an alignment that are the result of additions or deletions of amino acids. Thus, two copies of exactly the same sequence have 100% identity, but sequences that are less highly conserved, and have deletions, additions, or replacements, may have a lower degree of identity. Those skilled in the art will recognize that several computer

programs are available for determining sequence identity using standard parameters, for example Blast (Altschul, et al. (1997) *Nucleic Acids Res.* **25**, 3389-3402), Blast2 (Altschul, et al. (1990) *J. Mol. Biol.* **215**, 403-410), and Smith-Waterman (Smith, et al. (1981) *J. Mol. Biol.* **147**, 195-197).

[0040] The term "mutated" or "mutein" in reference to a nucleic acid or a polypeptide of the disclosure refers to the exchange, deletion, or insertion of one or more nucleotides or amino acids, respectively, compared to the naturally occurring nucleic acid or polypeptide. A mutein of the present disclosure includes at least three substitutions in comparison to the corresponding native human tear lipocalin.

[0041] In some embodiments, a mutein of human tear lipocalin according to the disclosure includes at least 2 including 3, 4, 5, 6, 8, 10, 12, 14, 15, 16, 17 or 18 mutated amino acid residues at any one of the sequence positions 26-34, 56-58, 80, 83, 104-106 and 108 of the linear polypeptide sequence of mature human tear lipocalin (SEQ ID NO: 1). The positions 26-34 are included in the AB loop, the positions 56-58 are included in the CD loop. The position 80 is located in a α-helical region. Position 83 is a single loop-defining amino acid between this α-helical region and a beta-sheet (βF). The positions 104-106 and 108 are included in the GH loop in the binding site at the open end of the β-barrel structure of tear lipocalin. The definition of these regions is used herein in accordance with Flower (Flower, 1996, supra, Flower, et al., 2000, supra) and Breustedt et al. (2005, supra).

[0042] In some embodiments, a human lipocalin mutein according to the disclosure may further include an amino acid substitution of a native cysteine residue at positions 61 and/or 153 by a serine residue. In this context it is noted that it has been found that removal of the structural disulfide bond (on the level of a respective native nucleic acid library) of mature human tear lipocalin that is formed by the cysteine residues 61 and 153 (cf. Breustedt, et al., 2005, supra) provides human tear lipocalin muteins that are not only stably folded but in addition are also able to bind a given non-natural ligand with high affinity. Without wishing to be bound by theory, it is also believed that the elimination of the structural disulfide bond provides the further advantage of allowing for the (spontaneous) generation or deliberate introduction of non-natural artifical disulfide bonds into muteins of the disclosure (see **Examples**), thereby increasing the stability of the muteins, for example. However, human tear lipocalin muteins that binds PCSK9 and that have the disulfide bond formed between Cys 61 and Cys 153 are also part of the present disclosure.

[0043] In some embodiments, a human tear lipocalin mutein of the disclosure includes the amino acid substitutions Cys 61 → Ala, Phe, Lys, Arg, Thr, Asn, Tyr, Met, Ser, Pro or Trp and/or Cys 153 → Ser or Ala.

[0044] In some embodiments, a human tear lipocalin mutein according to the disclosure includes an amino acid substitution of a native cysteine residue at position 101 by a serine residue. Further, in some embodiments, a human tear lipocalin mutein according to the disclosure includes an amino acid substitution of a native arginine residue at positions 111 by a proline residue. In some embodiments, a human tear lipocalin mutein according to the disclosure includes an amino acid substitution of a native lysine residue at positions 114 by a tryptophan residue.

[0045] In some embodiments, a human tear lipocalin mutein of the disclosure includes at least one amino acid substitution, which may be an additional amino acid substitution, selected from Arg 111 → Pro and Lys 114 → Trp. A human tear lipocalin mutein of the disclosure may further include the cysteine at position 101 of the sequence of mature human tear lipocalin substituted by another amino acid. This substitution may, for example, be the mutation Cys 101 → Ser or Cys 101 → Pro.

[0046] In some embodiments a human tear lipocalin mutein of the disclosure includes one or more of the following amino acid substitutions in comparison to mature human tear lipocalin: Arg 26 → Ser, Phe, Trp, His or Thr, Glu 34 → Asn, Thr, Arg or Gly, Leu 56 → Met, Ser, Gln, Phe, His or Asn and Ser 58 → Lys, Ala, Arg, Trp or Pro.

[0047] In some embodiments, a human tear lipocalin mutein according to the disclosure contains at least one of the following amino acid substitutions in comparison to mature human tear lipocalin: Met 31 → Ala, Gly, His, Pro, Ser Aps, Glu or Gln, Leu 33 → Tyr, Trp, Tyr, Phe, Pro or Ala, Ser 61 → Trp or Phe, Asp 80 → Ser, Met, Pro, Ile, Gln, Tyr, Ser, Val or Thr, Glu 104 → Leu, Pro, Ser, Ala, Asn, Thr, Lys or Asp, His 106 → Pro, Gln, Gly, Arg, Val, Thr, Asn or Leu and Lys 108 → Gln, Ala, Trp, Tyr, Arg, Asp, Asn, Ser, Glu or Thr.

[0048] In some embodiments, a human tear lipocalin mutein according to the disclosure includes one or more of the following amino acid substitutions in comparison to mature human tear lipocalin: Glu 27 → Arg, Ser, Gln, Thr, Phe, Lys, Ala or Arg, Pro 29 → Gly, Asp, Asn, Ile, Leu or Met, Asn 32 → Ile, Leu, Tyr, Met or Trp and Leu 105 → Cys, Tyr, Trp, Glu, Arg, Ser, His, Ala, Val, Asp, Pro, Gly or Lys.

[0049] In some embodiments, a human tear lipocalin mutein according to the disclosure contains at least one of the following amino acid substitutions in comparison to mature human tear lipocalin: Phe 28 → Cys, Arg, Lys, Trp, Asp, Gly, His, Leu or Asn; Glu 30 → Arg, Asp, Thr, Ser, Gly, Ala or Asn, Ile 57 → Tyr, Trp, His, Gln, Thr or Arg, Lys 83 → Arg, Ser, Gln, Thr or Glu.

[0050] In some embodiments, a human tear lipocalin mutein according to the disclosure includes the combination of amino acid substitutions: Arg 26 → Phe; Asn 32 → Ile; Glu 34 → Thr; Leu 56 → Met; Ser 58 → Ala and Lys 83 → Ser, in comparison to mature human tear lipocalin. In some embodiments, a human tear lipocalin mutein according to the disclosure includes the combination of amino acid substitutions: Arg 26 → Trp; Asn 32 → Leu; Glu 34 → Thr; Leu 56 → Ser and Ser 58 → Ala, in comparison to mature human tear lipocalin. In some embodiments, a human tear lipocalin mutein according to the disclosure includes the combination of amino acid substitutions: Arg 26 → His; Asn 32 → Tyr; Glu 34 → Thr; Leu 56 → Ser; Ser 58 → Arg and Lys 83 → Gln; in comparison to mature human tear lipocalin. In some embodiments, a human tear lipocalin mutein according to the disclosure includes the combination of amino acid substitutions: Arg 26 → Phe; Asn 32 → Met; Glu 34 → Thr; Leu 56 → Gln; Ser 58 → Ala and Lys 83 → Thr; in comparison to mature human tear lipocalin. In some embodiments, a human tear lipocalin mutein according to the disclosure includes the combination of amino acid substitutions: Asn 32 → Trp; Glu 34 → Arg; Leu 56 → Asn; Ser 58 → Trp and Lys 83 → Ser, in comparison to mature human tear lipocalin. In some embodiments, a human tear lipocalin mutein according to the disclosure includes the combination of amino acid substitutions: Arg 26 → Phe; Asn 32 → Leu; Glu 34 → Thr; Leu 56 → Phe; Ser 58 → Ala and Lys 83 → Arg, in comparison to mature human tear lipocalin. In some embodiments, a human tear lipocalin mutein according to the disclosure includes the combination of amino acid substitutions: Arg 26 → Thr; Asn 32 → Trp; Glu 34 → Asn; Leu 56 → His; Ser 58 → Pro and Lys 83 → Ser, in comparison to mature human tear lipocalin. In some embodiments, a human tear lipocalin mutein according to the disclosure includes the combination of amino acid substitutions: Asn 32 → Trp; Glu 34 → Asn; Leu 56 → Phe; Ser 58 → Arg and Lys 83 → Glu, in comparison to mature human tear lipocalin. In some embodiments, a human tear lipocalin mutein according to the disclosure includes the combination of amino acid substitutions: Arg 26 → Trp; Asn 32 → Leu; Glu 34 → Thr; Leu 56 → Met; Ser 58 → Ala and Lys 83 → Ser, in comparison to mature human tear lipocalin. In some embodiments, a human tear lipocalin mutein according to the disclosure

includes the combination of amino acid substitutions: Asn 32 → Trp; Glu 34 → Gly; Leu 56 → Gln; Ser 58 → Ala and Lys 83 → Gln, in comparison to mature human tear lipocalin.

[0051] In some embodiments, a human tear lipocalin mutein of the disclosure includes one of the following sets of amino acid substitutions:

(1) Glu 27 → Ser; Phe 28 → Arg; Pro 29 → Gly; Glu 30 → Asp; Met 31 → Ala; Leu 33 → Trp; Ile 57 → Tyr; Asp 80 → Met; Glu 104 → Pro; Leu 105 → Tyr; His 106 → Gln; Lys 108 → Ala,

(2) Glu 27 → Gln; Phe 28 → Cys; Pro 29 → Asp; Glu 30 → Thr; Met 31 → Gly; Leu 33 → Trp; Ile 57 → Tyr; Leu 105 → Cys; His 106 → Gly; Lys 108 → Trp,

(3) Glu 27 → Glu; Phe 28 → Trp; Pro 29 → Asn; Glu 30 → Gly; Met 31 → His; Leu 33 → Tyr; Ile 57 → Tyr; Asp 80 → Pro; Glu 104 → Ser; Leu 105 → Trp; His 106 → Pro; Lys 108 → Tyr,

(4) Glu 27 → Thr; Phe 28 → Asp; Pro 29 → Asn; Glu 30 → Ser; Met 31 → Pro; Leu 33 → Phe; Ile 57 → Tyr; Asp 80 → Ile; Glu 104 → Ala; Leu 105 → Glu; His 106 → Arg; Lys 108 → Arg,

(5) Glu 27 → Phe; Phe 28 → Lys; Pro 29 → Ile; Glu 30 → Ala; Met 31 → Ser; Leu 33 → Pro; Ile 57 → Trp; Asp 80 → Gln; Glu 104 → Asn; Leu 105 → Arg; His 106 → Gln; Lys 108 → Asp,

(6) Glu 27 → Lys; Phe 28 → Gly; Pro 29 → Pro; Glu 30 → Thr; Met 31 → Pro; Leu 33 → Trp; Ile 57 → His; Asp 80 → Tyr; Glu 104 → Ala; Leu 105 → Ser; His 106 → Val; Lys 108 → Asn,

(7) Glu 27 → Glu; Phe 28 → His; Pro 29 → Leu; Glu 30 → Ala; Met 31 → Asp; Leu 33 → Ala; Ile 57 → Gln; Asp 80 → Ile; Glu 104 → Ala; Leu 105 → Tyr; His 106 → Pro; Lys 108 → Ser,

(8) Glu 27 → Ala; Phe 28 → Asp; Pro 29 → Met; Glu 30 → Gly; Met 31 → Asp; Leu 33 → Pro; Ile 57 → Thr; Asp 80 → Thr; Glu 104 → Thr; His 106 → Thr; Lys 108 → Arg,

(9) Glu 27 → Arg; Phe 28 → Leu; Pro 29 → Asp; Glu 30 → Asn; Met 31 → Glu; Leu 33 → Trp; Ile 57 → Tyr; Asp 80 → Gln; Glu 104 → Pro; Leu 105 → Arg; His 106 → Asn; Lys 108 → Ala,

(10) Glu 27 → Lys; Phe 28 → Asn; Pro 29 → Met; Glu 30 → Gly; Met 31 → Gln; Leu 33 → Pro; Ile 57 → Arg; Asp 80 → Ile; Glu 104 → Asp; Leu 105 → Arg; His 106 → Leu; Lys 108 → Thr, or

(11) Glu 27 → Ser; Phe 28 → Arg; Pro 29 → Gly; Glu 30 → Asp; Met 31 → Ala; Leu 33 → Trp; Ile 57 → Tyr; Asp 80 → Met; Glu 104 → Pro; Leu 105 → Gly; His 106 → Gln; Lys 108 → Ala.

[0052] In a particular embodiment, a human tear lipocalin mutein according to the disclosure includes the combination of amino acid substitutions: Arg 26 → Phe; Glu 27 → Ser; Phe 28 → Arg; Pro 29 → Gly; Glu 30 → Asp; Met 31 → Ala; Asn 32 → Ile; Leu 33 → Trp; Glu 34 → Thr; Leu 56 → Met; Ile 57 → Tyr; Ser 58 → Ala; Lys 83 → Ser; Glu 104 → Pro and Lys 108 → Thr, in comparison to mature human tear lipocalin. In a still further embodiments, the human tear lipocalin mutein includes one or more of the following amino acid substitutions in comparison to mature human tear lipocalin: Thr 43 → Ile or Ala, Glu 45 → Gly, Asn 48 → Gly, Glu 63 → Gly, Ala 66 → Vla, Glu 69 → Vla, Lys 70 → Arg, Ala 79 → Thr, Met or Vla, Asp 80 → Met or Ser, Gly 82 → Ser, His 84 → Gln, Vla 85 → Gly, Tyr 87 → Ser, Ile 88 → Thr or Leu, His 92 → Pro, Leu 105 → His, Gly or Tyr and His 106 → Gln or Arg.

[0053] In yet another particular embodiment, a human tear lipocalin mutein according to the disclosure includes the combination of amino acid substitutions: Glu 27 → Phe; Phe 28 → Lys; Pro 29 → Ile; Asn 32 → Trp; Leu 33 → Pro; Glu 34 → Arg; Leu 56 → Asn; Ile 57 → Trp; His 106 → Gln and Lys 108 → Glu, in comparison to mature human tear lipocalin. In a still further embodiments, the human tear lipocalin mutein includes one or more of the following amino acid substitutions in comparison to mature human tear lipocalin: Glu 43 → Gly or Ala, Glu 45 → Gly, Ser 58 → Trp or Arg, Glu 63 → Asp, Glu 69 → Gly, Lys 70 → Arg, Asp 80 → Gln, Val or Thr, Gly 82 → Asp, Lys 83 → Ser or Arg, Ala 86 → Glu or Ser, Phe 99 → Leu, Glu 102 → Lys or Val, Glu 104 → Asn or Lys and Pro 106 → Thr.

[0054] In some further embodiments, a human tear lipocalin mutein according to the disclosure comprises one or more mutated amino acid residues at any one of the amino acid sequence positions 79, 92 and 105 of the linear polypeptide sequence of mature human tear lipocalin. For example, a human tear lipocalin mutein of the disclosure may include the following amino acid substitutions: Ala 79 → Met, Thr or Val, His 92 → Pro and/or Leu 105 → Ala, Val, Asp, Pro, Arg, Gly, Lys or His.

[0055] As defined above, a human tear lipocalin mutein of the disclosure includes at least one amino acid substitution, which is located at a sequence position of the positions 26, 27, 28, 30, 31, 33, 34, 57, 61, 80, 83, 104-106 and 108 of the linear polypeptide sequence of the mature human tear lipocalin (SEQ ID NO: 1). In some embodiments a mutein of the

disclosure includes two or more, such as 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15 or 16 amino acid substitutions of these sequence positions of the mature human tear lipocalin. In one particular embodiment, the mutein has a mutated amino acid residue at each of the sequence positions 26, 27, 28, 30, 31, 33, 53, 57, 61, 64, 66, 80, 83, 104-106 and 108 of the linear polypeptide sequence of the mature human tear lipocalin (see, for example, **Figure 10** and **Figure 14**).

[0056] In some embodiments, a human tear lipocalin mutein of the disclosure may also include with respect to the amino acid sequence of mature human tear lipocalin one or more, including at least two, at least three or at least four amino acid substitutions of native amino acid residues by cysteine residues at any of positions within the loop regions of mature human tear lipocalin. In some embodiments, a mutein according to the disclosure includes an amino acid substitution of a native amino acid by a cysteine residue at positions 28 or 105 with respect to the amino acid sequence of mature human tear lipocalin.

[0057] In the residual region, i.e. the region differing from sequence positions 26-34, 56-58, 80, 83, 104-106 and 108, a human tear lipocalin mutein of the disclosure may include the wild type (natural) amino acid sequence outside the mutated amino acid sequence positions. In some embodiments, a human tear lipocalin mutein according to the disclosure may also carry one or more amino acid mutations at a sequence position/ positions as long as such a mutation does, at least essentially not hamper or not interfere with the binding activity and the folding of the mutein. Such mutations can be accomplished very easily on DNA level using established standard methods. Illustrative examples of alterations of the amino acid sequence are insertions or deletions as well as amino acid substitutions. Such substitutions may be conservative, i.e. an amino acid residue is replaced with an amino acid residue of chemically similar poperties, in particular with regard to polarity as well as size. Examples of conservative substitutions are the replacements among the members of the following groups: 1) alanine, serine, and threonine; 2) aspartic acid and glutamic acid; 3) asparagine and glutamine; 4) arginine and lysine; 5) isoleucine, leucine, methionine, and valine; and 6) phenylalanine, tyrosine, and tryptophan. On the other hand, it is also possible to introduce non-conservative alterations in the amino acid sequence. In addition, instead of replacing single amino acid residues, it is also possible to either insert or delete one or more continuous amino acids of the primary structure of tear lipocalin as long as these deletions or insertion result in a stable folded/functional mutein (see for example, the experimental section in which muteins with truncated N- and C-terminus are generated).

[0058] Such modifications of the amino acid sequence include directed mutagenesis of single amino acid positions in order to simplify sub-cloning of the mutated lipocalin gene or its parts by incorporating cleavage sites for certain restriction enzymes. In addition, these mutations can also be incorporated to further improve the affinity of a lipocalin mutein for a given target. Furthermore, mutations can be introduced in order to modulate certain characteristics of the mutein such as to improve folding stability, serum stability, protein resistance or water solubility or to reduce aggregation tendency, if necessary. For example, naturally occurring cysteine residues may be mutated to other amino acids to prevent disulfide bond formation. It is also possible to deliberately mutate other amino acid sequence position to cysteine in order to introduce new reactive groups, for example for the conjugation to other compounds, such as polyethylene glycol (PEG), hydroxyethyl starch (HES), biotin, peptides or proteins, or for the formation of non-naturally occurring disulfide linkages. Exemplary possibilities of such a mutation to introduce a cysteine residue into the amino acid sequence of a human tear lipocalin mutein include the substitutions Thr 40→ Cys, Glu 73→ Cys, Arg 90→ Cys, Asp 95→ Cys, and Glu 131→ Cys. The generated thiol moiety at the side of any of the amino acid positions 40, 73, 90, 95 and/or 131 may be used to PEGylate or HESylate the mutein, for example, in order to increase the serum half-life of a respective tear lipocalin mutein.

[0059] The present disclosure also encompasses muteins as defined above, in which the first four N-terminal amino acid residues of the sequence of mature human tear lipocalin (His-His-Leu-Leu; positions 1-4) and/or the last two C-terminal amino acid residues (Ser at position 157 and Asp at positions 158) of the sequence of mature human tear lipocalin have been deleted (see **Figure 10** and **Figure 14**). Another possible mutation of the wild type sequence is to change the amino acid sequence at sequence positions 5 to 7 (Ala Ser Asp) to Gly Gly Asp as described in PCT publication WO 2005/019256.

[0060] The human tear lipocalin mutein of the disclosure may include, consist essentially of or consist of any one of the amino acid sequences set forth in SEQ ID NOs: 3-28, 62-71 and 82 or a fragment or variant thereof.

[0061] The term “fragment” as used herein in connection with the lipocalin muteins of the disclosure relates to proteins or peptides derived from full-length mature lipocalin that are N-terminally and/or C-terminally shortened, i.e. lacking at least one of the N-terminal and/or C-terminal amino acids. Such fragments may include at least 10, more such as 20 or 30 or

more consecutive amino acids of the primary sequence of the mature lipocalin and are usually detectable in an immunoassay of the mature lipocalin.

[0062] The term "variant" as used in the present disclosure relates to derivatives of a lipocalin mutein of the disclosure that include modifications of the amino acid sequence, for example by substitution, deletion, insertion or chemical modification. Such modifications do in some embodiments not reduce the functionality of the mutein. For example, to generate such variant, one or more amino acids of a mutein of the disclosure can be replaced by their respective D-stereoisomers or by amino acids other than the naturally occurring 20 amino acids, such as, e.g. ornithine, hydroxyproline, citrulline, homoserine, hydroxylysine, norvaline. However, such substitutions may also be conservative, i.e. an amino acid residue is replaced with a chemically similar amino acid residue. Examples of conservative substitutions are the replacements among the members of the following groups: 1) alanine, serine, and threonine; 2) aspartic acid and glutamic acid; 3) asparagine and glutamine; 4) arginine and lysine; 5) isoleucine, leucine, methionine, and valine; and 6) phenylalanine, tyrosine, and tryptophan.

[0063] A lipocalin mutein of the disclosure may exist as a monomeric protein. In some embodiments a lipocalin mutein according to the disclosure may be able to spontaneously dimerise or oligomerise. The use of lipocalin muteins that form stable monomers may be advantageous in some applications, e.g. because of faster diffusion and better tissue penetration. In other embodiments the use of a lipocalin mutein that spontaneously forms stable homodimers or multimers may be advantageous, since such multimers can provide (further) increased affinity and/or avidity to a given target. Furthermore, oligomeric forms of the lipocalin mutein may have slower dissociation rates or prolonged serum half-life. If dimerisation or multimerisation of muteins that form stable monomers is desired, this can for example be achieved by fusing respective oligomerization domains such as jun-fos domains or leucin-zippers to muteins of the disclosure or by the use of "Duocalins" (see also below).

[0064] A tear lipocalin mutein according to the present disclosure can be obtained by means of mutagenesis of a naturally occurring form of human tear lipocalin. The term "mutagenesis" as used herein means that the experimental conditions are chosen such that the amino acid naturally occurring at a given sequence position of human tear lipocalin (Swiss-Prot data bank entry P31025) can be substituted by at least one amino acid that is not present at this specific position in the respective natural polypeptide sequence. The term "mutagenesis" also includes the (additional) modification of the length of sequence segments

by deletion or insertion of one or more amino acids. Thus, it is within the scope of the disclosure that, for example, one amino acid at a chosen sequence position is replaced by a stretch of three random mutations, leading to an insertion of two amino acid residues compared to the length of the respective segment of the wild type protein. Such an insertion or deletion may be introduced independently from each other in any of the peptide segments that can be subjected to mutagenesis in the disclosure. In one exemplary embodiment of the disclosure, an insertion of several mutations may be introduced into the loop AB of the chosen lipocalin scaffold (cf. PCT publication WO 2005/019256 which is incorporated by reference in its entirety herein). The term "random mutagenesis" means that no predetermined single amino acid (mutation) is present at a certain sequence position but that at least two amino acids can be incorporated with a certain probability at a predefined sequence position during mutagenesis.

[0065] The coding sequence of human tear lipocalin (Redl, B. et al. (1992) *J. Biol. Chem.* **267**, 20282-20287) is used as a starting point for the mutagenesis of the peptide segments selected in the present disclosure. For the mutagenesis of the recited amino acid positions, the person skilled in the art has at his disposal the various established standard methods for site-directed mutagenesis. A commonly used technique is the introduction of mutations by means of PCR (polymerase chain reaction) using mixtures of synthetic oligonucleotides, which bear a degenerate base composition at the desired sequence positions. For example, use of the codon NNK or NNS (wherein N = adenine, guanine, cytosine or thymine; K = guanine or thymine; S = adenine or cytosine) allows incorporation of all 20 amino acids plus the amber stop codon during mutagenesis, whereas the codon VVS (wherein V = adenine, guanine or cytosine) limits the number of possibly incorporated amino acids to 12, since it excludes the amino acids Cys, Ile, Leu, Met, Phe, Trp, Tyr, Val from being incorporated into the selected position of the polypeptide sequence; use of the codon NMS (wherein M = adenine or cytosine), for example, restricts the number of possible amino acids to 11 at a selected sequence position since it excludes the amino acids Arg, Cys, Gly, Ile, Leu, Met, Phe, Trp, Val from being incorporated at a selected sequence position. In this respect it is noted that codons for other amino acids (than the regular 20 naturally occurring amino acids) such as selenocysteine or pyrrolysine can also be incorporated into a nucleic acid of a mutein. It is also possible, as described by Wang, L., et al. (2001) *Science* **292**, 498-500, or Wang, L., and Schultz, P.G. (2002) *Chem. Comm.* **1**, 1-11, to use "artificial" codons such as UAG which are usually recognized as stop codons in order to insert other unusual amino acids, for example o-methyl-L-tyrosine or p-aminophenylalanine.

[0066] The use of nucleotide building blocks with reduced base pair specificity, as for example inosine, 8-oxo-2'deoxyguanosine or 6(2'-deoxy-β-D-ribofuranosyl)-3,4-dihydro-8H-pyrimindo-1,2-oxazine-7-one (Zaccolo et al. (1996) *J. Mol. Biol.* **255**, 589-603), is another option for the introduction of mutations into a chosen sequence segment.

[0067] A further possibility is the so-called triplet-mutagenesis. This method uses mixtures of different nucleotide triplets, each of which codes for one amino acid, for incorporation into the coding sequence (Virnekäs B, et al., (1994) *Nucleic Acids Res* **22**, 5600-5607).

[0068] One possible strategy for introducing mutations in the selected regions of the respective polypeptides is based on the use of four oligonucleotides, each of which is partially derived from one of the corresponding sequence segments to be mutated. When synthesizing these oligonucleotides, a person skilled in the art can employ mixtures of nucleic acid building blocks for the synthesis of those nucleotide triplets which correspond to the amino acid positions to be mutated so that codons encoding all natural amino acids randomly arise, which at last results in the generation of a lipocalin peptide library. For example, the first oligonucleotide corresponds in its sequence - apart from the mutated positions - to the coding strand for the peptide segment to be mutated at the most N-terminal position of the lipocalin polypeptide. Accordingly, the second oligonucleotide corresponds to the non-coding strand for the second sequence segment following in the polypeptide sequence. The third oligonucleotide corresponds in turn to the coding strand for the corresponding third sequence segment. Finally, the fourth oligonucleotide corresponds to the non-coding strand for the fourth sequence segment. A polymerase chain reaction can be performed with the respective first and second oligonucleotide and separately, if necessary, with the respective third and fourth oligonucleotide.

[0069] The amplification products of both of these reactions can be combined by various known methods into a single nucleic acid that includes the sequence from the first to the fourth sequence segments, in which mutations have been introduced at the selected positions. To this end, both of the products can for example be subjected to a new polymerase chain reaction using flanking oligonucleotides as well as one or more mediator nucleic acid molecules, which contribute the sequence between the second and the third sequence segment. In the choice of the number and arrangement within the sequence of the oligonucleotides used for the mutagenesis, the person skilled in the art has numerous alternatives at his disposal.

[0070] The nucleic acid molecules defined above can be connected by ligation with the missing 5'- and 3'-sequences of a nucleic acid encoding a lipocalin polypeptide and/or the vector, and can be cloned in a known host organism. A multitude of established procedures are available for ligation and cloning. For example, recognition sequences for restriction endonucleases also present in the sequence of the cloning vector can be engineered into the sequence of the synthetic oligonucleotides. Thus, after amplification of the respective PCR product and enzymatic cleavage the resulting fragment can be easily cloned using the corresponding recognition sequences.

[0071] Longer sequence segments within the gene coding for the protein selected for mutagenesis can also be subjected to random mutagenesis via known methods, for example by use of the polymerase chain reaction under conditions of increased error rate, by chemical mutagenesis or by using bacterial mutator strains. Such methods can also be used for further optimization of the target affinity or specificity of a lipocalin mutein. Mutations possibly occurring outside the segments of experimental mutagenesis are often tolerated or can even prove to be advantageous, for example if they contribute to an improved folding efficiency or folding stability of the lipocalin mutein.

[0072] In an exemplary method according to the disclosure, a nucleic acid molecule encoding a human tear lipocalin is subjected to mutagenesis at one or more of the amino acid sequence positions 26-34, 56-58, 80, 83, 104-106 and 108 of the linear polypeptide sequence of mature human tear lipocalin (SEQ ID NO: 1). In some embodiments, the nucleic acid molecule is further subjected to mutagenesis at one or more of the amino acid sequence positions 61, 101, 111, 114 and 153 of the linear polypeptide sequence of the mature human tear lipocalin.

[0073] In one embodiment of the disclosure, a method for the generation of a mutein of human tear lipocalin includes mutating at least 2, 3, 4, 5, 6, 8, 10, 12, 14, 15, 16, or 17 of the codons of any of the amino acid sequence positions 26-34, 56-58, 80, 83, 104-106 and 108 of the linear polypeptide sequence of mature human tear lipocalin. In one embodiment, all 18 of the codons of amino acid sequence positions 26, 27, 28, 29, 30, 31, 32, 33, 34, 56, 57, 58, 80, 83, 104, 105, 106 and 108 of the linear polypeptide sequence of mature human tear lipocalin are mutated.

[0074] In a further embodiment of the disclosure, the methods according to the disclosure include the mutation of both of the codons encoding cysteine at positions 61 and

153 in the linear polypeptide sequence of mature human tear lipocalin (SEQ ID NO: 1). In one embodiment position 61 is mutated to encode an alanine, phenylalanine, lysine, arginine, threonin, asparagine, tyrosine, methionine, serine, proline or a tryptophane residue, to name only a few possibilities. In embodiments where position 153 is mutated, an amino acid such as a serine or alanine can be introduced at position 153.

[0075] In another embodiment of the disclosure as described herein, the codons encoding amino acid sequence positions 111 and/or 114 of the linear polypeptide sequence of mature human tear lipocalin are mutated to encode for example an arginine at position 111 and a tryptophane at position 114.

[0076] Another embodiment of the methods of the disclosure, involves mutagenesis of the codon encoding the cysteine at position 101 of the linear polypeptide sequence of mature human tear lipocalin so that this codon encodes any other amino acid. In one embodiment the mutated codon encoding position 101 encodes a serine. Accordingly, in some embodiments either two or all three of the cysteine codons at position 61, 101 and 153 are replaced by a codon of another amino acid.

[0077] According to the method of the disclosure, a lipocalin mutein is obtained starting from a nucleic acid molecule encoding human tear lipocalin. Such a nucleic acid molecule is subjected to mutagenesis and introduced into a suitable bacterial or eukaryotic host organism by means of recombinant DNA technology. Obtaining a nucleic acid library of lipocalin muteins can be carried out using any suitable technique that is known in the art for generating lipocalin muteins with antibody-like properties, i.e. muteins that have affinity towards a given target. Examples of such combinatorial methods are described in detail in the PCT publications WO 99/16873, WO 00/75308, WO 03/029471, WO 03/029462, WO 03/029463, WO 2005/019254, WO 2005/019255, WO 2005/019256, or WO 2006/56464 for instance. The content of each of these patent applications is incorporated by reference herein in its entirety. After expression of the nucleic acid sequences that were subjected to mutagenesis in an appropriate host, the clones carrying the genetic information for the plurality of respective lipocalin muteins, which bind a given target can be selected from the library obtained. Well known techniques can be employed for the selection of these clones, such as phage display (reviewed in Kay, B.K. et al. (1996) *supra*; Lowman, H.B. (1997) *supra* or Rodi, D.J., and Makowski, L. (1999) *supra*), colony screening (reviewed in Pini, A. et al. (2002) *Comb. Chem. High Throughput Screen.* **5**, 503-510), ribosome display (reviewed in Amstutz, P. et al. (2001) *Curr. Opin. Biotechnol.* **12**, 400-405) or mRNA display as reported in

Wilson, D.S. et al. (2001) *Proc. Natl. Acad. Sci. USA* **98**, 3750-3755 or the methods specifically described in WO 99/16873, WO 00/75308, WO 03/029471, WO 03/029462, WO 03/029463, WO 2005/019254, WO 2005/019255, WO 2005/019256, or WO 2006/56464.

[0078] The resulted nucleic acid molecules encoding one or more lipocalin muteins of the disclosure may be expressed using any suitable expression system. The obtained lipocalin mutein or lipocalin muteins can be further selected. The selection may for example be carried out under competitive conditions. Competitive conditions as used herein means that selection of lipocalin muteins encompasses at least one step in which the lipocalin muteins and the given non-natural ligand of wide-type lipocalin are brought in contact in the presence of an additional ligand, which competes with binding of the muteins to such non-natural ligand. This additional ligand may be a physiological ligand of the target, an excess of the target itself or any other non-physiological ligand of the target that binds at least an overlapping epitope to the epitope recognized by the muteins of the disclosure and thus interferes with target binding of the muteins. Alternatively, the additional ligand competes with binding of the muteins by complexing an epitope distinct from the binding site of the muteins to the target by allosteric effects.

[0079] An embodiment of the phage display technique (reviewed in Kay, B.K. et al. (1996), *supra*; Lowman, H. B. (1997) *supra* or Rodi, D.J., & Makowski, L. (1999), *supra*) using temperate M13 phage is given as an example of a selection method that can be employed in the present disclosure. Another embodiment of the phage display technology that can be used for selection of muteins of the disclosure is the hyperphage phage technology as described by Broders et al. (Broders et al. (2003) "Hyperphage. Improving antibody presentation in phage display." *Methods Mol. Biol.* **205**:295-302). Other temperate phage such as f1 or lytic phage such as T7 may be employed as well. For the exemplary selection method, M13 phagemids are produced which allow the expression of the mutated lipocalin nucleic acid sequence as a fusion with a signal sequence at the N-terminus, such as the OmpA-signal sequence, and with the capsid protein pIII of the phage M13 or fragments thereof capable of being incorporated into the phage capsid at the C-terminus. The C-terminal fragment ΔpIII of the phage capsid protein that includes amino acids 217 to 406 of the wild type sequence is may be used to produce the fusion proteins. In one embodiment a C-terminal fragment of pIII is used, in which the cysteine residue at position 201 is missing or is replaced by another amino acid.

[0080] Accordingly, a further embodiment of the methods of the disclosure involves operably fusing a nucleic acid molecule coding for the one or more lipocalin muteins and resulting from mutagenesis at the 3' end with a gene coding for the coat protein pIII of a filamentous bacteriophage of the M13-family or for a fragment of this coat protein, in order to select at least one mutein for the binding of a given ligand.

[0081] The fusion protein may include additional components such as an affinity tag, which allows the immobilization, detection and/or purification of the fusion protein or its parts. Furthermore, a stop codon can be located between the sequence regions encoding the lipocalin or its muteins and the phage capsid gene or fragments thereof, wherein the stop codon, such as an amber stop codon, is at least partially translated into an amino acid during translation in a suitable suppressor strain.

[0082] For example, the phasmid vector pTLPC27 (see, for example, Figure 20 and SEQ ID NO: 9 of PCT publication WO 2008/015239), also called pTlc27, can be used for the preparation of a phagemid library encoding human tear lipocalin muteins. The inventive nucleic acid molecules coding for the tear lipocalin muteins may be inserted into the vector using the two *Bst*XI restriction sites. After ligation a suitable host strain such as *E. coli* XL1-Blue is transformed with the resulting nucleic acid mixture to yield a large number of independent clones. A respective vector can be generated for the preparation of a hyperphagemid library, if desired.

[0083] The resulting library is subsequently superinfected in liquid culture with an appropriate M13-helper phage or hyperphage in order to produce functional phagemids. The recombinant phagemid displays the lipocalin mutein on its surface as a fusion with the coat protein pIII or a fragment thereof, while the N-terminal signal sequence of the fusion protein is normally cleaved off. On the other hand, it also bears one or more copies of the native capsid protein pIII supplied by the helper phage and is thus capable of infecting a recipient, in general a bacterial strain carrying an F- or F'-plasmid. In case of hyperphage display, the hyperphagemids display the lipocalin muteins on their surface as a fusion with the infective coat protein pIII but no native capsid protein. During or after infection with helper phage or hyperphage, gene expression of the fusion protein between the lipocalin mutein and the capsid protein pIII can be induced, for example by addition of anhydrotetracycline. The induction conditions are chosen such that a substantial fraction of the phagemids obtained displays at least one lipocalin mutein on their surface. In case of hyperphage display induction conditions result in a population of hyperphagemids carrying between three and five fusion proteins

consisting of the lipocalin mutein and the capsid protein pIII. Various methods are known for isolating the phagemids, such as precipitation with polyethylene glycol. Isolation typically occurs after an incubation period of 6-8 hours.

[0084] The isolated phasmids can then be subjected to selection by incubation with the desired target, wherein the target is presented in a form allowing at least temporary immobilization of those phagemids which carry muteins with the desired binding activity as fusion proteins in their coat. Among the various embodiments known to the person skilled in the art, the target can, for example, be conjugated with a carrier protein such as serum albumin and be bound via this carrier protein to a protein binding surface, for example polystyrene. Microtiter plates suitable for ELISA techniques or so-called "immuno-sticks" can for instance be used for such an immobilization of the target. Alternatively, conjugates of the target with other binding groups, such as biotin, can be used. The target can then be immobilized on a surface which selectively binds this group, for example microtiter plates or paramagnetic particles coated with streptavidin, neutravidin or avidin. If the target is fused to an Fc portion of an immunoglobulin, immobilization can also be achieved with surfaces, for example, microtiter plates or paramagnetic particles, which are coated with protein A or protein G.

[0085] Non-specific phagemid-binding sites present on the surfaces can be saturated with blocking solutions as they are known for ELISA methods. The phagemids are then typically brought into contact with the target immobilized on the surface in the presence of a physiological buffer. Unbound phagemids are removed by multiple washings. The phagemid particles remaining on the surface are then eluted. For elution, several methods are possible. For example, the phagemids can be eluted by addition of proteases or in the presence of acids, bases, detergents or chaotropic salts or under moderately denaturing conditions. One such method is the elution using buffers of pH 2.2, wherein the eluate is subsequently neutralized. Alternatively, a solution of the free target can be added in order to compete with the immobilized target for binding to the phagemids or target-specific phagemids can be eluted by competition with immunoglobulins or natural liganding proteins which specifically bind to the target of interest.

[0086] Afterwards, *E. coli* cells are infected with the eluted phagemids. Alternatively, the nucleic acid sequences can be extracted from the eluted phagemids and used for sequence analysis, amplification or transformation of cells in another manner. Starting from the *E. coli* clones obtained in this way, fresh phagemids or hyperphagemids are again produced by

superinfection with M13 helper phages or hyperphage according to the method described above and the phagemids amplified in this way are once again subjected to a selection on the immobilized target. Multiple selection cycles are often necessary in order to obtain the phagemids with the lipocalin muteins of the disclosure in optimized form. The number of selection cycles is in some embodiments chosen in such a way that in the subsequent functional analysis at least 0.1% of the clones studied produce muteins with detectable affinity for the given target. Depending on the size, i.e. the complexity of the library employed, 2 to 8 cycles are typically required to this end.

[0087] For the functional analysis of the selected muteins, an *E. coli* strain is infected with the phagemids obtained from the selection cycles and the corresponding double stranded phasmid DNA is isolated. Starting from this phasmid DNA, or also from the single-stranded DNA extracted from the phagemids, the nucleic acid sequences of the selected muteins of the disclosure can be determined by the methods known in the art and the amino acid sequence can be deduced therefrom. The mutated region or the sequence of the entire lipocalin mutein can be subcloned on another expression vector and expressed in a suitable host organism. For example, the vector pTLPC26 (as referred in the description of **Figure 9**), also called pTlc26, can be used for expression in *E. coli* strains such as *E.coli* TG1. A lipocalin mutein thus produced can be purified by various biochemical methods. A lipocalin mutein produced, for example with pTlc26, may carry an affinity peptide, a so called affinity tag, for instance at its C-terminus and can therefore be purified by affinity chromatography. Examples of an affinity tag include, but are not limited to biotin, the Strep-tag, Strep-tag II (Schmidt et al., supra), oligohistidine, polyhistidine, an immunoglobulin domain, maltose-binding protein, glutathione-S-transferase (GST) or calmodulin binding peptide (CBP).

[0088] Some affinity tags are haptens, for example but not limited to, dinitrophenol and digoxigenin. Some affinity tags are epitope tags, such as the FLAG®-peptide (Asp-Tyr-Lys-Asp-Asp-Asp-Asp-Lys-Gly), the T7 epitope (Ala-Ser-Met-Thr-Gly-Gly-Gln-Gln-Met-Gly), maltose binding protein (MBP), the HSV epitope of the sequence Gln-Pro-Glu-Leu-Ala-Pro-Glu-Asp-Pro-Glu-Asp of herpes simplex virus glycoprotein D, the hemagglutinin (HA) epitope of the sequence Tyr-Pro-Tyr-Asp-Val-Pro-Asp-Tyr-Ala, the VSV-G epitope of the Vesicular Stomatitis viral glycoprotein (Cys-Tyr-The-Asp-Ile-Glu-Met-Asn-Arg-Leu-Lys), the E epitope tag of the sequence Gly-Ala-Pro-Val-Pro-Tyr-Pro-Asp-Pro-Leu-Glu-Pro-Arg, the E2 epitope tag of the sequence Gly-Val-Ser-Ser-Thr-Ser-Ser-Asp-Phe-Arg-Asp-Arg, the Tag-100 epitope tag of C-termini of mammalian MAPK/ERK kinases of the sequence Glu-Glu-

Thr-Ala-Arg-Phe-Gln-Pro-Gly-Tyr-Arg-Ser, the S-tag of the sequence Lys-Glu-Thr-Ala-Ala-Ala-Lys-Phe-Glu-Arg-Gln-His-Met-Asp-Ser, the "myc" epitope of the transcription factor c-myc of the sequence Glu-Gln-Lys-Leu-Ile-Ser-Glu-Glu-Asp-Leu and the small V5 epitope present on the P and V proteins of the paramyxovirus of Simian Virus 5 (Gly-Lys-Pro-Ile-Pro-Asn-Pro-Leu-Leu-Gly-Leu-Asp-Ser-Thr). In addition, but generally not as a single tag, a solubility-enhancing tag such as NusA, thioredoxin (TRX), small ubiquitin-like modifier (SUMO), and ubiquitin (Ub) may be used. Haptens and epitope tags may be used in combination with a corresponding antibody or an antibody like proteinaceous molecule as binding partner. The S-peptide epitope of the sequence Lys-Glu-Thr-Ala-Ala-Ala-Lys-Phe-Glu-Arg-Gln-His-Met-Asp-Ser may be used as an epitope tag in connection with a respective antibody or in combination with the S-protein as a binding partner (Hackbarth, JS, et al., BioTechniques (2004) 37, 5, 835-839).

[0089] The selection can also be carried out by means of other methods. Many corresponding embodiments are known to the person skilled in the art or are described in the literature. Moreover, a combination of methods can be applied. For example, clones selected or at least enriched by "phage display" can additionally be subjected to "colony screening". This procedure has the advantage that individual clones can directly be isolated with respect to the production of a lipocalin mutein with detectable binding affinity for a target.

[0090] In addition to the use of *E. coli* as host organism in the "phage display" technique or the "colony screening" method, other bacterial strains, yeast or also insect cells or mammalian cells can be used for this purpose. Further to the selection of a lipocalin mutein from a random library as described above, evolutive methods including limited mutagenesis can also be applied in order to optimize a mutein that already possesses some binding activity for the target with respect to affinity or specificity for the target after repeated screening cycles.

[0091] It is readily apparent to the skilled person that complex formation is dependent on many factors such as concentration of the binding partners, the presence of competitors, ionic strength of the buffer system etc. Selection and enrichment is generally performed under conditions allowing the isolation of lipocalin muteins having, in complex with the desired target, a dissociation constant of at least 200 nM. However, the washing and elution steps can be carried out under varying stringency. A selection with respect to the kinetic characteristics is possible as well. For example, the selection can be performed under conditions, which favor complex formation of the target with muteins that show a slow dissociation from the target, or

in other words a low k_{off} rate. Alternatively, selection can be performed under conditions, which favor fast formation of the complex between the mutein and the target, or in other words a high k_{on} rate. As a further illustrative alternative, the screening can be performed under conditions that select for improved thermo-stability of the muteins (compared to either wild type lipocalin or a mutein that already has affinity towards a pre-selected target).

[0092] Once a lipocalin mutein with affinity to a given target has been selected, it is additionally possible to subject such a mutein to another mutagenesis in order to subsequently select variants of even higher affinity or variants with improved properties such as higher thermo-stability, improved serum stability, thermodynamic stability, improved solubility, improved monomeric behavior, improved resistance against thermal denaturation, chemical denaturation, proteolysis, or detergents, etc. This further mutagenesis, which in case of aiming at higher affinity can be considered as *in vitro* "affinity maturation", can be achieved by site specific mutation based on rational design or a random mutation. Another possible approach for obtaining a higher affinity or improved properties is the use of error-prone PCR, which results in point mutations over a selected range of sequence positions of the lipocalin mutein. The error-prone PCR can be carried out in accordance with any known protocol such as the one described by Zaccolo et al. (1996) *J. Mol. Biol.* **255**, 589-603. Other methods of random mutagenesis that are suitable for such purposes include random insertion/deletion (RID) mutagenesis as described by Murakami, H et al. (2002) *Nat.Biotechnol.* **20**, 76-81 or nonhomologous random recombination (NRR) as described by Bittker, J. A et al. (2002) *Nat. Biotechnol.* **20**,1024-1029. If desired, affinity maturation can also be carried out according to the procedure described in WO 00/75308 or Schlehuber, S. et al. (2000) *J. Mol. Biol.* **297**, 1105-1120, where muteins of the bilin-binding protein having high affinity to digoxigenin were obtained.

[0093] In this regard, it is clear to the skilled person that the affinity's K_D values (dissociation constant of the complex formed between the respective mutein and its ligand) may vary within a certain experimental range, depending on the method and experimental setup that is used for determining the affinity of a particular lipocalin mutein for a given ligand. This means, there may be a slight deviation in the measured K_D values or a tolerance range depending, for example, on whether the K_D value was determined by surface plasmon resonance (Biacore) or by competition ELISA.

[0094] Also included in the scope of the present disclosure are forms of the above muteins, in which the respective mutein has been altered or modified with respect to its potential immunogenicity.

[0095] Cytotoxic T-cells recognize peptide antigens on the cell surface of an antigen-presenting cell in association with a class I major histocompatibility complex (MHC) molecule. The ability of the peptides to bind to MHC molecules is allele specific and correlates with their immunogenicity. In order to reduce immunogenicity of a given protein, the ability to predict which peptides in a protein have the potential to bind to a given MHC molecule is of great value. Approaches that employ a computational threading approach to identify potential T-cell epitopes have been previously described to predict the binding of a given peptide sequence to MHC class I molecules (Altuvia et al. (1995) *J. Mol. Biol.* **249**, 244-250).

[0096] Such an approach may also be utilized to identify potential T-cell epitopes in the muteins of the disclosure and to make depending on its intended use a selection of a specific mutein on the basis of its predicted immunogenicity. It may be furthermore possible to subject peptide regions which have been predicted to contain T-cell epitopes to additional mutagenesis to reduce or eliminate these T-cell epitopes and thus minimize immunogenicity. The removal of amphipathic epitopes from genetically engineered antibodies has been described (Mateo et al. (2000) *Hybridoma* **19,** 6, 463-471) and may be adapted to the muteins of the present disclosure.

[0097] The muteins thus obtained may possess a minimized immunogenicity, which is desirable for their use in therapeutic and diagnostic applications, such as those described below.

[0098] For several applications of the lipocalin muteins disclosed herein, the inventive lipocalin muteins may be fused, for example at their N-terminus or their C-terminus, to a moiety, which can be protein, a protein domain or a peptide such as a signal sequence and/or an affinity tag.

[0099] Affinity tags such as the Strep-tag® or Strep-tag® II (Schmidt, T.G.M. et al. (1996) *J. Mol. Biol.* **255**, 753-766), the *myc*-tag, the FLAG-tag, the His_6-tag or the HA-tag or proteins such as glutathione-S-transferase also allow easy detection and/or purification of recombinant proteins are further examples of suitable fusion partners. Finally, proteins with

chromogenic or fluorescent properties such as the green fluorescent protein (GFP) or the yellow fluorescent protein (YFP) are suitable fusion partners for a lipocalin mutein of the disclosure as well. For example, when used in the experiments described in **Examples** below, the lipocalin muteins disclosed herein carry a C-terminal Strep-Tag®II purification tag (IBA GmbH) consisting of 10 amino acids (SAWSHPQFEK).

[00100] For some applications, it is also useful to employ the muteins of the disclosure in a labeled form. Accordingly, the disclosure is also directed to lipocalin muteins which are conjugated to a label moiety selected from the group consisting of enzyme labels, radioactive labels, colored labels, fluorescent labels, chromogenic labels, luminescent labels, haptens, digoxigenin, biotin, metal complexes, metals, and colloidal gold. The mutein may also be conjugated to a low molecular weight organic compound. The term "low molecular weight organic compound" as used herein denotes a monomeric carbon-based compound, which may have aliphatic, alicyclic and/or aromatic moieties. In typical embodiments the low molecular weight organic compound is an organic compound that has a main chain of at least two carbon atoms, and in some embodiments not more than 7 or 12 rotatable carbon bonds. Such a compound has a molecular weight in the range from about 100 to about 2000 Dalton, such as from about 100 to about 1000 Dalton. It may optionally include one or two metal atoms.

[00101] In general, it is possible to label the lipocalin mutein with any appropriate chemical substance or enzyme, which directly or indirectly generates a detectable compound or signal in a chemical, physical, optical, or enzymatic reaction. An example for a physical reaction and at the same time optical reaction/marker is the emission of fluorescence upon irradiation or the emission of X-rays when using a radioactive label. Alkaline phosphatase, horseradish peroxidase and β-galactosidase are examples of enzyme labels (and at the same time optical labels) which catalyze the formation of chromogenic reaction products. In general, all labels commonly used for antibodies (except those exclusively used with the sugar moiety in the Fc part of immunoglobulins) can also be used for conjugation to the muteins of the present disclosure. The muteins of the disclosure may also be conjugated with any suitable therapeutically active agent, e.g., for the targeted delivery of such agents to a given cell, tissue or organ or for the selective targeting of cells, e.g., of tumor cells without affecting the surrounding normal cells. Examples of such therapeutically active agents include radionuclides, toxins, small organic molecules, and therapeutic peptides (such as peptides acting as agonists/antagonists of a cell surface receptor or peptides competing for a protein binding site on a given cellular target). The lipocalin muteins of the disclosure may, however,

also be conjugated with therapeutically active nucleic acid molecules such as antisense nucleic acid molecules, small interfering RNAs, micro RNAs or ribozymes. Such conjugates can be produced by methods well known in the art.

[00102] In one embodiment, the muteins of the disclosure may also be coupled to a moiety that can target a specific body region, organism, tissue, organ or cell within a subject in order to deliver the inventive muteins of the disclosure to a desired body region, organism, tissue, organ or cell of such subject. One example wherein such modification may be desirable is the crossing of the blood-brain-barrier. In order to cross the blood-brain barrier, the muteins of the disclosure may be coupled to moieties that facilitate the active transport across this barrier (see Gaillard PJ, et al., Diphtheria-toxin receptor-targeted brain drug delivery. *International Congress Series,* 2005 1277, 185-198 or Gaillard PJ, et al. Targeted delivery across the blood-brain barrier. *Expert Opin Drug Deliv.* 2005 **2**, 299-309. Such moieties are for example available under the trade name 2B-Trans™ (to-BBB technologies BV, Leiden, NL).

[00103] As indicated above, a lipocalin mutein of the disclosure may in some embodiments be conjugated to a moiety that can extend the serum half-life of the mutein (in this regard see also PCT publication WO 2006/56464 where such conjugation strategies are described with references to muteins of human neutrophile gelatinase-associated lipocalin with binding affinity for CTLA-4). When used in this specification, the term "conjugate" or "conjugation" includes that a moiety is linked to a lipocalin mutein by way of a chemical agent, e.g., a cross-linking agent or an agent which couples a moiety to a side group of an amino acid or the like. Also, said term when used herein is understood to include that a moiety is genetically fused to a lipocalin mutein at the either terminal end by way of forming a covalent bond, e.g., by translationally fusing a moiety that extends the half-life to a lipocalin mutein. The skilled person will understand from the context where said term is used whether a chemical agent is used for conjugation or whether a translational fusion is meant which is achieved by genetic engineering. The moiety that extends the serum half-life may be a polyalkylene glycol molecule, hydroxyethyl starch, fatty acid molecules, such as palmitic acid (Vajo & Duckworth (2000) *Pharmacol. Rev.* **52**, 1-9), an Fc part of an immunoglobulin, a CH3 domain of an immunoglobulin, a CH4 domain of an immunoglobulin, albumin or a fragment thereof, an albumin binding peptide, or an albumin binding protein, transferrin to name only a few. The albumin binding protein may be a bacterial albumin binding protein, an albumin binding peptide, an engineered albumin binding polypeptide, an antibody, an

antibody fragment including domain antibodies (see US patent 6,696,245, for example), or a lipocalin mutein with binding activity for albumin. Accordingly, suitable conjugation partners for extending the half-life of a lipocalin mutein of the disclosure include albumin (Osborn, B.L. et al. (2002) *J. Pharmacol. Exp. Ther.* **303**, 540-548), or an albumin binding protein, for example, a bacterial albumin binding domain, such as the one of streptococcal protein G (König, T., & Skerra, A. (1998) *J. Immunol. Methods* **218**, 73-83). Examples of albumin binding peptides that can be used as conjugation partner are, for instance, those having a Cys-Xaa_1-Xaa_2-Xaa_3-Xaa_4-Cys consensus sequence, wherein Xaa_1 is Asp, Asn, Ser, Thr, or Trp; Xaa_2 is Asn, Gln, His, Ile, Leu, or Lys; Xaa_3 is Ala, Asp, Phe, Trp, or Tyr; and Xaa_4 is Asp, Gly, Leu, Phe, Ser, or Thr as described in US patent application 2003/0069395 or Dennis et al. (Dennis, M. S., Zhang, M., Meng, Y. G., Kadkhodayan, M., Kirchhofer, D., Combs, D. & Damico, L. A. (2002) *J. Biol. Chem.* **277**, 35035-35043).

[00104] Streptococcal protein G (SpG) is a bi-functional receptor present on the surface of certain strains of streptococci and is capable of binding to both IgG and serum albumin (Bjorck et al, Mol Immunol 24:1 1 13, 1987). The structure is highly repetitive with several structurally and functionally different domains (Guss et al, EMBO J 5:1567, 1986), more precisely three Ig-binding domains and three serum albumin binding domains (Olsson et al, Eur J Biochem 168:319, 1987). The structure of one of the three serum albumin binding domains in SpG has been determined, showing a three-helix bundle fold (Kraulis et al, FEBS Lett 378:190, 1996, Johansson et al, J. Biol. Chem. 277:81 14-20, 2002). A 46 amino acid motif was defined as ABD (albumin binding domain) and has subsequently also been designated G148-GA3 (GA for protein G-related albumin binding). For example, in PCT publication WO 2009/016043, albumin binding variants of the 46 amino acid motif ABD are disclosed.

[00105] Other bacterial albumin binding domains than the ones in protein G have also been identified, some of which are structurally similar to the ones of protein G. Examples of proteins containing such albumin binding domains are the PAB, PPL, MAG and ZAG proteins (Rozak et al, Biochemistry 45:3263- 3271 , 2006). Studies of structure and function of such albumin binding domains have been carried out and reported e.g. by Johansson and coworkers (Johansson et al, J Mol Biol 266:859-865, 1997). Furthermore, Rozak et al have reported on the creation of artificial variants of G148-GA3, which were selected and studied with regard to different species specificity and stability (Rozak et al, Biochemistry 45:3263-3271, 2006), whereas Jonsson et al developed artificial variants of G148-GA3 having very

much improved affinity for human serum albumin (Jonsson et al, Prot Eng Des Sel 21:515-27, 2008). For some of the variants a higher affinity was achieved at the cost of reduced thermal stability.

[00106] In addition to the three-helix containing proteins described above, there are also other unrelated bacterial proteins that bind albumin.

[00107] Recently, a few T- and B-cell epitopes were experimentally identified within the albumin binding region of Streptococcal protein G strain 148 (G148) (Goetsch et al, Clin Diagn Lab Immunol 10:125-32, 2003). The authors behind the study were interested in utilizing the T-cell epitopes of G148 in vaccines, i.e. to utilize the inherent immune-stimulatory property of the albumin binding region. Goetsch et al additionally found a B-cell epitope, i.e. a region bound by antibodies after immunization, in the sequence of G148.

[00108] However, in pharmaceutical compositions for human administration no immune-response is desired. Therefore, the albumin binding domain G148 is as such unsuitable for use in such compositions due to its abovementioned immune- stimulatory properties. Such drawbacks and deficiencies are overcome or alleviated by, for example, engineered albumin binding polypeptides disclosed in PCT publication WO 2012/004384, which is incorporated by reference in its entirety herein.

[00109] In this regard, lipocalin muteins of the disclosore may be conjugated to an albumin binding protein, which binds to human serum albumin ("HSA"), via one or more peptide-bond linkers, such as GGG and KLGGGG as unlimiting examaples. In some embodiments, such albumin binding protein may be an albumin binding domain such as Streptococcal protein G strain 148 (G148). In some other embodiments, the albumin binding protein may be an engineered albumin binding polypeptide. For example, the albumin binding polypeptide may have an amino acid sequence comprising SEQ ID NO: 85. The albumin binding polypeptide of SEQ ID NO. 85 may in some embodiments thus have additional amino acid residue(s) which is/are attached to the either terminal end, e.g. such as the three amino acids KLN. In this regard, the present disclosure provides exemplary conjugated lipocalin muteins, which comprises an amino acid sequence as set forth in any one of SEQ ID NOs: 83-84.

[00110] In other embodiments, albumin itself or a biological active fragment of albumin can be used as conjugation partner of a lipocalin mutein of the disclosure. The term "albumin" includes all mammal albumins such as human serum albumin ("HSA") or bovine

serum albumin or rat albumin. The albumin or fragment thereof can be recombinantly produced as described in US patent 5,728,553 or European patent applications EP 0 330 451 and EP 0 361 991. As a representative example, recombinant human albumin (Recombumin®) Novozymes Delta Ltd. (Nottingham, UK) can be conjugated or fused to a lipocalin mutein in order to extend the half-life of the mutein.

[00111] If the albumin-binding protein is an antibody fragment it may be a domain antibody. Domain Antibodies are engineered to allow precise control over biophysical properties and *in vivo* half-life to create the optimal safety and efficacy product profile. Domain Antibodies are for example commercially available from Domantis Ltd. (Cambridge, UK and MA, USA).

[00112] Using transferrin as a moiety to extend the serum half-life of the muteins of the disclosure, the muteins can be genetically fused to the N or C terminus, or both, of non-glycosylated transferrin. Non-glycosylated transferrin has a half-life of 14-17 days, and a transferrin fusion protein will similarly have an extended half-life. The transferrin carrier also provides high bioavailability, biodistribution and circulating stability. This technology is commercially available from BioRexis (BioRexis Pharmaceutical Corporation, PA, USA). Recombinant human transferrin (DeltaFerrin™) for use as a protein stabilizer/half-life extension partner is also commercially available from Novozymes Delta Ltd. (Nottingham, UK).

[00113] If an Fc part of an immunoglobulin is used for the purpose to prolong the serum half-life of the muteins of the disclosure, the *SynFusion*™ technology, commercially available from Syntonix Pharmaceuticals, Inc (MA, USA), may be used. The use of this Fc-fusion technology allows the creation of longer-acting biopharmaceuticals and may for example consist of two copies of the mutein linked to the Fc region of an antibody to improve pharmacokinetics, solubility and production efficiency.

[00114] Yet another alternative to prolong the half-life of a lipocalin mutein of the disclosure is to fuse long, unstructured, flexible glycine-rich sequences (for example, poly-glycine with about 20 to 80 consecutive glycine residues) to the N-or C-terminus of a lipocalin mutein of the disclosure. This approach disclosed in WO2007/038619, for example, has also been term "rPEG" (recombinant PEG).

[00115] If polyalkylene glycol molecule is used for the purpose to prolong the serum half-life of the muteins of the disclosure, the polyalkylene glycol can be substituted,

unsubstituted, linear or branched. It can also be an activated polyalkylene derivative. Examples of suitable compounds are polyethylene glycol (PEG) molecules or activated derivatives thereof as described in WO 99/64016, in US Patent 6,177,074 or in US Patent 6,403,564 in relation to interferon, or as described for other proteins such as PEG-modified asparaginase, PEG-adenosine deaminase (PEG-ADA) or PEG-superoxide dismutase (see for example, Fuertges et al. (1990) The Clinical Efficacy of Poly(Ethylene Glycol)-Modified Proteins *J. Control. Release* **11**, 139-148). The molecular weight of such a polymer, such as polyethylene glycol, may range from about 300 to about 70,000 Dalton, including, for example, polyethylene glycol with a molecular weight of about 10,000, of about 20,000, of about 30,000 or of about 40,000 Dalton. Moreover, as e.g. described in US patents 6,500,930 or 6,620,413, carbohydrate oligo- and polymers such as starch or hydroxyethyl starch (HES) can be conjugated to a mutein of the disclosure for the purpose of serum half-life extension. In some further embodiments, for the purpose to prolong the serum half-life of the muteins of the disclosure, PEG30 or PEG40 would be suggested in animals/humans with normal renal filtration rather than shorter PEGs, because i.e. the faster elimination of PEG12 or PEG20 may limit the effectiveness and duration of PEG-conjugated (PEGylated) lipocalin muteins of the disclosure. In this regard, the present disclosure provides exemplary lipocalin muteins as shown in SEQ ID NOs: 30-32 that can be PEG-conjugated.

[00116] In another embodiment, a lipocalin mutein of the disclosure may be fused to one or more moieties that can confer new characteristics to the fusion such as enzymatic activity or binding affinity for other molecules. Examples of such suitable moieties are alkaline phosphatase, horseradish peroxidase, glutathione-S-transferase, the albumin-binding domain of protein G, protein A, antibody fragments, oligomerization domains, lipocalin muteins of same or different binding specificity (which results in the formation of "Duocalins", cf. Schlehuber, S., and Skerra, A. (2001), Duocalins, engineered ligand-binding proteins with dual specificity derived from the lipocalin fold. *Biol. Chem.* **382**, 1335-1342) or toxins.

[00117] In particular, it may be possible to fuse a lipocalin mutein of the disclosure with a separate enzyme active site such that both "components" of the resulting fusion may act together on a given therapeutic target. For example, when fused together, the binding domain of the lipocalin mutein can attach to a disease-causing target, thereby allowing the enzyme domain to abolish the biological function of the target.

[00118] If one of the above moieties is conjugated to the human tear lipocalin mutein of the disclosure, conjugation to an amino acid side chain can be advantageous. Suitable amino acid side chains may occur naturally in the amino acid sequence of human tear lipocalin or may be introduced by mutagenesis. In case a suitable binding site is introduced via mutagenesis, one possibility is the replacement of an amino acid at the appropriate position by a cysteine residue. In one embodiment, such mutation includes at least one of Thr 40→ Cys, Glu 73→ Cys, Arg 90→ Cys, Asp 95→ Cys or Glu 131→ Cys substitution. The newly created cysteine residue at any of these positions can in the following be utilized to conjugate the mutein to moiety prolonging the serum half-life of the mutein, such as PEG or an activated derivative thereof.

[00119] In another embodiment, in order to provide suitable amino acid side chains for conjugating one of the above moieties to the muteins of the disclosure artificial amino acids may be introduced by mutagenesis. Generally, such artificial amino acids are designed to be more reactive and thus to facilitate the conjugation to the desired moiety. One example of such an artificial amino acid that may be introduced via an artificial tRNA is para-acetyl-phenylalanine.

[00120] In some embodiments, the lipocalin muteins according to the disclosure may contain a signal sequence. Signal sequences at the N-terminus of a polypeptide direct this polypeptide to a specific cellular compartment, for example the periplasm of *E. coli* or the endoplasmatic reticulum of eukaryotic cells. A large number of signal sequences are known in the art. An illustrative signal sequence for secretion a polypeptide into the periplasm of *E. coli* is the OmpA-signal sequence.

[00121] The present disclosure also relates to nucleic acid molecules (DNA and RNA) that include nucleotide sequences coding for muteins as described herein. Since the degeneracy of the genetic code permits substitutions of certain codons by other codons specifying the same amino acid, the disclosure is not limited to a specific nucleic acid molecule encoding a mutein of the disclosure but encompasses all nucleic acid molecules that include nucleotide sequences encoding a functional mutein. In this regard, the present disclosure provides nucleic acid sequences (as shown in SEQ ID NOs: 36-61, 72-81 and 86-89) encoding certain lipocalin muteins of the disclosure.

[00122] Therefore, the present disclosure includes a nucleic acid sequence encoding a mutein according to the disclosure that has a mutation at at least one codon of any of the

amino acid sequence positions 26-34, 56-58, 80, 83, 104-106 and 108 of the linear polypeptide sequence of mature human tear lipocalin, wherein the codons encoding at least one of the cysteine residues at sequence positions 61 and 153 of the linear polypeptide sequence of the mature human tear lipocalin have been mutated to encode any other amino acid residue. In some further embodiments, the nucleic acid sequence encoding a mutein according to the disclosure that has a mutation at at least one codon of any of the amino acid sequence positions 79, 92 and 105 of the linear polypeptide sequence of mature human tear lipocalin.

[00123] The disclosure as disclosed herein also includes nucleic acid molecules encoding tear lipocalin muteins of the disclosure, which include additional mutations outside the indicated sequence positions of experimental mutagenesis. Such mutations are often tolerated or can even prove to be advantageous, for example if they contribute to an improved folding efficiency, serum stability, thermal stability or ligand binding affinity of the mutein.

[00124] A nucleic acid molecule disclosed in this application may be "operably linked" to a regulatory sequence (or regulatory sequences) to allow expression of this nucleic acid molecule.

[00125] A nucleic acid molecule, such as DNA, is referred to as "capable of expressing a nucleic acid molecule" or capable "to allow expression of a nucleotide sequence" if it includes sequence elements which contain information regarding to transcriptional and/or translational regulation, and such sequences are "operably linked" to the nucleotide sequence encoding the polypeptide. An operable linkage is a linkage in which the regulatory sequence elements and the sequence to be expressed are connected in a way that enables gene expression. The precise nature of the regulatory regions necessary for gene expression may vary among species, but in general these regions include a promoter which, in prokaryotes, contains both the promoter *per se*, i.e. DNA elements directing the initiation of transcription, as well as DNA elements which, when transcribed into RNA, will signal the initiation of translation. Such promoter regions normally include 5' non-coding sequences involved in initiation of transcription and translation, such as the -35/-10 boxes and the Shine-Dalgarno element in prokaryotes or the TATA box, CAAT sequences, and 5'-capping elements in eukaryotes. These regions can also include enhancer or repressor elements as well as translated signal and leader sequences for targeting the native polypeptide to a specific compartment of a host cell.

[00126] In addition, the 3' non-coding sequences may contain regulatory elements involved in transcriptional termination, polyadenylation or the like. If, however, these termination sequences are not satisfactory functional in a particular host cell, then they may be substituted with signals functional in that cell.

[00127] Therefore, a nucleic acid molecule of the disclosure can include a regulatory sequence, such as a promoter sequence. In some embodiments a nucleic acid molecule of the disclosure includes a promoter sequence and a transcriptional termination sequence. Suitable prokaryotic promoters are, for example, the *tet* promoter, the *lac*UV5 promoter or the T7 promoter. Examples of promoters useful for expression in eukaryotic cells are the SV40 promoter or the CMV promoter.

[00128] The nucleic acid molecules of the disclosure can also be part of a vector or any other kind of cloning vehicle, such as a plasmid, a phagemid, a phage, a baculovirus, a cosmid or an artificial chromosome.

[00129] In one embodiment, the nucleic acid molecule is included in a phasmid. A phasmid vector denotes a vector encoding the intergenic region of a temperent phage, such as M13 or f1, or a functional part thereof fused to the cDNA of interest. After superinfection of the bacterial host cells with such an phagemid vector and an appropriate helper phage (e.g. M13K07, VCS-M13 or R408) intact phage particles are produced, thereby enabling physical coupling of the encoded heterologous cDNA to its corresponding polypeptide displayed on the phage surface (see e.g. Lowman, H.B. (1997) *Annu. Rev. Biophys. Biomol. Struct.* **26,** 401-424, or Rodi, D.J., and Makowski, L. (1999) *Curr. Opin. Biotechnol.* **10,** 87-93).

[00130] Such cloning vehicles can include, aside from the regulatory sequences described above and a nucleic acid sequence encoding a lipocalin mutein of the disclosure, replication and control sequences derived from a species compatible with the host cell that is used for expression as well as selection markers conferring a selectable phenotype on transformed or transfected cells. Large numbers of suitable cloning vectors are known in the art, and are commercially available.

[00131] The DNA molecule encoding lipocalin muteins of the disclosure, and in particular a cloning vector containing the coding sequence of such a lipocalin mutein can be transformed into a host cell capable of expressing the gene. Transformation can be performed using standard techniques. Thus, the disclosure is also directed to a host cell containing a nucleic acid molecule as disclosed herein.

[00132] The transformed host cells are cultured under conditions suitable for expression of the nucleotide sequence encoding a fusion protein of the disclosure. Suitable host cells can be prokaryotic, such as Escherichia coli (*E. coli*) or Bacillus subtilis, or eukaryotic, such as Saccharomyces cerevisiae, Pichia pastoris, SF9 or High5 insect cells, immortalized mammalian cell lines (e.g. HeLa cells or CHO cells) or primary mammalian cells.

[00133] The disclosure also relates to a method for the production of a mutein of the disclosure, wherein the mutein, a fragment of the mutein or a fusion protein of the mutein and another polypeptide is produced starting from the nucleic acid coding for the mutein by means of genetic engineering methods. The method can be carried out *in vivo*, the mutein can for example be produced in a bacterial or eukaryotic host organism and then isolated from this host organism or its culture. It is also possible to produce a protein *in vitro*, for example by use of an *in vitro* translation system.

[00134] When producing the mutein *in vivo* a nucleic acid encoding a mutein of the disclosure is introduced into a suitable bacterial or eukaryotic host organism by means of recombinant DNA technology (as already outlined above). For this purpose, the host cell is first transformed with a cloning vector that includes a nucleic acid molecule encoding a mutein of the disclosure using established standard methods. The host cell is then cultured under conditions, which allow expression of the heterologous DNA and thus the synthesis of the corresponding polypeptide. Subsequently, the polypeptide is recovered either from the cell or from the cultivation medium.

[00135] In some tear lipocalin muteins of the disclosure, the naturally occurring disulfide bond between Cys 61 and Cys 153 is removed. Accordingly, such muteins (or any other tear lipocalin mutein that does not include an intramolecular disulfide bond) can be produced in a cell compartment having a reducing redox milieu, for example, in the cytoplasm of Gram-negative bacteria. In case a lipocalin mutein of the disclosure includes intramolecular disulfide bonds, it may be desired to direct the nascent polypeptide to a cell compartment having an oxidizing redox milieu using an appropriate signal sequence. Such an oxidizing environment may be provided by the periplasm of Gram-negative bacteria such as *E. coli*, in the extracellular milieu of Gram-positive bacteria or in the lumen of the endoplasmatic reticulum of eukaryotic cells and usually favors the formation of structural disulfide bonds. It is, however, also possible to produce a mutein of the disclosure in the cytosol of a host cell, such as *E. coli*. In this case, the polypeptide can either be directly

obtained in a soluble and folded state or recovered in form of inclusion bodies, followed by renaturation *in vitro*. A further option is the use of specific host strains having an oxidizing intracellular milieu, which may thus allow the formation of disulfide bonds in the cytosol (Venturi M, et al. (2002) *J. Mol. Biol.* **315**, 1-6).

[00136] However, a lipocalin mutein of the disclosure may not necessarily be generated or produced only by use of genetic engineering. Rather, a lipocalin mutein can also be obtained by chemical synthesis such as Merrifield solid phase polypeptide synthesis or by *in vitro* transcription and translation. It is for example possible that promising mutations are identified using molecular modeling and then to synthesize the wanted (designed) polypeptide *in vitro* and investigate the binding activity for a given target. Methods for the solid phase and/or solution phase synthesis of proteins are well known in the art (see e.g. Bruckdorfer, T. et al. (2004) *Curr. Pharm. Biotechnol.* **5**, 29-43).

[00137] In another embodiment, the lipocalin muteins of the disclosure may be produced by *in vitro* transcription/translation employing well-established methods known to those skilled in the art.

[00138] As is evident from the above disclosure, a lipocalin mutein of the present disclosure or a fusion protein or a conjugate thereof can be employed in many applications. In general, the muteins disclosed herein and its derivatives can thus be used in many fields similar to antibodies or fragments thereof. Therefore, numerous possible applications for the inventive muteins exist in medicine.

[00139] For example, the disclosure encompasses the use of one or more lipocalin muteins of the disclosure or one or more compositions comprising such muteins for the binding of PCSK9 in a subject and/or inhibiting the binding of PCSK9 to the low-density lipoprotein receptor (LDL-R), in a subject. In some embodiments, such use comprises administering to the subject an effective amount of one or more muteins of the disclosure or one or more compositions comprising such muteins. In this regard, the current application also discloses methods of binding PCSK9 as well as inhibiting the binding of PCSK9 to LDL-R in a subject, comprising administering to said subject an effective amount of one or more lipocalin muteins of the disclosure one or more compositions comprising such muteins.

[00140] In another aspect of the disclosure, the present disclosure involves the use of the lipocalin muteins of the disclosure for complex formation with PCSK9. In this context it is also noted that the complex formation between the respective mutein and its ligand is

influenced by many different factors such as the concentrations of the respective binding partners, the presence of competitors, pH and the ionic strength of the buffer system used, and the experimental method used for determination of the K_D (for example fluorescence titration, competition ELISA or surface plasmon resonance, just to name a few) or even the mathematical algorithm which is used for evaluation of the experimental data.

[00141] In some embodiments, the invented lipocalin muteins as disclosed herein can be used for the detection of PCSK9. Such use may include the steps of contacting the mutein with a sample suspected of containing the given ligand under suitable conditions, thereby allowing formation of a complex between the mutein and the given ligand, and detecting the complexed mutein by a suitable signal.

[00142] The detectable signal can be caused by a label, as explained above, or by a change of physical properties due to the binding, i.e. the complex formation, itself. One example is surface plasmon resonance, the value of which is changed during binding of binding partners from which one is immobilized on a surface such as a gold foil.

[00143] In another aspect, the disclosure provides for a kit comprising at least one mutein of the disclosure and one or more instructions for using the kit.

[00144] In some embodiments, the kit further includes integrally thereto or as one or more separate documents, information pertaining to the contents or the kit and the use of one or more muteins of the disclosure. The kit may include one or more muteins of the disclosure that are formulated for reconstitution in a diluent. Such a diluent, e.g. a sterile diluent, may also be included in the kit, for example within a container.

[00145] The lipocalin muteins disclosed herein may also be used for the separation of PCSK9. Such use may include the steps of contacting the mutein with a sample supposed to contain said ligand under suitable conditions, thereby allowing formation of a complex between the mutein and the ligand, and separating the mutein/ligand complex from the sample.

[00146] In the use of a mutein of the disclosure for the detection of PCSK9 as well as for the separation of PCSK9, the mutein and/or PCSK9 may be immobilized on a suitable solid phase.

[00147] In some embodiment, one or more lipocalin muteins of the disclosure may also be used to target a compound to a preselected organism, tissue, organ or cell to be treated with

the compound, wherein PCSK9 is present in such organism, tissue, organ or cell. For such a purpose, the mutein is contacted with the compound of interest in order to allow complex formation. Then the complex that includes the mutein and the compound of interest are delivered to the preselected organism, tissue, organ or cell. This use is in particular suitable, but not restricted to, for delivering a drug (selectively) to a preselected organism, tissue, organ or cell, such as an infected body part, which is supposed to be treated with the drug. Besides formation of a complex between mutein and compound of interest, the mutein can also be reacted with the given compound to yield a conjugate of mutein and compound. Similar to the above complex, such a conjugate may be suitable to deliver the compound to the preselected organism, tissue, organ or cell. Such a conjugate of mutein and compound may also include a linker that covalently links mutein and compound to each other. Optionally, such a linker is stable in the bloodstream but is cleavable in a cellular environment.

[00148] Additional objects, advantages, and features of this disclosure will become apparent to those skilled in the art upon examination of the following Examples and the attached Figures thereof, which are not intended to be limiting. Thus, it should be understood that although the present disclosure is specifically disclosed by exemplary embodiments and optional features, modification and variation of the disclosures embodied therein herein disclosed may be resorted to by those skilled in the art, and that such modifications and variations are considered to be within the scope of this disclosure.

V. EXAMPLES

[00149] Example 1: Production and characterization of recombinant human PCSK9 and human PCSK9 mutant

[00150] Human PCSK9 (SEQ ID NO: 34) containing a C-terminal FLAG tag was expressed in transfected HEK293F cells. 600ml of transfected cells were cultivated in DMEM/TS/0.05% BSA for 6 days and the supernatant containing the hPCSK9 was recovered. hPCSK9 was bound to FLAG M2 resin, washed with 50CV wash buffer (10mM Tris/HCL pH7.4, 150ml NaCl, 2mM Cacl2, 10% glycerol) and eluted with 5 CV wash buffer containing 100µg/ml 3x FLAG peptide. The eluted protein was further purified via gel filtration using a Superdex 200 16/60 column (GE Healthcare). Functionality was tested with a LDL-R cell-ELISA using HepG2 cells.

[00151] For selection and screening of lipocalin muteins of interest, hPCSK9 may be biotinylated. hPCSK9 was incubated with a 5 times molar excess of EZ-Link NHS-Chromogenic Biotin reagent (Thermo Scientific) for 1 hr at room temperature. Excess of biotin was removed and the biotinylated protein was concentrated by ultrafiltration. A Streptacin pull-down assay confirmed biotinylation.

[00152] The gain of function hPCSK9_D374Y mutant, cynomolgus PCSK9 and mouse PCSK9 were produced and characterized in the same way.

[00153] Example 2: Generation of a library with $2x10^{10}$ independent lipocalin muteins and phagemid selection of lipocalin muteins against PCSK9

[00154] A random library of $2x10^{10}$ lipocalin muteins with high diversity was generated by random mutagenesis of mature human tear lipocalin (see, for example, WO2007/107563). For selection of PCSK9-specific lipocalin muteins, $2x10^{12}$ phagemids from this library were incubated with 200 nM biotinylated humand and/or cynomolgus PCSK9. Paramagnetic beads coated with neutravidin or streptavidin were used to capture PCSK9/phagemid complexes which were subsequently isolated with a magnet. Unbound phagemids were removed by washing the beads eight times with 1 ml PBS/T. Bound phagemids were eluted by incubation first with triethylamine and then with 0.1 M glycine pH 2.2. Four consecutive rounds of selection were performed.

[00155] The mutagenized central cassette of the phasmid preparation obtained after phage display selection was isolated by digestion of the DNA with BstX1 and subsequent purification via agarose gel electrophoresis using standard methods (Sambrook et al., (1989) *Molecular cloning: a laboratory manual*). The DNA was inserted into the likewise cut vector pTlc10 which allows bacterial production of the muteins under the control of a tetracyclin promoter. $CaCl_2$-competent TG1-F' cells were transformed with the ligation mixture and plated on LB/Amp plates. Individual colonies were used to inoculate 2xYT/Amp medium and grown overnight (14-18 h) to stationary phase. Subsequently, 50 µl 2xYT/Amp were inoculated from the stationary phase cultures and incubated for 3h at 37°C and then shifted to 22°C until an OD_{595} of 0.6-0.8 was reached. Anticalin production was induced by addition of 10 µl 2xYT/Amp supplemented with 1.2 µg/ml anhydrotetracyclin. Cultures were incubated at 22°C until the next day. After addition of 40 µl of 5% (w/v) BSA in PBS/T and incubation for 1h at 25°C cultures were ready for use in screening assays.

[00156] For selection of lipocalin muteins, human and cynomolgus PCSK9 (1µg/ml in PBS/T), which all carried a FLAG-tag, were captured on microtiterplates by means of an anti-FLAG-tag antibody (Sigma Aldrich, St. Louis, MO) which was coated on the plates the day before with an final concentration of 5 µg/ml in PBS. Anti-Flag-tag antibody alone served as negative control. Subsequently, 20 µl of BSA-blocked cultures were added and incubated for 1h at 25°C. Bound muteins were detected with a 1:10000 dilution of anti-T7 antibody conjugated with horseradish peroxidase ("HRP", Merck KgaA, Darmstadt) in PBS/T. For quantification, 20 µl QuantaBlu fluorogenic peroxidase substrate was added and measured at an excitation wavelength of 320 nm and an emission wavelength of 430 nm.

[00157] **Example 3: Generation of a biased maturation library for optimization of PCSK9-specific lipocalin muteins**

[00158] For optimization of PCSK9-specific muteins identified from the lipocalin library in above **Example 2**, additional libraries based on lipocalin muteins SEQ ID NO: 3, SEQ ID NO: 4 and SEQ ID NO: 7 (hereafter, named "mother clone(s)" in this example), respectively, were generated. The libraries were generated in a manner that leads to partial randomisation of selected positions only. The design was made such that, for each of the selected positions, the amino acid encoded corresponds to the amino acid found in the respective mother clone with a probability of 70%, while it can be a different amino acid with a 30% probability. With N the number of targeted positions and B as bias, the most probable number of exchanges per clone is N x (1-B). For example, if 20 amino acid positions are

partially randomised with a 70% bias on the amino acid of the mother clone, this will result in a library of mutants on average containing six mutations overall compared to the mother clone, but on the targeted positions only. However, not all of the clones would have six exchanges: the frequency of mutations per clone will follow a binomial distribution, as depicted in **Fig. 11 D**.

[00159] To assemble such libraries, recursive assembly of oligonucleotides in a polymerase chain reaction ("PCR") reaction (Stemmer et al., (1995) *Gene* 164:49-53) was used. The oligonucleotides are generated by standard phosphoramidite chemistry (Beaucage et al., (1981) *Tetrahedron Lett.* 22, 1859-62; McBride et al., (1983) *Tetrahedron Lett.* 24, 245-8). To allow an encoding of a 70% bias, we have calculated optimised mixtures for each position of a nucleotide triplet for each of the 20 canonical amino acids. For example, a mixture encoding serine with a bias of 70% and allowing various different amino acids in the remaining 30% is generated by the mixture of nucleoside phosphoramidite building blocks "*abc*", where *a* corresponds to a mixture of 85% thymidine, and 5% guaninidine, cytosine and adenosine each, *b* corresponds to a mixture of 85% cytosine and 5% of the other nucleosides each, and *c* corrresponds to a mixture of 50% guanidine and 50% thymidine (see **Figure 11**).

[00160] Using the technology described above, said libraries based on SEQ ID NO: 3, SEQ ID NO: 4 and SEQ ID NO: 7, respectively, were generated by recursive PCR. Subsequently, the generated lipocalin muteins were cloned with high efficiently into a phagemid vector essentially as described (see, for example, Kim et al., (2009) *J Am Chem Soc* 131(10):3565-76). The library size ranged from $7x10^9$ to $11x10^9$ mutants. The libraries were employed in subsequent phage panning (see **Example 4**).

[00161] **Example 4: Phagemid selection of optimized lipocalin muteins against PCSK9**

[00162] For selection of optimized PCSK9-specific lipocalin muteins, $2x10^{12}$ phagemids from the libraries described in **Example 3** were used. Phagemids were dissolved in PBS supplemented with 0.1% Tween-20 (v/v) (i.e. PBS/T), 50 mM benzamidine and 1% (w/v) casein. To select lipocalin muteins with increased affinity, phagemids were incubated with reduced concentrations of biotinylated PCSK9 proteins that ranged from 0.01 – 10 nM. In several instances, phagemids were incubated at 65°C for 10 min to select for muteins with increased heat-tolerance. Blocked phagemids were incubated for 40 min with biotinylated PCSK9 proteins before 0.3 mM desthiobiotin was added to the solution to saturate free

streptavidin binding sites and incubation was continued for 20 min. Subsequently, blocked (1% (w/v) casein in PBS/T) and drained paramagnetic beads that were either coated with streptavidin or neutravidin were added for 20 min to capture PCSK9-phagemid complexes. Uncomplexed phagemids were removed by washing the beads eight times with 1 ml PBS/T by thorough resuspension followed by collection of beads with a magnet. To specifically select muteins with reduced k_{off} rates either a more stringent wash protocol was applied by performing 5 additional wash steps after round 1, 10 after round 2, 15 after round 3 and 20 after round 4 or mutein-PCSK9 complexes were incubated with different amounts (10 nM – 5 µM) of purified parental mutein (e.g. SEQ ID NOs: 3, 4 or 7) to allow competition in PCSK9-binding between optimized and parental lipocalin muteins. Additionally, combinations of both methods were applied. Bound phagemids were first eluted with 300 µl 70 mM triethylamine for 10 min followed by immediate neutralization of the supernatant with 100 µl 1M Tris-Cl pH 6.0. After one intermediate wash cycle remaining phagemids were eluted with 100 mM glycin pH 2.2 for 10 min followed by immediate neutralization with 50 µl 0.5 M Tris-base. Both elution fractions were pooled and used to infect 4 ml of log-phase E. coli culture (OD_{550} 0.45-0.6) for reamplification. After incubation for 30 min under agitation bacteria were collected by centrifugation at 5000xg for 2 min, resuspended in 1 ml 2xYT medium and plated on three big LB/Amp agar plates (10 g/l bacto tryptone, 5 g/l yeast extract, 5 g/l NaCl, pH 7.5, 15 g/l agar, 100 µg/ml ampicillin). Plates were incubated overnight at 32°C. Infected cells were scraped from the agar plates using 50 ml 2xYT medium supplemented with 100 µg/ml ampicillin (2xYT/Amp). 50 ml 2xYT/Amp medium were inoculated with the appropriate volume of bacterial suspension to reach an OD_{550} of 0.08. The culture was incubated at 37°C on a shaker (160 rpm) until an OD_{550} of 0.5 was reached and then infected with helperphages ($1.5x10^{11}$ pfu) by incubation for 15 min with gentle agitation and for 45 min on a shaker at 37°C. Subsequently, kanamycin was added to a final concentration of 70 µg/ml to select for bacteria that were infected by helperphages. Finally, expression of the pIII-lipocalin proteins was induced by addition of 25 ng/ml anhydrotetracyclin.

[00163] Example 5: Identification of PCSK9-specific Tlc muteins by screening

[00164] The mutagenized central cassette of the phasmid preparation obtained after phage display selection, as described in **Example 4**, was isolated by digestion of the DNA with BstX1 and subsequent purification via agarose gel electrophoresis using standard methods (Sambrook et al. 1989). The DNA was inserted into a likewise-cut vector which allowed bacterial production of the muteins under the control of a tetracyclin promoter.

$CaCl_2$-competent TG1-F' cells were transformed with the ligation mixture and plated on LB/Amp plates. Individual colonies were used to inoculate 2xYT/Amp medium and grown overnight (14-18 h) to stationary phase. Subsequently, 50 µl 2xYT/Amp were inoculated from the stationary phase cultures and incubated for 3h at 37°C and then shifted to 22°C until an OD_{595} of 0.6-0.8 was reached. Lipocalin-mutein production was induced by addition of 10 µl 2xYT/Amp supplemented with 1.2 µg/ml anhydrotetracyclin. Cultures were incubated at 22°C until the next day. After addition of 40 µl of 5% (w/v) BSA in PBS/T and incubation for 1h at 25°C cultures were ready for use in screening assays.

[00165] For selection of lipocalin muteins, human and cynomolgus PCSK9 (1 µg/ml in PBS/T) as well as hPCSK9-D374Y mutant, which all carried a FLAG-tag, were captured on microtiterplates by means of an anti-FLAG-tag antibody (Sigma Aldrich, St. Louis, MO), which was coated on the plates the day before with an final concentration of 5 µg/ml in PBS. Subsequently, 20 µl of BSA-blocked cultures were added and incubated for 1 h at 25°C. Bound lipocalin muteins were detected with a 1:10000 dilution of anti-T7 antibody conjugated with HRP (Merck KgaA, Darmstadt) in PBS/T. For quantification, 20 µl QuantaBlu fluorogenic peroxidase substrate was added and measured at an excitation wavelength of 320 nm and an emission wavelength of 430 nm.

[00166] For affinity ranking of lipocalin muteins, anti-Strep-tag antibody (IBA, Goettingen) in PBS was coated on microtiterplates and 20 µl of BSA-blocked cultures were added, which allowed specific capture of lipocalin muteins on the plate. Different concentrations (0.5 – 5 nM) of biotinylated PCSK9 proteins were added and specifically-bound PCSK9 proteins were detected with extravidin-HRP (Sigma Aldrich, St. Louis, MO) after extensive washing. For quantification, 20 µl QuantaBlu was added and measured at an excitation wavelength of 320 nm and an emission wavelength of 430 nm.

[00167] Selection of competitive lipocalin muteins was performed by coating anti-FLAG-tag (5 µg/ml in PBS) on microtiterplates and subsequently capturing hPCSK9-D374Y mutant (1 µg/ml in PBS/T). Blocked cultures were adjusted to 30 nM purified LDL receptor and added for 72 h to plates with captured hPCSK9-D374Y mutant. This allowed equilibration of the system and reliable selection of competitive muteins. Bound receptor was detected with an HRP-conjugated anti-His-tag antibody (1 µg/ml in PBS/T; Abcam, Cambridge, UK). For quantification, 20 µl QuantaBlu fluorogenic peroxidase substrate was added and measured at an excitation wavelength of 320 nm and an emission wavelength of 430 nm.

[00168] Example 6: Affinity of representative lipocalin muteins to PCSK9

[00169] To measure the binding affinity of a representative group of lipocalin muteins to biotinylated PCSK9, a Surface Plasmon Resonance (SPR) based assay was employed utilizing a Biacore T200 instrument (GE Healthcare). For the SPR affinity assay (**Figure 1**), the Biotin CAPture Kit (GE Healthcare) was used.

[00170] In each measurement cycle, Biotin CAPture Reagent (GE Healthcare) was applied to the reference and measurement channels of Sensor Chip CAP (GE Healthcare) for 5 min at a flow rate of 2 µl/min. Biotinylated PCSK9 at a concentration of 4 µg/ml was injected on the measurement channel for 2 min at a flow rate of 10 µl/min. To determine the affinity, three to four dilutions of SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11 and SEQ ID NO: 12 were prepared in HBS-EP+ (0.01 M HEPES pH 7.4, 0.15 M NaCl, 3 mM EDTA, 0.005% Surfactant P20) buffer and applied to the chip surface, using concentrations of 500, 125, 31 and 8 nM for SEQ ID NO: 3, SEQ ID NO: 6, SEQ ID NO: 11, and SEQ ID NO: 12, concentrations of 300, 75, 19 and 5 nM for SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 8, SEQ ID NO: 9 and SEQ ID NO: 10, and concentrations of 75, 19 and 5 nM for SEQ ID NO: 7. The binding assay was carried out with a contact time of 3 min, dissociation time of 20 min and applying a flow rate of 30 µl/min. All measurements were performed at 25°C. Regeneration of the Sensor Chip CAP surface was achieved with an injection of 6 M guanidine-HCl with 0.25 M NaOH (2 min) followed by an extra wash with running buffer and a stabilization period of 2 min. Prior to the measurements, one conditioning cycle consisting of three consecutive regeneration steps was performed. Data were evaluated with Biacore T200 Evaluation software (V 1.0). Double referencing was used. The 1:1 binding model was used to fit the raw data.

[00171] The resulting fit curves for SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 6 and SEQ ID NO: 11 are shown in **Figure 1 (A-D)**, respectively. For example, the data shows that SEQ ID NO: 3 (**Fig. 1A**) bound with high affinity to PCSK9 (K_D = 0.85 nM). Association rate constants k_a or k_{on}, dissociation rate constants k_d or k_{off} and the resulting dissociation constants K_D for all lipocalin muteins are summarized in **Table 1** below.

[00172] **Table 1**:

Molecule	k_{on} [$M^{-1}*s^{-1}$]	k_{off} [s^{-1}]	K_D [nM]
SEQ ID NO: 3	1.77E+05	1.50E-04	0.85
SEQ ID NO: 4	4,79E+04	1,39E-04	2.89
SEQ ID NO: 5	3,40E+04	1,63E-04	4.8
SEQ ID NO: 6	5,66E+04	2,32E-04	4.1
SEQ ID NO: 7	7,24E+05	4,84E-03	6.69
SEQ ID NO: 8	1,54E+05	1,38E-03	8.96
SEQ ID NO: 9	2,33E+05	4,80E-03	20.59
SEQ ID NO: 10	5,70E+05	7,19E-03	12.61
SEQ ID NO: 11	4,70E+04	8,90E-05	1.89
SEQ ID NO: 12	2,44E+04	1,56E-04	6.4

[00173] **Example 7: Competitive mode of action of representative lipocalin muteins to PCSK9**

[00174] Whether lipocalin muteins disclosed in **Example 6** bind to PCSK9 in a competitive mode was tested *in vitro* using a competition ELISA format. In this experiment, a constant concentration of human PCSK9 (SEQ ID NO: 34) or human PCSK9_D374Y mutant was incubated with variable concentrations of lipocalin muteins for 1 h. After this pre-incubation in solution, an aliquot of the lipocalin mutein/PCSK9 mixture was transferred to an ELISA plate coated with human LDL-R to measure the concentration of hPCSK9 that was not blocked to bind hLDL-R.

[00175] All incubation steps were performed with shaking at 300 rpm, and the plate was washed after each incubation step with 100 µl PBS-T buffer (PBS (Phosphate buffered saline), 0.05% Tween 20) for five times using a Biotek ELx405 select CW washer. In the first step, a 384-well fluorescence plate was coated with 20 µl of recombinant human LDL-R (R&D Systems, Cat. No. 2148-LD/CF) at a concentration of 5 µg/ml in PBS over night at 4°C. After washing, the LDL-R-coated wells were blocked with 100 µl PBS-T/BSA (2% BSA (Bovine serum albumin) in PBS containing 0.05% Tween 20) for 1 h at room temperature ("RT").

[00176] A fixed concentration of 25 nM human PCSK9 or of 0.25 nM human PCSK9_D374Y mutant was incubated in solution with (i) varying concentrations of SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, or benchmark antibody of SEQ ID NO: 29 and SEQ ID NO: 33, or with (ii) SEQ ID NO: 2 as a negative control, using a starting concentration of 300 nM which was serially diluted at a 1:3 ratio

down to 5 pM in PBS-T/BSA buffer. After 1 h incubation at room temperature, 20 µl of the reaction mixture was transferred to the LDL-R-coated ELISA plate to capture unbound (free) or non-competitively bound PCSK9 for 20 min at RT. To allow for transformation of ELISA readout results into free hPCSK9 concentrations (cf. below), a standard curve containing varying concentrations of hPCSK9 or hPCSK9_ D374Y mutant starting with 25 / 50 nM (1:3 serially diluted in 11 steps) was prepared in PBS-T/BSA and incubated for 20 min on a MSD (MesoScaleDiscovery) plate as well.

[00177] To allow for detection and quantification of bound PCSK9, the residual supernatants were discarded and 20 µl mouse-anti-Flag M2-horseradish peroxidase ("HRP") (Sigma-Aldrich) was added in a 1:5000 dilution in PBS-T/BSA and incubated for 1 h at RT. After washing, 20 µl QuantaBlu Fluorogenic Peroxidase Substrate was added to each well and the fluorescence was measured at an excitation wavelength of 320 nm and an emission wavelength of 430 nM after 15 min using the GENios Plus plate reader (Tecan).

[00178] The evaluation was performed as follows: free hPCSK9 or the hPCSK9_D374Y mutant concentration c(hPCSK9)free / c(hPCSK9_D374Y)free was calculated from relative fluorescence signals using the standard curve determined in parallel and plotted versus the lipocalin mutein concentration, c(SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, or benchmark antibody of SEQ ID NO: 29 and SEQ ID NO: 33). To obtain the lipocalin mutein concentration at which formation of the PCSK9/LDL-R complex was blocked by 50% (IC50), the curves were fitted by nonlinear regression with a single-site binding model according to c(PCSK9)free =c(PCSK9)tot/(1+c(lipocalin mutein)/IC50)), with the total tracer concentration c(PCSK9)tot and the IC50 value obtained above as free parameters. Curve fitting was performed using GraphPad Prism 4 software.

[00179] In summary, the negative control SEQ ID NO: 2 did not bind to PCSK9; in contrast, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 7 and SEQ ID NO: 8 showed strong competitive binding to hPCSK9 and hPCSK9_D374Y mutant, when competed against hLDL-R. The fitted IC50 values are shown in **Table 2** below as well as in **Figure 2** (**A** and **B**). Competitive mode of action for the lipocalin muteins (SEQ ID NOs: 3, 4 and 6-9) was shown with both, wildtype and mutant PCSK9. The IC50 values in the competition ELISA using hPCSK9 are solely influenced by the fixed concentration of 25 nM. In the competition ELISA using 0.25 nM hPCSK9_D374Y mutant, IC50 values are affected by lipocalin muteins' affinity as well as by the fixed mutant concentration.

[00180] **Table 2**:

Molecule	hPCSK9 wt IC50 [nM]	hPCSK9_D374Y IC50 [nM]
SEQ ID NO: 3	13.8	0.13
SEQ ID NO: 4	6.2	0.37
SEQ ID NO: 6	10.1	0.21
SEQ ID NO: 7	13.2	0.13
SEQ ID NO: 8	10.7	0.32

[00181] **Example 8: Specificity and species crossreactivity of representative lipocalin muteins to PCSK9**

[00182] Specificity and species crossreactivity (**Figures 3** (**A-D**)) of lipocalin muteins was assayed in a binding ELISA, the principle of which was as follows: Biotinylated ligands (human PCSK9, human PCSK9_D374Y, mouse PCSK9, and cynomolgus PCSK9) were captured on Neutravidin-coated ELISA plates and variable concentrations of lipocalin muteins were added. Bound lipocalin muteins were detected with rabbit anti-Streptag II antibody (GenScript, Cat. No. A00626) and HRP-labeled anti-rabbit-IgG antibody (Jackson ImmunoResearch, Cat. No. 211-035-109).

[00183] In the following detailed experimental protocol, incubation and washing steps were performed as described above in the competition ELISA protocol of **Example 7**. A 384-well plate suitable for fluorescence measurements (Greiner FLUOTRAC™ 600, black flat bottom, high-binding) was coated with 20 µl of Neutravidin at a concentration of 5 µg/ml in PBS over night at 4°C. After washing, the Neutravidin-coated wells were blocked with 100 µl blocking buffer (PBS-T/BSA) for 1 h at room temperature. After washing again, 20 µl biotinylated ligand, either human PCSK9, human PCSK9_D374Y, mouse PCSK9 or cynomolgus PCSK9, at a concentration of 1 µg/ml in PBS-T/BSA was added for 1 h at room temperature. Excess ligand was removed by a further washing step.

[00184] Concentration of lipocalin mutein solutions was adjusted to 100 nM and then solutions were serially diluted at a 1:3 ratio down to 2 nM in PBS-T/BSA. A volume of 20 µl of the dilution was transferred to the 384-well plate and allowed to bind for 1 h at room temperature.

[00185] After incubation, the residual supernatants were discarded and 20 µl of the anti-StreptagII antibody in a 1:5.000 dilution in PBS-T/BSA was added and incubated for 1 h at room temperature. Supernatants were discarded again. To detect bound anti-Streptag II

antibody, 20 µl of the mouse anti-rabbit IgG-HRP were added and incubated for 1 h at room temperature. After washing, 20 µl fluorogenic HRP substrate (Quantablue, Pierce) was added to each well, and the reaction was allowed to proceed for 15 min. The fluorescence intensity in relative fluorescence units (RFU) of every well on the plate was read using a Safire Microplate reader (Tecan). To obtain the lipocalin mutein concentration at which the maximum fluorescence signal is reached by 50% (EC50), the curves were fitted by nonlinear regression with a single-site binding model according to RFU = RFUmax·c(Lipocalin mutein)/(EC50+c(lipocalin mutein)), with the maximum relative fluorescenc RFUmax and the EC50 value as free parameters. Curve fitting was performed using GraphPad Prism 4 software.

[00186] In summary, binding of SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8 and SEQ ID NO: 9 to human PCSK9, human PCSK9_D374Y mutant, mouse PCSK9 and cynomolgus PCKS9 could be detected, whereas negative control SEQ ID NO: 2 showed no binding to any of these targets. The fitted EC50 values are shown in **Table 3** below. The EC50 values for human PCSK9 and cynomolgus PCSK9 are comparable, showing that the lipocalin muteins are fully crossreactive with cynomolgus monkey PCSK9. Affinities to mouse PCSK9 are similar or up to 10-fold lower while EC50 values for human PCSK9_D374Y mutant are similar to those obtained for human PCSK9.

[00187] **Table 3**:

Molecule	hPCSK9 EC50 [nM]	hPCSK9 D374Y EC50 [nM]	mPCSK9 EC50 [nM]	cPCSK9 EC50 [nM]
SEQ ID NO: 3	1.6	1.2	4.4	1.8
SEQ ID NO: 4	2.4	1.6	21.8	2.9
SEQ ID NO: 5	5.1	2.9	30	5.7
SEQ ID NO: 6	3.1	2.1	20.1	3.7
SEQ ID NO: 7	2.8	0.8	16.3	3.8
SEQ ID NO: 8	4.4	1.4	10.1	6.1
SEQ ID NO: 9	5.6	1.1	16.2	8.4

[00188] **Example 9: Lipocalin mutein mediated restorage of downregulation of Dil-labeled LDL uptake in a cell-based assay**

[00189] A cell-based assay was employed to demonstrate the ability of PCSK9-binding lipocalin muteins (SEQ NO: 3, SEQ NO: 4, SEQ NO: 6, SEQ NO: 7 and SEQ NO: 8) to

neutralize the PCSK9-mediated reduction of number of surface LDL-R molecules and in consequence restore downregulated LDL uptake in HepG2 cells. SEQ ID NO: 2 served as negative control.

[00190] In this regard, HepG2 cells were plated in a 96-well poly-d-lysine-coated plate (Greiner, 955946) at a density of 60,000 cells/well in 100 µl/well DMEM (PAN P04-04510) containing 10% FCS (Fetal calf serum). After 24 h the medium was switched to DMEM containing 1% FCS (100 µl/well). After 18 h the medium was removed and switched (without washing step) to 50 µl DMEM containing 20 µg/ml LDL-Bodipy® FL (Invitrogen, L3483) but without FCS. Serial 1:2 dilution of lipocalin muteins starting at a concentration of 4000 nM was performed. One dilution series was prepared in DMEM containing 15 µg/ml PCSK9 and another one, as a control, in pure DMEM. Lipocalin muteins and PCSK9 were preincubated for 30 min. at room temperature and then 50 µl was added to the cells resulting in a final PCSK9 concentration of 100 nM. Total sample volume on the plate was 100 µl and all samples were measured in 5x replicates. Cells in DMEM without LDL and PCSK9, DMEM with LDL and PCSK9, and DMEM with LDL but without PCSK9 were used as controls.

[00191] Plates with samples were incubated at 37°C for 6 h before cells were washed with PBS. Wells were filled with 100 µl PBS and fluorescence of cells was read at 485/535 nm using a BMG PheraStar reader.

[00192] To determine IC50 values the highest and the lowest value of the 5 replicates were excluded and the mean and standard deviation for each remaining data point was calculated. The curves were fitted by GraphPad Prism 4 using nonlinear regression "sigmoidal dose – response, variable slope" model (5PL fit). Data were normalized by the value of stimulated and non-stimulated cells (cells with/without PCSK9). The fitted curves are shown in figure 4 and calculated IC50 values are summarized in **Table 4** below.

[00193] **Table 4**:

Molecule	IC50 [nM]
SEQ ID NO: 3	71.8
SEQ ID NO: 4	85.8
SEQ ID NO: 6	44.5
SEQ ID NO: 7	95.8
SEQ ID NO: 8	81.2

[00194] Example 10: Affinity of additional lipocalin muteins to PCSK9

[00195] To measure the binding affinity of additional lipocalin muteins to biotinylated human PCSK9 (hPCSK9-Bio), a Surface Plasmon Resonance (SPR) based assay was employed utilizing a Biacore T200 instrument (GE Healthcare). For the SPR affinity assay (**Figure 5 (A-C)**), the Biotin CAPture Kit (GE Healthcare) was used.

[00196] In each measurement, cycle Biotin CAPture Reagent (GE Healthcare) was applied to the reference and measurement channels of Sensor Chip CAP (GE Healthcare) for 5 min at a flow rate of 2 µl/min. hPCSK9-Bio at a concentration of 1 µg/ml was injected on the measurement channel for 2 min at a flow rate of 10 µl/min. To determine the affinity, three to four dilutions of lipocalin muteins of SEQ ID NOs: 13-28 (see **Table 5**) were prepared in HBS-EP+ buffer and applied to the chip surface, using concentrations of 128, 32, 8 and 2 nM for said muteins. The binding assay was carried out with a contact time of 3 min, dissociation time of 15 min and applying a flow rate of 30 µl/min. All measurements were performed at 25°C. Regeneration of the Sensor Chip CAP surface was achieved with an injection of 6 M guanidine-HCl with 0.25 M NaOH (2 min) followed by an extra wash with running buffer and a stabilization period of 2 min. Prior to the measurements, one conditioning cycle consisting of three consecutive regeneration steps was performed. Data were evaluated with Biacore T200 Evaluation software (V 1.0). Double referencing was used. The 1:1 binding model was used to fit the raw data.

[00197] The resulting fit curves for some of the lipocalin muteins are shown in **Figure 5.** Namelly, SEQ ID NO: 13 (**Fig. 5C**), SEQ ID NO: 20 (**Fig. 5A**), and SEQ ID NO: 22 (**Fig. 5B**) bound with high affinity to human PCSK9. Association rate constants k_a or k_{on}, dissociation rate constants k_d or k_{off} and resulting dissociation constants K_D for all muteins are summarized in **Table 5**.

[00198] **Table 5:**

Molecule	k_{on} [$M^{-1}*s^{-1}$]	k_{off} [s^{-1}]	K_D [nM]
SEQ ID NO: 13	2.75E+05	8.77E-05	0.32
SEQ ID NO: 14	2.56E+05	1.05E-04	0.41
SEQ ID NO: 15	2.78E+05	1.07E-04	0.38
SEQ ID NO: 16	2.55E+05	1.29E-04	0.51
SEQ ID NO: 17	2.49E+05	1.11E-04	0.45
SEQ ID NO: 18	3.13E+05	1.11E-04	0.35
SEQ ID NO: 19	2.47E+05	1.32E-04	0.53
SEQ ID NO: 20	3.13E+05	9.73E-05	0.31
SEQ ID NO: 21	2.45E+05	1.37E-04	0.56
SEQ ID NO: 22	7.53E+05	2.63E-04	0.35
SEQ ID NO: 23	8.36E+05	1.76E-04	0.21
SEQ ID NO: 24	3.67E+05	1.15E-04	0.31
SEQ ID NO: 25	4.36E+05	1.05E-04	0.24
SEQ ID NO: 26	6.68E+05	2.30E-04	0.34
SEQ ID NO: 27	7.34E+05	3.10E-04	0.42
SEQ ID NO: 28	6.84E+05	1.98E-04	0.29

[00199] **Example 11: Species crossreactivity of additional lipocalin muteins to PCSK9**

[00200] To measure the binding affinity of the lipocalin muteins SEQ ID NO: 13, SEQ ID NO: 20 and SEQ ID NO: 22 to biotinylated human, cynomolgus monkey and mouse PCSK9, a Surface Plasmon Resonance (SPR) based assay was employed utilizing a Biacore T200 instrument (GE Healthcare). For the SPR affinity assay (**Figure 6** (**A-C**)), the Biotin CAPture Kit (GE Healthcare) was used.

[00201] In the following experimental protocol, capture, sample binding and regeneration steps as well as data evaluation were performed as described above in **Example 10**. To determine the affinity, four dilutions of said muteins were prepared in HBS-EP+ buffer and applied to the chip surface, using concentrations of 128, 32, 8 and 2 nM, respectively.

[00202] The resulting fit curves for SEQ ID NO: 20 are shown in **Figure 6**. The data show that SEQ ID NO: 20 bound with high affinity to human PCSK9 (**Fig. 6A**) and to cynomolgus monkey PCSK9 (**Fig. 6B**). Affinity to mouse PCSK9 (**Fig. 6C**) is lower. Association rate constants k_a or k_{on}, dissociation rate constants k_d or k_{off} and resulting dissociation constants K_D are summarized in **Table 6** below.

[00203] **Table 6:**

Ligand	Molecule	k_{on}	k_{off}	K_D
		[M-1*s-1]	[s-1]	[nM]
human PCSK9	SEQ ID NO: 13	2.62E+05	8.31E-05	0.32
cyno PCSK9	SEQ ID NO: 13	2.16E+05	9.40E-05	0.44
mouse PCSK9	SEQ ID NO: 13	1.76E+05	3.12E-04	1.77
human PCSK9	SEQ ID NO: 20	2.49E+05	7.79E-05	0.31
cyno PCSK9	SEQ ID NO: 20	2.00E+05	1.03E-04	0.52
mouse PCSK9	SEQ ID NO: 20	1.77E+05	3.51E-04	1.98
human PCSK9	SEQ ID NO: 22	6.63E+05	2.58E-04	0.39
cyno PCSK9	SEQ ID NO: 22	3.86E+05	2.76E-04	0.71
mouse PCSK9	SEQ ID NO: 22	3.21E+05	6.38E-04	1.99

[00204] **Example 12: Binding of additional lipocalin muteins to PCSK9 in solution**

[00205] Binding of lipocalin muteins and PEGylated variants thereof (here, with branched PEG40), to biotinylated human PCSK9 (hPCSK9-Bio) in solution was tested *in vitro* using a competition electrochemiluminescence (ECL) assay format (**Figure 7**). In this experiment, a constant concentration of hPCSK9-Bio was incubated for 1 h with variable concentrations of lipocalin muteins SEQ ID NO: 13, SEQ ID NO: 20, and SEQ ID NO: 22 as well as the PEGylated variants SEQ ID NO: 30, SEQ ID NO: 31 and SEQ ID NO: 32. After this pre-incubation in solution, an aliquot of the lipocalin mutein/PCSK9 mixture was transferred to an ECL plate coated with a monoclonal benchmark antibody (comprising the light chain of SEQ ID NO: 29 and the heavy chain of SEQ ID NO: 33) to measure the concentration of hPCSK9 that was not blocked by the lipocalin muteins (PEGylated as well as non-PEGylated forms) and therefore could still be bound by the antibody (**Figure 7**). Competitive mode of action for those lipocalin muteins was shown with hPCSK9-Bio.

[00206] All incubation steps were performed with shaking at 300 rpm, and the plate was washed after each incubation step with 80 µl PBS-T buffer (PBS, 0.05% Tween 20) for five times using a Biotek ELx405 select CW washer. In the first step, a 384-well MSD plate was coated with 20 µl of the benchmark antibody at a concentration of 5 µg/ml in PBS over night at 4°C. After washing, the LDL-R-coated wells were blocked with 60 µl PBS-T/BSA (2% BSA in PBS containing 0.05% Tween 20) for 1 h at room temperature.

[00207] A fixed concentration of 10 pM hPCSK9-Bio was incubated in solution with varying concentrations of said muteins, using a starting concentration of 100 nM which was serially diluted at a 1:3 ratio down to 1.7 pM in PBS-T/BSA buffer. After 1 h of incubation at

room temperature, 20 µl of the reaction mixture were transferred to the antibody-coated ELISA plate to capture unbound (free) PCSK9 for 20 min at room temperature. To allow for transformation of ELISA readout results into free hPCSK9 concentrations (cf. detection and quantification of bound hPCSK9-Bio below), a standard curve containing varying concentrations of hPCSK9-Bio starting with 10 nM (1:3 serially diluted in 11 steps) was prepared in PBS-T/BSA and incubated for 20 min on a MSD plate (MesoScaleDiscovery).

[00208] To allow for detection and quantification of bound hPCSK9-Bio, the residual supernatants were discarded and 20 µl Sulfo-Tag-labeled Streptavidin (Meso Scale Discovery) was added at a concentration of 1 µg/ml in PBS-T/BSA and incubated for 1 h at room temperature. After washing, 35 µl 2x MSD read buffer with surfactant (Meso Scale Discovery) was added to each well and electrochemiluminescence (ECL) signals were measured within 15 min using the SECTOR Imager 2400 (Meso Scale Discovery).

[00209] The evaluation was performed as follows: free PCSK9 concentration $c(PCSK9)_{free}$ was calculated from ECL signals using the standard curve determined in parallel and plotted versus lipocalin mutein concentration, c(lipocalin mutein). To obtain the lipocalin mutein concentration at which formation of the PCSK9/benchmark antibody complex was blocked by 50% (IC50), the curves were fitted by nonlinear regression with a single-site binding model according to $c(PCSK9)_{free} = c(PCSK9)_{tot}/(1+c(\text{lipocalin mutein})/IC50))$, with the total tracer concentration $c(PCSK9)_{tot}$ and the IC50 value as free parameters. Curve fitting was performed using GraphPad Prism 4 software.

[00210] In summary, lipocalin muteins SEQ ID NO: 13, SEQ ID NO: 20 and SEQ ID NO: 22 as well as the PEGylated variants SEQ ID NO: 30, SEQ ID NO: 31 and SEQ ID NO: 32 showed strong competitive binding to hPCSK9-Bio, when competed against the benchmark antibody (comprising SEQ ID NOs: 29 and 33). The fitted IC50 values are summarized in **Table 7** below.

[00211] **Table 7**:

Molecule	IC50 [nM]
SEQ ID NO: 13	0.16
SEQ ID NO: 20	0.11
SEQ ID NO: 22	0.09
SEQ ID NO: 30	0.19
SEQ ID NO: 31	0.53
SEQ ID NO: 32	0.37

[00212] Example 13: Inhibition of PCSK9-mediated downregulation of LDL-R by additional lipocalin muteins

[00213] Human PCSK9 induces LDL-R internalization and therefore the depletion of LDL-R from the cell surface. Expression of LDL-R was assessed in this assay in presence of lipocalin muteins referred in **Example 12** (PEGylated (here, with branched PEG40) as well as non-PEGylated forms) to determine the lipocalin muteins' potency to inhibit PCSK9's activity in mediating LDL-R cell surface depletion, while SEQ ID NO: 2 was used as a negative control.

[00214] HEPG2 cells (10,000 cells/wells) were allowed to attach 24 h in 384-well MSD (Mesoscale Discovery) plate pre-coated with 100 µg/ml poly-d-lysine. Full medium (DMEM containing 1 mg/ml G418 and 10% FBS) was then switched to either DMEM lacking serum or containing 10% lipoprotein-deficient serum to allow maximal expression of LDL-R on the cell surface. Cells were then washed with PBS and dilution series of lipocalin muteins in the presence of 100 nM PCSK9 were incubated at 37°C for 6 h. The mixture was then discarded by gently tapping out and fixation of the cells was then performed by addition of Roti®-Histofix at room temperature for 20 min. Cells were washed twice with PBS and incubated overnight at 4°C with blocking buffer (PBS/FCS 4% / BSA 2%). Buffer was gently discarded and a mix of 1 µg/ml of a goat anti-hLDL-R (R&D systems, Cat. No. AF2148) and 2 µg/ml of a donkey anti-goat-Sulfotag (MSD, Cat. No. R32AG-1) in blocking buffer was incubated at room temperature for 1 h. Cells were then gently twice washed with PBS and Surfactant free reading buffer (MSD) was added. ECL signals were measured using the SECTOR Imager 2400 (MSD). The evaluation was performed as follows: ECL signals were transformed by setting the signals measured for PCSK9 activity in the absence of competitor (here, lipocalin mutein) to 100% PCSK9 activity. Data were fitted with a sigmoidal dose-response model with shared slope using GraphPad Prism 4 software (**Figure 8**). Resulting IC50 and IC90 values are summarized in **Table 8** below.

[00215] Table 8:

Molecule	IC50 [nM]	IC90 [nM]
SEQ ID NO: 13	103.3	216.1
SEQ ID NO: 20	91.7	192.0
SEQ ID NO: 22	76.9	160.9
SEQ ID NO: 30	82.6	172.8
SEQ ID NO: 31	82.6	172.8
SEQ ID NO: 32	70.7	147.8

[00216] Example 14: Generation of thermo-stabilized PCSK9-specific lipocalin muteins by positional saturation mutagenesis

[00217] For improvement of thermal stability of PCSK9-specific muteins, lipocalin mutein of SEQ ID NO: 13 was mutated at positions 79 and 105 (as shown in **Figure 14**). Libraries of thermo-stabilized derivatives of SEQ ID NO: 13were generated in a manner that led to saturated randomization of the mentioned positions either on their own or in combination with the use of recursive assembly of NNK oligonucleotides in a polymerase chain reaction (see, for example, WO2007/107563). For the same purpose, lipocalin mutein of SEQ ID NO: 22 was mutated at position 92 from Histidine to Proline (as shown in **Figure 14**).

[00218] Example 15: Identification of thermo-stabilized PCSK9-specific muteins by screening

[00219] The mutagenized central cassette of the libraries preparation obtained after PCR assembly, as described in **Example 14**, was inserted into a vector which allowed bacterial production of the lipocalin muteins under the control of a tetracyclin promoter (as described **Example 5**).

[00220] For affinity ranking of the optimized lipocalin muteins, anti-Strep-tag antibody (IBA, Goettingen) diluted in PBS was coated on microtiterplates and 20 µl of BSA-blocked cultures were added, which allowed specific capture of lipocalin muteins on the plate. Different concentrations (0.5 – 5 nM) of biotinylated PCSK9 proteins were added and specifically-bound PCSK9 proteins were detected with extravidin-HRP (Sigma Aldrich, St. Louis, MO) after extensive washing. For quantification, 20 µl QuantaBlu was added and measured at an excitation wavelength of 320 nm and an emission wavelength of 430 nm.

[00221] Selection of thermo-stabilized lipocalin muteins was performed in the same way as described above with the only difference that bacterial extracts containing lipocalin muteins were heated up to 65°C for 30 min prior to incubation with the PCSK9 target. Those muteins that showed unaffected binding signals after heating step compared to the non-heated samples were selected for sequencing.

[00222] Example 16: Measurement of melting temperatures of optimized PCSK9-specific muteins

[00223] To determine melting temperatures of PCSK9-specific muteins, samples at a protein concentration of 1mg/ml in PBS (Gibco) were scanned (25-100°C) at 1C/min using a capillary nanoDSC instrument (Q2000, TA Instruments). The integrated software calculated the melting temperature (Tm) from the displayed thermogram.

[00224] The resulting melting temperatures for the two lipcalin muteins (SEQ ID NO: 22 and SEQ ID NO: 13) together with the optimized derivatives therefrom (SEQ ID NOs: 62-71) are summarized in **Table 9** below. For example, the data shows that Tms of SEQ ID NO: 63, SEQ ID NO: 64 and SEQ ID NO: 65 were significantly higher compared to SEQ ID NO: 13 and the onset of melting was shifted by up to 13°C (**Fig. 12**).

[00225] Table 9:

SEQ ID	Tm [°C] nanoDSC	onset of melting [°C]
SEQ ID NO: 13	61	49
SEQ ID NO: 65	72,8	62
SEQ ID NO: 64	63,8	54
SEQ ID NO: 66	69	53
SEQ ID NO: 67	67,8	53
SEQ ID NO: 68	65,1	55
SEQ ID NO: 63	68,3	57
SEQ ID NO: 69	63,7	55
SEQ ID NO: 70	59,1	54
SEQ ID NO: 71	65	56
SEQ ID NO: 22	56	52
SEQ ID NO: 62	59	53

[00226] Example 17: Affinity of optimized lipocalin derivatives to PCSK9

[00227] To measure the binding affinity to biotinylated human PCSK9 of a representative group of lipocalin muteins, a Surface Plasmon Resonance (SPR) based assay was employed utilizing a Biacore T200 instrument (GE Healthcare). For the SPR affinity assay, the Biotin CAPture Kit (GE Healthcare) was used.

[00228] In each measurement cycle, Biotin CAPture Reagent (GE Healthcare) was applied to the reference and measurement channels of Sensor Chip CAP (GE Healthcare) for 5 min at a flow rate of 2 µl/min. Biotinylated PCSK9 at a concentration of 4 µg/ml was

injected on the measurement channel for 2 min at a flow rate of 10 µl/min. To determine the affinity, three to four dilutions of SEQ ID NOs: 62-71 were prepared in HBS-EP+ (0.01 M HEPES pH 7.4, 0.15 M NaCl, 3 mM EDTA, 0.005% Surfactant P20) buffer and applied to the chip surface, using final concentrations of 128 nM, 32 nM, 8 nM and 4 nM. The binding assay was carried out with a contact time of 3 min, dissociation time of 20 min and applying a flow rate of 30 µl/min. All measurements were performed at 25°C. Regeneration of the Sensor Chip CAP surface was achieved with an injection of 6 M guanidine-HCl with 0.25 M NaOH (2 min) followed by an extra wash with running buffer and a stabilization period of 2 min. Prior to the measurements, one conditioning cycle consisting of three consecutive regeneration steps was performed. Data were evaluated with Biacore T200 Evaluation software (V 1.0). Double referencing was used. The 1:1 binding model was used to fit the raw data.

[00229] The resulting fit curves for lipocalin muteins of SEQ ID NOs: 62-71 are shown in **Figure 13 (A-J)**, respectively. The data shows that affinities of thermo-stabilized lipocalin muteins (SEQ ID NOs: 62-71) are fully retained compared to lipocalin muteins of SEQ ID NO: 13 and SEQ ID NO: 22. Association rate constants k_a or k_{on} while dissociation rate constants k_d or k_{off}. The resulting dissociation constants K_D for said lipocalin muteins are summarized in **Table 10** below.

[00230] **Table 10**:

SEQ ID	kon [M-1*s-1]	koff [s-1]	KD [nM]
SEQ ID NO: 13	2,81E+05	6,84E-05	0,24
SEQ ID NO: 65	2,39E+05	7,61E-05	0,32
SEQ ID NO: 64	3,23E+05	7,25E-05	0,22
SEQ ID NO: 66	2,51E+05	8,17E-05	0,33
SEQ ID NO: 67	2,49E+05	7,60E-05	0,31
SEQ ID NO: 68	2,63E+05	8,03E-05	0,31
SEQ ID NO: 63	2,35E+05	7,84E-05	0,33
SEQ ID NO: 69	2,63E+05	7,66E-05	0,29
SEQ ID NO: 70	2,23E+05	7,39E-05	0,33
SEQ ID NO: 71	2,72E+05	8,81E-05	0,32
SEQ ID NO: 22	5,91E+05	2,19E-04	0,37
SEQ ID NO: 62	4,98E+05	1,65E-04	0,33

[00231] Example 18: Production of PCSK9-specific Tlc muteins in E. coli

[00232] PCSK9-specific lipocalin muteins (SEQ ID NOs: 62, 82, 83 and 84) were expressed in E. coli. DNA encoding each lipocalin mutein (SEQ ID NOs: 86, 87, 88 and 89, respectively) was inserted into a likewise-cut vector which allowed bacterial production of the muteins under the control of a T5 promoter (in case of SEQ ID NOs: 62, 82 and 84) or a T7A3 promoter (in case of SEQ ID NO: 83). The Muteins were purified from cell lysates by combination of column chromatography methods using anion exchange column, phenyl sepharose column, gel filtration column and chelating column (in the case of SEQ ID NOs: 82 and 84). The purified muteins were finally solubilized in PBS.

[00233] Example 19: Biacore analysis

[00234] All procedures were performed with Biacore T200 (GE Healthcare) at 25 °C. A HBS-EP+ buffer (10 mM HEPES, pH 7.4, 0.15 M NaCl, 3 mM EDTA, and 0.05% surfactant P20) was used as running buffer. A biotinylation of PCSK9 protein was performed in a general manner using a labeling reagent, EZ-Link Sulfo-NHS-LC-LC-Biotin (Thermo Scientific), and the unreacted reagents were removed by desalting spin columns. A Biotin CAPture kit (GE Healthcare) was used to immobilize the biotinylated PCSK9 ligand to sensor chips. Flowcells on the CAP sensor chips, pre-immobilized with a ss-DNA oligo, were hybridized with a complementary ss-DNA oligo conjugated with streptavidin, and followed by a biotinylated ligand injection.

[00235] For capture experiments, streptavidin-DNA conjugates were injected to two flowcells for 20 sec; and the biotinylated PCSK9 samples were diluted to 1 ng/µl in the running buffer and then injected to one flowcell for 1 min at 10 µl/min, whereas another flowcell was left without captured samples to provide a reference surface. The capture protocol was designed to yield capture levels of ligand samples that resulted in Rmax values no greater than 20 RU.

[00236] For each kinetic experiment, varying concentrations of purified PCSK9-specific lipocalin muteins ranging from 0.03 nM to 100 nM were prepared as the analytes, and injected for 300 sec at 30 µl/min followed by 30 min of dissociation. Captured and reference surfaces were regenerated with a 2 min pulse of 6 M guanidine hydrochloride in 0.25 M sodium hydroxide.

[00237] The dissociation constants (KDs) were calculated using a 1:1 Langmuir binding model. The raw data sets were analyzed using Biacore T200 Evaluation Software (version 1.0, GE Healthcare), and the sensorgrams of the reference flowcells were subtracted from the sensorgrams of the sample-captured flowcells.

[00238] **Example 20: Cell free PCSK9-LDLR TR-FRET assay**

[00239] Secreted PCSK9 facilitates the degradation of hepatic LDLR, leading to increase in serum LDL-C level. Thus the PCSK9-specific lipocalin muteins which interfere with the interaction between PCSK9 and LDLR, result in enhancement of the recycling of LDLR to plasma membrane, which activates LDL-C intake and eventually lower the circulating LDL-C levels.

[00240] Cell free TR-FRET assay was used to determine the inhibitory effect of the lipocalin muteins (SEQ ID NO: 62, SEQ ID NO: 82, SEQ ID NO: 83 and SEQ ID NO: 84) on the binding between PCSK9 and LDLR. Biotin-labeled hPCSK9 (biotin-hPCSK9) used in the assay was prepared by incubation with a 5 times molar excess of EZ-Link NHSChromogenic Biotin reagent (Thermo Scientific) for 1 hr at room temperature and excess of biotin was removed by illustra NAP column (GE Healthcare Life Science). Europium-labeled LDLR (Eu-LDLR) was prepared as described in the previous report (Fisher TS, et al., J. Biol. Chem. (2007) 282(28), 20502-20512).

[00241] Cell free PCSK9-LDLR TR-FRET assay was performed in 384 well format. A final concentration of 20 nM of Biotin-hPCSK9 was incubated with several concentrations of test lipocalin muteins in binding buffer (10 mM HEPES, pH 7.4, 150 mM NaCl, 0.1 mM $CaCl_2$, and 0.05% (w/v) BSA) for two hours at room temperature in the presence or absence of 34 mg/ml of human serum albumin. Then ten microliter of above biotin-hPCSK9-lipocalin solution and ten microliter of Eu-LDLR/Alexa-SA solution (1.0 nM of Eu-LDLR, 80 nM of streptavidin/Alexa Fluor 647 conjugate (Invitrogen), 10 mM HEPES, pH 7.4, 150 mM NaCl, 0.1 mM $CaCl_2$, and 0.05% (w/v) BSA) was mixed in the well and incubated for two hours at room temperature in the dark followed by incubation overnight in the refrigerator. Samples were read using a BMG Lab Systems Rubystar Reader set to read 20 flashes/well with a 50-μs integration delay and a 200-μs integration time for a total read time of 1100 ms/well. FRET was quantified by measurement of the emission ratio at 665/620 nm. TR-FRET ratio was calculated as following formulation.

[00242] TR-FRET Ratio = (counts at 665 nm/counts at 620 nm) x 10,000

[00243] To obtain the lipocalin mutein concentration at which formation of the PCSK9/LDLR complex was blocked by 50% (IC50), the curves were fitted by nonlinear regression with a single-site binding model. Curve fitting was performed using Kaleida Graph ver 4.1.1 software. (Synergy Software)

[00244] The resulting calculated IC50 values are summarized in **Table 11** below **Example 21**.

[00245] **Example 21: In vivo plasma half-life of PCSK9-specific lipocalin muteins**

[00246] The conjugation of lipocalin muteins with a moiety that can target a specific body region, organism, tissue, organ or cell may extend the half-life of the lipocalin muteins in the body. For example, half-life of human serum albumin (HSA) was reported to be ~19 days (Biochimica et Biophysica Acta 1830; 5526-5534, 2013) and therefore PCSK9-specific lipocalin muteins (SEQ ID NO: 62 and SEQ ID NO: 82) were conjugated to an albumin binding protein (such as G148 and SEQ ID NO: 85) that binds to HSA, and therefore, may exhibit long half-life in the body for the lipocalin muteins.

[00247] To observe the effect of conjugation with albumin binding protein and to determine plasma long half-life of PCSK9-specific lipocalin muteins, several tested lipocalin muteins were intravenously administered to normal rats and plasma concentrations of the lipocalin muteins were measured using sandwich ELISA. Blood sampling for determination of plasma half-life was conducted at various time points following administration of test lipocalin muteins.

[00248] The resulting plasma half-lifes for the four lipocalin muteins are summarized in Table 11 as below. For example the data shows that lipocalin muteins conjugated to a moiety that can bind to HSA exhibit longer half–life than lipocalin muteins alone.

[00249] **Table 11**:

Molecule	Biacore_Anti PCSK9			Biacore_Anti HSA			LDLR binding (IC50, nM)		T1/2 (h)
	ka (1/Ms)	ka (1/s)	KD (M)	ka (1/Ms)	ka (1/s)	KD (M)	w/o HSA	w/ HSA	
SEQ ID NO: 62	1.1 E+05	2.9 E-04	2.6 E-10	-	-	-	1.36	0.93	0.99
SEQ ID NO: 82	1.5 E+05	3.7 E-04	2.5 E-10	-	-	-	1.68	1.33	0.86
SEQ ID NO: 83	7.1 E+05	2.7 E-04	3.8 E-10	2.2 E+06	4.2 E-05	1.9 E-11	1.93	1.26	24
SEQ ID NO: 84	7.5 E+05	3.0 E-04	3.9 E-10	2.4 E+06	3.0 E-05	1.3 E-11	1.09	1.09	32

[00250] Embodiments illustratively described herein may suitably be practiced in the absence of any element or elements, limitation or limitations, not specifically disclosed herein. Thus, for example, the terms "comprising", "including", "containing", etc. shall be read expansively and without limitation. Additionally, the terms and expressions employed herein have been used as terms of description and not of limitation, and there is no intention in the use of such terms and expressions of excluding any equivalents of the features shown and described or portions thereof, but it is recognized that various modifications are possible within the scope of the invention claimed. Thus, it should be understood that although the present embodiments have been specifically disclosed by preferred embodiments and optional features, modification and variations thereof may be resorted to by those skilled in the art, and that such modifications and variations are considered to be within the scope of this invention. All patents, patent applications, textbooks and peer-reviewed publications described herein are hereby incorporated by reference in their entirety. Furthermore, where a definition or use of a term in a reference, which is incorporated by reference herein is inconsistent or contrary to the definition of that term provided herein, the definition of that term provided herein applies and the definition of that term in the reference does not apply. Each of the narrower

species and subgeneric groupings falling within the generic disclosure also forms part of the invention. This includes the generic description of the invention with a proviso or negative limitation removing any subject matter from the genus, regardless of whether or not the excised material is specifically recited herein. In addition, where features are described in terms of Markush groups, those skilled in the art will recognize that the disclosure is also thereby described in terms of any individual member or subgroup of members of the Markush group. Further embodiments will become apparent from the following claims

.

CLAIMS

1. A mutein of human tear lipocalin, wherein the mutein comprises:

   (a) a mutated amino acid residue at any one or more of the sequence positions 26-34, 56-58, 80, 83, 104-106 and 108 of the linear polypeptide sequence of the mature human tear lipocalin, and

   (b) a mutated amino acid residue at any one or more of the sequence positions 61, 101, 111, 114 and 153 of the linear polypeptide sequence of the mature human tear lipocalin,

   and wherein the mutein binds specifically to PCSK9.

2. A lipocalin mutein that is an antagonist of PCSK9.

3. A lipocalin mutein that is competitive for binding of LDL-R to PCSK9.

4. A lipocalin mutein that is competitive for binding of a monoclonal antibody comprising SEQ ID NO: 29 and SEQ ID NO: 33 to PCSK9.

5. A lipocalin mutein that is able to fully or partially inhibit PCSK9-mediated downregulation of LDL-R.

6. A lipocalin mutein that is able to restore LDL uptake in the presence of PCSK9.

7. The lipocalin mutein according to any one of the claims 1-6, wherein the mutein binds to a non-human primate PCSK9 or an immunogenic fragment thereof with a dissociation constant (K_D) equal to or less than 10 nM.

8. The lipocalin mutein according to any one of the claims 1-6, wherein the mutein binds to mouse PCSK9 or an immunogenic fragment thereof with a dissociation constant (K_D) equal to or less than 10 nM.

9. The lipocalin mutein according to any one of the claims 1-6, wherein the mutein binds to human PCSK9 or a fragment thereof with a dissociation constant (K_D) equal to or less than 10 nM.

10. The lipocalin mutein according to any one of the claims 1-6, wherein the mutein binds to human PCSK9 or a fragment thereof with a dissociation constant (K_D) equal to or less than 1 nM.

11. The lipocalin mutein according to any one of the claims 1-6, wherein the mutein binds to human PCSK9 or a fragment thereof with a dissociation constant (K_D) equal to or less than 0.1 nM.

12. The lipocalin mutein according to any one of the claims 1-6, wherein mutein binds to human PCSK9 or a fragment thereof with a dissociation constant (K_D) equal to or less than 1 pM.

13. The mutein according to any one of claims 1-12, wherein the mutein contains at least one of the following amino acid substitutions in comparison to mature human tear lipocalin: Arg 26 → Ser, Phe, Trp, His or Thr.

14. The mutein according to any one of claims 1-12, wherein the mutein contains at least one of the following amino acid substitutions in comparison to mature human tear lipocalin: Glu 34 → Asn, Thr, Arg or Gly, Leu 56 → Met, Ser, Gln, Phe, His or Asn.

15. The mutein according to any one of claims 1-12, wherein the mutein contains at least one of the following amino acid substitutions in comparison to mature human tear lipocalin: Ser 58 → Lys, Ala, Arg, Trp or Pro.

16. The mutein according to any one of claims 1-12, wherein the mutein contains at least one of the following amino acid substitutions in comparison to mature human tear lipocalin: Met 31 → Ala, Gly, His, Pro, Ser Aps, Glu or Gln.

17. The mutein according to any one of claims 1-12, wherein the mutein contains at least one of the following amino acid substitutions in comparison to mature human tear lipocalin: Leu 33 → Tyr, Trp, Tyr, Phe, Pro or Ala.

18. The mutein according to any one of claims 1-12, wherein the mutein contains at least one of the following amino acid substitutions in comparison to mature human tear lipocalin: Ser 61 → Trp or Phe, Asp 80 → Ser, Met, Pro, Ile, Gln, Tyr, Ser, Val or Thr.

19. The mutein according to any one of claims 1-12, wherein the mutein contains at least one of the following amino acid substitutions in comparison to mature human tear lipocalin: Glu 104 → Leu, Pro, Ser, Ala, Asn, Thr, Lys or Asp.

20. The mutein according to any one of claims 1-12, wherein the mutein contains at least one of the following amino acid substitutions in comparison to mature human tear lipocalin: His 106 → Pro, Gln, Gly, Arg, Val, Thr, Asn or Leu.

21. The mutein according to any one of claims 1-12, wherein the mutein contains at least one of the following amino acid substitutions in comparison to mature human tear lipocalin: Lys 108 → Gln, Ala, Trp, Tyr, Arg, Asp, Asn, Ser, Glu or Thr.

22. The mutein according to any one of claims 1-12, wherein the mutein contains at least one of the following amino acid substitutions in comparison to mature human tear lipocalin: Glu 27 → Arg, Ser, Gln, Thr, Phe, Lys, Ala or Arg.

23. The mutein according to any one of claims 1-12, wherein the mutein contains at least one of the following amino acid substitutions in comparison to mature human tear lipocalin: Pro 29 → Gly, Asp, Asn, Ile, Leu or Met.

24. The mutein according to any one of claims 1-12, wherein the mutein contains at least one of the following amino acid substitutions in comparison to mature human tear lipocalin: Asn 32 → Ile, Leu, Tyr, Met or Trp.

25. The mutein according to any one of claims 1-12, wherein the mutein contains at least one of the following amino acid substitutions in comparison to mature human tear lipocalin: Leu 105 → Cys, Tyr, Trp, Glu, Arg, Ser, His, Ala, Val, Asp, Pro, Gly or Lys.

26. The mutein according to any one of claims 1-12, wherein the mutein contains at least one of the following amino acid substitutions in comparison to mature human tear lipocalin: Phe 28 → Cys, Arg, Lys, Trp, Asp, Gly, His, Leu or Asn.

27. The mutein according to any one of claims 1-12, wherein the mutein contains at least one of the following amino acid substitutions in comparison to mature human tear lipocalin: Glu 30 → Arg, Asp, Thr, Ser, Gly, Ala or Asn.

28. The mutein according to any one of claims 1-12, wherein the mutein contains at least one of the following amino acid substitutions in comparison to mature human tear lipocalin: Ile 57 → Tyr, Trp, His, Gln, Thr or Arg,

29. The mutein according to any one of claims 1-12, wherein the mutein contains at least one of the following amino acid substitutions in comparison to mature human tear lipocalin: Lys 83 → Arg, Ser, Gln, Thr or Glu.

30. The mutein according to any one of claims 1-12, comprising one of the following sets of amino acid substitutions in comparison to mature human tear lipocalin:

(a) Arg 26 → Phe; Asn 32 → Ile; Glu 34 → Thr; Leu 56 → Met; Ser 58 → Ala and Lys 83 → Ser,

(b) Arg 26 → Trp; Asn 32 → Leu; Glu 34 → Thr; Leu 56 → Ser and Ser 58 → Ala,

(c) Arg 26 → His; Asn 32 → Tyr; Glu 34 → Thr; Leu 56 → Ser; Ser 58 → Arg and Lys 83 → Gln;

(d) Arg 26 → Phe; Asn 32 → Met; Glu 34 → Thr; Leu 56 → Gln; Ser 58 → Ala and Lys 83 → Thr;

(e) Asn 32 → Trp; Glu 34 → Arg; Leu 56 → Asn; Ser 58 → Trp and Lys 83 → Ser,

(f) Arg 26 → Phe; Asn 32 → Leu; Glu 34 → Thr; Leu 56 → Phe; Ser 58 → Ala and Lys 83 → Arg,

(g) Arg 26 → Thr; Asn 32 → Trp; Glu 34 → Asn; Leu 56 → His; Ser 58 → Pro and Lys 83 → Ser,

(h) Asn 32 → Trp; Glu 34 → Asn; Leu 56 → Phe; Ser 58 → Arg and Lys 83 → Glu,

(i) Arg 26 → Trp; Asn 32 → Leu; Glu 34 → Thr; Leu 56 → Met; Ser 58 → Ala and Lys 83 → Ser, or

(j) Asn 32 → Trp; Glu 34 → Gly; Leu 56 → Gln; Ser 58 → Ala and Lys 83 → Gln.

31. The mutein of according to any one of claims 1-12, comprising one of the following sets of amino acid substitutions in comparison to mature human tear lipocalin:

(a) Glu 27 → Ser; Phe 28 → Arg; Pro 29 → Gly; Glu 30 → Asp; Met 31 → Ala; Leu 33 → Trp; Ile 57 → Tyr; Asp 80 → Met; Glu 104 → Pro; Leu 105 → Tyr; His 106 → Gln; Lys 108 → Ala,

(b) Glu 27 → Gln; Phe 28 → Cys; Pro 29 → Asp; Glu 30 → Thr; Met 31 → Gly; Leu 33 → Trp; Ile 57 → Tyr; Leu 105 → Cys; His 106 → Gly; Lys 108 → Trp,

(c) Glu 27 → Glu; Phe 28 → Trp; Pro 29 → Asn; Glu 30 → Gly; Met 31 → His; Leu 33 → Tyr; Ile 57 → Tyr; Asp 80 → Pro; Glu 104 → Ser; Leu 105 → Trp; His 106 → Pro; Lys 108 → Tyr,

(d) Glu 27 → Thr; Phe 28 → Asp; Pro 29 → Asn; Glu 30 → Ser; Met 31 → Pro; Leu 33 → Phe; Ile 57 → Tyr; Asp 80 → Ile; Glu 104 → Ala; Leu 105 → Glu; His 106 → Arg; Lys 108 → Arg,

(e) Glu 27 → Phe; Phe 28 → Lys; Pro 29 → Ile; Glu 30 → Ala; Met 31 → Ser; Leu 33 → Pro; Ile 57 → Trp; Asp 80 → Gln; Glu 104 → Asn; Leu 105 → Arg; His 106 → Gln; Lys 108 → Asp,

(f) Glu 27 → Lys; Phe 28 → Gly; Pro 29 → Pro; Glu 30 → Thr; Met 31 → Pro; Leu 33 → Trp; Ile 57 → His; Asp 80 → Tyr; Glu 104 → Ala; Leu 105 → Ser; His 106 → Val; Lys 108 → Asn,

(g) Glu 27 → Glu; Phe 28 → His; Pro 29 → Leu; Glu 30 → Ala; Met 31 → Asp; Leu 33 → Ala; Ile 57 → Gln; Asp 80 → Ile; Glu 104 → Ala; Leu 105 → Tyr; His 106 → Pro; Lys 108 → Ser,

(h) Glu 27 → Ala; Phe 28 → Asp; Pro 29 → Met; Glu 30 → Gly; Met 31 → Asp; Leu 33 → Pro; Ile 57 → Thr; Asp 80 → Thr; Glu 104 → Thr; His 106 → Thr; Lys 108 → Arg,

(i) Glu 27 → Arg; Phe 28 → Leu; Pro 29 → Asp; Glu 30 → Asn; Met 31 → Glu; Leu 33 → Trp; Ile 57 → Tyr; Asp 80 → Gln; Glu 104 → Pro; Leu 105 → Arg; His 106 → Asn; Lys 108 → Ala,

(j) Glu 27 → Lys; Phe 28 → Asn; Pro 29 → Met; Glu 30 → Gly; Met 31 → Gln; Leu 33 → Pro; Ile 57 → Arg; Asp 80 → Ile; Glu 104 → Asp; Leu 105 → Arg; His 106 → Leu; Lys 108 → Thr, or

(k) Glu 27 → Ser; Phe 28 → Arg; Pro 29 → Gly; Glu 30 → Asp; Met 31 → Ala; Leu 33 → Trp; Ile 57 → Tyr; Asp 80 → Met; Glu 104 → Pro; Leu 105 → Gly; His 106 → Gln; Lys 108 → Ala.

32. The mutein according to any one of claims 1-12, comprising the following combination of amino acid substitutions: Arg 26 → Phe; Glu 27 → Ser; Phe 28 → Arg; Pro 29 → Gly; Glu 30 → Asp; Met 31 → Ala; Asn 32 → Ile; Leu 33 → Trp; Glu 34 → Thr; Leu 56 → Met; Ile 57 → Tyr; Ser 58 → Ala; Lys 83 → Ser; Glu 104 → Pro and Lys 108 → Thr, in comparison to mature human tear lipocalin.

33. The mutein according to claim 32, further includes one or more of the following amino acid substitutions in comparison to mature human tear lipocalin: Thr 43 → Ile or Ala, Glu 45 → Gly, Asn 48 → Gly, Glu 63 → Gly, Ala 66 → Vla, Glu 69 → Vla, Lys 70 → Arg, Ala 79 → Thr, Met or Vla, Asp 80 → Met or Ser, Gly 82 → Ser, His 84 → Gln, Vla 85 → Gly, Tyr 87 → Ser, Ile 88 → Thr or Leu, His 92 → Pro, Leu 105 → His, Gly or Tyr and His 106 → Gln or Arg.

34. The mutein according to any one of claims 1-12, comprising the following combination of amino acid substitutions: Glu 27 → Phe; Phe 28 → Lys; Pro 29 → Ile; Asn 32 → Trp; Leu 33 → Pro; Glu 34 → Arg; Leu 56 → Asn; Ile 57 → Trp; His 106 → Gln and Lys 108 → Glu, in comparison to mature human tear lipocalin.

35. The mutein according to claim 34, further includes one or more of the following amino acid substitutions in comparison to mature human tear lipocalin: Glu 43 → Gly or Ala, Glu 45 → Gly, Ser 58 → Trp or Arg, Glu 63 → Asp, Glu 69 → Gly, Lys 70 → Arg, Asp 80 → Gln, Val or Thr, Gly 82 → Asp, Lys 83 → Ser or Arg, Ala 86 → Glu or Ser, Phe 99 → Leu, Glu 102 → Lys or Val, Glu 104 → Asn or Lys and Pro 106 → Thr.

36. The mutein according to any one of claims 1 to 35, wherein the mutein comprises an amino acid substitution of a native amino acid by a cysteine residue at positions 28 or 105 with respect to the amino acid sequence of mature human tear lipocalin.

37. The mutein according to one of claims 1 to 36, wherein the mutein has at least 75% identity to the sequence of mature human tear lipocalin.

38. The mutein of any one of claims 1 to 12, wherein the mutein has an amino acid sequence as set forth in any one of SEQ ID NOs: 3-28, 62-71 and 82 or of a fragment or variant thereof.

39. The mutein of any one of claims 1 to 12, wherein the mutein has an amino acid sequence as set forth in SEQ ID NO: 23 or of a fragment or variant thereof.

40. The mutein of any one of claims 1 to 12, wherein the mutein has an amino acid sequence as set forth in SEQ ID NO: 13 or of a fragment or variant thereof.

41. The mutein of any one of claims 1 to 12, wherein the mutein has an amino acid sequence as set forth in SEQ ID NO: 20 or of a fragment or variant thereof.

42. The mutein of any one of claims 1 to 12, wherein the mutein has an amino acid sequence as set forth in SEQ ID NO: 22 or of a fragment or variant thereof.

43. The mutein of any one of claims 1-42, wherein the mutein is conjugated to a label moiety.

44. The mutein of any one of claims 1-42, wherein the mutein is conjugated to a moiety that can target a specific body region, organism, tissue, organ or cell wihtin a subject.

45. The mutein of any one of claims 1-42, wherein the mutein is conjugated to a moiety that can extend the serum half-life of the mutein.

46. The mutein of any one of claims 1-42, wherein the mutein is conjugated to a polyalkylene glycol molecule.

47. The conjugated mutein of claim 46, wherein the conjugated mutein comprises an amino acid sequence as set forth in any one of SEQ ID NOs: 30-32.

48. The mutein of any one of claims 1-42, wherein the mutein is conjugated to an albumin binding protein.

49. The conjugated mutein of claim 48, wherein the conjugated mutein comprises an amino acid sequence as set forth in any one of SEQ ID NOs: 83-84.

50. The mutein of any one of claims 1-42, wherein the mutein is fused to a moiety can confer new characteristics to the fusion.

51. A method of generating one or more muteins of human tear lipocalin, wherein the one or more mutein bind to PCSK9, comprising:

(a) subjecting a nucleic acid molecule encoding a human tear lipocalin to mutagenesis at:

(i) any one or more of the amino acid sequence positions 26-34, 56-58, 80, 83, 104-106 and 108 of the linear polypeptide sequence of mature human tear lipocalin, and

(ii) any one or more of the amino acid sequence positions 61, 101, 111, 114 and 153 of the linear polypeptide sequence of the mature human tear lipocalin,

thereby obtaining one or more nucleic acids molecule(s) encoding one or more mutein(s) of human tear lipocalin,

(b) expressing the one or more nucleic acid molecule(s) obtained in (a) in an expression system, thereby obtaining one or more mutein(s) of human tear lipocalin, and

(c) further selecting the one or more mutein(s) obtained in (b).

52. The method according to claim 51, wherein step (c) further comprises:

(ci) providing PCSK9 or an immunogenic fragment thereof,

(cii) contacting the one or more mutein(s) obtained through selection with the PCSK9 or the immunogenic fragment thereof, thereby allowing the formation of a complex between the PCSK9 or the immunogenic fragment thereof and the mutein having binding affinity for the same, and

(ciii) removing one or more mutein(s) having no or no substantial binding affinity.

53. The method of claims 51 or 52, wherein the selection in step (c) is carried out under competitive conditions.

54. The method of any one of claims 51-53, wherein step (a) further comprises: (a)(iii) subjecting the nucleic acid molecule encoding a human tear lipocalin to mutagenesis at any one or more of the amino acid sequence positions 79, 92 and 105 of the linear polypeptide sequence of mature human tear lipocalin.

55. A nucleic acid molecule comprising a nucleotide sequence encoding a mutein of any one of claims 1-50.

56. A nucleic acid molecule as set forth in any one of SEQ ID NOs: 36-61, 72-81 and 86-89.

57. A host cell containing a nucleic acid molecule of claim 55 or 56.

58. The use of a mutein according to any one of claims 1-50 or a composition comprising such mutein for the binding of PCSK9 in a subject.

59. The use of a mutein according to any one of claims 1-50 or a composition comprising such mutein for inhibiting the binding of PCSK9 to LDL-R in a subject.

60. The use of a mutein according to any one of claims 1-50 for the detection of PCSK9, comprising:
    (a) contacting the mutein with a test sample suspected to contain PCSK9 under suitable conditions, thereby allowing the formation of a complex between the mutein and PCSK9 or a domain or fragment thereof, and
    (b) detecting the complex by a suitable signal.

61. The use of a mutein according to any one of claims 1-50 for the separation of PCSK9, comprising:
    (a) contacting the mutein with a sample supposed to contain PCSK9 under suitable conditions, thereby allowing formation of a complex between the mutein and PCSK9 or a domain or fragment thereof, and
    (b) separating the complex from the sample.

62. The use of a mutein according to any one of claims 1-50 for targeting a compound to a preselected organism, tissue, organ or cell to be treated with the compound, comprising the steps of:
    (a) conjugating the mutein with said compound, and
    (b) delivering the mutein/compound complex to the preselected organism, tissue, organ or cell.

63. A kit comprising a mutein according to any one of claims 1-50.

Figure 1

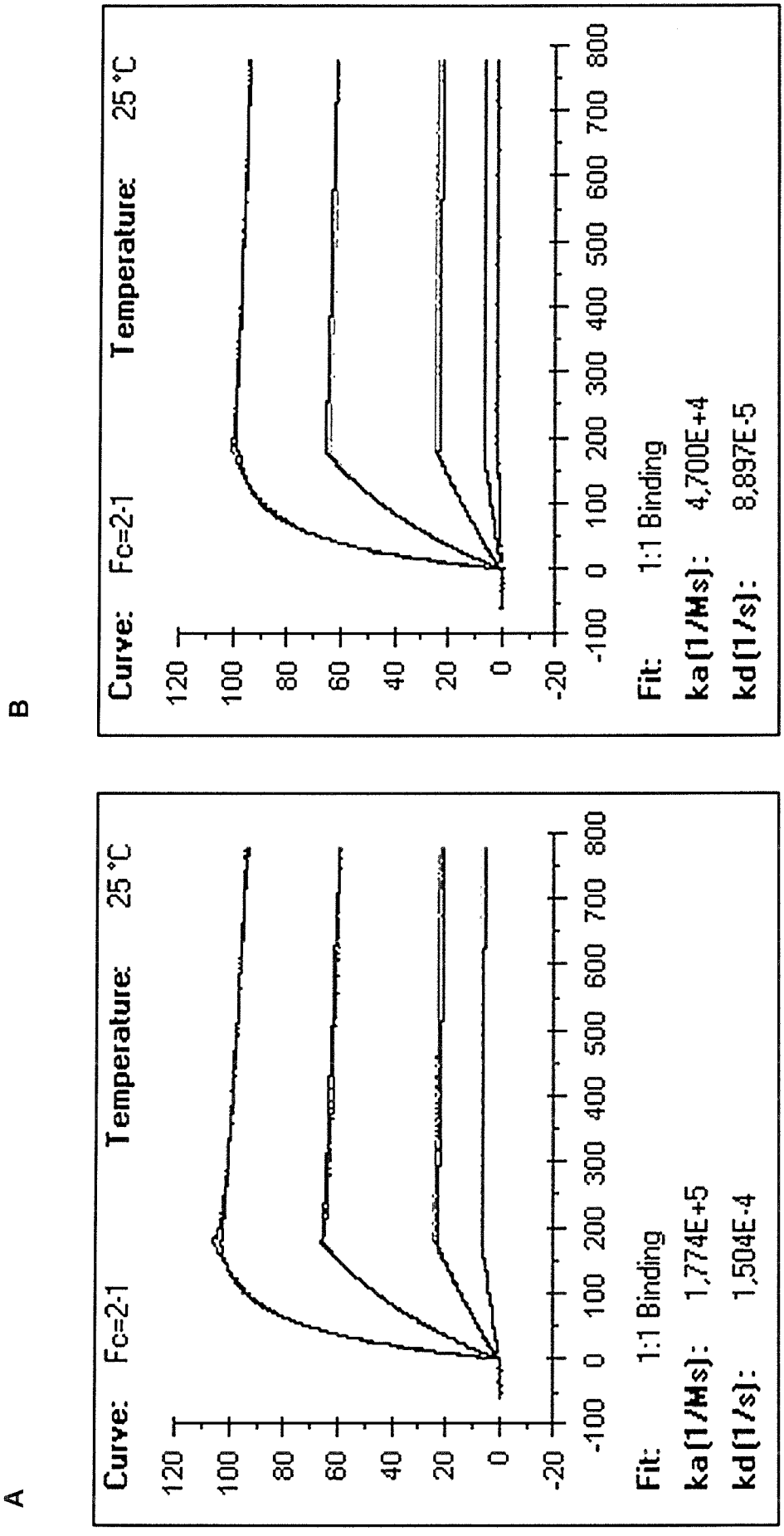
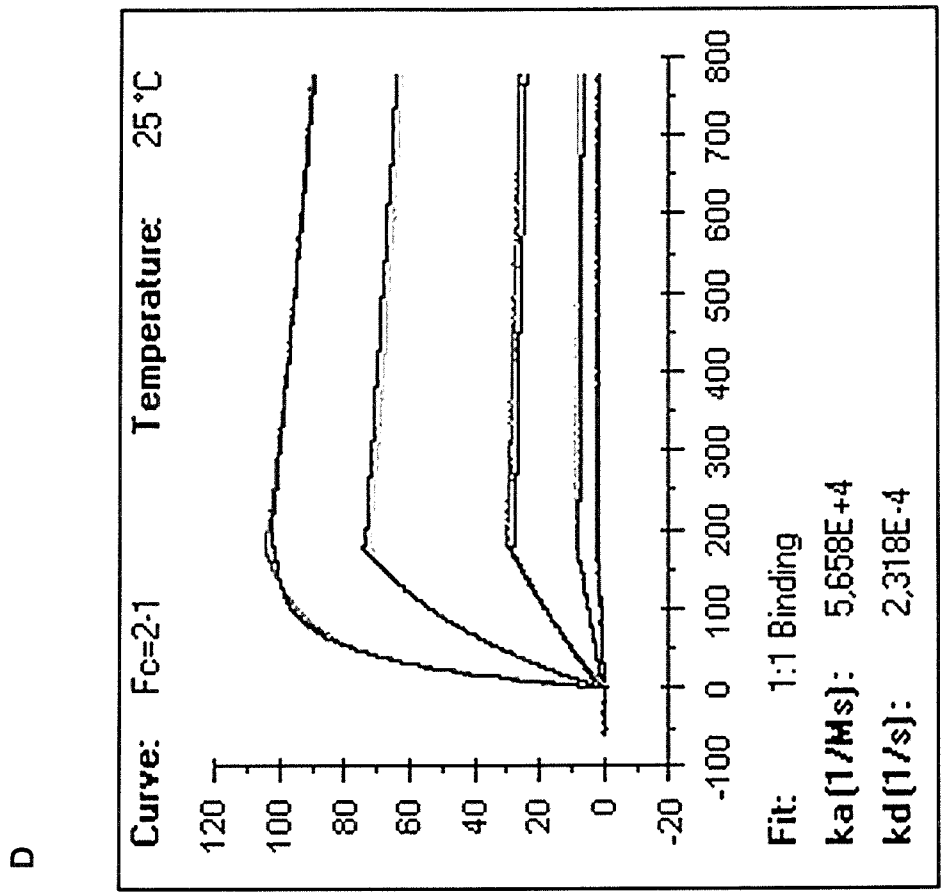

A
Curve: Fc=2-1 Temperature: 25 °C
120
100
80
60
40
20
0
-20
-100 0 100 200 300 400 500 600 700 800
Fit: 1:1 Binding
ka[1/Ms]: 1,774E+5
kd[1/s]: 1,504E-4
B
Curve: Fc=2-1 Temperature: 25 °C
120
100
80
60
40
20
0
-20
-100 0 100 200 300 400 500 600 700 800
Fit: 1:1 Binding
ka[1/Ms]: 4,700E+4
kd[1/s]: 8,897E-5

Figure 1 (cont'd)



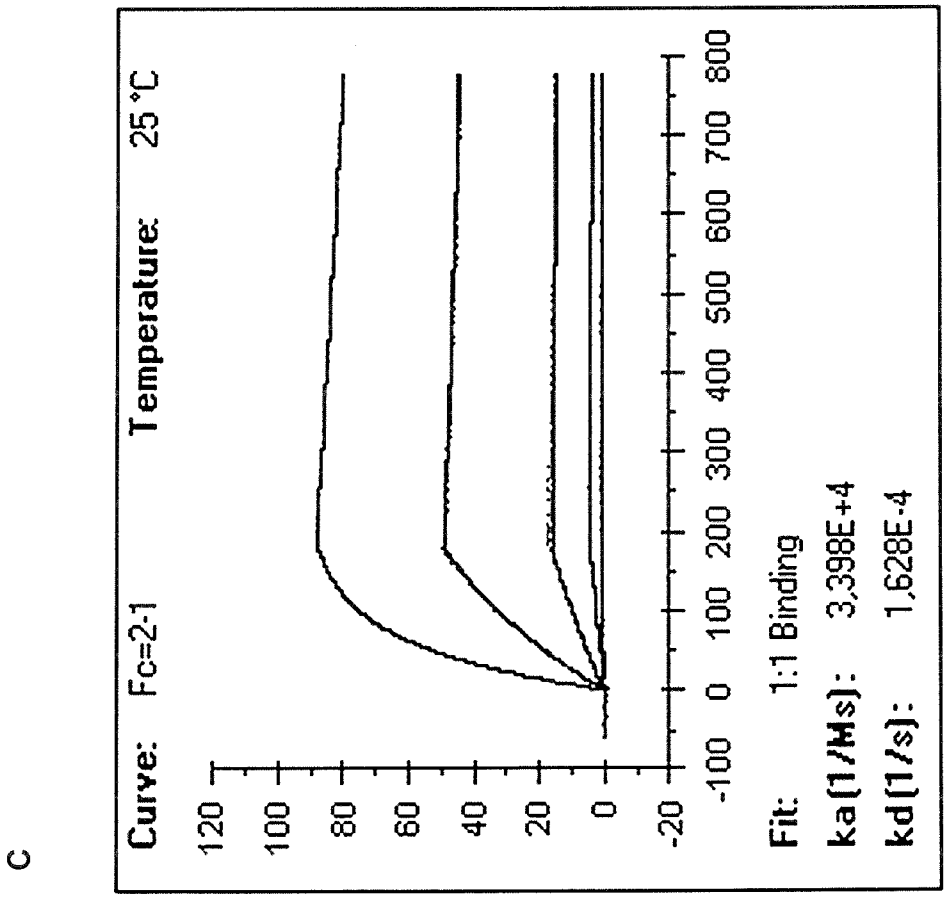
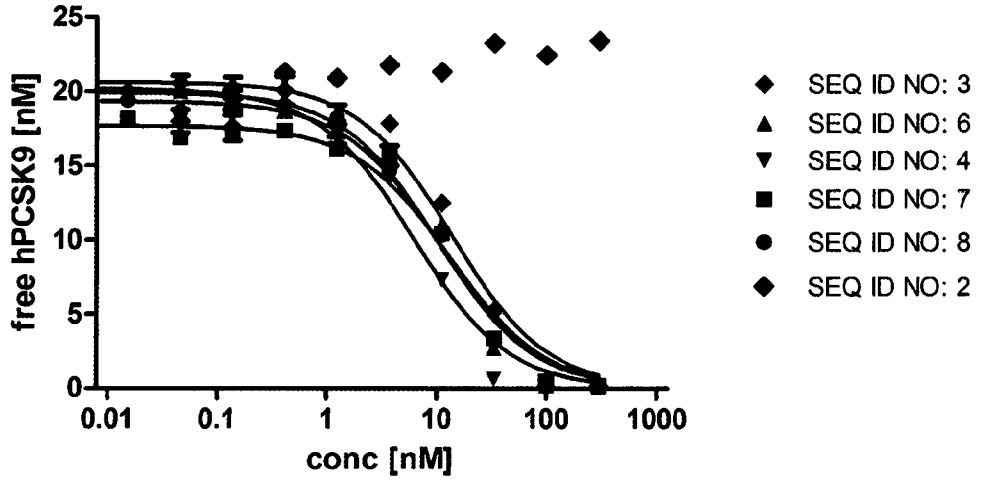


Figure 2

A


free hPCSK9 [nM]
25
20
15
10
5
0
0.01
0.1
1
10
100
1000
conc [nM]
SEQ ID NO: 3
SEQ ID NO: 6
SEQ ID NO: 4
SEQ ID NO: 7
SEQ ID NO: 8
SEQ ID NO: 2

B

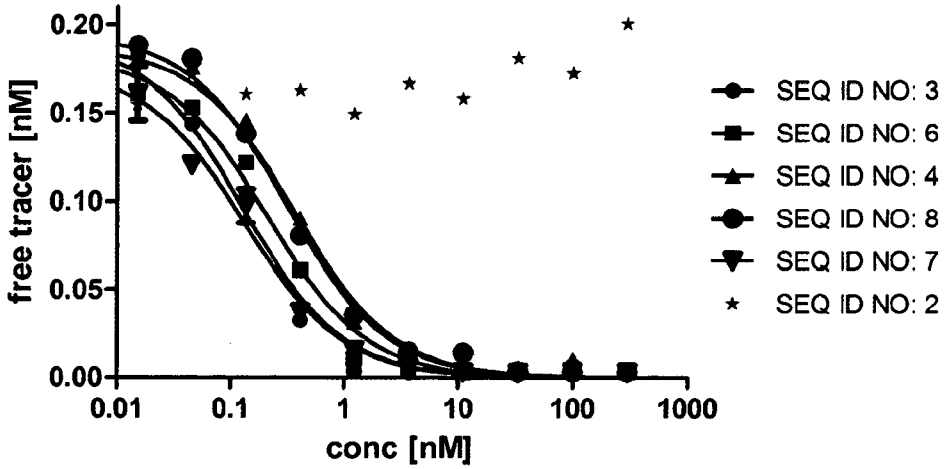
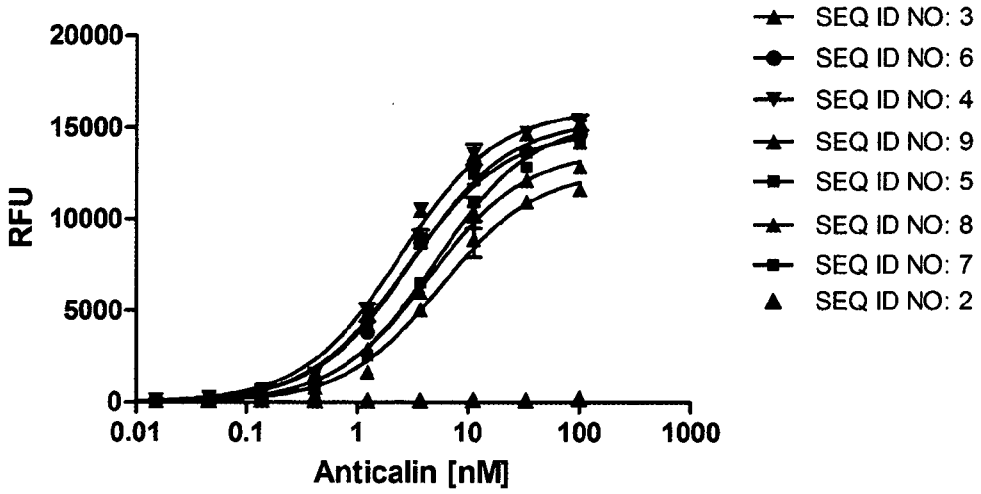

free tracer [nM]
0.20
0.15
0.10
0.05
0.00
0.01
0.1
1
10
100
1000
conc [nM]
SEQ ID NO: 3
SEQ ID NO: 6
SEQ ID NO: 4
SEQ ID NO: 8
SEQ ID NO: 7
SEQ ID NO: 2

Figure 3

A


20000
15000
10000
5000
0
RFU
0.01
0.1
1
10
100
1000
Anticalin [nM]
SEQ ID NO: 3
SEQ ID NO: 6
SEQ ID NO: 4
SEQ ID NO: 9
SEQ ID NO: 5
SEQ ID NO: 8
SEQ ID NO: 7
SEQ ID NO: 2

B

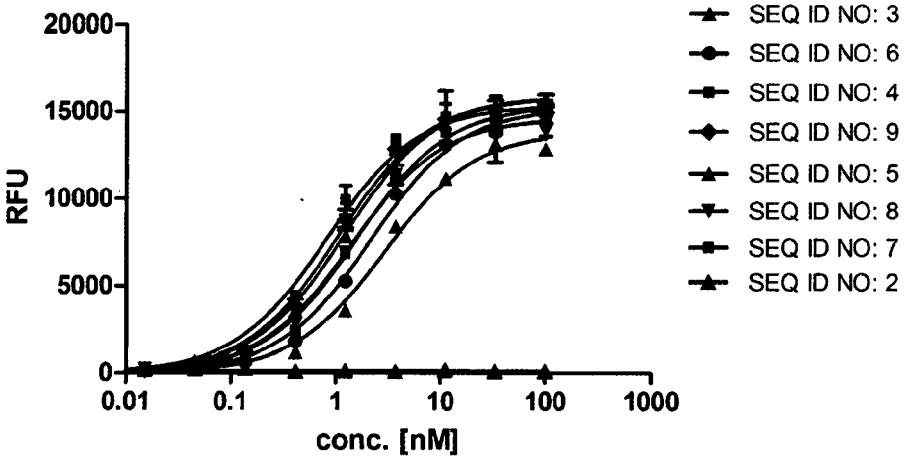

20000
15000
10000
5000
0
RFU
0.01
0.1
1
10
100
1000
conc. [nM]
SEQ ID NO: 3
SEQ ID NO: 6
SEQ ID NO: 4
SEQ ID NO: 9
SEQ ID NO: 5
SEQ ID NO: 8
SEQ ID NO: 7
SEQ ID NO: 2

Figure 3 (cont'd)

Fig. 3C

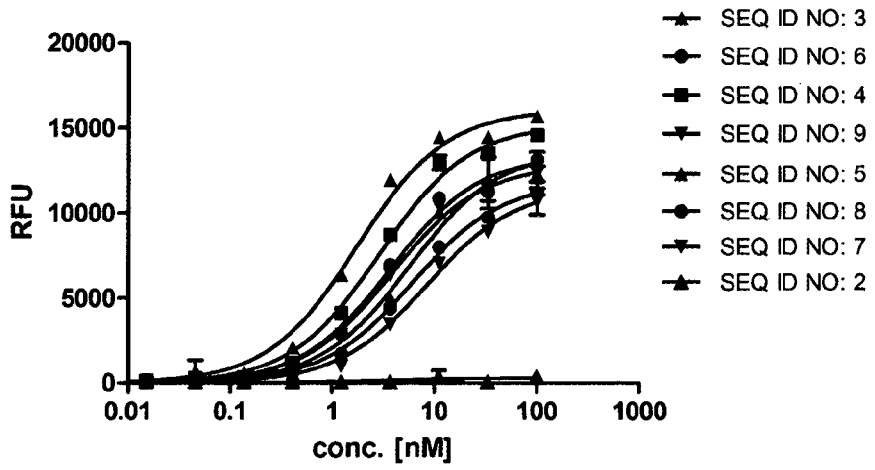


Fig. 3D

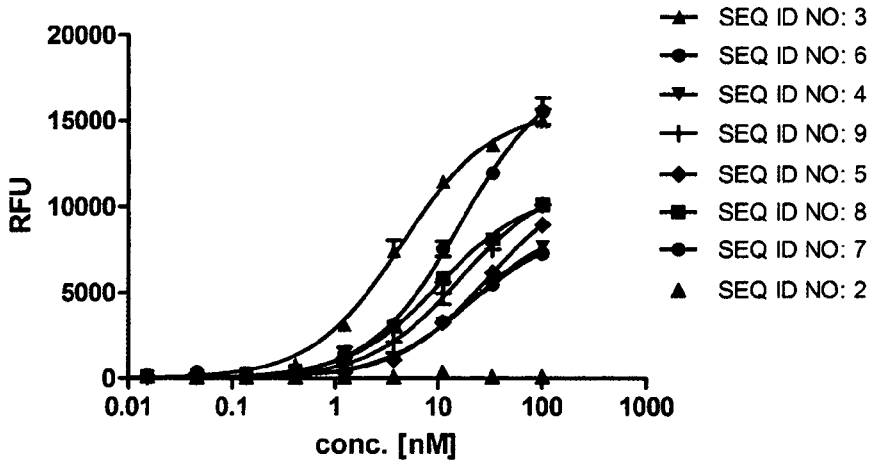


Figure 4

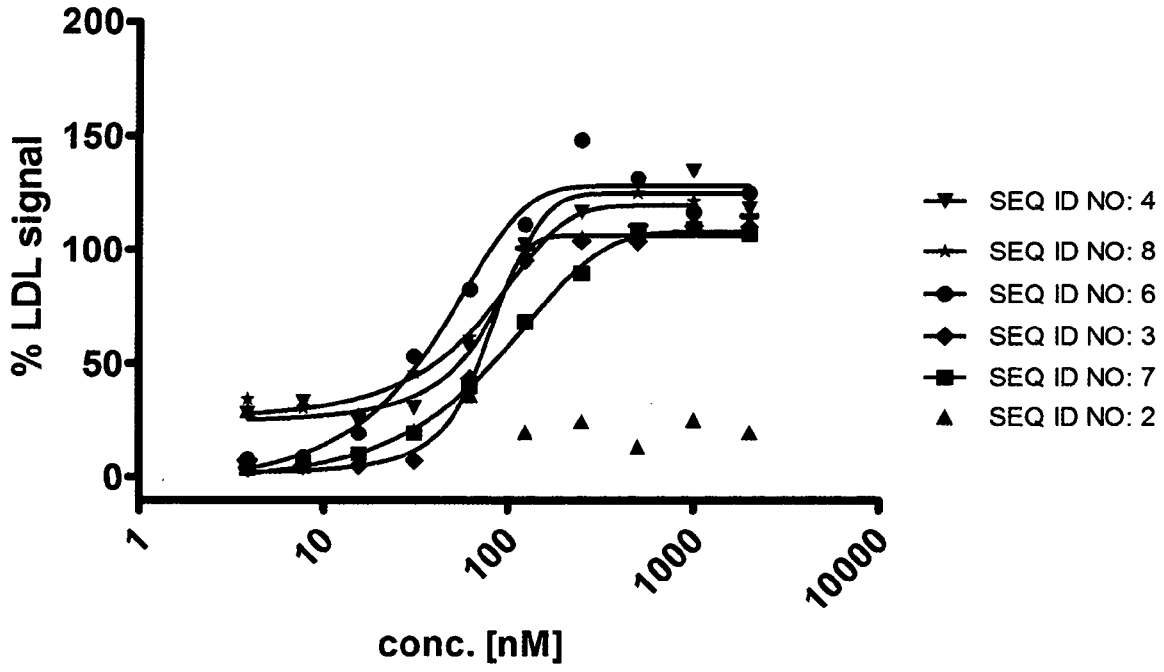

200
150
100
50
0
% LDL signal
1
10
100
1000
10000
conc. [nM]
SEQ ID NO: 4
SEQ ID NO: 8
SEQ ID NO: 6
SEQ ID NO: 3
SEQ ID NO: 7
SEQ ID NO: 2

Figure 5

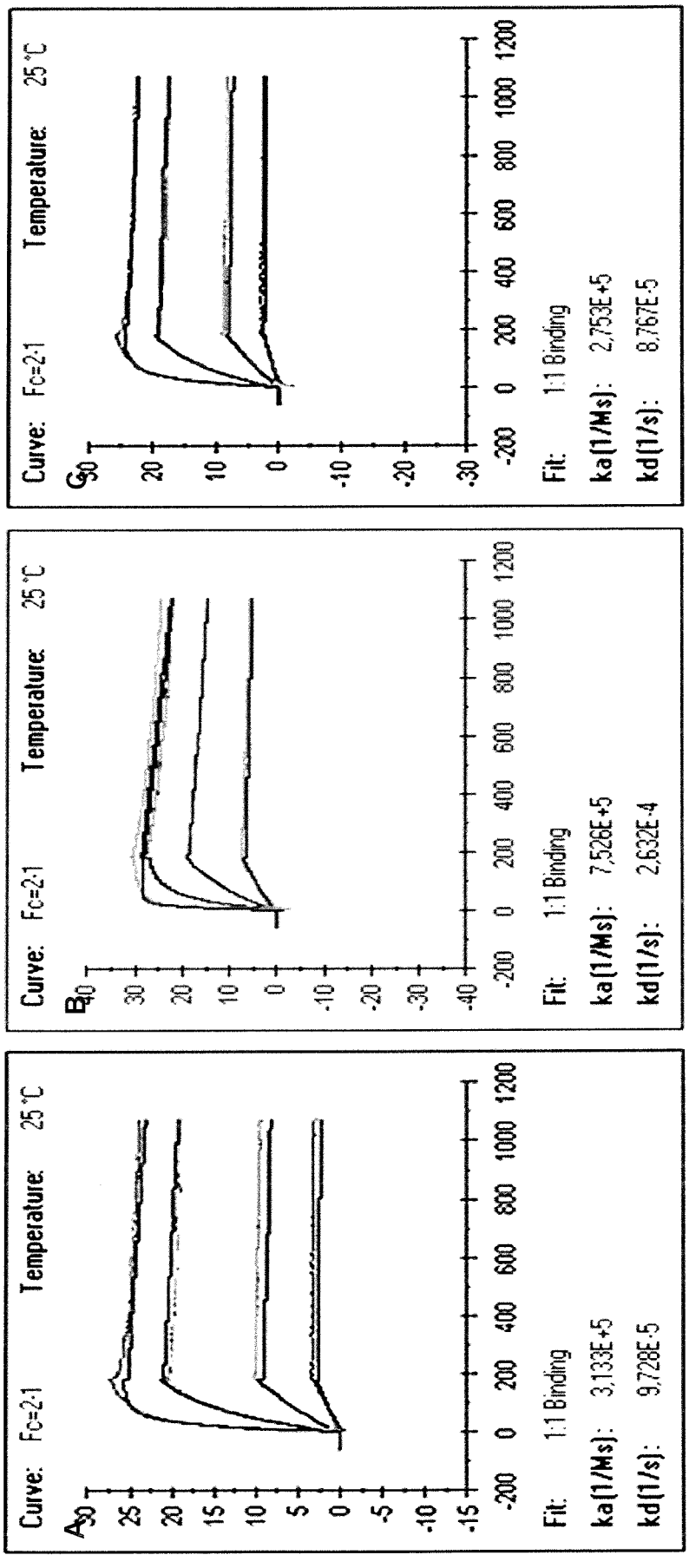

Curve: Fc=2:1
Temperature: 25 °C
A50
B40
G50
Fit: 1:1 Binding
ka(1/Ms): 3,133E+5
kd(1/s): 9,728E-5
ka(1/Ms): 7,526E+5
kd(1/s): 2,632E-4
ka(1/Ms): 2,753E+5
kd(1/s): 8,767E-5

Figure 6

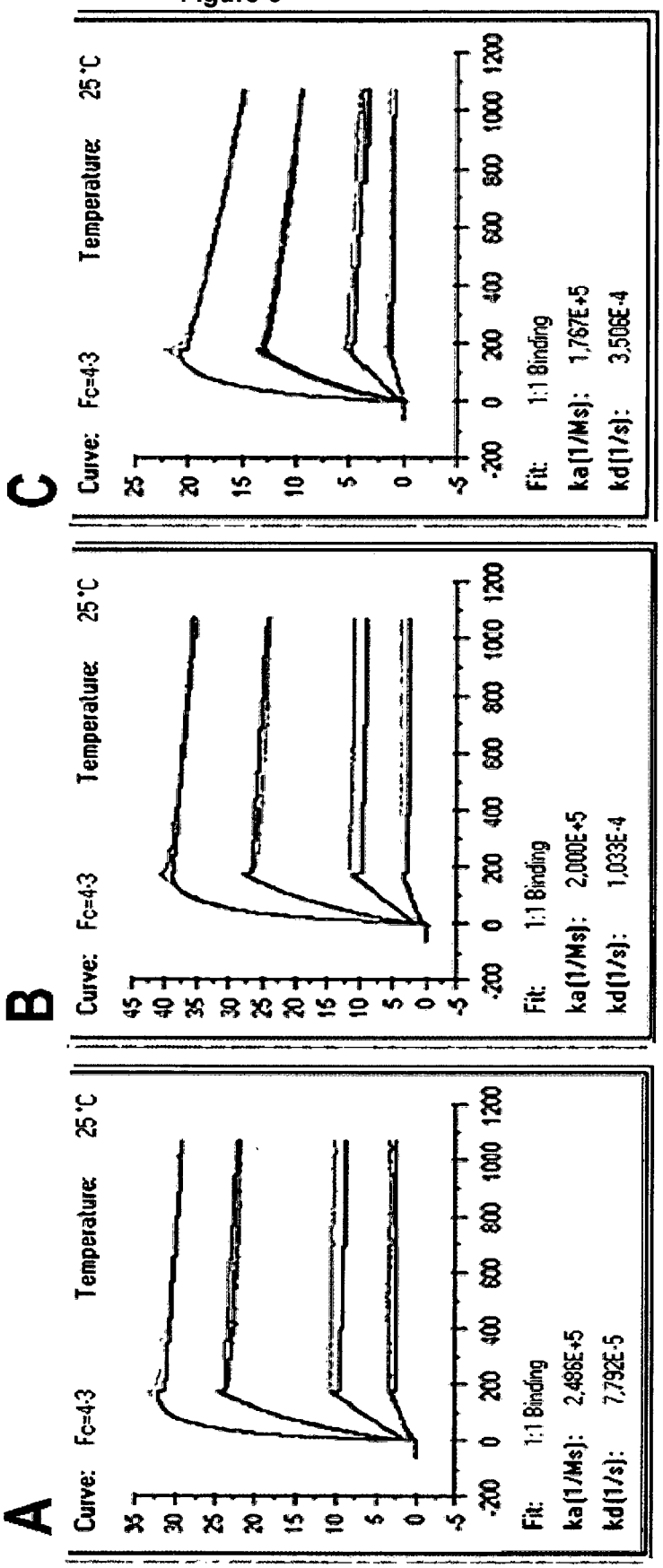

A
Curve: Fc=4:3 Temperature: 25°C
Fit: 1:1 Binding
ka[1/Ms]: 2,486E+5
kd[1/s]: 7,792E-5
B
Curve: Fc=4:3 Temperature: 25°C
Fit: 1:1 Binding
ka[1/Ms]: 2,000E+5
kd[1/s]: 1,033E-4
C
Curve: Fc=4:3 Temperature: 25°C
Fit: 1:1 Binding
ka[1/Ms]: 1,767E+5
kd[1/s]: 3,508E-4

Figure 7

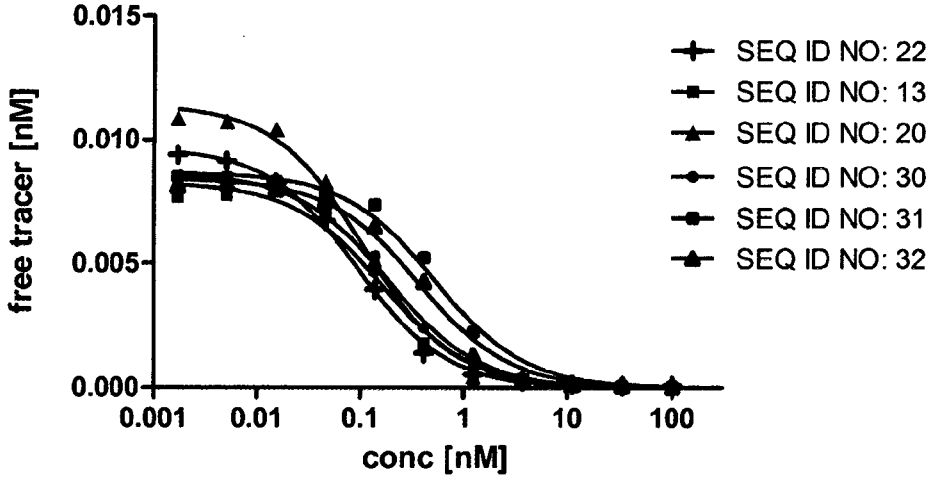


Figure 8

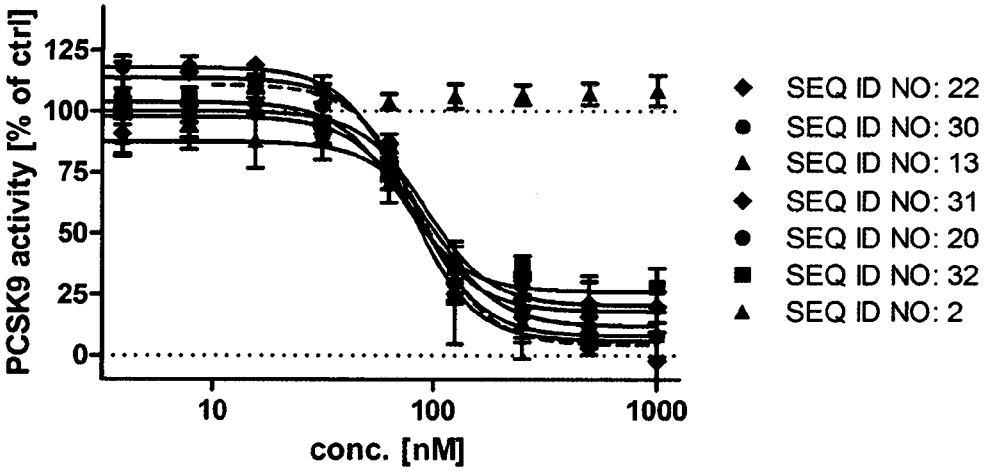


Figure 9

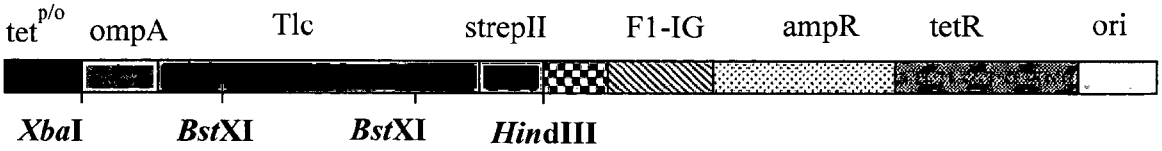


Figure 10

Molecule	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23
SEQ ID NO: 1	H	H	L	L	A	S	D	E	E	I	Q	D	V	S	G	T	W	Y	L	K	A	M	T
SEQ ID NO: 2					A	S	D	E	E	I	Q	D	V	S	G	T	W	Y	L	K	A	M	T
SEQ ID NO: 3					A	S	D	E	E	I	Q	D	V	S	G	T	W	Y	L	K	A	M	T
SEQ ID NO: 4					A	S	D	E	E	I	Q	D	V	S	G	T	W	Y	L	K	A	M	T
SEQ ID NO: 5					A	S	D	E	E	I	Q	D	V	S	G	T	W	Y	L	K	A	M	T
SEQ ID NO: 6					A	S	D	E	E	I	Q	D	V	S	G	T	W	Y	L	K	A	M	T
SEQ ID NO: 7					A	S	D	E	E	I	Q	D	V	S	G	T	W	Y	L	K	A	M	T
SEQ ID NO: 8					A	S	D	E	E	I	Q	D	V	S	G	T	W	Y	L	K	A	M	T
SEQ ID NO: 9					A	S	D	E	E	I	Q	D	V	S	G	T	W	Y	L	K	A	M	T
SEQ ID NO: 10					A	S	D	E	E	I	Q	D	V	S	G	T	W	Y	L	K	A	M	T
SEQ ID NO: 11					A	S	D	E	E	I	Q	D	V	S	G	T	W	Y	L	K	A	M	T
SEQ ID NO: 12					A	S	D	E	E	I	Q	D	V	S	G	T	W	Y	L	K	A	M	T
SEQ ID NO: 13					A	S	D	E	E	I	Q	D	V	S	G	T	W	Y	L	K	A	M	T
SEQ ID NO: 14					A	S	D	E	E	I	Q	D	V	S	G	T	W	Y	L	K	A	M	T
SEQ ID NO: 15					A	S	D	E	E	I	Q	D	V	S	G	T	W	Y	L	K	A	M	T
SEQ ID NO: 16					A	S	D	E	E	I	Q	D	V	S	G	T	W	Y	L	K	A	M	T
SEQ ID NO: 17					A	S	D	E	E	I	Q	D	V	S	G	T	W	Y	L	K	A	M	T
SEQ ID NO: 18					A	S	D	E	E	I	Q	D	V	S	G	T	W	Y	L	K	A	M	T
SEQ ID NO: 19					A	S	D	E	E	I	Q	D	V	S	G	T	W	Y	L	K	A	M	T
SEQ ID NO: 20					A	S	D	E	E	I	Q	D	V	S	G	T	W	Y	L	K	A	M	T
SEQ ID NO: 21					A	S	D	E	E	I	Q	D	V	S	G	T	W	Y	L	K	A	M	T
SEQ ID NO: 22					A	S	D	E	E	I	Q	D	V	S	G	T	W	Y	L	K	A	M	T
SEQ ID NO: 23					A	S	D	E	E	I	Q	D	V	S	G	T	W	Y	L	K	A	M	T
SEQ ID NO: 24					A	S	D	E	E	I	Q	D	V	S	G	T	W	Y	L	K	A	M	T
SEQ ID NO: 25					A	S	D	E	E	I	Q	D	V	S	G	T	W	Y	L	K	A	M	T
SEQ ID NO: 26					A	S	D	E	E	I	Q	D	V	S	G	T	W	Y	L	K	A	M	T
SEQ ID NO: 27					A	S	D	E	E	I	Q	D	V	S	G	T	W	Y	L	K	A	M	T
SEQ ID NO: 28					A	S	D	E	E	I	Q	D	V	S	G	T	W	Y	L	K	A	M	T

Figure 10 (cont'd)

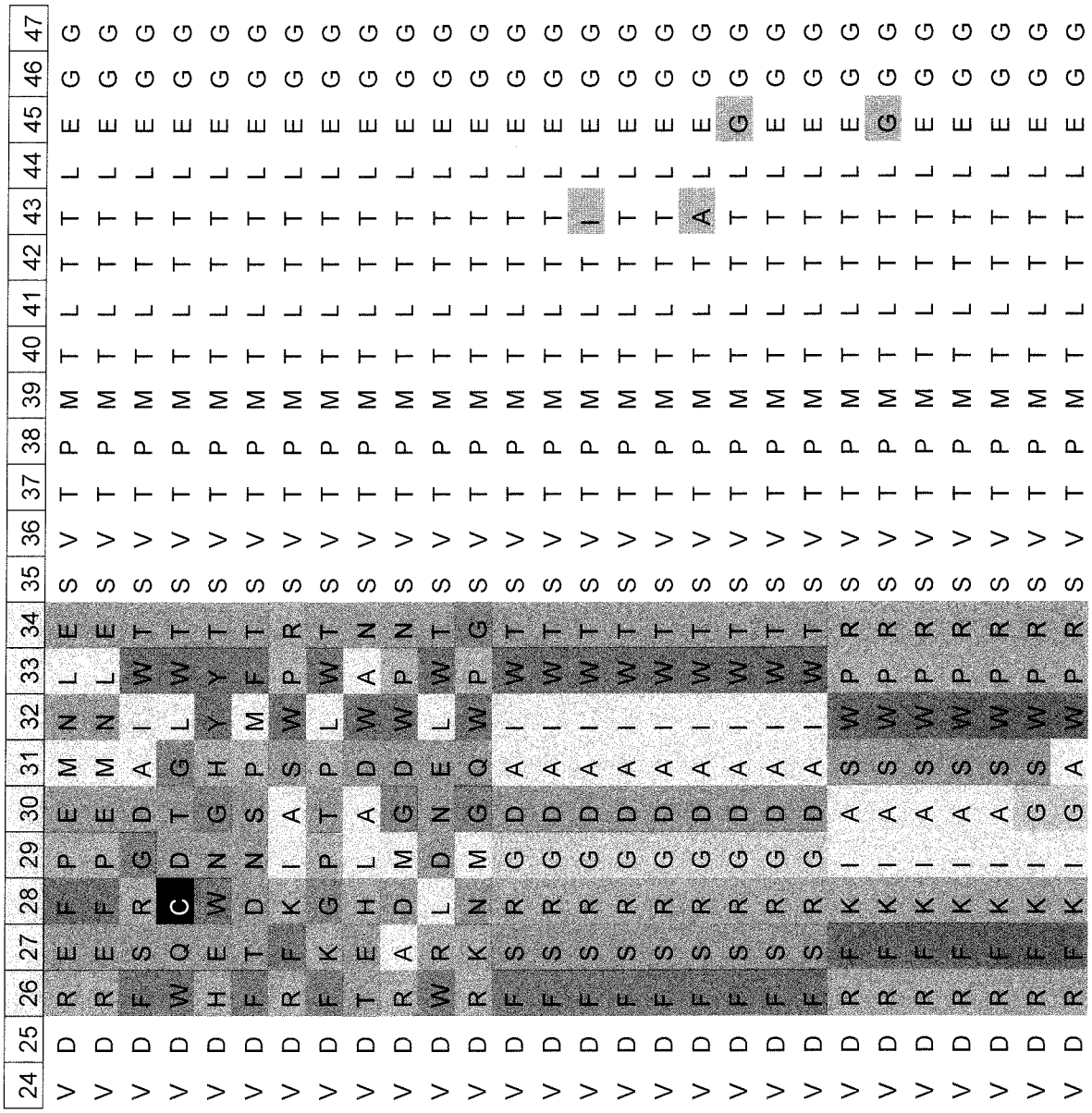


Figure 10 (cont'd)

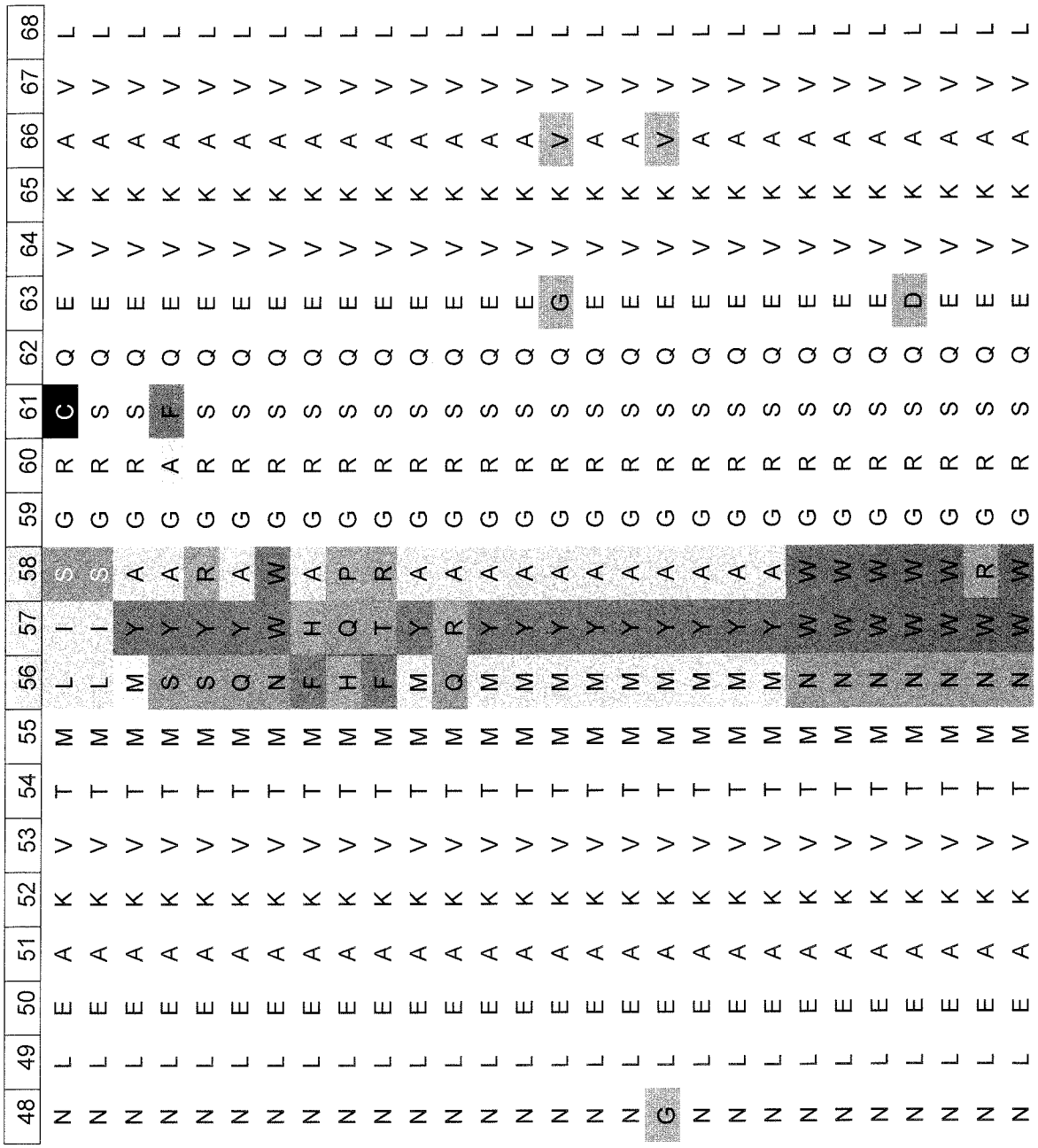


Figure 10 (cont'd)

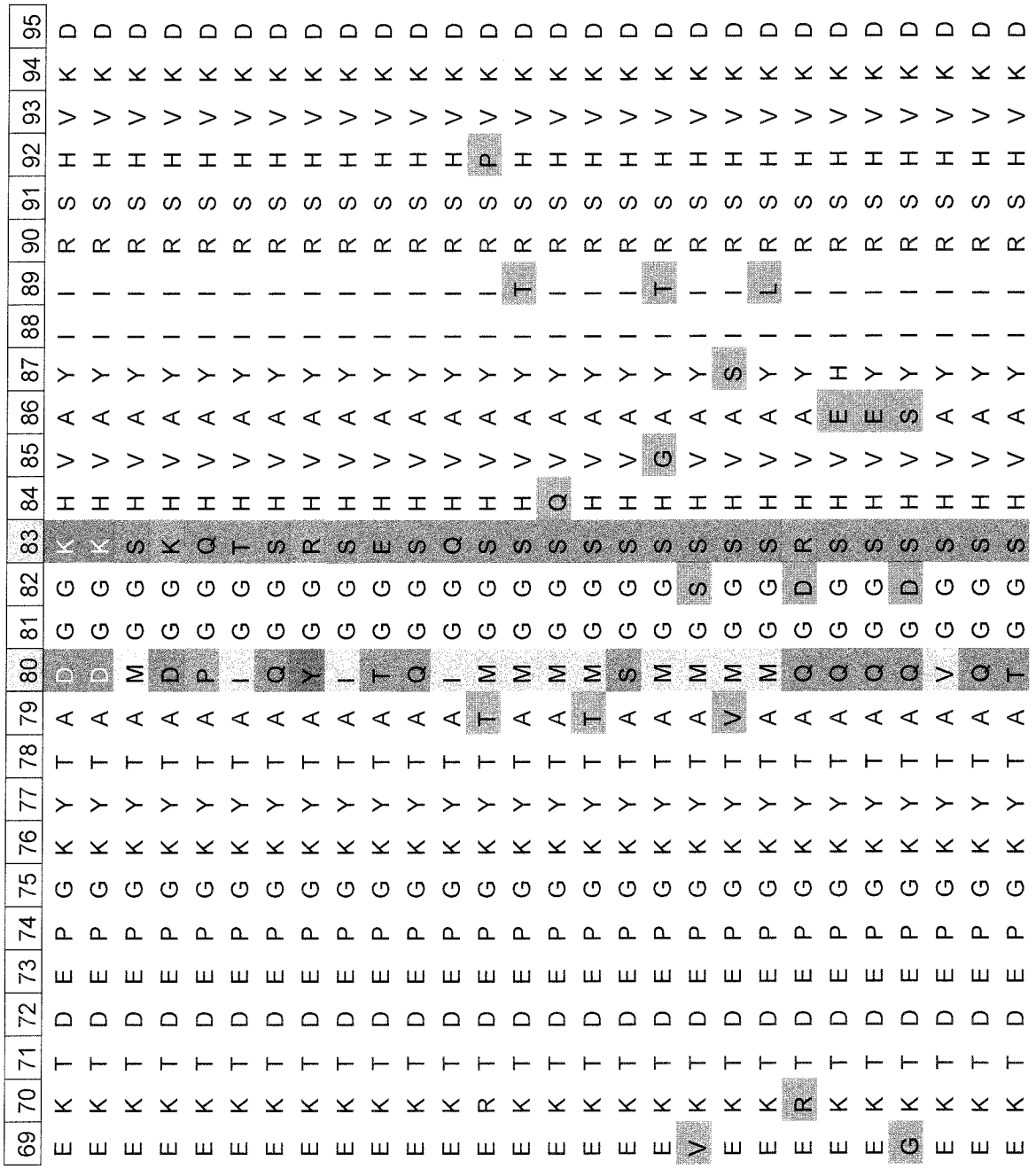


Figure 10 (cont'd)

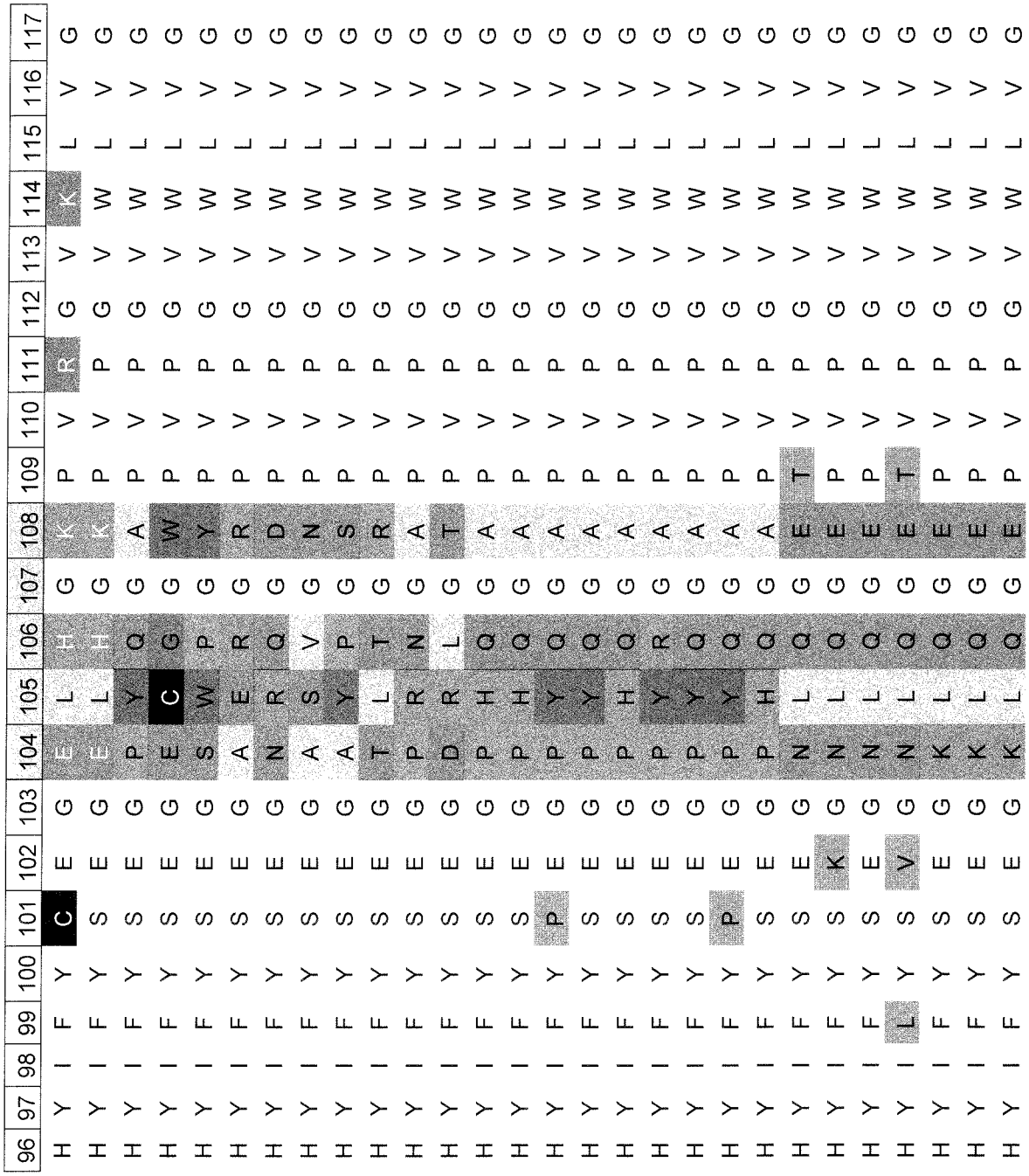


Figure 10 (cont'd)

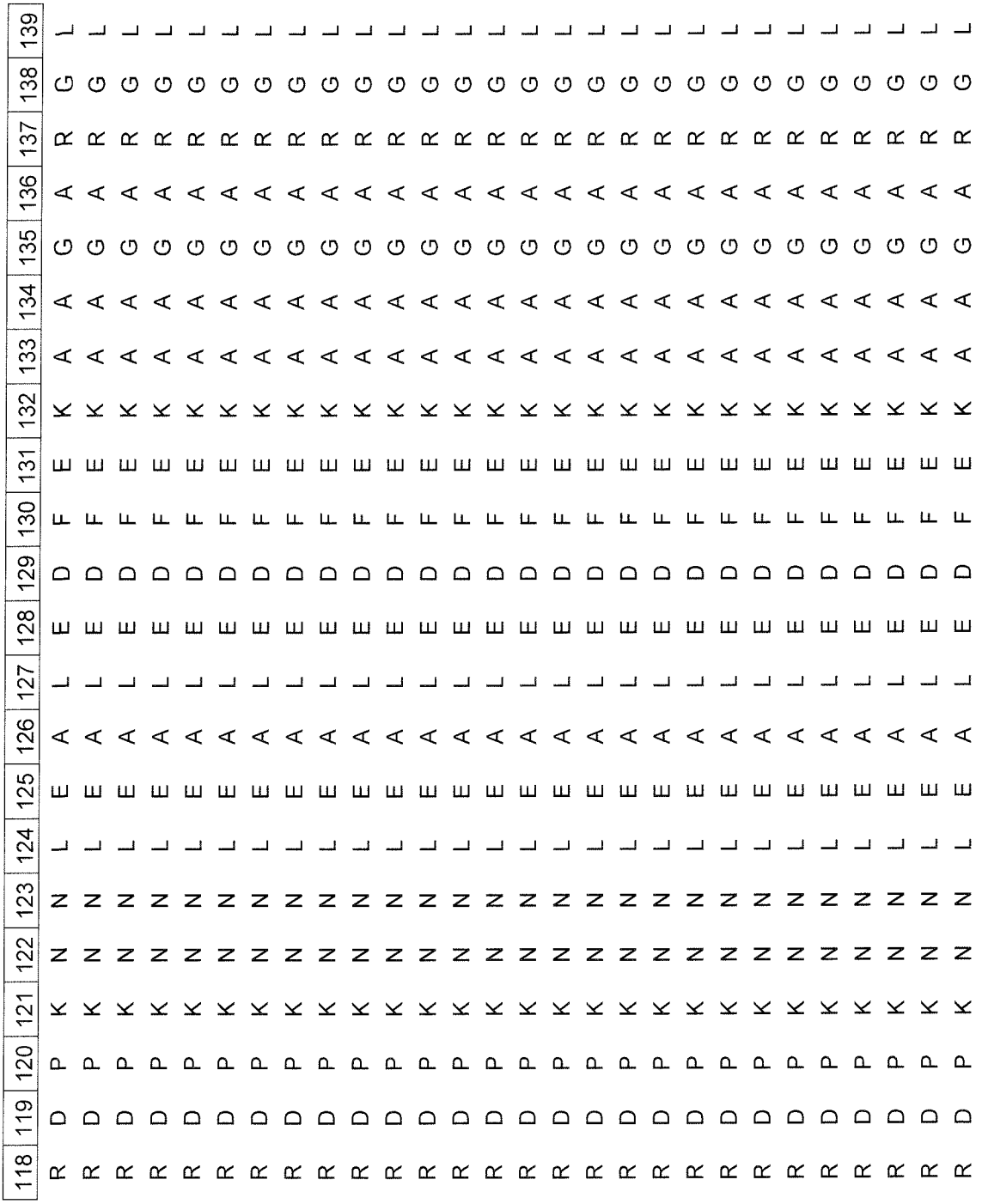


Figure 10 (cont'd)

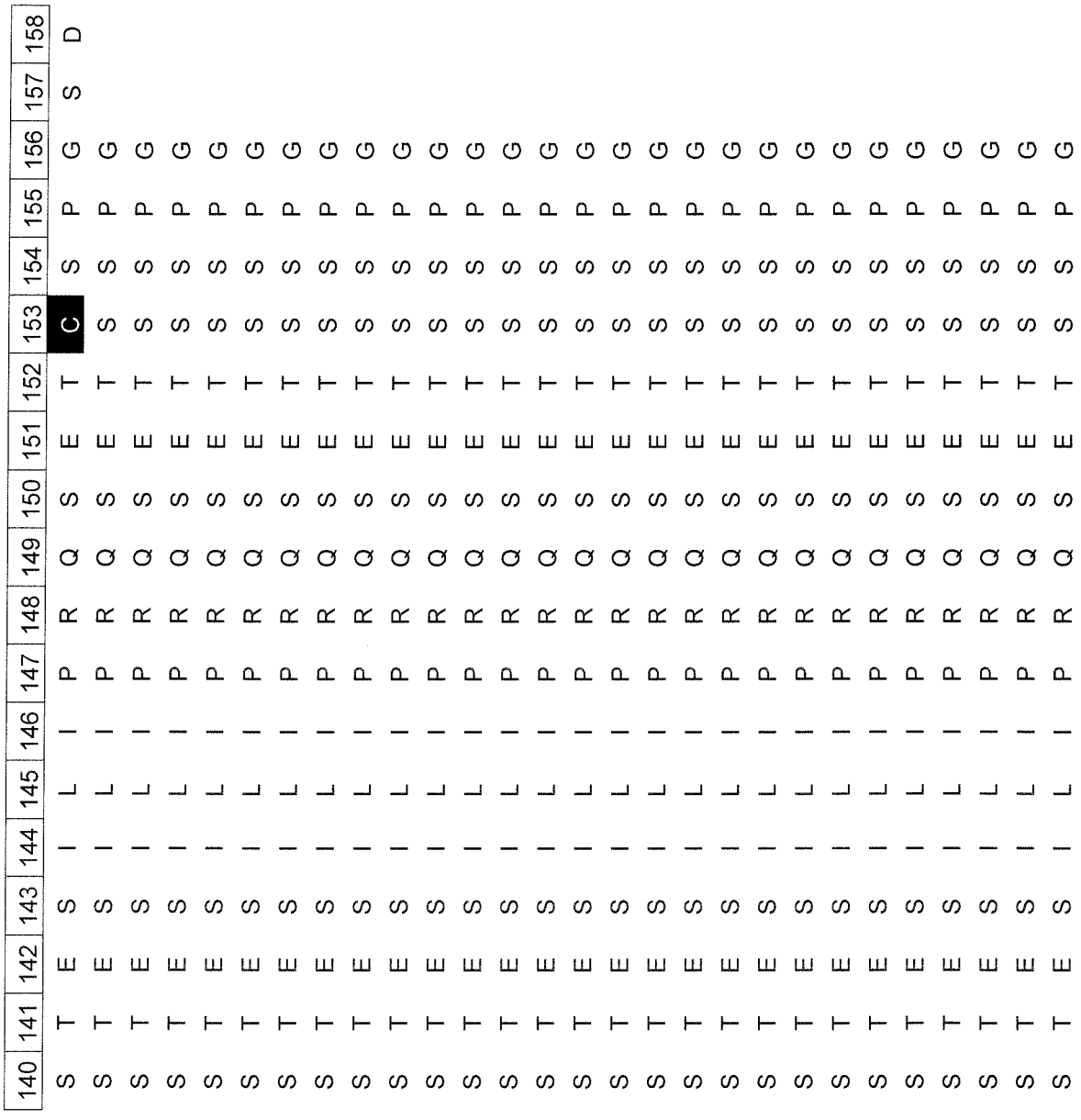


Figure 11

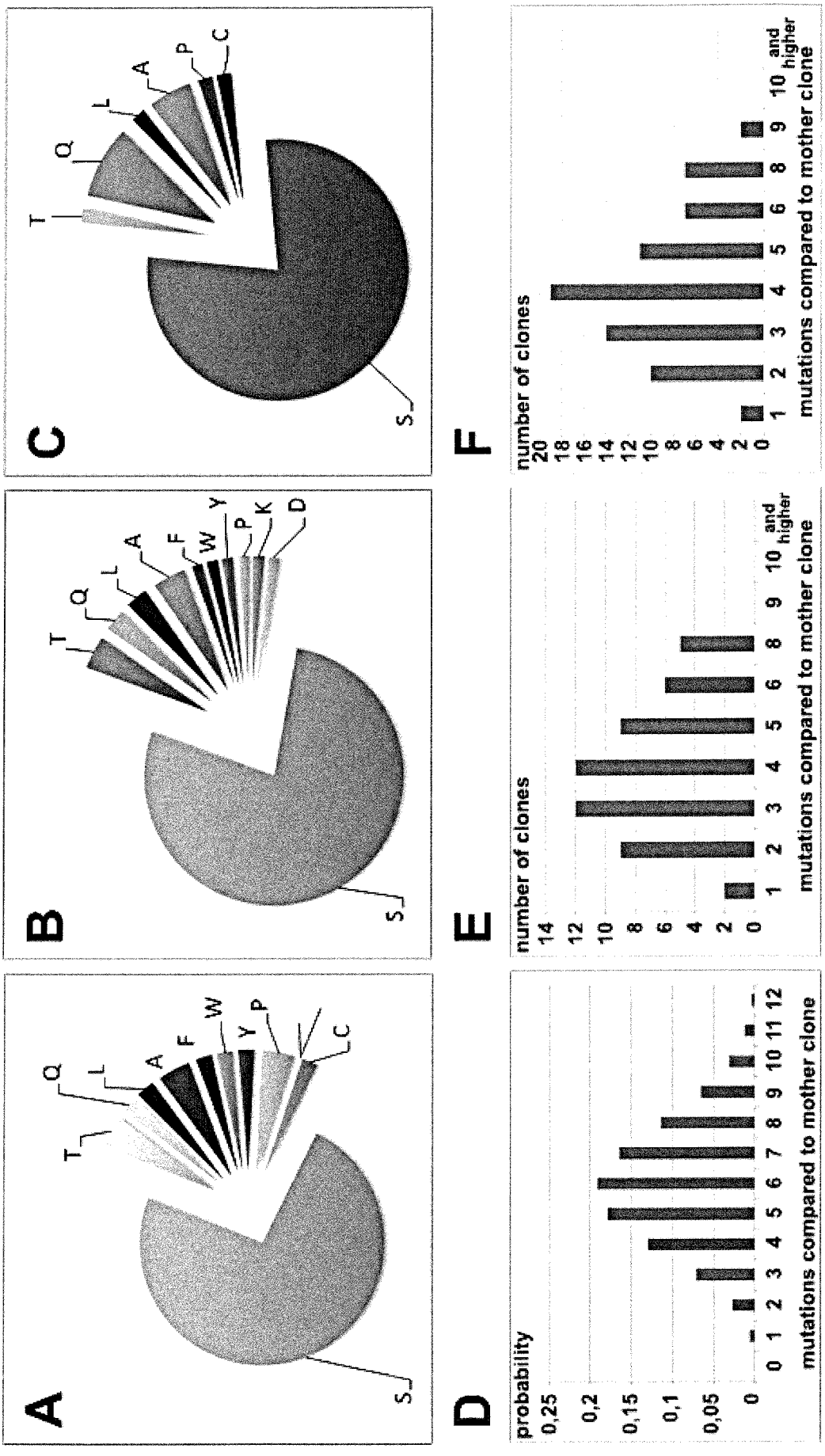

A
T
Q
L
A
F
W
Y
P
C
S
B
T
Q
L
A
F
W
Y
P
K
D
S
C
T
Q
L
A
P
C
S
D
probability
0,25
0,2
0,15
0,1
0,05
0
0 1 2 3 4 5 6 7 8 9 10 11 12
mutations compared to mother clone
E
number of clones
14
12
10
8
6
4
2
0
1 2 3 4 5 6 8 9 10 and higher
mutations compared to mother clone
F
number of clones
20
18
16
14
12
10
8
6
4
2
0
1 2 3 4 5 6 8 9 10 and higher
mutations compared to mother clone

Figure 12

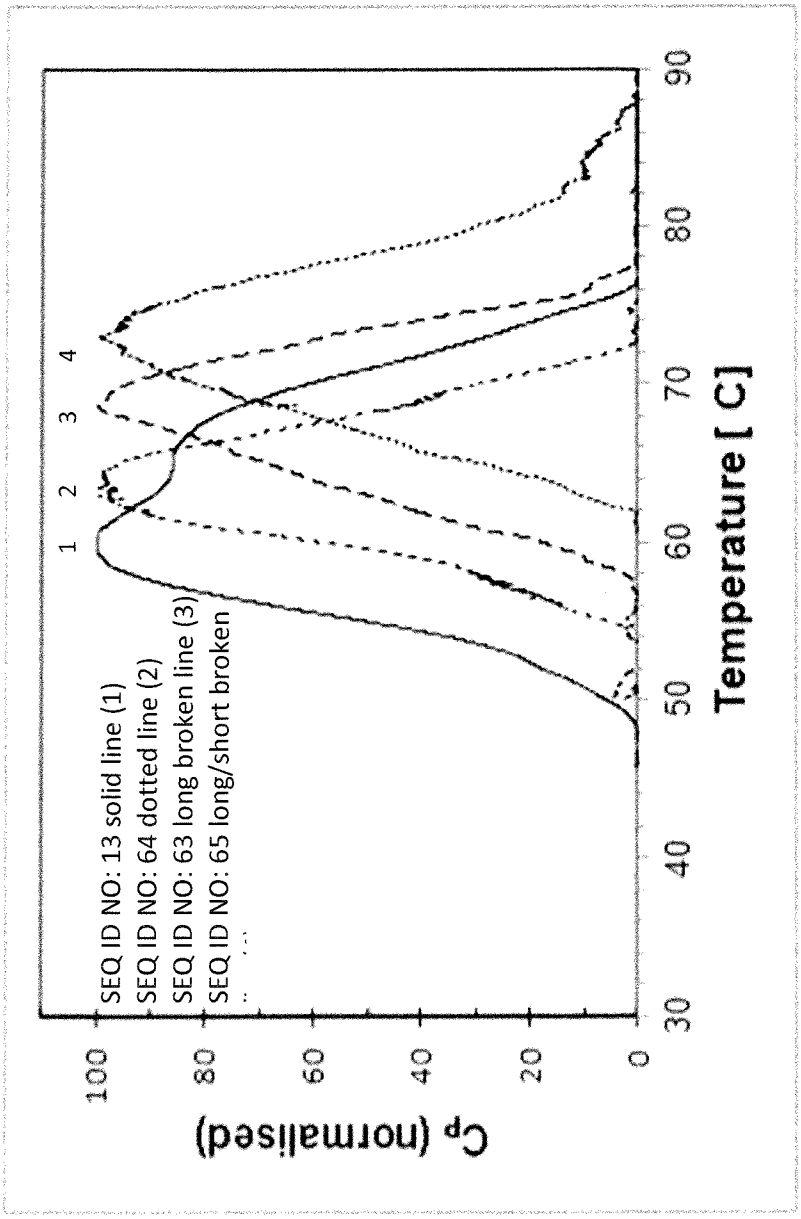

Cp (normalised)
Temperature [C]
SEQ ID NO: 13 solid line (1)
SEQ ID NO: 64 dotted line (2)
SEQ ID NO: 63 long broken line (3)
SEQ ID NO: 65 long/short broken
1
2
3
4
0
20
40
60
80
100
30
40
50
60
70
80
90

Figure 13

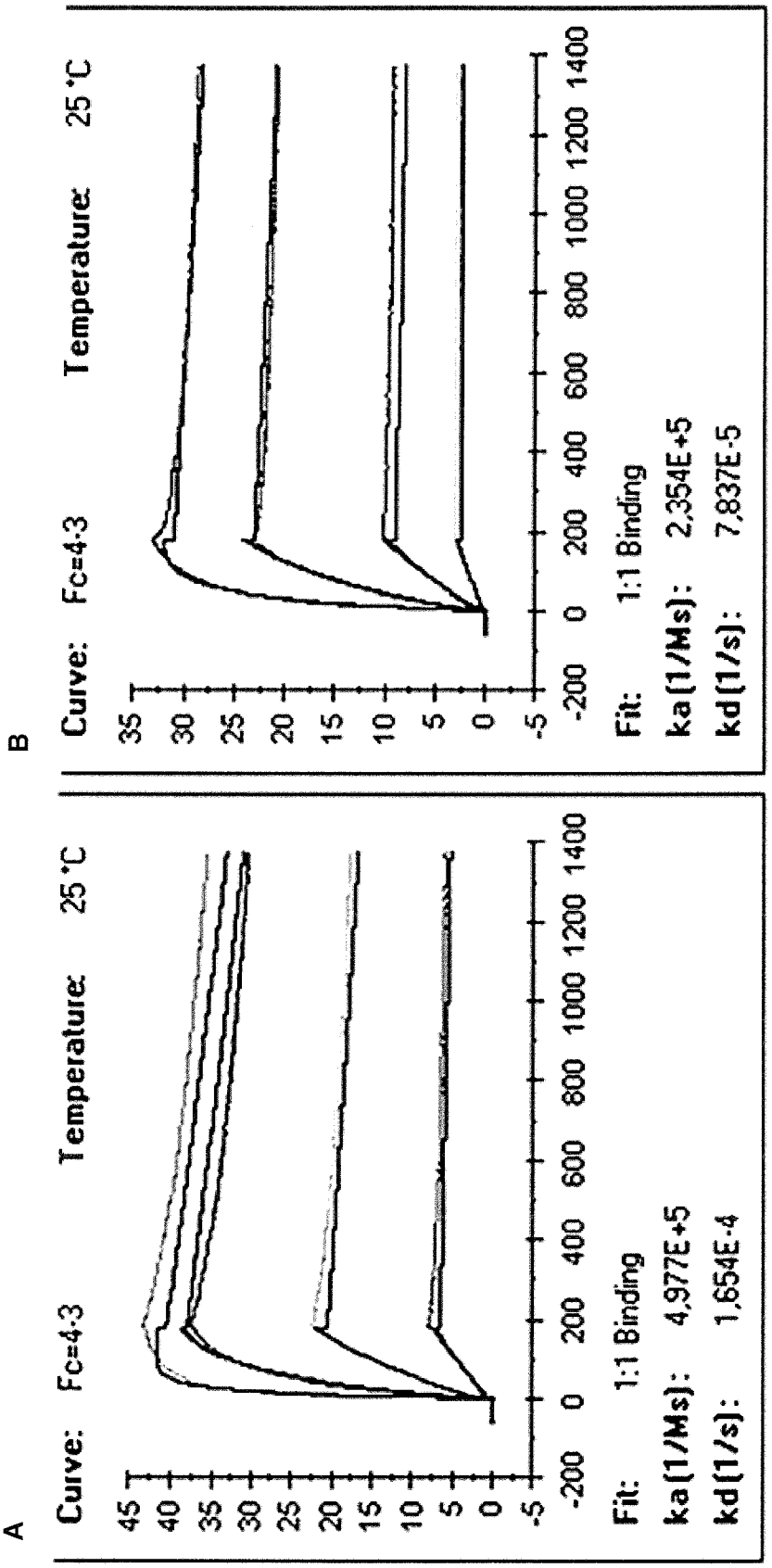

A
Curve: Fc=4-3 Temperature: 25 °C
45
40
35
30
25
20
15
10
5
0
-5
-200 0 200 400 600 800 1000 1200 1400
Fit: 1:1 Binding
ka(1/Ms): 4,977E+5
kd(1/s): 1,654E-4
B
Curve: Fc=4-3 Temperature: 25 °C
35
30
25
20
15
10
5
0
-5
-200 0 200 400 600 800 1000 1200 1400
Fit: 1:1 Binding
ka(1/Ms): 2,354E+5
kd(1/s): 7,837E-5

Figure 13 (cont'd)

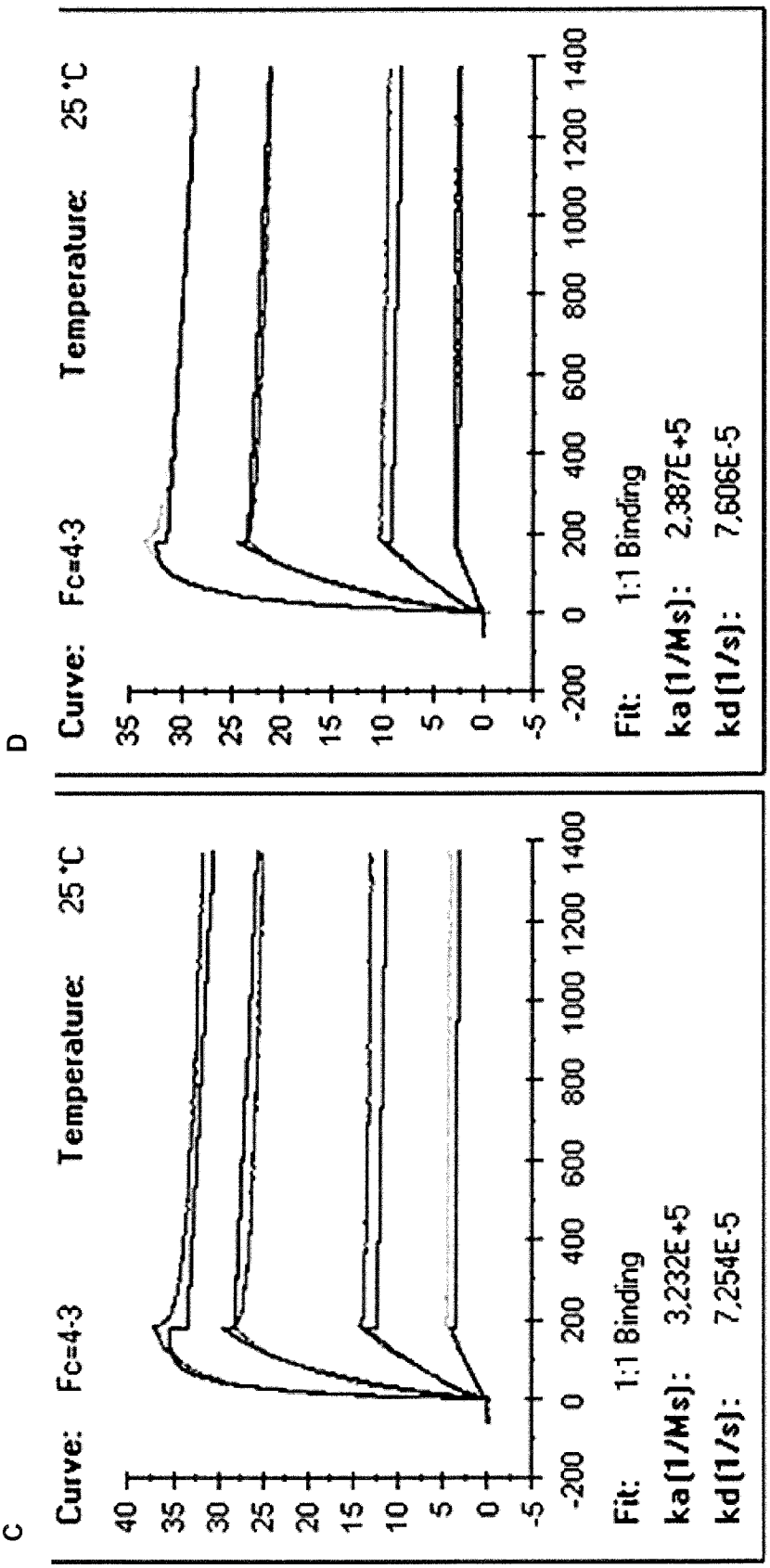


Figure 13 (cont'd)

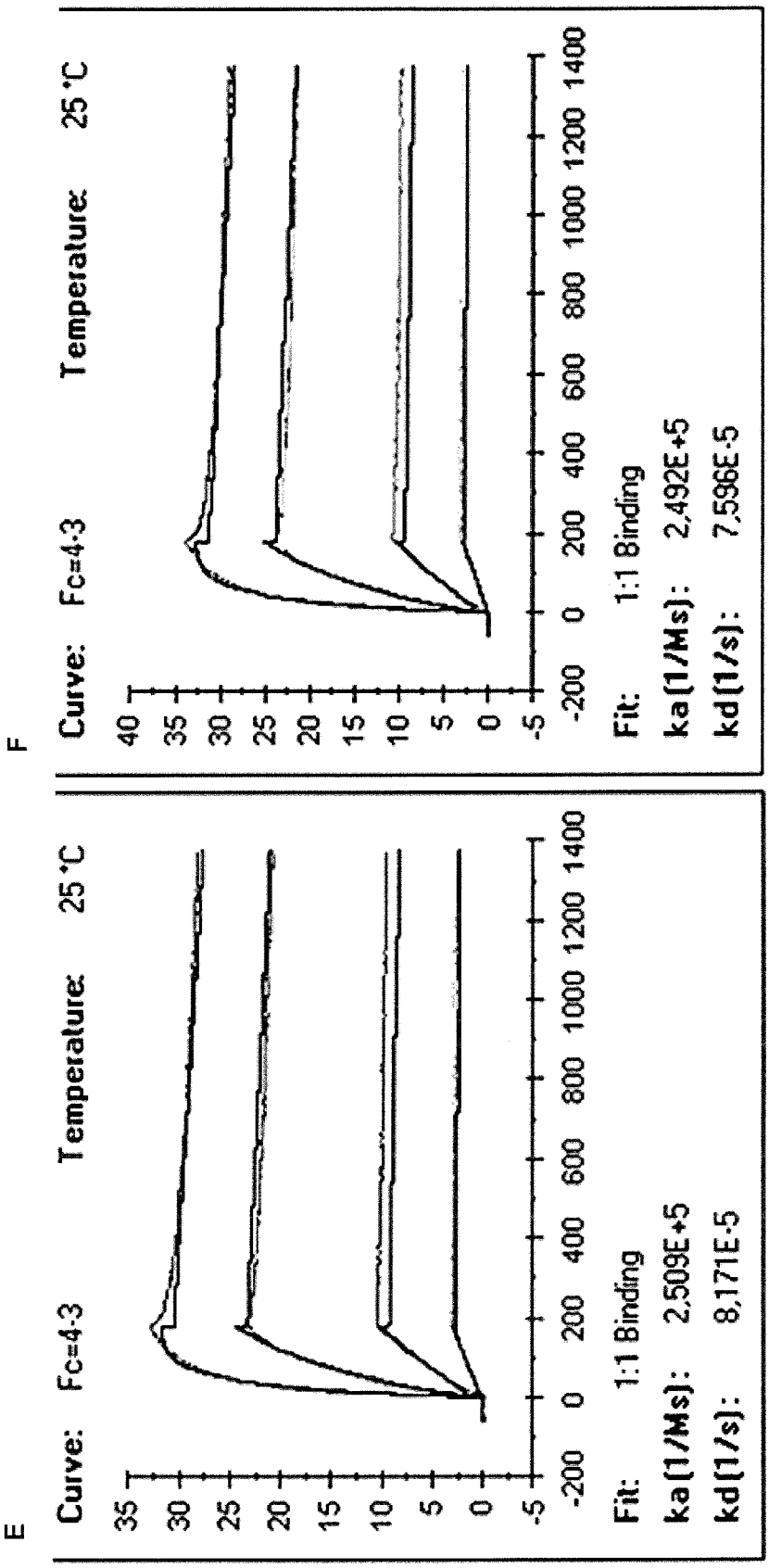


Figure 13 (cont'd)

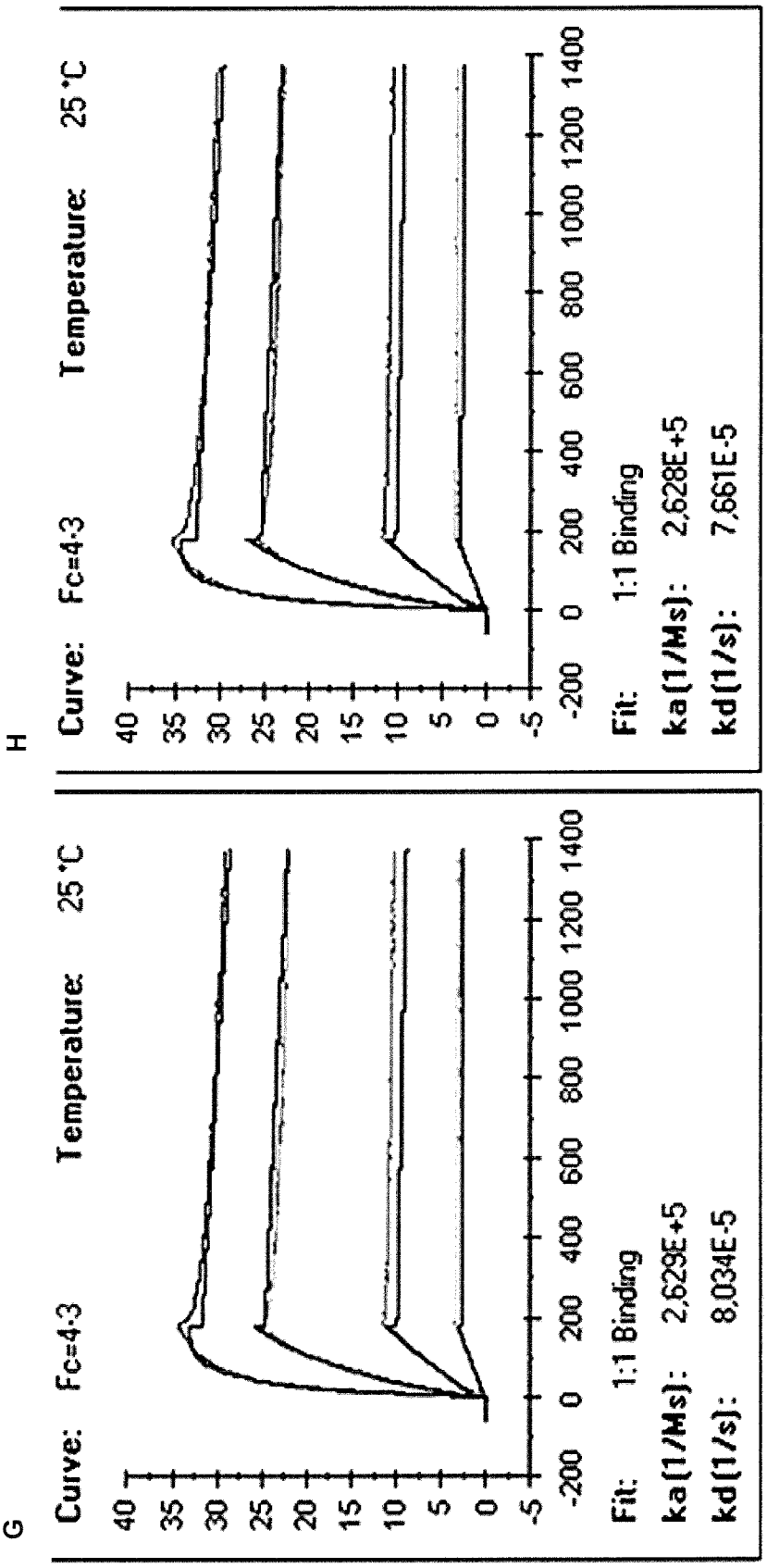


Figure 13 (cont'd)

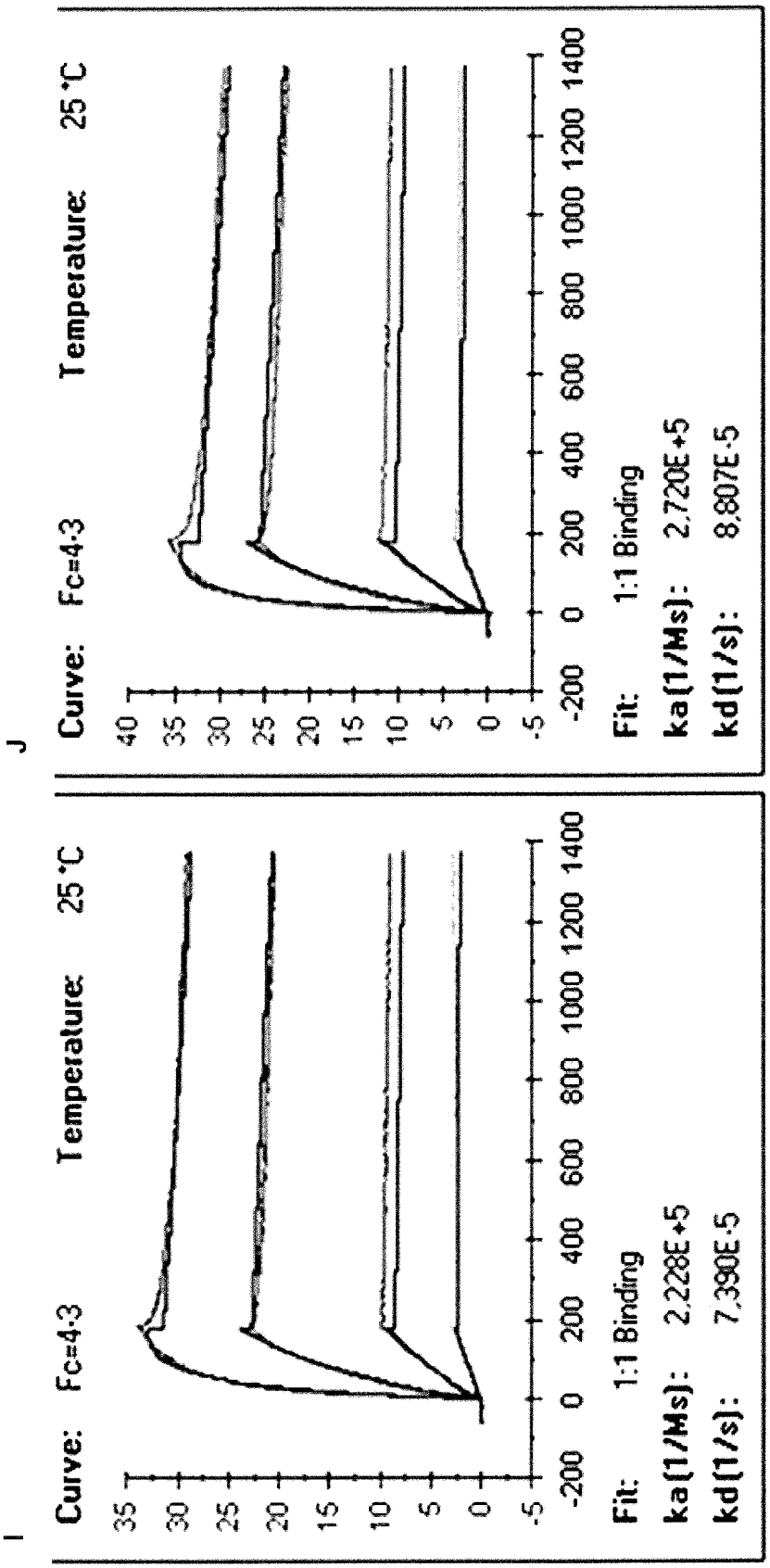


Figure 14

Molecule	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47
SEQ ID NO: 1	H	H	L	L	A	S	D	E	E	I	Q	D	V	S	G	T	W	Y	L	K	A	M	T	V	D	R	E	F	P	E	M	N	L	E	S	V	T	P	M	T	L	T	T	L	E	G	G
SEQ ID NO: 13					A	S	D	E	E	I	Q	D	V	S	G	T	W	Y	L	K	A	M	T	V	D	F	S	R	G	D	A	I	W	T	S	V	T	P	M	T	L	T	T	L	E	G	G
SEQ ID NO: 63					A	S	D	E	E	I	Q	D	V	S	G	T	W	Y	L	K	A	M	T	V	D	F	S	R	G	D	A	I	W	T	S	V	T	P	M	T	L	T	T	L	E	G	G
SEQ ID NO: 64					A	S	D	E	E	I	Q	D	V	S	G	T	W	Y	L	K	A	M	T	V	D	F	S	R	G	D	A	I	W	T	S	V	T	P	M	T	L	T	T	L	E	G	G
SEQ ID NO: 65					A	S	D	E	E	I	Q	D	V	S	G	T	W	Y	L	K	A	M	T	V	D	F	S	R	G	D	A	I	W	T	S	V	T	P	M	T	L	T	T	L	E	G	G
SEQ ID NO: 66					A	S	D	E	E	I	Q	D	V	S	G	T	W	Y	L	K	A	M	T	V	D	F	S	R	G	D	A	I	W	T	S	V	T	P	M	T	L	T	T	L	E	G	G
SEQ ID NO: 67					A	S	D	E	E	I	Q	D	V	S	G	T	W	Y	L	K	A	M	T	V	D	F	S	R	G	D	A	I	W	T	S	V	T	P	M	T	L	T	T	L	E	G	G
SEQ ID NO: 68					A	S	D	E	E	I	Q	D	V	S	G	T	W	Y	L	K	A	M	T	V	D	F	S	R	G	D	A	I	W	T	S	V	T	P	M	T	L	T	T	L	E	G	G
SEQ ID NO: 69					A	S	D	E	E	I	Q	D	V	S	G	T	W	Y	L	K	A	M	T	V	D	F	S	R	G	D	A	I	W	T	S	V	T	P	M	T	L	T	T	L	E	G	G
SEQ ID NO: 70					A	S	D	E	E	I	Q	D	V	S	G	T	W	Y	L	K	A	M	T	V	D	F	S	R	G	D	A	I	W	T	S	V	T	P	M	T	L	T	T	L	E	G	G
SEQ ID NO: 71					A	S	D	E	E	I	Q	D	V	S	G	T	W	Y	L	K	A	M	T	V	D	F	S	R	G	D	A	I	W	T	S	V	T	P	M	T	L	T	T	L	E	G	G
SEQ ID NO: 22					A	S	D	E	E	I	Q	D	V	S	G	T	W	Y	L	K	A	M	T	V	D	F	S	R	G	D	A	I	W	T	S	V	T	P	M	T	L	T	T	L	E	G	G
SEQ ID NO: 62					A	S	D	E	E	I	Q	D	V	S	G	T	W	Y	L	K	A	M	T	V	D	R	F	K	I	A	S	W	P	R	S	V	T	P	M	T	L	T	T	L	E	G	G
																								V	D	R	F	K	I	A	S	W	P	R	S	V	T	P	M	T	L	T	T	L	E	G	G

Figure 14 (cont'd)

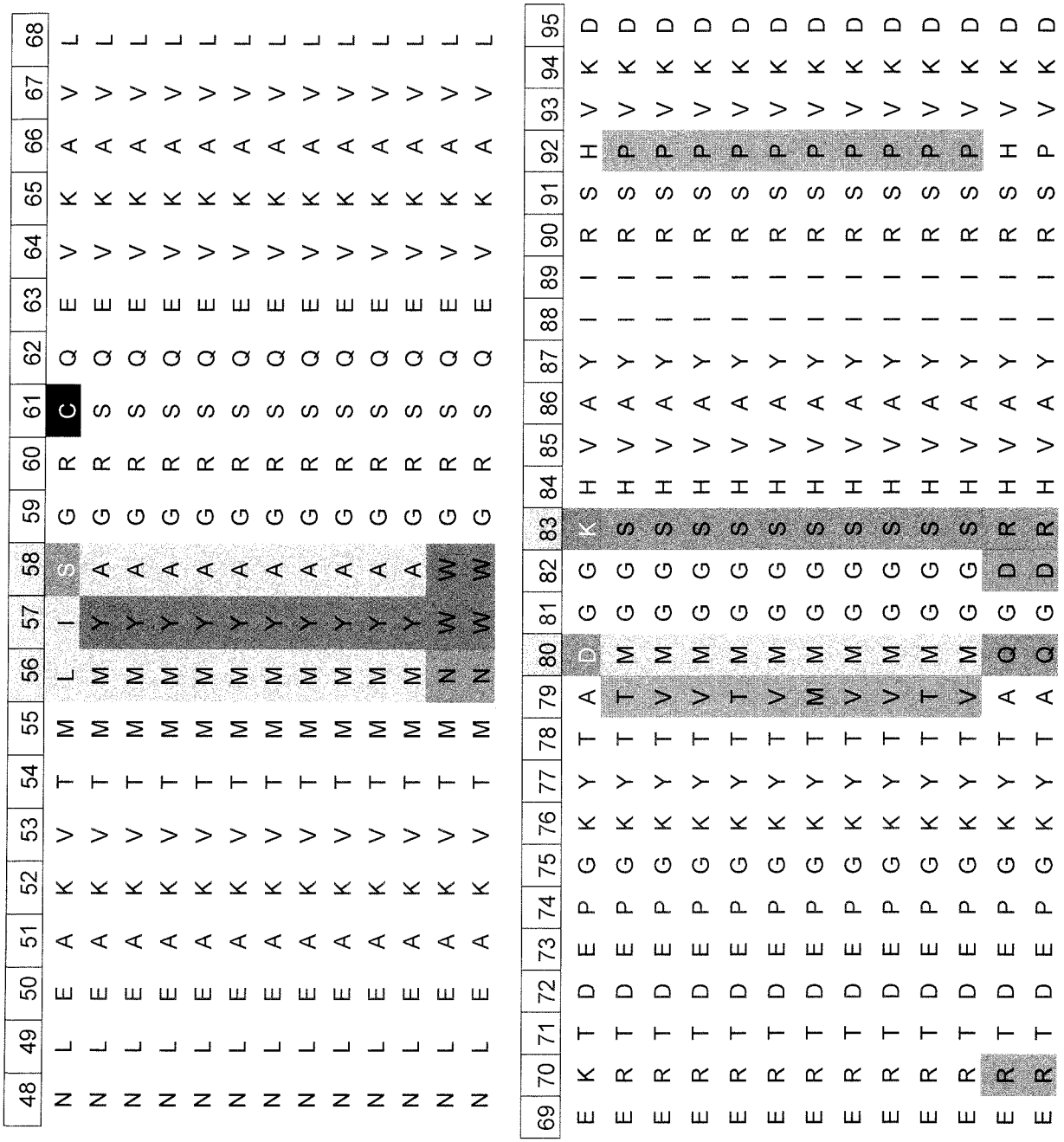
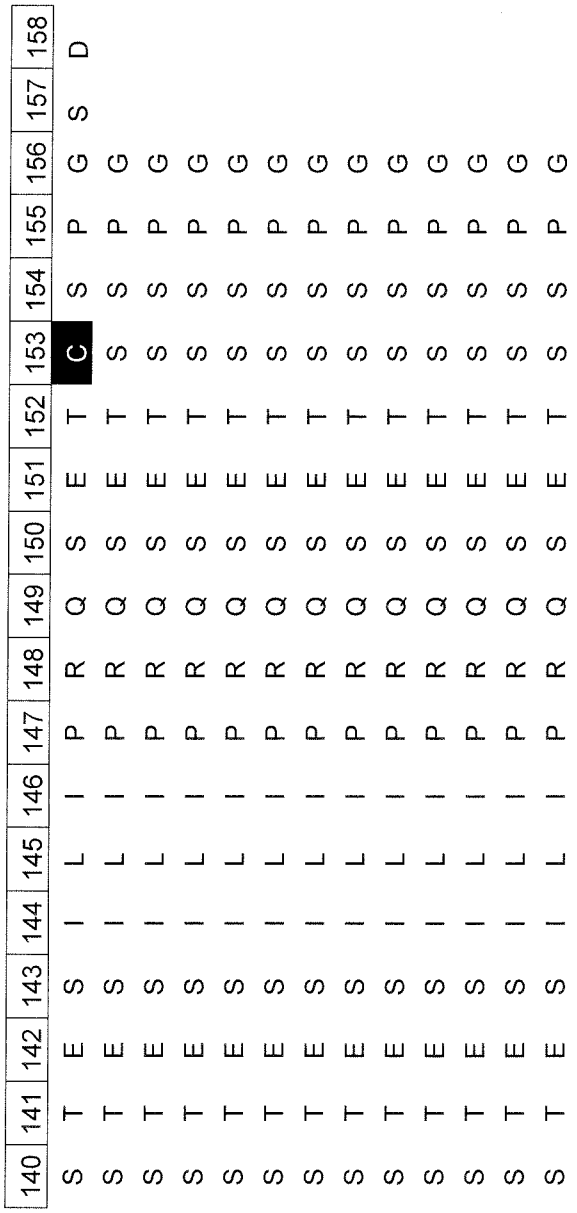


Figure 14 (cont'd)

96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117
H	Y	I	F	Y	C	E	G	E	L	H	G	K	P	V	R	G	V	K	L	V	G
H	Y	I	F	Y	S	E	G	P	H	Q	G	A	P	V	P	G	V	W	L	V	G
H	Y	I	F	Y	S	E	G	P	G	Q	G	A	P	V	P	G	V	W	L	V	G
H	Y	I	F	Y	S	E	G	P	R	Q	G	A	P	V	P	G	V	W	L	V	G
H	Y	I	F	Y	S	E	G	P	A	Q	G	A	P	V	P	G	V	W	L	V	G
H	Y	I	F	Y	S	E	G	P	D	Q	G	A	P	V	P	G	V	W	L	V	G
H	Y	I	F	Y	S	E	G	P	V	Q	G	A	P	V	P	G	V	W	L	V	G
H	Y	I	F	Y	S	E	G	P	P	Q	G	A	P	V	P	G	V	W	L	V	G
H	Y	I	F	Y	S	E	G	P	K	Q	G	A	P	V	P	G	V	W	L	V	G
H	Y	I	F	Y	S	E	G	P	R	Q	G	A	P	V	P	G	V	W	L	V	G
H	Y	I	F	Y	S	E	G	P	L	Q	G	A	P	V	P	G	V	W	L	V	G
H	Y	I	F	Y	S	E	G	N	L	Q	G	E	T	V	P	G	V	W	L	V	G
H	Y	I	F	Y	S	E	G	N	L	Q	G	E	T	V	P	G	V	W	L	V	G

118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139
R	D	P	K	N	N	L	E	A	L	E	D	F	E	K	A	A	G	A	R	G	L
R	D	P	K	N	N	L	E	A	L	E	D	F	E	K	A	A	G	A	R	G	L
R	D	P	K	N	N	L	E	A	L	E	D	F	E	K	A	A	G	A	R	G	L
R	D	P	K	N	N	L	E	A	L	E	D	F	E	K	A	A	G	A	R	G	L
R	D	P	K	N	N	L	E	A	L	E	D	F	E	K	A	A	G	A	R	G	L
R	D	P	K	N	N	L	E	A	L	E	D	F	E	K	A	A	G	A	R	G	L
R	D	P	K	N	N	L	E	A	L	E	D	F	E	K	A	A	G	A	R	G	L
R	D	P	K	N	N	L	E	A	L	E	D	F	E	K	A	A	G	A	R	G	L
R	D	P	K	N	N	L	E	A	L	E	D	F	E	K	A	A	G	A	R	G	L
R	D	P	K	N	N	L	E	A	L	E	D	F	E	K	A	A	G	A	R	G	L
R	D	P	K	N	N	L	E	A	L	E	D	F	E	K	A	A	G	A	R	G	L
R	D	P	K	N	N	L	E	A	L	E	D	F	E	K	A	A	G	A	R	G	L
R	D	P	K	N	N	L	E	A	L	E	D	F	E	K	A	A	G	A	R	G	L

Figure 14 (cont'd)



INTERNATIONAL SEARCH REPORT

International application No
PCT/EP2014/055013

A. CLASSIFICATION OF SUBJECT MATTER
INV. A61K39/00 C07K14/435 C07K14/47
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)
A61K 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, BIOSIS, Sequence Search, EMBASE, FSTA, WPI Data

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 2011/154420 A2 (PIERIS AG [DE]; HOHLBAUM ANDREAS [DE]; BAEHRE ALEXANDRA [NL]; MATSCHIN) 15 December 2011 (2011-12-15)	22,25, 26, 43-46, 48,50, 55,57,63
Y	the whole document	51-54
X	-& DATABASE REGISTRY [Online] CHEMICAL ABSTRACTS SERVICE, COLUMBUS, OHIO, US; 15 December 2011 (2011-12-15), Seq ID No: 21 of WO 2011/154420: "Lipocalin 1 [9-arginine]", XP002726601, Database accession no. 1352249-02-5 -/--	22

[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
3 July 2014	21/07/2014

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	Voigt-Ritzer, Heike

1

Form PCT/ISA/210 (second sheet) (April 2005)

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	-& DATABASE REGISTRY [Online] CHEMICAL ABSTRACTS SERVICE, COLUMBUS, OHIO, US; Seq ID No: 21 of WO 2011/154420: "Lipocalin 1 [87-cystein]", XP002726602, Database accession no. 1352249-12-7	25
X	-& DATABASE REGISTRY [Online] CHEMICAL ABSTRACTS SERVICE, COLUMBUS, OHIO, US; Seq ID No: 21 of WO 2011/154420: "Lipocalin 1 [10-cystein]", XP002726603, Database accession no. 1352249-03-6	26

X	WO 2008/125623 A2 (NOVARTIS AG [CH]; MIKHAILOV DMITRI [US]; YOWE DAVID LANGDON [US]; FLEM) 23 October 2008 (2008-10-23)	1-12, 38-46, 48,50, 55,57-63
Y	example 5 page 1, line 5 - line 20	47,49,56

Y	SCHLEHUBER STEFFEN ET AL: "Anticalins in drug development", BIODRUGS: CLINICAL IMMUNOTHERAPEUTICS, BIOPHARMACEUTICALS AND GENE THERAPY, ADIS INTERNATIONAL, FR, vol. 19, no. 5, 1 January 2005 (2005-01-01), pages 279-288, XP009101206, ISSN: 1173-8804, DOI: 10.2165/00063030-200519050-00001	47,49,56
A	abstract page 281, column 2, paragraph 2 - page 282, column 1, paragraph 2 page 284, column 2, paragraph 3 - page 286, column 1, paragraph 3	1-46,48, 50-55, 57-63

Y	BASAK AJOY ET AL: "Proprotein Convertase Subtilisin Kexin9 (PCSK9): A Novel Target For Cholesterol Regulation", PROTEIN AND PEPTIDE LETTERS, BENTHAM SCIENCE PUBLISHERS, NL, vol. 19, no. 6, 1 January 2012 (2012-01-01), pages 575-585, XP008155110, ISSN: 0929-8665, DOI: 10.2174/092986612800494020	47,49, 51-54,56
A	the whole document	1-46,48, 50,55, 57-63

	-/--	

1

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	PALMER-SMITH H ET AL: "Regulatory effects of peptides from the pro and catalytic domains of proprotein convertase subtilisin/kexin 9 (PCSK9) on low-density lipoprotein receptor (LDL-R)", CURRENT MEDICINAL CHEMISTRY, BENTHAM SCIENCE PUBLISHERS, NL, vol. 17, no. 20, 1 January 2010 (2010-01-01), pages 2168-2182, XP009166099, ISSN: 0929-8673 the whole document -----	1-63

1

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No
PCT/EP2014/055013

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 2011154420 A2	15-12-2011	AU 2011263786 A1	29-11-2012
		CA 2800026 A1	15-12-2011
		CN 103038249 A	10-04-2013
		EP 2580236 A2	17-04-2013
		JP 2013537400 A	03-10-2013
		SG 186161 A1	30-01-2013
		US 2013085113 A1	04-04-2013
		WO 2011154420 A2	15-12-2011
WO 2008125623 A2	23-10-2008	AR 066042 A1	22-07-2009
		AU 2008237940 A1	23-10-2008
		CA 2681428 A1	23-10-2008
		CN 101679527 A	24-03-2010
		CO 6231040 A2	20-12-2010
		EA 200901376 A1	30-12-2010
		EC SP099688 A	30-11-2009
		EP 2137218 A2	30-12-2009
		GT 200900264 A	12-08-2011
		JP 2010523135 A	15-07-2010
		KR 20100019440 A	18-02-2010
		MA 31304 B1	01-04-2010
		PE 01452009 A1	23-04-2009
		TW 200906439 A	16-02-2009
		US 2010233177 A1	16-09-2010
		WO 2008125623 A2	23-10-2008
		ZA 200906489 A	26-05-2010

摘要

本发明涉及新颖的脂质运载蛋白突变蛋白，其與 PCSKP 结合。本发明还提供了相应的核酸分子，其编码脂质运载蛋白突变蛋白和，脂质运载蛋白突变蛋白的制备方法以及它们的编码核酸分子。