Abstract:

Novel antibodies and antigen binding fragments that specifically bind to clusterin are described. In some embodiments, the antibodies block the biological activity of clusterin and are useful in composition in certain cancers, more particularly in cancers, such as endometrial carcinoma, breast carcinoma, hepatocellular carcinoma, prostate carcinoma, a renal cell carcinoma, ovarian carcinoma, pancreatic carcinoma, and colorectal carcinoma. The invention also relates to cells expressing the humanized or hybrid antibodies. Additionally, methods of detecting and treating cancer using the antibodies and fragments are also disclosed.
TITLE: ANTI-CLUSTERIN ANTIBODIES AND ANTIGEN BINDING FRAGMENTS AND THEIR USE TO REDUCE TUMOR VOLUME

FIELD OF THE INVENTION

The invention relates to anti-clusterin antibodies and their use to reduce tumor volume. The invention more particularly relates to humanized antibodies, hybrid antibodies and antigen binding fragment which bind to clusterin and their use to reduce tumor volume, to inhibit tumor growth and metastasis.

BACKGROUND OF THE INVENTION

Carcinomas, the most common human malignancy, arise from epithelial cells. Progression of epithelial cancers begins with the disruption of cell-cell contacts as well as the acquisition of a migratory (mesenchymal-like) phenotype. This phenomenon, which is called an epithelial-to-mesenchymal transition (EMT), is considered to be a crucial event in late stage tumor progression and metastasis.

The secreted protein TGF-β suppresses tumor growth initially largely due to its growth inhibitory action on tumor cells of epithelial origin, then at later stages promotes tumor cell progression and metastasis. One mechanism by which TGF-β can promote tumor progression is through the induction of an EMT.

Due to the dual role that TGF-β plays in carcinogenesis, direct inhibitors of TGF-β may be risky since, while they could benefit late stage tumors, they could also accelerate preneoplastic lesions. A better therapeutic may be one that inhibits the pro-oncogenic EMT-promoting action of TGF-β, while leaving the tumor suppressor growth-inhibitory action of TGF-β unaffected. To develop such an inhibitor it would be necessary to identify the point at which there is a bifurcation of the TGF-β signaling pathway such that the mediators in one branch of the pathway participate in the EMT response, but not the growth inhibitory response to TGF-β. Therapeutics that inhibit mediators that lie exclusively in the EMT-promoting branch of the TGF-β signaling pathway will reduce metastasis while having little or no effect on the acceleration of preneoplastic lesions.

No TGF-β signal pathway specific components have been generally identified that promote or mediate the EMT-promoting action of TGF-β, yet are not involved in the growth inhibitory action of TGF-β.
In contrast, an endogenous protein (the YY1 nuclear factor) has been identified that is able to interfere with (as opposed to promote) the protumorigenic EMT action of TGF-β, while leaving the tumor-suppressing action (growth inhibition) intact (Kurisaki et al., 2004).

Inhibitors that target TGF-β ligands, receptors and the Smad signaling proteins are known. Specifically, soluble receptor ectodomains, antibodies and other binding proteins are able to act as antagonists by interacting with TGF-β ligands and sequestering them away from cell surface receptors. Small molecules are available that inhibit the kinase activity of the Type I TGF-β receptor and endogenous inhibitors of the Smad signaling proteins are also known. Since all of these signaling pathway components are involved in both the pro- and anti-carcinogenic actions of TGF-β, these inhibitors that target them may benefit late stage tumors, however, they could also accelerate preneoplastic lesions.

International patent application No. PCT/CA2006/001505 filed on September 13, 2006 and published on March 22, 2007 under No. WO2007/030930 describes anti-clusterin antibodies and antigen binding fragments that are directed to a specific epitope of clusterin and that are capable of inhibiting epithelial-to-mesenchymal transition of carcinoma cells. This patent application more particularly shows the ability of anti-clusterin antibodies at inhibiting EMT in prostate carcinoma and breast carcinoma.

**SUMMARY OF THE INVENTION**

The present invention relates in one aspect thereof to an antibody which is capable of specific binding to clusterin and which comprises a humanized light chain variable region and/or a humanized heavy chain variable region.

More particularly, the present invention provides a humanized antibody of a non-human parent antibody that is capable of specific binding to clusterin as well as hybrid antibodies and antigen binding fragment thereof.

The humanized or hybrid antibodies of the present invention comprise light chain variable region and a heavy chain variable region which may include non-human complementarity determining region amino acid residues and human framework region amino acid residues of a natural human antibody.

The present invention also relates to an antigen binding fragment comprising a light chain variable region and a heavy chain variable region, which may include non-human complementarity determining region amino acid residues and human framework region amino acid residues.
The antibodies and antigen binding fragment of the present invention may be used to inhibit epithelial-to-mesenchymal transition induced by clusterin.

In another aspect, the present invention relates to an anti-clusterin antibody (a polyclonal antibody, a monoclonal antibody, a chimeric antibody, a humanized antibody, an isolated human antibody, a hybrid antibody or a fragment thereof) for use in reducing tumor volume and methods for doing so.

Also encompassed by the present invention are isolated nucleic acids encoding the light chain variable region and/or the heavy chain variable region of the humanized antibody, the hybrid antibody or the antigen binding fragment described herein or the isolated antibody described herein.

Also encompassed herewith is a vector or construct, comprising the nucleic acid described herein. In accordance with the present invention, the vector may be, for example and without limitation, a mammalian expression vector, a bacterial expression vector etc.

The invention also relates to cells comprising or expressing the antibody or antigen binding fragment of the present invention or comprising the nucleic acids or vectors of the present invention.

In yet a further aspect, the present invention provides a kit comprising a vial or vials which may comprise, for example, the humanized antibody described herein, the hybrid antibody described herein, the antigen binding fragment described herein, the isolated antibody described herein, the isolated nucleic acid described herein or the vector described herein.

In another aspect, the present invention relates to a pharmaceutical composition which may comprise, for example, the humanized antibody described herein, the hybrid antibody described herein, the antigen binding fragment described herein or the isolated antibody described herein and a pharmaceutically acceptable carrier.

Yet another aspect of the invention relates to a combination therapy which includes the pharmaceutical composition described herein and a chemotherapeutic agent.

Also encompassed herewith are methods of producing humanized or hybrid anti-clusterin antibodies or antigen binding fragments as well as method of treating a disease associated with clusterin expression or secretion using the humanized or hybrid anti-clusterin antibodies or antigen binding fragments.
Further scope, applicability and advantages of the present invention will become apparent from the non-restrictive detailed description given hereinafter. It should be understood, however, that this detailed description, while indicating exemplary embodiments of the invention, is given by way of example only, with reference to the accompanying drawings.

5 BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1. Homology 3D model of the variable region of the mouse 16B5 anti-clusterin antibody. CDRs are labeled (L1, L2, L3 in the light chain, and H1, H2, H3 in the heavy chain). Mouse framework residues replaced by human framework residues are indicated as sphere models.

Figure 2. Sequence alignment of the mouse 16B5, humanized 16B5 and the selected human framework (NCBI database links provided). Kabat numbering is shown at the top. CDRs are highlighted. Candidate residues for back-mutations are highlighted below the sequence alignment according to proximity to CDRs (5: within 5 Angstrom), surface exposure (B: Buried), and contact with the pairing variable domain.

Figure 3. Kinetic analysis of 16B5 murine and humanized anti-clusterin antibodies.

Figure 4. hl6B5 blocks the migration of cancer cell lines. The hl6B5 is at least as active as the mouse 16B6 in the scratch assay against mouse mammary carcinoma cells. The figure shows the ability of the antibodies in various configurations to block the migration of the cells in vitro.

Figure 5. Inhibition of hl6B5 reduces the invasiveness of human prostate cancer cells. The bottom of 12-well plates was covered with 200 µL Growth factor reduced matrigel (Becton Dickinson). Cells (2.5 x 10⁴) were resuspended in 200 µL matrigel, which was layered on top of this, and finally 500 µL of cell specific growth medium was added on top of the matrigel. hl6B5 was added to every layer of matrigel as well as the medium in a concentration of 8 µg/mL. Plates were incubated at 37°C for up to 3 weeks during which the growth medium (+/- hl6B5) was replenished weekly. The arrows indicate the areas of epithelial-like cells.

Figure 6. Treatment of prostate cancer tumors with hl6B5 reduces the growth of the tumors and increases their response to chemotherapy. DU145 prostate cancer cells (2 x 10⁶) were implanted s.c. into SCID mice and allowed to grow until the tumor sizes were approximately 100 mm³. Tumors were measured bi-weekly with a digital caliper and tumor volumes were calculated as L x W x H. Each group contained 8 animals that were randomized
prior to the beginning of the treatments. The results were expressed as mm$^3 \pm $ SEM. The $P$ values were calculated using the Student's T test.

**Figure 7** Homology 3D model of the variable region of the mouse 21B12 anti-clusterin antibody. CDRs are labeled (L1, L2, L3 in the light chain, and H1, H2, H3 in the heavy chain). Mouse framework residues replaced by human framework residues are indicated as sphere models.

**Figure 8.** Sequence alignment of the mouse 16B5, humanized 21B12 and the selected human framework (NCBI database links provided). Kabat numbering is shown at the top. CDRs are highlighted. Candidate residues for back-mutations are highlighted below the sequence alignment according to proximity to CDRs (5: within 5 Angstrom), surface exposure (B: Buried), and contact with the pairing variable domain.

**Figure 9.** Kinetic analysis of the 21B12 murine and humanized anti-clusterin antibodies.

**Figure 10.** *hl6B5 inhibits the growth of PC-3 prostate tumors.* PC-3 prostate cancer cells ($2 \times 10^6$) were implanted s.c. into SCID mice and allowed to grow until the tumor sizes were approximately 100 mm$^3$. Tumors were measured bi-weekly with a digital caliper and tumor volumes were calculated as $L \times W \times H$. Each group contained 8 animals that were randomized prior to the beginning of the treatments. The results were expressed as mm$^3 \pm $ SEM.

**Figure 11.** *Clusterin is expressed in human pancreatic tumors.* Tumors derived from pancreatic cancer cell lines (as indicated) were grown in SCID mice, harvested, fixed in formalin, sections and examined using immunohistochemistry with hl6B5. Positive staining was visualized by standard methods using a HRP-conjugated secondary antibody. The negative control was performed under identical conditions with an isotype control antibody.

**Figure 12.** *H16B5 inhibits the migration of pancreatic cancer cell lines.* PANC-1 cells were seeded in serum-free medium in the upper chamber of a 24-well Transwell plate containing a Matrigel barrier. The lower wells were filled with medium containing 10% FBS as a chemo-attractant. After a 24h incubation in the presence or absence of TGFβ and/or hl6B5 (as indicated), the number of cells in the Matrigel layer were stained and counted.

**Figure 13.** *Secreted clusterin is internalized in cancer cells.* Recombinant human clusterin was expressed in 293-6E cells, purified, and labelled with Alexa Fluor 488 using a commercial labelling kit (Invitrogen). BRI-JM01 mouse mammary carcinoma cells were seeded on coverslips and treated with 250 ng/ml of labelled secreted clusterin. At the indicated times, the cells were washed with ice-cold PBS and fixed in 2% paraformaldehyde.
The slides were mounted with Antifade Gold and images were generated with a fluorescence microscope.

**Figure 14.** H16B5 inhibits the internalization of secreted clusterin in cancer cells. The experiment was performed as described for Figure 13. H16B5 was added at 10 µg/ml.

**Figure 15.** Shows the region of homology between human clusterin (NP_001822) and murine clusterin (NP_038520).

**Figure 16.** Shows the binding of h16B5 (labeled as AB-16B5 in the figure) to murine clusterin that is expressed in fixed frozen sections generated from 4T1 mouse mammary tumors. The experiment was performed using immunohistochemistry and detection was accomplished using a HRP-conjugated secondary antibody.

**DETAILED DESCRIPTION OF THE INVENTION**

The present invention relates in one aspect thereof to antibodies which are capable of specific binding to clusterin and which comprise a humanized light chain variable region and/or a humanized heavy chain variable region.

The sequence of human clusterin may be found at RefSeq accession number; NM_001831.2 (protein id.: NP_001822) whereas the sequence of murine clusterin may be found at RefSeq accession number; NM_013492.2 (protein id.: NP_038520).

The antibodies or antigen binding fragment of the present invention may be able to bind to the murine and/or the human form of clusterin. The antibodies or antigen binding fragment of the present invention may also be able to bind naturally occurring variant as well as synthetic variants of clusterin having for example at least 75% (e.g., 80%, 85%, 90%, 95%, 99%) amino acid identity with human or murine clusterin.

The present invention therefore provides a humanized antibody of a non-human parent antibody that is capable of specific binding to clusterin or an antigen binding fragment thereof as well as hybrid antibodies and antigen binding fragments thereof.

In accordance with an embodiment of the invention, the humanized or hybrid antibody may inhibit (lower) the growth of a tumor cell expressing or secreting clusterin.

In accordance with a further embodiment of the invention, the humanized or hybrid antibody may reduce the volume of a tumor comprising cells expressing or secreting clusterin.
In accordance with another embodiment of the invention, the humanized or hybrid antibody may inhibit (lower) migration or invasion of a tumor cell expressing or secreting clusterin.

Therefore in accordance with yet another embodiment of the invention, the humanized or hybrid antibody may inhibit (lower) metastasis occurring from a tumor cell expressing or secreting clusterin.

In another aspect, the present invention relates to a method for reducing the volume of a tumor comprising clusterin-expressing cells which may comprise administering an anti-clusterin antibody (a polyclonal antibody, a monoclonal antibody, a chimeric antibody, a humanized antibody, an isolated human antibody, a hybrid antibody or a fragment thereof) to a mammal in need. The method more particularly contemplates administering a chimeric, humanized or hybrid antibody.

In one embodiment, the hybrid antibody or fragment thereof may comprise, for example, a light chain variable region of a non-human antibody and a heavy chain variable region of a humanized antibody.

In another embodiment, the hybrid antibody or fragment thereof may comprise, for example, a light chain variable region of a non-human antibody and a heavy chain variable region of a humanized antibody.

The term "antibody" refers to intact antibody, monoclonal, (fully or partially) humanized, hybrid, chimeric or polyclonal antibodies as well as isolated human antibodies. The term "antibody" also encompasses multispecific antibodies such as bispecific antibodies. Human antibodies are usually made of two light chains and two heavy chains each comprising variable regions and constant regions. The light chain variable region comprises 3 CDRs, identified herein as CDRL1, CDRL2 and CDRL3 flanked by framework regions. The heavy chain variable region comprises 3 CDRs, identified herein as CDRH1, CDRH2 and CDRH3 flanked by framework regions.

The term "humanized antibody" refers to an antibody comprising from one to six CDR(s) comprising non-human CDR amino acid residues and substantial portion of its heavy chain and/or light chain framework region that is from the human antibody repertoire. In some instance, the totality of the heavy chain and/or light chain framework region of the humanized antibody may be identical to those of an antibody that is encoded (encodable) by the human antibody repertoire (a natural human antibody). In other instances, the heavy chain and/or light chain framework region of the humanized antibody may comprises from one to thirty amino acids from the non-human antibody which is sought to be humanized and the remaining
portion being of from a natural human antibody. In additional instances, the humanized antibody may comprise from 1 to 6 fully non-human CDRs and often the six CDRs are fully non-human. In yet other instances, a "humanized antibody" may comprise a constant region that is or human or other origin (from a mammal).

The term "hybrid antibody" refers to an antibody comprising one of its heavy or light chain variable region (its heavy or light chain) that is humanized or from a natural human antibody (having affinity for clusterin) while the other of the heavy or light chain variable region (the heavy or light chain) remains non-human.

The term "chimeric antibody" refers to an antibody having non-human variable region(s) and human constant region.

The term "natural human antibody" refers to an antibody that is encoded (encodable) by the human antibody repertoire, i.e., germline sequence.

As used herein, an isolated human antibody is "derived from" a particular germline sequence if the antibody is obtained from a system using human immunoglobulin sequences, e.g., by immunizing a transgenic mouse carrying human immunoglobulin genes or by screening a human immunoglobulin gene library. An isolated human antibody that is "derived from" a human germline immunoglobulin sequence can be identified as such by comparing the amino acid sequence of the human antibody to the amino acid sequence of human germline immunoglobulins. A selected human antibody typically is at least 90% identical in amino acids sequence to an amino acid sequence encoded by a human germline immunoglobulin gene and contains amino acid residues that identify the human antibody as being human when compared to the germline immunoglobulin amino acid sequences of other species (e.g., murine germline sequences). In certain cases, a human antibody may be at least 95%, or even at least 96%, 97%, 98%, or 99% identical in amino acid sequence to the amino acid sequence encoded by the germline immunoglobulin gene. Typically, a human antibody derived from a particular human germline sequence will display no more than 10 amino acid differences from the amino acid sequence encoded by the human germline immunoglobulin gene. In certain cases, the human antibody may display no more than 5, or even no more than 4, 3, 2, or 1 amino acid difference from the amino acid sequence encoded by the germline immunoglobulin gene.

The term "antigen-binding fragment", as used herein, refers to one or more fragments of an antibody that retain the ability to bind to an antigen. It has been shown that the antigen-binding function of an antibody can be performed by fragments of an intact antibody.
Examples of binding fragments encompassed within the term "antigen-binding fragment" of an antibody include (i) a Fab fragment, a monovalent fragment consisting of the $V_L$, $V_H$, $C_L$, and $C_H$ domains; (ii) a F(ab')$_2$ fragment, a bivalent fragment comprising two Fab fragments linked by a disulfide bridge at the hinge region; (iii) a Fd fragment consisting of the $V_H$ and $C_H$ domains; (iv) a Fv fragment consisting of the $V_L$ and $V_H$ domains of a single arm of an antibody, and (v) a dAb fragment (Ward et al., (1989) Nature 341:544-546), which consists of a $V_H$ domain. Furthermore, although the two domains of the Fv fragment, $V_L$ and $V_H$, are coded for by separate genes, they can be joined, using recombinant methods, by a synthetic linker that enables them to be made as a single polypeptide chain in which the $V_L$ and $V_H$ regions pair to form monovalent molecules (known as single chain Fv (scFv); see e.g., Bird et al. (1988) Science 242:423-426; and Huston et al. (1988) Proc. Natl. Acad. Sci. USA 85:5879-5883). Such single chain antibodies are also intended to be encompassed within the term "antigen-binding fragment" of an antibody. Furthermore, the antigen-binding fragments include binding-domain immunoglobulin fusion proteins comprising (i) a binding domain polypeptide (such as a heavy chain variable region, a light chain variable region, or a heavy chain variable region fused to a light chain variable region via a linker peptide) that is fused to an immunoglobulin hinge region polypeptide, (ii) an immunoglobulin heavy chain CH2 constant region fused to the hinge region, and (iii) an immunoglobulin heavy chain CH3 constant region fused to the CH2 constant region. The hinge region may be modified by replacing one or more cysteine residues with serine residues so as to prevent dimerization.

Such binding-domain immunoglobulin fusion proteins are further disclosed in US 2003/01 18592 and US 2003/0133939. These antibody fragments are obtained using conventional techniques known to those with skill in the art, and the fragments are screened for utility in the same manner as are intact antibodies.

A typical antigen binding site is comprised of the variable regions formed by the pairing of a light chain immunoglobulin and a heavy chain immunoglobulin. The structure of the antibody variable regions is very consistent and exhibits very similar structures. These variable regions are typically comprised of relatively homologous framework regions (FR) interspaced with three hypervariable regions termed Complementarity Determining Regions (CDRs). The overall binding activity of the antigen binding fragment is often dictated by the sequence of the CDRs. However, the FRs often play a role in the proper positioning and alignment in three dimensions of the CDRs for optimal antigen binding.

A humanized or hybrid antibody of the present invention may comprise a heavy chain variable region which may include non-human complementarity determining region amino
acid residues and human framework region amino acid residues of a natural human antibody and a complementary light chain.

A humanized or hybrid antibody of the present invention may comprise a light chain variable region which may include non-human complementarity determining region amino acid residues and human framework region amino acid residues of a natural human antibody and a complementary heavy chain.

A humanized or hybrid antibody of the present invention may inhibit metastasis, tumor cell migration or invasion or may inhibit the growth of clusterin-expressing cells including, for example, carcinoma cells. In fact, the Applicant came to the unexpected discovery that anti-clusterin antibodies including the humanized or hybrid antibodies of the present invention reduce tumor volume in vivo. Alternatively, the humanized or hybrid antibody of the present invention may be used to detect clusterin-expressing cells.

The natural human antibody that is selected for humanization of the non-human parent antibody may comprise a variable region having a three-dimensional structure similar to that of (superimposable to) a (modeled) variable region of the non-human parent antibody. As such, the humanized or hybrid antibody has a greater chance of having a three-dimensional structure similar to that of the non-human parent antibody.

The humanized antibody of the present invention has a high affinity for clusterin. In fact, it has been shown herein that the humanized antibody binds to recombinant monomeric clusterin with an affinity of $4.49 \times 10^{-4} \text{ M} \pm 8.5 \times 10^{-10}$ or better.

In accordance with the present invention, the human framework region amino acid residues of the humanized or hybrid antibody light chain are from a natural human antibody light chain framework region. The light chain framework region of the natural human antibody selected for humanization purposes, may have, for example, at least 70% identity with a light chain framework region of the non-human parent antibody. Preferably, the natural human antibody selected for humanization purposes may have the same or substantially the same number of amino acids in its light chain complementarity determining region to that of a light chain complementarity determining region of the non-human parent antibody.

In other embodiments of the invention, the human framework region amino acid residues of the humanized or hybrid antibody light chain are from a natural human antibody light chain framework region having at least 75, 80, 83% identity (or more) with the light chain framework region of the non-human parent antibody.
Also in accordance with the present invention, the human framework region amino acid
residues of the humanized or hybrid antibody heavy chain are from a natural human antibody
heavy chain framework region having at least 70% identity with a heavy chain framework
region of the non-human parent antibody. Preferably, the natural human antibody selected for
humanization purposes may have the same or substantially the same number of amino acids in
its heavy chain complementarity determining region to that of a heavy chain complementarity
determining region of the non-human parent antibody.

In other embodiments of the invention, the human framework region amino acid residues of
the humanized or hybrid antibody heavy chain are from a natural human antibody heavy chain
framework region having at least 73, 75, 80 % identity with the heavy chain framework
region of the non-human parent antibody.

In an embodiment of the invention, the heavy chain variable region of the humanized or
hybrid antibody may thus comprise at least one non-human complementarity determining
region.

Alternatively, in other embodiments of the invention, the heavy chain variable region of the
humanized or hybrid antibody may comprise at least two non-human complementarity
determining regions or even three non-human complementarity determining regions.

In an additional embodiment of the invention, the light chain variable region may comprise at
least one non-human complementarity determining region.

Alternatively, in yet additional embodiments of the invention, the light chain variable region
comprise at least two non-human complementarity determining regions or even three non-
human complementarity determining regions.

The humanized antibody may thus advantageously comprise all six CDRs of the non-human
antibody. In the case of a divalent humanized antibody, all twelve CDRs may be from the
non-human antibody.

Clusterin-expressing cells which may be detected by a humanized or hybrid antibody
comprises carcinoma cells. The humanized or hybrid antibody may also be used to inhibit the
growth of clusterin-expressing carcinoma cells and especially, human carcinoma cells.

Several types of human carcinoma cells have been shown to express or secrete clusterin,
amongst which, cells of endometrial carcinoma, of breast carcinoma, of hepatocellular
carcinoma, of prostate carcinoma, of renal cell carcinoma, of ovarian carcinoma, of colorectal
cancer, of pancreatic carcinoma, etc.
An exemplary embodiment of the invention includes, for example, the humanized or hybrid antibody comprising human framework region amino acid residues of the natural human antibody heavy chain as described herein and heavy chain CDR selected from the group consisting of a CDRH1 having an amino acid sequence of SEQ ID NO.:1, a CDRH2 having an amino acid sequence of SEQ ID NO.:2 and a CDRH3 having an amino acid sequence of SEQ ID NO.:3 and combination thereof or heavy chain CDR selected from the group consisting of a CDRH1 having an amino acid sequence of SEQ ID NO.:11, a CDRH2 having an amino acid sequence of SEQ ID NO.:12 and a CDRH3 having an amino acid sequence of SEQ ID NO.:13 and combination thereof.

In another exemplary embodiment, the humanized or hybrid antibody may comprise human framework region amino acid residues of the natural human antibody heavy chain as described herein and at least two heavy chain CDRs selected from the group consisting of a CDRH1 having an amino acid sequence of SEQ ID NO.:1, a CDRH2 having an amino acid sequence of SEQ ID NO.:2 and a CDRH3 having an amino acid sequence of SEQ ID NO.:3 or at least two heavy chain CDRs selected from the group consisting of a CDRH1 having an amino acid sequence of SEQ ID NO.:11, a CDRH2 having an amino acid sequence of SEQ ID NO.:12 and a CDRH3 having an amino acid sequence of SEQ ID NO.:13 and combination thereof.

Alternatively, in another exemplary embodiment, the humanized or hybrid antibody of the present invention may comprise human framework region amino acid residues of the natural human antibody heavy chain as described herein and a CDRH1 having an amino acid sequence of SEQ ID NO.:1, a CDRH2 having an amino acid sequence of SEQ ID NO.:2 and a CDRH3 having an amino acid sequence of SEQ ID NO.:3 or a CDRH1 having an amino acid sequence of SEQ ID NO.:11, a CDRH2 having an amino acid sequence of SEQ ID NO.:12 and a CDRH3 having an amino acid sequence of SEQ ID NO.:13.

In a more specific embodiment of the invention, the humanized or hybrid antibody (or any antigen binding fragment derived therefrom) may comprise a light chain variable region comprising SEQ ID NO.:26 (hl6B5 VL consensus 1):

DIVMXQSPXSALVSXGEXXXCKSSQSLNSRTRKNYLAWYQQKPGQXPKLLY

WASTRESGVPDRFXGSNGTDFLTISSXQAEDXAVYYCKQSYNLWTGFXTKLEX

K; wherein at least one of the amino acid identified by X is an amino acid substitution in comparison with a corresponding amino acid in the polypeptide set forth in SEQ ID NO.:25 (the murine 16B5 VL). The amino acid substitution may be, for example conservative or non-conservative. In accordance with the invention, the amino acid substitution may be conservative.
The humanized or hybrid antibody (or any antigen binding fragment derived therefrom) may comprise a light chain variable region comprising SEQ ID NO.:27 (16B5 VL consensus2):

DIVMX_a1QSPX_a2SLAVSX_a3GEX_a4X_5TX_a6X_a7CKSSQLLSRTRKNYLAWYQQKPGQX

a8PKLLIYWASTRESGVPDRFX_a9GSGSGTDLTTLTISSX_a0QAEDX_a11AVYYCKQSYNLW

TFGX_a12GTKLEX_a13K;

Wherein X_a1 may be a neutral hydrophilic amino acid such as for example, T or S;
Wherein X_a2 may be for example D or S;
Wherein X_a3 may be an hydrophobic amino acid such as for example, L or A;
Wherein X_a4 may be a basic amino acid such as for example R or K;
Wherein X_a5 may be an hydrophobic amino acid such as for example A or V;
Wherein X_a6 may be an hydrophobic amino acid as for example I or M;
Wherein X_a7 may be for example N or S;
Wherein X_a8 may be for example P or S;
Wherein X_a9 may be a neutral hydrophilic amino acid such as for example S or T;
Wherein X_a10 may be an hydrophobic amino acid such as for example L or V;
Wherein X_a11 may be an hydrophobic amino acid such as for example V or L;
Wherein X_a12 may be for example Q or G;
Wherein X_a13 may be for example I or F and;

wherein the light chain variable region may comprise at least one of the above amino acid substitution in comparison with SEQ ID NO.:25.

The humanized or hybrid antibody (or any antigen binding fragment derived therefrom) may comprise a light chain variable region comprising SEQ ID NO.:28 (16B5 VL consensus3):

DIVMX_a1QSPX_a2SLAVSX_a3GEX_a4X_5TX_a6X_a7CKSSQLLSRTRKNYLAWYQQKPGQX

a8PKLLIYWASTRESGVPDRFX_a9GSGSGTDLTTLTISSX_a0QAEDX_a11AVYYCKQSYNLW

TFGX_a12GTKLEX_a13K;

Wherein X_a1 may be for example, T or S;
Wherein X_a2 may be for example D or S;
Wherein X_a3 may be for example, L or A;
Wherein X_a4 may be for example R or K;
Wherein X_a5 may be for example A or V;
Wherein X_a6 may be for example I or M;
Wherein X_a7 may be for example N or S;
Wherein X_a8 may be for example P or S;
Wherein X_a9 may be for example S or T;
Wherein X_a10 may be for example L or V;
Wherein $X_{11}$ may be for example V or L;
Wherein $X_{12}$ may be for example Q or G;
Wherein $X_{13}$ may be for example I or F and;
wherein the light chain variable region may comprise at least one of the above amino acid
substitution in comparison with SEQ ID NO.:25.

In another more specific embodiment of the invention, the humanized or hybrid antibody (or any antigen binding fragment derived therefrom) may comprise a heavy chain variable region comprising SEQ ID NO.:30 (16B5 VH consensus 1):

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XVQLQSGAEXXKPGAXVXXSCXXSGFNKDIYMHWVXQXPXXGLEXWXGRIDPA
YGNTKYDPKFGQXXTITADTSXXTAYXXLSSLXSEDATVYYCARRYDTAMDYWG
QGTXVTVSS;
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wherein at least one of the amino acid identified by X is an amino acid substitution in comparison with a corresponding amino acid in the polypeptide set forth in SEQ ID NO.:29 (the murine 16B5 VH). The amino acid substitution may be, for example conservative or non-conservative. In accordance with the invention, the amino acid substitution may be conservative.

The humanized or hybrid antibody (or any antigen binding fragment derived therefrom) may comprise a heavy chain variable region comprising SEQ ID NO.:31 (16B5 VH consensus 2):

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X_{b1}QVLX_{b2}QSGAEX_{b3}Xb4KPGAX_{b5}VX_{b6}X_{b7}SCX_{b8}X_{b9}SGFNKDIYMHWVX_{b10}QbXb11pb2
X_{b12}GLEXWX_{b13}GRIDPA YGNTKYDPKFGQX_{b14}X_{b15}TTADTSX_{b16}X_{b17}TAYX_{b18}X_{b19}LSLX_{b20}X_{b21}SEDATVYYCARRYDTAMDYWG QGTX_{b22}VTVSS;
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Wherein $X_{b1}$ may be for example Q or E;

Wherein $X_{b2}$ may be for example V or Q;

Wherein $X_{b3}$ may be an hydrophobic amino acid such as for example V or L;
Wherein $X_{b4}$ may be for example K or V;

Wherein $X_{b5}$ may be a neutral hydrophilic amino acid such as for example T or S;
Wherein $X_{b6}$ may be a basic amino acid such as for example K or R;

Wherein $X_{b7}$ may be an hydrophobic amino acid such as for example I or L;
Wherein $X_{b8}$ may be for example K or T;
Wherein $X_{b9}$ may be for example V or T;

Wherein $X_{b10}$ may be a basic amino acid such as for example Q or K;
Wherein $X_{b11}$ may be for example A or R;

Wherein $X_{b12}$ may be for example G or E;
Wherein $X_{b13}$ may be a basic amino acid such as for example K or Q;
Wherein $X_{b14}$ may be an hydrophobic amino acid such as for example M or I;
Wherein $X_{b1}$ may be a basic amino acid such as for example R or K;
Wherein $X_{b6}$ may be an hydrophobic amino acid such as for example V or A;
Wherein $X_{b17}$ may be a neutral hydrophobic amino acid such as for example T or S;
Wherein $X_{b18}$ may be for example D or N;
Wherein $X_{b19}$ may be an hydrophobic amino acid such as for example M or L;
Wherein $X_{b30}$ may be for example E or Q;
Wherein $X_{b21}$ may be for example R or T;
Wherein $X_{b22}$ may be for example L or S and;
wherein the heavy chain variable region may comprise at least one of the above amino acid substitution in comparison with SEQ ID NO.:29.

The humanized or hybrid antibody (or any antigen binding fragment derived therefrom) may comprise a heavy chain variable region comprising SEQ ID NO.:32 (16B5 VH consensus3):

$X_{b3}$ VQLX$b$12QSGAE$X_{b3}$$X_{b4}$ KPGAX$X_{b5}$ VX$X_{b7}$ SCX$X_{b8}$ X$X_{b9}$ SGFNKDIYMHVWX$X_{b10}$ QX$X_{b11}$ PX$X_{b12}$

$X_{b3}$ GLEWX$X_{b14}$ I4GRIDPAYNTKYPKFGX$X_{b6}$ TITADTSX$X_{b7}$ TAYX$X_{b8}$ TAYX$X_{b9}$ L20LSSL

$X_{b2}$ SEDTAVYYC ARRYDT AMD YWGQGTX$X_{b22}$ VTVSS;

Wherein $X_{b1}$ may be for example Q or E;
Wherein $X_{b2}$ may be for example V or Q;
Wherein $X_{b3}$ may be for example V or L;
Wherein $X_{b4}$ may be for example K or V;
Wherein $X_{b5}$ may be for example T or S;
Wherein $X_{b6}$ may be for example K or R;
Wherein $X_{b7}$ may be for example I or L;
Wherein $X_{b8}$ may be for example K or T;
Wherein $X_{b9}$ may be for example V or T;
Wherein $X_{b10}$ may be for example Q or K;
Wherein $X_{b11}$ may be for example A or R;
Wherein $X_{b12}$ may be for example G or E;
Wherein $X_{b13}$ may be for example K or Q;
Wherein $X_{b14}$ may be for example M or L;
Wherein $X_{b15}$ may be for example R or K;
Wherein $X_{b16}$ may be for example V or A;
Wherein $X_{b17}$ may be for example T or S;
Wherein $X_{b18}$ may be for example D or N;
Wherein $X_{b19}$ may be for example M or L;
Wherein $X_{b20}$ may be for example E or Q;
Wherein $X_{b21}$ may be for example R or T;
Wherein $X_{t,22}$ may be for example L or S and;
wherein the heavy chain variable region may comprise at least one of the above amino acid substitution in comparison with SEQ ID NO.:39.

In an additional specific embodiment of the invention the humanized or hybrid antibody (or any antigen binding fragment derived therefrom) may comprise a light chain variable region comprising SEQ ID NO.:34 (2IB12 VL consensus 1):

```
DIVMXQSPXS(ALVSXGEXXTXCKSSQSLLYSSNQKNYLAHYQQXPGQXPKL

WASTRESTGVPPDFXGSGSTDFTLTISSXXAEDXAVYYCQQYYIYPR

TFGXXGTKEI
```

$K$;

wherein at least one of the amino acid identified by X is an amino acid substitution in comparison with a corresponding amino acid in the polypeptide set forth in SEQ ID NO.:33 (the murine 2IB12 VL). The amino acid substitution may be, for example conservative or non-conservative. In accordance with the invention, the amino acid substitution may be conservative.

The humanized or hybrid antibody (or any antigen binding fragment derived therefrom) may comprise a light chain variable region comprising SEQ ID NO.:35 (2IB12 VL consensus 2):

```
DIVMX_e1QSPX_e2SLAVS_e3GEX_e4X_e5TX_e6X_e7C

KSSQSLLYSSNQKNYLAHYQQXP

GQXPKL

X_e8PGQ

X_e9ASTRESTGVPPDFX_e10GSGSTDFTLTISSXX_e11AED

X_e12AVYYCQQYYIY

YPRTFGX_e13GTKEIK
```

Wherein $X_{e1}$ may be a neutral hydrophilic amino acid such as for example T or S;
Wherein $X_{e2}$ may be for example D or S;
Wherein $X_{e3}$ may be an hydrophobic amino acid such as for example L or V;
Wherein $X_{e4}$ may be a basic amino acid such as for example R or $K$;
Wherein $X_{e5}$ may be an hydrophobic amino acid such as for example A or V;
Wherein $X_{e6}$ may be an hydrophobic amino acid such as for example I or M;
Wherein $X_{e7}$ may be for example N or S;
Wherein $X_{e8}$ may be a basic amino acid such as for example $K$ or $R$;
Wherein $X_{e9}$ may be for example P or S;
Wherein $X_{e10}$ may be a neutral hydrophilic amino acid such as for example S or T;
Wherein $X_{e11}$ may be an hydrophobic amino acid such as for example L or V;
Wherein $X_{e12}$ may be a basic amino acid such as for example Q or $K$;
Wherein $X_{e13}$ may be an hydrophobic amino acid such as for example V or L;
Wherein $X_{e14}$ may be for example Q or G and;
wherein the light chain variable region may comprise at least one of the above amino acid substitution in comparison with SEQ ID NO.:33.
The humanized or hybrid antibody (or any antigen binding fragment derived therefrom) may comprise a light chain variable region comprising SEQ ID NO.:36 (21B12 VL consensus):

\[
\text{DIVMX_iQSPX_e^cSLAVSX_c^eGEX}_i^c4Xc5TX_e^cX_c^eC\text{KSSQSLLYSSNQKNLYAWYQQX}_e^c8PGQ}
\]

\[
X_{e_9}^PKLLIYWASTREGVPDX_c^oGSGSGTDFTLTISSX_{c_11}^X_{c_12}^X_{c_13}^AVYYCQQYYIYPRTFGX_{c_14}^GTKLIEK;
\]

Wherein \(X_{e_1}\) may be T or S;
Wherein \(X_{e_2}\) may be for example D or S;
Wherein \(X_{e_3}\) may be L or V;
Wherein \(X_{e_4}\) may be R or K;
Wherein \(X_{e_5}\) may be for example A or V;
Wherein \(X_{e_6}\) may be for example 1 or M;
Wherein \(X_{e_7}\) may be for example N or S;
Wherein \(X_{e_8}\) may be for example K or R;
Wherein \(X_{e_9}\) may be for example P or S;
Wherein \(X_{e_{10}}\) may be for example S or T;
Wherein \(X_{e_11}\) may be for example L or V;
Wherein \(X_{e_{12}}\) may be for example Q or K;
Wherein \(X_{e_{13}}\) may be for example V or L;
Wherein \(X_{e_{14}}\) may be for example Q or G and;

wherein the light chain variable region may comprise at least one of the above amino acid substitution in comparison with SEQ ID NO.:33.

In a further exemplary embodiment of the invention, the humanized or hybrid antibody (or any antigen binding fragment derived therefrom) may comprise a heavy chain variable region comprising SEQ ID NO.:38 (21B12 VH consensus):

\[
\text{QXQLVQSGXELKKPGVXXVXXSCKASGYTFTNYGMHWVXQAPGXLXWMGWINT}
\]

\[
\text{YTGEPTYADDFKGRFXSLXTSSTAYLQIXXLKXEDTAXYXCARDGFLYFFDYW}
\]

\[
\text{GQGTXXTVSS;}
\]

wherein at least one of the amino acid identified by X is an amino acid substitution in comparison with a corresponding amino acid in the polypeptide set forth in SEQ ID NO.:37 (the murine 21B12 VH). The amino acid substitution may be, for example conservative or non-conservative. In accordance with the invention, the amino acid substitution may be conservative.

The humanized or hybrid antibody (or any antigen binding fragment derived therefrom) may comprise a heavy chain variable region comprising SEQ ID NO.:39 (21B12 VH consensus):
QX_{d1}QLVQSGX_{2}ELKKPGX_{3}Xa4vKX_{4}SCKASGYTFTNYGMHWVX_{5}QAPGX_{6}GLX_{7}GLX_{8}
WMGWINTYTEPADDKGRFX_{d9}FSLX_{d10}TSX_{d11}STAYLQIX_{d12}X_{d3}LKKX_{d4}EDTAX_{d5}YX_{d6}CARDGFLYFFDYWGQGTX_{d7}X_{d18}STVSS;

Wherein X_{d1} may be an hydrophobic amino acid such as for example V or I;

5 Wherein X_{d2} may be for example S or P;
Wherein X_{d3} may be for example A or E;
Wherein X_{d4} may be a neutral hydrophilic amino acid such as for example S or T;
Wherein X_{d5} may be an hydrophobic amino acid such as for example V or I;
Wherein X_{d6} may be a basic amino acid such as for example R or K;

10 Wherein X_{d7} may be a basic amino acid such as for example Q or K;
Wherein X_{d8} may be for example E or K;
Wherein X_{d9} may be an hydrophobic amino acid such as for example V or A;
Wherein X_{d10} may be an acidic amino acid such as for example D or E;
Wherein X_{d11} may be an hydrophobic amino acid such as for example V or A;

15 Wherein X_{d12} may be for example S or N;
Wherein X_{d13} may be for example S or N;
Wherein X_{d14} may be for example A or N;
Wherein X_{d15} may be for example V or T;
Wherein X_{d16} may be an aromatic amino acid such as for example Y or F;

20 Wherein X_{d17} may be for example L or T;
Wherein X_{d18} may an hydrophobic amino acid such as for example V or L and;
wherein the heavy chain variable region may comprise at least one of the above amino acid substitution in comparison with SEQ ID NO.:37.

The humanized or hybrid antibody (or any antigen binding fragment derived therefrom) may comprise a heavy chain variable region comprising SEQ ID NO.:40(21B12 VH consensus3):

QX_{d1}QLVQSGX_{d2}ELKKPGX_{d3}VX_{d4}SVKX_{d5}SCKASGYTFTNYGMHWVX_{d6}QAPGX_{d7}GLX_{d8}
WMGWINTYTEPADDKGRFX_{d9}FSLX_{d10}TSX_{d11}STAYLQIX_{d12}X_{d13}LKKX_{d14}EDTAX_{d15}YX_{d16}CARDGFLYFFDYWGQGTX_{d17}X_{d18}TVSS;

Wherein X_{d1} may be for example V or I;

25 Wherein X_{d2} may be for example S or P;
Wherein X_{d3} may be for example A or E;
Wherein X_{d4} may be for example S or T;
Wherein X_{d5} may be for example V or I;
Wherein X_{d6} may be for example R or K;

30 Wherein X_{d7} may be for example Q or K;
Wherein X_{d8} may be for example E or K;
Wherein $X_{40}$ may be for example V or A;
Wherein $X_{d10}$ may be for example D or E;
Wherein $X_{d11}$ may be for example V or A;
Wherein $X_{d2}$ may be for example S or N;
5
Wherein $X_{d13}$ may be for example S or N;
Wherein $X_{d14}$ may be for example A or N;
Wherein $X_{d15}$ may be for example V or T;
Wherein $X_{d16}$ may be for example Y or F;
Wherein $X_{d17}$ may be for example L or T;
10
Wherein $X_{d18}$ may be for example V or L and;
wherein the heavy chain variable region may comprise at least one of the above amino acid
substitution in comparison with SEQ ID NO.:37.

In a more specific embodiment, the humanized or hybrid antibody may comprise a heavy
chain variable region having an amino acid sequence of SEQ ID NO.:7 or SEQ ID NO.:17.
15
Yet a more specific embodiment of the invention includes a humanized or hybrid antibody
which may comprise a heavy chain having an amino acid sequence of SEQ ID NO.:9 or SEQ
ID NO.:19.

The humanized or hybrid antibody of the present invention may have a heavy chain or heavy
chain variable region as specified herein and a complementary light chain or light chain
variable region.

On the other hand, the humanized or hybrid antibody of the present invention may have a
light chain or light chain variable region as specified herein and a complementary heavy chain
or heavy chain variable region.

The humanized or hybrid antibody of the present invention may thus comprise human
framework region amino acid residues of the natural human antibody light chain as described
herein and a light chain CDR selected, for example, from the group consisting of a CDRL1
having an amino acid sequence of SEQ ID NO.:4, a CDRL2 having an amino acid sequence
of SEQ ID NO.:5 and a CDRL3 having an amino acid sequence of SEQ ID NO.:6 or heavy
chain CDR selected from the group consisting of a CDRL1 having an amino acid sequence of
SEQ ID NO.:14, a CDRL2 having an amino acid sequence of SEQ ID NO.:15 and a CDRL3
having an amino acid sequence of SEQ ID NO.:16 and combination thereof.

In a further embodiment, the humanized or hybrid antibody may comprise human framework
region amino acid residues of the natural human antibody light chain as described herein and
at least two light chain CDRs selected from the group consisting of a CDRL1 having an amino acid sequence of SEQ ID NO.:4, a CDRL2 having an amino acid sequence of SEQ ID NO.:5 and a CDRL3 having an amino acid sequence of SEQ ID NO.:6 or at least two heavy chain CDRs selected from the group consisting of a CDRL1 having an amino acid sequence of SEQ ID NO.:14, a CDRL2 having an amino acid sequence of SEQ ID NO.:15 and a CDRL3 having an amino acid sequence of SEQ ID NO.:16 and combination thereof.

In yet a further embodiment, the humanized or hybrid antibody may comprise human framework region amino acid residues of the natural human antibody light chain as described herein and a CDRL1 having an amino acid sequence of SEQ ID NO.:4, a CDRL2 having an amino acid sequence of SEQ ID NO.:5 and a CDRL3 having an amino acid sequence of SEQ ID NO.:6 or a CDRL1 having an amino acid sequence of SEQ ID NO.:14, a CDRL2 having an amino acid sequence of SEQ ID NO.:15 and a CDRL3 having an amino acid sequence of SEQ ID NO.:16 and combination thereof.

In a more particular embodiment, the humanized or hybrid antibody may comprise a light chain variable region having an amino acid sequence of SEQ ID NO.:8 or SEQ ID NO.:18.

In an even more particular embodiment, the humanized or hybrid antibody of the present invention may comprise a light chain having an amino acid sequence of SEQ ID NO.:10 or SEQ ID NO.:20.

Other specific embodiments of the invention encompass a humanized antibody having a heavy chain variable region having an amino acid sequence of SEQ ID NO.:7 or SEQ ID NO.:17 and a light chain variable region having an amino acid sequence of SEQ ID NO.:8 or SEQ ID NO.:18.

An additional specific embodiment of the invention encompass a humanized antibody having a heavy chain having an amino acid sequence of SEQ ID NO.:9 and a light chain having an amino acid sequence of SEQ ID NO.:10.

Yet, an additional specific embodiment of the invention encompass a humanized antibody having a heavy chain having an amino acid sequence of SEQ ID NO.:19 and a light chain having an amino acid sequence of SEQ ID NO.:20.

The present invention relates in a further aspect to an antibody or antigen binding fragment thereof which may be capable of specific binding to clusterin and which may be selected from the group consisting of:
an antibody or antigen binding fragment thereof which may have a light chain variable region at least 80% identical (e.g., 85%, 90%, 95%, 99%) to SEQ ID NO.:25 and/or a heavy chain variable region at least 80% identical (e.g., 85%, 90%, 95%, 99%) to SEQ ID NO.:29 wherein the antibody or antigen binding fragment thereof may comprise, for example, at least one amino acid substitution in comparison with SEQ ID NO.:25 or SEQ ID NO.:29 and wherein the amino acid substitution may be, for example, outside of a complementarity determining region (CDR) and;

an antibody or antigen binding fragment thereof which may have a light chain variable region at least 80% identical (e.g., 85%, 90%, 95%, 99%) to SEQ ID NO.:33 and/or a heavy chain variable region at least 80% identical (e.g., 85%, 90%, 95%, 99%) to SEQ ID NO.:37 wherein the antibody or antigen binding fragment thereof may comprise at least one amino acid substitution in comparison with SEQ ID NO.:33 or SEQ ID NO.:37 and wherein the amino acid substitution may be, for example, outside of a complementarity determining region (CDR).

In accordance with the present invention, the at least one amino acid substitution may be, for example, in the light chain variable region.

In accordance with the present invention, the at least one amino acid substitution may be, for example, in the heavy chain variable region.

The amino acid substitution may be conservative or non-conservative. In a more specific embodiment, the amino acid substitution may be conservative.

In accordance with an embodiment of the invention, the antibodies and antigen binding fragments of the present invention bind human clusterin. In accordance with another embodiment of the invention, the antibodies and antigen binding fragments of the present invention bind murine clusterin. The antibodies and antigen binding fragment of the present invention may also bind a naturally occurring or synthetic variant of murine or human clusterin. Such variant may have, for example, at least 75% amino acid sequence identity with human clusterin or with murine clusterin.

The CDRs of SEQ ID NO.:29 (identical to those of SEQ ID NOs. 30, 31, 32 and 7) were identified using the Kabat and Chothia definitions. The corresponding CDR sequences are identified herein as follow; the CDR1 of the heavy chain variable region corresponds to SEQ ID NO.:1, the CDR2 of the heavy chain variable region corresponds to SEQ ID NO.:2 and the CDR3 of the heavy chain variable region corresponds to SEQ ID NO.:3.
Shorter versions of SEQ ID NOs.1, 2 and 3 were presented in international application No. PCT/CA2006/001505 filed on September 13, 2006 (i.e., the 1505 appl.) and published under No. WO2007/030930. In this patent application, the CDRs of SEQ ID NO.:29 (corresponding to SEQ ID NO.:23 in the '1505 appl.) were identified with the IMGT/V quest software that implements the IMGT definition. The corresponding sequences are identified herein as follow; the CDR1 of the heavy chain variable region corresponds to SEQ ID NO.:44, the CDR2 of the heavy chain variable region corresponds to SEQ ID NO.:45 and the CDR3 of the heavy chain variable region corresponds to SEQ ID NO.:46.

As used herein the term "amino acid substitution... outside of a complementarity determining region (CDR)" with respect to SEQ ID NO.:29 generally refers to amino acids (outside of) surrounding SEQ ID NOs.:1, 2 and 3. In some embodiments this term may alternatively refer to amino acids (outside of) surrounding SEQ ID NOs.:44, 45 and 46.

The CDRs of SEQ ID NO.:25 (identical to those of SEQ ID NOs. 26, 27, 28 and 8) were identified using the Kabat and Chothia definitions. The corresponding CDR sequences are identified herein as follow; the CDR1 of the light chain variable region corresponds to SEQ ID NO.:4, the CDR2 of the light chain variable region corresponds to SEQ ID NO.:5 and the CDR3 of the light chain variable region corresponds to SEQ ID NO.:6.

Shorter versions of SEQ ID NOs. 4, 5 and 6 were presented in international application No. PCT/CA2006/001505 filed on September 13, 2006 (i.e., the 1505 appl.) and published under No. WO2007/030930. In this patent application, the CDRs of SEQ ID NO.:25 (corresponding to SEQ ID NO.:12 in the '1505 appl.) were identified with the IMGT/V quest software that implements the IMGT definition. The corresponding sequences are identified herein as follow; the CDR1 of the light chain variable region corresponds to SEQ ID NO.:47, the CDR2 of the light chain variable region corresponds to amino acid sequence "WAS" and the CDR3 of the light chain variable region corresponds to SEQ ID NO.:49.

As used herein the term "amino acid substitution... outside of a complementarity determining region (CDR)" with respect to SEQ ID NO.:25 generally refers to amino acids (outside of) surrounding SEQ ID NOs.:4, 5 and 6. In some embodiments this term may alternatively refer to amino acids (outside of) surrounding SEQ ID NOs.:47, the CDR2 of the light chain variable region and 49.

The CDRs of SEQ ID NO.:37 (identical to those of SEQ ID NOs. 38, 39, 40 and 17) were identified using the Kabat and Chothia definitions. The corresponding CDR sequences are identified herein as follow; the CDR1 of the heavy chain variable region corresponds to SEQ
ID NO.:11, the CDR2 of the heavy chain variable region corresponds to SEQ ID NO.:12 and the CDR3 of the heavy chain variable region corresponds to SEQ ID NO.:13.

Shorter versions of SEQ ID NOs.:1, 12 and 13 were presented in international application No. PCT/CA2006/001505 filed on September 13, 2006 (i.e., the 1505 appl.) and published under No. WO2007/030930. In this patent application, the CDRs of SEQ ID NO.:37 (corresponding to SEQ ID NO.:22 in the 1505 appl.) were identified with the IMGT/V quest software that implements the IMGT definition. The corresponding sequences are identified herein as follow; the CDR1 of the heavy chain variable region corresponds to SEQ ID NO.:50, the CDR2 of the heavy chain variable region corresponds to SEQ ID NO.:51 and the CDR3 of the heavy chain variable region corresponds to SEQ ID NO.:52.

As used herein the term "amino acid substitution... outside of a complementarity determining region (CDR)" with respect to SEQ ID NO.:37 generally refers to amino acids (outside of) surrounding SEQ ID NOs.:1, 12 and 13. In some embodiments this term may alternatively refer to amino acids (outside of) surrounding SEQ ID NOs.:50, 51 and 52.

The CDRs of SEQ ID NO.:33 (identical to those of SEQ ID NOs. 34, 35, 36 and 18) were identified using the Kabat and Chothia definitions. The corresponding CDR sequences are identified herein as follow; the CDR1 of the light chain variable region corresponds to SEQ ID NO.:14, the CDR2 of the light chain variable region corresponds to SEQ ID NO.:15 and the CDR3 of the light chain variable region corresponds to SEQ ID NO.:16.

Shorter versions of SEQ ID NOs. 14, 15 and 16 were presented in international application No. PCT/CA2006/001505 filed on September 13, 2006 (i.e., the 1505 appl.) and published under No. WO2007/030930. In this patent application, the CDRs of SEQ ID NO.:33 (corresponding to SEQ ID NO.:11 in the 1505 appl.) were identified with the IMGT/V quest software that implements the IMGT definition. The corresponding sequences are identified herein as follow; the CDR1 of the light chain variable region corresponds to SEQ ID NO.:53, the CDR2 of the light chain variable region corresponds to amino acid sequence "WAS" and the CDR3 of the light chain variable region corresponds to SEQ ID NO.:55.

As used herein the term "amino acid substitution... outside of a complementarity determining region (CDR)" with respect to SEQ ID NO.:33 generally refers to amino acids (outside of) surrounding SEQ ID NOs.:14, 15 and 16. In some embodiments this term may alternatively refer to amino acids (outside of) surrounding SEQ ID NOs.:53, the CDR2 of the light chain variable region and 55.

The humanized antibody of the present invention (or any antigen binding fragment derived therefrom) may comprise a light chain variable region selected from the group consisting of
SEQ ID NO.:7, SEQ ID NO.:26 or SEQ ID NO.:27 and a heavy chain variable region selected from the group consisting of SEQ ID NO.:8, SEQ ID NO.:29 or SEQ ID NO.:30.

The hybrid antibody of the present invention (or any antigen binding fragment derived therefrom) may comprise a light chain variable region selected from the group consisting of SEQ ID NO.:7, SEQ ID NO.:26 or SEQ ID NO.:27 and a heavy chain variable region comprising SEQ ID NO.:28.

Alternatively the hybrid antibody of the present invention (or any antigen binding fragment derived therefrom) may comprise a light chain variable region comprising SEQ ID NO.:25 and a heavy chain variable region selected from the group consisting of SEQ ID NO.:8, SEQ ID NO.:29 or SEQ ID NO.:30.

The humanized antibody of the present invention (or any antigen binding fragment derived therefrom) may comprise a light chain variable region selected from the group consisting of SEQ ID NO.:18, SEQ ID NO.:32 or SEQ ID NO.:33 and a heavy chain variable region selected from the group consisting of SEQ ID NO.:17, SEQ ID NO.:35 or SEQ ID NO.:36.

The hybrid antibody of the present invention (or any antigen binding fragment derived therefrom) may comprise a light chain variable region selected from the group consisting of SEQ ID NO.:18, SEQ ID NO.:32 or SEQ ID NO.:33 and a heavy chain variable region comprising SEQ ID NO.:34.

Alternatively the hybrid antibody of the present invention (or any antigen binding fragment derived therefrom) may comprise a light chain variable region comprising SEQ ID NO.:31 and a heavy chain variable region selected from the group consisting of SEQ ID NO.:17, SEQ ID NO.:35 or SEQ ID NO.:36.

Another exemplary embodiment of the humanized antibody or antigen binding fragment of the present invention includes for example, an antibody or antigen binding fragment having a light chain variable region which may comprise at least 90 consecutive amino acids of any of SEQ ID NO.:26, SEQ ID NO.:27, SEQ ID NO.:28 or SEQ ID NO.:8.

As used herein the term "at least 90 consecutive amino acids of SEQ ID NO.:26" also includes the terms "at least 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111 or at least 112 consecutive amino acids". The term "at least 90 consecutive amino acids of SEQ ID NO.:26" encompasses any possible sequence of at least 90 consecutive amino acids found in SEQ ID NO.:26 and especially those sequences which
include the 3 CDRs of SEQ ID NO.:26, such as, for example a sequence comprising amino acids 6 to 108, 5 to 109, 13 to 103, 9 to 111 of SEQ ID NO.:26 and so on.

As used herein the term "at least 90 consecutive amino acids of SEQ ID NO.:27" also includes the terms "at least 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111 or at least 112 consecutive amino acids". The term "at least 90 consecutive amino acids of SEQ ID NO.:27" encompasses any possible sequence of at least 90 consecutive amino acids found in SEQ ID NO.:27 and especially those sequences which include the 3 CDRs of SEQ ID NO.:27, such as, for example a sequence comprising amino acids 7 to 109, 12 to 104, 22 to 113, 18 to 112 of SEQ ID NO.:27 and so on.

The terms "at least 90 consecutive amino acids of SEQ ID NO.:28" or "at least 90 consecutive amino acids of SEQ ID NO.:8" has a similar meaning.

In accordance with the present invention, the antibody or antigen binding fragment of the present invention may have, for example, a light chain variable region as set forth in SEQ ID NO.:8.

Also in accordance with the present invention, the antibody or antigen binding fragment of the present invention may have, for example, a light chain as set forth in SEQ ID NO.:TO.

The humanized antibody or antigen binding fragment of the invention includes (or further includes) for example, a heavy chain variable region which may comprise at least 90 consecutive amino acids of any of SEQ ID NOs.:30, 31, 32 or 7.

As used herein the term "at least 90 consecutive amino acids of SEQ ID NO.:30" also includes the terms "at least 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116 or at least 117 consecutive amino acids". The term "at least 90 consecutive amino acids of SEQ ID NO.:30" encompasses any possible sequence of at least 90 consecutive amino acids found in SEQ ID NO.:30 and especially those sequences which include the 3 CDRs of SEQ ID NO.:30, such as, for example a sequence comprising amino acids 1 to 108, 2 to 112, 11 to 113, 7 to 109 of SEQ ID NO.:30 and so on.

As used herein the term "at least 90 consecutive amino acids of SEQ ID NO.:31" also includes the terms "at least 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116 or at least 117 consecutive amino acids". The term "at least 90 consecutive amino acids of SEQ ID NO.:31" encompasses any possible sequence of at least 90 consecutive amino acids found in SEQ ID NO.:31 and
especially those sequences which include the 3 CDRs of SEQ ID NO.:31, for example a sequence comprising amino acids 6 to 109, 8 to 113, 1 to 108, 2 to 115 of SEQ ID NO.:31 and so on.

The terms "at least 90 consecutive amino acids of SEQ ID NO.:32" or "at least 90 consecutive amino acids of SEQ ID NO.:7" has a similar meaning.

In accordance with the present invention, the antibody or antigen binding fragment of the present invention may have, for example, a heavy chain variable region as set forth in SEQ ID NO.:7.

Also in accordance with the present invention, the antibody or antigen binding fragment of the present invention may have, for example, a heavy chain as set forth in SEQ ID NO.:9.

In accordance with the present invention the antibody or antigen binding fragment may comprise, for example,

a) a light chain variable region which may comprise at least 90 consecutive amino acids of SEQ ID NO.:26 and a heavy chain variable region which may comprise at least 90 consecutive amino acids of any of SEQ ID NO.:30, SEQ ID NO.:31, SEQ ID NO.:32 or SEQ ID NO.:7;

b) a light chain variable region which may comprise at least 90 consecutive amino acids of SEQ ID NO.:27 and a heavy chain variable region which may comprise at least 90 consecutive amino acids of any of SEQ ID NO.:30, SEQ ID NO.:31, SEQ ID NO.:32 or SEQ ID NO.:7;

c) a light chain variable region which may comprise amino acids at least 90 consecutive amino acids of SEQ ID NO.:28 and a heavy chain variable region which may comprise at least 90 consecutive amino acids of any of SEQ ID NO.:30, SEQ ID NO.:31, SEQ ID NO.:32 or SEQ ID NO.:7 or;

d) a light chain variable region which may comprise at least 90 consecutive amino acids of SEQ ID NO.:8 and a heavy chain variable region which may comprise at least 90 consecutive amino acids of any of SEQ ID NO.:30, SEQ ID NO.:31, SEQ ID NO.:32 or SEQ ID NO.:7.

In accordance with a more specific embodiment of the invention, the light chain variable region may comprise at least 90 consecutive amino acids of SEQ ID NO.:8 and the heavy chain variable region may comprise at least 90 consecutive amino acids of SEQ ID NO.:7.
In accordance with an even more specific embodiment of the invention, the light chain
variable region may be as set forth in SEQ ID NO.: 8 and the heavy chain variable region may
be as set forth in SEQ ID NO.: 7.

Other exemplary embodiments of the humanized antibodies or antigen binding fragments of
the invention are those which may comprise a light chain variable region which may comprise
at least 90 consecutive amino acids of any of SEQ ID Nos. 34, 35, 36 or 18.

As used herein the term "at least 90 consecutive amino acids of SEQ ID NO.: 34" also
includes the terms "at least 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105,
106, 107, 108, 109, 110, 111, 112 or at least 113, consecutive amino acids". The term "at least
90 consecutive amino acids of SEQ ID NO.: 34" encompasses any possible sequence of at
least 90 consecutive amino acids found in SEQ ID NO.: 34 and especially those sequences
which include the 3 CDRs of SEQ ID NO.: 34, for example a sequence comprising amino
acids 6 to 103, 11 to 106, 1 to 106, 3 to 110, 5 to 107 of SEQ ID NO.: 34 and so on.

As used herein the term "at least 90 consecutive amino acids of SEQ ID NO.: 35" also
includes the terms "at least 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105,
106, 107, 108, 109, 110, 111, 112 or at least 113, consecutive amino acids". The term "at least
90 consecutive amino acids of SEQ ID NO.: 35" encompasses any possible sequence of at
least 90 consecutive amino acids found in SEQ ID NO.: 35 and especially those sequences
which include the 3 CDRs of SEQ ID NO.: 35, for example a sequence comprising amino
acids 9 to 106, 10 to 113, 11 to 109, 20 to 110, 7 to 107 of SEQ ID NO.: 35 and so on.

The terms "at least 90 consecutive amino acids of SEQ ID NO.: 36" or "at least 90
consecutive amino acids of SEQ ID NO.: 18" has a similar meaning.

In accordance with the present invention, the antibody or antigen binding fragment of the
present invention may have, for example, a light chain variable region as set forth in SEQ ID
NO.: 18.

Also in accordance with the present invention, the antibody or antigen binding fragment of
the present invention may have, for example, a light chain as set forth in SEQ ID NO.: 20.

The humanized antibody or antigen binding fragment of the invention includes (or further
includes) for example, a heavy chain variable region which may comprise at least 90
consecutive amino acids of any of SEQ ID Nos.: 38, 39, 40 or 17.

As used herein the term "at least 90 consecutive amino acids of SEQ ID NO.: 38" also
includes the terms "at least 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105,
106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117 or at least 118 consecutive amino acids". The term "at least 90 consecutive amino acids of SEQ ID NO.:38" encompasses any possible sequence of at least 90 consecutive amino acids found in SEQ ID NO.:38 and especially those sequences which include the 3 CDRs of SEQ ID NO.:38, such as, for example a sequence comprising amino acids 6 to 111, 1 to 114, 12 to 109, 5 to 113, 10 to 107 of SEQ ID NO.:38 and so on.

As used herein the term "at least 90 consecutive amino acids of SEQ ID NO.:39" also includes the terms "at least 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117 or at least 118 consecutive amino acids". The term "at least 90 consecutive amino acids of SEQ ID NO.:39" encompasses any possible sequence of at least 90 consecutive amino acids found in SEQ ID NO.:39 and especially those sequences which include the 3 CDRs of SEQ ID NO.:39, such as, for example a sequence comprising amino acids 3 to 109, 1 to 115, 1 to 110, 22 to 116, 20 to 115 of SEQ ID NO.:39 and so on.

The terms "at least 90 consecutive amino acids of SEQ ID NO.:40" or "at least 90 consecutive amino acids of SEQ ID NO.:17" has a similar meaning.

In accordance with the present invention, the antibody or antigen binding fragment of the present invention may have, for example, a heavy chain variable region as set forth in SEQ ID NO.:17.

Also in accordance with the present invention, the antibody or antigen binding fragment of the present invention may have, for example, a heavy chain as set forth in SEQ ID NO.:19. In accordance with the present invention the antibody or antigen binding fragment may comprise, for example,

a) a light chain variable region which may comprise at least 90 consecutive amino acids of SEQ ID NO.:34 and a heavy chain variable region which may comprise at least 90 consecutive amino acids of any of SEQ ID NO.:38, SEQ ID NO.:39, SEQ ID NO.:40 or SEQ ID NO.:17;

b) a light chain variable region which may comprise at least 90 consecutive amino acids of SEQ ID NO.:35 and a heavy chain variable region which may comprise at least 90 consecutive amino acids of any of SEQ ID NO.:38, SEQ ID NO.:39, SEQ ID NO.:40 or SEQ ID NO.:17;
c) a light chain variable region which may comprise amino acids at least 90 consecutive amino acids of SEQ ID NO.:36 and a heavy chain variable region which may comprise at least 90 consecutive amino acids of any of SEQ ID NO.:38, SEQ ID NO.:39, SEQ ID NO.:40 or SEQ ID NO.:17 or;

d) a light chain variable region which may comprise at least 90 consecutive amino acids of SEQ ID NO.:18 and a heavy chain variable region which may comprise at least 90 consecutive amino acids of any of SEQ ID NO.:38, SEQ ID NO.:39, SEQ ID NO.:40 or SEQ ID NO.:17.

In accordance with a more specific embodiment of the invention, the light chain variable region may have at least 90 consecutive amino acids of SEQ ID NO.: 18 and the heavy chain variable region may have at least 90 consecutive amino acids of SEQ ID NO.:17.

In accordance with an even more specific embodiment of the invention, the light chain variable region may be as set forth in SEQ ID NO.: 18 and the heavy chain variable region may be as set forth in SEQ ID NO.:17.

Of course, the light chain or heavy chain or their variable region described herein may also contain a signal peptide. Such signal peptide may be from an original sequence or may be designed to optimize a particular cellular localization of the polypeptide. Of course, desirable signal peptides are those which may allow secretion of the polypeptide (e.g., cleavable).

The humanized or hybrid antibody of the present invention may have a constant region, preferably a human constant region. Although other subtypes may be selected, the humanized or hybrid antibody may comprise amino acids residues of a constant region of an immunoglobulin of an IgGl, IgG2 or IgG3 subtype.

The present invention also relates in another aspect, to an antigen binding fragment comprising a light chain variable region (or a fragment thereof) and a heavy chain variable region (or a fragment thereof), which may include non-human complementarity determining region amino acid residues and human framework region amino acid residues.

The antigen binding fragment of the present invention may bind to clusterin and may advantageously have a better affinity than an antigen binding fragment of a non-human parent antibody.

In fact, it has been shown herein that the antigen binding fragment binds to recombinant monomeric clusterin with an affinity of $1.7 \times 10^9 \text{ M} \pm 2.97 \times 10^9$ or better.
In an exemplary embodiment, the antigen binding fragment may comprise human framework region amino acid residues of the natural human antibody heavy chain as described herein and a heavy chain CDR selected from the group consisting of a CDRH1 having an amino acid sequence of SEQ ID NO.:1, a CDRH2 having an amino acid sequence of SEQ ID NO.:2 and a CDRH3 having an amino acid sequence of SEQ ID NO.:3 or a heavy chain CDR selected from the group consisting of a CDRH1 having an amino acid sequence of SEQ ID NO.:11, a CDRH2 having an amino acid sequence of SEQ ID NO.:12 and a CDRH3 having an amino acid sequence of SEQ ID NO.:13.

In another exemplary embodiment, the antigen binding fragment may comprise human framework region amino acid residues of the natural human antibody heavy chain as described herein and at least two heavy chain CDRs selected from the group consisting of a CDRH1 having an amino acid sequence of SEQ ID NO.:1, a CDRH2 having an amino acid sequence of SEQ ID NO.:2 and a CDRH3 having an amino acid sequence of SEQ ID NO.:3 or at least two heavy chain CDR selected from the group consisting of a CDRH1 having an amino acid sequence of SEQ ID NO.:11, a CDRH2 having an amino acid sequence of SEQ ID NO.:12 and a CDRH3 having an amino acid sequence of SEQ ID NO.:13.

In yet another exemplary embodiment, the antigen binding fragment may comprise human framework region amino acid residues of the natural human antibody heavy chain as described herein and a CDRH1 having an amino acid sequence of SEQ ID NO.:1, a CDRH2 having an amino acid sequence of SEQ ID NO.:2 and a CDRH3 having an amino acid sequence of SEQ ID NO.:3 or a CDRH1 having an amino acid sequence of SEQ ID NO.:11, a CDRH2 having an amino acid sequence of SEQ ID NO.:12 and a CDRH3 having an amino acid sequence of SEQ ID NO.:13.

In a more particular embodiment, the antigen binding fragment may comprise a heavy chain variable region having an amino acid sequence of SEQ ID NO:7 or SEQ ID NO.:17 (or a fragment thereof).

In a further exemplary embodiment, the antigen binding fragment may comprise human framework region amino acid residues of the natural human antibody light chain as described herein and a light chain CDR selected from the group consisting of a CDRL1 having an amino acid sequence of SEQ ID NO.:4, a CDRL2 having an amino acid sequence of SEQ ID NO.:5 and a CDRL3 having an amino acid sequence of SEQ ID NO.:6 or a light chain CDR selected from the group consisting of a CDRL1 having an amino acid sequence of SEQ ID NO.:14, a CDRL2 having an amino acid sequence of SEQ ID NO.:15 and a CDRL3 having an amino acid sequence of SEQ ID NO.:16.
In yet a further exemplary embodiment, the antigen binding fragment may comprise human framework region amino acid residues of the natural human antibody light chain as described herein and at least two light chain CDRs selected from the group consisting of a CDRL1 having an amino acid sequence of SEQ ID NO.:4, a CDRL2 having an amino acid sequence of SEQ ID NO.:5 and a CDRL3 having an amino acid sequence of SEQ ID NO.:6 or at least two light chain CDRs selected from the group consisting of a CDRL1 having an amino acid sequence of SEQ ID NO.:14, a CDRL2 having an amino acid sequence of SEQ ID NO.:15 and a CDRL3 having an amino acid sequence of SEQ ID NO.:16.

In still a further exemplary embodiment, the antigen binding fragment may comprise human framework region amino acid residues of the natural human antibody light chain as described herein and a CDRL1 having an amino acid sequence of SEQ ID NO.:4, a CDRL2 having an amino acid sequence of SEQ ID NO.:5 and a CDRL3 having an amino acid sequence of SEQ ID NO.:6 or a CDRL1 having an amino acid sequence of SEQ ID NO.:14, a CDRL2 having an amino acid sequence of SEQ ID NO.:15 and a CDRL3 having an amino acid sequence of SEQ ID NO.:16.

In a more specific embodiment, the antigen binding fragment may comprise a light chain variable region having an amino acid sequence of SEQ ID NO.:8 or SEQ ID NO.:18 or a fragment thereof.

In accordance with the present invention, the antigen binding fragment may be, for example, a Fab fragment, a F(ab')2 fragment, a Fd fragment, a Fv fragment or a dAb fragment.

Preferably, the antigen binding fragment may be, for example, a Fab fragment or a F(ab')2 fragment.

The present invention also encompasses an isolated antibody comprising the amino acid sequence of the antigen binding fragment described herein. The isolated antibody may also comprise a constant region.

**Variant antibody and antigen binding fragments.**

still exists. For example, in United States Patent No. 7,537,931, attempts at transferring the CDRs of a murine antibody into a human antibody resulted in loss of binding to the antigen.

If the humanization process does not result in a humanized or hybrid antibody having the desired characteristics (i.e., specificity, affinity, etc.), it is possible to substitute non-human amino acid framework residues for human amino acid framework residues.

The present invention therefore encompasses variants of the humanized or hybrid antibodies or antigen binding fragments described herein. Variant antibodies or antigen binding fragments included are those having a variation in the amino acid sequence of the humanized or hybrid antibody or antigen binding fragments described herein. For example, variant antibodies or antigen binding fragments encompassed by the present invention are those having a light chain variable region and a heavy chain variable region which may include non-human complementarity determining region amino acid residues and human framework region amino acid residues of a natural human antibody and further comprising at least one amino acid variation (preferably in the framework region).

Variant antibodies or antigen binding fragments included in the present invention are those having, for example, similar or improved characteristics in comparison with the humanized or hybrid antibody or antigen binding fragment but which carries at least one amino acid variation in comparison with the humanized or hybrid antibody described herein.

Variant antibodies or antigen binding fragments encompassed by the present invention are those which may comprise an insertion, a deletion or an amino acid substitution (conservative or non-conservative). Some variants may thus have at least one amino acid residue in its amino acid sequence removed and a different residue inserted in its place.

The sites of interest for substitutional mutagenesis may include the hypervariable regions (CDRs), the framework region or even the constant region. Conservative substitutions may be made by exchanging an amino acid from one of the groups listed below (group 1 to 6) for another amino acid of the same group.

Other exemplary embodiments of conservative substitutions are shown in Table 1A under the heading of "preferred substitutions". If such substitutions result in an undesired property, then more substantial changes, denominated "exemplary substitutions" in Table 1A, or as further described below in reference to amino acid classes, may be introduced and the products screened.
Examples of substitutions identified as "conservative substitutions" are shown in Table 1A. If such substitutions result in a change not desired, then other type of substitutions, denominated "exemplary substitutions" in Table 1A, or as further described herein in reference to amino acid classes, are introduced and the products screened.

Substantial modifications in function or immunological identity may be accomplished by selecting substitutions that differ significantly in their effect on maintaining (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. Naturally occurring residues are divided into groups based on common side chain properties:

- (group 1) hydrophobic: norleucine, methionine (Met), Alanine (Ala), Valine (Val), Leucine (Leu), Isoleucine (He)
- (group 2) neutral hydrophilic: Cysteine (Cys), Serine (Ser), Threonine (Thr)
- (group 3) acidic: Aspartic acid (Asp), Glutamic acid (Glu)
- (group 4) basic: Asparagine (Asn), Glutamine (Gin), Histidine (His), Lysine (Lys), Arginine (Arg)
- (group 5) residues that influence chain orientation: Glycine (Gly), Proline (Pro);
- (group 6) aromatic: Tryptophan (Trp), Tyrosine (Tyr), Phenylalanine (Phe)

Non-conservative substitutions will entail exchanging a member of one of these classes for another.

**Table 1A. Amino acid substitution**

<table>
<thead>
<tr>
<th>Original residue</th>
<th>Exemplary substitution</th>
<th>Conservative substitution</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ala (A)</td>
<td>Val, Leu, Ile</td>
<td>Val</td>
</tr>
<tr>
<td>Arg (R)</td>
<td>Lys, Gln, Asn</td>
<td>Lys</td>
</tr>
<tr>
<td>Asn (N)</td>
<td>Gln, His, Lys, Arg, Asp</td>
<td>Gln</td>
</tr>
<tr>
<td>Asp (D)</td>
<td>Glu, Asn</td>
<td>Glu</td>
</tr>
<tr>
<td>Cys (C)</td>
<td>Ser, Ala</td>
<td>Ser</td>
</tr>
<tr>
<td>Gln (Q)</td>
<td>Asn; Glu</td>
<td>Asn</td>
</tr>
<tr>
<td>Glu (E)</td>
<td>Asp, Gln</td>
<td>Asp</td>
</tr>
<tr>
<td>Gly (G)</td>
<td>Ala</td>
<td>Ala</td>
</tr>
<tr>
<td>His (H)</td>
<td>Asn, Gln, Lys, Arg,</td>
<td>Arg</td>
</tr>
<tr>
<td>Ile (I)</td>
<td>Leu, Val, Met, Ala, Phe,</td>
<td>Leu</td>
</tr>
<tr>
<td>Original residue</td>
<td>Exemplary substitution</td>
<td>Conservative substitution</td>
</tr>
<tr>
<td>------------------</td>
<td>------------------------</td>
<td>--------------------------</td>
</tr>
<tr>
<td>norleucine</td>
<td>of norleucine, He, Val, Met, Ala, Phe</td>
<td>of He</td>
</tr>
<tr>
<td>Leu (L)</td>
<td>Arg, Gin, Asn</td>
<td>of Arg</td>
</tr>
<tr>
<td>Met (M)</td>
<td>Leu, Phe, Ile</td>
<td>of Leu</td>
</tr>
<tr>
<td>Phe (F)</td>
<td>Leu, Val, Ile, Ala, Tyr</td>
<td>of Tyr</td>
</tr>
<tr>
<td>Pro (P)</td>
<td>Ala</td>
<td>of Ala</td>
</tr>
<tr>
<td>Ser (S)</td>
<td>Thr</td>
<td>of Thr</td>
</tr>
<tr>
<td>Thr (T)</td>
<td>Ser</td>
<td>of Ser</td>
</tr>
<tr>
<td>Trp (W)</td>
<td>Tyr, Phe</td>
<td>of Tyr</td>
</tr>
<tr>
<td>Tyr (Y)</td>
<td>Trp, Phe, Thr, Ser</td>
<td>of Phe</td>
</tr>
<tr>
<td>Val (V)</td>
<td>Ile, Leu, Met, Phe, Ala, norleucine</td>
<td>of Leu</td>
</tr>
</tbody>
</table>

Variation in the amino acid sequence of the variant antibody or antigen binding fragment may include an amino acid addition, deletion, insertion, substitution etc., one or more modification in the backbone or side-chain of one or more amino acid, or an addition of a group or another molecule to one or more amino acids (side-chains or backbone).

Variant antibody or antigen binding fragment may have substantial sequence similarity and/or sequence identity in its amino acid sequence in comparison with that the original antibody or antigen binding fragment amino acid sequence. The degree of similarity between two sequences is based upon the percentage of identities (identical amino acids) and of conservative substitution.

When determining percent identity of a framework region in comparison with another framework region, the CDRs amino acid sequence should preferably not be taken into account. The percent identity of a framework region in comparison with another is preferably determined over the entire framework region and not framework by framework.

Generally, the degree of similarity and identity between variable chains has been determined herein using the Blast2 sequence program (Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250) using default settings, i.e., blastp program, BLOSUM62 matrix (open gap 11 and extension gap penalty 1; gapx dropoff 50, expect 10.0, word size 3) and activated filters.
Percent identity will therefore be indicative of amino acids which are identical in comparison with the original peptide and which may occupy the same or similar position.

Percent similarity will be indicative of amino acids which are identical and those which are replaced with conservative amino acid substitution in comparison with the original peptide at the same or similar position.

Variants of the present invention therefore comprise those which may have at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity with an original sequence or a portion of an original sequence.

Exemplary embodiments of variants are those having at least 81% sequence identity to a sequence described herein and 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence similarity with an original sequence or a portion of an original sequence.

Other exemplary embodiments of variants are those having at least 82% sequence identity to a sequence described herein and 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence similarity with an original sequence or a portion of an original sequence.

Further exemplary embodiments of variants are those having at least 85% sequence identity to a sequence described herein and 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence similarity with an original sequence or a portion of an original sequence.

Other exemplary embodiments of variants are those having at least 90% sequence identity to a sequence described herein and 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence similarity with an original sequence or a portion of an original sequence.

Additional exemplary embodiments of variants are those having at least 95% sequence identity to a sequence described herein and 95%, 96%, 97%, 98%, 99% or 100% sequence similarity with an original sequence or a portion of an original sequence.

Yet additional exemplary embodiments of variants are those having at least 97% sequence identity to a sequence described herein and 97%, 98%, 99% or 100% sequence similarity with an original sequence or a portion of an original sequence.
For a purpose of concision the applicant provides herein a Table 1B illustrating exemplary embodiments of individual variants encompassed by the present invention and comprising the specified \% sequence identity and \% sequence similarity. Each "X" is to be construed as defining a given variant.

<table>
<thead>
<tr>
<th>Table 1B</th>
<th>Percent (%) sequence identity</th>
</tr>
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<tbody>
<tr>
<td></td>
<td>80</td>
</tr>
<tr>
<td>Percent (%) sequence similarity</td>
<td></td>
</tr>
<tr>
<td>80</td>
<td>X</td>
</tr>
<tr>
<td>81</td>
<td>X</td>
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<tr>
<td>82</td>
<td>X</td>
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<tr>
<td>83</td>
<td>X</td>
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<td>84</td>
<td>X</td>
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<td>X</td>
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<tr>
<td>99</td>
<td>X</td>
</tr>
<tr>
<td>100</td>
<td>X</td>
</tr>
</tbody>
</table>

The present invention thus encompasses humanized or hybrid antibody in which non-human amino acid framework residues are reintroduced or where other types of amino acid modifications are made. Those amino acids that are particularly selected to optimize the characteristics of the antibody include those that are involved in antigen binding. Examples, of such amino acids are provided in Figure 2.

In an exemplary embodiment, the humanized or hybrid antibody of the present invention may thus comprise from one to twenty-one non-human framework region amino acid residues in the heavy chain variable region (back mutations).

In another exemplary embodiment, the humanized or hybrid antibody may comprise from one to twelve non-human framework region amino acid residues in the light chain variable region (back mutations).

As used herein the term "from one to twenty" includes every individual values and ranges such as for example, 1, 2, 3, and up to 20; 1 to 20; 1 to 19; 1 to 18; 1 to 17; 1 to 16; 1 to 15 and so on; 2 to 20; 2 to 19; 2 to 18; 2 to 17 and so on; 3 to 20; 3 to 19; 3 to 18 and so on; 4 to 20; 4 to 19; 4 to 18; 4 to 17; 4 to 16 and so on; 5 to 20; 5 to 19; 5 to 18; 5 to 17 and so on, etc.
Likewise, the term "from one to twelve" includes every individual values and ranges such as for example, 1, 2, 3, and up to 12; 1 to 12; 1 to 11; 1 to 10 and so on; 2 to 12; 2 to 11, 2 to 10; 2 to 9; 2 to 8 and so on; 3 to 12; 3 to 11; 3 to 10; 3 to 9 and so on; 4 to 12; 4 to 11 and so on; 5 to 12; 5 to 11; 5 to 10; 5 to 9; 5 to 8; 5 to 7; and so on, etc.

Similar terms are to be interpreted in a similar manner.

The invention encompasses or uses amino acid sequence having a desired % identity with another amino acid sequence, for example, "a natural human antibody light chain framework region having at least 70% identity with the light chain framework region of the non-human parent antibody" or "a natural human antibody heavy chain framework region having at least 70% identity with the heavy chain framework region of the non-human parent antibody".

The term "a natural human antibody light chain framework region having at least 70% identity with the light chain framework region of the non-human parent antibody" encompasses a natural human antibody light chain framework region having 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity with the light chain framework region of the non-human parent antibody. The % identity is preferably determined over the entire framework regions (i.e., excluding the CDRs).

As mentioned above for with respect to variants, the term "a light chain framework region having at least 70% identity with the light chain framework region of the non-human parent antibody" encompasses a light chain framework region having 70% identity with the light chain framework region of the non-human parent antibody and which may also have 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence similarity with the light chain framework region of the non-human parent antibody.

The term "a natural human antibody heavy chain framework region having at least 70% identity with the heavy chain framework region of the non-human parent antibody" encompasses a natural human antibody heavy chain framework region having 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity with the heavy chain framework region of the non-human parent antibody.

As mentioned above for with respect to variants, the term "a heavy chain framework region having at least 70% identity with the heavy chain framework region of the non-human parent antibody" encompasses a heavy chain framework region having 70% identity with the heavy
chain framework region of the non-human parent antibody and which may also have 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, ..., immunoglobulin chains described herein may be ligated into a single expression vector and expressed simultaneously.

5 Production of the antibodies in cells

The antibodies that are disclosed herein can be made by a variety of methods familiar to those skilled in the art (recombinant DNA methods, chemical synthesis etc.).

In order to express the antibodies, nucleotide sequences able to encode any one of a light and heavy immunoglobulin chains described herein may be inserted into an expression vector, e.g., a vector that contains the elements for transcriptional and translational control of the inserted coding sequence in a particular host. These elements may include regulatory sequences, such as enhancers, constitutive and inducible promoters, and 5′ and 3′ un-translated regions. Methods that are well known to those skilled in the art may be used to construct such expression vectors. These methods include in vitro recombinant DNA techniques, synthetic techniques, and in vivo genetic recombination.

A variety of expression vector/host cell systems known to those of skill in the art may be utilized to express a polypeptide or RNA derived from nucleotide sequences able to encode any one of a light and heavy immunoglobulin chains described herein. These include, but are not limited to, microorganisms such as bacteria transformed with recombinant bacteriophage, plasmid, or cosmid DNA expression vectors; yeast transformed with yeast expression vectors; insect cell systems infected with baculovirus vectors; plant cell systems transformed with viral or bacterial expression vectors; or animal cell systems. For long-term production of recombinant proteins in mammalian systems, stable expression in cell lines may be effected. For example, nucleotide sequences able to encode any one of a light and heavy immunoglobulin chains described herein may be transformed into cell lines using expression vectors that may contain viral origins of replication and/or endogenous expression elements and a selectable or visible marker gene on the same or on a separate vector. The invention is not to be limited by the vector or host cell employed. In certain embodiments of the present invention, the nucleotide sequences able to encode any one of a light and heavy immunoglobulin chains described herein may each be ligated into a separate expression vector and each chain expressed separately. In another embodiment, both the light and heavy chains able to encode any one of a light and heavy immunoglobulin chains described herein may be ligated into a single expression vector and expressed simultaneously.
Alternatively, RNA and/or polypeptide may be expressed from a vector comprising nucleotide sequences able to encode any one of a light and heavy immunoglobulin chains described herein using an in vitro transcription system or a coupled in vitro transcription/translation system.

In general, host cells that contain nucleotide sequences able to encode any one of a light and heavy immunoglobulin chains described herein and/or that express a polypeptide encoded by the nucleotide sequences able to encode any one of a light and heavy immunoglobulin chains described herein, or a portion thereof, may be identified by a variety of procedures known to those of skill in the art. These procedures include, but are not limited to, DNA/DNA or DNA/RNA hybridizations, PCR amplification, and protein bioassay or immunoassay techniques that include membrane, solution, or chip based technologies for the detection and/or quantification of nucleic acid or amino acid sequences. Immunological methods for detecting and measuring the expression of polypeptides using either specific polyclonal or monoclonal antibodies are known in the art. Examples of such techniques include enzyme-linked immunosorbent assays (ELISAs), radioimmunoassays (RIAs), and fluorescence activated cell sorting (FACS). Those of skill in the art may readily adapt these methodologies to the present invention.

Host cells comprising nucleotide sequences able to encode any one of a light and heavy immunoglobulin chains described herein may thus be cultured under conditions for the transcription of the corresponding RNA and/or the expression of the polypeptide from cell culture. The polypeptide produced by a cell may be secreted or may be retained intracellularly depending on the sequence and/or the vector used. In an exemplary embodiment, expression vectors containing nucleotide sequences able to encode any one of a light and heavy immunoglobulin chains described herein may be designed to contain signal sequences that direct secretion of the polypeptide through a prokaryotic or eukaryotic cell membrane.

An exemplary embodiment of a nucleic acid encoding a heavy chain variable region is provided in SEQ ID NO.:21 and SEQ ID NO.:22.

An exemplary embodiment of a nucleic acid encoding a light chain variable region is provided in SEQ ID NO.:23 and SEQ ID NO.:24.

Due to the inherent degeneracy of the genetic code, other DNA sequences that encode the same, substantially the same or a functionally equivalent amino acid sequence may be produced and used, for example, to express a polypeptide encoded by nucleotide sequences able to encode any one of a light and heavy immunoglobulin chains described herein. The
nucleotide sequences of the present invention may be engineered using methods generally
known in the art in order to alter the nucleotide sequences for a variety of purposes including,
but not limited to, modification of the cloning, processing, and/or expression of the gene
product. DNA shuffling by random fragmentation and PCR reassembly of gene fragments and
synthetic oligonucleotides may be used to engineer the nucleotide sequences. For example,
oligonucleotide-mediated site-directed mutagenesis may be used to introduce mutations that
create new restriction sites, alter glycosylation patterns, change codon preference, produce
splice variants, and so forth.

In addition, a host cell strain may be chosen for its ability to modulate expression of the
inserted sequences or to process the expressed polypeptide in the desired fashion. Such
modifications of the polypeptide include, but are not limited to, acetylation, carboxylation,
glycosylation, phosphorylation, lipidation, and acylation. In an exemplary embodiment,
antibodies that contain particular glycosylation structures or patterns may be desired. Post-
translational processing, which cleaves a "prepro" form of the polypeptide, may also be used
to specify protein targeting, folding, and/or activity. Different host cells that have specific
cellular machinery and characteristic mechanisms for post-translational activities (e.g., CHO,
HeLa, MDCK, HEK293, and W138) are available commercially and from the American Type
Culture Collection (ATCC) and may be chosen to ensure the correct modification and
processing of the expressed polypeptide.

Those of skill in the art will readily appreciate that natural, modified, or recombinant nucleic
acid sequences may be ligated to a heterologous sequence resulting in translation of a fusion
polypeptide containing heterologous polypeptide moieties in any of the aforementioned host
systems. Such heterologous polypeptide moieties may facilitate purification of fusion
polypeptides using commercially available affinity matrices. Such moieties include, but are
not limited to, glutathione S-transferase (GST), maltose binding protein, thioredoxin,
calmodulin binding peptide, 6-His (His), FLAG, c-myc, hemaglutinin (HA), and antibody
epitopes such as monoclonal antibody epitopes.

In yet a further aspect, the present invention relates to a polynucleotide which may comprise a
nucleotide sequence encoding a fusion protein. The fusion protein may comprise a fusion
partner (e.g., HA, Fc, etc.) fused to the polypeptide (e.g., complete light chain, complete heavy
chain, variable regions, CDRs etc.) described herein.

Those of skill in the art will also readily recognize that the nucleic acid and polypeptide
sequences may be synthesized, in whole or in part, using chemical or enzymatic methods well
known in the art. For example, peptide synthesis may be performed using various solid-phase
techniques and machines such as the ABI 431 A Peptide synthesizer (PE Biosystems) may be used to automate synthesis. If desired, the amino acid sequence may be altered during synthesis and/or combined with sequences from other proteins to produce a variant protein.

When only one of the light chain variable domain or the heavy chain variable domain is available, an antibody or antigen-binding fragment may be reconstituted by screening a library of complementary variable domains using methods known in the art (Portolano et al. The Journal of Immunology (1993) 150:880-887, Clarkson et al., Nature (1991) 352:624-628). As such, knowing only one of the variable region amino acid sequence (heavy chain variable region or light chain variable region) is often enough to reconstitute an intact antibody having the desired antigen binding specificity. Therefore, nucleic acids encoding a light chain variable region or a heavy chain variable region of an antibody may be useful in identifying a complementary chain which when assembled with one another forms an antigen binding fragment or antibody having sufficient antigen binding specificity. A single stranded nucleic acid (e.g., oligo) or its complement having a high level of sequence identity with the nucleic acids encoding a light chain variable region or a heavy chain variable region of an antibody may be useful to detect the latter or to detect any other nucleic acid sequence sharing a high level of sequence identity.

Therefore, in an additional aspect, the present invention also provides an isolated nucleic acid encoding the light chain variable region and/or the heavy chain variable region of the humanized or hybrid antibody described herein, encoding the antigen binding fragment described herein or the isolated antibody described herein.

In yet another aspect, the present invention provides a vector or construct, comprising the (isolated) nucleic acid described herein. In accordance with the present invention, the vector may be, for example, a mammalian expression vector, a bacterial expression vector etc.

The present invention also encompasses, an isolated cell comprising the isolated nucleic acid described herein or the vector described herein. Isolated cells expressing the antibody or antigen binding fragment of the present invention are also encompassed herewith. Suitable cells, include for example, a mammalian cell, a bacterial cell, etc.

Yet another aspect of the invention relate to a method for making a humanized or hybrid anti-clusterin antibody which may comprise introducing non-human heavy chain CDR amino acid residues of a non-human antibody capable of specific binding to clusterin into a framework region of a natural human antibody heavy chain variable region.
Yet an additional aspect of the invention relates to a method for making a humanized or hybrid anti-clusterin antibody which may comprise transforming a cell with a nucleic acid encoding a heavy chain variable region (or a complete heavy chain) comprising non-human heavy chain CDR amino acid residues of a non-human antibody capable of specific binding to clusterin and framework region amino acids of a natural human antibody heavy chain variable region. The method may also comprise transforming the cell with a nucleic acid encoding a complementary light chain variable region (or a complete light chain).

In another aspect, the invention relates to a method for making a humanized or hybrid anti-clusterin antibody which may comprise expressing a heavy chain variable region (or a complete heavy chain) comprising non-human heavy chain CDR amino acid residues of a non-human antibody capable of specific binding to clusterin and framework region amino acids of a natural human antibody heavy chain variable region. The method may also comprise expressing a complementary light chain variable region (or a complete light chain).

The natural human antibody heavy chain variable region which may be selected for humanization purposes may have the following characteristics: a) a three-dimensional structure similar to or identical (superimposable) to that of a heavy chain of the non-human antibody, b) a framework region having an amino acid sequence at least 70% identical to a heavy chain framework region of the non-human antibody, and/or; c) (a number of) amino acid residues in a heavy chain CDR (e.g., all three CDRs) that is the same or substantially the same as that of the non-human heavy chain CDR amino acid residues.

The method may thus comprise, for example, introducing non-human heavy chain CDR amino acid residues of at least two CDRs of the non-human antibody. The nucleic acid used in methods of making humanized or hybrid antibodies may thus encode at least two CDRs of the non-human antibody. The heavy chain variable region that is expressed in methods of making humanized or hybrid antibodies may thus comprise at least two CDRs of the non-human antibody.

The method may preferably comprise introducing non-human heavy chain CDR amino acid residues of all three CDRs. The nucleic acid used in methods of making humanized or hybrid antibodies may thus encode three CDRs of the non-human antibody. The heavy chain variable region that is expressed in methods of making humanized or hybrid antibodies may thus comprise three CDRs of the non-human antibody.

The method thus includes introducing the non-human CDRs comprising the amino acid sequence of SEQ ID NO.:1, SEQ ID NO.:2 and SEQ ID NO.:3. The nucleic acid used in
methods of making humanized or hybrid antibodies may thus encode SEQ ID NO.:1, SEQ ID NO.:2 and SEQ ID NO.:3. The heavy chain variable region that is expressed in methods of making humanized or hybrid antibodies may thus comprise SEQ ID NO.:1, SEQ ID NO.:2 and SEQ ID NO.:3.

The method thus also includes introducing the non-human CDRs comprising the amino acid sequence of SEQ ID NO.:11, SEQ ID NO.:12 and SEQ ID NO.:13. The nucleic acid used in methods of making humanized or hybrid antibodies may thus encode SEQ ID NO.:11, SEQ ID NO.:12 and SEQ ID NO.:13. The heavy chain variable region that is expressed in methods of making humanized or hybrid antibodies may thus comprise SEQ ID NO.:11, SEQ ID NO.:12 and SEQ ID NO.:13.

Alternatively, shorter versions of the above-mentioned CDRs may be introduced into a framework region of a natural human antibody heavy chain variable region.

The method of the present invention may further comprise introducing non-human light chain CDR amino acid residues of a non-human antibody capable of specific binding to clusterin into a framework region of a natural human antibody light chain variable region.

The method of the present invention may comprise allowing expression of a nucleic acid encoding a light chain variable region (or a complete light chain) comprising non-human light chain CDR amino acid residues of a non-human antibody capable of specific binding to clusterin and framework region amino acids of a natural human antibody light chain variable region. The method may also comprise transforming the cell with a nucleic acid encoding a complementary heavy chain variable region (or a complete heavy chain).

In another aspect, the invention relates to a method for making a humanized or hybrid anti-clusterin antibody which may comprise expressing a light chain variable region (or a complete heavy chain) comprising non-human light chain CDR amino acid residues of a non-human antibody capable of specific binding to clusterin and framework region amino acids of a natural human antibody light chain variable region. The method may also comprise expressing a complementary heavy chain variable region (or a complete heavy chain).

The natural human antibody light chain variable region which may be selected for humanization purposes may have the following characteristics: a) a three-dimensional structure similar to or identical (superimposable) to that of a light chain of the non-human antibody, b) a framework region having an amino acid sequence at least 70% identical to a light chain framework region of the non-human antibody, and/or; c) (a number of) amino acid
residues in a light chain CDR (e.g., all three CDRs) that is the same or substantially the same as that of the non-human light chain CDR amino acid residues.

The method may thus comprise, for example, introducing non-human light chain CDR amino acid residues of at least two CDRs of the non-human antibody. The nucleic acid used in methods of making humanized or hybrid antibodies may thus encode at least two CDRs of the non-human antibody. The light chain variable region that is expressed in methods of making humanized or hybrid antibodies may thus comprise at least two CDRs of the non-human antibody.

The method may preferably comprise introducing non-human light chain CDR amino acid residues of all three CDRs. The nucleic acid used in methods of making humanized or hybrid antibodies may thus encode three CDRs of the non-human antibody. The light chain variable region that is expressed in methods of making humanized or hybrid antibodies may thus comprise three CDRs of the non-human antibody.

The method thus includes introducing the non-human CDRs comprising the amino acid sequence of SEQ ID NO.:4, SEQ ID NO.:5 and SEQ ID NO.:6. The nucleic acid used in methods of making humanized or hybrid antibodies may thus encode SEQ ID NO.:4, SEQ ID NO.:5 and SEQ ID NO.:6. The light chain variable region that is expressed in methods of making humanized or hybrid antibodies may thus comprise SEQ ID NO.:4, SEQ ID NO.:5 and SEQ ID NO.:6.

The method thus also includes introducing the non-human CDRs comprising the amino acid sequence of SEQ ID NO.:14, SEQ ID NO.:15 and SEQ ID NO.:16. The nucleic acid used in methods of making humanized or hybrid antibodies may thus encode SEQ ID NO.:14, SEQ ID NO.:15 and SEQ ID NO.:16. The light chain variable region that is expressed in methods of making humanized or hybrid antibodies may thus comprise SEQ ID NO.:14, SEQ ID NO.:15 and SEQ ID NO.:16.

Alternatively, shorter versions of the above-mentioned CDRs may be introduced into a framework region of a natural human antibody heavy chain variable region.

An additional aspect of the invention concerns a method for making a humanized anti-clusterin antibody which may comprise introducing non-human heavy chain CDR amino acid residues of a non-human antibody capable of specific binding to clusterin into a framework region of a natural human antibody heavy chain variable region and introducing non-human light chain CDR amino acid residues of a non-human antibody capable of specific binding to clusterin into a framework region of a natural human antibody light chain variable region.
Yet, an additional aspect of the invention concerns a method for making a humanized anti-clusterin antibody which may comprise allowing expression of a nucleic acid encoding non-human heavy chain CDR amino acid residues of a non-human antibody capable of specific binding to clusterin and a framework region of a natural human antibody heavy chain variable region and allowing expression of a nucleic acid encoding a non-human light chain CDR amino acid residues of a non-human antibody capable of specific binding to clusterin and a framework region of a natural human antibody light chain variable region.

The natural human antibody heavy chain variable region which may be selected for humanization purposes may have the following characteristics: a) comprising a framework region having an amino acid sequence at least 70% identical to a heavy chain framework region of the non-human antibody, and; b) having (a number of) amino acid residues in a heavy chain CDR (e.g., all three CDRs) that is the same or substantially the same as that of the non-human heavy chain CDR amino acid residues, while the natural human antibody light chain variable region which may be selected for humanization purposes may have the following characteristics: a) comprising a framework region having an amino acid sequence at least 70% identical to a light chain framework region of the non-human antibody, and; b) having (a number of) amino acid residues in a light chain CDR (e.g., all three CDRs) that is the same or substantially the same as that of the non-human light chain CDR amino acid residues. The natural human antibody variable region(s) preferably has a three-dimensional structure similar to or identical (superimposable) to that of the non-human antibody variable region(s).

In accordance with the present invention, the method may comprise introducing non-human heavy chain CDR amino acid residues of at least two CDRs of the non-human antibody. The nucleic acid used in methods of making humanized or hybrid antibodies may thus encode at least two CDRs of the non-human antibody. The heavy chain variable region that is expressed in methods of making humanized or hybrid antibodies may thus comprise at least two CDRs of the non-human antibody.

Alternatively, the method may comprise introducing non-human heavy chain CDR amino acid residues of all three CDRs. The nucleic acid used in methods of making humanized or hybrid antibodies may thus encode three CDRs of the non-human antibody. The heavy chain variable region that is expressed in methods of making humanized or hybrid antibodies may thus comprise three CDRs of the non-human antibody.

Also in accordance with the present invention, the method may comprise introducing non-human light chain CDR amino acid residues of at least two CDRs of the non-human antibody.
The nucleic acid used in methods of making humanized or hybrid antibodies may thus encode at least two CDRs of the non-human antibody. The light chain variable region that is expressed in methods of making humanized or hybrid antibodies may thus comprise at least two CDRs of the non-human antibody.

Alternatively, the method may comprise introducing non-human light chain CDR amino acid residues of all three CDRs. The nucleic acid used in methods of making humanized or hybrid antibodies may thus encode three CDRs of the non-human antibody. The light chain variable region that is expressed in methods of making humanized or hybrid antibodies may thus comprise three CDRs of the non-human antibody.

Using the method described herein, CDRs comprising the amino acid sequence of SEQ ID NO.:1, SEQ ID NO.:2 and SEQ ID NO.:3 are advantageously imported into the natural human antibody heavy chain variable region. The nucleic acid used in methods of making humanized or hybrid antibodies may thus encode SEQ ID NO.:1, SEQ ID NO.:2 and SEQ ID NO.:3. The light chain variable region that is expressed in methods of making humanized or hybrid antibodies may thus comprise SEQ ID NO.:1, SEQ ID NO.:2 and SEQ ID NO.:3.

Using the method described herein, CDRs comprising the amino acid sequence of SEQ ID NO.:11, SEQ ID NO.:12 and SEQ ID NO.:13 are advantageously imported into the natural human antibody heavy chain variable region. The nucleic acid used in methods of making humanized or hybrid antibodies may thus encode SEQ ID NO.:11, SEQ ID NO.:12 and SEQ ID NO.:13. The light chain variable region that is expressed in methods of making humanized or hybrid antibodies may thus comprise SEQ ID NO.:11, SEQ ID NO.:12 and SEQ ID NO.:13.

Using the method described herein, CDRs comprising the amino acid sequence of SEQ ID NO.:4, SEQ ID NO.:5 and SEQ ID NO.:6 are advantageously imported into the natural human antibody light chain variable region. The nucleic acid used in methods of making humanized or hybrid antibodies may thus encode SEQ ID NO.:4, SEQ ID NO.:5 and SEQ ID NO.:6. The light chain variable region that is expressed in methods of making humanized or hybrid antibodies may thus comprise SEQ ID NO.:4, SEQ ID NO.:5 and SEQ ID NO.:6.

Using the method described herein, CDRs comprising the amino acid sequence of SEQ ID NO.:14, SEQ ID NO.:15 and SEQ ID NO.:16 are advantageously imported into the natural human antibody light chain variable region. The nucleic acid used in methods of making humanized or hybrid antibodies may thus encode SEQ ID NO.:14, SEQ ID NO.:15 and SEQ ID NO.:16. The light chain variable region that is expressed in methods of making humanized
or hybrid antibodies may thus comprise SEQ ID NO.:14, SEQ ID NO.:115 and SEQ ID NO.:16.

In another aspect, the present invention, concerns a method for making a humanized or hybrid anti-clusterin antibody which may comprise transforming a host cell with a nucleic acid encoding the heavy chain variable region described herein.

Exemplary embodiments of suitable heavy chain variable region are those of the non-human antibody which may comprise three CDRs having the amino acid sequence of SEQ ID NO.:1, SEQ ID NO.:2 and SEQ ID NO.:3 and natural human antibody heavy chain framework region having an amino acid sequence at least 70% identical to a heavy chain framework region of the non-human antibody. Preferably, the natural human antibody may comprise (a number of) heavy chain CDR amino acid residues that is the same or substantially the same as that of a CDR (e.g., all three CDRs) of the non-human heavy chain.

Exemplary embodiments of suitable heavy chain variable region are those of the non-human antibody which may comprise three CDRs having the amino acid sequence of SEQ ID NO.:11, SEQ ID NO.:12 and SEQ ID NO.:13 and natural human antibody heavy chain framework region having an amino acid sequence at least 70% identical to a heavy chain framework region of the non-human antibody. Preferably, the natural human antibody may comprise (a number of) heavy chain CDR amino acid residues that is the same or substantially the same as that of a CDR (e.g., all three CDRs) of the non-human heavy chain.

The method of the present invention may further comprise transforming a host cell with a nucleic acid encoding a complementary light chain.

If desirable, the complementary light chain may be encoded by the same nucleic acid as that encoding the heavy chain.

Such complementary light chain may comprise a light chain variable region of a non-human antibody which may comprise three CDRs having the amino acid sequence of SEQ ID NO.:4, SEQ ID NO.:5 and SEQ ID NO.:6 and natural human antibody light chain framework region having an amino acid sequence at least 70% identical to a light chain framework region of the non-human antibody. Preferably, the natural human antibody may comprise (a number of) light chain CDR amino acid residues that is the same or substantially the same as that of a CDR (e.g., all three CDRs) of the non-human light chain.
Such complementary light chain may comprise a light chain variable region of a non-human antibody which may comprise three CDRs having the amino acid sequence of SEQ ID NO.:14, SEQ ID NO.:15 and SEQ ID NO.:16 and natural human antibody light chain framework region having an amino acid sequence at least 70% identical to a light chain framework region of the non-human antibody. Preferably, the natural human antibody may comprise (a number of) light chain CDR amino acid residues that is the same or substantially the same as that of a CDR (e.g., all three CDRs) of the non-human light chain.

In yet another aspect, the present invention relates to a method for making a humanized or hybrid anti-clusterin antibody which may comprise transforming a host cell with a nucleic acid encoding a light chain variable region.

Exemplary embodiments of suitable light chain variable region are those of a non-human antibody which may comprise three CDRs having the amino acid sequence of SEQ ID NO.:4, SEQ ID NO.:5 and SEQ ID NO.:6 and natural human antibody light chain framework region having an amino acid sequence at least 70% identical to a light chain framework region of the non-human antibody. Preferably, the natural human antibody comprises (a number of) light chain CDR amino acid residues that is the same or substantially the same as that of a CDR (e.g., all three CDRs) of the non-human light chain.

Exemplary embodiments of suitable light chain variable region are those of a non-human antibody which may comprise three CDRs having the amino acid sequence of SEQ ID NO.:14, SEQ ID NO.:15 and SEQ ID NO.:16 and natural human antibody light chain framework region having an amino acid sequence at least 70% identical to a light chain framework region of the non-human antibody. Preferably, the natural human antibody comprises (a number of) light chain CDR amino acid residues that is the same or substantially the same as that of a CDR (e.g., all three CDRs) of the non-human light chain.

The method of the present invention may further comprise transforming a host cell with a nucleic acid encoding a complementary heavy chain.

If desirable, the complementary heavy chain may be encoded by the same nucleic acid as that encoding the light chain.

Pharmaceutical compositions of the antibodies and their use

In another aspect, the present invention relates to a pharmaceutical composition which may comprise, for example, the humanized or hybrid antibody described herein, the antigen
binding fragment described herein or the isolated antibody described herein and a pharmaceutically acceptable carrier.

Yet other aspects of the invention relate to the use of the isolated antibody or antigen binding fragment described herein in the treatment or diagnosis of diseases.

Yet another aspect of the invention relates to a combination therapy which includes the pharmaceutical composition described herein and a chemotherapeutic agent.

In accordance with the present invention, the pharmaceutical composition may be administered (is administrable) concurrently with the chemotherapeutic agent.

Also in accordance with the present invention, the pharmaceutical composition and the chemotherapeutic agent may be administered (is administrable) at different time intervals.

Further in accordance with the present invention, the chemotherapeutic agent may be conjugated with the antibody or antigen binding fragment.

In addition to the active ingredients, a pharmaceutical composition may contain pharmaceutically acceptable carriers comprising water, PBS, salt solutions, gelatins, oils, alcohols, and other excipients and auxiliaries that facilitate processing of the active compounds into preparations that may be used pharmaceutically. In other instances, such preparations may be sterilized.

As used herein, "pharmaceutical composition" means therapeutically effective amounts of the agent together with pharmaceutically acceptable diluents, preservatives, solubilizers, emulsifiers, adjuvant and/or carriers. A "therapeutically effective amount" as used herein refers to that amount which provides a therapeutic effect for a given condition and administration regimen. Such compositions are liquids or lyophilized or otherwise dried formulations and include diluents of various buffer content (e.g., Tris-HCl, acetate, phosphate), pH and ionic strength, additives such as albumin or gelatin to prevent absorption to surfaces, detergents (e.g., Tween 20, Tween 80, Pluronic F68, bile acid salts). Solubilizing agents (e.g., glycerol, polyethylene glycerol), anti-oxidants (e.g., ascorbic acid, sodium metabisulfite), preservatives (e.g., thimerosal, benzyl alcohol, parabens), bulking substances or tonicity modifiers (e.g., lactose, mannitol), covalent attachment of polymers such as polyethylene glycol to the protein, complexation with metal ions, or incorporation of the material into or onto particulate preparations of polymeric compounds such as polyactic acid, polyglycolic acid, hydrogels, etc, or onto liposomes, microemulsions, micelles, unilamellar or multilamellar vesicles, erythrocyte ghosts, or spheroplasts. Such compositions will influence
the physical state, solubility, stability, rate of in vivo release, and rate of in vivo clearance. Controlled or sustained release compositions include formulation in lipophilic depots (e.g., fatty acids, waxes, oils). Also comprehended by the invention are particulate compositions coated with polymers (e.g., poloxamers or poloxamines). Other embodiments of the compositions of the invention incorporate particulate forms protective coatings, protease inhibitors or permeation enhancers for various routes of administration, including parenteral, pulmonary, nasal, oral, vaginal, rectal routes. In one embodiment the pharmaceutical composition is administered parenterally, paracancerally, transmucosally, transdermally, intramuscularly, intravenously, intradermal ly, subcutaneously, intraperitonealy, intraventricularly, intracranially and intratumorally.

Further, as used herein "pharmaceutically acceptable carrier" or "pharmaceutical carrier" are known in the art and include, but are not limited to, 0.01-0.1 M or 0.05 M phosphate buffer or 0.8 % saline. Additionally, such pharmaceutically acceptable carriers may be aqueous or non-aqueous solutions, suspensions, and emulsions. Examples of non-aqueous solvents are propylene glycol, polyethylene glycol, vegetable oils such as olive oil, and injectable organic esters such as ethyl oleate. Aqueous carriers include water, alcoholic/aqueous solutions, emulsions or suspensions, including saline and buffered media. Parenteral vehicles include sodium chloride solution, Ringer's dextrose, dextrose and sodium chloride, lactated Ringer's or fixed oils. Intravenous vehicles include fluid and nutrient replenishers, electrolyte replenishers such as those based on Ringer's dextrose, and the like. Preservatives and other additives may also be present, such as, for example, antimicrobials, antioxidants, collating agents, inert gases and the like.

The pharmaceutical compositions utilized in this invention may be administered by any number of routes including, but not limited to, oral, intravenous, intramuscular, intra-arterial, intramedullary, intrathecal, intraventricular, transdermal, subcutaneous, intraperitoneal, intranasal, enteral, topical, sublingual, or rectal means.

The term "treatment" for purposes of this disclosure refers to both therapeutic treatment and prophylactic or preventative measures, wherein the object is to prevent or slow down (lessen) the targeted pathologic condition or disorder. Those in need of treatment include those already with the disorder as well as those prone to have the disorder or those in whom the disorder is to be prevented.

The antibodies and antigen binding fragments may have therapeutic uses in the treatment of various diseases. In certain instances, the antibodies or antigen binding fragments may interact with cells that express an antigen of interest and induce an immunological reaction by
mediating ADCC. In other instances, the antibodies or fragments may block the interaction of the antigen with its protein partners. In yet other instances, the antibodies or fragments may sequester the antigen.

A "chemotherapeutic agent" is a compound useful in the treatment of cancer. Examples of chemotherapeutic agents include alkylating agents such as thiotepa and cyclophosphamide; alkyl sulfonates such as busulfan, imposulfan and piposulfan; aziridines such as benzodopa, carboquone, meturedopa, and uredopa; ethylenimines and methylamines including altretamine, triethylenemelamine, triethylene phosphoramidate, triethylene thiophosphoramidate and trimethylolomelamine; nitrogen mustards such as chlorambucil, chlomaphazine, chlophosphamide, estramustine, ifosfamide, mechlorethamine, mechlorethamine oxide hydrochloride, melphalan, novembichin, pheneisterine, prednimustine, trofosfamide, uracil mustard; nitrosureas such as carmustine, chlorozotocin, fotemustine, lomustine, nimustine, ranimustine; antibiotics such as aclacinomysins, actinomycin, authramycin, azaserine, bleomycins, cactinomycin, calicheamicin, carabion, carminomycin, carzinophilin, chromomycins, dactinomycin, daunorubicin, detorubicin, 6-diazo-5-oxo-L-norleucine, doxorubicin, epirubicin, esorubicin, idarubicin, marcellomycin, mitomycins, mycophenolic acid, nogalamycin, oliomycins, peplomycin, potfiromycin, puromycin, quelamycin, rodorubicin, streptonigrin, streptozocin, tubercidin, ubenimex, zinostatin, zorubicin; anti-metabolites such as methotrexate and 5-fluorouracil (5-FU); folic acid analogues such as denopterin, methotrexate, pteropterin, trimetrexate; purine analogs such as fludarabine, 6-mercaptopurine, thiamiprine, thioguanine; pyrimidine analogs such as ancitabine, azacitidine, 6-azauridine, carmofur, cytarabine, dideoxyuridine, doxifluridine, enocitabine, flouxuridine; androgens such as calusterone, dromostanolone propionate, epitiostane, testolactone; anti-adrenals such as aminoglutethimide, mitotane, trilostane; folic acid replenisher such as frolinic acid; aceglatone; aldrophosphamide glycoside; aminolevulinic acid; amsacrine; bestrabucil; bisantren; edatraxate; defofamine; demecolcine; diaziouquone; elfomithine; ellipitinum acetate; etogluclid; gallium nitrate; hydroxyurea; lentinan; lonidamine; mitoguazone; mitoxantrone; mopiynamol; nitracrine; pentostatin; phenamet; pirarubicin; podophyllinic acid; 2-ethylhydrazide; procarbazine; PSK7; razoxane; sizofiran; spirogermanium; tenuazonic acid; triaziquone; 2,2',2''-trichloroetriethylamine; urethan; vindesine; dacarbazine; mannomustine; mitobronitol; mitolactol; pipobroman; gacytosine; arabinoside ("Ara-C"); cyclophosphamide; thiotepe; taxanes, e.g. paclitaxel and doxetaxel; chlorambucil; gemcitabine; 6-thioguanine; mercaptopurine; methotrexate; platinum analogs such as cisplatin and carboplatin; vinblastine; platinum; etoposide (VP-16); ifosfamide; mitomycinc C; mitoxantrone; vincristine; vinorelbine; navelbine; novantrone; teniposide; daunomycin; aminopterin; xeloda; ibandronate; CPT-11; topoisomerase inhibitor RFS 2000;
difluoromethylornithine (DMFO); retinoic acid; esperamicins; capecitabine; and pharmaceutically acceptable salts, acids or derivatives of any of the above. Also included in this definition are anti-hormonal agents that act to regulate or inhibit hormone action on tumors such as anti-estrogens including for example tamoxifen, raloxifene, aromatase inhibiting 4(5)-imidazoles, 4-hydroxytamoxifen, trioxifene, keoxifene, LY17018, onapristone, and toremifene (Fareston); and anti-androgens such as flutamide, nilutamide, bicalutamide, leuprolide, and goserelin; and pharmaceutically acceptable salts, acids or derivatives of any of the above.

**Antibody conjugates**

The antibody or antigen binding fragment of the present invention may be conjugated with a detectable moiety (i.e., for detection or diagnostic purposes) or with a therapeutic moiety (for therapeutic purposes, e.g., chemotherapeutic agent)

A "detectable moiety" is a moiety detectable by spectroscopic, photochemical, biochemical, immunochemical, chemical and/or other physical means. A detectable moiety may be coupled either directly and/or indirectly (for example via a linkage, such as, without limitation, a DOTA or NHS linkage) to antibodies and antigen binding fragments thereof of the present invention using methods well known in the art. A wide variety of detectable moieties may be used, with the choice depending on the sensitivity required, ease of conjugation, stability requirements and available instrumentation. A suitable detectable moiety include, but is not limited to, a fluorescent label, a radioactive label (for example, without limitation, $^{125}$I, $^{111}$In, $^{99}$Tc, $^{11}$I and including positron emitting isotopes for PET scanner etc.), a nuclear magnetic resonance active label, a luminiscent label, a chemiluminescent label, a chromophore label, an enzyme label (for example and without limitation horseradish peroxidase, alkaline phosphatase, etc.), quantum dots and/or a nanoparticle. Detectable moiety may cause and/or produce a detectable signal thereby allowing for a signal from the detectable moiety to be detected.

In another exemplary embodiment of the invention, the antibody or antigen binding fragment thereof may be coupled (modified) with a therapeutic moiety (e.g., drug, cytotoxic moiety).

In an exemplary embodiment, the antibodies and antigen binding fragments may comprise a chemotherapeutic agent or cytotoxic agent. For example, the antibody and antigen binding fragments may be conjugated to the chemotherapeutic agent or cytotoxic agent. In addition to those listed elsewhere in the present application, such chemotherapeutic or cytotoxic agents include, but are not limited to, Yttrium-90, Scandium-47, Rhenium-186, Iodine-131, Iodine-
125, and many others recognized by those skilled in the art (e.g., lutetium (e.g., Lu¹⁷⁷), bismuth (e.g., Bi¹⁵³), copper (e.g., Cu⁶¹)). In other instances, the chemotherapeutic or cytotoxic agent may be comprised of, among others known to those skilled in the art, 5-fluorouracil, adriamycin, irinotecan, taxanes, pseudomonas endotoxin, ricin and other toxins.

Alternatively, in order to carry out the methods of the present invention and as known in the art, the antibody or antigen binding fragment of the present invention (conjugated or not) may be used in combination with a second molecule (e.g., a secondary antibody, etc.) which is able to specifically bind to the antibody or antigen binding fragment of the present invention and which may carry a desirable detectable, diagnostic or therapeutic moiety.

Methods of treatment

A further aspect of the invention relates to a method of reducing the growth of a cancer cell expressing clusterin or of reducing volume of a tumor comprising clusterin-expressing cells. The method may comprise, for example, administering to a mammal in need an anti-clusterin antibody such as a polyclonal antibody, a monoclonal antibody, a chimeric antibody, a humanized antibody, an isolated human antibody, a hybrid antibody and a fragment thereof.

The method may further comprise administering a chemotherapeutic agent.

The present invention also relates in an additional aspect thereof to a method of treating a disease associated with increased clusterin expression or secretion. The method may comprise administering the humanized or hybrid antibody described herein, the antigen binding fragment described herein or the isolated antibody described herein to a mammal in need.

A mammal in need which would benefit from such method of treatment may include, for example, a mammal having a carcinoma, a mammal having an elevated level of clusterin, a mammal having an elevated level of plasma or blood clusterin, a mammal carrying or susceptible of carrying cells capable of epithelial-to-mesenchymal transition, a mammal having a disease related to an increased level of clusterin (pre-clusterin or secreted clusterin) or of clusterin expression or secretion (including blood or plasma clusterin) etc.

Another aspect of the invention concerns the use of the humanized or hybrid antibody described herein, the antigen binding fragment described herein or the isolated antibody described herein in the manufacture of a medicament for the treatment of a disease associated with clusterin expression or secretion.
Kits and assays

In yet a further aspect, the present invention provides a kit comprising a vial or vials which
could comprise, for example, the humanized or hybrid antibody described herein, the antigen
binding fragment described herein or the isolated antibody described. The kit may be used for
detection purposes or for therapeutic purposes.

In another exemplary embodiment, the kit may comprise the isolated nucleic acid described
herein or the vector described herein. Such kit may find utility for detecting complementary
nucleic acids, expressing the protein which it encodes or else.

The present invention therefore also relates to a method of detecting clusterin (pre-clusterin
and secreted clusterin) by contacting a sample containing or suspected of containing clusterin
with the humanized or hybrid antibody described herein, the antigen binding fragment
described herein or the isolated antibody described. Detection is carried out with an apparatus
having appropriate sensors which may detect the binding of an antigen to an antibody (e.g.,
BIAcore™, microplate reader, spectrophotometer, etc.). Such apparatus may be provided
with a computer system.

As used herein the term "three-dimensional structure similar to that of or superimposable to"
with respect to a variable region means that upon using a computerized model, a specified
variable region has a conformation that allows for the antigen binding site to be exposed in a
similar manner as another variable region. The variable regions are said to be superimposable
when the computerized representation of the variable region amino acids occupies a similar
position in space as the corresponding amino acids of another variable region.

As used herein the term "a modeled variable region" means a computerized representation of
a variable region that is obtained from known three dimensional structures of closely related
antibody variable region.

As used herein the term "non-human" encompasses without limitation rodent (e.g., mouse,
rats, etc.), rabbit or nonhuman primate etc.

As used wherein the term "non-human complementarity determining region amino acid
residues" therefore means that amino acid residues of the complementarity determining
region originates from a non-human, typically a rodent such as a mouse.

As used herein the term "non-human parent antibody" therefore encompasses an antibody
obtained from a non-human which is used as starting material for humanization procedures.
The term "transforming a host cell" includes several techniques known in the art for transferring or introducing a desired nucleic acid into a host cell. Such techniques include, without limitation, transfection, infection, lipofection, injection, transduction, nucleofection, electroporation, sonoporation, heat shock, magnetofection, etc.

The term "importing" with respect to non-human heavy chain or light chain CDR amino acid residues encompasses physical and computerized methods, e.g., cloning techniques, chemical synthesis of a nucleic acid or protein, computer generated humanized antibodies, etc. As used herein the term "substantially the same" with respect to the number of amino acids, means that a variation of +/- 3 amino acids or preferable +/- 2 amino acids or even more preferably +/- 1 amino acid may be tolerated.

**Example 1- Humanization by design of the anti-clusterin mouse monoclonal antibodies**

3D modeling of the variable regions of the mouse 16B5 monoclonal antibody.

This task was readily accomplished by mutating 3 light-chain residues and 7 heavy-chain residues in the available crystal structures of two different mouse antibodies (Protein Data Bank (PDB) codes 1Q9Q and 1TY7, respectively) followed by assembly of the light and heavy chains by superimposing the template structures. Part of the CDR-H3 loop was based on another antibody structure (PDB code 1UJ3, a humanized antibody) that also has high sequence similarity to the heavy chain of 16B5 but, unlike the mouse template structure, displays the same length for the CDR-H3 loop. The resulting structure was refined by energy minimization with the AMBER force-field and then used in the subsequent analysis. A good quality of the resulting homology model is expected in this case, given the high homology of the mouse 16B5 sequence to available structural templates. Nonetheless, comparable results were obtained in parallel control homology modeling experiments where we modeled the mouse 16B5 variable region by employing generic 3D homology modeling programs like Modeller or Composer, or antibody- specialized 3D homology modeling as implemented in the WAM software. A representation of the modeled variable regions of the mouse 16B5 antibody is given in Figure 1.

Characterization of the 16B5 source donor (mouse) amino-acid sequences and modeled structure.

This step was carried out to estimate the humanness index, to delineate the CDRs, canonical residues, inter-chain packing (VH/VL interface residues), variable-/constant-region packing (VH/CH and VL/CL interface residues), unusual framework residues, potential N- and O-
glycosylation sites, buried residues, Vernier zone residues, and proximity to CDRs. Internet-available resources and local software were used to assess these properties.

**Selection of the best human light-chain and heavy-chain frameworks for the mouse CDRs.**

Selection of the best human light-chain and heavy-chain frameworks was done by standard sequence homology comparison against a local copy of human germline databases (VBASE), against other sequence libraries (Genbank and SwissProt), as well as the set of human framework consensus sequences. BLAST searches were conducted to retrieve sequence matches with highest homology in the framework region only (thus excluding CDRs) while matching the length of the CDR loops. The structures of the human or humanized variable sequences most similar to the 16B5 variable sequences identified from PDB were superimposed onto the modeled structure of the 16B5 variable region for structural comparison. Several most similar human framework sequences were initially retained in order to assess the amino-acid variability at candidate positions for mutation, as well as to provide a pool of suitable framework sequences as backup in the event of affinity loss upon humanization. The closest human framework sequences are aligned to the murine 16B5 sequences in Figure 2.

**Identifying mouse-framework residues that can influence conformation and antigen binding.**

The identification mouse framework residues that can influence conformation and antigen binding is an important step that flags amino-acid residues that should be mutated to the corresponding human sequences with particular care. These residues represent primary candidates for back-mutations to the mouse sequences in case of affinity loss. This is the most difficult and unpredictable step of humanization by design, particularly in the absence of an experimental structure of the antibody-antigen complex. This step relies on the identification of residues in one or more of the following categories: canonical, CDR-H3, Vernier zone, unusual, CDR-proximal (within 5 Å), inter-chain packing, and glycosylation-site residues. These residues might affect antigen-binding site and affinity directly or indirectly. The final humanized sequences of the 16B5 anti-clusterin mAb require 13 framework mutations in the light chain and 22 framework mutations in the heavy chain relative to the murine sequences, while not altering the CDRs regions. Surprisingly, a careful structural and comparative sequence analyses indicated a high probability of retaining high antigen-binding affinity by introducing all these mutations, thus aiming at reaching the highest degree of humanization allowed by the CDR grafting technique (i.e., 100%, excluding CDRs). 3D modeling of the designed humanized antibody supports this prediction. Nonetheless, we have identified candidate residues for back-mutations, including CDR-proximal residues (3 in the light chain...
and 9 in the heavy chain within 5 Å from CDRs), one light-chain residue in contact with the heavy chain, as well as several buried residues (and hence likely not be immunogenic) that may be converted back to the mouse sequence (4 in the light chain and 6 in the heavy chain). Mutated residues and candidate residues for back-mutations are indicated in Figure 1 and Figure 2.

Additional structural analysis.

Prior to submitting the humanized sequence for recombinant expression, additional structural analysis included selection of signal peptide, selection of isotype, and analysis of structural compatibility at the variable-/constant-region junctions. In addition, a comparative analysis of inter-chain packing and variable-/constant-region packing between mouse and humanized antibodies indicated that in the case of 16B5 humanization it will be feasible to generate hybrid antibodies combining humanized and chimeric (mouse variable region) chains, i.e., mouse/mouse (M/M), mouse/humanized (M/H), humanized/mouse (H/M) and humanized/humanized (H/H) as light-chain/heavy-chain pairing. The isotype selected for the anti-clusterin antibodies was human IgG2. Human IgG2 do not harbor potent effector functions which is the hallmark of blocking antibodies as those disclosed here. In addition, human IgG2 are less susceptible to proteolytic cleavage which makes provides antibodies of this isotype more stability in vivo.

3D modeling of the variable regions of the mouse 21B12 monoclonal antibody.

Modeling of the 21B12 mouse anti-clusterin antibody was conducted according to the teachings describes above for 16B5. The resulting humanized 21B12 was 100 humanized and required 18 mutations in the heavy chain and 14 mutations in the light chain. Mutated residues and candidate residues for back-mutations are indicated in Figure 7 and Figure 8.

Example 2. Kinetic analysis of anti-clusterin antibodies

The purpose of these investigations is to determine the kinetics parameters of anti-clusterin antibodies. In particular, to determine whether the humanization of the 16B5 and 21B12 anti-clusterin monoclonal antibody affects the kinetics parameters of its binding to human clusterin. To this end, a kinetic analysis method was developed using the BIAcore 3000. Human clusterin was immobilized on a sensor chip. Full length antibodies or Fab fragments were injected and allowed to interact with the immobilized clusterin. This example described the exemplary antibody 16B5 but the 21B12 exemplary antibody was prepared and tested in a similar manner.
**Immobilization of clusterin**

HBST (10mM Hepes pH 7.4, 135 mM NaCl, 3.4 mM EDTA, 0.005% Tween 20) was used as running buffer for all BIAcore experiments. Recombinant monomeric clusterin was immobilized on a CM3 chip with normal amine coupling method at a flow of 5 µl/min. Surface was activated with 35 µl of a mixture of 50mM NHS/0.2M EDC. Clusterin in 10mM Na-acetate pH 4.5 was injected until a desired amount was captured (below 60RU). Unreacted esters were deactivated with 35 µl of 1M ethanolamine hydrochloride-NaOH pH8.5. A control surface was prepared by injecting NHS/EDC and ethanolamine in the same manner.

**Preparation of humanized anti-clusterin IgG2 antibodies**

Expression vectors containing the cDNAs encoding the light and heavy chain immunoglobulins were expressed in 293 cells using transient transfection methods familiar to those skilled in the art. By virtue of the signal peptides incorporated at the amino-termini of both immunoglobulin chains, the mature IgG2 was harvested from the serum-free culture medium of the cells. Growth of the cells was continued for 5 days post-transfection after which the culture medium was harvested for purification of the IgG2 chimeric monoclonal antibodies. The protein was purified using Protein-A agarose as instructed by the manufacturer (Sigma-Aldrich Canada Ltd., Oakville, ON).

**Preparation of mouse 16B5 and HH 16B5 Fab**

Mouse 16B5 IgG was treated with papain at a molar ratio of 1:100 for 4 hours at room temperature. The digestion was stopped by addition of a 4:1 molar ratio of the papain inhibitor E64. Fab fragments were separated from Fc fragments by chromatography on a 1 ml HiTrap Protein G column. The Fab fragments were eluted from the column with 0.1 M glycine, pH 2.7. The pH was neutralized immediately by collection of 1 ml fractions into tubes containing 100 µl of 2 M Tris, pH 9. Fab containing fractions were pooled and concentrated on an Amicon Ultra 4 centrifugal concentrator with a 30 kDa MW cutoff. The samples were passed through a Superose 12 size exclusion column (10 X 300 mm) in 20 mM HEPES, pH 7.5, 200 mM NaCl to separate the Fab and F(ab’)2 fractions. The Fab-containing fractions were pooled and concentrated on an Amicon Ultra 4 centrifugal concentrator with a 30 kDa MW cutoff.

For preparation of HH 16B5 Fab, the protocol was very similar to that of mouse Fab, except that the digestion time was 20 hours at room temperature and the Fab and Fc fragments were separated on a HiTrap Protein A column instead of a HiTrap Protein G column. The digestion time was increased based on results from a small scale test in an effort to try to eliminate the
presence of F(ab')2. The size exclusion profile showed that the longer digestion reduced, but
did not eliminate completely, the presence of F(ab')2 fragments. The switch to Protein A
rather than Protein G was done to avoid exposure of the Fab fragments to the low pH required
to elute the Fab fragments from the Protein G. The Fab fragments flowed through the Protein
A column and the Fc fragments were retained by the Protein A. The size exclusion separation
was done in PBS instead of HEPES buffer. The same methods were used to prepare 21B12
Fab fragments.

Kinetics analysis of mouse 16B5 and HH16B5 and Fab

Kinetics analysis was conducted at a flow of 50 µl/min. Full length antibodies (mouse or
humanized) or Fab were diluted in HBST. Concentration range was from 1.953-3 1.25nM for
the full length antibodies and 15.625-250 nM for the Fab. Each concentration was injected
over the clusterin and a control surface for 5 min followed with a 5 min dissociation wash.
The clusterin surface was regenerated between each antibody injection with 50 µl of 20mM
HCl.

Kinetics analysis of antibodies binding to clusterin

Figure 3 summarizes the results obtained for the determination of the kinetics parameters for
16B5 full length and Fab anti-clusterin antibodies.

The kinetics parameters of the full length humanized 16B5 (HH16B5) is very similar to the
kinetics of the full length mouse antibody (16B5), suggesting that the humanization did not
affect the binding of the antibody to the clusterin. However, the kinetics parameters of the
humanized 16B5 Fab (HH16B5 Fab) is slightly better the kinetics of the Fab mouse antibody
(16B5 Fab), again suggesting that the humanization did not affect the binding of the antibody
to the clusterin. The $K_D$ of the interaction between immobilized human clusterin and mouse
16B5 or humanized 16B5 is in the low nM range. The method develop can be use to compare
the kinetics parameters during the humanization process of anti-clusterin antibodies.

Figure 9 summarizes the results obtained for the determination of the kinetics parameters for
21B12 full length and Fab anti-clusterin antibodies. As was described for the 16B5, the
humanization of 21B12 (HH21B12) resulted in binding parameters that were similar to the
parent mouse 21B12 antibody. The $K_D$ of the interaction between immobilized human
clusterin and mouse 21B12 or humanized 21B12 is in the low nM range. The method
developed can be used to compare the kinetics parameters during the humanization process of
anti-clusterin antibodies.
Example 3. Biological activity of hl6B5 in cell based assays

These studies were conducted to compare the biological activity of hl6B5 with that of the mouse 16B5. To test the hl6B5, two assays were used that had previously shown that blocking clusterin with a monoclonal antibody could reduce the migration and invasion of cancer cell lines.

To test the activity of anti-clusterin antibodies against cancer cell migration, a standard wound healing, or scratch assay, was used. In this assay, EMT6 cells, a mouse mammary carcinoma cell line, was plated at high density and subjected to wounding by the creation of a scratch in the cell layer. At time 0, a wide denuded area is evident that quickly fills up after incubation of the cells at 37°C for 15h (see upper left-hand panels in Fig. 4). Incubation of the cells in the presence of either a commercial anti-clusterin polyclonal (C-18, Santa Cruz Biotech, Santa Cruz, CA) or the mouse 16B5 purified from the original hybridoma resulted in a reduced number of cells in the denuded area (see upper right-hand panels in Fig. 4, labeled commercial and hybridoma 16B5). Incubation of the wounded EMT6 cells with the chimeric 16B5 (see Fig. 4 lower panel MM), a hybrid antibody containing the chimeric light chain with the humanized heavy chain (see Fig. 4 lower panel MH), a hybrid antibody containing the chimeric heavy chain with the humanized light chain (see Fig. 4 lower panel HM), or the complete humanized 16B5 (see Fig. 4 lower panel HH) also resulted in blockage of migration of the cells into the denuded area. In fact, the humanized 16B5 appeared to be the most effective inhibitor. Additionally, the ability of the chimeric and the mouse-human hybrid antibodies to inhibit migration shows that interaction with clusterin was the same irrespective of which immunoglobulin chain was contained in the 16B5 antibody.

We then determined whether other cell lines such as the human prostate PC3 and DU145 cell lines, which secrete various levels of endogenous clusterin, could be affected in their invasive behavior and growth by the hl6B5. When seeded in Matrigel (Fig. 5, upper left hand panel), the PC3 tumor cell line displayed a stellate morphology with protrusions sprouting into the Matrigel, a feature that has been correlated with increased invasive potential (Thompson et al., 1992). Treatment with hl6B5 (Fig. 5, upper right hand panel) significantly reduced this stellate morphology strongly suggesting that clusterin secretion contributes to the invasive phenotype of the PC3 cells. DU145 cells did not display the stellate morphology observed in the PC3 cells, but rather formed sphere-like structures in Matrigel (Fig. 5, lower left hand panel), which seemed to be smaller and fewer in number in the presence of hl6B5 (Fig. 5, lower right hand panel). These results show that the ability of the hl6B5 to reduce the invasive potential of cancer cell lines is comparable to the original mouse 16B5 and shows
that the humanization process did not alter the ability of the antibody to interact with and block the activity of secreted clusterin.

Tumors derived from 4 different human pancreatic cell lines were obtained which were fixed in formalin, embedded in paraffin, and section on glass slides. Immunohistochemistry was conducted with hl6B5 antibody to determine if tumors derived from this cancer indication expressed clusterin. The tumors were derived from Aspc-1, BxPC-3, PANC-1, and MiaPaCa-2 all of which were derived from pancreatic cancer patients (ATCC, Manassas, VA). Paraffin-embedded epithelial pancreatic tumor samples were placed on glass slides and fixed for 15 min at 50 °C. Deparaffinization was conducted by treating 2x with xylene followed by dehydration in successive 5 min washes in 100%, 80%, and 70% ethanol. The slides were washed 2x in PBS for 5 min and treated with antigen retrieval solution (citrate-EDTA) to unmask the antigen. Endogenous peroxide reactive species were removed by incubating slides with $\text{H}_2\text{O}_2$ in methanol and blocking was performed by incubating the slides with serum-free blocking solution (Dakocytomation) for 20 min at room temperature. The primary mAb (a control IgG or hl6B5) was added at 5 μg/ml for 1 h at room temperature. H16B5-reactive clusterin was detected by incubating with biotin-conjugated human anti-kappa followed by streptavidin-HRP tertiary antibody. Positive staining was revealed by treating the slides with DAB-hydrogen peroxide substrate for less than 5 min and subsequently counterstained with hematoxylin. As shown in Fig. 11, all four tumors stained positive for clusterin expression (see right hand panels in Fig. 11). Interestingly, the tumors that were known to be resistant to chemotherapy (PANC-1 and MisPaCa-2) contained the highest level of secreted clusterin. The PANC-1 cell line was cultured and grown in Matrigel as described for the prostate cancer cell lines (see above). The cells were stimulated with TGFβ, and inducer of the epithelial-to-mesenchymal transition and a growth factor that causes the cells to migrate across the membrane into the Matrigel (see Fig. 12, upper right hand panel). When the stimulated cells were treated with hl6B5, migration was severely inhibited (Fig. 12, lower right hand panel). This result indicates that hl6B5 can block the migration of pancreatic cancer cells and shows that the antibody has the potential to be therapeutically active in this cancer indication as well.

### Example 4. Biological activity of hl6B5 in animal models of cancer

These studies were performed to measure the in vivo efficacy of hl6B5 in models of human cancer. Antisense oligonucleotides and small interfering RNAs targeting clusterin have been reported to induce apoptosis and chemosensitivity in vitro in prostate cancer xenografts [1-4]. The model system that was used comprised the DU145 human prostate cancer cell line that is
androgen-insensitive and represents one of the most well characterized models for this disease. Thus, 2 million cells were implanted sub-cutaneously into the flanks of SCID mice and the tumors were allowed to grow to approximately 100 mm³. Starting on day 1, hl6B5 was injected intra-peritoneally (i.p.) at a dosage of 5 mg/kg and from day 4, taxotere (TxT) was injected i.p. at a dosage of 10 mg/kg. The hl6B5 injections were continued twice per week while the TxT was administered weekly. As depicted in Fig. 6, the growth of the (primary) tumors was significantly reduced in the animals that received hl6B5 treatments compared to the control. This effect occurred both in the monotherapy group (compare control with hl6B5, \( P = 0.0104 \)) and in the combination group with TxT (compare TxT-with hl6B5+TxT, \( P = 0.0395 \)). This result shows that blocking clusterin with the hl6B5 causes tumor growth reduction and increases the chemo-sensitivity of the tumors for TxT.

A second prostate cancer model study was conducted in a different tumor model by implanting PC-3 prostate cancer cells. PC-3 cells are also hormone-insensitive but are documented as being slightly more invasive than the DU145 cells. As was described above, the cells were implanted sub-cutaneously in SCID mice and treatments were initiated when the tumors reached a volume of approximately 100 mm³ (designated day 1). The hl6B5 injections were administered i.p. on day 1 at 5 mg/kg and continued twice per week thereafter whereas a single TxT injection at 10 mg/kg was administered i.p. on day 5. This modification in the TxT schedule was performed because it was found that PC-3 cells are significantly more susceptible to this chemotherapeutic drug compared to the DU145 tumors.

The results of this study are depicted in Fig. 10. As before, it was observed that the tumors in the animals that received hl6B5 alone had an almost immediate response to the antibody compared to the untreated animals. The significant decrease in the average tumor size in the hl6B5 treatment group was found to result in a 37% reduction compared to the control group on day 43. Survival was also monitored and it was observed that on the day that there were no remaining animals in the control group (day 43), greater than 60% of the mice remained alive in the AB-16B5 treatment group. This increase in overall survival translated into a 47% increase in the animals that received hl6B5.

The cytotoxic effect of TxT against prostate cancer cells was observed but the tumors appeared to recover from this treatment approximately 18 days following the injection. The growth of the tumors in the TxT group even surpassed that of the tumors in the group that received the AB-16B5 (see day 50, Fig. 10). However, the combination of hl6B5 with TxT significantly slowed the growth of the tumors resulting in tumors that were 41% smaller compared to the TxT alone group. Again, the presence of hl6B5 extended the survival of the animals. Taken together, the results from these in vivo studies indicate that the hl6B5
humanized antibody that inhibits the function of secreted clusterin in tumors can significantly slow the growth of solid tumors.

Example 5. H16B5 inhibits the internalization of secreted clusterin in cancer cells.

The results disclosed above indicate that induction of the epithelial-to-mesenchymal transition (EMT) leads to the secretion of clusterin by cancer cells. Additionally, our data also showed that clusterin secreted by these cancer cells is a potent inducer of EMT. These findings imply that secreted clusterin is mediating this effect either indirectly by interacting with other tumor-associated factors in the extra-cellular matrix or directly by interacting with a receptor on the cell surface of cancer cells. Although secreted clusterin present in normal serum is known to associate with many different proteins such as members of the complement cascade, leptin, various apolipoproteins, the presence of protein partners for secreted clusterin in cancer cells or in the tumor micro-environment remains relatively unexplored. Some examples include a published report by Jo and co-workers (Jo et al., 2008) showed that tumor-secreted clusterin associated with IGF-1 under conditions of stress induced by serum deprivation. In addition, clusterin contained in prostate cancer cell lines was found to interact with a protein called COMMD1 (Zoubeidi et al., 2010). This interaction resulted in increased activation of NF-kappaB-related pathways which in turn promoted prostate cancer cell survival. These findings begin to elucidate some of the ways secreted clusterin might contribute to tumorigenesis but the molecular mechanism for how it promotes EMT is unknown.

In order to begin to address this question, cell-based experiments were undertaken to determine if secreted clusterin interacted with cancer cells directly or via other secreted factors in the cell medium. In order to measure this, secreted clusterin was fluorescently labelled and incubated with BRI-JM01 mouse mammary carcinoma cells. It was found that after approximately 24 hours of treatment, that the fluorescence signal was contained inside the cells. Analysis of these cells over shorter time points revealed that the fluorescently labelled secreted clusterin was internalized by the cells (see Fig. 13). As shown, the internalization increases over time in manner that is consistent with a receptor-mediated endocytic pathway. Furthermore, the punctate and perinuclear pattern of staining that results after 24 hours (see white arrows in Fig. 13) that is often observed in proteins that are internalized along the endosomal pathway. Similar results were observed in DU145 human prostate cancer cells.
This secreted clusterin internalization was further examined by testing if hl6B5 could block this activity. The cells were treated with secreted clusterin -Alexa480 in the presence of hl6B5 or an isotype control IgG. As shown, in Fig. 14, the internalization of secreted clusterin into JMOI cells was blocked by the addition of hl6B5. Internal perinuclear staining of secreted clusterin was still observed in the cells treated with the control IgG (see white arrows in Fig. 14).

Taken together, these results which show that this the internalization of secreted clusterin can be inhibited by the addition of hl6B5 suggests that this might be one of the mechanism by which the antibody prevents secreted clusterin from mediating EMT in cancer cells.

The experiments described herein may be carried out to determine how specific mutations in the amino acid sequence of an antibody (e.g., in the variable region(s), the constant region, the framework region or in the CDR(s)) affect the biological activity of the antibody. For example, one or more mutations may be introduced in the framework region of the variable light chain or variable heavy chain of hl6B5 (or in the murine 16B5) and tumor growth may be assed as described herein.

Binding of variant antibodies and antigen binding fragments to human or murine clusterin may be tested by several methods known in the art such as, for example, ELISA, Western blot, surface plasmon resonance, etc.

**Example 6. anti-clusteriii antibodies may bind to clusterin variants.**

The antibodies and antigen binding fragments of the present invention bind to both the human and murine form of clusterin. These two proteins share 77% amino acid sequence identity and 89% similarity (see Figure 15). By comparing the amino acid sequence of the murine and human form, one may understand that the antibody probably binds a linear or a conformational epitope preserved in both proteins. It is expected that the antibodies and antigen binding fragments may bind to other naturally occurring variants as well as synthetic variants (including recombinant proteins) having at least 75% amino acid identity (including 80%, 85%, 90%, 95%, 99%, 100%) with human or murine clusterin. For example, the antibodies and antigen binding fragments may bind a clusterin variant having an amino acid sequence comprising SEQ ID NO.:56 (wherein + represent an amino acid substitution, such as for example a conservative amino acid substitution) or SEQ ID NO.:57.

The present invention shows that anti-clusterin antibodies target clusterin that is expressed in human tumors. To demonstrate that the interaction of the anti-clusterin antibodies, such as hl6B5, with murine tumor clusterin, frozen sections prepared from 4T1 mouse mammary
tumors were incubated with hl6B5. Briefly, the frozen sections were fixed with ice-cold acetone for 10 minutes and non-specific binding was blocked with a reagent supplied in a commercially available kit (Dako Canada, Inc., Burlington, ON). H16B5 was incubated with the mouse tumor section for 1h at a concentration of 5 μg/ml. After washing, specific staining was revealed by incubating with a HRP-conjugated anti-human IgG. A control sample was processed in an identical manner with a human isotype control IgG. As shown in Figure 16, hl6B5 detected murine clusterin in the 4T1 tumors (see right panel, labeled as 4T1-AB-16B5) as evidenced by the brown staining resulting from the horseradish peroxidase coloring. The control antibody did not reveal any antigens (see left panel, labeled as 4T1-ctl). This result demonstrates that anti-clusterin antibodies, as exemplified by hl6B5, interact with murine clusterin that is expressed in mouse tumors. In addition, other studies using immunofluorescence showed that hl6B5 detected murine clusterin that was expressed in BRI-JM01 cells, another mouse mammary carcinoma cell line.

Binding of the antibodies and antigen binding fragments of the present invention to naturally occurring variant or synthetic variants of clusterin may also be tested by methods known in the art, including for example, the above mentioned methods.

The CLU gene is conserved in human, chimpanzee, dog, cow, mouse, rat, chicken and zebrafish. Testing of the antibodies and antigen binding fragments in these models is encompassed by the present invention.
SEQUENCE LISTING:

SEQ ID NO.: 1
16B5 CDRH1: GFNIKDIYMH

SEQ ID NO.: 2
16B5 CDRH2: R1DPAYGNTKYDPKFQG

SEQ ID NO.: 3
16B5 CDRH3: RYDTAMDY

SEQ ID NO.: 4
16B5 CDRL1: KSSQSLNSRTRKNYL

SEQ ID NO.: 5
16B5 CDRL2: WASTRES

SEQ ID NO.: 6
16B5 CDRL3: KQSYNLWT

SEQ ID NO.: 7
16B5 Humanized heavy chain variable region
QVQLVQSGAEVKPGATVKISCKVSQGFLIKDIYMHWVQQAPKGEWMGRIDPAY
GNTKYDPKFQGRVTITADTSTDAYMELSSLRSEDTAVVYYCARRYDTAMDYWQG

SEQ ID NO.: 8
16B5 Humanized light chain variable region
DIVMTQSPDSLAVSLGERATINCKSSQSLNSRTRKNYLAWYQQKPGQPPKLLJYW

SEQ ID NO.: 9
Complete heavy chain immunoglobulin sequences for hl6B5
QVQLVQSGAEVKPGATVKISCKVSQGFLIKDIYMHWVQQAPKGEWMGRIDPAY
GNTKYDPKFQGRVTITADTSTDAYMELSSLRSEDTAVVYYCArRYDTAMDYWQG
SASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPDPEVTSPWNLGALTSGVHTFPAV
LQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPCPPAPPV
AGPSVFLFPKKPDKTLMSRTPEVTCVVDVSHEDPEVQFNYVGDVEVHNAKTKPR
EEQFNSTFRVSVLTVHVDWLNGKEYKCKVSNKGPLAPIEKTIKTKGQPREEQVY
TLPPSREEMTKQVSLTCLVKGFYPDS1AVEWESNGQPENNYKTTPMLDSDGSFFL
YSKLTVDKSRWQQGNNFSVMHEALHNHYTQKSLSPGK

SEQ ID NO.: 10

**Complete light chain immunoglobulin sequences for hl6B5**

DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKQVLYQKPGQPPKLLYWA
STRESGVPDRFSGSGSTDDFTLISLQAEAVYYCKQSYNLWTFGGQGTLKLEIKVAA
PSVFIFPSDEQLKSGTASVCLNLNFYPREAVQVKVQVNALQSGNSQESVTEQDSK
DSTYLSSTLTLSKDYEKHKVACEVTHQGLSSPVTKSNRGE

SEQ ID NO.: 11

21B12 CDRH1: GYTFTNYGMH

SEQ ID NO.: 12

21B12 CDRH2: WINTYTGEPTYADDPKG

SEQ ID NO.: 13

21B12 CDRH3: DGFLYFFDY

SEQ ID NO.: 14

21B12 CDRL1: KSSQSLYSSNQKNYLA

SEQ ID NO.: 15

21B12 CDRL2: WASTRES

SEQ ID NO.: 16

21B12 CDRL3: QQYYIYPRT

SEQ ID NO.: 17

21B12 Humanized heavy chain variable region
SEQ ID NO.:18
21B12 Humanized light chain variable region
DIVMTQSPSDLAVSLGERATINCKSSQLLYSSNQKNYAWYQQKPGQPPKLIYWA
STRESGVIPRFSGSQSGTDFTLTISLQAEDVAVYYCQYYIYPRTFGQGTKLEIK

SEQ ID NO.:19
Complete heavy chain immunoglobulin sequences for h21B12
QVQLVQSGELKPGASVKSCKASGYTFTNYGHWVRQAPGQGLEWGMWINTY
TGEPTYADDFKGRFVFLDTSVSTAYLQISSLKAEDTAVYYCARdGFYFDDYWGQG
TLVTVSSASTKGSVPFLAPCSRSTSEASTALLGCLVKDYFPEPVTWSNWGALTSGVH

SEQ ID NO.:20
Complete light chain immunoglobulin sequences for h21B12
DIVMTQSPSDLAVSLGERATINCKSSQLLYSSNQKNYAWYQQKPGQPPKLIYWA
STRESGVIPRFSGSQSGTDFTLTISLQAEDVAVYYCQYYIYPRTFGQGTKLEIKRTV
AAPSVFIFPSDEQLKSHTASVVCVCLNNFYPREAKVQWVDNALQSGNQESVTEQD
SKDSTYLSLSTLTSKADYEKHKVYACEVTQHQLSSPVTQFSRGEC

SEQ ID NO.:21
Complete nucleotide sequence of the heavy chain of hl6B5
ATGGACTGAGACCTGGCGATCTCTCTGTGCGGCTCACCGCA ACCACG
CCCAGGTGCACTGCTGGCAGTCTCTGCGTCGCTGCCGACCCG
TCAAGATCAGCTGCAAGGTGTCCGGCTTCAACATCAAGGACATCTACATGCACTGGTGCAGCAGGCTCCAGGCAAGGGACTGGAGTGGATGGGCCGGATCGACCCTGCCTACGGCAACACCAAGTACGACCCTAAGTTCCAGGGCCGGGTGACCATCACCGCCGACACCTCCACCGACACCGCCTACATGGAACTGTCCTCCCTGCGGTCCGAGGACACCGCCGTGTACTACTGCGCCCGGAGATACGACACCGCCATGGATTACTGGGGCC

AGGGGACACCTGGTGACTCCCTCGCTTCCCAACAGGGCCCTGCTGGCCGGATCGACCCTGCCTACGGCAACACCAAGTACGACCCTAAGTTCCAGGGCCGGGTGACCATCACCGC

5

AGCAGCGTGGTGACCGTGCCCTCCAGCACTTCCGGCACCACAGCTAAGCTGCA

ACGTAGATCACAAGCCCAGCAACACCAAGGTGAGCAAGACAGTTGAGCGGAAAT

10

AGCAGCGTGGTGACCGTGCCCTCCAGCACTTCCGGCACCACAGCTAAGCTGCA

ACGTAGATCACAAGCCCAGCAACACCAAGGTGAGCAAGACAGTTGAGCGGAAAT

15

TACGTGGACGGCCTGGGAGGATGCTAATGCAAGACAAAGCCACGGGAGGAGCAG

TTCAACAGCAGTTCCGTGTTGTCAGCTGCTCTCACCGTTGGTGCACCAGGACTGGC

TGAACGGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCTCCG

20

TCTCCCTGTCTCCGGGTAAATGA
SEQ ID NO.: -22

Complete nucleotide sequence of the heavy chain of h21B12

ATGGACTGGACCTGGCGGATCCTGTTTCTGGTGCGCTACCAGGCACACACG
CCCAGGTGAGCTGGTGCAGTCCCGAGCTCCGAGCTGAAGAACCCTGGCGCCTCCGT
GAAGGTGTCCTGCAAGGCGGCTACACTTCAACCAACTACGGCAGTGCACGCT
5
GTGCAGCGGAGGGCCACACTGGGACAGGAGGTGAATGGATGGCTGATCAAACACTAC
ACCGGCGAGCCATCTACCTCCGGCAGCTGGTGCAAGTCCGGCTGACGACTTCAAG
ACACCTCCTGTCCACCCGCTACCTCGAGATCTCTCTCCTGAAGCCGAGAGAGAC
CGCCCGTGAATCTACTGCGGCCGAGCCGACGCTTCCTTGACTCTCTCTCGACTCTGC
10
CAGGGGACCCCTGCTGAGCGCTGTCCTCTGCTCCTCCACCAAGGCCCTCCGCTGGCTCC
CTCTGGGCTCGCTCCGCTACCCGCTCGTCCCTCTGACTCTCTGGCTCCCTCCTGCC
GTAAGGACTTCTTCCCTGAGCTGAGCGCTGGAGACTCTGCTGGAGACTCCTGCTG
15
ACGTGGACCAAGCCTTCAACACCAACCAAGGAGAGCGGAGGGGAAAT
GTCGACGGGTGCTCCCCTCTCTTTGTCTCTCCTCTCTGCTGCTGCTGGCCCTAGCGTGT
20
CTGTTCCCTCTCTGCTCGCTGACGAGCTGGCTGGAGGGAAAT
CAACTCCACCTTGGGATGGGACTGGGATGGAGGACTGGATGGGAAGGAGGAGG
25
TGAAGGGTCTTCACCTCTCCGAGCTGCAAGGACTCCGACCGCTGACTCTTGGTCTCCTG
TGACTGGCAGGGCTGCTGCAAGGACTCCGACCGCTGACTCTTGGTCTCCTG
30
SEQ ID NO.:23

**Complete nucleotide sequence of the light chain of hl6B5**

5
ATGGTGCTGCAGACCCAGGTGGTTCATCTCCCTCTGCTGTGATCTCCGGCCGCT
ACGGCGACATCGTGATGACCAGCTCCCAGACTCCCTGGCAGTGTCCTGGCCGA
GAGAGCCACCATCAACTGCAAGTCCTCCCAGTCCCTGCTGACTCCTCCAACCAGA
AGAACTACCTGGCTTGATACGCGAAGCCCTGGCAGCTCTAAGCTGCTGAT
CTACTGGGCCTCCACCCCCGAGTCCGGGCTGCCTGACCGGTTCTCCGGCTCTGGC
TCCGGCACCGACTTCACCCTGACCATCAGCTCCCTGCAGGCCGAGGAGGTGGCC
GTGTACTACTGCCAGCAGTACTACATCTACCCTCGGACCTTCGGCCAGGGCACCA
AAGTACGTCAGACGGACTACGAGTCACCTACAGGCGAGAGCCCAAGGACCGA

10
CAGCGGCACCCGACTTCACCCCTGACCATACGCTCCCCTGACGGCCAGGACGTGGCC
GTGTACTACTGCAAGCAGTCCTACAACCTGTGGACCTTCCCCCAGCAGACCTGAG
TGGAGATCAAGGGACTGTGTGCACCATCTGTCTTCTTATCTTCCCGCATCTGAT
GAGCAGTTGAAATCTCGAATACTGCTGTGTTGCTGGCTGCTGAATAACTTCTATCC
CAGAGAGGCCAAATGGTATGGAAGGTTGGAATACGCCCTCCAATCGGGTAACCT
CCAGGAGAGTGTGTCAGACGAGCAGAGGACGCAAGCCCCCTTCAGCAGCTCGCGA
AGTCACCATCAGGGCTTGACGCTCGCCCGTCACAAAGAGTGTTG

15
CAGCGGCACCCGACTTCACCCCTGACCATACGCTCCCCTGACGGCCAGGACGTGGCC
GTGTACTACTGCAAGCAGTCCTACAACCTGTGGACCTTCCCCCAGCAGACCTGAG
TGGAGATCAAGGGACTGTGTGCACCATCTGTCTTCTTATCTTCCCGCATCTGAT
GAGCAGTTGAAATCTCGAATACTGCTGTGTTGCTGGCTGCTGAATAACTTCTATCC
CAGAGAGGCCAAATGGTATGGAAGGTTGGAATACGCCCTCCAATCGGGTAACCT
CCAGGAGAGTGTGTCAGACGAGCAGAGGACGCAAGCCCCCTTCAGCAGCTCGCGA
AGTCACCATCAGGGCTTGACGCTCGCCCGTCACAAAGAGTGTTG

20
SEQ ID NO.:24

**Complete nucleotide sequence of the light chain of h21B12**

ATGGTGCTGCAGACCCAGGTGGTTCATCTCCCTCTGCTGTGATCTCCGGCCGCT
ACGGCGACATCGTGATGACCAGCTCCCAGACTCCCTGGCAGTGTCCTGGCCGA
GAGAGCCACCATCAACTGCAAGTCCTCCCAGTCCCTGCTGACTCCTCCAACCAGA
AGAACTACCTGGCTTGATACGCGAAGCCCTGGCAGCTCTAAGCTGCTGAT
CTACTGGGCCTCCACCCCCGAGTCCGGGCTGCCTGACCGGTTCTCCGGCTCTGGC
TCCGGCACCGACTTCACCCCTGACCATACGCTCCCCTGACGGCCAGGACCGA

25
AGAAGCTACTCCCGGCTTGATACGCGAAGCCCTGGCAGCTCTAAGCTGCTGAT
CTACTGGGCCTCCACCCCCGAGTCCGGGCTGCCTGACCGGTTCTCCCGGCTCTGAG
TCCGGCACCGACTTCACCCCTGACCATACGCTCCCCTGACGGCCAGGACCGA
GCGATCTGACTGCAGCTCATCTACCTCAGGACCGGACCTGAGCTGCTGAT

71
GCTGGAAATCAAGCGGACCGTGGCCGCTCCTTCCGTGTTCATCTTCCCCCCTTCCG
ACGAGCAGCTGAAGTCCGGCACCGCCTCTGTGGTGTGCCTGCTGAACAACTTCTA
CCCCCGGGAGGCCAAGGTGCAGTGGAAGGTGGACAACGCCCTGCAGTCCGGCAA
CTCCCAGGAATCCGGCAGCAGGACTCCAAGGACTCTACTCTCTTCTTGCC
TCCACCCCTGACCCCTGACGCCAAGGGCAGTACGAGAAGCACAAGGTGTCGCCTGC
G AAGTGACCACCCAGGCTGCTCGTCACCAGTGACTCCAGGACTCTACTCCCTTGCC
AAGTGACCCACCACCCGTGCCTCTGACCGTACCAAACTCTTCCACCCGCGGA
GTGCTGA

SEQ ID NO.:25 (murine 16B5 VL)

10 DIVMSQSPSSLA VSAGEKVTMSCKSSQSLNSRTRK NYLAWYQQKPQGSPKLLIYW
ASTRESGVPDRTGSGGTDFTLTISSVQAEDLAVYYCKQSY NLWTFFGGT KLEFK

SEQ ID NO.:26 (hl6B5 VL consensus)

DIVMXQSPXSLAVSXEXXTXXCKSSQSLNSRTRKNYLAWYQQKPQGXP KLLIY

15 WASTRESGVPD FXGSGSTDF TLTISSX Q AEDXAVYYCKQSY NLWTFFGX G TKLEK

X is an amino acid substitution in comparison with a corresponding amino acid in the polypeptide set forth in SEQ ID NO.:25.

SEQ ID NO.:27 (hl6B5 VL consensus)

DIVM X_1 Q S P X a_2 SLAVSX_{a3} GE X_{a4} X_{a5} X_{a6} X_{a7} CKSSQS LLNSRTRKNYLAWYQQKPQGX

_{a8} PKLLIY WASTRESGVPD RX_{a9} GSGSTDF TLTISSX_{a10} QAEDX_{a11} AVYYCKQSY NL-

WTFGX_{a12}GTKLEX_{a13}K

_X_{a1} is a neutral hydrophilic amino acid such as for example, T or S;

_X_{a2} is D or S;

_X_{a3} is an hydrophobic amino acid such as for example, L or A;

_X_{a4} is a basic amino acid such as for example R or K;

_X_{a5} is an hydrophobic amino acid such as for example A or V;

_X_{a6} is an hydrophobic amino acid as for example I or M;
**X_0** is **N** or **S**;

**X_1** is **P** or **S**;

**X_2** is a neutral hydrophilic amino acid such as for example **S** or **T**;

**X_3** is a hydrophobic amino acid such as for example **L** or **V**;

**X_4** is an hydrophobic amino acid such as for example **V** or **L**;

**X_5** is **Q** or **G** and;

**X_6** is **I** or **F**.

SEQ ID NO.:28 (hl6B5  VL consensus3)

```
DIVMX_1 OSPX_2 SLAVSX_3 GEX_4 TX_5 X_6 CKSSQSLNRSRTRKNLYAWYQQKPGQX
```

**X_7** is **T** or **S**; **X_8** is **D** or **S**; **X_9** is **L** or **A**; **X_10** is **R** or **K**; **X_11** is **A** or **V**; **X_12** is **I** or **M**; **X_13** is **N** or **S**; **X_14** is **P** or **S**; **X_15** is **S** or **T**; **X_16** is **L** or **V**; **X_17** is **V** or **L**; **X_18** is **Q** or **G** and; **X_19** is **I** or **F**.

SEQ ID NO.:29 (murine 16B5 VH)

```
EVQLQSGAEVLKPGASVRLSCCTTSGFNKIDYMHWVKQREPEQGLEWGRIDPA
```

**SEQ ID NO.:30 (h!6B5 VH consensus1)**

```
XVQLXQSGAEXXKPGAXVXXSCHXXSGFNKIDYMHWVXQXPXXGLEXGEXGRIDPA
```

**SEQ ID NO.:31 (hl6B5 VH consensus2)**

```
Xb1 QVXLXb2 QSGAEb3 KPGAXb4 5VXB5 Xb6 Xb7 SCXb8 Xb9 SGFNKIDYMHWVX
```

**Xb10** is **Q** or **E**;

**Xb11** is **V** or **Q**;

**Xb12** is **S** and;

**Xb13** is **I** or **M**;

**Xb14** is a neutral hydrophilic amino acid such as for example **T** or **S**;

**Xb15** is an hydrophobic amino acid such as for example **V** or **L**;

**Xb16** is **K** or **V**;

**Xb17** is a neutral hydrophilic amino acid such as for example **T** or **S**;

**Xb20** is **Q** or **G** and;

**Xb21** is **I** or **F**.

**Xb22** is **V** or **Q**;

**Xb23** is **S** and;

**Xb24** is **I** or **M**;

**Xb25** is **K** or **V**;

**Xb26** is **S** and;
X_{36} is a basic amino acid such as for example K or R;
X_{87} is a hydrophobic amino acid such as for example I or L;
X_{88} is K or T;
X_{89} is V or T;
X_{90} is a basic amino acid such as for example Q or K;
X_{91} is A or R;
X_{92} is G or E;
X_{93} is a basic amino acid such as for example K or Q;
X_{94} is a hydrophobic amino acid such as for example M or I;
X_{95} is a basic amino acid such as for example R or K;
X_{96} is a hydrophobic amino acid such as for example V or A;
X_{97} is a neutral hydrophilic amino acid such as for example T or S;
X_{98} is for example D or N;
X_{99} is a hydrophobic amino acid such as for example M or L;
X_{100} is E or Q;
X_{101} is R or T and;
X_{102} is L or S.

SEQ ID NO.:32 (hl6B5 VH consensus3)

X_{36}VQLX_{92}QSGAE{X_{93}X_{94}KPGAX}_{5\beta X_{95}AVQX_{96}KPGAX} X_{97}LEWX_{98}GRIDPAYGNTKYDPKFQGX
TITADTX_{101}X_{102}TAYX_{103}VQX_{104}S_{105}LSS
X_{106}SEDATAVYX{ARRYDTAMDYGQGTX}_{20 VTVS S};
X_{107}Q or E; X_{108}V or Q; X_{109}K or V; X_{110}T or S; X_{111}K or R; X_{112}V or I;
X_{113}K or T; X_{114}V or T; X_{115}Q or K; X_{116}A or R; X_{117}G or E; X_{118}M or L;
X_{119}M or I; X_{120}R or K; X_{121}V or A; X_{122}E or T or S; X_{123}D or N; X_{124}M or L;
X_{125}E or Q; X_{126}R or T and; X_{127}L or S.

SEQ ID NO.:33 (murine 2IB12 VL)

DIVMSQSPSSLAVSVGKVTMSCKSSQSLLYSNQKNLYAWYQQRPGQPXLKLYWA
STRESGVPDRFTGSGTDTFTLIISSVKAEDLAVYQQYIYPRTFGGTKLEIK

SEQ ID NO.:34 (h2 1B12 VL consensus 1)

DIVMX_{QSPXSLLASVGKVTMSCKSSQSLLYSNQKNLYAWYQQRPGQPXLKLYWA
WASTRESGVPDRFTGSGTDTFTLIISSVKAEDLAVYQQYIYPRTFGGTKLEIK
X is an amino acid substitution in comparison with a corresponding amino acid in the polypeptide set forth in SEQ ID NO.:33.
SEQ ID NO.:35 (h21B12 VL consensus2)
DIVMX_{cl}QSPX_{cl}SLAVSX_{e1}GEX_{e1}X_{e1\theta}TX_{e6}X_{e7}CKSSQSLLYSSNQKNYLAWYQQX_{e8}PGQ
X_{e9}PKLLIYWASTREGVPDRFX_{e10}GSGSGTDLTISXX_{e11}X_{e12}AEDX_{e13}AVYYCQQY YI
YPRTFGX_{e14}GTKLEIK;

5  X_{e1} is a neutral hydrophilic amino acid such as for example T or S;
  X_{e2} is D or S;
  X_{e3} is an hydrophobic amino acid such as for example L or V;
  X_{e4} is a basic amino acid such as for example R or K;
  X_{e5} is an hydrophobic amino acid such as for example A or V;
  X_{e6} is an hydrophobic amino acid such as for example I or M;
  X_{e7} is N or S;
  X_{e8} is a basic amino acid such as for example K or R;
  X_{e9} is P or S;
  X_{e10} is a neutral hydrophilic amino acid such as for example S or T;

10 X_{e11} is an hydrophobic amino acid such as for example L or V;
  X_{e12} is a basic amino acid such as for example Q or K;
  X_{e13} is an hydrophobic amino acid such as for example V or L and;
  X_{e14} is Q or G.

20 SEQ ID NO.:36 (h21B12 VL consensus3)
DIVMX_{cl}QSPX_{cl}SLAVSX_{e1}GEX_{e1}X_{e1\theta}TX_{e6}X_{e7}CKSSQSLLYSSNQKNYLAWYQQX_{e8}PGQ
X_{e9}PKLLIYWASTREGVPDRFX_{e10}GSGSGTDLTISXX_{e11}X_{e12}AEDX_{e13}AVYYCQQY YI
YPRTFGX_{e14}GTKLEIK;
  X_{e1} is T or S;  X_{e2} is D or S;  X_{e3} is L or V;  X_{e4} is R or K;  X_{e5} is A or V;  X_{e6} is I or M;  X_{e7} is N or S;  X_{e8} is K or R;  X_{e9} is P or S;  X_{e10} is S or T;  X_{e11} is L or V;  X_{e12} is Q or K;  X_{e13} is V or L and;  X_{e14} is Q or G.

SEQ ID NO.:37 (murine 21B12 VH)
QIQLVQSGPELKKPGETVKISCKASGYTFTNYGMHWVKQAPGKLKWGMWINTYT

30 GEPTYADDFKGRFAFSLETASTAYLQINNLKNEGTATYFC ARDFLYFFDY WQGQT
TLTVSS
SEQ ID NO.:38 (h2 IB 12 VH consensus 1)
QXQLVQSGXELKKPGEVXKXCSCKASGYTFTNYGMHWVQAPGXGLXWMGWINT
YTGEPYADDFKGRFXFSLXTSXSTAYLQISSLKXEDTAXYXCARDGFLYFFDYW

35 GQGTXXTVSS
X is an amino acid substitution in comparison with a corresponding amino acid in the polypeptide set forth in SEQ ID NO.:37.
SEQ ID NO.:39 (h21B12 VH consensus2)

QX_{d1}QLVQSGX_{d2}ELKKPGX_{d3}Xd_{d4}VKX_{d5}SCKASGYTFTNYGMHWVX_{d6}QAPGX_{d7}GLX_{d8}
WMGWINTYTGEPTYADDFKGRFX_{d9}FSLX_{d10}TSX_{d11}STAYLQIX_{d12}2X_{d13}LKX_{d14}EDTAX_{d15}
\ldots\text{YX}_{d16}\text{CARDGFLYFFDYWGQGTX}_{d17}\text{X}_{d18}\text{TVSS;}

X_{d1} is an hydrophobic amino acid such as for example V or I;
X_{d2} is S or P;
X_{d3} is A or E;
X_{d4} is a neutral hydrophilic amino acid such as for example S or T;
X_{d5} is an hydrophobic amino acid such as for example V or I;

X_{d6} is a basic amino acid such as for example R or K;
X_{d7} is a basic amino acid such as for example Q or K;
X_{d8} is E or K;
X_{d9} is an hydrophobic amino acid such as for example V or A;
X_{d10} is an acidic amino acid such as for example D or E;

X_{d11} is an hydrophobic amino acid such as for example V or A;
X_{d12} is S or N;
X_{d13} is S or N;
X_{d14} is A or N;
X_{d15} is V or T;

X_{d16} is an aromatic amino acid such as for example Y or F;
X_{d17} is L or T and;
X_{d18} is hydrophobic amino acid such as for example V or L.

SEQ ID NO.:40 (h21B12 VH consensus3)

QX_{d1}QLVQSGX_{d2}ELKKPGX_{d3}Xd_{d4}VKX_{d5}SCKASGYTFTNYGMHWVX_{d6}QAPGX_{d7}GLX_{d8}
WMGWINTYTGEPTYADDFKGRFX_{d9}FSLX_{d10}TSX_{d11}STAYLQIX_{d12}2X_{d13}LKX_{d14}EDTAX_{d15}
\ldots\text{YX}_{d16}\text{CARDGFLYFFDYWGQGTX}_{d17}\text{X}_{d18}\text{TVSS;}

X_{d1} is V or I; X_{d2} is S or P; X_{d3} is A or E; X_{d4} is S or T; X_{d5} is V or I; X_{d6} is R or K; X_{d7} is Q or K; X_{d8} is E or K; X_{d9} is V or A; X_{d10} is D or E; X_{d11} is V or A; X_{d12} is S or N; X_{d13} is S or N;
X_{d14} is A or N; X_{d15} is V or T; X_{d16} is Y or F; X_{d17} is L or T and; X_{d18} is V or L.

SEQ ID NO.: 41 (human model of 16B5VL)

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNSKNLYAWYQQKPQPPKLIYWA
STRESGVPDVFSGSGTDFTLTISSLQAEDVAVYCYQQYYSTPYSFGQQGTKLEIK

76
SEQ ID NO.: 42 (human model of 16B5VH)
QVQLVQSGAEVKKPGATVKISCKVSGYTVFTDYYMHVWQQAPGKGGLEWMGLVDPEDGETIY
AEKFQGRVTITAUTADTDAYMELSSLRSEDATAVYCARPLFIQRGRDHWQGTLVTVSR

SEQ ID NO.: 43 (human model of 21B12VL)
DIVMTQSPDSLAVSLGERATINCKSSQSVLSSNSKNYLAWYQQPKGPPKLLIYWASTRES
GVPDRFGSGSGTDLFTISSLAEDVAVVYCMQPPYSTPSFGQGTLEIK

SEQ ID NO.: 58 (human model of 21B12VH)
QVQLVQSGSELKKPGGSKASGYSQFTSYRNWVVRQAPGQGLEWFGWINTNTGNPT
YAQGFTGRFVFLDSSTAYLQISSLKAEVATAVYCARIDWQGTLVTVSSVATIDENWFDP

SEQ ID NO.: 44
16B5 CDRH1: GFNIKDIY

SEQ ID NO.: 45
16B5 CDRH2: IDPAYGNT

SEQ ID NO.: 46
16B5 CDRH3: X,X$_2$RYDTAMDY
$X_1$ is A;
$X_2$ is R;

or $X_1$ and $X_2$ are outside the CDRH3

SEQ ID NO.: 47
16B5 CDRL1: QSLLNSRTRKNY

16B5 CDRL2: WAS

SEQ IDNO.: 49
16B5 CDRL3: KQSYNLWT

SEQ ID NO.: 50
21B12 CDRH1: GYTFTNYG
SEQ ID NO.: 51
21B12 CDRH2: INTYTGEP

SEQ ID NO.: 52
21B12 CDRH3: X_3X_4DGFLYFFDY
X_3 is A;
X_4 is R;
or X_3 and X_4 are outside the CDRH3

SEQ ID NO.: 53
21B12 CDRL1: QSLLYSSNQKNY

21B12 CDRL2: WAS

SEQ ID NO.: 55
21B12 CDRL3: QQYYIYPRT
References


CLAIMS:

1. Use of an anti-clusterin antibody for reducing volume of a tumor comprising cells expressing or secreting clusterin.

2. The use as defined in claim 1, wherein the anti-clusterin antibody is selected from the group consisting of a polyclonal antibody, a monoclonal antibody, a chimeric antibody, a humanized antibody, an isolated human antibody, a hybrid antibody and a fragment thereof.

3. The use as defined in claim 2, wherein the hybrid antibody or fragment thereof comprises a light chain variable region of a non-human antibody and a heavy chain variable region of a humanized antibody.

4. The use as defined in claim 2, wherein the hybrid antibody or fragment thereof comprises a heavy chain variable region of a non-human antibody and a light chain variable region of a humanized antibody.

5. The use as defined in any one of claims 1 to 4, wherein the tumor is a carcinoma selected from the group consisting of endometrial carcinoma, breast carcinoma, hepatocellular carcinoma, prostate carcinoma, a renal cell carcinoma, ovarian carcinoma, pancreatic carcinoma, and colorectal carcinoma.

6. The use as defined in claim 5, wherein the carcinoma is a prostate carcinoma.

7. The use as defined in claim 5, wherein the carcinoma is a breast carcinoma.

8. A humanized or hybrid antibody of a non-human parent antibody, wherein said humanized antibody comprises a heavy chain variable region comprising non-human complementarity determining region amino acid residues and human framework region amino acid residues of a natural human antibody and a complementary light chain and wherein the humanized or hybrid antibody specifically binds to clusterin.

9. The humanized or hybrid antibody of claim 8, wherein the natural human antibody comprises a variable region having a three-dimensional structure similar to that of a variable region of the non-human parent antibody.

10. The humanized or hybrid antibody of claim 8, wherein the humanized antibody inhibits the migration, invasion or the growth of clusterin-expressing cells or clusterin-secreting cells.
11. The humanized or hybrid antibody of any one of claims 8 to 10, characterized by an affinity of $4.49 \times 10^{-9} \text{ M} \pm 8.5 \times 10^{-9}$ or better.

12. The humanized or hybrid antibody of any one of claims 8 to 11, wherein the complementary light chain comprises human framework region amino acid residues that are from a natural human antibody light chain framework region having at least 70% identity with a light chain framework region of the non-human parent antibody and having amino acids in a light chain complementarity determining region that is the same or substantially the same to that of a corresponding light chain complementarity determining region of the non-human parent antibody.

13. The humanized or hybrid antibody of claim 12, wherein the human framework region amino acid residues are from a natural human antibody light chain framework region having at least 80% identity with the light chain framework region of the non-human parent antibody.

14. The humanized or hybrid antibody of claim 13, wherein the human framework region amino acid residues are from a natural human antibody light chain framework region having at least 83% identity with the light chain framework region of the non-human parent antibody.

15. The humanized or hybrid antibody of any one of claims 8 to 14, wherein the human framework region amino acid residues of the humanized antibody heavy chain are from a natural human antibody heavy chain framework region having at least 70% identity with a heavy chain framework region of the non-human parent antibody and having a number of amino acids in a heavy chain complementarity determining region that is the same or substantially the same to that of a corresponding heavy chain complementarity determining region of the non-human parent antibody.

16. The humanized or hybrid antibody of claim 15, wherein the human framework region amino acid residues of the humanized antibody heavy chain are from a natural human antibody heavy chain framework region having at least 73% identity with the heavy chain framework region of the non-human parent antibody.

17. The humanized or hybrid antibody of claim 16, wherein the human framework region amino acid residues of the humanized antibody heavy chain are from a natural human antibody heavy chain framework region having at least 80% identity with the heavy chain framework region of the non-human parent antibody.
18. The humanized or hybrid antibody of any one of claims 8 to 17, wherein the heavy chain variable region comprises at least one non-human complementarity determining region.

19. The humanized or hybrid antibody of claim 18, wherein the heavy chain variable region comprises at least two non-human complementarity determining regions.

20. The humanized or hybrid antibody of claim 19, wherein the heavy chain variable region comprises three non-human complementarity determining regions.

21. The humanized or hybrid antibody of any one of claims 8 to 20, wherein the light chain variable region comprise at least one non-human complementarity determining region.

22. The humanized or hybrid antibody of claim 21, wherein the light chain variable region comprise at least two non-human complementarity determining regions.

23. The humanized or hybrid antibody of claim 22, wherein the light chain variable region comprise three non-human complementarity determining regions.

24. The humanized or hybrid antibody of claim 8, wherein the clusterin-expressing cells are carcinoma cells.

25. The humanized or hybrid antibody of claim 24, wherein the carcinoma cells are human carcinoma cells.

26. The humanized or hybrid antibody of claim 25, wherein the human carcinoma cells are from a carcinoma selected from the group consisting of endometrial carcinoma, breast carcinoma, hepatocellular carcinoma, prostate carcinoma, renal cell carcinoma, ovarian carcinoma, melanoma, pancreatic carcinoma, lung carcinoma, bladder carcinoma, and colorectal cancer.

27. The humanized or hybrid antibody of claim 26, wherein the carcinoma is prostate carcinoma.

28. The humanized or hybrid antibody of claim 26, wherein the carcinoma is breast carcinoma.

29. An antibody or antigen binding fragment thereof capable of specific binding to clusterin and selected from the group consisting of:
a. an antibody or antigen binding fragment thereof having a light chain variable region at least 80% identical to SEQ ID NO.:25 and/or a heavy chain variable region at least 80% identical to SEQ ID NO.:29 wherein said antibody or antigen binding fragment thereof comprises at least one amino acid substitution in comparison with SEQ ID NO.:25 or SEQ ID NO.:29 and wherein said amino acid substitution is outside of a complementarity determining region (CDR) and;

b. an antibody or antigen binding fragment thereof having a light chain variable region at least 80% identical to SEQ ID NO.:33 and/or a heavy chain variable region at least 80% identical to SEQ ID NO.:37 wherein said antibody or antigen binding fragment thereof comprises at least one amino acid substitution in comparison with SEQ ID NO.:33 or SEQ ID NO.:37 and wherein said amino acid substitution is outside of a complementarity determining region (CDR).

30. The antibody or antigen binding fragment of claim 29, wherein the at least one amino acid substitution is in the light chain variable region.

31. The antibody or antigen binding fragment of claim 29 or 30, wherein the amino acid substitution is in the heavy chain variable region.

32. The antibody or antigen binding fragment of any one of claims 29 to 31, wherein said amino acid substitution is conservative.

33. The antibody or antigen binding fragment of any one of claims 29 to 32, wherein the light chain variable region comprises at least 90 consecutive amino acids of SEQ ID NO.:26.

34. The antibody or antigen binding fragment of claim 33, wherein the light chain variable region comprises at least 90 consecutive amino acids of SEQ ID NO.:27.

35. The antibody or antigen binding fragment of claim 34, wherein the light chain variable region comprises at least 90 consecutive amino acids of SEQ ID NO.:28.

36. The antibody or antigen binding fragment of claim 35, wherein the light chain variable region comprises at least 90 consecutive amino acids of SEQ ID NO.:8.

37. The antibody or antigen binding fragment of claim 36, wherein the light chain variable region is as set forth in SEQ ID NO.:8.
38. The antibody or antigen binding fragment of any one of claims 29 to 37 wherein the heavy chain variable region comprises at least 90 consecutive amino acids of SEQ ID NO.:30.

39. The antibody or antigen binding fragment of claim 38, wherein the heavy chain variable region comprises at least 90 consecutive amino acids of SEQ ID NO.:31.

40. The antibody or antigen binding fragment of claim 39, wherein the heavy chain variable region comprises at least 90 consecutive amino acids of SEQ ID NO.:32.

41. The antibody or antigen binding fragment of claim 40, wherein the heavy chain variable region comprises at least 90 consecutive amino acids of SEQ ID NO.:7.

42. The antibody or antigen binding fragment of claim 41, wherein the heavy chain variable region is as set forth in SEQ ID NO.:7.

43. The antibody or antigen binding fragment of claim 29, wherein the light chain variable region comprises at least 90 consecutive amino acids of SEQ ID NO.:26 and wherein the heavy chain variable region comprises at least 90 consecutive amino acids of SEQ ID NO.:30.

44. The antibody or antigen binding fragment of claim 43, wherein the light chain variable region comprises at least 90 consecutive amino acids of SEQ ID NO.:27 and wherein the heavy chain variable region comprises at least 90 consecutive amino acids of SEQ ID NO.:31.

45. The antibody or antigen binding fragment of claim 44, wherein the light chain variable region comprises amino acids at least 90 consecutive amino acids of SEQ ID NO.:28 and wherein the heavy chain variable region comprises at least 90 consecutive amino acids of SEQ ID NO.:32.

46. The antibody or antigen binding fragment of claim 45, wherein the light chain variable region comprises at least 90 consecutive amino acids SEQ ID NO.:8 and wherein the heavy chain variable region comprises at least 90 consecutive amino acids of SEQ ID NO.:7.

47. The antibody or antigen binding fragment of claim 46, wherein the light chain variable region is as set forth in SEQ ID NO.:8 and wherein the heavy chain variable region is as set forth in SEQ ID NO.:7.
48. The antibody or antigen binding fragment of any one of claims 29 to 32, wherein the
light chain variable region comprises at least 90 consecutive amino acids of SEQ ID
NO.:34.

49. The antibody or antigen binding fragment of claim 48, wherein the light chain
variable region comprises at least 90 consecutive amino acids of SEQ ID NO.:35.

50. The antibody or antigen binding fragment of claim 49, wherein the light chain
variable region comprises at least 90 consecutive amino acids of SEQ ID NO.:36.

51. The antibody or antigen binding fragment of claim 50, wherein the light chain
variable region comprises at least 90 consecutive amino acids of SEQ ID NO.:18.

52. The antibody or antigen binding fragment of claim 51, wherein the light chain
variable region is as set forth in SEQ ID NO.:18.

53. The antibody or antigen binding fragment of any one of claims 29 to 32 or 48 to 52,
wherein the heavy chain variable region comprises at least 90 consecutive amino
acids of SEQ ID NO.:38.

54. The antibody or antigen binding fragment of claim 53, wherein the light chain
variable region comprises at least 90 consecutive amino acids of SEQ ID NO.:39.

55. The antibody or antigen binding fragment of claim 54, wherein the light chain
variable region comprises at least 90 consecutive amino acids of SEQ ID NO.:40.

56. The antibody or antigen binding fragment of claim 55, wherein the light chain
variable region comprises at least 90 consecutive amino acids of SEQ ID NO.:17.

57. The antibody or antigen binding fragment of claim 56, wherein the light chain
variable region is as set forth in SEQ ID NO.:17.

58. The antibody or antigen binding fragment of claim 29, wherein the light chain
variable region comprises at least 90 consecutive amino acids of SEQ ID NO.:34 and
wherein the heavy chain variable region comprises at least 90 consecutive amino
acids of SEQ ID NO.:38.

59. The antibody or antigen binding fragment of claim 58, wherein the light chain
variable region comprises at least 90 consecutive amino acids of SEQ ID NO.:35 and
wherein the heavy chain variable region comprises at least 90 consecutive amino
acids of SEQ ID NO.:39.
60. The antibody or antigen binding fragment of claim 59, wherein the light chain variable region comprises at least 90 consecutive amino acids of SEQ ID NO.:36 and wherein the heavy chain variable region comprises at least 90 consecutive amino acids of SEQ ID NO.:40.

61. The antibody or antigen binding fragment of claim 60, wherein the light chain variable region comprises at least 90 consecutive amino acids of SEQ ID NO.:18 and wherein the heavy chain variable region comprises at least 90 consecutive amino acids of SEQ ID NO.:17.

62. The antibody or antigen binding fragment of claim 61, wherein the light chain variable region is as set forth in SEQ ID NO.:18 and wherein the heavy chain variable region is as set forth in SEQ ID NO.:17.

63. The antibody or antigen binding fragment of any one of claims 8 to 62, wherein said antibody comprises amino acids of a constant region.

64. The antibody or antigen binding fragment of claim 63, wherein the amino acids of the constant region are from a human antibody.

65. The antibody or antigen binding fragment of any one of claims 8 to 64, comprising a human IgG2 constant region.

66. The antibody or antigen binding fragment of any one of claims 8 to 65, wherein the antigen binding fragment is a scFv, a Fab, a Fab' or a (Fab')2.

67. The antibody or antigen binding fragment of any one of claims 8 to 66, conjugated with a cytotoxic moiety.

68. The antibody or antigen binding fragment of any one of claims 8 to 66, conjugated with a detectable moiety.

69. The antibody or antigen binding fragment of any one of claims 8 to 67, for use in the treatment of cancer comprising tumor cells expressing clusterin or a clusterin variant.

70. The antibody or antigen binding fragment of any one of claims 8 to 68, for use in the detection of cancer comprising tumor cells expressing clusterin or a clusterin variant.

71. The antibody or antigen binding fragment of any one of claims 1 to 68, for use in preventing or treating metastasis.
72. An isolated antibody or antigen binding fragment capable of competing with the antibody or antigen binding fragment of any one of claims 1 to 68.

73. An antigen binding fragment comprising a light chain variable region and a heavy chain variable region non-human complementarity determining region amino acid residues and human framework region amino acid residues and wherein the antigen binding fragment specifically binds to clusterin and has a better affinity than an antigen binding fragment of a non-human parent antibody.

74. The antigen binding fragment of claim 73 wherein said antigen binding fragment is from the humanized or hybrid antibody of any one of claims 8 to 28.

75. The antigen binding fragment of claim 73 or 74, characterized by an affinity of $17 \times 10^9 \text{ M} \leq 2.97 \times 10^9$ or better.

76. An isolated antibody comprising the amino acid sequence of the antigen binding fragment of any one of claims 73 or 75.

77. An isolated nucleic acid encoding the light chain variable region and/or the heavy chain variable region of the antibody of any one of claims 8 to 72, of the antigen binding fragment of any one of claims 73 to 75 or of the isolated antibody of claim 76.

78. A vector comprising the isolated nucleic acid of claim 77.

79. The vector of claim 78, wherein said vector is a mammalian expression vector.

80. An isolated cell comprising the isolated nucleic acid of claim 77, or the vector of claim 78 or 79 or expressing the humanized or hybrid antibody of any one of claims 8 to 72, the antigen binding fragment of any one of claims 73 to 75 or the isolated antibody of claim 76.

81. The isolated cell of claim 80, wherein said cell is a mammalian cell.

82. A pharmaceutical composition comprising the antibody of any one of claims 8 to 72, the antigen binding fragment of any one of claims 73 to 75 or the isolated antibody of claim 76 and a pharmaceutically acceptable carrier.

83. A combination therapy comprising the pharmaceutical composition of claim 82 and a chemotherapeutic agent.
84. The combination therapy of claim 83, wherein the chemotherapeutic agent comprises a taxane.

85. The combination therapy of claim 84, wherein the taxane is paclitaxel or docetaxel.

86. The combination therapy of any one of claims 83 to 85, wherein the pharmaceutical composition is administered concurrently with the chemotherapeutic agent.

87. The combination therapy of any one of claims 83 to 86, wherein the pharmaceutical composition and the chemotherapeutic agent are administered at different time intervals.

88. A method of reducing the growth of a cancer cell expressing clusterin, the method comprising administering an anti-clusterin antibody to a mammal in need.

89. The method of claim 88, comprising administering the antibody of any one of claims 8 to 72, the antigen binding fragment of any one of claims 73 to 75 or the isolated antibody of claim 76.

90. The method of claim 88 or 89, further comprising administering a chemotherapeutic agent.

91. The method of any one of claims 88 to 90, wherein the mammal in need has an elevated level of clusterin.

92. The method of any one of claims 88 to 90, wherein the mammal in need has a disease associated with an elevated level of clusterin.

93. The method of any one of claims 88 to 90, wherein the mammal in need is susceptible of carrying cells capable of epithelial-to-mesenchymal transition.

94. The method of any one of claims 88 to 90, wherein the mammal in need has a tumor expressing or secreting clusterin.

95. The method of any one of claims 88 to 94, wherein the mammal in need has a carcinoma.

96. The method of claim 95, wherein the carcinoma is prostate carcinoma.

97. The method of claim 95, wherein the carcinoma is breast carcinoma.
98. A method of treating a disease associated with clusterin expression, the method comprising administering the humanized or hybrid antibody of any one of claims 8 to 72, the antigen binding fragment of any one of claims 73 to 75 or the isolated antibody of claim 76 to a mammal in need.

99. Use of the humanized or hybrid antibody of any one of claims 8 to 72, the antigen binding fragment of any one of claims 73 to 75 or the isolated antibody of claim 76 in the manufacture of a medicament for the treatment of a disease associated with clusterin expression.

100. A method for making a humanized or hybrid anti-clusterin antibody comprising expressing a heavy chain variable region comprising non-human heavy chain CDR amino acid residues of a non-human antibody capable of specific binding to clusterin and framework region amino acids of a natural human antibody heavy chain variable region and expressing a complementary light chain variable region.

101. The method of claim 100, wherein the natural human antibody heavy chain variable region has: a) a three-dimensional structure similar to or identical to that of a heavy chain of the non-human antibody, b) a framework region having an amino acid sequence at least 70% identical to a heavy chain framework region of the non-human antibody, and/or; c) a number of amino acid residues in a heavy chain CDR that is the same or substantially the same as that of the non-human heavy chain CDR amino acid residues.

102. A method for making a humanized or hybrid anti-clusterin antibody comprising expressing a light chain variable region comprising non-human light chain CDR amino acid residues of a non-human antibody capable of specific binding to clusterin and framework region amino acids of a natural human antibody light chain variable region and expressing a complementary heavy chain variable region.

103. The method of claim 102, wherein the natural human antibody light chain variable region has: a) a three-dimensional structure similar to or identical to that of a light chain of the non-human antibody, b) a framework region having an amino acid sequence at least 70% identical to a light chain framework region of the non-human antibody, and/or; c) a number of amino acid residues in a light chain CDR that is the same or substantially the same as that of the non-human light chain CDR amino acid residues.
104. A kit comprising a vial or vials comprising antibody of any one of claims 8 to 72, the antigen binding fragment of any one of claims 73 to 75, the isolated antibody of claim 76, the isolated nucleic acid of claim 77 or the vector of claim 78 or 79.

105. A method for reducing the volume of a tumor comprising cells expressing or secreting clusterin in an individual in need, the method comprising administering an anti-clusterin antibody.

106. The method of claim 105, wherein the anti-clusterin antibody is selected from the group consisting of a polyclonal antibody, a monoclonal antibody, a chimeric antibody, a humanized antibody, an isolated human antibody, a hybrid antibody and a fragment thereof.

107. The method of claim 106, wherein the hybrid antibody or fragment thereof comprises a light chain variable region of a non-human antibody and a heavy chain variable region of a humanized antibody or human antibody.

108. The method of claim 106, wherein the hybrid antibody or fragment thereof comprises a heavy chain variable region of a non-human antibody and a light chain variable region of a humanized antibody or human antibody.

109. The method of any one of claims 105 to 108, wherein the tumor is a carcinoma selected from the group consisting of endometrial carcinoma, breast carcinoma, hepatocellular carcinoma, prostate carcinoma, a renal cell carcinoma, ovarian carcinoma, of pancreatic carcinoma, and colorectal carcinoma.

110. The method of claim 109, wherein the carcinoma is prostate carcinoma.

111. The method of claim 109, wherein the carcinoma is breast carcinoma.
### FIGURE 2

**VL**

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<th>DIVY5QS5PSSLAVASAGKVTNSCKSSQSSLNN3RT3K3NYLAWQKFGQSFPRLL1IYWASTE3GVPORFTGGS8GTDTPLTIS3SVQAE3DLAVVYYCKQSYNL-WTFQGCGTFLEEK</th>
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| VH |

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16B5 murine VL—SEQ ID NO.:25 (CDRs are highlighted)

16B5 humanized VL = SEQ ID NO.:8 (CDRs are highlighted)

Human model of 16B5 VL—SEQ ID NO.:41

16B5 murine VH=SEQ ID NO.:29 (CDRs are highlighted)

15B5 humanized VH=SEQ ID NO.:7 (CDRs are highlighted)

Human model of 16B5 VH—SEQ ID NO.:42
FIGURE 3

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FIGURE 4

Murine 16B5

T = 0h

T = 15h

commercial

hybridoma 16B5

Humanized 16B5

T = 15h

EMT6 cells

MM

MH

HM

HH
FIGURE 8

21B12 humanization

VL (14 mutations, 100% framework humanization):

Mouse D1VMQGSFSLLAVEGVKTMSCKSSQSLYSSQHQLQWYQPRQKGSQPKLTVKWASTRESGVDFRTFGSOGTDFTLTISSVCAEDLAVYQQYYFRTSGGFKLEIK
Humanized D1VMQGSFSLLAVERATINCSKSSQSLYSSQHQLQWYQPRQKGSQPKLTVKWASTRESGVDFRTFGSOGTDFTLTISSVCAEDLAVYQQYYFRTSGGFKLEIK
Human FR 8a D1VMQGSFSLLAVERATINCSKSSQSLYSSQHQLQWYQPRQKGSQPKLTVKWASTRESGVDFRTFGSOGTDFTLTISSVCAEDLAVYQQYYFRTSGGFKLEIK
Back mutations S S V KV ME R S T VK L G

VH (18 mutations, 100% framework humanization):

Mouse Q1LVQSGPELKKFGETVKKISSSQTTITYQG5H5WQAFKGLFWMQWINTTFEPTADDFFKGRFAFSELTASASTLQIQINNLKEDTTATYFCAKDFLY---FFDYWSQQTTLT
Humanized Q1LVQSGPELKKFGETVKKISSSQTTITYQG5H5WQAFKGLFWMQWINTTFEPTADDFFKGRFAFSELTASASTLQIQINNLKEDTTATYFCAKDFLY---FFDYWSQQTTLT
Human FR 8b Q1LVQSGPELKKFGETVKKISSSQTTITYQG5H5WQAFKGLFWMQWINTTFEPTADDFFKGRFAFSELTASASTLQIQINNLKEDTTATYFCAKDFLY---FFDYWSQQTTLT
Back mutations I P E T I K K K A E A NN N NF TL

21B12 murine VL = SEQ ID NO.:33 (CDRs are highlighted)
21B12 humanized VL = SEQ ID NO.:18 (CDRs are highlighted)
Human model of 21B12 VL = SEQ ID NO.:43
21B12 murine VH = SEQ ID NO.:37 (CDRs are highlighted)
21B12 humanized VH = SEQ ID NO.:17 (CDRs are highlighted)
Human model of 21B12 VH = SEQ ID NO.:58


buried within 5Å from CDRs (Kabat definition)
close to VH
close to VL
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<th>$K_d$ (1/s)</th>
<th>$K_D$ (M)</th>
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FIGURE 10

The figure shows the growth of tumor volume over time for different cell lines and treatments. The x-axis represents time in days, ranging from 0 to 50. The y-axis represents tumor volume in mm³, ranging from 0 to 3000. Different symbols and lines are used to represent different groups:
- PC-3 (black circles)
- TxF (black triangles)
- AB-16B5 (grey circles)
- TxF + AB-16B5 (grey triangles)

Error bars are shown at each data point, indicating the variability in the observed tumor volumes.
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<td>IgG ctl</td>
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**FIGURE 15**

Query is human clusterin (NP_001822)
Sbjct is murine clusterin (NP_038520)

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<th>Gaps</th>
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<td>334/435 (77%)</td>
<td>384/435 (89%)</td>
<td>0/435 (0%)</td>
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<th>WESGCQVLGDQTVSDNELQMSNQSGKSYVKQEIQNAVNGVQVQIKTLIEKTNEERKTLSSNL</th>
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<td>W++G VLQ+Q VSDNELQ+SE CGS+Y+NKEIQNAV GVK IKTLIEKTN ERK++L+L</td>
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<tr>
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<td>57</td>
<td>W G VLQ Q VSDNELQ E CGS Y NKEIQNAV GVK IKTLIEKTN ERK LL L</td>
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<tr>
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<td>LVG+QLEFLQSSPFYFWMNGDRDSLLE+DQQ+ +LD WQD P+RAS IID LFQDR</td>
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INTERNATIONAL SEARCH REPORT

A. CLASSIFICATION OF SUBJECT MATTER

IPC: C07K 16/18 (2006.01) . A61K 39/395 (2006.01) . A61P 35/00 (2006.01) . C07K 16/46 (2006.01) . C12N 15/13 (2006.01) . C07K 14-775 (2006.01)

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)

IPC: C07K 16/18 (2006.01) . A61K 39/395 (2006.01) . A61P 35/00 (2006.01) . C07K 16/46 (2006.01) . C12N 15/13 (2006.01) . C07K 14-775 (2006.01)

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

Electronic database(s) consulted during the international search (name of database(s) and, where practicable, search terms used)

Canadian Patents Database, TotalPatent, PubMed, Google Scholar, GQPAT, RefSeq, NCBI GenPept, ENSEMBL, NCBI IBLAST, PDB Protein. Keywords: clusterin, apolipoprotein J, antibody, cancer. Authors: Tremblay, Filion, Sulea.

C. DOCUMENTS CONSIDERED TO BE RELEVANT

<table>
<thead>
<tr>
<th>Category</th>
<th>Citation of document, with indication, where appropriate, of the relevant passages</th>
<th>Relevant to claim No.</th>
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[ ] Further documents are listed in the continuation of Box C. [X] See patent family annex.

Date of the actual completion of the international search:
7 February 2011 (07-02-2011)

Date of mailing of the international search report:
16 February 2011 (16-02-2011)

Name and mailing address of the ISA/CA:
Canadian Intellectual Property Office
Place du Portage 1, C1 14 - 1st Floor, Box PCT
50 Victoria Street
Gatineau, Quebec K1A 0C9
Facsimile No.: 001-819-953-2476

Authorized officer

Ernest Tan (819) 994-4148
<table>
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<tr>
<th>Box No. 1</th>
<th>Nucleotide and/or amino acid sequence(s) (Continuation of item l.c of the first sheet)</th>
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<td>1.</td>
<td>With regard to any nucleotide and/or amino acid sequence disclosed in the international application, the international search was carried out on the basis of a sequence listing filed or furnished:</td>
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<td>a. (means)</td>
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<td>[ ] in the international application as filed</td>
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<td>[ ] together with the international application in electronic form</td>
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<td>[X] subsequently to this Authority for the purposes of search</td>
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<td>2.</td>
<td>[ ] In addition, in the case that more than one version or copy of a sequence listing has been filed or furnished, the required statements that the information in the subsequent or additional copies is identical to that in the application as filed or does not go beyond the application as filed, as appropriate, were furnished.</td>
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<td>3.</td>
<td>Additional comments:</td>
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<td>The electronic form of the sequence listing submitted on 12-01-2011 was used for the sequence search purposes.</td>
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INTERNATIONAL SEARCH REPORT

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

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

1. [X] Claim Nos. : 88-98 and 105-111
   because they relate to subject matter not required to be searched by this Authority, namely:
   Although claims 88-98 and 105-111 are directed to a method of medical treatment of the human/animal body which this Authority is not required to search in view of Rule 39.3(iv) of the PCT, the search has nevertheless been carried out based on the alleged effect of the antibody defined therein.

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

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

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

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

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

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

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

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

Remark on Protest  [ ] The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.

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

[ ] No protest accompanied the payment of additional search fees.
<table>
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<tr>
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