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(54) Title: LIPOSOMAL COMPOSITIONS AND USES OF SAME

(57) Abstract: Compositions comprising liposomes composed of whole cell membrane fraction are provided. The liposomes may be attached to, or encapsulate a pharmaceutical agent. Also provided are methods of generating and using these liposomes.

LIPOSOMAL COMPOSITIONS AND USES OF SAME

RELATED APPLICATION/S

This application claims the benefit of priority under 35 USC 119(e) of U.S. Provisional Patent Application No. 61/237,306 filed August 27, 2009, the contents of which are incorporated herein by reference in their entirety.

FIELD AND BACKGROUND OF THE INVENTION

The present invention, in some embodiments thereof, relates to liposomal compositions and uses of same.

Liposome based DNA and drug delivery systems have been extensively investigated in the last four decades, and used as a mean to treat various conditions. Liposomal systems allow the efficient entrapment of both hydrophilic and hydrophobic compounds in a well-characterized, biocompatible and non-immunogenic lipid vesicle that can range from nanometers to micrometers in diameter. Liposomes can also be targeted using specific ligands such as protein conjugates or antibodies that bind specific cellular receptors. In cancer therapy, liposomal systems are of the most popular and well-investigated drug carriers. This is mainly due to the enhanced permeability and retention (EPR) effect, which refers to the increased vascular permeability of tumor vessels due to tumor angiogenesis. The EPR effect results in the accumulation of liposomes in the tumor extracellular fluid, which is exploited as a passive targeting mechanism. State of the art technologies in liposomal drug delivery for cancer therapy primarily include drugs that are approved for clinical use (e.g., DaunoXome™, Myocet™, Doxil™, Caelyx™). Several approaches are currently investigated for the targeting of liposomal systems to cancer, which include the binding of targeting moieties to the liposome surface (e.g., antibodies). Synthetic cationic liposomes are the most common vectors for DNA delivery although their cytotoxicity remains a concern irrespective of the preferred route of DNA transfer both *in vitro* and *in vivo*. On the other hand, anionic liposomes that better resemble cell-derived liposomes (in term of their electric charge) were also shown to mediate gene transfer, but suffer from poor encapsulation efficiency due to the large size and the negative charge of the

uncondensed DNA. Improving encapsulation efficiency and protecting DNA from degradation was achieved by complexation of the DNA with cations or poly-cations that subsequently also significantly improved the transfection efficiencies.

In the last decade several studies have revealed that certain primary cells, such as adult mesenchymal stem cells (MSC), adult hematopoietic stem cells (HSC) and endothelial cells, accumulate at tumor microenvironments, when administered to tumor bearing animals. Recent data suggests that isolated membrane fractions of tumor cells appear to contain potent MSC attractants, more so than the cytoplasmic fractions isolated from the same cells. This data implies that the mechanism of MSC targeting to tumor cells is mainly governed by cell-to-cell interactions via the binding of surface molecules found on tumors and MSC. However, cellular response to different soluble factors (i.e., chemokines) secreted by angiogenic blood vessels and tumor cells is suggested to take some part in the MSC homing mechanism as well. The homing mechanism motivated studies on the use of these cells as a targeted delivery vehicle for cancer therapy. In these studies, primary cells were isolated and transduced with different genes of interest, either anti-cancer or reporter genes. The cells were transplanted to tumor bearing animals and their homing to the tumor microenvironment was demonstrated using the expressed reporter proteins. Tumor inhibition was achieved using the expressed anti-cancer proteins.

Liposomes, which are derived from the cytoplasmatic membrane of mammalian cells, have been commonly used as a tool in the study of membranes and cellular mechanisms. Cell derived liposomes (CDL or CDLs in plural) have been also investigated as a tool for cancer immunotherapy. In these studies, liposomes were prepared from the membranes of tumor cells and were used as adjuvant to evoke the immune system towards tumor antigens located on the liposome membrane. However, cell derived liposomes have never been produced from stem cells, nor used as a delivery vehicle. Furthermore, no CDL system has ever been developed as a targeting platform.

Related Art:

Boone, C.W., Ford, L.E., Bond, H.E., Stuart, D.C. & Lorenz, D. Isolation of plasma membrane fragments from HeLa cells. J Cell Biol 41, 378-392 (1969).

Westerman and Jensen Methods Enzymol. 2003;373:118-27.

SUMMARY OF THE INVENTION

According to an aspect of some embodiments of the present invention there is provided a composition-of matter comprising a liposome attached to, or encapsulating a pharmaceutical agent, the liposome being composed of a whole cell membrane fraction.

According to some embodiments of the invention, the cell is a human cell.

According to some embodiments of the invention, a cell source for the whole cell membrane is selected from the group consisting of a stem cell, a primary cell, a cell-line, a non-tumorigenic cell, a cancer cell and an immune cell.

According to an aspect of some embodiments of the present invention, there is provided a composition-of matter comprising a liposome composed of a whole cell membrane fraction of a stem cell.

According to some embodiments of the invention, the stem cell comprises a human mesenchymal stem cell.

According to an aspect of some embodiments of the present invention there is provided a composition-of matter comprising a liposome composed of a whole cell membrane fraction of a primary human cell.

According to an aspect of some embodiments of the present invention there is provided a composition-of matter comprising a liposome composed of a whole cell membrane fraction of a non-tumorigenic human cell.

According to some embodiments of the invention, the cell membrane is genetically modified to express an exogenous protein.

According to some embodiments of the invention, the exogenous protein is selected from the group consisting of a cell marker, a targeting moiety and the pharmaceutical agent.

According to some embodiments of the invention, the liposome encapsulates, or attached to a pharmaceutical agent.

According to some embodiments of the invention, the pharmaceutical agent is a therapeutic agent.

According to some embodiments of the invention, the composition-of-matter is non-immunogenic in a human subject.

According to some embodiments of the invention, a cell source of the whole cell membrane fraction comprises cells autologous to a host subject.

According to some embodiments of the invention, a cell source of the whole cell membrane fraction comprises cells non-autologous to a host subject.

According to some embodiments of the invention, said liposome is attached to a synthetic polymer at an external surface thereof.

According to some embodiments of the invention, the pharmaceutical agent is a diagnostic agent.

According to some embodiments of the invention, the liposome is unilamellar.

According to some embodiments of the invention, the liposome is attached to a synthetic polymer at an external surface thereof.

According to some embodiments of the invention, the synthetic polymer is a poly-ethylene-glycol (PEG).

According to some embodiments of the invention, the liposome has a size range of 30-1000 nm.

According to an aspect of some embodiments of the present invention there is provided a method of producing liposomes comprising,

(a) subjecting cells to hypotonic conditions, so as to obtain ruptured cell membranes and/or ghosts; and

(b) homogenizing the ruptured cell membranes and/or ghosts to thereby produce liposomes.

According to some embodiments of the invention, the homogenizing is effected by:

(c) sonicating the ruptured cell membrane and/or ghosts; and optionally

(d) extruding the ruptured membrane and/or ghosts through a matrix of pre-determined porosity.

According to some embodiments of the invention, the method further comprises conjugating a synthetic polymer to the liposomes following step (c).

According to an aspect of some embodiments of the present invention there is provided a method of encapsulating a pharmaceutical agent in a liposome, the method comprising making the liposomes according to the method above and adding the pharmaceutical agent prior to the step of homogenizing.

According to an aspect of some embodiments of the present invention there is provided a pharmaceutical composition comprising as an active ingredient the composition-of-matter and a pharmaceutically acceptable carrier.

According to an aspect of some embodiments of the present invention there is provided a method of delivering a pharmaceutical agent, the method comprising administering to a subject in need thereof the composition of matter, thereby delivering the pharmaceutical agent.

According to some embodiments of the invention, the cell source of the whole cell membrane fraction is autologous to the subject.

According to some embodiments of the invention, a cell source of the whole cell membrane fraction is non-autologous to said subject.

Unless otherwise defined, all technical and/or scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which the invention pertains. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of embodiments of the invention, exemplary methods and/or materials are described below. In case of conflict, the patent specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and are not intended to be necessarily limiting.

BRIEF DESCRIPTION OF THE DRAWINGS

Some embodiments of the invention are herein described, by way of example only, with reference to the accompanying images and drawings. [1-10 images, 11 drawing]. With specific reference now to the images/drawings in detail, it is stressed that the particulars shown are by way of example and for purposes of illustrative discussion of embodiments of the invention. In this regard, the description taken with the images/drawings makes apparent to those skilled in the art how embodiments of the invention may be practiced.

In the drawings:

FIGs. 1A-C characterize human MSCs. Cell morphology as visualized by Giemsa staining (Figures 1A,B) and typical MSC (positive and negative) surface markers analyzed by flow cytometry (Figure 1C).

FIG. 2 is a photograph showing the migration of hMSCs towards cancer cells. DiI (red) labeled hMSC and DiO (green) labeled BHK, PC3, Cf2Th and COS-7 cells were drop-wise seeded. Maestro imaging following 72 hrs incubation demonstrated specific migration of the hMSCs towards PC3 prostate cells while "avoiding" other cell-lines.

FIG. 3 is a graph showing targeting of MCF7 breast cancer cell-line by hMSCs stimulated by MCF7-derived condition media.

FIGs. 4A-B are Cryo-TEM images of cell-derived liposomes. Cell-derived liposomes were prepared from the cytoplasmatic membranes of hMSCs and were PEGylated by conjugation with monomethoxy-PEG. The resulting PEGylated (Figure 4A) and un-PEGylated (Figure 4B) CDLs were then imaged by Cryo-TEM.

FIGs. 5A-C are graphs showing DLS and Zeta-Potential analysis of CDLs. Un-PEGyltated and PEGylated hMSC derived CDLs were analyzed for size, size distribution and charge by Number-weight DLS (Figure 5A), Volume-Weight DLS (Figure 5B) and Zeta-potential (Figure 5C).

FIG. 6 shows the surface marker characterization of hMSCs derived liposomes. CDL's were prepared from hMSCs, conjugated with Tosyl-activated Dynabeads™ and analyzed by FACS for hMSCs specific membranal markers (i.e., CD44, CD29, CD90 and CD105).

FIGs. 7A-B show the binding of CDLs prepared from hMSCs to prostate cancer cell-line (PC3). PC3 cells were labeled with DiO (green) and incubated with CDLs that were previously labeled with DiI (red). Cultures were imaged following 12 hrs incubation. Representative 3D-projection (Figure 7A) and single-slice (Figure 7B) images are presented.

FIGs. 8A-B are graphs and FACS histograms showing concentration-dependent binding of CDLs prepared from hMSCs to prostate cancer cell-line (PC3). PC3 cells were incubated with various concentrations of CDLs that were previously labeled with a red fluorescent dye (DiI). Following 24 hrs incubation, cells were washed, harvested and analyzed by FACS (Figure 8A). The mean fluorescence intensity of the cells was calculated and plotted vs. the natural logarithm of CDLs concentration (Figure 8B).

FIG. 9 show the specific binding of CDLs, prepared from conditioned hMSCs (i.e cell cultured with conditioned media of cancer cells), to prostate cancer cell-line

(PC3). DiI-labeled CDLs were prepared from hMSCs which were previously incubated for 24 hrs with condition media derived from a prostate cancer cell-line (PC3) and from a non-human cell-line (BHK). The resulting "conditioned" CDLs, as well as CDLs prepared from unconditioned hMSCs (control, NO CM), were incubated with PC3 and BHK cells for 15 min, 1 hr and 3 hrs. Following incubation, the cells were washed, harvested and analyzed by FACS. The percentage in the marker refers to the ratio of DiI-labeled cells within the marker. The percentage in brackets, designated on the upper-left histogram only, refers to the ratio of unlabeled cells within the marker. The marker and the ratio of unlabeled cells within the marker are identical for all histograms.

FIGs. 10A-B are cryo-TEM images of hMSCs derived liposomes entrapping soluble Tumor necrosis factor-related apoptosis-inducing ligand (sTRAIL). sTRAIL-containing CDLs (Figure 10A) and empty CDLs (Figure 10B) were prepared at the same final concentration and imaged by Cryo-TEM under the same conditions. To emphasize CDLs' content, the original grey-scale Cryo-TEM images (left pane) were re-colored to black and white (right pane).

FIG. 11 is a schematic illustration of the overall design of targeted carriers based on cell-derived liposomes (CDL). Origin cells that naturally and specifically interact with target cells are selected as a source for cell derived liposomes. For example, MSC membranally interact with cancer cells therefore are selected as a source for cancer targeting carriers. Source cells undergo hypotonic treatment to generate ghost cells, which are then homogenized to produce CDL. Resulting CDL are then able to specifically bind their target cells in a similar manner to the cells they are derived from.

DESCRIPTION OF SPECIFIC EMBODIMENTS OF THE INVENTION

The present invention, in some embodiments thereof, relates to liposomal compositions and uses of same.

Before explaining at least one embodiment of the invention in detail, it is to be understood that the invention is not necessarily limited in its application to the details set forth in the following description or exemplified by the Examples. The invention is capable of other embodiments or of being practiced or carried out in various ways.

A major challenge facing cancer therapy is achieving a cytotoxic effect towards

cancer cells, while sparing the healthy ones. The importance of the development of novel targeted therapeutic delivery strategies for cancer therapy has long been recognized worldwide.

The present inventors have designed a novel delivery vehicle for targeted delivery of therapeutic and diagnostic agents into cells and tissues. The delivery vehicle is liposome-based composed of a whole cell membrane fraction which comprises both natural lipids and proteins. By employing native cell membranes, the delivery vehicles of the present invention may be formulated to be of low immunogenic potential, easily home to the target tissue and can be genetically modified to express therapeutic or targeting moieties.

As is illustrated below and in the examples section, which follows and further depicted in Figure 12, the present inventors have generated liposomes composed of whole cell membranes of mesenchymal stem cells, which are well-known for their homing capacities as well as their immuno-suppressive abilities (i.e., their ability to reduce inflammation and suppress immune cells) and hypo-immunogenic features (i.e., stealth-like features that makes them less immunogenic and less recognizable as foreign matter when heterologously transplanted). The liposomes exhibit the protein signature of mesenchymal stem cells and as such are expected to mediate similar immunosuppression and migratory properties as intact mesenchymal stem cells. These cell derived liposomes were further PEGylated to increase their bioavailability and dispersion and reduce their coagulation. The cell derived liposomes were also treated to encapsulate a therapeutic agent. Altogether these findings, place the present delivery system as a pivotal tool in the diagnosis and treatment of human disease such as cancer.

Thus, according to an aspect of the present invention there is provided a composition-of-matter comprising a liposome attached to, or encapsulating a pharmaceutical agent, said liposome being composed of a whole cell membrane fraction.

As used herein the term "liposome" refers to fully closed carrier molecules comprising a spherical lipid membrane which itself is in a liquid crystalline phase or a liquid gel phase, in which an entrapped liquid volume is contained. The two liquid phases are immiscible. Thus, liposomes of the present invention (also referred to herein as cell derived liposomes (CDLs), similar to membranes of cells, are in an entirely gel/liquid state and/or liquid crystal state and not in a solid state.

The liposomes of some embodiments of the present invention have an expected protein to lipid ration of about 0.8 w/w.

Of note, the protein content of hMSCc CDLs is about 0.8 mg/10^8 cells (as determined by Bradford assay). The lipid content can be easily determined using the Stewart phospholipids assay. It is expected to be about 1 mg/ 10^8 cells.

The following calcultation can be used to determine the theoretical phospholipids content. Since the dry mass of a single mammalian cell is in the magnitude of 10^{-7} mg [1] and since phospholipids constitutes approximately 10% of the dry cell mass [2] then the theoretical yield of the cell derived liposomes' production process (assumed 100% efficiency) should be in the magnitude of 10^{-8} mg phospholipids per single cell or 1 mg per 10^8 cells.

Liposomes include niosomes, transfersomes, emulsions, foams, micelles, liquid crystals, dispersions, lamellar layers and the like.

The liposomes may be unilamellar or multilamellar.

According to a specific embodiment of the invention, the liposomes are unilamellar, as determined by Cryo-TEM.

According to a specific embodiment of the invention, the liposomes exhibit native membrane symmetry and expression of native markers.

Liposomes of the present invention are composed of a whole cell membrane fraction.

As used herein the phrase "cell membrane" or "cellular membrane" (which may be interchangeably used) refers to a biological membrane, which surrounds the cell or is an integral part of an organelle thereof (e.g., chloroplast, ER, golgi, mitochondrion, vacuole, nucleus and a lysosome).

According to a specific embodiment of the present invention the cell membrane refers to the plasma membrane. The use of plasma membrane is of a specific advantage since it presents proteins, which are associated with cell-to-cell interactions, as well as other recognition molecules, such as receptors that bind soluble ligands.

As used herein "a whole cell membrane fraction" refers to a fraction, which does not include lipids alone but also includes membrane proteins.

Examples of membrane proteins include, but are not limited to, integral proteins, transmembrane proteins, lipid anchored proteins and glycoproteins.

According to an embodiment of the invention the whole cell membrane fraction also includes carbohydrates.

According to a specific embodiment the cell is a eukaryotic cell [e.g., mammalian (such as human), plant, insect cell].

According to an additional specific embodiment the eukaryotic cell is a mammalian cell.

According to yet an additional embodiment the cell can be a primary cell (i.e., non-immortalized and at times not cultured) or a cell-line.

According to yet an additional embodiment the cell can be an embryonic cell.

Use of a primary cell may be advantageous for clinical use where non-cultured cells are used in autologous or non-autologous (syngeneic allogeneic or xenogeneic) settings.

According to a specific embodiment the eukaryotic cell is a stem cell.

As used herein, the phrase "stem cells" refers to cells, which are capable of remaining in an undifferentiated state (*e.g.,* pluripotent or multipotent stem cells) for extended periods of time in culture until induced to differentiate into other cell types having a particular, specialized function (*e.g.,* fully differentiated cells). Preferably, the phrase "stem cells" encompasses embryonic stem cells (ESCs), induced pluripotent stem cells (iPS), adult stem cells, mesenchymal stem cells and hematopoietic stem cells.

According to a specific embodiment the stem cell is a mesenchymal stem cell.

Mesenchymal stem cells are the formative pluripotent blast cells. Mesenchymal stem cells (MSCs) give rise to one or more mesenchymal tissues (e.g., adipose, osseous, cartilaginous, elastic and fibrous connective tissues, myoblasts, cardiac like cells) as well as to tissues other than those originating in the embryonic mesoderm (e.g., neural cells) depending upon various influences from bioactive factors such as cytokines. MSCs can be isolated from embryonic yolk sac, placenta, umbilical cord, fetal and adolescent skin, blood, bone marrow, adipose and other tissues, although their abundance in the bone marrow far exceeds their abundance in other tissues. MSCs have been shown to have immunosuppressive functions in various settings, including autoimmune diseases and transplantation, rendering liposomes generated therefrom ultimate tools in inflammatory and autoimmune settings.

Methods of isolating, purifying and expanding mesenchymal stem cells (MSCs) are known in the arts and include, for example, those disclosed by Caplan and Haynesworth in U.S. Pat. No. 5,486,359 and Jones E.A. et al., 2002, Isolation and characterization of bone marrow multipotential mesenchymal progenitor cells, Arthritis Rheum. 46(12): 3349-60.

Preferably, mesenchymal stem cell cultures are generated by diluting BM aspirates (usually 20 ml) with equal volumes of Hank's balanced salt solution (HBSS; GIBCO Laboratories, Grand Island, NY, USA) and layering the diluted cells over about 10 ml of a Ficoll column (Ficoll-Paque; Pharmacia, Piscataway, NJ, USA). Following 30 minutes of centrifugation at 2,500 x g, the mononuclear cell layer is removed from the interface and suspended in HBSS. Cells are then centrifuged at 1,500 x g for 15 minutes and resuspended in a complete medium (MEM, α medium without deoxyribonucleotides or ribonucleotides; GIBCO); 20 % fetal calf serum (FCS) derived from a lot selected for rapid growth of MSCs (Atlanta Biologicals, Norcross, GA); 100 units/ml penicillin (GIBCO), 100 μg/ml streptomycin (GIBCO); and 2 mM L-glutamine (GIBCO). Resuspended cells are plated in about 25 ml of medium in a 10 cm culture dish (Corning Glass Works, Corning, NY) and incubated at 37 °C with 5 % humidified CO_2. Following 24 hours in culture, nonadherent cells are discarded, and the adherent cells are thoroughly washed twice with phosphate buffered saline (PBS). The medium is replaced with a fresh complete medium every 3 or 4 days for about 14 days. Adherent cells are then harvested with 0.25 % trypsin and 1 mM EDTA (Trypsin/EDTA, GIBCO) for 5 min at 37 °C, replated in a 6-cm plate and cultured for another 14 days. Cells are then trypsinized and counted using a cell counting device such as for example, a hemocytometer (Hausser Scientific, Horsham, PA). Cultured cells are recovered by centrifugation and resuspended with 5 % DMSO and 30 % FCS at a concentration of 1 to 2 X 10^6 cells per ml. Aliquots of about 1 ml each are slowly frozen and stored in liquid nitrogen.

To expand the mesenchymal stem cell fraction, frozen cells are thawed at 37 °C, diluted with a complete medium and recovered by centrifugation to remove the DMSO. Cells are resuspended in a complete medium and plated at a concentration of about 5,000 cells/cm^2. Following 24 hours in culture, nonadherent cells are removed and the adherent cells are harvested using Trypsin/EDTA, dissociated by passage through a

narrowed Pasteur pipette, and preferably replated at a density of about 1.5 to about 3.0 cells/cm^2. Under these conditions, MSC cultures can grow for about 50 population doublings and be expanded for about 2000 fold [Colter DC., et al. Rapid expansion of recycling stem cells in cultures of plastic-adherent cells from human bone marrow. Proc Natl Acad Sci USA. 97: 3213-3218, 2000].

MSC cultures utilized by the present invention preferably include three groups of cells, which are defined by their morphological features: small and agranular cells (referred to as RS-1, herein below), small and granular cells (referred to as RS-2, herein below) and large and moderately granular cells (referred to as mature MSCs, herein below). The presence and concentration of such cells in culture can be assayed by identifying a presence or absence of various cell surface markers, by using, for example, immunofluorescence, *in situ* hybridization, and activity assays.

When MSCs are cultured under the culturing conditions of the present invention they exhibit negative staining for the hematopoietic stem cell markers CD34, CD11B, CD43 and CD45. A small fraction of cells (less than 10 %) are dimly positive for CD31 and/or CD38 markers. In addition, mature MSCs are dimly positive for the hematopoietic stem cell marker, CD117 (c-Kit), moderately positive for the osteogenic MSCs marker, Stro-1 [Simmons, P. J. & Torok-Storb, B. (1991). Blood 78, 5562] and positive for the thymocytes and peripheral T lymphocytes marker, CD90 (Thy-1). On the other hand, the RS-1 cells are negative for the CD117 and Stro1 markers and are dimly positive for the CD90 marker, and the RS-2 cells are negative for all of these markers.

Other cells, which may be used as an effective source for whole cell membrane fraction include, but are not limited to, endothelial cells, hepatic cells, pancreatic cells, bone cells, chondrocytes, neuronal cells and the like.

The cells can be used native (i.e., not manipulated by genetic modification) or genetically modified to manipulate the membrane composition of the cell.

The advantage of genetic modification is in its increased efficiency. Essentially all (> 95 %) the CDLs generated from genetically modified cells express the gene-of-interest. The gene-of-interest may be constitutively expressed on the cell source (by integration to the cells genome) or transiently expressed (episomal expression) such as to

avoid hazardous implications of stable transfection agents (e.g., lentiviral and retroviral vectors).

Thus, the cells may be genetically modified to express a gene-of-interest (i.e., not naturally expressed in the native membrane but also in order to enhance the expression of endogenous proteins that are naturally expressed on the cell's membrane but in lower levels).

According to specific embodiments, the gene-of-interest encodes a membrane protein. The gene-of-interest may be a native membrane protein or modified to have a membrane localization signal and other motifs needed for membrane anchorage e.g., a transmembrane domain.

Examples of membrane proteins which may be heterologously (exogenously) expressed include, but are not limited to, a targeting protein (e.g., antibodies, receptors, membrane anchored ligands, decoys), a protein which affects the chemistry of the membrane (e.g., structural proteins, charged proteins), a diagnostic protein (e.g., an enzyme as described in length below) and a therapeutic protein (as described in length below).

A targeting moiety includes a targeting protein such as an antibody, a receptor ligand and a non-proteinecious molecule such as carbohydrates, which binds cell surface or extra-cellular matrix markers. For example, prostate-specific membrane antigen (PSMA) that is over-expressed on prostate cancer cells can be targeted by its ligand NAAG[3] conjugated to a transmembranal motif (e.g, truncated LIME)[4]. This may be achieved, by genetically engineering the cells (of which the CDLs are derived from) to express the chimeric or natural form of NAAG. For example, the expression plasmid encoding LIME is constructed by PCR and subsequent insertion of the corresponding fragment into pcDNA3.1 (Invitrogen). The primers also have BamHI (5′ primer and 3′ primer) site extension to facilitate the subcloning. The PCR product is digested with BamHI and inserted into corresponding sites in pcDNA3.1(+) (CLONTECH Laboratories, Inc.). For expression vector encoding LIME-acetylaspartylglutamate (NAAG), the open reading frame can be inserted into plasmid coding LIME such that the NAAG is conjugated trough its N-terminus and maintains its C-terminus free to react with PSMA [i.e., LIME(C)-(N)NAAG-COOH]. Alternatively, expression plasmid encoding NAAG–LIME chimera can be constructed following the method described

previously described for CD8-LIME chimera[5]. Fragments corresponding to NAAG and LIME transmembrane region were generated by PCR. Primers encoding the 3′ sequences of the NAAG and the 5′ sequences of the LIME fragment were designed to overlap, such that annealing of the two products yielded a hybrid template. From this template, the chimera is amplified using external primers containing XbaI sites. The NAAG–LIME chimera is inserted into pcDNA3.1(+).

As used herein, the phrase "surface marker", refers to any chemical structure, which is specifically displayed at uniquely high density, and/or displayed in a unique configuration by a cell surface or extracellular matrix of the target cell/tissue.

For example, the targeting moiety may be useful for targeting to tumor cells. For example, it is generally accepted that the intracellular environment of tumor cells is more alkaline compared to their immediate extracellular environment, which in turn is more acidic than the microenvironment found in the angiogenic blood vessels feeding the tumor. In addition, many previous studies have shown that the surface charges of tumor cells is more negative compared to benign normal cells and even less invasive tumor cells. Accordingly, it may be useful to express membrane-bound enzymes and/or proteins, which will render the liposomes with a positive charge only in the acidic intermediate extracellular environment of the tumor. For example, any membranal protein with a pI of about 7.2-7.4 that falls between the high alkaline pH of the angiogenic blood vessels (pH>7.4) and the low acidic pH of the tumor immediate extracellular environment (pH<7.2) can be used. Such proteins can be specifically identified by cross referencing the RCSB Protein Data Bank (PDB) for human plasma membrane proteins. The expected desirable pI (7.2-7.4) for those proteins can be calculated using the standard iterative algorithm [10, 11] that gives relatively precise results of pI calculations for raw protein sequences [12, 13]. The algorithm is used in the Compute pI/Mw tool at the ExPASy server. Such liposomes are expected to have negative or neutral charge in the alkaline microenvironment of the angiogenic tumor vessels and positive charge in the more acidic immediate extracellular environment of the tumor. Accordingly, this charge alteration will assist both liposomal extravasation, which is significantly enhanced for negative of neutral particles, and intra-tumor delivery which is more easily accomplished with positively charge particles [8, 14, 15].

Ample guidance regarding surface markers specifically over-expressed in diseases such as cancer, and antibodies specific for such surface markers is provided in the literature of the art (for example, refer to: A M Scott, C Renner. "Tumour Antigens Recognised by Antibodies." In: Encyclopedia of Life Sciences, Nature Publishing Group, Macmillan, London, UK, www.els.net, 2001).

Diseases associated with a target cell/tissue specifically displaying a growth factor receptor/TAA surface marker which are amenable to treatment by the method of the present invention include, for example, some of the numerous diseases which specifically display growth factor receptors/TAAs, such as EGF receptor, platelet derived growth factor (PDGF) receptor, insulin like growth factor receptor, vascular endothelial growth factor (VEGF) receptor, fibroblast growth factor (FGF) receptor, transferrin receptor, and folic acid receptor. Specific examples of such diseases and the growth factor receptors/TAAs which these specifically display are listed in Table 1, below.

Table 1

Review reference	*Malignancy type*	*Receptor**
Kim, E. S. *et al.*, 2001. Curr Opin Oncol 13, 506-13; Kuan *et al.*, 2000. Brain Tumor Pathol. 2000;17:71-8	Malignant glioma, glioblastoma, head and neck, breast, colon, lung, prostate, kidney, ovary, brain, pancreas, bladder	EGF receptor
George, D., 2001. Semin Oncol 28, 27-33	Brain, prostate	PDGF receptor
Wang, Y., and Sun, Y., 2002. Curr Cancer Drug Targets 2, 191-207	Breast, lung, colon, prostate	IGF receptor
Rosen, L. S., 2001. Cancer J 7 Suppl 3, S120-8; Giles, F. J., 2001. Oncologist 6, 32-9	Solid tumors, acute and chronic leukemias, myeloproliferative diseases, multiple myeloma, non-Hodgkin's lymphomas, and Hodgkin's disease	VEGF receptor
Lappi, D. A., 1995. Semin Cancer Biol 6, 279-88	Melanoma, Caposi sarcoma, pancreas	FGF receptor
Singh, M., 1999. Curr Pharm Des 5, 443-51	Leukemia, brain, colon, kidney, bladder	Transferrin receptor

* Abbreviations: EGF – epidermal growth factor, PDGF – platelet derived growth factor, IGF – insulin like growth factor, VEGF – vascular endothelial growth factor, FGF – fibroblast growth factor.

In a preferred embodiment, the ligand is an antibody or an antibody fragment, targeting antigens specific to a receptor on a target cell. Antibodies can be monoclonal antibodies, polyclonal antibodies or antibody fragments, which are target specific. In an embodiment, the antibodies attached to the liposomes are anti-CD19, anti-CD20, or anti-CD22, for specific binding to a B-cell epitope. These antibodies or antibody fragments

are typically derived from hybridomas that show positive reactivity toward the affected B-cells. It is contemplated that other antibodies or antibody fragments targeting any other cell in the body can be similarly used. For example, anti-CD19 antibodies are used to target liposome containing an entrapped agent to malignant B-cells. The antibody recognizes a unique epitope, the CD19 surface antigen, on the B-cells.

Methods of expressing heterologous proteins in eukaryotic cells are well known in the art.

Thus, an exogenous polynucleotide sequence designed and constructed to express at least a functional portion of the gene-of-interest may be expressed in the cells from which membranes are later extracted. Accordingly, the exogenous polynucleotide sequence may be a DNA or RNA sequence of the gene-of-interest.

The phrase "functional portion" as used herein refers to part of the encoded protein (*i.e.*, a polypeptide), which exhibits functional properties of the enzyme such as binding to a substrate. For example, the functional portion of an antibody may be the variable region conferring specificity and additional/or alternatively the constant region, i.e., Fc, which may activate complement and induce cell killing. For example, cells can be transfected with genes encoding one or more members from the GPCRs family (e.g., CCR5, CXCR4 etc.) that will render the liposomes targeted against abundant of cellular pathologies including auto-immune and viral diseases (e.g., HIV/AIDS).

To express exogenous gene-of-interest in eukaryotic (e.g., mammalian) cells, a polynucleotide sequence encoding the gene-of-interest is preferably ligated into a nucleic acid construct suitable for eukaryotic cell expression. Such a nucleic acid construct includes a promoter sequence for directing transcription of the polynucleotide sequence in the cell in a constitutive or inducible manner.

Constitutive promoters suitable for use for mammalian expression with the present invention are promoter sequences, which are active under most environmental conditions and most types of cells such as the cytomegalovirus (CMV) and Rous sarcoma virus (RSV). Inducible promoters suitable for use with the present invention include for example the inducible promoter of the tetracycline-inducible promoter (Zabala M, et al., Cancer Res. 2004, 64(8): 2799-804).

The nucleic acid construct (also referred to herein as an "expression vector") of the present invention includes additional sequences, which render this vector suitable

for replication and integration in prokaryotes, eukaryotes, or preferably both (e.g., shuttle vectors). In addition, a typical cloning vector may also contain a transcription and translation initiation sequence, transcription and translation terminator and a polyadenylation signal. By way of example, such constructs will typically include a 5' LTR, a tRNA binding site, a packaging signal, an origin of second-strand DNA synthesis, and a 3' LTR or a portion thereof.

The nucleic acid construct of the present invention typically includes a signal sequence for directing the translated polypeptide to the membrane and additionally a membrane anchor domain such as a transmembrane domain or a lipid based anchor (e.g., GPI).

Eukaryotic promoters typically contain two types of recognition sequences, the TATA box and upstream promoter elements. The TATA box, located 25-30 base pairs upstream of the transcription initiation site, is thought to be involved in directing RNA polymerase to begin RNA synthesis. The other upstream promoter elements determine the rate at which transcription is initiated.

Preferably, the promoter utilized by the nucleic acid construct of the present invention is active in the specific cell population transformed. Examples of cell type-specific and/or tissue-specific promoters include promoters such as albumin that is liver specific [Pinkert et al., (1987) Genes Dev. 1:268-277], lymphoid specific promoters [Calame et al., (1988) Adv. Immunol. 43:235-275]; in particular promoters of T-cell receptors [Winoto et al., (1989) EMBO J. 8:729-733] and immunoglobulins; [Banerji et al. (1983) Cell 33729-740], neuron-specific promoters such as the neurofilament promoter [Byrne et al. (1989) Proc. Natl. Acad. Sci. USA 86:5473-5477], pancreas-specific promoters [Edlunch et al. (1985) Science 230:912-916] or mammary gland-specific promoters such as the milk whey promoter (U.S. Pat. No. 4,873,316 and European Application Publication No. 264,166).

Enhancer elements can stimulate transcription up to 1,000 fold from linked homologous or heterologous promoters. Enhancers are active when placed downstream or upstream from the transcription initiation site. Many enhancer elements derived from viruses have a broad host range and are active in a variety of tissues. For example, the SV40 early gene enhancer is suitable for many cell types. Other enhancer/promoter combinations that are suitable for the present invention include those derived from

polyoma virus, human or murine cytomegalovirus (CMV), the long term repeat from various retroviruses such as murine leukemia virus, murine or Rous sarcoma virus and HIV. See, Enhancers and Eukaryotic Expression, Cold Spring Harbor Press, Cold Spring Harbor, N.Y. 1983, which is incorporated herein by reference.

In the construction of the expression vector, the promoter is preferably positioned approximately the same distance from the heterologous transcription start site as it is from the transcription start site in its natural setting. As is known in the art, however, some variation in this distance can be accommodated without loss of promoter function.

Polyadenylation sequences can also be added to the expression vector in order to increase the efficiency of mRNA translation. Two distinct sequence elements are required for accurate and efficient polyadenylation: GU or U rich sequences located downstream from the polyadenylation site and a highly conserved sequence of six nucleotides, AAUAAA, located 11-30 nucleotides upstream. Termination and polyadenylation signals that are suitable for the present invention include those derived from SV40.

In addition to the elements already described, the expression vector of the present invention may typically contain other specialized elements intended to increase the level of expression of cloned nucleic acids or to facilitate the identification of cells that carry the recombinant DNA. For example, a number of animal viruses contain DNA sequences that promote the extra chromosomal replication of the viral genome in permissive cell types. Plasmids bearing these viral replicons are replicated episomally as long as the appropriate factors are provided by genes either carried on the plasmid or with the genome of the host cell.

The vector may or may not include a eukaryotic replicon. If a eukaryotic replicon is present, then the vector is amplifiable in eukaryotic cells using the appropriate selectable marker. If the vector does not comprise a eukaryotic replicon, no episomal amplification is possible. Instead, the recombinant DNA integrates into the genome of the engineered cell, where the promoter directs expression of the desired nucleic acid.

The expression vector of the present invention can further include additional polynucleotide sequences that allow, for example, the translation of several proteins

from a single mRNA such as an internal ribosome entry site (IRES) and sequences for genomic integration of the promoter-chimeric polypeptide.

Examples for mammalian expression vectors include, but are not limited to, pcDNA3, pcDNA3.1(+/-), pGL3, pZeoSV2(+/-), pSecTag2, pDisplay, pEF/myc/cyto, pCMV/myc/cyto, pCR3.1, pSinRep5, DH26S, DHBB, pNMT1, pNMT41, pNMT81, which are available from Invitrogen, pCI which is available from Promega, pMbac, pPbac, pBK-RSV and pBK-CMV which are available from Strategene, pTRES which is available from Clontech, and their derivatives.

Expression vectors containing regulatory elements from eukaryotic viruses such as lentiviruses and retroviruses can be also used. SV40 vectors include pSVT7 and pMT2. Vectors derived from bovine papilloma virus include pBV-1MTHA, and vectors derived from Epstein Bar virus include pHEBO, and p2O5. Other exemplary vectors include pMSG, pAV009/A^+, pMTO10/A^+, pMAMneo-5, baculovirus pDSVE, and any other vector allowing expression of proteins under the direction of the SV-40 early promoter, SV-40 later promoter, metallothionein promoter, murine mammary tumor virus promoter, Rous sarcoma virus promoter, polyhedrin promoter, or other promoters shown effective for expression in eukaryotic cells.

Alternatively, cells, membranes, ghosts or CDLs (either of which may be native or genetically modified), may be chemically treated such as to present a protein, a saccharide, a synthetic polymer, a peptide or any combination of same. Methods of modifying the membrane with a synthetic polymer are described herein below and in the examples section, which follows. Such a chemical attachment may be effected at any stage from live cultured or suspended cells to produced CDLs.

For example, the CDLs may be also chemically conjugated with folate that may further enhance their targeting and attachment to tumor cells, which are known to express higher levels of folate receptors compared to benign cells.

According to another example, it is also possible to permanently modulate the CDLs to have a more positive surface charge by treating them with cations, salts or polycations (e.g., Polybrene®, polyethyleneimine and Poly-L-Lysine) rendering them more positive to better target the tumor angiogenic vasculature.

Non-native material can be also introduced to the surface of the CDLs by fusion (e.g., PEG or detergent induced) with other liposomes (e.g., cell-derived or synthetic)

that may be comprised of well characterized lipids, proteins and additives. Such fusion, creating hybrid CDLs, can be used to conjugate any moieties (e.g., targeting, therapeutic, diagnostic, stealth-rendering etc.) to the CDLs and to alter their surface properties. See Example 5 for further guidance on liposomal fusion.

Synthetic polymers are typically used to prevent or reduce coagulation, increase dispersion, reduce interaction with blood components, evade non-specific uptake by the mononuclear phagocytic system and prolong the particle circulation time to a large extent thus, rendering the liposomes with properties and features that are commonly referred to as stealth properties or long-circulating liposomes. Accordingly, the pH nano-environment at the particle surface may also be dependent upon the length of these molecules.

There are numerous polymers, which may be attached to lipids. Polymers typically used as lipid modifiers include, without being limited thereto: polyethylene glycol (PEG), polysialic acid, polylactic (also termed polylactide), polyglycolic acid (also termed polyglycolide), apolylactie- polyglycolic acid' polyvinyl alcohol, polyvinylpyrrolidone, polymethoxazoline, polyethyloxazoline, polyllydroxyetlyloxazolille, solyhydroxypryloxazoline, polyaspartarllide, polyhydroxypropyl methacrylamide, polymethacrylamide, polydimethylacrylamide, polyvinylmethylether, polyhydroxyethyl acrylate, derivatized celluloses such as hydroxymethylcellulose or hydroxyethylcellulose.

The polymers may be employed as homopolymers or as block or random copolymers.

The most commonly used and commercially available lipids derivatized into lipopolymers are those based on phosphatidyl ethanolamine (PE), usually distearylphosphatidylethanolamine (DSPE).

A specific family of lipopolymers, which may be employed by the invention include PEG-DSPE (with different lengths of PEG chains) in which the PEG polymer is linked to the lipid via a carbamate linkage and Polyethyleneglycol distearoylglycerol. The PEG moiety headgroup preferably has a molecular weight from about 750 Da to about 20,000 Da. More preferably, the molecular weight is from about 750 Da to about 12, 000 Da and most preferably between about 1,000 Da to about 5,000 Da. Two exemplary DSPE-PEG are those wherein PEG has a molecular weight of 2000 Da, and

of 5000a designated herein DSPE-PEG(2000) (DSPE-PEG2k) and DSPE-PEG(5000) (DSPE-PEG5k).

Specific families of lipopolymers, which may be also employed by the invention, include C8 and C16 mPEG Ceramides (with different lengths of PEG chains) in which the PEG-Ceramides contain ester linkages between the PEG and ceramide moieties that allow the compound to be easily metabolized. The PEG moiety headgroup preferably has a molecular weight from about 750 Da to about 2,000 Da. More preferably, the molecular weight is about 2,000 Da.

Conventional post-insertion PEGylation of common liposomes requires heating or solublization in a detergent containing solution that might damage surface proteins and lead to encapsulate leakage. Therefore, CDLs may be also PEGylated by the two following described methods or their combination. Primarily, PEGylated CDLs will be prepared by detergent-dialysis incorporation of PEGylated lipids into the ghost cell membrane (prior to CDLs preparation). Following, direct PEGylation of the CDLs may be performed with monomethoxy-PEG activated by succinimidyl succinate, which has been proven to increase the trasnfection efficiency and reduce serum mediated inactivation of PEGylated lentiviral particles, used as gene transduction vectors[16].

Chemical binding of non-proteinaceous components (e.g., synthetic polymers, carbohydrates and the like) to the liposomal surface may be employed. Thus, a non-proteinaceous moiety, may be covalently or non-covalently linked to, embedded or adsorbed onto the liposome using any linking or binding method and/or any suitable chemical linker known in the art. The exact type and chemical nature of such cross-linkers and cross linking methods is preferably adapted to the type of affinity group used and the nature of the liposome. Methods for binding or adsorbing or linking the enzyme and/or targeting moiety are also well known in the art.

For example, the enzyme and/or targeting moiety may be attached to a group at the interface via, but not limited to, polar groups such as amino, SH, hydroxyl, aldehyde, formyl, carboxyl, His-tag or other polypeptides. In addition, the enzyme and/or targeting moiety may be attached via, but not limited to, active groups such as succinimidyl succinate, cyanuric chloride, tosyl activated groups, imidazole groups, CNBr, NHS, Activated CH, ECH, EAH, Epoxy, Thiopropyl, Activated Thiol, etc. Moreover, the enzyme and/or targeting moiety may be attached via, but not limited to,

hydrophobic bonds (Van Der Waals) or electrostatic interactions that may or may not include cross-linking agents (e.g., bivalent anions, poly-anions, poly-cations etc.).

Once the cell source is available the liposomes are made. Thus, there is provided a method of producing liposomes comprising,

(a) subjecting cells to hypotonic conditions, so as to obtain ruptured cell membranes and/or ghost cells (also termed ghosts); and

(b) homogenizing the ruptured cell membranes and/or ghosts to thereby produce liposomes.

The method may be practiced according to other well accepted protocols known in the art such as that of Boone, C.W., Ford, L.E., Bond, H.E., Stuart, D.C. & Lorenz, D. Isolation of plasma membrane fragments from HeLa cells. J Cell Biol 41, 378-392 (1969); and Westerman and Jensen Methods Enzymol. 2003;373:118-27 (each of which is incorporated herein by reference) with or without modifications.

As used herein, the term "ghosts" refers to a cell that all of its cytoplasmic contents and/or nucleolus were removed by cell lysis and/or membrane rapture so that only its outer cytoplasmatic/cell membrane remains; and

Without being bound to a specific protocol it is suggested in a specific embodiment that liposomes of the present invention are made in a step-wise manner. First, plasma membranes are isolated from cells (10^9 cells) primarily by using hypotonic treatment such that the cell ruptures and ghost cells are formed. Altrnatively, ghost cells can be formed using mild sonication, freeze-thaw, French-press, needle-passaging or solublization in detergent-containing solutions. According to a specific embodiment hypotonic treatment is effected in Tris-magnesium buffer (e.g., pH 7.4 or pH 8.6 at 4 °C, pH adjustment made with HCl). Cell swelling is monitored by phase-contrast microscopy. Once the cells swell and ghosts are formed, the suspension is placed in a homogenizer. Typically, about 95% cell rupture is sufficient. The membranes/ghosts are then placed in Sucrose (0.25 M or higher) for preservation. To avoid adherence, the ghosts are placed in plastic tubes and centrifuged. A laminated pellet is produced in which the topmost lighter gray lamina consists only entirely of ghosts. However, the entire pellet is processed, to increase yields. Centrifugation (e.g., 3,000 rpm for 15 min at 4 °C) and washing (e.g., 20 volumes of Tris magnesium/TM-sucrose pH 7.4) may be repeated.

In the next step, the ghost fraction is separated by floatation in a discontinuous sucrose density gradient. A small excess of supernatant is left over the washed pellet, which now contains ghosts, nuclei, and incompletely ruptured whole cells. Additional 60% w/w sucrose in TM, pH 8.6 is added to the suspension to give a reading of 45 % sucrose on a refractometer. After this step, all solutions contain TM pH 8.6. 15 ml of suspension are placed in SW-25.2 cellulose nitrate tubes and discontinuous gradient is formed over the suspension by adding 15 ml layers, respectively, of 40% and 35% w/w sucrose, and then adding 5 ml of TM-sucrose (0.25 M). The material is now centrifuged at 20,000 rpm for 10 min, 4°C. The nuclei sediment form a pellet, the incompletely ruptured whole cells are collect at the 40%-45% interface, and the ghosts are collected at the 35%-40% interface. The ghosts are collected and pooled.

In the next step, the ghosts are homogenized such as by sonication which may be followed by extrusion.

A specific sonication protocol relates to 5 second sonication using an MSE sonicator with microprobe at an amplitude setting of 8 (Instrumentation Associates, N.Y.). This short period of sonication is enough to cause the plasma membrane of the ghosts to break up into cell derived liposomes (CDLs). Under these specific conditions organelle membranes are not disrupted and these are removed by centrifugation (3,000 rpm, 15 min 4 °C). Plasma membrane vesicles (CDLs) are then purified by sedimentation in a continuous sucrose density gradient.

Liposomes comprising one or more pharmaceutical agent of the present invention are preferably in the size range of 20-1000 nm e.g., 30-1000 nm, 0.02-1.0 μm, more preferably 0.05-1.0 μm, more preferably 0.07-0.5 μm and more preferably 0.1-0.3 μm. An advantage of liposomes smaller or about 0.2 μm is that they can easily permeate through tumor vasculature (due to the EPR effect), they are not readily uptaken by macrophages and they can undergo filter sterilization.

Extrusion of liposomes through a commercially available polycarbonate membrane (e.g., from Sterlitech, Washington) or an asymmetric ceramic membrane (e.g., Membralox), commercially available from Pall Execia, France is an effective method for reducing liposome sizes to a relatively well defined size distribution. Typically, the suspension is cycled through the membrane one or more times until the desired liposome size distribution is achieved. The liposomes may be extruded through

successively smaller pore membranes (e.g., 400 nm, 100 nm and/or 50 nm pore size) to achieve a gradual reduction in liposome size and uniform distribution.

At any step prior to the homogenization, sonication and/or extrusion, that is, typically following ghosts preparation, a pharmaceutical agent may be added to the reaction mixture such that the resultant liposomes encapsulate the pharmaceutical agent.

As used herein the phrase "pharmaceutical agent" refers to a therapeutic agent or diagnostic agent, which can be used to treat or diagnose a medical condition, respectively.

According to a specific embodiment, the composition comprising the pharmaceutical agent and the liposome is hypo or non-immunogenic especially when the cell source is a mesenchymal stem cell.

Thus, the liposome of the present invention may have a pharmaceutical agent adsorbed to a surface thereof or encapsulated therein either within the intra-liposomal polar phase or the lamellar non-polar lipid phase.

Methods of conjugating molecules (e.g., targeting moieties, pharmaceutical agents, synthetic polymers and the like) to liposomes are well known in the art. For example, a the pharmaceutical agent (or any other molecule) may be attached, conjugated or adsorbed to surface of the liposomes, ghosts or the cells of which the liposomes derive from based on hydrophobic interactions (Van Der Waals bonds) or electrostatic interactions with or without the use of cross-linking agents (e.g. anions and poly-anions). Hydrophobic and/or amphipathic pharmaceutical agent (or any other hydrophobic and/or amphipathic molecule) may be soulibilized, partially soulibilized or partitioned into the cells, ghosts or liposomal lipid membranes with or without the use of detergent and/or by detergent dialysis. A pharmaceutical agent (or any other molecule) may be attached, conjugated or adsorbed to surface of the liposomes, ghosts or the cells of which the liposomes derive from based on covalent bonds with active groups. A pharmaceutical agent may be attached, conjugated or adsorbed to surface of the liposomes, ghosts or the cells of which the liposomes derive from as a conjugate of an antibody or part of that specifically recognized a natural moiety found on the liposomes, ghosts or cells. For example, pharmaceutical agent may be adsorbed to the surface (inner or outer) of the liposomes via, but not limited to, polar groups such as amino, SH, hydroxyl, aldehyde, formyl, carboxyl, His-tag or other polypeptides. In addition, the

pharmaceutical agents may be adsorbed via, but not limited to, active groups such as succinimidyl succinate, cyanuric chloride, tosyl activated groups, imidazole groups, CNBr, NHS, Activated CH, ECH, EAH, Epoxy, Thiopropyl, Activated Thiol, etc.

Entrapped in, adsorbed, expressed, conjugated, attached, and/or solubilzed on the liposomes' surface or membrane is a therapeutic agent for delivery to the target cells and/or tissues by one or more of ,but not limited to, the following mechanisms:

Direct intracellular delivery of the agent by means of membrane fusion between the liposomes and cells and/or liposomal uptake by endocytosis, phagocytosis or by any kind of transmembranal transport mechanism.

Diffusion and/or leakage of the agent from the liposome and consequent binding to the surface of the target cells/tissue and/or uptake into the target cell/tissue by diffusion, endocytosis, phagocytosis or by any kind of transmembranal transport mechanism.

Binding to the surface of the target cells and/or tissues of an agent which is permanently, constantly or transiently expressed, attached, adsorbed, conjugated and/or solubilzed on the liposomes' surface or membrane.

A variety of therapeutic agents can be entrapped in lipid vesicles, including water-soluble agents that can be stably encapsulated in the aqueous compartment of the liposome, lipophilic compounds that stably partition in the lipid phase of the vesicles, or agents that can be stably or transiently attached, conjugated, adsorbed or expressed on to the outer or inner surfaces of the liposomes, e.g., by electrostatic, covalent or hydrophobic interactions.

Exemplary water-soluble compounds include small molecules (i.e., less than 1000 Daltons) or large molecules (i.e., above 1000 Daltons); biomolecules (e.g. proteinaceous molecules, including, but not limited to, peptide, polypeptide, post-translationally modified protein, antibodies etc.) or a nucleic acid molecule (e.g. double-stranded DNA, single-stranded DNA, ds/ss RNA (e.g., siRNA, antisense, ribozymes), or triple helix nucleic acid molecules or chemicals. Therapeutic agents may be natural products derived from any known organism (including, but not limited to, animals, plants, bacteria, fungi, protista, or viruses) or from a library of synthetic molecules. Therapeutic agents can be monomeric as well as polymeric compounds.

As mentioned above, the therapeutic agent may be a protein, such as an enzyme which compensates for loss in activity or poor expression of an endogenous enzyme e.g., the enzyme hexosaminidase A, a shortage of which results in Tay-Sachs disease.

Examples of therapeutic agents which may be delivered across a blood barrier to the brain, eye, testis or mammary gland include, but are not limited to antibiotic agents, anti-neoplastic agents, anti-inflammatory agents, antiparasitic agents, antifungal agents, antimycobacterial agents, antiviral agents, anticoagulant agents, radiotherapeutic agents, chemotherapeutic agents, cytotoxic agents, cytostatic agents, vasodilating agents, anti-oxidants, analeptic agents, anti-convulsant agents, antihistamine agents, neurotrophic agents, psychotherapeutic agents, anxiolytic sedative agents, stimulant agents, sedative agents, analgesic agents, anesthetic agents, birth control agents, neurotransmitter agents, neurotransmitter analog agents, scavenging agents and fertility-enhancing agents.

The liposome-entrapped compound may also be a diagnostic agent such as an imaging or a contrast agent as indium and technetium, enzymes such as horseradish peroxidase and alkaline phosphatase, MRI contrast media containing gadolinium, X-ray contrast media containing iodine, ultrasonography contrast media such as CO_2, europium derivatives, fluorescent substances such as carboxyfluorescein and illuminants such as N-methylacrydium derivatives.

Once the liposomes are formed (i.e., with or without a pharmaceutical agent), they may be characterized for their size distribution, composition, concentration, zeta potential, electrical surface potential, surface (local) pH, protein to lipid ratio and therapeutic efficacy in vitro and in vivo.

Experimentally tested liposomes of the present invention have the following size values as described on Table 2 below:

Table 2

Without PEGylation:	With PEGylation:
Avg. by number 30 nm	Avg. by number 100 nm
Avg. by volume 200 nm	Avg. by volume 215 nm
Aggregation factor: 200/30=7	Aggregation factor: 215/100=2

Empty liposomes or liposomes comprising one or more pharmaceutical agent of the present invention are preferably in the size range of 30-3000-nm, more preferably 50-500 nm, more preferably 30-300 nm, more preferably 50-200 nm and more preferably 70-150 nm. An advantage of liposomes smaller or about 100-nm is its ability

to penetrate through very narrow blood vessels which is of great significance in diagnostic and treatment.

Any method known in the art can be used to determine the size of the liposome. For example, a Nicomp Submicron Particle Sizer (model 370, Nicomp, Santa Barabara, Calif.) utilizing laser light scattering can be used. Other methods of measuring liposome size include photocorrelation spectroscopy, laser diffraction, low-angle laser light scattering (LALLS), medium-angle laser light scattering (MALLS), light obscuration methods (Coulter method, for example), rheology, or microscopy (light or electron). The preferred average effective particle size depends on factors such as the intended route of administration, formulation, solubility, toxicity and bioavailability of the compound.

Values of Zeta potential in experimentally tested liposomes are provided infra. CDLs without PEGylation -17.9 to -15.5 mV.

With PEGylation (of ghosts-indirect): -13.2 mV. With PEGylation (of CDls-direct): -10.2 mV.

Thus, liposomes of the present invention are characterized by a zeta potential of -20 to -15 mV without PEGylation and -15 to -10 mV with PEGylation.

As mentioned, liposomes of the present invention are advantageously used in the clinic.

Thus, according to an aspect of the invention there is provided a method of delivering a pharmaceutical agent, the method comprising administering to a subject in need thereof the above-describe liposome, wherein the pharmaceutical agent is enclosed therein or adsorbed thereon, thereby delivering the pharmaceutical agent.

According to an embodiment, the cells are target cells and the liposomes contain a targeting moiety, either chemically conjugated, heterologously added, as described above, or natively presented in the membranes from which the liposome is comprised (e.g., as in MSCs, which migrate to tumor cells).

The cell source for the liposomes may be autologous or non-autologous (e.g., allogeneic, xenogeneic) to the subject.

The "target cell" referred to herein is a cell or a cluster of cells (of homogenous or heterogeneous population) and/or tissue to which a substance is to be delivered by using the liposome. Examples thereof include cancer cells, vascular endothelial cells of angiogenic cancer tissues, cancer stem cells, interstitial cells of cancer tissues, cells

affected by genetic abnormality, cells infected by a pathogen and the like. The "target molecule" may be any molecule presented the surface of the target cells or cells adjacent to the target cells. Another form of the target molecule includes molecules which are released from cells. Examples thereof includes extracellular matrix components, secretions or architectures of cancer cells or interstitial cells of cancer tissues, and specific examples thereof include tumor markers, structures between cells and the like.

Delivering can be for diagnostic reasons (e.g., the liposome includes a diagnostic agent) or for treating (i.e., as a drug delivery tool, delivering a therapeutic agent).

The liposomes may be administered to the subject per se, or as part of a pharmaceutical composition.

As used herein a "pharmaceutical composition" refers to a preparation of one or more of the active ingredients described herein with other chemical components such as physiologically suitable carriers and excipients. The purpose of the pharmaceutical composition is to facilitate administration of the active ingredients to the subject.

Herein the term "active ingredient" refers to the therapeutic agent (with or without the liposome) accountable for the biological effect. It is to be appreciated that the liposome *per se* may have immunomodulatory function such as when prepared from membranes of MSCs or other immunomodulatory cells (e.g., immune B and T lymphocytes etc.). It is also to be appreciated that the liposome *per se* may have a cytoxoic effect on the target cells as due to membrane fusion with target cells and consequent disruption to cell membrane, cytoskeleton and functions. In such a case measures are taken to include a targeting moiety such that the cytotoxic effect becomes specific.

Hereinafter, the phrases "physiologically acceptable carrier" and "pharmaceutically acceptable carrier" which may be interchangeably used refer to a carrier or a diluent that does not cause significant irritation to the subject and does not abrogate the biological activity and properties of the administered active ingredients. An adjuvant is included under these phrases.

Herein, the term "excipient" refers to an inert substance added to the pharmaceutical composition to further facilitate administration of an active ingredient of the present invention or to increase shelf-life stability. Examples, without limitation, of excipients include calcium carbonate, calcium phosphate, various sugars and salts and

types of starch, cellulose derivatives, gelatin, vegetable oils, EDTA, EGTA, Poly-L-Lysine, polyethyleneimine, Polybrene (hexadimethrine bromide), polyethylene glycols and other poly or single anions. The pharmaceutical composition may advantageously take the form of foam, aerosol or a gel.

Techniques for formulation and administration of drugs may be found in "Remington's Pharmaceutical Sciences," Mack Publishing Co., Easton, PA, latest edition, which is incorporated herein by reference.

Suitable routes of administration include any of various suitable systemic and/or local routes of administration.

Suitable routes of administration may, for example, include the inhalation, oral, buccal, rectal, transmucosal, topical, transdermal, intradermal, transnasal, intestinal and/or parenteral routes; the intramuscular, subcutaneous and/or intramedullary injection routes; the intrathecal, direct intraventricular, intravenous, intraperitoneal, intranasal, and/or intraocular injection routes, Catheterization with or without angio balloons; and/or the route of direct injection into a tissue region of the subject.

The pharmaceutical composition may be manufactured by processes well known in the art, e.g., by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes.

Pharmaceutical compositions for use in accordance with the present invention thus may be formulated in conventional manner using one or more physiologically acceptable carriers comprising excipients and auxiliaries, which facilitate processing of the active ingredients into preparations which, can be used pharmaceutically. Proper formulation is dependent upon the route of administration chosen.

For injection, the active ingredients of the pharmaceutical composition may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hank's solution, Ringer's solution, or physiological salt buffer.

For transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

For oral administration, the pharmaceutical composition can be formulated readily by combining the active ingredients with pharmaceutically acceptable carriers well known in the art. Such carriers enable the pharmaceutical composition to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions,

and the like, for oral ingestion by a patient. Pharmacological preparations for oral use can be made using a solid excipient, optionally grinding the resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carbomethylcellulose; and/or physiologically acceptable polymers such as polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be added, such as cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate.

Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, titanium dioxide, lacquer solutions and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active ingredient doses.

Pharmaceutical compositions which can be used orally include push-fit capsules made of gelatin as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules may contain the active ingredients in admixture with filler such as lactose, binders such as starches, lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active ingredients may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added. All formulations for oral administration should be in dosages suitable for the chosen route of administration.

For buccal administration, the compositions may take the form of tablets or lozenges formulated in conventional manner.

For administration via the inhalation route, the active ingredients for use according to the present invention can be delivered in the form of an aerosol/spray presentation from a pressurized pack or a nebulizer with the use of a suitable propellant, e.g., a fluorochlorohydrocarbon such as dichlorodifluoromethane, trichlorofluoromethane, dichloro-tetrafluoroethane; carbon dioxide; or a volatile hydrocarbon such as butane, propane, isobutane, or mixtures thereof. In the case of a

pressurized aerosol, the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, e.g., gelatin for use in a dispenser may be formulated containing a powder mix of the active ingredients and a suitable powder base such as lactose or starch.

The pharmaceutical composition may be formulated for parenteral administration, e.g., by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, e.g., in ampoules or in multidose containers with optionally, an added preservative. The compositions may be suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents.

A pharmaceutical composition for parenteral administration may include an aqueous solution of the active ingredients in water-soluble form. Additionally, suspensions of the active ingredients may be prepared as appropriate oily or water based injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acids esters such as ethyl oleate, triglycerides or liposomes. Aqueous injection suspensions may contain substances, which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the active ingredients to allow for the preparation of highly concentrated solutions.

Alternatively, the active ingredients may be in powder form for constitution with a suitable vehicle, e.g., sterile, pyrogen-free water based solution, before use.

The pharmaceutical composition may also be formulated in rectal compositions such as suppositories or retention enemas, using, e.g., conventional suppository bases such as cocoa butter or other glycerides.

The pharmaceutical composition should contain the active ingredients in an amount effective to achieve disease treatment.

Determination of a therapeutically effective amount is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein.

For any preparation used in the methods of the invention, the therapeutically effective amount or dose can be estimated initially from in vitro and cell culture and in vivo assays. For example, a dose can be formulated in animal models to achieve a

desired concentration or titer. Such information can be used to more accurately determine useful doses in humans.

Toxicity and therapeutic efficacy of the active ingredients described herein can be determined by standard pharmaceutical procedures *in vitro*, in cell cultures or experimental animals. The data obtained from these *in vitro* and cell culture assays and animal studies can be used in formulating a range of dosage for use in human. The dosage may vary depending upon the dosage form employed and the route of administration utilized. The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. (See e.g., Fingl, *et al.*, 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p.1).

Dosage amount and interval may be adjusted individually to provide plasma or brain levels of the active ingredients which are sufficient to achieve the desired therapeutic effect (minimal effective concentration, MEC). The MEC will vary for each preparation, but can be estimated from *in vitro* data. Dosages necessary to achieve the MEC will depend on individual characteristics and route of administration. Detection assays can be used to determine plasma concentrations.

Depending on the severity and responsiveness of the condition to be treated, dosing can be of a single or a plurality of administrations, with course of treatment lasting from several days to several weeks or until cure is effected or diminution of the disease state is achieved.

The amount of the composition to be administered will be dependent on the subject being treated, the severity of the affliction, the manner of administration, the judgment of the prescribing physician, etc.

Compositions of the present invention may, if desired, be presented in a pack or dispenser device, such as an FDA approved kit, which may contain one or more unit dosage forms containing the active ingredients. The pack may, for example, comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration. The pack or dispenser may also be accommodated by a notice associated with the container in a form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals, which notice is reflective of approval by the agency of the form of the compositions or human or veterinary administration. Such notice, for example, may be of labeling approved by

the U.S. Food and Drug Administration for prescription drugs or of an approved product insert.

As used herein the term "about" refers to ± 10 %.

The terms "comprises", "comprising", "includes", "including", "having" and their conjugates mean "including but not limited to".

The term "consisting of" means "including and limited to".

The term "consisting essentially of" means that the composition, method or structure may include additional ingredients, steps and/or parts, but only if the additional ingredients, steps and/or parts do not materially alter the basic and novel characteristics of the claimed composition, method or structure.

As used herein, the singular form "a", "an" and "the" include plural references unless the context clearly dictates otherwise. For example, the term "a compound" or "at least one compound" may include a plurality of compounds, including mixtures thereof.

Throughout this application, various embodiments of this invention may be presented in a range format. It should be understood that the description in range format is merely for convenience and brevity and should not be construed as an inflexible limitation on the scope of the invention. Accordingly, the description of a range should be considered to have specifically disclosed all the possible subranges as well as individual numerical values within that range. For example, description of a range such as from 1 to 6 should be considered to have specifically disclosed subranges such as from 1 to 3, from 1 to 4, from 1 to 5, from 2 to 4, from 2 to 6, from 3 to 6 etc., as well as individual numbers within that range, for example, 1, 2, 3, 4, 5, and 6. This applies regardless of the breadth of the range.

Whenever a numerical range is indicated herein, it is meant to include any cited numeral (fractional or integral) within the indicated range. The phrases "ranging/ranges between" a first indicate number and a second indicate number and "ranging/ranges from" a first indicate number "to" a second indicate number are used herein interchangeably and are meant to include the first and second indicated numbers and all the fractional and integral numerals there between.

As used herein the term "method" refers to manners, means, techniques and procedures for accomplishing a given task including, but not limited to, those manners,

means, techniques and procedures either known to, or readily developed from known manners, means, techniques and procedures by practitioners of the chemical, pharmacological, biological, biochemical and medical arts.

As used herein, the term "treating" includes abrogating, substantially inhibiting, slowing or reversing the progression of a condition, substantially ameliorating clinical or aesthetical symptoms of a condition or substantially preventing the appearance of clinical or aesthetical symptoms of a condition.

It is appreciated that certain features of the invention, which are, for clarity, described in the context of separate embodiments, may also be provided in combination in a single embodiment. Conversely, various features of the invention, which are, for brevity, described in the context of a single embodiment, may also be provided separately or in any suitable subcombination or as suitable in any other described embodiment of the invention. Certain features described in the context of various embodiments are not to be considered essential features of those embodiments, unless the embodiment is inoperative without those elements.

Various embodiments and aspects of the present invention as delineated hereinabove and as claimed in the claims section below find experimental support in the following examples.

EXAMPLES

Reference is now made to the following examples, which together with the above descriptions illustrate some embodiments of the invention in a non limiting fashion.

Generally, the nomenclature used herein and the laboratory procedures utilized in the present invention include molecular, biochemical, microbiological and recombinant DNA techniques. Such techniques are thoroughly explained in the literature. See, for example, "Molecular Cloning: A laboratory Manual" Sambrook et al., (1989); "Current Protocols in Molecular Biology" Volumes I-III Ausubel, R. M., ed. (1994); Ausubel et al., "Current Protocols in Molecular Biology", John Wiley and Sons, Baltimore, Maryland (1989); Perbal, "A Practical Guide to Molecular Cloning", John Wiley & Sons, New York (1988); Watson et al., "Recombinant DNA", Scientific American Books, New York;

Birren et al. (eds) "Genome Analysis: A Laboratory Manual Series", Vols. 1-4, Cold Spring Harbor Laboratory Press, New York (1998); methodologies as set forth in U.S. Pat. Nos. 4,666,828; 4,683,202; 4,801,531; 5,192,659 and 5,272,057; "Cell Biology: A Laboratory Handbook", Volumes I-III Cellis, J. E., ed. (1994); "Current Protocols in Immunology" Volumes I-III Coligan J. E., ed. (1994); Stites et al. (eds), "Basic and Clinical Immunology" (8th Edition), Appleton & Lange, Norwalk, CT (1994); Mishell and Shiigi (eds), "Selected Methods in Cellular Immunology", W. H. Freeman and Co., New York (1980); available immunoassays are extensively described in the patent and scientific literature, see, for example, U.S. Pat. Nos. 3,791,932; 3,839,153; 3,850,752; 3,850,578; 3,853,987; 3,867,517; 3,879,262; 3,901,654; 3,935,074; 3,984,533; 3,996,345; 4,034,074; 4,098,876; 4,879,219; 5,011,771 and 5,281,521; "Oligonucleotide Synthesis" Gait, M. J., ed. (1984); "Nucleic Acid Hybridization" Hames, B. D., and Higgins S. J., eds. (1985); "Transcription and Translation" Hames, B. D., and Higgins S. J., Eds. (1984); "Animal Cell Culture" Freshney, R. I., ed. (1986); "Immobilized Cells and Enzymes" IRL Press, (1986); "A Practical Guide to Molecular Cloning" Perbal, B., (1984) and "Methods in Enzymology" Vol. 1-317, Academic Press; "PCR Protocols: A Guide To Methods And Applications", Academic Press, San Diego, CA (1990); Marshak et al., "Strategies for Protein Purification and Characterization - A Laboratory Course Manual" CSHL Press (1996); all of which are incorporated by reference as if fully set forth herein. Other general references are provided throughout this document. The procedures therein are believed to be well known in the art and are provided for the convenience of the reader. All the information contained therein is incorporated herein by reference.

EXAMPLE 1

Characterization of MSC migratory and targeting abilities

Human MSCs were purchased from Lonza® (Switzerland) and characterized using Giemsa staining and FACS analysis for human mesenchymal stem cells (hMSCs)

typical cell surface markers. As seen from Figures 1A-C the cells appear to be positive for CD90, CD105, CD44, and CD29 and negative for CD133, CD31, CD34 and CD144, as expected for hMSCs.

The migratory abilities of the hMSCs towards cancer cells were tested as well. For these experiments, hMSCs were labeled by a red-fluorescent dye (DiI) while several other cell lines (including a prostate cancer cell-line - PC3) were labeled by a green fluorescent dye (DiO). Labeled cells were drop-wise seeded on tissue culture plates, incubated for 72 hrs and imaged using the Maestro in vivo Imager (Figure 2). As seen, specific migration of hMSCs towards PC3 cancer cells was demonstrated while "avoiding" interaction with other cell-lines (BHK, Cf2Th, and COS-7).

Additional experiments were conducted to validate the targeting abilities of conditioned hMSCs to breast cancer cell-line MCF7. For that, human hMSCs were cultured with or without MCF7-derived conditioning media, labeled with DiI (red) and co-cultured with MCF7 cells labeled with DiO (green). Following 2 hr incubation, cultures were washed and the coverage areas of each cell type and cell overlay (yellow) were determined using fluorescent microscopy image analysis. Assuming that the overlay of DiI and DiO is a consequence of physical interaction between the two cell types, the percent of overlay may represent the amount of membranal interactions between the two cell types. As can be seen from Figure 3, the incubation of conditioned hMSCs with MCF7 cells resulted in 7% overlay, out of the total cell coverage area, compared to no overlay when using unconditioned hMSCs ($p<0.001$). This apparent targeting evidently differs from the migration described in Figure 2 as it is mainly governed by membranal interactions between the hMSCs and the cancerous cells and not based on the migratory abilities of hMSCs that is largely mediated by soluble factors.

EXAMPLE 2

Characterization of cell derived liposomes prepared from hMSCs

Cell Derived Liposome preparation - About 10^7 Cells were harvested and washed with PBS. Cells were then hypotonically treated by re-suspension in ice cold Tris-magnesium (TM buffer, 0.01 M Tris, 0.001 M $MgCl_2$) pH 7.4 for 15min at 4°C. Following hypotonic treatment, the cells were homogenized by rotor-stator mechanical

homogenizer (IKA®, Taquara, RJ, Brazil) for 1 min at 22,000 rpm and turned into ghosts (95% ruptured cell membranes as confirmed by phase-contrast microscopy). For stabilizing the ghosts' suspension, 60% (w/w) sucrose solution was immediately added to the suspension to make a final concentration of 0.25M or 10% by volume. Ghosts were then centrifuged at 3000 rpm for 15 min at 4°C. The supernatant was discarded and the pellet of ghosts was then washed twice with 0.25 M sucrose in TM-buffer pH 7.4, by repeated suspension and centrifugation at 3,000 rpm for 15 min at 4°C. In order to create sonicated ghosts, the re-suspended pellet was then sonicated for 5 seconds at 27% amplitude using VibraCell VCX750 (Sonics & Materials Inc., Newtown, CT) and centrifuged at 3,000 rpm for 15 min at 4°C. The pellet of sonicated ghosts was then washed twice again with 0.25 M sucrose in TM-buffer pH 8.6, by repeated suspension and centrifugation at 3,000 rpm for 15 min at 4°C. For the formation of unilamellar liposomes, the resuspeded pellet of sonicated ghosts was manually extruded by 21 successive passages trough polycarbonate membranes with pore sizes of 0.4 μm and 0.1 μm (Osmonics Inc., Minnesota USA). The extruded liposomes were then centrifuged for 45 min at 150,000 g at 4°C. The supernatant was discarded and the resulting liposomes pellet was resuspended with TM buffer pH 8.6.

Cell derived liposomes surface protein PEGylation (according to the methof of Croyle, M.A. et al., 2004) - About 10^7 Cells were harvested and washed with PBS. Cells were then hypotonically treated by re-suspension in ice cold Tris-magnesium (TM buffer, 0.01 M Tris, 0.001 M $MgCl_2$) pH 7.4 for 15min at 4°C. Following hypotonic treatment, the cells were homogenized by rotor-stator mechanical homogenizer (IKA®, Taquara, RJ, Brazil) for 1 min at 22,000 rpm and turned into ghosts (95% ruptured cell membranes as confirmed by phase-contrast microscopy). For stabilizing the ghosts' suspension, 60% (w/w) sucrose solution was immediately added to the suspension to make a final concentration of 0.25M or 10% by volume. Ghosts were then centrifuged at 3000 rpm for 15 min at 4°C. The supernatant was discarded and the pellet of ghosts was then washed twice with 0.25 M sucrose in TM-buffer pH 7.4, by repeated suspension and centrifugation at 3,000 rpm for 15 min at 4°C. In order to create sonicated ghosts, the re-suspended pellet was then sonicated for 5 seconds at 27% amplitude using VibraCell VCX750 (Sonics & Materials Inc., Newtown, CT) and centrifuged at 3,000 rpm for 15 min at 4°C. The pellet of sonicated ghosts was then

washed twice again with 0.25 M sucrose in TM-buffer pH 8.6, by repeated suspension and centrifugation at 3,000 rpm for 15 min at 4°C. For the formation of unilamellar liposomes, the resuspeded pellet of sonicated ghosts was manually extruded by 21 successive passages trough polycarbonate membranes with pore sizes of 0.4 μm and 0.1 μm (Osmonics Inc., Minnesota USA). The extruded liposomes were then centrifuged for 45 min at 150,000 g at 4°C. The supernatant was discarded and the resulting liposomes pellet was resuspended with TM buffer pH 8.6.

The protein content on the liposome's surface was determined using the Bradford protein assay, referring to bovine serum albumin (BSA) as standard. Succinimidyl succinate activated Monomethoxy-PEG was obtained from Sigma Chemicals (St. Louis, Mo.) and was added to the resuspended liposomes at a 10:1 ratio relative to the liposomes' protein content as previously determined by the Bradford assay. For example, 10 μg of Monomethoxy-PEG were added for each 1 μg of protein. The conjugation reaction between the Monomethoxy-PEG and the liposomes was performed at 25°C with gentle agitation. The reaction was stopped by the addition of 10X L-lysine (Sigma Chemicals) with respect to the amount of Monomethoxy-PEG added. Un-reacted free PEG, excess lysine, and reaction byproducts were eliminated by buffer exchange over a Micro-Bio Spin P-30 chromatography column (Bio-Rad) equilibrated with TM buffer pH 8.6.

CDL FACS analysis. **Materials -** Coupling Buffer - used for pre-washing and conjugating Dynabeads M-280 to the liposomes. The buffer was composed of 0.1M Na-phosphate buffer pH 7.4, 2.62 g $NaH_2PO_4 \times H_2O$ (MW 137.99) and 14.42 g Na2HPO4 × 2H2O (MW 177.99) dissolved in distilled water and adjusted to 1 liter. Washing, blocking and Storage Buffer - PBS pH 7.4 with 0.1% (w/v) BSA: Add 0.88 g NaCl (MW 58.4) and 0.1% (w/v) BSA to 80 ml 0.01M Na-phosphate pH 7.4. Mix thoroughly and adjust volume to 100 ml with 0.01M Na-phosphate pH 7.4.

Method: Liposomes were created form $2x10^7$ hMSCs as previously described. Tosyl-activated paramagnetic Dynabeads® M-280 (invitrogen) were used as they were able to non-specifically and covalently bind any protein and/or liposomes conjugated with proteins and to be later analyzed by flow-cytometry. Using magnetic separation device (MACS, Dynal™ Magnetic Particle Separator – Invitrogen), the beads were washed with the coupling buffer. To increase their ability to conjugate proteins, the

beads were then further washed with 3M ammonium sulfate added to the coupling Buffer. later, 4 samples were prepared containing 10^7 beads each: Beads only, beads with liposomes, beads with liposomes to be labeled with secondary antibody (isotype control) and beads conjugated with liposomes to be labeled with primary and secondary antibody (test sample). About $5x10^6$ cell equivalent liposomes were added to each sample. Liposomes and beads were then incubated for at least 12 hr at 4^0C. After attachment, samples were re-suspended in the washing\blocking buffer. Each sample was suspended in total volume of 200 µl. First, mouse MABs anti-human CD29, CD44, CD90 or CD105 were added to the appropriate samples in a ratio 1:100. Samples were incubated for 30 min in RT. Next, samples were washed twice using the magnetic device. Then secondary ABs (FITC-conjugated goat anti mouse) were added and the samples were incubated for 30 min at RT in the dark. All antibodies, primary and secondary, were purchased from BD - Becton, Dickinson and Company. Following washing of the samples as mentioned before, the samples were run and analyzed using FACSCalibur and CellQuest Pro (BD).

Results

PEGylated Cell-Derived Liposomes (PEG-CDLs) are expected to be protected from opsonization and degradation, thus, having stealth properties and longer circulation time *in vivo*. Also, PEGylation may reduce the risk of non-specific binding and fusion of liposomes as with non-target cells[17-19].

Cryo-TEM imaging of the CDLs demonstrated that the PEGylation had no apparent effect on the desirable small unilamellar morphology of the CDLs (Figures 4A-B). However, the PEGylated liposomes (Figure 4A) seemed more dispersed and less coagulated than the un-PEGylated liposomes (Figure 4B), that were imaged at the same concentration and under the same conditions. Apparently, not only that the PEGylation does not damage liposomes' morphology but it may also improve their dispersion and stability. The size and size distribution of the CDLs were further analyzed using number and volume weighing DLS analysis (Dynamic Light Scattering, Malvern Nanosize). While number-weight DLS analysis (Figure 5A) demonstrated an increase in liposomes' size following PEGylation (from ~30 nm to ~100 nm), volume-weight DLS analysis (Figure 5b) demonstrated that the addition of PEG had a homogenizing effect on the system, exhibiting a significant reduction in the liposomes' size distribution.

Evidently, the addition of PEG groups stabilized the system and prevented aggregation even though the Zeta-potential decreased from -17.9 mV to -10.2 mV (Figure 5C).

Finally, the expression of MSC-specific surface markers, on the surface of hMSCs derived liposomes, was validated by FACS analysis (Figure 6). As seen, the CDLs retained their cytoplasmatic membrane symmetry and the expression of correctly oriented typical hMSCs surface markers (i.e., CD44, CD29, CD90 and CD105).

EXAMPLE 3

Binding and specific targeting of cancerous cell-lines by CDLs

Confocal microscopy imaging and flow cytometry analysis were used to determine the binding of fluorescently labeled CDLs prepared from hMSCs to prostate cancer cells (PC3). As can be seen from Figure 7A, most vesicles favored cell binding. In addition, the vesicles were detected inside and fused with the cell membranes (Figure 7A).

Flow cytometry analysis demonstrates that most cells bind the vesicles (Figure 8A) in a concentration-dependent manner (Figure 8A), thus allowing to determine the extent of liposomal binding according to the cells' mean fluorescence intensity.

To test the specific targeting of cancerous cell-lines, DiI-labeled CDLs were prepared from hMSCs, which were previously incubated for 24 hrs with condition media derived from a prostate cancer cell-line (PC3) and from a non-human cell-line (BHK). The resulting "conditioned" CDLs, as well as CDLs prepared from unconditioned hMSCs (control), were incubated with PC3 and BHK cells for 15 min, 1 hr and 3 hrs. Following incubation, cells were washed, harvested and analyzed by flow cytometry (Figure 9).

The specificity index for every experiment, given a certain conditioning media (NO CM, BHK-derived and PC3-derived) and incubation time (15 min, 1 hr and 3 hrs), was calculated according to the following equation:

$$\begin{pmatrix}\text{Specificity}\\ \text{index}\end{pmatrix} = \frac{\dfrac{\%\ \text{PC3 cells in the marker following incubation with CDLs}}{\%\ \text{PC3 cells in the marker withot CDLs}}}{\dfrac{\%\ \text{BHK cells in the marker following incubation with CDLs}}{\%\ \text{BHK cells in the marker withot CDLs}}}$$

The specificity index results, summarized in Table 3 below, not only illustrates that the system exhibits specificity towards cancerous cells but that this specificity, as excepted, decreases with incubation time. In addition, the specificity index values show that the system's specific affinity towards cancer cells can be largely affected by subjecting the cells to various conditioning media prior to CDLs preparation.

Table 3-Specificity index of CDLs binding to prostate cancer PC3 cell-line

hMSCs Conditioning media	CDL incubation time with PC3 and BHK cells		
	15 min	1 hr	3 hr
No CM	1.91	1.50	1.25
BHK derived	3.45	3.43	1.10
PC3 derived	2.92	2.31	1.50

EXAMPLE 4

Protein entrapment within CDLs

sTRAIL production

Mediums and buffers – 1L 2YT medium was prepared from 16 gr Bacto™ Tryptone (BD number 211705), 10 gr Bacto™ Yeast Extract (DIFCO number 212750) and 5 gr NaCl (Chemically Pure). Medium used for culturing in Petri dished contained 16 gr Agar Granulated (DIFCO number 214530) on top of the above components. The medium was autoclaved for sterility. PBSX10 was prepred from 2 gr KCl, 2.4 gr KH_2PO_4, 14.4 gr $Na_2HPO_4 \cdot 7H_2O$ and 80 gr NaCl. Volume was adjusted to 1L with DDW and the buffer was filter sterilized through 0.2 μm filter.

Plasmids, DNA, bacteria and antibiotics - GST-sTRAIL coding DNA was kindly supplied by Dr. Stanley Lipkowitz, Bethesda, MD in pGEX-2TK plasmid introduced into *E. coli* BL21 using Ampicillin 100 μg/ml as a selection agent. Ampicillin stock was prepared from ampicillin Sodium Salt (Sigma number A9518) dissolved in Ultra Pure DDW (UP-water) to a final concentration of 100 mg/ml and filtered through 0.2μm filters.

Additional materials: Ethyl Alcohol 99% Dehydrated (FRUTAROM number 2355516400); D(+)GLUCOSE (Sigma number G5146); IPTG (Ornat Biochemicals number INA-1758-1400); Complete Mini EDTA-Free Protease inhibitor cocktail tablets (Roche Applied Science number 04693159001); DTT - DL-Dithiothereitol solution (Sigma number 43816); GSH BEADS (GE Healthcare); Glutathione Sepharose 4B (10

ml, Danyel Biotech number 17-0756-01); and L-Glutathione-reduced (Sigma number G4251).

Equipment - Amicon Ultra-15 centrifugal filters (Millipore number UFC901024); and French Press cell disruption system. All solutions were filtered for sterility through a 0.2 μm filters; all procedures up to Day 2 (step 4, pellet of bacteria after IPTG O/N induction) were carried out in a Sterile Hood.

Swith 1/100 GST-TRAIL glycerol stock (e.g., 400 μl GST-trail glycerol stock in 40 ml medium). The solution was incubated O/N 37^0C in a shaking incubator at 250 RPM.

Day 2

STEP 2: The "starter" culture was spun down at 1000 g for 15 min to remove the antibiotics. The supernatant was discarded and resuspended in 40 ml of fresh 2YT. In a Sterile Hood, the resuspended 40 ml of the O/N preparation from step number 1 was added to 2L of 2YT in a 4L flask (alternatively add the resuspended pellet of 20 ml of the O/N preparation from step number 1 to two 2L flasks each containing 1L of 2YT). The solution was incubated for 2-3 hours in a 37^0C shaking incubator at 250 RPM. Measures are taken not incubate for more than 3 hours until O.D. is 2.5-3.0 (it is recommended to measure $O.D._{595}$ after 2 hours).

STEP 3: Just before IPTG induction, PBS was added to a final concentration of 0.1X to maintain the pH of the culture. EtOH (99% Dehydrated) was added to a final concentration of 2% (40 ml in 2L culture) to increase the solubility of the protein. 10 ml/L of 0.5M Glucose was added as a carbon source to a final concentration of 5mM.

STEP 4: 500 μM IPTG were added to the supplemented culture. The culture was incubated over night in a shaking incubator (250 RPM) at 20-25^0 C.

Day 3

STEP 5: Bacteria was pelleted at 6,000 g for 10 min and the supernatant was discarded. All bacteria were resuspended in a 50 ml Falcon Tube using 40 ml PBS supplemented with 4 protease inhibitor tablets (Roche Applied Science) 1 tablet per 10 ml PBS.

STEP 6: Cells were lyzed by running the bacteria from step number 5 twice through a French Press cell disruption system. Alternatively, 10 ml aliquots in 50 ml tubes were sonicated on ice at 30% power by 4 bursts of 10 sec each. After Cell

disruption, the following was added to each 40 ml of cell lysate: 0.1% Triton-X (40 µl of TritonX100), 1 mM $MgCl_2$ (40 µl of 1M stock $MgCl_2$) and 1 mM DTT (40 µl of 1M stock DTT). The solution was mixed thoroughly and incubated at RT for 15 min on a rocker or shaker.

STEP 7: The bacterial lysate was spun down for 10 min at 16,900 g and 4 °C. Supernatants were aspirated and collected in 50 ml tubes.

STEP 8: Binding to GSH (Glutathione – Sepharose 4B Beads) - In a 15ml Falcon Tube, 3 ml of GSH Beads were washed three times with PBS. Collected supernatant was centrifuged again because of mass bead loss. The washed beads were added to the bacterial cell lysate from step number 7 and incubated with tumbling for 1 hour at 4°C.

STEP 9: The bacterial cell lysate, containing the sepharose beads from step number 8, was spun down at 2000 RPM for 1min in a MULTI CENTRIFUGE CM 6M ELMI to separate the protein-conjugated beads from the cell-lysate. The supernatant was collected and was centrifuged again to pellet the remaining sepharose beads in the supernatant (that might have not pelleted during the first centrifugation). The pellet from both centrifugations, containing the sTRAIL-conjugated beads, was washed 5 times with 5 ml of PBS supplemented with 0.1% Triton-X100, 150 mM NaCl and 1 proteinase inhibitor tablets per 20 ml PBS.

STEP 10: Elution of GST-sTRAIL – The beads were spun down as before and the supernatant was aspirated. 3 ml of 50 mM Glutathione (pH 8.5) in 10 mM Tris-HCl and 100 mM NaCl were added. Each 3 ml was vortexed for 2 min and the protein was eluted into the supernatant. The supernatant was aspirated as before and the supernatant kept. The procedure of elution was repeated 3-4 times.

STEP 11: The protein was concentrated using Amicon Ultra-15 10K NMWLnumber UFC9010, giving a protein yield of about 5 mg/L culture. sTRAIL was produced at a final concentration of 0.2 mg/ml

sTRAIL entrapment -About 10^7 Cells were harvested and washed with PBS. Cells were then hypotonically treated by re-suspension in ice cold Tris-magnesium (TM buffer, 0.01 M Tris, 0.001 M $MgCl_2$) pH 7.4 for 15min at 4°C. Following hypotonic treatment, the cells were homogenized by rotor-stator mechanical homogenizer (IKA®, Taquara, RJ, Brazil) for 1 min at 22,000 rpm and turned into ghosts (95% ruptured cell

membranes as confirmed by phase-contrast microscopy). For stabilizing the ghosts' suspension, 60% (w/w) sucrose solution was immediately added to the suspension to make a final concentration of 0.25M or 10% by volume. Ghosts were then centrifuged at 3000 rpm for 15 min at 4°C. The supernatant was discarded and the pellet of ghosts was then washed twice with 0.25 M sucrose in TM-buffer pH 7.4, by repeated suspension and centrifugation at 3,000 rpm for 15 min at 4°C. In order to create sonicated ghosts, the re-suspended pellet was then sonicated for 5 seconds at 27% amplitude using VibraCell VCX750 (Sonics & Materials Inc., Newtown, CT) and centrifuged at 3,000 rpm for 15 min at 4°C. The pellet of sonicated ghosts was then washed twice again with 0.25 M sucrose in TM-buffer pH 8.6, by repeated suspension and centrifugation at 3,000 rpm for 15 min at 4°C. After, sTRAIL was added to the suspended sonicated ghosts (in TM buffer pH 8.6) to a final concentration of 1 μg per 1 ml of ghost suspension. For the formation of unilamellar liposomes containing sTRAIL, the sTRAIL-containing resuspeded pellet of sonicated ghosts was manually extruded by 21 successive passages trough polycarbonate membranes with pore sizes of 0.4 μm and 0.1 μm (Osmonics Inc., Minnesota USA). The extruded liposomes containing sTRAIL were then centrifuged for 45 min at 150,000 g at 4°C. The supernatant containing excess non-encapsulated sTRAIL was discarded and the resulting liposomes pellet was resuspended with TM buffer pH 8.6.

Results

TRAIL - tumor necrosis factor-related apoptosis-inducing agent is a type II transmembrane protein that induces apoptosis in tumor cells of diverse origins, while sparing most normal cells [20-24]. Delivery of both full length and truncated, secreted forms of TRAIL (sTRAIL) were shown to induce apoptosis in a variety of cancer cells both in culture and *in vivo*[25, 26]. Our preliminary experiments with sTRAIL included its production and passive encapsulation within hMSCs CDLs at a final concentration of 1 μg/ml. Cryo-TEM imaging of the resulting sTRAIL-containing CDLs (Figure 10A left pane), compared to empty CDLs (Figure 10B, left pane) prepared and imaged under the same conditions, demonstrates the accumulation of 14-20 nm protein micelles within the CDLs. The sTRAIL micelles are even more clearly visible after digitally re-coloring the images from grey-scale to black-and-white (Figures 10A and 10B, right panel).

EXAMPLE 5

Preparation of "Hybrid CDLs" by fusion with other liposomes

Various molecules (e.g., proteins, lipids, additives and even encapsulates) can be introduced, conjugated or attached onto the surface of the CDLs by means of fusion between the CDLs and other liposomes (synthetic or cell-derive), thus creating – "Hybrid CDLs" . For example, a liposomal formulation made from synthetic well characterized lipids may be conjugated with a protein on its surface or may contain a desirable encapsulate. Then, by means of induced membrane fusion between the said synthetic liposomes and CDLs a hybrid CDL may be formed. These hybrid CDLs contain both lipids and proteins from the cell-membrane they derive from and the lipids and proteins that were originally formulated on the fused synthetic liposomes. Such introduction of 'non-native' materials onto the Hybrid CDLs may be used to attach or conjugate any molecule or moieties related, but not limited to, liposomal targeting, therapeutic effect, diagnostic effect, stealth-rendering properties etc. Such fusion may be also used to change the biochemical or chemophysical properties of the CDLs membranes by introduction of synthetic lipids, additives (e.g., cholesterol, ceramides) etc. Such fusion may be also used to increase the encapsulation efficiency in the said CDLs. Since encapsulation in CDLs is mainly limited to passive encapsulation, fusion with synthetic liposomes that were actively loaded with high concentration of encapsulates may significantly improve the CDLs' encapsulation efficiency.

Methods for preparation of synthetic liposomes are well known in the art and mainly include hydration of dehydrated lipids to form lamellar structures and consequent homogenization of those lamellar structures to create liposomes. Synthetic liposomes of the said application can be produced by any method known in the art including, but not limited to, solvent evaporation, solvent replacement, detergent dialysis, extrusion, sonication, freeze-drying, reverse phase evaporation, ethanol/ether injection, agitation and/or any other form of mechanical homogenization. Liposomes can be prepared from a variety of synthetic and naturally derived lipids and may or may not contain additional additives (e.g., cholesterol, ceramides etc.). Methods for active encapsulation of matter in such synthetic liposomes, which are mainly based on membrane pH gradient or active transporters, are also well known in the art and may be used to create synthetic liposomes with high encapsulation efficiency.

Fusion between CDLs and other liposomes to create "Hybrid CDLs" can be readily and easily accomplished by adding short chain free PEG (~200-500 Da) to the liposomes. The mechanism of PEG-induced vesicle fusion is believed to be related to the reduction of water activity and the dehydration of the lipid headgroups which consequently leads to vesicle coagulation and fusion. Fusion can also be artificially induced through electroporation in a process known as electrofusion. It is believed that this phenomenon results from the energetically active edges formed during electroporation, which can act as the local defect point to nucleate stalk growth between two bilayers. Fusion can also be achieved by addition of detergents (usually under 2%) to the liposomal mixture (e.g., Cymal-5™, 1-S-Octyl Beta-D-thioglucopyranoside etc.), incubation with mild agitation and consequent detergent dialysis.

EXAMPLE 6

Proteomics analysis of hMSCc ghost and derived CDLs

Method

Proteomics analysis was conducted on 4 samples containing ghost cells and CDLs derived from hMSCc that were either conditioned or unconditioned by a medium derived from a prostate cancer cell-line (PC3). For the production of conditioned ghosts and CDLs, hMSCs were incubated for 24 prior to harvesting in medium composed of 50% conditioning media derived from PC3 cells. Cells were then harvested and sonicated ghosts and CDLs were prepared thereof by the method previously described. Sonicated ghosts from conditioned and unconditioned hMSCs (10^6 cells) were resuspended for analysis in 1 ml TM-buffer, pH 7.4. Cell-derived liposomes derived from $7x10^6$ conditioned and unconditioned hMSCc were resuspended in 50 μL TM buffer, pH 8.6.

The samples were sent for proteomics analysis at the proteomics center of the TECHNION – Israel Institute of Technology. Briefly, the samples were digested by Trypsin and the resulting peptides were analyzed by LC-MS/MS. Peptide mix was fractionated by HPLC and electro-sprayed onto an ion-trap mass spectrometer (Orbitrap™). Mass spectrometry was performed in order to analyze the peptides' mass to charge ratio spectra and to determine the proteins' mass. For additional analysis and identification, the peptides were further fragmented by collision induced dissociation (CID) and analyzed again. The peptides were identified by Sequest 3.31 software

against the human part of the uniprot database. All protein results are given as Uniport Accession Numbers. The following values were determined for each protein/accession number:

MW - Molecular weight

P_{pro} - The probability of finding a match as good as or better than the observed match by chance. The value displayed for the protein is the probability of the best peptide match (the peptide with the lowest score).

Pep Count - The total number of identified peptides.

Mean - The Average of the peak areas of top 3 identified peptides per protein.

Mean.SE - Mean standard error.

Med - Median of the peak area of all identified peptides per protein

MedErr - Median absolute deviation.

Protein Name.

Results

The hundreds of proteins that were identified on one or more of the four samples can be divided into 4 distinct groups:

1. Proteins that were prevalent in all four samples (Table 7), i.e. conditioned and unconditioned ghosts and CDLs.
2. Proteins that were prevalent in the ghosts or conditioned ghosts but were missing from the CDLs (Table 5). These proteins are probably or mostly the remains of cytoplasmatic matter that was not completely removed from the ghosts.
3. Proteins that were prevalent only on the conditioned ghosts and CDLs (Table 6). These proteins are probably or mostly membarnal proteins which are only expressed after induction or exposure to condition media.
4. Proteins that were prevalent in all samples but CDLs that were produced from unconditioned hMSCs (Table 7). These proteins are probably or mostly membarnal proteins which are expressed in lower levels on unconditioned hMSCs and which are completely depleted on their derived CDLs. Inducing the hMSCs with condition media probably elevates these proteins level to the extent they become more apparent on the conditioned CDLs.

Table 4 – Proteins prevalent on conditioned and unconditioned ghosts and CDLs.

Uniport Accession Number	MW	Fold expression on conditioned CDLs relative to unconditioned CDLS	Protein name
P04179	24706.6	30	Moesin
P62899	14453.9	26	Myosin regulatory light chain 12A
P09622	54143.1	26	Sodium/potassium-transporting ATPase subunit alpha-1
P02545	74094.8	24	40S ribosomal protein S28
P05023	112824.1	14	Integrin beta-1
P11142	70854.4	14	Cathepsin D
P62701	29579.1	12	Sulfide:quinone oxidoreductase
P07602	58073.9	12	Histone H4
P21589	63327.6	11	Major vault protein
P27797	48111.9	10	Keratin
O75396	24724.8	10	Elongation factor 2
P13674	61011.1	10	Erlin-2
P24752	45170.7	9	60S ribosomal protein L4
P30044	22012.5	9	60S ribosomal protein L18a
P51659	79636.4	9	40S ribosomal protein S21
P61604	10924.9	8	Actin
P17301	129213.8	8	Acetyl-CoA acetyltransferase
P38117	27826.2	8	Leucine-rich PPR motif-containing protein
P10809	61016.5	8	Ras-related protein Rab-7a
P14314	59387.9	7	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2
P62736	41981.8	7	60S ribosomal protein L14
Q96D15	37470	7	Voltage-dependent anion-selective channel protein 3
P62241	24190.2	7	Annexin A4
Q9Y2Q3	25480.3	7	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1
P02786	84818	7	Pyruvate kinase isozymes M1/M2
P38646	73634.8	7	40S ribosomal protein S19
P62829	14856.1	7	Annexin A2
Q9H4B7	50294.6	7	Reticulocalbin-3
P40926	35480.7	7	Peroxiredoxin-1
P08648	114464.9	7	Malate dehydrogenase
P07237	57080.8	7	Prenylcysteine oxidase 1
Q70UQ0	39285	7	40S ribosomal protein S4
Q9NZM1	234558.8	7	Proactivator polypeptide
Q07020	21621.1	7	Heat shock cognate 71 kDa protein
P30040	28975.2	6	Integrin alpha-V
Q09666	628705.2	6	Annexin A11
Q32P28	83341.2	6	60S ribosomal protein L7a
Q15155	134267.4	6	Serine hydroxymethyltransferase
P04040	59718.9	6	Tubulin alpha-1B chain
P30048	27675.2	6	60S ribosomal protein L26-like 1
P68104	50109.2	6	Integrin alpha-2
Q00325	40068.8	6	Myoferlin
P30443	40820.2	6	Trifunctional enzyme subunit beta

P06756	115964.5	6	Thioredoxin-dependent peroxide reductase
Q15149	531465.9	6	ATP synthase subunit O
P16615	114682.7	6	Elongation factor Tu
P14625	92411.2	6	60S ribosomal protein L11
P19105	19781.5	6	60S acidic ribosomal protein P0-like
P34897	55957.8	6	40S ribosomal protein S3
P45880	31546.5	6	Signal recognition particle receptor subunit beta
O15118	142073.5	6	Serpin H1
P62805	11360.4	6	Isocitrate dehydrogenase [NADP]
Q99536	41893.5	6	Endoplasmin
P36957	48698.6	6	Tubulin beta chain
P02751	262439.5	5	CD44 antigen
P13639	95277.1	5	60S ribosomal protein L30
P49411	49510.2	5	60S ribosomal protein L12
Q00610	191491.7	5	Plectin-1
P55072	89265.9	5	Aldehyde dehydrogenase X
P21281	56465	5	ATP synthase subunit alpha
Q16698	36044.8	5	Collagen alpha-1(I) chain
P26038	67777.9	5	40S ribosomal protein S8
P14854	10185.7	5	ATP synthase subunit d
P50454	46411.3	5	Erlin-1
P08670	53619.2	5	Vesicle-trafficking protein SEC22b
Q13423	113822.9	5	Procollagen-lysine
P62847	15413.4	5	Synaptic vesicle membrane protein VAT-1 homolog
P00505	47445.3	5	Protein disulfide-isomerase A6
P05556	88357	5	Niemann-Pick C1 protein
P30837	57202.3	5	Annexin A1
P13667	72887.1	5	Cytochrome c oxidase subunit 6B1
P06733	47139.4	5	Voltage-dependent anion-selective channel protein 2
P68363	50119.6	5	10 kDa heat shock protein
Q15084	48091.3	5	Heme oxygenase 1
P04844	69241.1	5	Lysosome membrane protein 2
P36578	47667.5	5	60S ribosomal protein L22
P11021	72288.5	5	Dipeptidyl peptidase 4
O60568	84731.7	5	ATP synthase subunit beta
P04406	36030.4	5	Keratin
O95816	23757.2	5	Calreticulin
Q04837	17249	5	60S acidic ribosomal protein P2
P09601	32798	5	Transitional endoplasmic reticulum ATPase
Q06830	22096.3	5	Lamin-A/C
Q9H9B4	35596.4	5	Protein disulfide-isomerase A3
P09525	35860.1	5	40S ribosomal protein S5
P16070	81503.4	5	Tubulin beta-1 chain
P04075	39395.3	5	Annexin A5
P14649	22749.7	5	Electron transfer flavoprotein subunit beta
Q02809	83497.5	5	Peptidyl-prolyl cis-trans isomerase B
P10606	13686.9	5	Collagen alpha-1(VI) chain
P48735	50876.9	5	Translocon-associated protein subunit delta
P07339	44523.7	5	Keratin
Q9Y6N5	49928.9	5	Peroxisomal multifunctional enzyme type 2

Q7KZF4	101933.6	5	Prohibitin-2
P50213	39566.1	5	Leucine-rich repeat-containing protein 59
Q9UNX3	17245.6	5	Prolyl 3-hydroxylase 1
P14618	57900.2	5	Lysosome-associated membrane glycoprotein 2
Q96AG4	34908.9	5	40S ribosomal protein S18
P07355	38579.8	4	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1
P61803	12488.6	4	Dihydrolipoyl dehydrogenase
Q13162	30520.8	4	60S ribosomal protein L5
P63220	9105.6	4	Guanine nucleotide-binding protein subunit beta-2-like 1
P62263	16262.5	4	60S ribosomal protein L18
Q14108	54255.6	4	Histone H2B type 1-B
P63244	35054.6	4	5'-nucleotidase
P49748	70345.5	4	ADP/ATP translocase 2
P55084	51261.6	4	Aminopeptidase N
P42704	157804.6	4	L-lactate dehydrogenase A chain
P00338	36665.4	4	Voltage-dependent anion-selective channel protein 1
Q02543	20748.9	4	Glucosidase 2 subunit beta
Q13885	49875	4	Annexin A6
P30101	56746.8	4	ATP synthase subunit delta
P35268	14777.8	4	Peroxiredoxin-5
Q9P2E9	152380	4	Very long-chain specific acyl-CoA dehydrogenase
P62424	29977	4	Prolow-density lipoprotein receptor-related protein 1
P36543	26128.8	4	Inhibitor of nuclear factor kappa-B kinase-interacting protein
P62857	7836.2	4	40S ribosomal protein S24
P62753	28663	4	Elongation factor 1-alpha 1
Q9UHG3	56603.8	4	Aspartate aminotransferase
P50914	23417	4	60S ribosomal protein L13
P60174	26652.7	4	Adipocyte plasma membrane-associated protein
P27487	88222.5	4	Fibronectin
P62269	17707.9	4	Myosin light chain 6B
P36542	32975.3	4	Transgelin
P39656	50769	4	Staphylococcal nuclease domain-containing protein 1
Q99623	33275.9	4	Sideroflexin-3
P26373	24246.5	4	60S ribosomal protein L31
Q9HDC9	46450.9	4	Phosphate carrier protein
Q71U36	50103.7	4	ADP/ATP translocase 1
P08865	32833.4	4	Lysosome-associated membrane glycoprotein 1
P00387	34212.7	4	Hexokinase-1
Q9Y5M8	29683.8	4	Protein disulfide-isomerase A4
P25705	59713.7	4	Catalase
P23284	23727.5	4	Cytochrome c oxidase subunit 5A
P05387	11657.9	4	40S ribosomal protein SA
P43307	32215.4	4	Isocitrate dehydrogenase [NAD] subunit alpha
P49755	24960	4	2
P04083	38690	4	Tubulin beta-2C chain
P04843	68526.9	4	V-type proton ATPase subunit E 1
P08133	75825.7	4	40S ribosomal protein S6
P68371	49799	4	V-type proton ATPase catalytic subunit A
O75477	38901.4	4	Trifunctional enzyme subunit alpha
P21796	30753.6	4	Ribosome-binding protein 1

P62873	37353	4	Vimentin
P12235	33043.2	4	Protein S100-A11
P20674	16751.7	4	Procollagen-lysine
Q9BWM7	35480.5	4	Mitochondrial inner membrane protein
P23396	26671.4	4	60S ribosomal protein L23
P05141	32874.2	4	60 kDa heat shock protein
P61247	29925.8	3	Alpha-enolase
Q16891	83626.5	3	Transmembrane emp24 domain-containing protein 9
P51571	18986.6	3	Collagen alpha-2(I) chain
O75489	30222.7	3	Endoplasmic reticulum resident protein 29
P31930	52612.5	3	Cytochrome b-c1 complex subunit 1
P48047	23262.7	3	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3
P62888	12775.7	3	Neuroblast differentiation-associated protein AHNAK
P12111	343450.3	3	Prohibitin
Q8NHW5	34342.7	3	40S ribosomal protein S14
P12109	108462	3	V-type proton ATPase subunit B
P30050	17807.5	3	Triosephosphate isomerase
P40939	82947	3	Integrin alpha-5
O75947	18479.5	3	Fructose-bisphosphate aldolase A
P31040	72645.4	3	Calnexin
P19367	102420.2	3	Cytochrome b-c1 complex subunit 2
P30049	17479.2	3	Prolyl 4-hydroxylase subunit alpha-1
P46782	22862.1	3	Transmembrane emp24 domain-containing protein 10
P39019	16050.5	3	Peroxiredoxin-4
Q07065	65982.9	3	Stomatin-like protein 2
P35232	29785.9	3	BAG family molecular chaperone regulator 2
P62913	20239.7	3	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2
P06576	56524.7	3	Clathrin heavy chain 1
P51149	23474.9	3	Collagen alpha-3(VI) chain
P27824	67526	3	60S ribosomal protein L9
P31949	11732.8	3	HLA class I histocompatibility antigen
P35579	226390.6	3	NADH-ubiquinone oxidoreductase 75 kDa subunit
P02452	138826.8	3	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit
Q01995	22596.4	3	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1
Q14764	99266.1	3	Transferrin receptor protein 1
Q9UJZ1	38510.2	3	40S ribosomal protein S3a
P08123	129209.8	3	NADH-cytochrome b5 reductase 3
P50995	54355.1	2	Sideroflexin-1
P11279	44853.9	2	Actin
Q9BVK6	27260.2	2	Myosin-9
P38606	68260.6	2	NAD(P) transhydrogenase
P08758	35914.4	2	60S ribosomal protein L7
P28331	79416.7	2	CD59 glycoprotein
P15144	109470.8	2	Cytochrome c oxidase subunit 5B
P22695	48412.9	2	Glyceraldehyde-3-phosphate dehydrogenase
P35908	65393.2	2	Glutathione S-transferase kappa 1
P35527	62026.7	2	Tubulin alpha-1A chain

Q07954	504243.2	2	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex
P33778	13941.6	2	Succinate dehydrogenase [ubiquinone] flavoprotein subunit
P13645	58791.6	1	Cytoskeleton-associated protein 4
P60709	41709.7	1	Keratin
P46777	34340.7	1	Stress-70 protein
Q9Y277	30639.3	1	Protein disulfide-isomerase
P32969	21849.8	1	ATP synthase subunit gamma
P18124	29207.2	1	Translocon-associated protein subunit alpha
O94905	37815.5	1	Single-stranded DNA-binding protein
P13987	14167.8	1	78 kDa glucose-regulated protein
P07437	49639	1	Nodal modulator 1
P13473	44932.3	1	Superoxide dismutase [Mn]
P04264	65998.9	1	Tubulin beta-2A chain

Table 5 - Proteins that were prevalent in the ghosts or conditioned ghosts but were missing from the CDLs

Uniport Accession Number	MW	Prevalent in ghosts	Prevalent in conditioned ghosts	Protein name
P78527	468786.9	+	+	Actin-related protein 2/3 complex subunit 1B
Q99715	332939.7	+	+	rRNA 2'-O-methyltransferase fibrillarin
Q14573	303910.4	+	+	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8
P24821	240697.7	+	+	E3 ubiquitin-protein ligase MARCH5
P35580	228856.9	+	+	Acyl carrier protein
P07942	197935.7	+	+	Fibrillin-1
P55268	195853.3	+	+	Extracellular sulfatase Sulf-1
Q8WWI1	192589.5	+	+	Protein kinase C alpha type
P20908	183446.3	+	+	Cytosol aminopeptidase
P11047	177487.9	+	+	Beta-galactosidase
Q6YHK3	161586.8	+	+	Histone H3.1t
Q7L576	145088.6	+	+	GDP-fucose protein O-fucosyltransferase 1
Q08211	140868.9	+	+	Protein S100-A6
P23634	137832.9	+	+	Protein tyrosine phosphatase-like protein PTPLAD1
Q12768	134200.9	+	+	39S ribosomal protein L43
P00533	134190.2	+	+	Radixin
O43795	131901.9	+	+	Putative ribosomal RNA methyltransferase NOP2
Q9BSJ8	122780.1	+	+	Trophoblast glycoprotein
P26006	118680.2	+	+	Galectin-3
P54707	115437.2	+	+	ATP synthase subunit f
Q8N766	111689.2	+	+	Calponin-2
O60313	111560.7	+	+	Tumor necrosis factor receptor superfamily member 10B
Q9Y4L1	111266.2	+	+	Probable glutathione peroxidase 8
Q6P179	110391.1	+	+	Hydroxyacyl-coenzyme A dehydrogenase
P22413	104856.7	+	+	Medium-chain specific acyl-CoA dehydrogenase
Q6ZXV5	103941.9	+	+	SH3 domain-binding glutamic acid-rich-like protein 3
A0FGR8	102294.1	+	+	V-type proton ATPase 116 kDa subunit a isoform 3
P11586	101495.6	+	+	U5 small nuclear ribonucleoprotein 200 kDa helicase
Q15063	93255.4	+	+	Transducin beta-like protein 2

Q13488	92908.6	+	+	Extended synaptotagmin-2
O95479	88836.6	+	+	Mitochondrial import inner membrane translocase subunit Tim8 A
Q9UBV2	88698.6	+	+	Histone H1.2
Q9NR30	87290.5	+	+	Vesicular integral-membrane protein VIP36
Q15436	86105.3	+	+	SRA stem-loop-interacting RNA-binding protein
Q99798	85372	+	+	Nuclear pore complex protein Nup205
P08238	83212.2	+	+	DnaJ homolog subfamily B member 1
P13010	82652.4	+	+	HEAT repeat-containing protein 1
Q96TA1	82631.1	+	+	Pyruvate dehydrogenase E1 component subunit alpha
Q8IVL6	81785.8	+	+	Pre-mRNA-processing-splicing factor 8
Q9UH99	80261.7	+	+	Collagen alpha-1(XIV) chain
Q9BU23	79647.6	+	+	Probable saccharopine dehydrogenase
Q96AC1	77810.7	+	+	Nucleoside diphosphate kinase B
P21980	77279.8	+	+	Protein DEK
Q6NUQ4	77101.6	+	+	Nascent polypeptide-associated complex subunit alpha
P17252	76714.3	+	+	LIM domain only protein 7
P23246	76101.8	+	+	NADH dehydrogenase [ubiquinone] iron-sulfur protein 6
Q99805	75725.7	+	+	Peptidyl-tRNA hydrolase 2
O75746	74715	+	+	Deoxyribonuclease-2-alpha
P46063	73410	+	+	Alpha-L-iduronidase
Q8NBJ5	71590.6	+	+	Cytochrome c oxidase subunit 6C
P17066	70984.4	+	+	Signal peptidase complex subunit 2
O43390	70899.2	+	+	60S ribosomal protein L35
P43155	70812.5	+	+	Adenosine 3'-phospho 5'-phosphosulfate transporter 1
P34931	70331.5	+	+	Proliferation-associated protein 2G4
P54652	69978	+	+	Splicing factor
P17844	69104.8	+	+	Ras-related protein Ral-A
Q96CM8	68080.8	+	+	60S ribosomal protein L10-like
Q03252	67647.6	+	+	ATP-binding cassette sub-family E member 1
O94826	67412.2	+	+	Actin-related protein 2/3 complex subunit 2
P20700	66367.7	+	+	Cathepsin Z
Q5JTV8	66208.4	+	+	Acyl-coenzyme A thioesterase 1
O00567	66008.8	+	+	Signal peptidase complex catalytic subunit SEC11A
P23368	65402	+	+	Acetyl-coenzyme A transporter 1
Q10471	64691.5	+	+	4F2 cell-surface antigen heavy chain
Q10472	64177.5	+	+	Tropomyosin beta chain
P14866	64092.4	+	+	Coiled-coil domain-containing protein 47
Q14956	63882	+	+	Myb-binding protein 1A
P07686	63071.3	+	+	ADP-ribosylation factor 1
O95302	63043.6	+	+	Synaptonemal complex protein SC65
Q969V3	62934.7	+	+	Signal peptidase complex subunit 3
P30038	61680.7	+	+	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2
Q96S52	61617.3	+	+	Ras-related protein Rab-8A
Q9HCC0	61294.5	+	+	EH domain-containing protein 2
Q5SSJ5	61169.3	+	+	Rho GTPase-activating protein 1
Q9P0J1	61015.7	+	+	Putative 40S ribosomal protein S26-like 1
Q9H857	60679.8	+	+	Mitochondrial chaperone BCS1
P04062	59678.4	+	+	Calcium-binding mitochondrial carrier protein Aralar2
Q9Y2X3	59540.6	+	+	Ribosome-releasing factor 2

Q7Z4H8	58535.3	+	+	39S ribosomal protein L46
Q13217	57544.3	+	+	Cytochrome c1
P49257	57513.1	+	+	Transmembrane 9 superfamily member 4
P26599	57185.8	+	+	60S ribosomal protein L36a
P05091	56345.7	+	+	Metaxin-2
Q96A33	55838.4	+	+	Heterogeneous nuclear ribonucleoprotein L
Q9UMS4	55146.4	+	+	ES1 protein homolog
O60701	54989.3	+	+	Replication protein A 14 kDa subunit
O76021	54939	+	+	60S ribosomal protein L37a
P10619	54431.2	+	+	Neuron-specific calcium-binding protein hippocalcin
Q96HE7	54358.1	+	+	Translocation protein SEC63 homolog
Q15233	54197.4	+	+	Protein transport protein Sec61 subunit beta
Q02818	53846.4	+	+	Torsin-1A-interacting protein 2
P22570	53803.1	+	+	NADH dehydrogenase [ubiquinone] iron-sulfur protein 7
Q96N66	52730.3	+	+	Fatty aldehyde dehydrogenase
P20073	52705.8	+	+	All-trans-retinol 13
P61619	52230.6	+	+	H/ACA ribonucleoprotein complex subunit 4
Q9Y512	51943.4	+	+	Multidrug resistance-associated protein 1
O43615	51323.6	+	+	Neuroplastin
Q07960	50404.3	+	+	Heterochromatin protein 1-binding protein 3
Q13509	50400.3	+	+	Transmembrane emp24 domain-containing protein 3
Q9P2R7	50285.3	+	+	Phosphoglycerate mutase 1
P80303	50164.4	+	+	Putative heterogeneous nuclear ribonucleoprotein A1-like 3
P36551	50120.1	+	+	Isovaleryl-CoA dehydrogenase
P13489	49941.2	+	+	ATP synthase subunit b
Q9Y305	49869.6	+	+	Ras-related protein Rab-5A
Q9BUF5	49825	+	+	Poly(rC)-binding protein 2
P04350	49553.9	+	+	Actin-related protein 2/3 complex subunit 5
P31943	49198.4	+	+	60S ribosomal protein L13a
P62495	49000.2	+	+	Mitochondrial import inner membrane translocase subunit Tim13
P82675	47976.2	+	+	Beta-actin-like protein 2
P09543	47548.7	+	+	Protein disulfide-isomerase TMX3
P45954	47455.3	+	+	Acid ceramidase
Q8NBX0	47121.5	+	+	Lipase maturation factor 2
O60664	47018	+	+	Ras-related C3 botulinum toxin substrate 1
P28300	46914.5	+	+	Golgin subfamily B member 1
P11310	46558.6	+	+	Ectonucleotide pyrophosphatase/phosphodiesterase family member 1
O75718	46532	+	+	Ras-related protein Rab-18
O14979	46409	+	+	High mobility group protein B1
P26440	46289.7	+	+	Coproporphyrinogen-III oxidase
P60842	46124.6	+	+	Contactin-associated protein 1
Q58FF3	45829.9	+	+	Protein S100-A16
Q96HD1	45408.9	+	+	Isocitrate dehydrogenase [NAD] subunit beta
Q6YN16	45365.5	+	+	CDP-diacylglycerol--inositol 3-phosphatidyltransferase
Q8NC51	44938.5	+	+	Follistatin-related protein 1
Q96G23	44847.4	+	+	Ribose-phosphate pyrophosphokinase 1
Q9BTV4	44847.3	+	+	Eukaryotic initiation factor 4A-III

P61160	44732.3	+	+	Probable cation-transporting ATPase 13A1
P09110	44263.9	+	+	High mobility group protein HMGI-C
P07093	43974.3	+	+	Mesoderm-specific transcript homolog protein
Q9H488	43927.2	+	+	Cytoplasmic FMR1-interacting protein 1
O75521	43557.4	+	+	Matrin-3
Q6NVY1	43454.4	+	+	Polypeptide N-acetylgalactosaminyltransferase 1
P17302	42980.9	+	+	39S ribosomal protein L1
Q13336	42499.8	+	+	Dolichol-phosphate mannosyltransferase
Q16795	42482.6	+	+	Peptidyl-prolyl cis-trans isomerase C
P35613	42174.1	+	+	Gamma-glutamyl hydrolase
P29992	42096.6	+	+	V-type proton ATPase 16 kDa proteolipid subunit
Q9BYX7	41988.9	+	+	Ribosome biogenesis regulatory protein homolog
Q562R1	41976	+	+	28S ribosomal protein S5
Q9BRK5	41780.5	+	+	Lanosterol synthase
P30533	41440.9	+	+	Glyoxylate reductase/hydroxypyruvate reductase
P82650	41254.4	+	+	Transforming growth factor-beta-induced protein ig-h3
Q15050	41168.2	+	+	Beta-actin-like protein 3
Q12907	40203.1	+	+	Nucleolar RNA helicase 2
O75367	39592.5	+	+	CAAX prenyl protease 1 homolog
Q9NYL9	39570.3	+	+	RNA-binding protein FUS
P09972	39431.3	+	+	ADP-ribosylation factor-like protein 6-interacting protein 1
Q5EB52	38805.5	+	+	Glia-derived nexin
Q15366	38555.6	+	+	Tubulin beta-6 chain
Q9H0U3	38011.4	+	+	Magnesium transporter protein 1
O15121	37841.1	+	+	60S ribosomal protein L6
Q9UDY4	37783.2	+	+	Peptidyl-prolyl cis-trans isomerase FKBP3
P62136	37487.8	+	+	Up-regulated during skeletal muscle growth protein 5
Q14257	36853.7	+	+	Thioredoxin-related transmembrane protein 1
P05198	36089.4	+	+	28S ribosomal protein S31
Q9NZ01	36010.8	+	+	High mobility group protein HMG-I/HMG-Y
P27695	35532.2	+	+	Antigen peptide transporter 1
P08574	35367	+	+	DnaJ homolog subfamily C member 3
P31937	35305.8	+	+	Peroxisomal acyl-coenzyme A oxidase 1
Q08257	35184.6	+	+	Chloride intracellular channel protein 1
Q15006	34811.4	+	+	N-acetylglucosamine-6-sulfatase
P09486	34609.7	+	+	Probable transcription factor PML
O15144	34311.5	+	+	Mitochondrial import receptor subunit TOM70
Q16836	34255.9	+	+	Endoplasmic reticulum aminopeptidase 2
Q9UHQ9	34073.2	+	+	LDLR chaperone MESD
P53007	33991	+	+	Acyl-coenzyme A thioesterase 13
Q9UBR2	33846.2	+	+	Lamin-B1
Q8NBJ7	33835.8	+	+	116 kDa U5 small nuclear ribonucleoprotein component
P62995	33645.6	+	+	Proteolipid protein 2
Q9BPW8	33288.9	+	+	Collagen triple helix repeat-containing protein 1
P07951	32830.6	+	+	Isocitrate dehydrogenase [NAD] subunit gamma
P42126	32795.2	+	+	RNA-binding Raly-like protein
Q02878	32707.6	+	+	Sphingolipid delta(4)-desaturase DES1
Q86SE5	32310.6	+	+	3
Q9Y639	31271.9	+	+	Mitochondrial import inner membrane translocase subunit TIM44

P15559	30848	+	+	Mammalian ependymin-related protein 1
O75431	29744.1	+	+	Aldehyde dehydrogenase
O60762	29615.8	+	+	Urea transporter 1
P22090	29437	+	+	Retinol dehydrogenase 11
P62258	29155.4	+	+	T-complex protein 1 subunit delta
P24539	28890.3	+	+	Ribonuclease inhibitor
P18669	28785.9	+	+	Splicing factor
P67936	28504.5	+	+	60S ribosomal protein L28
Q9UFN0	28448.5	+	+	Calpain small subunit 1
Q9UHQ4	28302.2	+	+	Histone H1.1
P30042	28152.7	+	+	Pre-mRNA-processing factor 19
P57088	27959.8	+	+	NADH dehydrogenase [ubiquinone] iron-sulfur protein 5
Q9P0L0	27875.2	+	+	OCIA domain-containing protein 2
Q07955	27727.8	+	+	Histone H1.0
P63104	27727.7	+	+	Glycylpeptide N-tetradecanoyltransferase 1
Q9NR28	27113.7	+	+	Putative 60S ribosomal protein L13a-like MGC87657
P33316	26689.7	+	+	Major facilitator superfamily domain-containing protein 10
O75352	26620.5	+	+	Transmembrane emp24 domain-containing protein 1
P54819	26460.8	+	+	Cystatin-B
P17931	26136.1	+	+	Integrin alpha-3
P60033	25792.1	+	+	Signal peptidase complex subunit 1
Q9UM22	25420.6	+	+	NAD(P)H dehydrogenase [quinone] 1
Q13445	25189.7	+	+	Mannose-P-dolichol utilization defect 1 protein
Q00688	25161.3	+	+	DnaJ homolog subfamily B member 4
Q15005	24986.7	+	+	Heat shock 70 kDa protein 6
P09429	24878.2	+	+	Heterogeneous nuclear ribonucleoprotein D-like
P62906	24815.5	+	+	Protein Mpv17
Q9Y3Q3	24761.3	+	+	Tubulin beta-3 chain
P27635	24587.9	+	+	Anoctamin-10
Q96L21	24502.7	+	+	Acyl-CoA synthetase family member 2
P62826	24407.6	+	+	Heat shock protein beta-1
B2RPK0	24222.8	+	+	Peptidyl-prolyl cis-trans isomerase FKBP7
O43402	23757.7	+	+	Thioredoxin reductase 2
P20339	23643.8	+	+	Acyl-coenzyme A thioesterase 9
P40429	23562.4	+	+	Heterogeneous nuclear ribonucleoprotein H
P11233	23552	+	+	Probable ATP-dependent RNA helicase DDX5
O14735	23523.1	+	+	Hydroxysteroid dehydrogenase-like protein 2
Q8N983	23416.2	+	+	WASH complex subunit strumpellin
P45877	22748.8	+	+	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9
P46781	22577.6	+	+	Nucleosome assembly protein 1-like 1
P84074	22413	+	+	Lysosomal protective protein
Q96AB3	22322.8	+	+	Beta-hexosaminidase subunit alpha
O43399	22224.3	+	+	Serum albumin
Q02539	21828.9	+	+	B-cell receptor-associated protein 29
O75915	21600.4	+	+	Mitochondrial import inner membrane translocase subunit TIM50
Q9H061	21513.5	+	+	NADH dehydrogenase [ubiquinone] flavoprotein 2
P16403	21351.8	+	+	Protein sel-1 homolog 1
P84077	20683.7	+	+	Beta-hexosaminidase subunit beta

P67812	20612.1	+	+	Nucleolar protein 56
P18085	20497.7	+	+	Sterol-4-alpha-carboxylate 3-dehydrogenase
P24844	19814.5	+	+	WASH complex subunit 7
O60831	19245.5	+	+	Glycine cleavage system H protein
P46778	18553.1	+	+	Putative hexokinase HKDC1
P62280	18419	+	+	SWI/SNF complex subunit SMARCC2
P62277	17211.7	+	+	39S ribosomal protein L38
Q9BX68	17151.2	+	+	Ganglioside GM2 activator
P15531	17137.7	+	+	Oligosaccharyltransferase complex subunit OSTC
P62841	17029.2	+	+	Small nuclear ribonucleoprotein-associated proteins B and B'
P63241	16821.4	+	+	Regulator of chromosome condensation
Q9NRP0	16817.8	+	+	Nucleoside diphosphate kinase A
Q86SX6	16617.5	+	+	60S ribosomal protein L34
O15511	16310.3	+	+	Tubulin beta-4 chain
P46779	15737.7	+	+	Tropomyosin alpha-4 chain
P26885	15639.3	+	+	Receptor expression-enhancing protein 5
O60361	15519	+	+	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15
Q9NS69	15511.8	+	+	Four and a half LIM domains protein 2
Q9Y3E0	15415.4	+	+	ATP-dependent RNA helicase DHX29
P69905	15247.9	+	+	Leucyl-cystinyl aminopeptidase
P42766	14542.6	+	+	Heterogeneous nuclear ribonucleoprotein R
P55769	14164.6	+	+	Histidyl-tRNA synthetase
P04908	14127	+	+	Small nuclear ribonucleoprotein Sm D3
P61769	13705.9	+	+	Prostacyclin synthase
Q5JNZ5	12994	+	+	[Pyruvate dehydrogenase [acetyl-transferring]]-phosphatase 1
Q9GZT3	12341.4	+	+	Protein transport protein Sec23A
P84090	12251	+	+	Abhydrolase domain-containing protein 10
Q96FQ6	11794	+	+	Putative endoplasmin-like protein
P99999	11741.1	+	+	60S acidic ribosomal protein P1
P17096	11669.2	+	+	Trans-2
O60220	10991.3	+	+	GDH/6PGL endoplasmic bifunctional protein
P56134	10910.7	+	+	Potassium-transporting ATPase alpha chain 2
Q9Y5L4	10493	+	+	Eukaryotic peptide chain release factor subunit 1
Q9H299	10431.3	+	+	Transmembrane and TPR repeat-containing protein 3
P61513	10268.5	+	+	Ribosomal L1 domain-containing protein 1
O75531	10052	+	+	Regulator of microtubule dynamics protein 1
P60468	9968.1	+	+	Adenylate kinase 2
P62979	9411.9	+	+	Alpha-2-macroglobulin
P63173	8212.7	+	+	72 kDa type IV collagenase
P04732	6009.2	+	+	SUN domain-containing protein 1
P35555	312082	+	-	Laminin subunit beta-1
Q05707	193393	+	-	SUN domain-containing protein 2
Q7Z478	155138.3	+	-	Vesicle transport protein GOT1B
Q9HD20	132869.9	+	-	Actin-related protein 2
Q9UIQ6	117274.2	+	-	Hemoglobin subunit alpha
Q9UGP8	87941.5	+	-	ERO1-like protein alpha
Q9UJS0	74128.8	+	-	Glucosylceramidase

P27658	73317.2	+	-	Metaxin-1
P35475	72624.8	+	-	ATP-dependent DNA helicase Q1
P02768	69321.6	+	-	Tumor protein D54
P35241	68521.5	+	-	Epidermal growth factor receptor
P08195	67951.9	+	-	Polypeptide N-acetylgalactosaminyltransferase 2
Q6NUM9	66776.8	+	-	Annexin A7
Q9NNW7	66320.8	+	-	Neighbor of COX4
Q86UE4	63798.8	+	-	Actin-related protein 2/3 complex subunit 3
P12081	57374.3	+	-	NHP2-like protein 1
Q9UBM7	54453.8	+	-	Cleft lip and palate transmembrane protein 1
P49189	53767.1	+	-	ATP-binding cassette sub-family D member 3
O15269	52710.6	+	-	Arylsulfatase A
O75306	52511.8	+	-	Delta-1-pyrroline-5-carboxylate dehydrogenase
P12694	50439.2	+	-	ADP-dependent glucokinase
Q92791	50349.3	+	-	Peptidyl-prolyl cis-trans isomerase FKBP9
Q15113	47942	+	-	Prostaglandin E synthase 2
Q8TB61	47483.6	+	-	Carnitine O-acetyltransferase
P55209	45346	+	-	40S ribosomal protein S9
Q92665	45290.5	+	-	Eukaryotic translation initiation factor 2 subunit 1
Q96DV4	44568.4	+	-	40S ribosomal protein S13
Q13561	44203.9	+	-	Coiled-coil domain-containing protein 109A
Q9UQ80	43759.2	+	-	Heat shock 70 kDa protein 1-like
P29803	42905.6	+	-	Niban-like protein 1
P51553	42767.1	+	-	3-hydroxyisobutyryl-CoA hydrolase
P61163	42586.9	+	-	Splicing factor
P25685	38020.4	+	-	Heat shock protein HSP 90-beta
Q9H2U2	37896	+	-	CD166 antigen
Q9H7B2	35560.2	+	-	Transient receptor potential cation channel subfamily V member 2
Q8TC12	35363.5	+	-	40S ribosomal protein S4
Q12841	34962.9	+	-	Plasminogen activator inhibitor 1 RNA-binding protein
P60891	34811.9	+	-	LAG1 longevity assurance homolog 2
Q99439	33675.3	+	-	Uncharacterized protein KIAA0090
Q86WA6	32522	+	-	Putative phospholipase B-like 2
Q14192	32170.6	+	-	Mitochondrial import receptor subunit TOM22 homolog
P16152	30355.9	+	-	28S ribosomal protein S23
Q9Y680	29990.1	+	-	Putative high mobility group protein B1-like 1
O60613	27629	+	-	ATP-dependent RNA helicase DDX18
Q96CG8	26207.1	+	-	Protein NipSnap homolog 1
Q14696	26060.3	+	-	NADH-cytochrome b5 reductase 1
Q13765	23369.7	+	-	Transmembrane protein 214
P09211	23341	+	-	40S ribosomal protein S29
P04792	22768.5	+	-	GTP-binding nuclear protein Ran
Q9Y3D9	21757.3	+	-	Carbonyl reductase [NADPH] 1
Q00765	21479.1	+	-	Peptidyl-prolyl cis-trans isomerase FKBP2
P63000	21436.3	+	-	Perilipin-3
P05976	21131.8	+	-	Nuclear pore complex protein Nup155
P30086	21043.7	+	-	Vesicle-associated membrane protein 2
Q9ULC4	20541.8	+	-	Succinyl-CoA ligase [ADP-forming] subunit beta
P61009	20300.5	+	-	Nicalin

P51970	20092.1	+	-	Inositol 1
P84103	19317.9	+	-	Malignant T cell-amplified sequence 1
Q9Y6H1	15502.7	+	-	U1 small nuclear ribonucleoprotein C
Q9NPJ3	14950.9	+	-	Tricarboxylate transport protein
P35244	13559.9	+	-	UDP-glucose 6-dehydrogenase
O43920	12509.4	+	-	Transmembrane protein 33
Q6NVV1	12126.9	+	-	Diablo homolog
P04080	11132.6	+	-	Non-POU domain-containing octamer-binding protein
O43678	10914.8	+	-	Ankycorbin
P09669	8775.7	+	-	Procollagen galactosyltransferase 1
Q15738	NA	-	+	ADP-ribosylation factor 4
P17900	NA	-	+	Histidine triad nucleotide-binding protein 2
P46087	NA	-	+	Myosin-Ib
O00299	NA	-	+	Quinone oxidoreductase
P39210	NA	-	+	60S ribosomal protein L10a
Q9P035	NA	-	+	Plasma membrane calcium-transporting ATPase 4
Q9NUJ1	NA	-	+	Enhancer of rudimentary homolog
O43837	NA	-	+	Cysteine-rich with EGF-like domain protein 1
Q9Y5S1	NA	-	+	Ribosome production factor 2 homolog
Q16647	NA	-	+	Beta-2-microglobulin
Q96JJ7	NA	-	+	2'
P23434	NA	-	+	PRA1 family protein 2
P0C7M2	NA	-	+	Nucleobindin-2
P15289	NA	-	+	Serine palmitoyltransferase 1
O75844	NA	-	+	Core histone macro-H2A.1
P09234	NA	-	+	Coiled-coil-helix-coiled-coil-helix domain-containing protein 2
P08253	NA	-	+	60S ribosomal protein L38
P04632	NA	-	+	Protein NipSnap homolog 3A
Q03518	NA	-	+	DNA-(apurinic or apyrimidinic site) lyase
Q8NFQ8	NA	-	+	Nucleobindin-1
P07305	NA	-	+	Splicing factor
Q15029	NA	-	+	Sulfatase-modifying factor 2
O75643	NA	-	+	C-1-tetrahydrofolate synthase
Q9Y276	NA	-	+	5'-nucleotidase domain-containing protein 2
Q9BYD6	NA	-	+	Gap junction alpha-1 protein
Q8IWU6	NA	-	+	Laminin subunit beta-2
Q9UBQ7	NA	-	+	Alpha-2-macroglobulin receptor-associated protein
P61221	NA	-	+	Lamin-B2
P63027	NA	-	+	Periostin
Q9Y4P3	NA	-	+	Phosphatidylethanolamine-binding protein 1
P30419	NA	-	+	14-3-3 protein zeta/delta
P50991	NA	-	+	14-3-3 protein epsilon
O94901	NA	-	+	Metallothionein-1E
Q9H7Z7	NA	-	+	Procollagen C-endopeptidase enhancer 1
P22087	NA	-	+	Collagen alpha-1(XII) chain
P28288	NA	-	+	4-trimethylaminobutyraldehyde dehydrogenase
Q13505	NA	-	+	Collagen alpha-1(VIII) chain
Q9Y3E5	NA	-	+	Transmembrane 9 superfamily member 2
P27449	NA	-	+	Guanine nucleotide-binding protein subunit alpha-11

Q13510	NA	-	+	Short/branched chain specific acyl-CoA dehydrogenase
P62318	NA	-	+	Histone H2A type 1-B/E
O00115	NA	-	+	Calcium-binding mitochondrial carrier protein Aralar1
P33527	NA	-	+	Sorting and assembly machinery component 50 homolog
Q8NE86	NA	-	+	Dynactin subunit 2
O60832	NA	-	+	Protein transport protein Sec61 subunit alpha isoform 1
Q15582	NA	-	+	28S ribosomal protein S22
Q13740	NA	-	+	Inorganic pyrophosphatase 2
Q9NVP1	NA	-	+	15 kDa selenoprotein
P22392	NA	-	+	Fermitin family homolog 2
P43243	NA	-	+	Peroxisomal 3
P38919	NA	-	+	Transmembrane protein 43
Q04941	NA	-	+	Transformer-2 protein homolog beta
P05386	NA	-	+	Cytochrome c
Q8NHP8	NA	-	+	40S ribosomal protein S11
Q8TAQ2	NA	-	+	Valacyclovir hydrolase
O15145	NA	-	+	Protein LYRIC
Q86TX2	NA	-	+	Torsin-1A-interacting protein 1
Q16629	NA	-	+	Alpha-centractin
P35637	NA	-	+	Tropomodulin-3
Q9NX47	NA	-	+	Cartilage-associated protein
Q9NP72	NA	-	+	Tenascin
Q9NZN4	NA	-	+	Methylcrotonoyl-CoA carboxylase beta chain
P51648	NA	-	+	Lysophospholipid acyltransferase 7
O15143	NA	-	+	DNA-dependent protein kinase catalytic subunit
Q92820	NA	-	+	Basigin
Q9Y6A9	NA	-	+	CD81 antigen
P29590	NA	-	+	SPARC
Q6P2Q9	NA	-	+	Prolyl 3-hydroxylase 3
Q13641	NA	-	+	60S ribosomal protein L21
Q2TB90	NA	-	+	Extended synaptotagmin-1
Q14789	NA	-	+	Protein-lysine 6-oxidase
P15586	NA	-	+	Tetratricopeptide repeat protein 35
O75694	NA	-	+	Myosin light chain 1/3
Q56VL3	NA	-	+	Vesicle-associated membrane protein-associated protein A
P61006	NA	-	+	GPI transamidase component PIG-S
P49207	NA	-	+	Glutaredoxin-related protein 5
P14678	NA	-	+	40S ribosomal protein S15
Q96IX5	NA	-	+	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit
O75380	NA	-	+	Splicing factor
Q969S9	NA	-	+	Nucleolar protein 58
P52926	NA	-	+	3-ketoacyl-CoA thiolase
Q9H2W6	NA	-	+	KDEL motif-containing protein 2
Q08170	NA	-	+	Heat shock-related 70 kDa protein 2
O14763	NA	-	+	Dynamin-like 120 kDa protein
Q15067	NA	-	+	3-hydroxyisobutyrate dehydrogenase
Q2M389	NA	-	+	Myosin regulatory light polypeptide 9
Q3ZCQ8	NA	-	+	PRA1 family protein 3

Q9BRR6	NA	-	+	2-oxoisovalerate dehydrogenase subunit alpha
P78357	NA	-	+	Eukaryotic initiation factor 4A-I
P19404	NA	-	+	Transmembrane protein 126A
P35659	NA	-	+	Protein-glutamine gamma-glutamyltransferase 2
P16278	NA	-	+	Laminin subunit gamma-1
Q9P0K7	NA	-	+	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2
P18754	NA	-	+	Eukaryotic translation initiation factor 5A-1
P62273	NA	-	+	Glutathione S-transferase P
Q14728	NA	-	+	Deoxyuridine 5'-triphosphate nucleotidohydrolase
O75251	NA	-	+	Reticulocalbin-2
Q9H3N1	NA	-	+	NADPH:adrenodoxin oxidoreductase
P06703	NA	-	+	ATP-dependent RNA helicase A
O96005	NA	-	+	7-dehydrocholesterol reductase
P28838	NA	-	+	Collagen alpha-1(V) chain
P83881	NA	-	+	Polypyrimidine tract-binding protein 1
O43143	NA	-	+	Putative nucleoside diphosphate kinase
O00400	NA	-	+	NAD-dependent malic enzyme
Q8TED1	NA	-	+	Hypoxia up-regulated protein 1
Q9H583	NA	-	+	X-ray repair cross-complementing protein 5
Q16695	NA	-	+	CD109 antigen
Q96DB5	NA	-	+	Barrier-to-autointegration factor
Q9NW15	NA	-	+	60S ribosomal protein L10
P01023	NA	-	+	40S ribosomal protein S27a
Q92544	NA	-	+	Protein ERGIC-53
Q9BQG0	NA	-	+	Transmembrane glycoprotein NMB
P48449	NA	-	+	Fructose-bisphosphate aldolase C
P06865	NA	-	+	45 kDa calcium-binding protein
O14561	NA	-	+	Isochorismatase domain-containing protein 2
Q15041	NA	-	+	Aconitate hydratase
Q92621	NA	-	+	Myosin-10

Table 6 - Proteins that were prevalent only on the conditioned ghosts and CDLs

Uniport Accession Number	MW	Ratio of expression: conditioned CDLs / conditioned ghost	Protein name
Q15717	NA	100%	Endoplasmic reticulum lectin 1
P14136	NA	100%	Signal recognition particle receptor subunit alpha
Q32P51	NA	17%	Long-chain-fatty-acid--CoA ligase 3
Q9NVA2	NA	16%	Cation-independent mannose-6-phosphate receptor
O75131	NA	11%	Granulins
Q96DZ1	NA	10%	Heterogeneous nuclear ribonucleoprotein K
P01889	NA	9%	DnaJ homolog subfamily C member 10
Q16270	NA	9%	Copine-3
P61978	NA	7%	Flotillin-1
P21912	NA	6%	Metalloproteinase inhibitor 3
P28799	NA	6%	Glial fibrillary acidic protein
Q8IXB1	NA	6%	Translational activator GCN1
Q5KU26	NA	5%	Heterogeneous nuclear ribonucleoprotein A1-like 2
O75955	NA	4%	Protein FAM98A

P35625	NA	4%	Septin-11
Q92616	NA	4%	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit
O95573	NA	3%	Collectin-12
Q8NCA5	NA	3%	Insulin-like growth factor-binding protein 7
P11717	NA	2%	HLA class I histocompatibility antigen

Table 7 - Proteins that were prevalent in ghosts, conditioned ghosts and conditioned CDLs but were missing from unconditioned CDLs.

Uniport Accession Number	MW	Ratio of expression		Protein name
		Cond Ghosts / Ghosts	Cond. CDLs / Cond. Ghosts	
Q53EP0	132803.2	302%	2%	Calumenin
P52272	77464.3	262%	2%	Nucleophosmin
P12956	69799.2	248%	1%	Cytochrome c oxidase subunit 2
O60716	108103.3	220%	4%	Glutaminase kidney isoform
P05121	45031.1	218%	5%	Integrin beta-5
P18621	21383.3	218%	13%	Plasma membrane calcium-transporting ATPase 1
Q9H845	68716.8	209%	7%	Nucleolin
Q14103	38410.3	198%	0%	60S acidic ribosomal protein P0
P61916	16559.5	195%	2%	Atlastin-3
Q02978	34039.9	193%	3%	NADH dehydrogenase [ubiquinone] iron-sulfur protein 8
Q969X5	32571.5	186%	8%	Neutral alpha-glucosidase AB
P07858	37796.8	179%	2%	Cytochrome c oxidase subunit 4 isoform 1
O95831	66859	176%	4%	Complement component 1 Q subcomponent-binding protein
P51148	23467.8	161%	6%	3-hydroxyacyl-CoA dehydrogenase type-2
Q9H0U4	22157.2	161%	1%	AP-2 complex subunit alpha-1
O75390	51679.6	157%	3%	Adenylyl cyclase-associated protein 1
Q8TCJ2	93613.8	155%	1%	Collagen alpha-1(III) chain
P21964	30017.6	148%	0%	Mitochondrial carrier homolog 2
O43852	37083.6	143%	2%	Fibronectin type III domain-containing protein 3B
O95782	107477.9	142%	5%	Ras-related protein Rab-1B
P50416	88310.8	142%	2%	Alpha-actinin-1
Q9NYU2	177077.4	140%	1%	Hydroxymethylglutaryl-CoA lyase
P46977	80476.9	138%	3%	40S ribosomal protein S12
P49821	50784.9	137%	5%	Actin-related protein 3
Q12797	85809.5	135%	5%	40S ribosomal protein S20
P46940	189132.9	133%	1%	Thy-1 membrane glycoprotein
Q9ULV4	53215.1	131%	3%	Coronin-1C
O00159	121648.1	129%	4%	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10
P07996	129299.2	129%	2%	Mitochondrial-processing peptidase subunit beta
O14773	61209.7	129%	6%	Mesencephalic astrocyte-derived neurotrophic factor
P10620	17587.2	128%	3%	60S ribosomal protein L8
Q9NSE4	113719.1	121%	4%	Peptidyl-prolyl cis-trans isomerase A
O00469	84631.8	120%	2%	39S ribosomal protein L49
P20340	23577.9	100%	100%	60S ribosomal protein L3
P80723	22680	100%	33%	Endoplasmic reticulum resident protein 44
Q96AQ6	80594.2	100%	27%	40S ribosomal protein S7

P08962	25619.1	100%	25%	Prolyl 4-hydroxylase subunit alpha-2
P50281	65842	100%	25%	Transmembrane emp24 domain-containing protein 4
P62988	8559.6	100%	23%	Electron transfer flavoprotein subunit alpha
P21291	20553.8	100%	21%	Protein S100-A10
P62879	37307.1	100%	21%	40S ribosomal protein S23
Q92499	82379.9	100%	15%	Myosin-11
P05388	34251.8	100%	14%	Heterogeneous nuclear ribonucleoprotein D0
O96000	20763.2	100%	12%	Catenin beta-1
P23528	18490.7	100%	12%	Seprase
P15313	56797	100%	12%	Translocation protein SEC62
Q9UBS4	40488.7	100%	12%	Mitochondrial 2-oxoglutarate/malate carrier protein
P62917	28007.3	100%	12%	Microsomal glutathione S-transferase 1
P00403	25548.2	100%	12%	X-ray repair cross-complementing protein 6
P17813	70533.2	100%	11%	Talin-1
P61353	15787.8	100%	11%	Mannosyl-oligosaccharide glucosidase
Q00341	141368	100%	11%	Neutral cholesterol ester hydrolase 1
P0C7P4	30796.1	100%	11%	Probable ATP-dependent RNA helicase DDX17
P49368	60495.4	100%	11%	Cytochrome b-c1 complex subunit 7
Q9NQC3	129851.2	100%	10%	40S ribosomal protein S15a
Q9NX63	26136.2	100%	10%	Interleukin enhancer-binding factor 3
P84098	23451.3	100%	10%	Protein ETHE1
Q12906	95279.2	100%	10%	Coiled-coil-helix-coiled-coil-helix domain-containing protein 3
P11166	54048.7	100%	9%	Estradiol 17-beta-dehydrogenase 12
P06748	32554.9	100%	9%	Heterogeneous nuclear ribonucleoprotein M
Q99584	11464.1	100%	9%	Mitochondrial import receptor subunit TOM40 homolog
P14927	13522	100%	8%	T-complex protein 1 subunit gamma
Q9UBI6	8001.2	100%	8%	Pyruvate dehydrogenase E1 component subunit alpha
P83731	17767.9	100%	8%	Protein canopy homolog 2
Q02218	115861.5	100%	8%	Spectrin alpha chain
P61026	22526.6	100%	7%	Filamin-A
O95299	40725	100%	7%	Myosin-Ic
P22626	37406.7	100%	7%	Ras-related protein Rap-1A
Q9UBG0	166548.2	100%	7%	Succinyl-CoA ligase [GDP-forming] subunit beta
P07099	52915	100%	7%	RNA-binding protein Raly
O95182	12543.6	100%	7%	Collagen alpha-2(VI) chain
P04216	17923.4	100%	7%	Ras GTPase-activating-like protein IQGAP1
P62266	15797.7	100%	7%	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2
P35221	100008.6	100%	7%	V-type proton ATPase subunit B
Q13405	19186	100%	7%	Procollagen-lysine
P18859	12579.6	100%	7%	60S ribosomal protein L32
P25398	14505.5	100%	7%	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A
O00571	73198.1	100%	7%	Alpha-soluble NSF attachment protein
P00367	61359.3	100%	7%	ATPase family AAA domain-containing protein 3A
P62081	22113.3	100%	6%	Pre-B-cell leukemia transcription factor-interacting protein 1
Q15293	38866.2	100%	6%	Delta-1-pyrroline-5-carboxylate synthase
P21333	280561.4	100%	6%	Ras-related protein Rab-10

P54920	33211.3	100%	6%	ATP-dependent RNA helicase DDX3X
P62249	16435	100%	6%	DnaJ homolog subfamily B member 11
P62834	20973.7	100%	6%	Heterogeneous nuclear ribonucleoproteins A2/B1
O00264	21657.8	100%	6%	Thioredoxin domain-containing protein 5
Q16718	13450.2	100%	6%	Calmodulin
Q9Y3B3	25155.6	100%	6%	40S ribosomal protein S27-like
Q01518	51822.8	100%	6%	Citrate synthase
P35222	85442.3	100%	6%	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10
Q9UKM9	32443.6	100%	6%	Epoxide hydrolase 1
P51991	39570.5	100%	6%	60S ribosomal protein L36
P04899	40425.1	100%	6%	UPF0027 protein C22orf28
P62244	14830	100%	6%	Reticulon-4
P32322	33339.6	100%	5%	Sarcoplasmic/endoplasmic reticulum calcium ATPase 1
P52815	21334.7	100%	5%	Peptidyl-prolyl cis-trans isomerase FKBP11
Q15019	41461.3	100%	5%	Histone H2A type 1-A
Q13011	35793.4	100%	5%	Gelsolin
P00558	44586.2	100%	5%	ATP synthase subunit g
O75439	54331.6	100%	5%	Thrombospondin-1
P43304	80801.7	100%	5%	Histone H1.5
P18084	87996.2	100%	5%	Plasminogen activator inhibitor 1
Q7Z7H5	25926.4	100%	5%	Matrix metalloproteinase-14
Q14554	59556.2	100%	5%	Peptidyl-prolyl cis-trans isomerase FKBP10
O60506	69559.6	100%	5%	Enoyl-CoA hydratase
Q9Y3U8	12245.9	100%	5%	Heterogeneous nuclear ribonucleoprotein A3
P62820	22663.4	100%	5%	Fumarate hydratase
Q13813	284362.5	100%	5%	2-oxoglutarate dehydrogenase
Q6P587	24826.7	100%	5%	Interleukin enhancer-binding factor 2
O75964	11421.2	100%	5%	Phosphoglycerate kinase 1
Q9Y2B0	20639.2	100%	4%	60S ribosomal protein L24
Q12931	80059.8	100%	4%	Myeloid-associated differentiation marker
P51572	27974	100%	4%	Alpha-actinin-4
Q5JRX3	117380.3	100%	4%	Ornithine aminotransferase
P36776	106422.5	100%	4%	UPF0556 protein C19orf10
O95571	27855.1	100%	4%	60S ribosomal protein L19
P61158	47341	100%	4%	NADH dehydrogenase [ubiquinone] flavoprotein 1
Q9BS26	46941.5	100%	4%	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7
P10515	68953.3	100%	4%	40S ribosomal protein S2
Q71UM5	9470.9	100%	4%	Transmembrane emp24 domain-containing protein 7
Q12905	43035.2	100%	4%	Fumarylacetoacetate hydrolase domain-containing protein 1
P54886	87247.7	100%	4%	Reticulocalbin-1
P13073	19564.1	100%	4%	Cathepsin B
P15880	31304.6	100%	4%	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex
P60866	13364.3	100%	4%	Aspartyl/asparaginyl beta-hydroxylase
Q96I99	46481.5	100%	3%	Catechol O-methyltransferase
O96008	37869.2	100%	3%	Protein S100-A13
P61313	24131.1	100%	3%	Alpha-aminoadipic semialdehyde dehydrogenase

Q6PIU2	45778.8	100%	3%	Vigilin
Q8NBS9	47598.7	100%	3%	Membrane-associated progesterone receptor component 1
Q14165	32213.6	100%	3%	Galectin-1
P04181	48504.3	100%	3%	Presequence protease
Q9NVI7	71324.8	100%	3%	Glutamate dehydrogenase 1
Q92896	134463.3	100%	3%	Pyruvate dehydrogenase E1 component subunit beta
Q99653	22442.4	100%	3%	Profilin-1
P54709	31492.1	100%	3%	Serine beta-lactamase-like protein LACTB
Q92520	24664.6	100%	3%	40S ribosomal protein S17
P53597	36226.9	100%	3%	3-ketoacyl-CoA thiolase
P15311	69369.8	100%	3%	Myosin light polypeptide 6
P13804	35057.6	100%	3%	Ubiquitin
O00217	23689.6	100%	3%	40S ribosomal protein S16
Q9UIJ7	25549.6	100%	3%	Microsomal glutathione S-transferase 3
P62158	16826.8	100%	3%	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5
Q969H8	18783.3	100%	3%	Lon protease homolog
P83111	60655.1	100%	3%	Sodium/potassium-transporting ATPase subunit beta-3
Q12884	87656.8	100%	3%	Cofilin-1
P07954	54602.2	100%	3%	Ras-related protein Rab-1A
Q14697	106806.8	100%	3%	Endoplasmic reticulum-Golgi intermediate compartment protein 1
O14983	110181.8	100%	2%	Pyrroline-5-carboxylate reductase 1
Q99714	26906.1	100%	2%	Ras-related protein Rab-5C
P20020	138667.9	100%	2%	60S ribosomal protein L17
P62910	15849.8	100%	2%	ATP synthase-coupling factor 6
P39023	46079.8	100%	2%	Ras-related protein Rab-6A
Q9NYL4	22166.3	100%	2%	39S ribosomal protein L12
O14880	16505.6	100%	2%	GTP:AMP phosphotransferase mitochondrial
Q92841	72326	100%	2%	Putative cytochrome b-c1 complex subunit Rieske-like protein 1
Q96QV6	14224.9	100%	2%	Septin-2
Q9Y224	28050.7	100%	2%	Catenin alpha-1
P55809	56122	100%	2%	Transmembrane emp24 domain-containing protein 2
Q13724	91860.9	100%	1%	60S ribosomal protein L27
Q6DD88	60503.5	100%	1%	Epididymal secretory protein E1
Q96AY3	64204.3	100%	1%	Protein disulfide-isomerase A5
Q9Y6C9	33308.9	100%	1%	C-type mannose receptor 2
O15460	60863.7	100%	1%	CD63 antigen
Q53GQ0	34302.2	100%	1%	Solute carrier family 2
Q07021	31342.6	100%	1%	Apoptosis-inducing factor 1
P60660	16919.1	100%	0%	Ezrin
P35749	227197.9	100%	0%	ATP-dependent RNA helicase DDX1
P08559	43267.7	100%	0%	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-12
O15260	30373.8	100%	0%	Tropomyosin alpha-1 chain
P16401	22566.5	100%	0%	Glycerol-3-phosphate dehydrogenase
P11177	39208.1	82%	4%	Golgi apparatus protein 1
P12110	108511.9	81%	3%	Brain acid soluble protein 1
P42765	41897.7	79%	2%	Succinyl-CoA ligase [GDP-forming] subunit alpha

O94925	73414	76%	3%	Catenin delta-1
Q9Y3I0	55175	72%	8%	Guanine nucleotide-binding protein G(i) subunit alpha-2
P55145	20243.6	71%	2%	Tripeptidyl-peptidase 1
O43707	104788.5	71%	4%	B-cell receptor-associated protein 31
P12814	102992.7	70%	4%	Carnitine O-palmitoyltransferase 1
P49419	58450.2	66%	3%	60S ribosomal protein L15
P09493	32688.7	66%	27%	Surfeit locus protein 4
P35914	34337.8	62%	8%	UDP-glucose:glycoprotein glucosyltransferase 1
P37802	22377.2	61%	4%	60S ribosomal protein L23a
P07737	15044.6	57%	7%	Calcium-binding protein p22
P08708	15540.4	57%	5%	Protein FAM3C
P30084	31367.1	57%	3%	Heterogeneous nuclear ribonucleoprotein Q
P62937	18000.9	54%	9%	Isoleucyl-tRNA synthetase
P19338	76568.5	50%	42%	Acyl-CoA dehydrogenase family member 9
P09382	14706.2	45%	28%	Malectin
P06396	85644.3	36%	2%	Delta(3
P02461	138479.2	35%	6%	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B
Q9Y490	269596.3	34%	5%	Endoglin
P62750	17684.1	24%	31%	Transgelin-2

Although the invention has been described in conjunction with specific embodiments thereof, it is evident that many alternatives, modifications and variations will be apparent to those skilled in the art. Accordingly, it is intended to embrace all such alternatives, modifications and variations that fall within the spirit and broad scope of the appended claims.

All publications, patents and patent applications mentioned in this specification are herein incorporated in their entirety by reference into the specification, to the same extent as if each individual publication, patent or patent application was specifically and individually indicated to be incorporated herein by reference. In addition, citation or identification of any reference in this application shall not be construed as an admission that such reference is available as prior art to the present invention. To the extent that section headings are used, they should not be construed as necessarily limiting.

Reference (other references are cited throughout the application)

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WHAT IS CLAIMED IS:

1. A composition-of matter comprising a liposome attached to, or encapsulating a pharmaceutical agent, said liposome being composed of a whole cell membrane fraction.

2. The composition-of-matter of claim 1, wherein said cell is a human cell.

3. The composition-of-matter of claim 1, wherein a cell source for said whole cell membrane is selected from the group consisting of a stem cell, a primary cell, a cell-line, a non-tumorigenic cell, a cancer cell and an immune cell.

4. A composition-of matter comprising a liposome composed of a whole cell membrane fraction of a stem cell.

5. The composition-of-matter of claim 4, wherein said stem cell comprises a human mesenchymal stem cell.

6. A composition-of matter comprising a liposome composed of a whole cell membrane fraction of a primary human cell.

7. A composition-of matter comprising a liposome composed of a whole cell membrane fraction of a non-tumorigenic human cell.

8. The composition-of matter of claim 1-6, wherein said cell membrane is genetically modified to express an exogenous protein.

9. The composition-of matter of claim 8, wherein said exogenous protein is selected from the group consisting of a cell marker, a targeting moiety and said pharmaceutical agent.

10. The composition-of-matter of claim 4-8, wherein said liposome encapsulates, or attached to a pharmaceutical agent.

11. The composition-of-matter of claim 1, wherein said pharmaceutical agent is a therapeutic agent.

12. The composition-of-matter of claim 11, being non-immunogenic in a human subject.

13. The composition-of-matter of claim 1-12, wherein a cell source of said whole cell membrane fraction comprises cells autologous to a host subject.

14. The composition-of-matter of claim 1-12, wherein a cell source of said whole cell membrane fraction comprises cells non-autologous to a host subject.

15. The composition-of-matter of claim 11, wherein said pharmaceutical agent is a diagnostic agent.

16. The composition-of-matter of claim 1-11, wherein said liposome is unilamellar.

17. The composition-of-matter of claim 1-16, wherein said liposome is attached to a synthetic polymer at an external surface thereof.

18. The composition-of-matter of claim 1-17, wherein said synthetic polymer is a poly-ethylene-glycol (PEG).

19. The composition-of-matter of claims 1-18, wherein said liposome has a size range of 30-1000 nm.

20. The composition-of-matter of claims 1-19, wherein said liposome is further composed of synthetic lipids.

21. A method of producing liposomes comprising,

(a) subjecting cells to hypotonic conditions, so as to obtain ruptured cell membranes and/or ghosts; and

(b) homogenizing said ruptured cell membranes and/or ghosts to thereby produce liposomes.

22. The method of claim 21, wherein said homogenizing is effected by:

(c) sonicating said ruptured cell membrane and/or ghosts; and optionally

(d) extruding said ruptured membrane and/or ghosts through a matrix of pre-determined porosity.

23. The method of claim 21 further comprising conjugating a synthetic polymer to said liposomes following step (c).

24. A method of encapsulating a pharmaceutical agent in a liposome, the method comprising making the liposomes according to the method of claim 21 and adding the pharmaceutical agent prior to the step of homogenizing.

25. A pharmaceutical composition comprising as an active ingredient the composition-of-matter of claim 1 and a pharmaceutically acceptable carrier.

26. A method of delivering a pharmaceutical agent, the method comprising administering to a subject in need thereof the composition of matter of claim 1, thereby delivering the pharmaceutical agent.

27. The method of claim 26, wherein a cell source of said whole cell membrane fraction is autologous to said subject.

28. The method of claim 26, wherein a cell source of said whole cell membrane fraction is non-autologous to said subject.

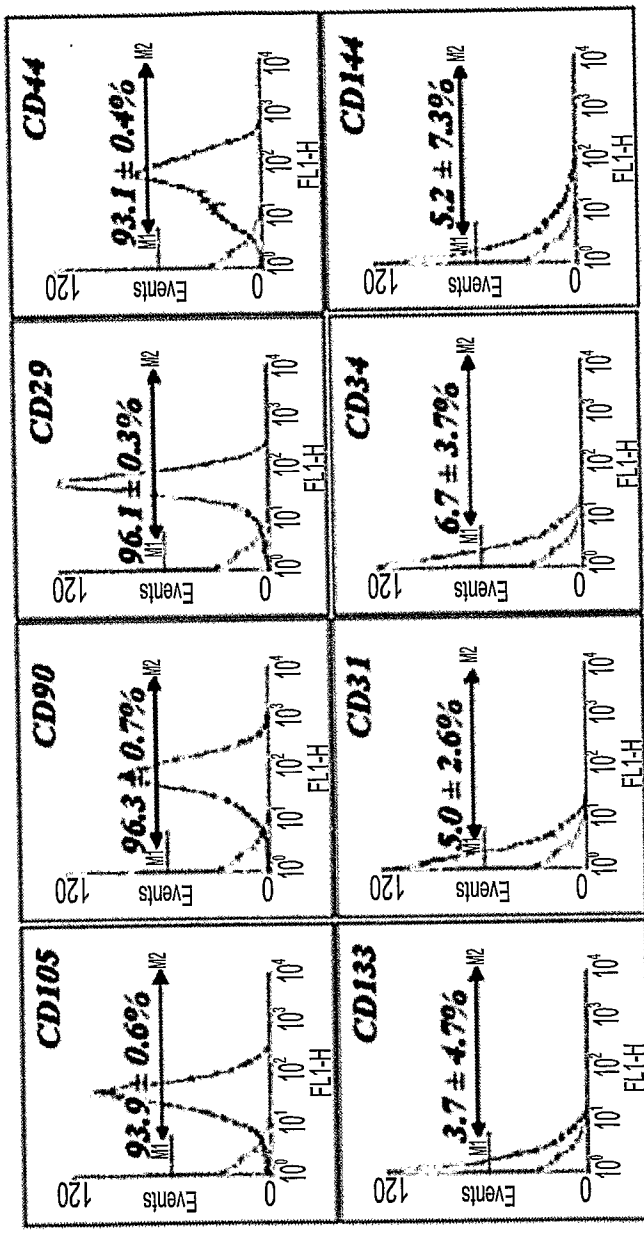


FIG. 1C

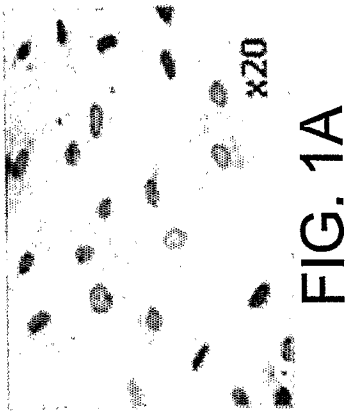


FIG. 1A

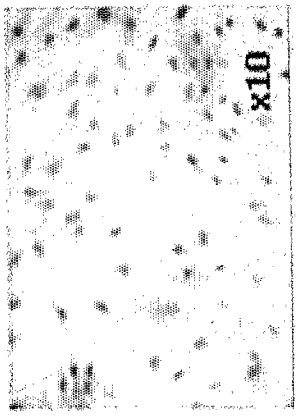


FIG. 1B

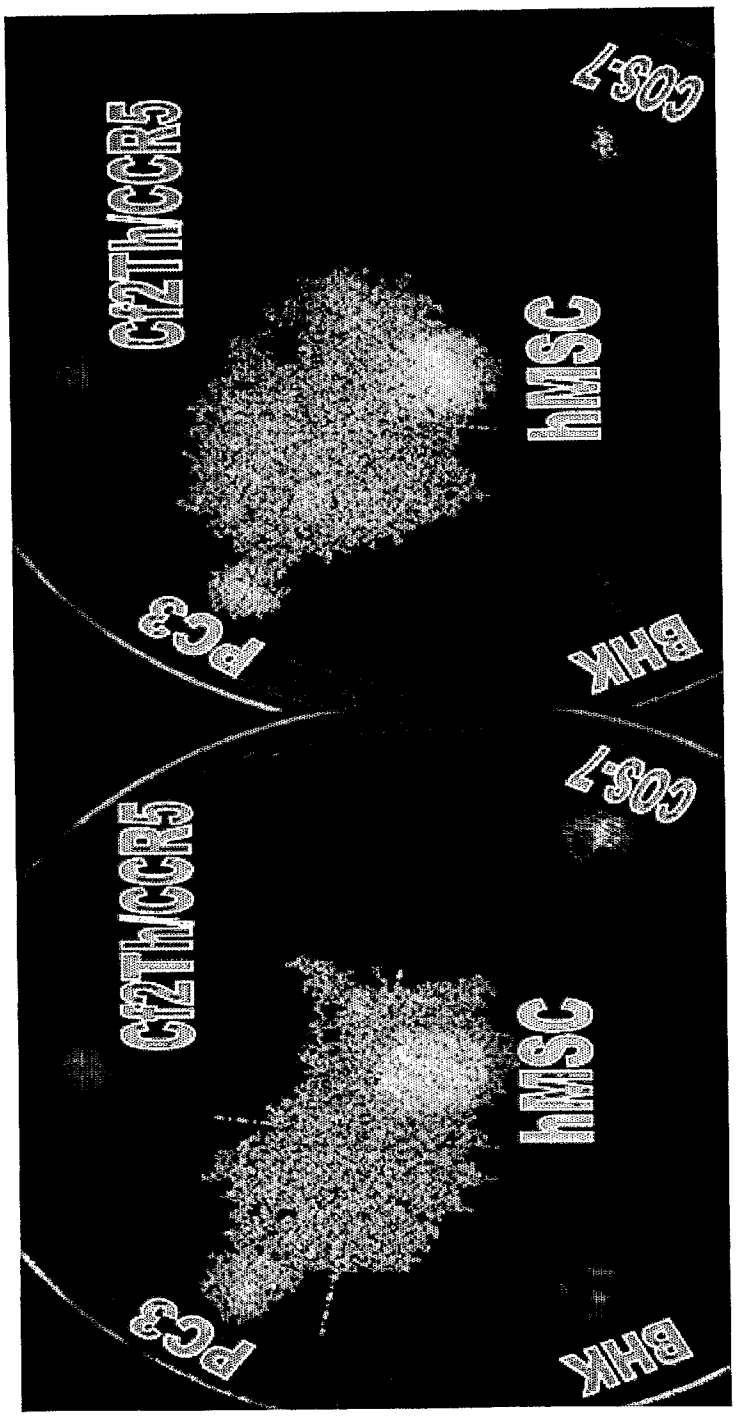


FIG. 2

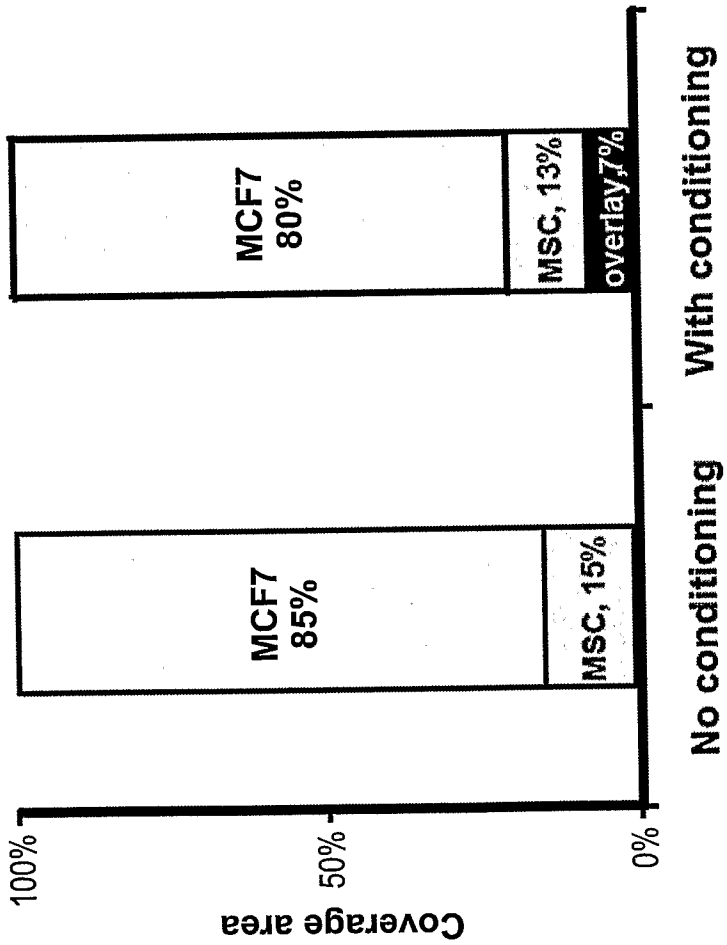

Coverage area
100%
50%
0%
No conditioning
With conditioning
MCF7
85%
MSC, 15%
MCF7
80%
MSC, 13%
overlay,7%

FIG. 3

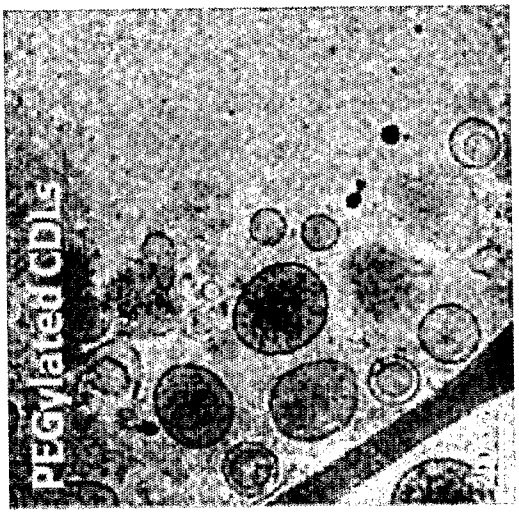

PEGylated CDLs

FIG. 4A

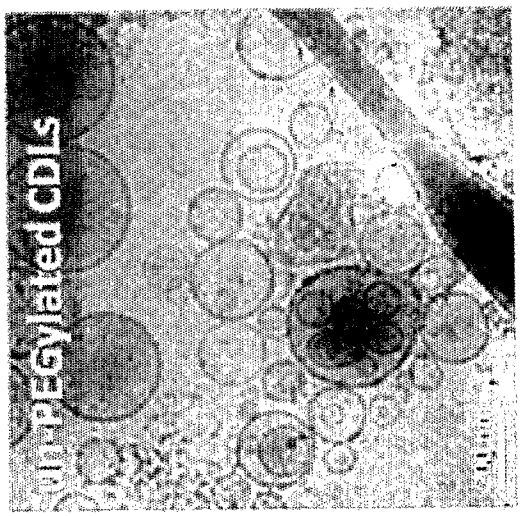
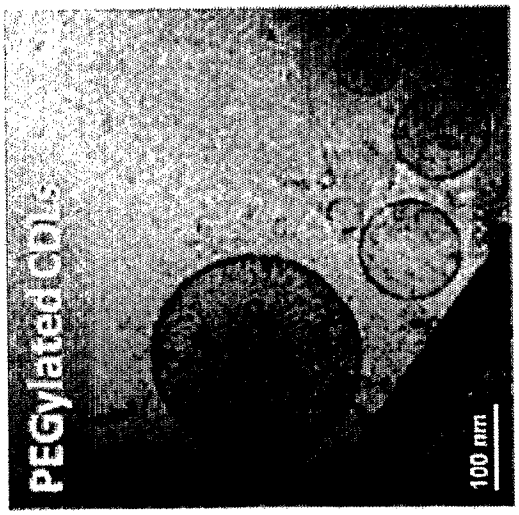
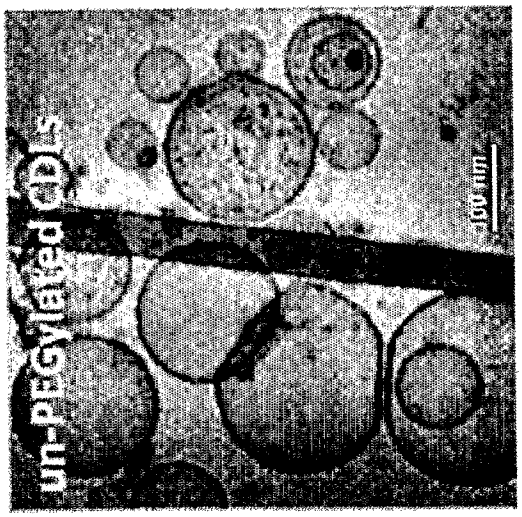

un-PEGylated CDLs

FIG. 4B


PEGylated CDLs
100 nm


un-PEGylated CDLs
100 nm

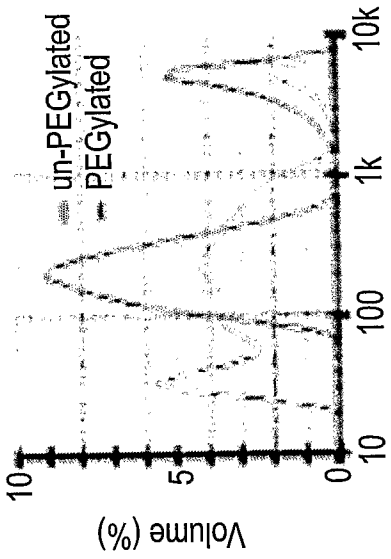


FIG. 5B

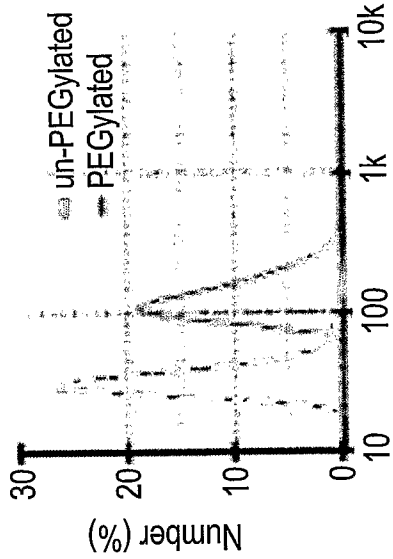


FIG. 5A

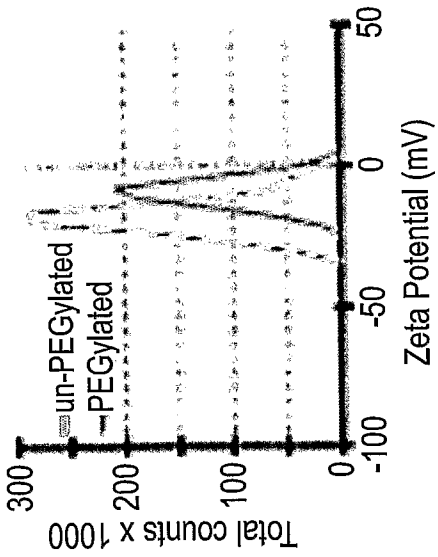


FIG. 5C

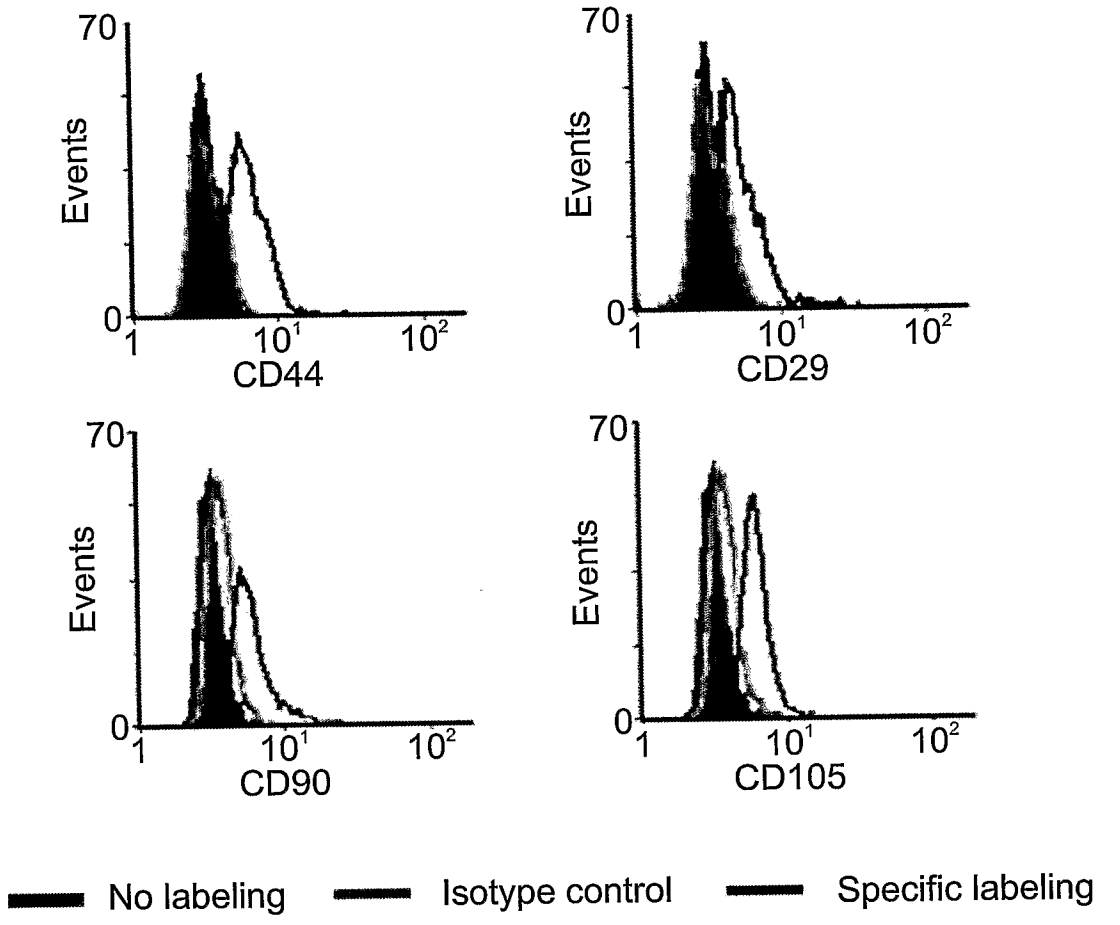


FIG. 6

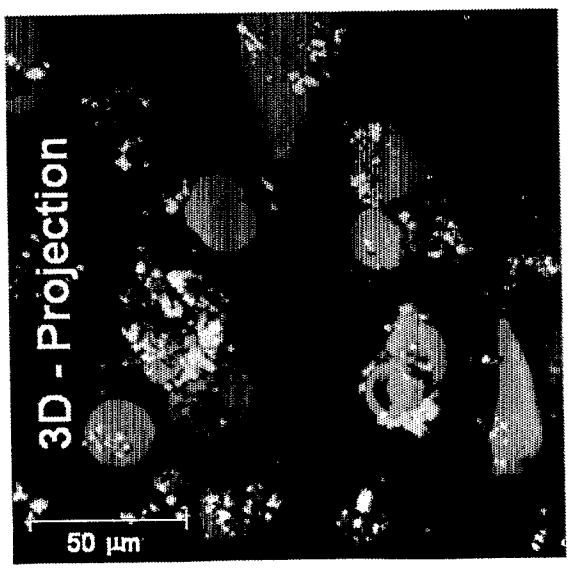


FIG. 7A

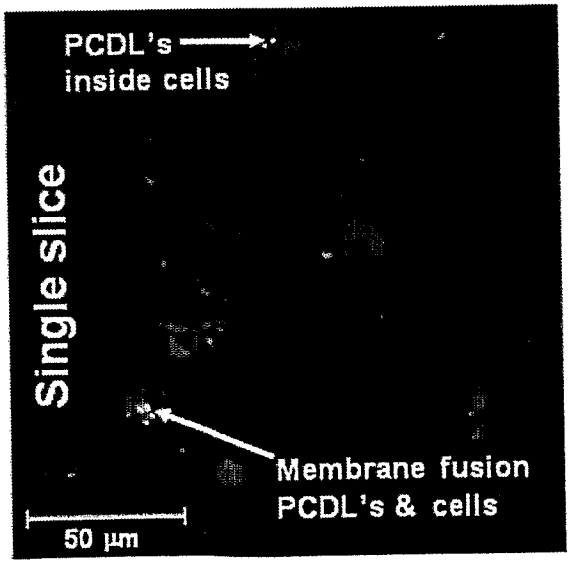


FIG. 7B

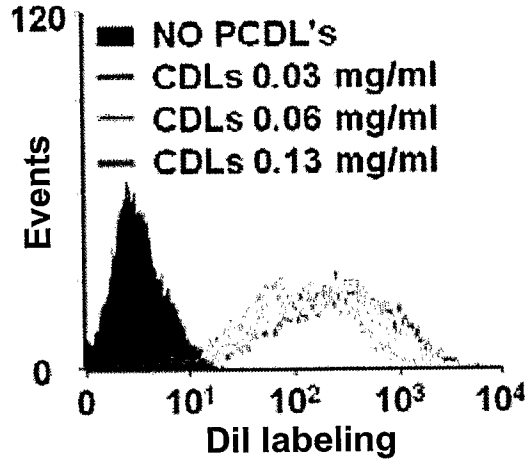


FIG. 8A

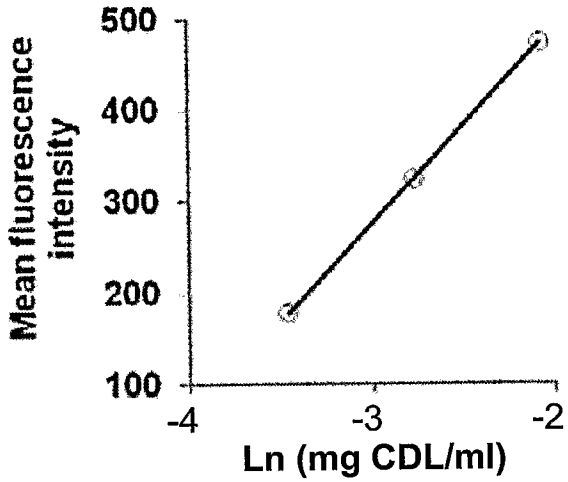


FIG. 8B

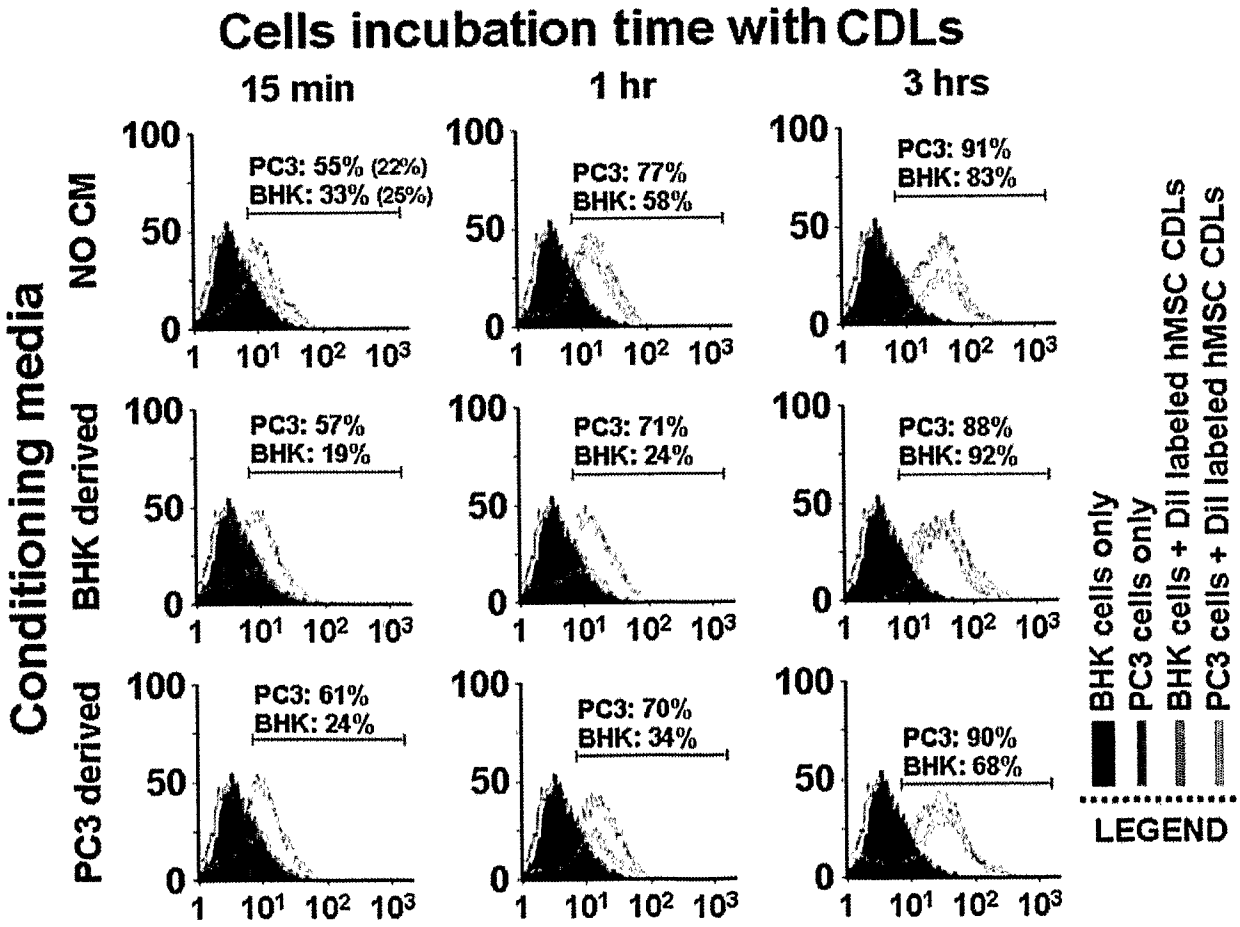


FIG. 9

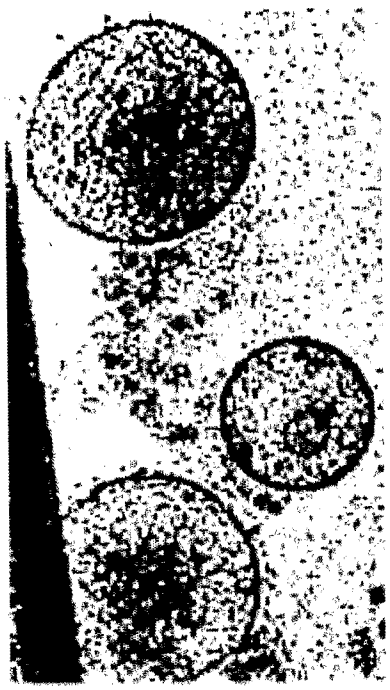


FIG. 10A

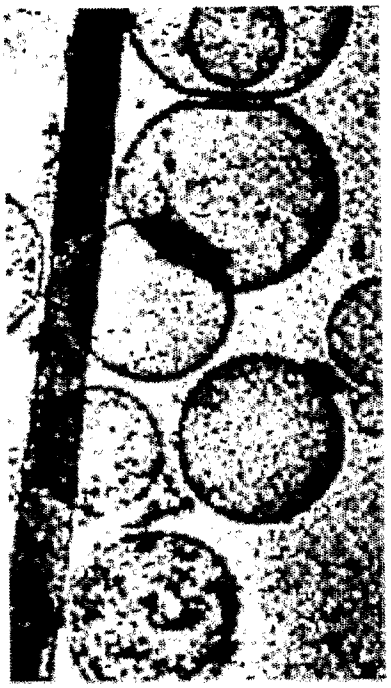
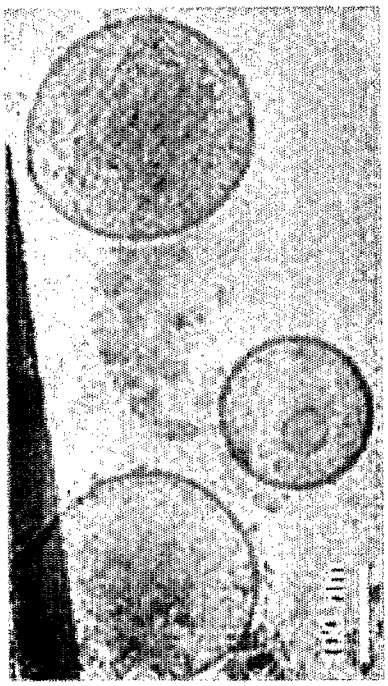
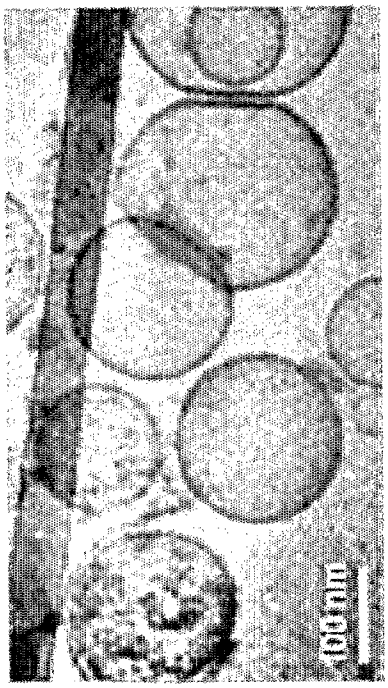


FIG. 10B





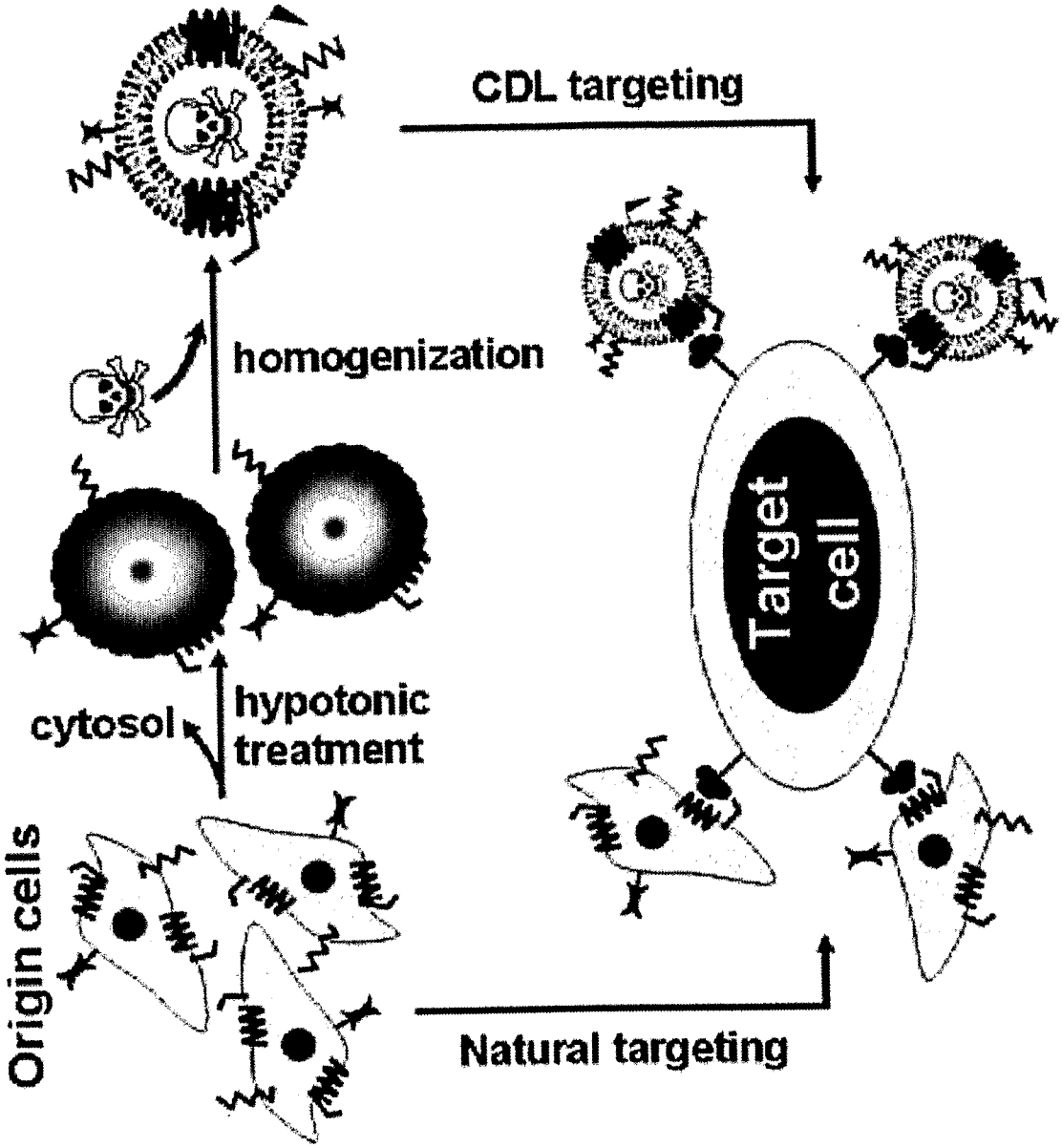

CDL targeting
homogenization
Target cell
cytosol
hypotonic treatment
Origin cells
Natural targeting

FIG. 11