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(54) Title: 18892, A NOVEL HUMAN LIPASE

(57) **Abstract:** The present invention relates to a newly identified human lipase belonging to the family of mammalian lipases. The invention also relates to polynucleotides encoding the lipase. The invention further relates to methods using the lipase polypeptides and polynucleotides as a target for diagnosis and treatment in lipase-mediated or -related disorders. The invention further relates to drug-screening methods using the lipase polypeptides and polynucleotides to identify agonists and antagonists for diagnosis and treatment. The invention further encompasses agonists and antagonists based on the lipase polypeptides and polynucleotides. The invention further relates to procedures for producing the lipase polypeptides and polynucleotides.



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18892, A NOVEL HUMAN LIPASE

FIELD OF THE INVENTION

The present invention relates to a newly identified human lipase. The invention also relates to polynucleotides encoding the human lipase. The invention further relates to methods using the lipase polypeptides and polynucleotides as a target for diagnosis and treatment in lipase-mediated or -related disorders. The invention further relates to drug-screening methods using the lipase polypeptides and polynucleotides to identify agonists and antagonists for diagnosis and treatment. The invention further encompasses agonists and antagonists based on the lipase polypeptides and polynucleotides. The invention further relates to procedures for producing the lipase polypeptides and polynucleotides.

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BACKGROUND OF THE INVENTION

Lipases are indispensable for the bioconversion of lipids within an organism through the catalysis of a variety of reactions that include hydrolysis, alcoholysis, acidolysis, esterification and aminolysis. In humans, several lipases have been identified which possess lipolytic activities that regulate levels of triglycerides and cholesterol in the body. Enzymes from this superfamily, include lipoprotein lipase (LPL), hepatic lipase (HL), and pancreatic lipase (PL). While all three enzymes hydrolyze lipid emulsions and have similar aqueous-lipid interfacial catalytic activities, they each possess unique properties and physiological functions. All three enzymes act preferentially on the sn-1 and sn-3 bonds of triglycerides, to release fatty acids from the glycerol backbone (Dolphin *et al.* (1992) *Structure and Function of Apolipoproteins*, Rosseneu, M. (ed) CRC Press, Inc, Boca Ratan, 295-362). However, while PL completes the hydrolysis of alimentary triglycerides, the LPL and HL enzymes hydrolyze triglycerides found in circulating lipoproteins.

Due to the insolubility of lipids in water, the plasma transports complex lipids among various tissues as components of lipoproteins. Each lipoprotein contains a neutral lipid core composed of triacylglycerol and/or a cholesterol ester. Surrounding the core is a layer of proteins, phospholipids, and cholesterol. The proteins associated

with the lipoprotein comprise a class of proteins referred to as apoproteins (apo). Based on apoprotein composition and density, lipoproteins have been classified into five major types that include chylomicrons, high-density lipoproteins (HDL), intermediate-density lipoproteins (IDL), low-density lipoproteins (LDL), and very-low density lipoproteins (VLDL).

Lipoprotein lipase (LPL) is the major enzyme responsible for the hydrolysis of triglyceride molecules present in circulating lipoproteins. LPL is associated with the luminal side of capillaries and arteries through an interaction with heparin-sulfate chains of proteoglycans and/or by glycerol phosphatidylinositol. With the help of the activator apo CII, LPL hydrolyzes triglycerides of lipoproteins to produce free fatty acids. Muscle and adipose tissue assimilate these fatty acids. Alternatively, the fatty acids can be bound to albumin and transported to other tissues. As the lipase hydrolyzes the triglycerides of the lipoprotein, the particles become smaller and are often referred to as lipoprotein remnants. Within the plasma compartment, LPL converts chylomicrons to remnants and begins the cascade requirements for conversion of VLDL to LDL.

In its active form, LPL is a glycosylated non-covalent homodimer, with each subunit containing a binding site for heparin and apolipoprotein (apo) CII, an activator protein required for LPL activity. In addition to hydrolysis of triglycerides, LPL can hydrolyze a variety of other substrates, for example, long and short chain glycerides, phospholipids and various synthetic substrates (Olivecrona *et al.* (1987) *Lipoprotein Lipase* Borensztajn, J. (ed) Elsevier Publisher, Inc., pages 15-58).

In addition to the lipolytic activity of LPL described above, LPL plays additional roles in lipid metabolism. After sufficient hydrolysis, lipoprotein lipase is released from proteoglycans and travels with the remnants of the chylomicrons or VLDL. In the plasma LPL may then act to sequester the remnant particles on surface proteoglycans. Subsequently LPL can act as a ligand for receptors such as the LDL receptor, LDL-receptor related protein, gp330, or the VLDL receptor. This interaction with the cell surface receptor facilitates the uptake and degradation of plasma lipoproteins by cells (Williams *et al.* (1992) *J. Biol. Chem* 267:13284-13292 and Nykjaer *et al.* (1993) *J. Biol. Chem.* 268:15048-15055).

Furthermore, LPL expressed in macrophages has been implicated in the cellular uptake of lipoprotein lipids and fat soluble vitamins, the degradation of lipid-containing

pathogens and cell debris, and the creation of fatty acids for the energy requirements of the cell.

Disruption of LPL activity has also been implicated in other biological functions including, for example, enhanced oxidative stress in blood cells, increased fluidity of the membrane components of these cells and increases the susceptibility of their mitochondrial DNA to structural alterations (Ven Murthy *et al.* (1996) *Acta Biochimica Polonica* 43:227-40).

Hepatic lipase (HL) has functions in lipid metabolism similar to those of LPL. HL is located on the surface of liver sinusoids through glycosaminoglycan links where it interacts with lipoproteins and hydrolyzes triglycerides into free fatty acids. Unlike LPL, the activity of HL does not require an activator, but its activity may be stimulated by apo E. Thus, the preferred substrates of HL are the triglycerides of apo E-containing lipoproteins, such as chylomicron remnants, IDL, and HDL. Furthermore, the actions of HL on HDL is important in the reverse cholesterol transport process, a mechanism thought to reduce excess accumulation of cholesterol in hepatic tissue.

Like LPL, hepatic lipase has also been implicated in the uptake and degradation of lipoprotein in the hepatic tissue. Evidence suggests that HL may interact with cell surface receptors, such as those described above, and direct hepatic cellular uptake of lipoproteins and lipoprotein remnants. (Chappell *et al.* (1998) *Progress in Lipid Research* 37: 363-422).

In its active form, HL exists as a monomer comprising both triglyceride lipase activity and phospholipase activity. As with LPL, treatment with heparin, results in the release of HL from the cell surfaces. While glycosylation plays an important role in secretion and affinity of LPL, it does not seem to be crucial for HL activity.

Pancreatic lipase (PL) is synthesized in acinar cells of the exocrine pancreas along with its protein activator, colipase. The pancreatic duct transports glycosylated PL and colipase into the duodenum. PL does not become anchored to membrane surfaces like LPL or HL. Instead, the free monomer of PL interacts with colipase which helps to anchor the PL to the lipid-water interface where the enzyme completes the hydrolysis of alimentary triglycerides.

In summary, lipases play a key role in lipid metabolism by regulating levels of cholesterol and triglycerides and therefore influence major metabolic processes including effects on lipid and lipoprotein concentrations, energy homeostasis, body

Accordingly, lipases are a major target for drug action and development. Thus, it is valuable to the field of pharmaceutical development to identify and characterize previously unknown lipases. The present invention advances the state of the art by providing a previously unidentified human lipase enzyme.

It is an object of the invention to identify novel lipases.

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It is a further object of the invention to provide polynucleotides corresponding to the novel lipase polypeptides that are useful as targets and reagents in assays applicable to treatment and diagnosis of lipase or lipase-mediated or -related disorders and useful for producing novel lipase polypeptides by recombinant methods.

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A further specific object of the invention is to provide compounds that modulate expression of the lipase for treatment and diagnosis of lipase and lipase-related disorders.

The invention provides isolated lipase polypeptides, including a polypeptide having the amino acid sequence shown in SEQ ID NO:1 or the amino acid sequence encoded by the cDNA deposited as ATCC No. PTA-1870 on May 12, 2000 (“the deposited cDNA”).

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The invention also provides variant polypeptides having an amino acid sequence that is substantially homologous to the amino acid sequence shown in SEQ ID NO:1 or encoded by the deposited cDNA.

5 The invention also provides variant nucleic acid sequences that are substantially homologous to the nucleotide sequence shown in SEQ ID NO:2 or in the deposited cDNA.

The invention also provides fragments of the polypeptide shown in SEQ ID NO:1 and nucleotide sequence shown in SEQ ID NO:2, as well as substantially homologous fragments of the polypeptide or nucleic acid.

10 The invention further provides nucleic acid constructs comprising the nucleic acid molecules described herein. In a preferred embodiment, the nucleic acid molecules of the invention are operatively linked to a regulatory sequence.

The invention also provides vectors and host cells for expressing the lipase nucleic acid molecules and polypeptides, and particularly recombinant vectors and host
15 cells.

The invention also provides methods of making the vectors and host cells and methods for using them to produce the lipase nucleic acid molecules and polypeptides.

The invention also provides antibodies or antigen-binding fragments thereof that selectively bind the lipase polypeptides and fragments.

20 The invention also provides methods of screening for compounds that modulate expression or activity of the lipase polypeptides or nucleic acid (RNA or DNA).

The invention also provides a process for modulating lipase polypeptide or nucleic acid expression or activity, especially using the screened compounds. Modulation of the 18892 gene may be used to treat conditions related to aberrant activity
25 or expression of the lipase polypeptides or nucleic acids or aberrant activity resulting in the altered accumulation/degradation of lipids. Also, modulation of 18892 may permit control of tumor cell proliferation and invasion in mammalian tissues including but not limited to breast, ovary, lung, colon, liver, and prostate.

The invention also provides assays for determining the activity of or the presence
30 or absence of the lipase polypeptides or nucleic acid molecules in a biological sample, including for disease diagnosis.

The invention also provides assays for determining the presence of a mutation in the polypeptides or nucleic acid molecules, including for disease diagnosis.

In still a further embodiment, the invention provides a computer readable means containing the nucleotide and/or amino acid sequences of the nucleic acids and polypeptides of the invention, respectively.

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DESCRIPTION OF THE DRAWINGS

Figure 1 shows the nucleotide sequence (SEQ ID NO:2) and the deduced amino acid sequence (SEQ ID NO:1) of the novel lipase.

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Figure 2 shows an analysis of the lipase amino acid sequence: $\alpha\beta$ turn and coil regions; hydrophilicity; amphipathic regions; flexible regions; antigenic index; and surface probability plot.

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Figure 3 shows a hydrophobicity plot of the lipase (SEQ ID NO:1). The analysis predicted an 18 amino acid signal peptide sequence at the amino terminus of the protein. Transmembrane segments of both the full length lipase and the mature lipase are also shown.

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Figure 4 shows an analysis of the lipase open reading frame for amino acids corresponding to specific functional sites of SEQ ID NO:1. Glycosylation sites are found from about amino acid 50 to 53, with the modified amino acid at position 53; about amino acid 58 to 61, with the modified amino acid at position 58; from about amino acid 66 to 69 with the modified amino acid at position 66, from about 357 to 360 with the modified amino acid at position 357. A cAMP and cGMP dependent protein kinase phosphorylation site is found from about amino acid 69 to 72. Protein kinase C phosphorylation sites are found from about amino acid 47 to 49; from about amino acid 68 to 70; from about amino acid 121 to 123; from about amino acid 124 to 126; from about amino acid 258 to 260; from about amino acid 287 to 289; from about amino acid 348 to 350. Casein kinase II phosphorylation sites are found from about amino acid 14 to 17; from amino acid 97 to 100; from amino acid 144 to 147; from amino acid 175 to 178; from amino acid 206 to 209; from amino acid 258 to 261; from amino acid 272 to 275; from amino acid 287 to 290; from amino acid 320 to 323. N-myristoylation sites are found from about amino acid from about 36 to 41, with the modified amino acid at

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position 36; from about amino acid 152 to 157, with the modified amino acid at position 152; from about amino acid 176 to 181, with the modified amino acid at position 176, from about amino acid 232 to 237, with the modified amino acid at position 232. An RGD cell attachment sequence is found from about amino acid 344 to 346. In addition,
5 an amino acid signature corresponding to a leucine zipper is found from amino acids 394 to 415.

Figure 5 shows an amino acid alignment of the lipase (SEQ ID NO: 1) against the top-scoring protein family domain from the ProSite database (SEQ ID NO:3).
10

Figure 6 shows transcriptional profiling data. Graph shows relative expression of gene 18892 in samples collected from five different patients. The three samples on the left represent the relative quantitative expression levels in normal ovarian epithelial cells from three different normal patients. The two samples on the right
15 were collected from the malignant ascites from two different diseased patients with ovarian cancer.

Figure 7 shows transcriptional profiling data for gene 18892 in normal and diseased patients. The five samples at the left were collected from patients with
20 normal (Norm) ovarian epithelial cells. The next 15 samples were collected from patients with tumors. Four samples were collected from patients with endometriod type (Endo) ovarian cancer. Two samples were collected from patients with mucinous (Mucin) type ovarian cancer. Nine samples were collected from patients with serous (Ser) type ovarian cancer.
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Figure 8 shows 18892 gene expression in Taqman phase I data. Pooled clinical tissue samples (2-4 patients per sample). High expression is noted in normal breast, normal ovary, prostate tumor, normal colon, colon tumor, fibrotic liver, fetal liver and COPD lung.
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Figure 9 shows gene 18892 expression with Taqman data in different clinical tissue samples, including: breast, ovary, lung, colon, liver, and prostate. 18892 is overexpressed in 2/5 ovarian tumors, 2/5 breast tumors, 3/7 lung tumors, 1/2 colon

metastasis, 1/3 prostate tumors, and 1/1 prostate metastasis samples. The panels covering breast, ovary, lung and colon are shown in Figure 10.

Figure 10 shows gene 18892 expression in oncology samples collected from patients with breast, ovary, lung, and colon cancers. Samples from normal (N) patients are shown at the left of each panel in the series. Samples from patients with tumors (T) are shown at the right in each panel from the different tissue types.

Figure 11 shows gene 18892 expression using a Taqman panel specific for the cardiovascular (CV) group. High expression in both normal and hypertensive kidney and normal fetal adrenal is indicated.

Figure 12 shows gene 18892 expression using a Taqman panel specific for the cardiovascular group. High expression in one normal vein sample, one monkey (MK) artery sample and one normal kidney sample is indicated.

DETAILED DESCRIPTION OF THE INVENTION

Polypeptides

The invention is based on the identification of a novel human lipase. Specifically, an expressed sequence tag (EST) clone was selected based on homology to lipase sequences. This EST was used to design primers based on sequences that it contains and used to identify a cDNA from the Stratagene column library #937204. Analysis of the assembled sequence revealed that the cloned cDNA molecule encodes a lipase.

The invention thus relates to a novel lipase having the deduced amino acid sequence shown in Figure 1 (SEQ ID NO:1) or having the amino acid sequence encoded by the deposited cDNA, ATCC No. PTA-1870.

“Lipase polypeptide” or “lipase protein” refers to the polypeptide in SEQ ID NO:1 or encoded by the deposited cDNA. The term “lipase protein” or “lipase polypeptide”, however, further includes the numerous variants described herein, as well as fragments derived from the full-length lipase and variants.

A plasmid containing the 18892 cDNA insert was deposited with the American Type Culture Collection (ATCC), 10801 University Boulevard, Manassas, Virginia, on May 12, 2000 and assigned Accession Number PTA-1870. This deposit will be maintained under the terms of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purposes of the Patent Procedure. This deposit was made merely as a convenience for those of skill in the art and is not an admission that a deposit is required under 35 U.S.C. § 112. The deposited sequences, as well as the polypeptides encoded by the sequences, are incorporated herein by reference and controls in the event of any conflict, such as a sequencing error, with description in this application.

The present invention thus provides an isolated or purified lipase polypeptide and variants and fragments thereof.

Based on Clustal W sequence alignment, highest homology was shown to soares fetal heart NbHH19W Homo sapiens EST clones (Acc. No. W69437 and W69436).

As used herein, a polypeptide is said to be "isolated" or "purified" when it is substantially free of cellular material when it is isolated from recombinant and non-recombinant cells, or free of chemical precursors or other chemicals when it is chemically synthesized. A polypeptide, however, can be joined to another polypeptide with which it is not normally associated in a cell and still be considered "isolated" or "purified."

The lipase polypeptides can be purified to homogeneity. It is understood, however, that preparations in which the polypeptide is not purified to homogeneity are useful and considered to contain an isolated form of the polypeptide. The critical feature is that the preparation allows for the desired function of the polypeptide, even in the presence of considerable amounts of other components. Thus, the invention encompasses various degrees of purity.

In one embodiment, the language "substantially free of cellular material" includes preparations of the lipase having less than about 30% (by dry weight) other proteins (i.e., contaminating protein), less than about 20% other proteins, less than about 10% other proteins, or less than about 5% other proteins. When the polypeptide is recombinantly produced, it can also be substantially free of culture medium, i.e., culture medium represents less than about 20%, less than about 10%, or less than about 5% of the volume of the protein preparation.

A lipase polypeptide is also considered to be isolated when it is part of a membrane preparation or is purified and then reconstituted with membrane vesicles or liposomes.

The language “substantially free of chemical precursors or other chemicals” includes preparations of the lipase polypeptide in which it is separated from chemical precursors or other chemicals that are involved in its synthesis. In one embodiment, the language “substantially free of chemical precursors or other chemicals” includes preparations of the polypeptide having less than about 30% (by dry weight) chemical precursors or other chemicals, less than about 20% chemical precursors or other chemicals, less than about 10% chemical precursors or other chemicals, or less than about 5% chemical precursors or other chemicals. In one embodiment, the lipase polypeptide comprises the amino acid sequence shown in SEQ ID NO:1 or the mature form of the polypeptide. However, the invention also encompasses sequence variants. Variants include a substantially homologous protein encoded by the same genetic locus in an organism, i.e., an allelic variant.

Variants also encompass proteins derived from other genetic loci in an organism, but having substantial homology to the lipase of SEQ ID NO:1. Variants also include proteins substantially homologous to the lipase but derived from another organism, i.e., an ortholog. Variants also include proteins that are substantially homologous to the lipase that are produced by chemical synthesis. Variants also include proteins that are substantially homologous to the lipase that are produced by recombinant methods. It is understood, however, that variants exclude any amino acid sequences disclosed prior to the invention.

As used herein, two proteins (or a region of the proteins) are substantially homologous when the amino acid sequences are at least about 70-75%, typically at least about 80-85%, and most typically at least about 90-95% or more homologous. A substantially homologous amino acid sequence, according to the present invention, will be encoded by a nucleic acid sequence hybridizing to the nucleic acid sequence, or portion thereof, of the sequence shown in SEQ ID NO:2 under stringent conditions as more fully described below.

To determine the percent identity of two amino acid sequences or of two nucleic acid sequences, the sequences are aligned for optimal comparison purposes (e.g., gaps can be introduced in one or both of a first and a second amino acid or

nucleic acid sequence for optimal alignment and non-homologous sequences can be disregarded for comparison purposes). In a preferred embodiment, the length of a reference sequence aligned for comparison purposes is at least 30%, preferably at least 40%, more preferably at least 50%, even more preferably at least 60%, and even more preferably at least 70%, 80%, or 90% of the length of the reference sequence (i.e., 100% = the entire coding sequence). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the second sequence, then the molecules are identical at that position (as used herein amino acid or nucleic acid "identity" is equivalent to amino acid or nucleic acid "homology"). The percent identity between the two sequences is a function of the number of identical positions shared by the sequences, taking into account the number of gaps, and the length of each gap, which need to be introduced for optimal alignment of the two sequences.

The invention also encompasses polypeptides having a lower degree of identity but having sufficient similarity so as to perform one or more of the same functions performed by the lipase. Similarity is determined by conserved amino acid substitution. Such substitutions are those that substitute a given amino acid in a polypeptide by another amino acid of like characteristics. Conservative substitutions are likely to be phenotypically silent. Typically seen as conservative substitutions are the replacements, one for another, among the aliphatic amino acids Ala, Val, Leu, and Ile; interchange of the hydroxyl residues Ser and Thr, exchange of the acidic residues Asp and Glu, substitution between the amide residues Asn and Gln, exchange of the basic residues Lys and Arg and replacements among the aromatic residues Phe, Tyr. Guidance concerning which amino acid changes are likely to be phenotypically silent are found in Bowie *et al.*, *Science* 247:1306-1310 (1990).

TABLE 1. Conservative Amino Acid Substitutions.

Aromatic	Phenylalanine
	Tryptophan
	Tyrosine
Hydrophobic	Leucine
	Isoleucine
	Valine
Polar	Glutamine
	Asparagine
Basic	Arginine
	Lysine
	Histidine
Acidic	Aspartic Acid
	Glutamic Acid
Small	Alanine
	Serine
	Threonine
	Methionine
	Glycine

The comparison of sequences and determination of percent identity and
 5 similarity between two sequences can be accomplished using a mathematical
 algorithm. (*Computational Molecular Biology*, Lesk, A.M., ed., Oxford University
 Press, New York, 1988; *Biocomputing: Informatics and Genome Projects*, Smith, D.W.,
 ed., Academic Press, New York, 1993; *Computer Analysis of Sequence Data, Part I*,
 Griffin, A.M., and Griffin, H.G., eds., Humana Press, New Jersey, 1994; *Sequence*
 10 *Analysis in Molecular Biology*, von Heinje, G., Academic Press, 1987; and *Sequence*
Analysis Primer, Gribskov, M. and Devereux, J., eds., M Stockton Press, New York,
 1991).

A preferred, non-limiting example of such a mathematical algorithm is described in Karlin *et al.* (1993) *Proc. Natl. Acad. Sci. USA* 90:5873-5877. Such an algorithm is incorporated into the NBLAST and XBLAST programs (version 2.0) as described in Altschul *et al.* (1997) *Nucleic Acids Res.* 25:3389-3402. When utilizing BLAST and
5 Gapped BLAST programs, the default parameters of the respective programs (e.g., NBLAST) can be used. See <http://www.ncbi.nlm.nih.gov>. In one embodiment, parameters for sequence comparison can be set at score = 100, wordlength = 12, or can be varied (e.g., W = 5 or W = 20).

In a preferred embodiment, the percent identity between two amino acid
10 sequences is determined using the Needleman *et al.* (1970) (*J. Mol. Biol.* 48:444-453) algorithm which has been incorporated into the GAP program in the GCG software package (available at <http://www.gcg.com>), using either a BLOSUM 62 matrix or a PAM250 matrix, and a gap weight of 16, 14, 12, 10, 8, 6, or 4 and a length weight of 1, 2, 3, 4, 5, or 6. In yet another preferred embodiment, the percent identity between two
15 nucleotide sequences is determined using the GAP program in the GCG software package (Devereux *et al.* (1984) *Nucleic Acids Res.* 12(1):387) (available at <http://www.gcg.com>), using a NWSgapdna.CMP matrix and a gap weight of 40, 50, 60, 70, or 80 and a length weight of 1, 2, 3, 4, 5, or 6.

Another preferred, non-limiting example of a mathematical algorithm utilized for
20 the comparison of sequences is the algorithm of Myers and Miller, CABIOS (1989). Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the CGC sequence alignment software package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used. Additional algorithms for sequence analysis
25 are known in the art and include ADVANCE and ADAM as described in Torellis *et al.* (1994) *Comput. Appl. Biosci.* 10:3-5; and FASTA described in Pearson *et al.* (1988) *PNAS* 85:2444-8.

A variant polypeptide can differ in amino acid sequence by one or more substitutions, deletions, insertions, inversions, fusions, and truncations or a combination
30 of any of these.

Variant polypeptides can be fully functional or can lack function in one or more activities. Thus, in the present case, variations can affect the function of the lipase at a variety of biological levels, including, disrupting interactions with the proteoglycans,

such as CSPG, HSPG, DSPG, disrupting interactions with cell surface receptors, such as the LDL receptor, LDL-receptor related protein, gp330, or the VLDL receptor, disrupting interactions with activator molecules, such as apo CII or colipase, disrupting interaction with heparin, disrupting interactions with lipoproteins or apoproteins, 5 disrupting triglyceride lipase activity or phospholipase activity, or disrupting homodimer formation. Variant polypeptides having such defects have been identified for LPL and are described in, for example, Murthy *et al.* (1996) *Pharmacol. Ther.* 70: 101-135, incorporated herein by reference for teaching these variations.

Fully functional variants typically contain only conservative variation or 10 variation in non-critical residues or in non-critical regions. Functional variants can also contain substitution of similar amino acids, which results in no change or an insignificant change in function. Alternatively, such substitutions may positively or negatively affect function to some degree.

Non-functional variants typically contain one or more non-conservative amino 15 acid substitutions, deletions, insertions, inversions, or truncation or a substitution, insertion, inversion, or deletion in a critical residue or critical region.

As indicated, variants can be naturally-occurring or can be made by recombinant means or chemical synthesis to provide useful and novel characteristics for the lipase polypeptide. This includes preventing immunogenicity from pharmaceutical 20 formulations by preventing protein aggregation.

Useful variations further include alteration of catalytic activity. For example, one embodiment involves a variation at the binding site that results in binding but not hydrolysis, or slower hydrolysis, of the triglyceride or phospholipid. A further useful variation results in an increased rate of hydrolysis of the triglycerides or phospholipids. 25 Additional variations include altered affinity for co-activator proteins, cell surface receptors, proteoglycans, heparin, triglycerides, phospholipids, lipoproteins or apoproteins. A further useful variation at the same site can result in higher or lower affinity for substrates. Useful variations also include changes that result in affinity to a different lipoprotein or lipoprotein remnant than that normally recognized. Other 30 variations could result in altered recognition of apoproteins thereby changing the preferred lipoproteins hydrolyzed by the lipase. Further useful variations affect the ability of the lipase to be induced by various activators, including, but not limited to, those disclosed herein. Specific variations include truncations in which a catalytic

domain or substrate binding domain is deleted. This variation results in a decrease or loss of lipid hydrolytic activity. Another useful variation includes one that prevents glycosylation. Further useful variations provide a fusion protein in which one or more domains or subregions are operationally fused to one or more domains or subregions from another lipase. Specifically, a domain or subregion can be introduced that provides a rescue function to an enzyme not normally having this function or for recognition of a specific substrate wherein recognition is not available to the original enzyme. Further variations could affect specific subunit interaction, particularly required for homodimerization or interaction with activator proteins. Other variations would affect developmental, temporal, or tissue-specific expression. Other variations would affect the interaction with cellular components, such as transcriptional regulatory factors.

Amino acids that are essential for function can be identified by methods known in the art, such as site-directed mutagenesis or alanine-scanning mutagenesis (Cunningham *et al.* (1985) *Science* 244:1081-1085). The latter procedure introduces single alanine mutations at every residue in the molecule. The resulting mutant molecules are then tested for biological activity, such as the ability to hydrolyze triglyceride or phospholipid *in vitro*. Alternatively, lipase *in vitro* activity may be measured by the ability of the lipase to interact with molecules such as, but not limited to, heparin, proteoglycans, cell surface receptors, lipoproteins, apoproteins, or activator proteins. Sites that are critical for binding or recognition can also be determined by structural analysis such as crystallization, nuclear magnetic resonance or photoaffinity labeling (Smith *et al.* (1992) *J. Mol. Biol.* 224:899-904; de Vos *et al.* (1992) *Science* 255:306-312).

The assays for lipase enzyme activity are well known in the art and can be found, for example, in Brun *et al.* (1989) *Metabolism* 38:1005-1009, Brunzell *et al.* (1992) *Atherosclerosis IX*, Stein (eds.) R&L Creative Communications Ltd., Tel Aviv 271-273, Peeva *et al.* (1992) *Int. J. Obes. Relat. Metab. Disord.* 16: 737-744, Ma *et al.* (1991) *N. Engl. J. Med.* 324: 1761-1766, Ma *et al.* (1992) *J. Biol. Chem.* 267: 1918-1923, Connelly *et al.* (1987) *J. Clin. Invest.* 80: 1597-1606, Huff *et al.* (1990) *J. Lipid Res.* 31: 385-396, and Hixson *et al.* (1990) *J. Lipid Res.* 31: 545-548. These assays include measurements of triglyceride or lipoprotein concentrations in the blood stream. For lipases associated with proteoglycans, plasma lipolytic activity may be determined following heparin treatment. In this protocol, lipase activity is measured

with a synthetic triglyceride substrate using plasma samples obtained following heparin administration. Post-heparin plasma may also be used to measure the lipase mass by immunoassay to determine if a catalytically defective lipase enzyme is released into the plasma. Lipase activity can also be determined in s.c. biopsies of adipose tissue and through the detection of lipase gene mutations. Additional assays include measuring lipase activation by the co-activator molecules.

Substantial homology can be to the entire nucleic acid or amino acid sequence or to fragments of these sequences.

The invention thus also includes polypeptide fragments of the lipase. Fragments can be derived from the amino acid sequence shown in SEQ ID NO:1. However, the invention also encompasses fragments of the variants of the lipase as described herein.

The fragments to which the invention pertains, however, are not to be construed as encompassing fragments that may be disclosed prior to the present invention.

Accordingly, a fragment can comprise at least about 13, 15, 20, 25, 30, 35, 40, 45, 50 or more contiguous amino acids. Fragments can retain one or more of the biological activities of the protein, for example the ability to bind to polyglycan, interact with cell surface receptors, interact with activator molecules, catalyze triglyceride hydrolysis, or retain phospholipase activity. Fragments can be used as an immunogen to generate lipase antibodies.

Biologically active fragments (peptides which are, for example, 5, 7, 10, 12, 15, 20, 30, 35, 36, 37, 38, 39, 40, 50, 100 or more amino acids in length) can comprise a domain or motif, e.g., catalytic sites, signal peptides, transmembrane segments, leucine zipper signature, RGD cell attachment sequences, and sites for glycosylation, cAMP and cGMP-dependent protein kinase phosphorylation, protein kinase C phosphorylation, casein kinase II phosphorylation, and N-myristoylation. Additional domains include catalytic domains involved in triglyceride hydrolysis and phospholipase activity, heparin binding sites, cell-surface receptor binding sites, triglyceride binding sites, sites important for homodimerization or activator interaction, and sites important for carrying out the other functions of the lipase as described herein.

Such domains or motifs can be identified by means of routine computerized homology searching procedures.

Fragments, for example, can extend in one or both directions from the functional site to encompass 5, 10, 15, 20, 30, 40, 50, or up to 100 amino acids. Further, fragments

can include sub-fragments of the specific domains mentioned above, which sub-fragments retain the function of the domain from which they are derived.

These regions can be identified by well-known methods involving computerized homology analysis.

5 The invention also provides fragments with immunogenic properties. These contain an epitope-bearing portion of the lipase and variants. These epitope-bearing peptides are useful to raise antibodies that bind specifically to a lipase polypeptide or region or fragment. These peptides can contain at least 13, 14, at least 14, or between at least about 16 to about 30 amino acids.

10 Non-limiting examples of antigenic polypeptides that can be used to generate antibodies include but are not limited to peptides derived from an extracellular site. Regions having a high antigenicity index are shown in Figure 2. However, intracellularly-made antibodies ("intrabodies") are also encompassed, which would recognize intracellular peptide regions.

15 The epitope-bearing lipase polypeptides may be produced by any conventional means (Houghten, R.A. (1985) *Proc. Natl. Acad. Sci. USA* 82:5131-5135). Simultaneous multiple peptide synthesis is described in U.S. Patent No. 4,631,211.

 Fragments can be discrete (not fused to other amino acids or polypeptides) or can be within a larger polypeptide. Further, several fragments can be comprised within a
20 single larger polypeptide. In one embodiment a fragment designed for expression in a host can have heterologous pre- and pro-polypeptide regions fused to the amino terminus of the lipase fragment and an additional region fused to the carboxyl terminus of the fragment.

 The invention thus provides chimeric or fusion proteins. These comprise a lipase
25 peptide sequence operatively linked to a heterologous peptide having an amino acid sequence not substantially homologous to the lipase. "Operatively linked" indicates that the lipase peptide and the heterologous peptide are fused in-frame. The heterologous peptide can be fused to the N-terminus or C-terminus of the lipase or can be internally located.

30 In one embodiment the fusion protein does not affect lipase function *per se*. For example, the fusion protein can be a GST-fusion protein in which the lipase sequences are fused to the N-or C-terminus of the GST sequences. Other types of fusion proteins include, but are not limited to, enzymatic fusion proteins, for example beta-galactosidase

fusions, yeast two-hybrid GAL-4 fusions, poly-His fusions and Ig fusions. Such fusion proteins, particularly poly-His fusions, can facilitate the purification of a recombinant lipase protein. In certain host cells (e.g., mammalian host cells), expression and/or secretion of a protein can be increased by using a heterologous signal sequence.

- 5 Therefore, in another embodiment, the fusion protein contains a heterologous signal sequence at its N-terminus.

EP-A-O 464 533 discloses fusion proteins comprising various portions of immunoglobulin constant regions. The Fc is useful in therapy and diagnosis and thus results, for example, in improved pharmacokinetic properties (EP-A 0232 262). In drug
10 discovery, for example, human proteins have been fused with Fc portions for the purpose of high-throughput screening assays to identify antagonists (Bennett *et al.* (1995) *J. Mol. Recog.* 8:52-58 (1995) and Johanson *et al.* *J. Biol. Chem.* 270:9459-9471). Thus, this invention also encompasses soluble fusion proteins containing a lipase polypeptide and various portions of the constant regions of heavy or light chains of immunoglobulins of
15 various subclass (IgG, IgM, IgA, IgE). Preferred as immunoglobulin is the constant part of the heavy chain of human IgG, particularly IgG1, where fusion takes place at the hinge region. For some uses it is desirable to remove the Fc after the fusion protein has been used for its intended purpose, for example when the fusion protein is to be used as antigen for immunizations. In a particular embodiment, the Fc part can be removed in a
20 simple way by a cleavage sequence, which is also incorporated and can be cleaved with factor Xa.

A chimeric or fusion protein can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different protein sequences are ligated together in-frame in accordance with conventional techniques. In another
25 embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers which give rise to complementary overhangs between two consecutive gene fragments which can subsequently be annealed and re-amplified to generate a chimeric gene sequence (see Ausubel *et al.* (1992) *Current*
30 *Protocols in Molecular Biology*). Moreover, many expression vectors are commercially available that already encode a fusion moiety (e.g., a GST protein). A lipase-encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the lipase.

Another form of fusion protein is one that directly affects lipase functions.

Accordingly, a lipase polypeptide is encompassed by the present invention in which one or more of the lipase domains (or parts thereof) has been replaced by homologous lipase domains (or parts thereof) from another species. Accordingly, various permutations are possible. One or more functional sites as disclosed herein from the specifically disclosed lipase can be replaced by one or more functional sites from a corresponding lipase of another species. Thus, chimeric lipases can be formed in which one or more of the native domains or subregions has been replaced by another. For example, the catalytic domain of the lipase of the present invention may be replaced by the catalytic domain of a different lipase polypeptide. Alternatively, protein domains that mediate the interaction with lipoproteins or domains that mediated the uptake of lipoproteins by cell surface receptors can be used to replace homologous domains of the lipase of the present invention. In doing so the binding affinity to various substrates and/or the rate of catalysis may be altered.

Additionally, chimeric lipase proteins can be produced in which one or more functional sites is derived from a different member of the lipase superfamily. It is understood however that sites could be derived from lipase families that occur in the mammalian genome but which have not yet been discovered or characterized. Such sites include but are not limited to any of the functional sites disclosed herein.

The isolated lipase can be purified from any of the cells that naturally express it, including, but not limited to liver, pancreas, muscle, such as skeletal and cardiac, adipose tissue, heart, lung, lactating mammary glands, embryonic liver, macrophages, adenayls, steroidogenic cells, brain. Additional tissues expressing LPL are reviewed in, for example, Borenzztajn (1987) *Lipoprotein Lipase* Evener Publisher, Inc., Chicago. Alternatively, the lipase may be purified from cells that have been altered to express it (recombinant), or synthesized using known protein synthesis methods.

In one embodiment, the protein is produced by recombinant DNA techniques. For example, a nucleic acid molecule encoding the lipase polypeptide is cloned into an expression vector, the expression vector introduced into a host cell and the protein expressed in the host cell. The protein can then be isolated from the cells by an appropriate purification scheme using standard protein purification techniques.

Polypeptides often contain amino acids other than the 20 amino acids commonly referred to as the 20 naturally-occurring amino acids. Further, many amino acids,

including the terminal amino acids, may be modified by natural processes, such as processing and other post-translational modifications, or by chemical modification techniques well known in the art. Common modifications that occur naturally in polypeptides are described in basic texts, detailed monographs, and the research literature, and they are well known to those of skill in the art.

Accordingly, the polypeptides also encompass derivatives or analogs in which a substituted amino acid residue is not one encoded by the genetic code, in which a substituent group is included, in which the mature polypeptide is fused with another compound, such as a compound to increase the half-life of the polypeptide (for example, polyethylene glycol), or in which the additional amino acids are fused to the mature polypeptide, such as a leader or secretory sequence or a sequence for purification of the mature polypeptide or a pro-protein sequence.

Known modifications include, but are not limited to, acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphatidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent crosslinks, formation of cystine, formation of pyroglutamate, formylation, gamma carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination.

Such modifications are well-known to those of skill in the art and have been described in great detail in the scientific literature. Several particularly common modifications, glycosylation, lipid attachment, sulfation, gamma-carboxylation of glutamic acid residues, hydroxylation and ADP-ribosylation, for instance, are described in most basic texts, such as *Proteins - Structure and Molecular Properties*, 2nd ed., T.E. Creighton, W. H. Freeman and Company, New York (1993). Many detailed reviews are available on this subject, such as by Wold, F., *Posttranslational Covalent Modification of Proteins*, B.C. Johnson, Ed., Academic Press, New York 1-12 (1983); Seifter *et al.* (1990) *Meth. Enzymol.* 182: 626-646) and Rattan *et al.* (1992) *Ann. N.Y. Acad. Sci.* 663:48-62).

As is also well known, polypeptides are not always entirely linear. For instance, polypeptides may be branched as a result of lipase, and they may be circular, with or without branching, generally as a result of post-translation events, including natural processing events and events brought about by human manipulation which do not occur naturally. Circular, branched and branched circular polypeptides may be synthesized by non-translational natural processes and by synthetic methods.

Modifications can occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. Blockage of the amino or carboxyl group in a polypeptide, or both, by a covalent modification, is common in naturally-occurring and synthetic polypeptides. For instance, the aminoterminal residue of polypeptides made in *E. coli*, prior to proteolytic processing, almost invariably will be N-formylmethionine.

The modifications can be a function of how the protein is made. For recombinant polypeptides, for example, the modifications will be determined by the host cell posttranslational modification capacity and the modification signals in the polypeptide amino acid sequence. Accordingly, when glycosylation is desired, a polypeptide should be expressed in a glycosylating host, generally a eukaryotic cell. Insect cells often carry out the same posttranslational glycosylations as mammalian cells and, for this reason, insect cell expression systems have been developed to efficiently express mammalian proteins having native patterns of glycosylation. Similar considerations apply to other modifications.

The same type of modification may be present in the same or varying degree at several sites in a given polypeptide. Also, a given polypeptide may contain more than one type of modification.

Polypeptide Uses

The protein sequences of the present invention can be used as a "query sequence" to perform a search against public databases to, for example, identify other family members or related sequences. Such searches can be performed using the NBLAST and XBLAST programs (version 2.0) of Altschul *et al.* (1990) *J. Mol. Biol.* 215:403-10. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to the nucleic acid molecules of the invention. BLAST protein searches can be

performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to the proteins of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.*, (1997) *Nucleic Acids Res.* 25(17):3389-3402. When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used. See <http://www.ncbi.nlm.nih.gov>.

The lipase polypeptides are useful for producing antibodies specific for the lipase protein, regions, or fragments. Regions having a high antigenicity index score are shown in Figure 2.

10 The lipase polypeptides are useful for biological assays related to lipase function. Such assays involve any of the known functions or activities or properties useful for diagnosis and treatment of lipase- or lipase-related conditions or conditions in which expression of the lipase is relevant, such as in hypertriacylglycerolaemia, obesity, atherogenesis, chylomicronemia syndrome, and the various other conditions described
15 herein. Potential assays have been disclosed herein.

The lipase polypeptides are also useful in drug screening assays, in cell-based or cell-free systems. Cell-based systems can be native, i.e., cells that normally express the lipase, as a biopsy or expanded in cell culture. In one embodiment, however, cell-based assays involve recombinant host cells expressing the lipase.

20 Determining the ability of the test compound to interact with the lipase can also comprise determining the ability of the test compound to preferentially bind to the polypeptide as compared to the ability of a known binding molecule (e.g., an activator (such as colipase, apo CII), cell surface receptors, heparin, triglycerides, phospholipids, proteoglycans, or lipoproteins) to bind to the polypeptide.

25 The polypeptides can be used to identify compounds that modulate lipase activity. Modulators of lipase activity comprise agents that influence the enzyme at a variety of biological levels, including, but not limited to agents that disrupt the interaction with the proteoglycans of the cell wall, such as HSPG-degrading enzymes, heparin, chlorate, or APOE; agents that disrupt the interaction with cell surface
30 receptors; agents which disrupt the interaction with activator molecules or homodimer formation; agents that disrupt interaction with lipoproteins; or agents that disrupt triglyceride hydrolysis or phospholipase activity.

The lipase polypeptides can be used to treat certain cancers in mammalian patients. One method for treating cancer in a patient involves introducing into the vicinity of the cancer in the patient an expression vector comprising the nucleotide sequence of SEQ ID NO:2. The vector would comprise a promoter operably linked to a
5 heterologous nucleotide sequence encoding a polypeptide of SEQ ID NO:1 and fragments thereof. Also, one method of delivering a chemotherapeutic agent to a vertebrate cancer cell which is abnormally expressing a lipase molecule involves contacting the cell with a polypeptide comprising the amino acid of SEQ ID NO:1. The sorts of cancers which may be amenable to such treatment include, but are not limited to,
10 ovarian, breast, lung, colon, liver, and prostate.

The tissue specific regulation of lipase regulation is complex with identical modulators regulating activity differently under various metabolic conditions. While specific modulators of lipase activity have been described above, additional modulators include, but are not limited to, apoproteins and a non-proteoglycan LPL-binding protein
15 having sequence homology to apo B and apo B (Sivaram *et al.* (1992) *J. Biol. Chem.* 267:16517-16552; Sivaram *et al.* (1994) *J. Biol. Chem.* 269:9409-9412). It has also been postulated that the lipolysis-stimulated receptor (LSR) plays a role in LPL activation (Yen *et al.* (1994) *Biochemistry* 33:1172-1180). Additional modulators of lipase activity include, fasting, feeding, growth hormone, insulin, exercise, estrogen,
20 thyroid hormone, catecholamines, hormones of the adrenergic system, vitamin D derivatives, glucagon, catecholamines, glucocorticoids, and 1, 25 dihydroxy-vitamin D. Further modulators comprise inflammatory mediators such as cytokines, interleukins, and interferons.

Modulators associated with an increase activity of lipase activity include, but are
25 not limited to, apo CII, and glycosylation. Furthermore, lipase enzymatic activity is stabilized in the presence of lipids or by binding to lipid-water interfaces and detergents, such as deoxycholate. Modulators associated with a decrease in lipase activity include, but are not limited to, increased concentrations of apo CII or apo CIII (Shirari *et al.* (1981) *Biochim. Biophys. Acta* 665:504-510), TNF (Kern *et al.* (1997) *Journal of*
30 *Nutrition* 127:1917S-1922S), fatty acids, high salt concentrations, and Orlistar (La Roche, Basle).

Both transcription and post-transcriptional levels of lipase expression are regulated by various dietary, environmental, and developmental factors and include,

for example, hormones, such as insulin, thyroid hormone, and glucocorticoids (Pykalisto *et al.* (1976) *J. clin. Endocrinol. Metab.* 43:591-600; Nillson-Ehle *et al.* (1980) *Annual Rev Biochem* 49:667-693; and Cryer *et al.* (1981) *Int. J. Biochem* 13:525-541). Various transcriptional factors such as CEBP, ADD-1, SREBP-1 and
5 PPAR δ also regulates expression of specific lipases. It is understood, therefore, that such compounds can be identified not only by means of direct interaction with the lipase, but by means of any of the components that functionally interact with the disclosed lipase. This includes, but is not limited to, any of those components disclosed herein.

10 Both lipase and appropriate variants and fragments can be used in high-throughput screens to assay candidate compounds for the ability to bind to the lipase. These compounds can be further screened against a functional lipase to determine the effect of the compound on the lipase activity. Compounds can be identified that activate (agonist) or inactivate (antagonist) the lipase to a desired degree. Modulatory methods
15 can be performed *in vitro* (e.g., by culturing the cell with the agent) or, alternatively, *in vivo* (e.g., by administering the agent to a subject).

The lipase polypeptides can be used to screen a compound for the ability to stimulate or inhibit interaction between the lipase protein and a target molecule that normally interacts with the lipase protein. The target can be a lipoprotein, lipoprotein
20 remnant, apoprotein, cell surface receptors, heparin, proteoglycan, triglyceride, phospholipid or another component of the pathway with which the lipase protein normally interacts. The assay includes the steps of combining the lipase protein with a candidate compound under conditions that allow the lipase protein or fragment to interact with the target molecule, and to detect the formation of a complex between the
25 lipase protein and the target or to detect the biochemical consequence of the interaction with the lipase and the target. Any of the associated effects of triglyceride hydrolysis or phospholipase function can be assayed. This includes the production of fatty acids from triglycerides and phospholipids.

Determining the ability of the lipase to bind to a target molecule can also be
30 accomplished using a technology such as real-time Bimolecular Interaction Analysis (BIA). Sjolander *et al.* (1991) *Anal. Chem.* 63:2338-2345 and Szabo *et al.* (1995) *Curr. Opin. Struct. Biol.* 5:699-705. As used herein, "BIA" is a technology for studying biospecific interactions in real time, without labeling any of the interactants

(e.g., BIAcore™). Changes in the optical phenomenon surface plasmon resonance (SPR) can be used as an indication of real-time reactions between biological molecules.

The test compounds of the present invention can be obtained using any of the numerous approaches in combinatorial library methods known in the art, including:
5 biological libraries; spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the 'one-bead one-compound' library method; and synthetic library methods using affinity chromatography selection. The biological library approach is limited to polypeptide
10 libraries, while the other four approaches are applicable to polypeptide, non-peptide oligomer or small molecule libraries of compounds (Lam, K.S. (1997) *Anticancer Drug Des.* 12:145).

Examples of methods for the synthesis of molecular libraries can be found in the art, for example in DeWitt *et al.* (1993) *Proc. Natl. Acad. Sci. USA* 90:6909; Erb
15 *et al.* (1994) *Proc. Natl. Acad. Sci. USA* 91:11422; Zuckermann *et al.* (1994). *J. Med. Chem.* 37:2678; Cho *et al.* (1993) *Science* 261:1303; Carell *et al.* (1994) *Angew. Chem. Int. Ed. Engl.* 33:2059; Carell *et al.* (1994) *Angew. Chem. Int. Ed. Engl.* 33:2061; and in Gallop *et al.* (1994) *J. Med. Chem.* 37:1233. Libraries of compounds may be presented in solution (e.g., Houghten (1992) *Biotechniques* 13:412-421), or on
20 beads (Lam (1991) *Nature* 354:82-84), chips (Fodor (1993) *Nature* 364:555-556), bacteria (Ladner USP 5,223,409), spores (Ladner USP '409), plasmids (Cull *et al.* (1992) *Proc. Natl. Acad. Sci. USA* 89:1865-1869) or on phage (Scott and Smith (1990) *Science* 249:386-390); (Devlin (1990) *Science* 249:404-406); (Cwirla *et al.* (1990) *Proc. Natl. Acad. Sci.* 97:6378-6382); (Felici (1991) *J. Mol. Biol.* 222:301-
25 310); (Ladner *supra*).

Candidate compounds include, for example, 1) peptides such as soluble peptides, including Ig-tailed fusion peptides and members of random peptide libraries (see, e.g., Lam *et al.* (1991) *Nature* 354:82-84; Houghten *et al.* (1991) *Nature* 354:84-86) and combinatorial chemistry-derived molecular libraries made of D- and/or L- configuration
30 amino acids; 2) phosphopeptides (e.g., members of random and partially degenerate, directed phosphopeptide libraries, see, e.g., Songyang *et al.* (1993) *Cell* 72:767-778); 3) antibodies (e.g., polyclonal, monoclonal, humanized, anti-idiotypic, chimeric, and single chain antibodies as well as Fab, F(ab')₂, Fab expression library fragments, and epitope-

binding fragments of antibodies); and 4) small organic and inorganic molecules (e.g., molecules obtained from combinatorial and natural product libraries).

One candidate compound is a soluble full-length lipase or fragment that competes for substrate binding. Other candidate compounds include mutant lipases or
5 appropriate fragments containing mutations that affect lipase function and compete for substrate. Accordingly, a fragment that competes for substrate, for example with a higher affinity, or a fragment that binds substrate but does not hydrolyze the triglyceride or phospholipid, is encompassed by the invention.

Other candidate compounds include lipase protein or protein analog that binds
10 to the lipid, lipoprotein, proteoglycan, cell surface receptors, or other substrates identified herein but is not released or released slowly. Other candidate compounds include analogs of the other natural substrates, such as substrates that bind to but are not released or released more slowly. Further candidate compounds include activators of the lipases, including but not limited to, those disclosed herein.

15 The invention provides other end points to identify compounds that modulate (stimulate or inhibit) lipase activity. The assays typically involve an assay of events in the pathway that indicate lipase activity. This can include cellular events that are influenced by lipid metabolism, such as but not limited to, lipid or lipoprotein concentrations. Specific phenotypes include metabolic consequences including effects
20 on energy homeostasis, body weight and body composition-parameters.

Assays are based on the multiple cellular functions of lipase enzymes. As described herein, these enzymes act at various levels in the regulation of lipid metabolism. Accordingly, assays can be based on detection of any of the products produced by the lipase enzyme.

25 Further, the expression of genes that are up- or down-regulated by action of the lipase can be assayed. In one embodiment, the regulatory region of such genes can be operably linked to a marker that is easily detectable, such as luciferase.

Accordingly, any of the biological or biochemical functions mediated by the lipase can be used as an endpoint assay. These include all of the biochemical or
30 biochemical/biological events described herein, in the references cited herein, incorporated by reference for these endpoint assay targets, and other functions known to those of ordinary skill in the art.

Binding and/or activating compounds can also be screened by using chimeric lipase proteins in which one or more domains, sites, and the like, as disclosed herein, or parts thereof, can be replaced by their heterologous counterparts derived from other lipase protein. For example, a recognition or binding region can be used that interacts with different substrate specificity and/or affinity than the native lipase. Accordingly, a different set of pathway components is available as an end-point assay for activation. Further, sites that are responsible for developmental, temporal, or tissue specificity can be replaced by heterologous sites such that the lipase can be detected under conditions of specific developmental, temporal, or tissue-specific expression.

10 The lipase polypeptides are also useful in competition binding assays in methods designed to discover compounds that interact with the lipase. Thus, a compound is exposed to a lipase polypeptide under conditions that allow the compound to bind to or to otherwise interact with the polypeptide. A lipase target, comprising a polypeptide or agent which is known to interact with lipase, is also added to the mixture. If the test compound interacts with the soluble lipase polypeptide, it decreases the amount of complex formed or the activity from the lipase target. This type of assay is particularly useful in cases in which compounds are sought that interact with specific regions of the lipase. Thus, the soluble polypeptide that competes with the target lipase region is designed to contain peptide sequences corresponding to the region of interest.

20 Another type of competition-binding assay can be used to discover compounds that interact with specific functional sites. As an example, a candidate compound can be added to a sample of the lipase. Compounds that interact with the lipase at the same site as a lipase substrate disclosed herein will reduce the amount of complex formed between the lipase and substrate. Accordingly, it is possible to discover a compound that specifically prevents interaction between the lipase and its various substrates. A compound that competes with lipase catalytic activity will reduce the rate of triglyceride or phospholipid hydrolysis. Alternatively, a compound may also compete at the level of substrate interaction. Accordingly, compounds can be discovered that directly interact with the lipase and interfere with its function. Such assays can involve any other component that interacts with the lipase such as heparin, proteoglycans, lipoproteins, lipoprotein remnants, cell surface receptors, triglycerides, phospholipids, activator proteins, and other compounds described herein.

To perform cell free drug screening assays, it is desirable to immobilize either the lipase, or fragment, or its target molecule to facilitate separation of complexes from uncomplexed forms of one or both of the proteins, as well as to accommodate automation of the assay.

- 5 Techniques for immobilizing proteins on matrices can be used in the drug screening assays. In one embodiment, a fusion protein can be provided which adds a domain that allows the protein to be bound to a matrix. For example, glutathione-S-transferase/lipase fusion proteins can be adsorbed onto glutathione sepharose beads (Sigma Chemical, St. Louis, MO) or glutathione derivatized microtitre plates, which are
10 then combined with the cell lysates (e.g., ³⁵S-labeled) and the candidate compound, and the mixture incubated under conditions conducive to complex formation (e.g., at physiological conditions for salt and pH). Following incubation, the beads are washed to remove any unbound label, and the matrix immobilized and radiolabel determined directly, or in the supernatant after the complexes is dissociated. Alternatively, the
15 complexes can be dissociated from the matrix, separated by SDS-PAGE, and the level of lipase-binding protein found in the bead fraction quantitated from the gel using standard electrophoretic techniques. For example, either the polypeptide or its target molecule can be immobilized utilizing conjugation of biotin and streptavidin using techniques well known in the art. Alternatively, antibodies reactive with the protein but which do not
20 interfere with binding of the protein to its target molecule can be derivatized to the wells of the plate, and the protein trapped in the wells by antibody conjugation. Preparations of a lipase-binding target component, such as, activator proteins, cell surface receptors, lipoproteins, apoproteins, triglycerides, phospholipids, and a candidate compound are incubated in the lipase-presenting wells and the amount of complex trapped in the well
25 can be quantitated. Methods for detecting such complexes, in addition to those described above for the GST-immobilized complexes, include immunodetection of complexes using antibodies reactive with the lipase target molecule, or which are reactive with lipase and compete with the target molecule; as well as enzyme-linked assays which rely on detecting an enzymatic activity associated with the target molecule.
- 30 Modulators of lipase activity identified according to these drug screening assays can be used to treat a subject with a disorder mediated or affected by a lipase, by treating cells that express the lipase or cells in which lipase expression is desirable. These methods of treatment include the steps of administering the modulators of lipase activity

in a pharmaceutical composition as described herein, to a subject in need of such treatment.

Lipases play critical roles in lipid metabolism and are associated with various lipid-related pathologies in humans such as, but not limited to, Wolman's disease ,
5 hypertension, Type II diabetes, retinopathy, and cholesterol ester storage disease. Furthermore, a decrease in LPL activity impairs the catabolism of chylomicrons and VLDL resulting in massive hypertriglyceridemia. Decreased LPL activity has been also associated with many disorders, including for example, chylomicronemia syndrome. This syndrome has multiple clinical symptoms and manifestations review by Murthy *et al.* (1996) *Pharmacol. Ther.* 70:101-135. Additional disorders resulting from defective
10 LPL activity include, familial lipoprotein lipase deficiency with fasting chylomicronemia (type I hyperlipidemia) (Santamarina *et al.* (1992) *Curr Opin Lipidology* 3:186), LPL deficiency, familial combined hyperlipidaemia (FCHL) (Babirak *et al.* (1992) *Arteriosclerosis thromb.* 12:1176; Seed *et al.* (1994) *Clin Invest* 72:100),
15 hypertriglyceridemia, pancreatitis and abnormalities in post prandial lipemia. In addition, LPL activity is abnormally regulated in obesity (Kern *et al.* (1997) *J. Nut.* 127: 1917S-1922S) and is also affected by alcohol and several hormones (Taskinen *et al.* (1987) *Lipoprotein Lipase*, Borensztajn J. (ed) Evener Chicago). Furthermore, changes in circulating lipoprotein and creation of lipolytic products have been implicated
20 in a number of processes that affect the biology of vessel walls. For example, atherogenesis is associated with increased LPL activity. In addition, autoantibodies against LPL have been reported in patients with idiopathic thrombocytopenic purpura and Grave's disease (Kihara *et al.* (1989) *N. Engl. J. Med.* 320:1255-1259) and heparin resistance was noted in a case of disseminated lupus erythematosus (Glueck *et al.* (1969) *Am. J. Med.* 47:318-324). Polymorphisms in LDL gene have also been
25 associated with altered levels of total and HDL cholesterol (Mitchell *et al.* (1994) *Hum. Biol.* 66:383-397), coronary heart disease (Mattu *et al.* (1994) *Arterioscler. Thromb.* 14:1090-1097), and insulin resistance (Cole *et al.* (1993) *Genet. Epidemiol.* 10:177-188).
30 Clinical situations in which LPL activity is increased include, but are not limited to, weight loss of obese subjects (Ginsberg *et al.* (1985) *J. Clin. Invest.* 75:614-623), treatment of diabetes mellitus (Ginsberg *et al.* (1991) *Diabetes Care* 14:839-855), and fibric acid therapy (Boberg *et al.* (1977) *Arteriosclerosis* 27:499-503).

The hydrolysis of HDL by hepatic lipase regulates cholesterol levels in hepatic tissue. Pathologies associated with cholesterol include, but are not limited to, atherosclerosis, xanthomas, inflammation and necrosis, cholesterosis and gall stone formation.

5 Lipases are expressed in a variety of tissues including, for example, liver, pancreas, muscle, such as skeletal and cardiac, adipose tissue, heart, lung, lactating mammary glands, embryonic liver, macrophages, adenoids, steroidogenic cells, brain. Additional tissues expressing LPL are reviewed in, for example, Borenztein (1987) *Lipoprotein Lipase* Elsevier Publisher, Inc., Chicago. Furthermore, lipases are known to
10 influence many biological roles in both blood vessel walls and the pancreas. Hence, the lipase is related to disorders involving these tissues.

Disorders involving the spleen include, but are not limited to, splenomegaly, including nonspecific acute splenitis, congestive splenomegaly, and splenic infarcts; neoplasms, congenital anomalies, and rupture. Disorders associated with
15 splenomegaly include infections, such as nonspecific splenitis, infectious mononucleosis, tuberculosis, typhoid fever, brucellosis, cytomegalovirus, syphilis, malaria, histoplasmosis, toxoplasmosis, kala-azar, trypanosomiasis, schistosomiasis, leishmaniasis, and echinococcosis; congestive states related to partial hypertension, such as cirrhosis of the liver, portal or splenic vein thrombosis, and cardiac failure;
20 lymphohematogenous disorders, such as Hodgkin disease, non-Hodgkin lymphomas/leukemia, multiple myeloma, myeloproliferative disorders, hemolytic anemias, and thrombocytopenic purpura; immunologic-inflammatory conditions, such as rheumatoid arthritis and systemic lupus erythematosus; storage diseases such as Gaucher disease, Niemann-Pick disease, and mucopolysaccharidoses; and other
25 conditions, such as amyloidosis, primary neoplasms and cysts, and secondary neoplasms.

Disorders involving the lung include, but are not limited to, congenital anomalies; atelectasis; diseases of vascular origin, such as pulmonary congestion and edema, including hemodynamic pulmonary edema and edema caused by
30 microvascular injury, adult respiratory distress syndrome (diffuse alveolar damage), pulmonary embolism, hemorrhage, and infarction, and pulmonary hypertension and vascular sclerosis; chronic obstructive pulmonary disease, such as emphysema, chronic bronchitis, bronchial asthma, and bronchiectasis; diffuse interstitial

(infiltrative, restrictive) diseases, such as pneumoconioses, sarcoidosis, idiopathic pulmonary fibrosis, desquamative interstitial pneumonitis, hypersensitivity pneumonitis, pulmonary eosinophilia (pulmonary infiltration with eosinophilia), *Bronchiolitis obliterans*-organizing pneumonia, diffuse pulmonary hemorrhage syndromes, including Goodpasture syndrome, idiopathic pulmonary hemosiderosis and other hemorrhagic syndromes, pulmonary involvement in collagen vascular disorders, and pulmonary alveolar proteinosis; complications of therapies, such as drug-induced lung disease, radiation-induced lung disease, and lung transplantation; tumors, such as bronchogenic carcinoma, including paraneoplastic syndromes, bronchioloalveolar carcinoma, neuroendocrine tumors, such as bronchial carcinoid, miscellaneous tumors, and metastatic tumors; pathologies of the pleura, including inflammatory pleural effusions, noninflammatory pleural effusions, pneumothorax, and pleural tumors, including solitary fibrous tumors (pleural fibroma) and malignant mesothelioma.

Disorders involving the colon include, but are not limited to, congenital anomalies, such as atresia and stenosis, Meckel diverticulum, congenital aganglionic megacolon-Hirschsprung disease; enterocolitis, such as diarrhea and dysentery, infectious enterocolitis, including viral gastroenteritis, bacterial enterocolitis, necrotizing enterocolitis, antibiotic-associated colitis (pseudomembranous colitis), and collagenous and lymphocytic colitis, irritable bowel syndrome, miscellaneous intestinal inflammatory disorders, including parasites and protozoa, acquired immunodeficiency syndrome, transplantation, drug-induced intestinal injury, radiation enterocolitis, neutropenic colitis (typhlitis), and diversion colitis; idiopathic inflammatory bowel disease, such as Crohn disease and ulcerative colitis; tumors of the colon, such as non-neoplastic polyps, adenomas, familial syndromes, colorectal carcinogenesis, colorectal carcinoma, and carcinoid tumors.

Disorders involving the liver include, but are not limited to, hepatic injury; jaundice and cholestasis, such as bilirubin and bile formation; hepatic failure and cirrhosis, such as cirrhosis, portal hypertension, including ascites, portosystemic shunts, and splenomegaly; infectious disorders, such as viral hepatitis, including hepatitis A-E infection and infection by other hepatitis viruses, clinicopathologic syndromes, such as the carrier state, asymptomatic infection, acute viral hepatitis, chronic viral hepatitis, and fulminant hepatitis; autoimmune hepatitis; drug- and

toxin-induced liver disease, such as alcoholic liver disease; inborn errors of metabolism and pediatric liver disease, such as hemochromatosis, Wilson disease, α_1 -antitrypsin deficiency, and neonatal hepatitis; intrahepatic biliary tract disease, such as secondary biliary cirrhosis, primary biliary cirrhosis, primary sclerosing cholangitis, and anomalies of the biliary tree; circulatory disorders, such as impaired blood flow into the liver, including hepatic artery compromise and portal vein obstruction and thrombosis, impaired blood flow through the liver, including passive congestion and centrilobular necrosis and peliosis hepatis, hepatic vein outflow obstruction, including hepatic vein thrombosis (Budd-Chiari syndrome) and veno-occlusive disease; hepatic disease associated with pregnancy, such as preeclampsia and eclampsia, acute fatty liver of pregnancy, and intrahepatic cholestasis of pregnancy; hepatic complications of organ or bone marrow transplantation, such as drug toxicity after bone marrow transplantation, graft-versus-host disease and liver rejection, and nonimmunologic damage to liver allografts; tumors and tumorous conditions, such as nodular hyperplasias, adenomas, and malignant tumors, including primary carcinoma of the liver and metastatic tumors.

Disorders involving the uterus and endometrium include, but are not limited to, endometrial histology in the menstrual cycle; functional endometrial disorders, such as anovulatory cycle, inadequate luteal phase, oral contraceptives and induced endometrial changes, and menopausal and postmenopausal changes; inflammations, such as chronic endometritis; adenomyosis; endometriosis; endometrial polyps; endometrial hyperplasia; malignant tumors, such as carcinoma of the endometrium; mixed Müllerian and mesenchymal tumors, such as malignant mixed Müllerian tumors; tumors of the myometrium, including leiomyomas, leiomyosarcomas, and endometrial stromal tumors.

Disorders involving the brain include, but are not limited to, disorders involving neurons, and disorders involving glia, such as astrocytes, oligodendrocytes, ependymal cells, and microglia; cerebral edema, raised intracranial pressure and herniation, and hydrocephalus; malformations and developmental diseases, such as neural tube defects, forebrain anomalies, posterior fossa anomalies, and syringomyelia and hydromyelia; perinatal brain injury; cerebrovascular diseases, such as those related to hypoxia, ischemia, and infarction, including hypotension, hypoperfusion, and low-flow states--global cerebral ischemia and focal cerebral ischemia--infarction

- from obstruction of local blood supply, intracranial hemorrhage, including intracerebral (intraparenchymal) hemorrhage, subarachnoid hemorrhage and ruptured berry aneurysms, and vascular malformations, hypertensive cerebrovascular disease, including lacunar infarcts, slit hemorrhages, and hypertensive encephalopathy;
- 5 infections, such as acute meningitis, including acute pyogenic (bacterial) meningitis and acute aseptic (viral) meningitis, acute focal suppurative infections, including brain abscess, subdural empyema, and extradural abscess, chronic bacterial meningoencephalitis, including tuberculosis and mycobacterioses, neurosyphilis, and neuroborreliosis (Lyme disease), viral meningoencephalitis, including arthropod-
- 10 borne (Arbo) viral encephalitis, *Herpes simplex* virus Type 1, *Herpes simplex* virus Type 2, *Varicella-zoster* virus (*Herpes zoster*), cytomegalovirus, poliomyelitis, rabies, and human immunodeficiency virus 1, including HIV-1 meningoencephalitis (subacute encephalitis), vacuolar myelopathy, AIDS-associated myopathy, peripheral neuropathy, and AIDS in children, progressive multifocal leukoencephalopathy,
- 15 subacute sclerosing panencephalitis, fungal meningoencephalitis, other infectious diseases of the nervous system; transmissible spongiform encephalopathies (prion diseases); demyelinating diseases, including multiple sclerosis, multiple sclerosis variants, acute disseminated encephalomyelitis and acute necrotizing hemorrhagic encephalomyelitis, and other diseases with demyelination; degenerative diseases, such
- 20 as degenerative diseases affecting the cerebral cortex, including Alzheimer disease and Pick disease, degenerative diseases of basal ganglia and brain stem, including Parkinsonism, idiopathic Parkinson disease (paralysis agitans), progressive supranuclear palsy, corticobasal degeneration, multiple system atrophy, including striatonigral degeneration, Shy-Drager syndrome, and olivopontocerebellar atrophy,
- 25 and Huntington disease; spinocerebellar degenerations, including spinocerebellar ataxias, including Friedreich ataxia, and ataxia-telangiectasia, degenerative diseases affecting motor neurons, including amyotrophic lateral sclerosis (motor neuron disease), bulbospinal atrophy (Kennedy syndrome), and spinal muscular atrophy; inborn errors of metabolism, such as leukodystrophies, including Krabbe disease,
- 30 metachromatic leukodystrophy, adrenoleukodystrophy, Pelizaeus-Merzbacher disease, and Canavan disease, mitochondrial encephalomyopathies, including Leigh disease and other mitochondrial encephalomyopathies; toxic and acquired metabolic diseases, including vitamin deficiencies such as thiamine (vitamin B₁) deficiency and

vitamin B₁₂ deficiency, neurologic sequelae of metabolic disturbances, including hypoglycemia, hyperglycemia, and hepatic encephatopathy, toxic disorders, including carbon monoxide, methanol, ethanol, and radiation, including combined methotrexate and radiation-induced injury; tumors, such as gliomas, including astrocytoma, including fibrillary (diffuse) astrocytoma and glioblastoma multiforme, pilocytic astrocytoma, pleomorphic xanthoastrocytoma, and brain stem glioma, oligodendroglioma, and ependymoma and related paraventricular mass lesions, neuronal tumors, poorly differentiated neoplasms, including medulloblastoma, other parenchymal tumors, including primary brain lymphoma, germ cell tumors, and pineal parenchymal tumors, meningiomas, metastatic tumors, paraneoplastic syndromes, peripheral nerve sheath tumors, including schwannoma, neurofibroma, and malignant peripheral nerve sheath tumor (malignant schwannoma), and neurocutaneous syndromes (phakomatoses), including neurofibromatosis, including Type 1 neurofibromatosis (NF1) and TYPE 2 neurofibromatosis (NF2), tuberous sclerosis, and Von Hippel-Lindau disease.

Disorders involving T-cells include, but are not limited to, cell-mediated hypersensitivity, such as delayed type hypersensitivity and T-cell-mediated cytotoxicity, and transplant rejection; autoimmune diseases, such as systemic lupus erythematosus, Sjögren syndrome, systemic sclerosis, inflammatory myopathies, mixed connective tissue disease, and polyarteritis nodosa and other vasculitides; immunologic deficiency syndromes, including but not limited to, primary immunodeficiencies, such as thymic hypoplasia, severe combined immunodeficiency diseases, and AIDS; leukopenia; reactive (inflammatory) proliferations of white cells, including but not limited to, leukocytosis, acute nonspecific lymphadenitis, and chronic nonspecific lymphadenitis; neoplastic proliferations of white cells, including but not limited to lymphoid neoplasms, such as precursor T-cell neoplasms, such as acute lymphoblastic leukemia/lymphoma, peripheral T-cell and natural killer cell neoplasms that include peripheral T-cell lymphoma, unspecified, adult T-cell leukemia/lymphoma, mycosis fungoides and Sézary syndrome, and Hodgkin disease.

Diseases of the skin, include but are not limited to, disorders of pigmentation and melanocytes, including but not limited to, vitiligo, freckle, melasma, lentigo, nevocellular nevus, dysplastic nevi, and malignant melanoma; benign epithelial tumors, including but not limited to, seborrheic keratoses, acanthosis nigricans,

fibroepithelial polyp, epithelial cyst, keratoacanthoma, and adnexal (appendage) tumors; premalignant and malignant epidermal tumors, including but not limited to, actinic keratosis, squamous cell carcinoma, basal cell carcinoma, and merkel cell carcinoma; tumors of the dermis, including but not limited to, benign fibrous

5 histiocytoma, dermatofibrosarcoma protuberans, xanthomas, and dermal vascular tumors; tumors of cellular immigrants to the skin, including but not limited to, histiocytosis X, mycosis fungoides (cutaneous T-cell lymphoma), and mastocytosis; disorders of epidermal maturation, including but not limited to, ichthyosis; acute inflammatory dermatoses, including but not limited to, urticaria, acute eczematous

10 dermatitis, and erythema multiforme; chronic inflammatory dermatoses, including but not limited to, psoriasis, lichen planus, and lupus erythematosus; blistering (bullous) diseases, including but not limited to, pemphigus, bullous pemphigoid, dermatitis herpetiformis, and noninflammatory blistering diseases: epidermolysis bullosa and porphyria; disorders of epidermal appendages, including but not limited to, acne

15 vulgaris; panniculitis, including but not limited to, erythema nodosum and erythema induratum; and infection and infestation, such as verrucae, molluscum contagiosum, impetigo, superficial fungal infections, and arthropod bites, stings, and infestations.

In normal bone marrow, the myelocytic series (polymorphoneuclear cells) make up approximately 60% of the cellular elements, and the erythrocytic series, 20-

20 30%. Lymphocytes, monocytes, reticular cells, plasma cells and megakaryocytes together constitute 10-20%. Lymphocytes make up 5-15% of normal adult marrow. In the bone marrow, cell types are add mixed so that precursors of red blood cells (erythroblasts), macrophages (monoblasts), platelets (megakaryocytes), polymorphoneuclear leucocytes (myeloblasts), and lymphocytes (lymphoblasts) can

25 be visible in one microscopic field. In addition, stem cells exist for the different cell lineages, as well as a precursor stem cell for the committed progenitor cells of the different lineages. The various types of cells and stages of each would be known to the person of ordinary skill in the art and are found, for example, on page 42 (Figure 2-8) of *Immunology, Immunopathology and Immunity*, Fifth Edition, Sell *et al.* Simon

30 and Schuster (1996), incorporated by reference for its teaching of cell types found in the bone marrow. According, the invention is directed to disorders arising from these cells. These disorders include but are not limited to the following: diseases involving hematopoietic stem cells; committed lymphoid progenitor cells; lymphoid cells

including B and T-cells; committed myeloid progenitors, including monocytes, granulocytes, and megakaryocytes; and committed erythroid progenitors. These include but are not limited to the leukemias, including B-lymphoid leukemias, T-lymphoid leukemias, undifferentiated leukemias; erythroleukemia, megakaryoblastic leukemia, monocytic; [leukemias are encompassed with and without differentiation]; chronic and acute lymphoblastic leukemia, chronic and acute lymphocytic leukemia, chronic and acute myelogenous leukemia, lymphoma, myelo dysplastic syndrome, chronic and acute myeloid leukemia, myelomonocytic leukemia; chronic and acute myeloblastic leukemia, chronic and acute myelogenous leukemia, chronic and acute promyelocytic leukemia, chronic and acute myelocytic leukemia, hematologic malignancies of monocyte-macrophage lineage, such as juvenile chronic myelogenous leukemia; secondary AML, antecedent hematological disorder; refractory anemia; aplastic anemia; reactive cutaneous angioendotheliomatosis; fibrosing disorders involving altered expression in dendritic cells, disorders including systemic sclerosis, E-M syndrome, epidemic toxic oil syndrome, eosinophilic fasciitis localized forms of scleroderma, keloid, and fibrosing colonopathy; angiomatoid malignant fibrous histiocytoma; carcinoma, including primary head and neck squamous cell carcinoma; sarcoma, including kaposi's sarcoma; fibroadenoma and phyllodes tumors, including mammary fibroadenoma; stromal tumors; phyllodes tumors, including histiocytoma; erythroblastosis; neurofibromatosis; diseases of the vascular endothelium; demyelinating, particularly in old lesions; gliosis, vasogenic edema, vascular disease, Alzheimer's and Parkinson's disease; T-cell lymphomas; B-cell lymphomas.

Disorders involving the heart, include but are not limited to, heart failure, including but not limited to, cardiac hypertrophy, left-sided heart failure, and right-sided heart failure; ischemic heart disease, including but not limited to angina pectoris, myocardial infarction, chronic ischemic heart disease, and sudden cardiac death; hypertensive heart disease, including but not limited to, systemic (left-sided) hypertensive heart disease and pulmonary (right-sided) hypertensive heart disease; valvular heart disease, including but not limited to, valvular degeneration caused by calcification, such as calcific aortic stenosis, calcification of a congenitally bicuspid aortic valve, and mitral annular calcification, and myxomatous degeneration of the mitral valve (mitral valve prolapse), rheumatic fever and rheumatic heart disease,

infective endocarditis, and noninfected vegetations, such as nonbacterial thrombotic endocarditis and endocarditis of systemic lupus erythematosus (Libman-Sacks disease), carcinoid heart disease, and complications of artificial valves; myocardial disease, including but not limited to dilated cardiomyopathy, hypertrophic
5 cardiomyopathy, restrictive cardiomyopathy, and myocarditis; pericardial disease, including but not limited to, pericardial effusion and hemopericardium and pericarditis, including acute pericarditis and healed pericarditis, and rheumatoid heart disease; neoplastic heart disease, including but not limited to, primary cardiac tumors, such as myxoma, lipoma, papillary fibroelastoma, rhabdomyoma, and sarcoma, and
10 cardiac effects of noncardiac neoplasms; congenital heart disease, including but not limited to, left-to-right shunts--late cyanosis, such as atrial septal defect, ventricular septal defect, patent ductus arteriosus, and atrioventricular septal defect, right-to-left shunts--early cyanosis, such as tetralogy of fallot, transposition of great arteries, truncus arteriosus, tricuspid atresia, and total anomalous pulmonary venous
15 connection, obstructive congenital anomalies, such as coarctation of aorta, pulmonary stenosis and atresia, and aortic stenosis and atresia, and disorders involving cardiac transplantation.

Disorders involving blood vessels include, but are not limited to, responses of vascular cell walls to injury, such as endothelial dysfunction and endothelial
20 activation and intimal thickening; vascular diseases including, but not limited to, congenital anomalies, such as arteriovenous fistula, atherosclerosis, and hypertensive vascular disease, such as hypertension; inflammatory disease--the vasculitides, such as giant cell (temporal) arteritis, Takayasu arteritis, polyarteritis nodosa (classic), Kawasaki syndrome (mucocutaneous lymph node syndrome), microscopic
25 polyanglitis (microscopic polyarteritis, hypersensitivity or leukocytoclastic angitis), Wegener granulomatosis, thromboanglitis obliterans (Buerger disease), vasculitis associated with other disorders, and infectious arteritis; Raynaud disease; aneurysms and dissection, such as abdominal aortic aneurysms, syphilitic (luetetic) aneurysms, and aortic dissection (dissecting hematoma); disorders of veins and lymphatics, such as
30 varicose veins, thrombophlebitis and phlebothrombosis, obstruction of superior vena cava (superior vena cava syndrome), obstruction of inferior vena cava (inferior vena cava syndrome), and lymphangitis and lymphedema; tumors, including benign tumors and tumor-like conditions, such as hemangioma, lymphangioma, glomus tumor

(glomangioma), vascular ectasias, and bacillary angiomatosis, and intermediate-grade (borderline low-grade malignant) tumors, such as Kaposi sarcoma and hemangioendothelioma, and malignant tumors, such as angiosarcoma and hemangiopericytoma; and pathology of therapeutic interventions in vascular disease, such as balloon angioplasty and related techniques and vascular replacement, such as coronary artery bypass graft surgery.

Disorders involving red cells include, but are not limited to, anemias, such as hemolytic anemias, including hereditary spherocytosis, hemolytic disease due to erythrocyte enzyme defects: glucose-6-phosphate dehydrogenase deficiency, sickle cell disease, thalassemia syndromes, paroxysmal nocturnal hemoglobinuria, immunohemolytic anemia, and hemolytic anemia resulting from trauma to red cells; and anemias of diminished erythropoiesis, including megaloblastic anemias, such as anemias of vitamin B12 deficiency: pernicious anemia, and anemia of folate deficiency, iron deficiency anemia, anemia of chronic disease, aplastic anemia, pure red cell aplasia, and other forms of marrow failure.

Disorders involving the thymus include developmental disorders, such as DiGeorge syndrome with thymic hypoplasia or aplasia; thymic cysts; thymic hypoplasia, which involves the appearance of lymphoid follicles within the thymus, creating thymic follicular hyperplasia; and thymomas, including germ cell tumors, lymphomas, Hodgkin disease, and carcinoids. Thymomas can include benign or encapsulated thymoma, and malignant thymoma Type I (invasive thymoma) or Type II, designated thymic carcinoma.

Disorders involving B-cells include, but are not limited to precursor B-cell neoplasms, such as lymphoblastic leukemia/lymphoma. Peripheral B-cell neoplasms include, but are not limited to, chronic lymphocytic leukemia/small lymphocytic lymphoma, follicular lymphoma, diffuse large B-cell lymphoma, Burkitt lymphoma, plasma cell neoplasms, multiple myeloma, and related entities, lymphoplasmacytic lymphoma (Waldenström macroglobulinemia), mantle cell lymphoma, marginal zone lymphoma (MAL Toma), and hairy cell leukemia.

Disorders involving the kidney include, but are not limited to, congenital anomalies including, but not limited to, cystic diseases of the kidney, that include but are not limited to, cystic renal dysplasia, autosomal dominant (adult) polycystic kidney disease, autosomal recessive (childhood) polycystic kidney disease, and cystic diseases

of renal medulla, which include, but are not limited to, medullary sponge kidney, and nephronophthisis-uremic medullary cystic disease complex, acquired (dialysis-associated) cystic disease, such as simple cysts; glomerular diseases including pathologies of glomerular injury that include, but are not limited to, in situ immune complex deposition, that includes, but is not limited to, anti-GBM nephritis, Heymann nephritis, and antibodies against planted antigens, circulating immune complex nephritis, antibodies to glomerular cells, cell-mediated immunity in glomerulonephritis, activation of alternative complement pathway, epithelial cell injury, and pathologies involving mediators of glomerular injury including cellular and soluble mediators, acute glomerulonephritis, such as acute proliferative (poststreptococcal, postinfectious) glomerulonephritis, including but not limited to, poststreptococcal glomerulonephritis and nonstreptococcal acute glomerulonephritis, rapidly progressive (crescentic) glomerulonephritis, nephrotic syndrome, membranous glomerulonephritis (membranous nephropathy), minimal change disease (lipoid nephrosis), focal segmental glomerulosclerosis, membranoproliferative glomerulonephritis, IgA nephropathy (Berger disease), focal proliferative and necrotizing glomerulonephritis (focal glomerulonephritis), hereditary nephritis, including but not limited to, Alport syndrome and thin membrane disease (benign familial hematuria), chronic glomerulonephritis, glomerular lesions associated with systemic disease, including but not limited to, systemic lupus erythematosus, Henoch-Schönlein purpura, bacterial endocarditis, diabetic glomerulosclerosis, amyloidosis, fibrillary and immunotactoid glomerulonephritis, and other systemic disorders; diseases affecting tubules and interstitium, including acute tubular necrosis and tubulointerstitial nephritis, including but not limited to, pyelonephritis and urinary tract infection, acute pyelonephritis, chronic pyelonephritis and reflux nephropathy, and tubulointerstitial nephritis induced by drugs and toxins, including but not limited to, acute drug-induced interstitial nephritis, analgesic abuse nephropathy, nephropathy associated with nonsteroidal anti-inflammatory drugs, and other tubulointerstitial diseases including, but not limited to, urate nephropathy, hypercalcemia and nephrocalcinosis, and multiple myeloma; diseases of blood vessels including benign nephrosclerosis, malignant hypertension and accelerated nephrosclerosis, renal artery stenosis, and thrombotic microangiopathies including, but not limited to, classic (childhood) hemolytic-uremic syndrome, adult hemolytic-uremic syndrome/thrombotic thrombocytopenic purpura, idiopathic

HUS/TTP, and other vascular disorders including, but not limited to, atherosclerotic ischemic renal disease, atheroembolic renal disease, sickle cell disease nephropathy, diffuse cortical necrosis, and renal infarcts; urinary tract obstruction (obstructive uropathy); urolithiasis (renal calculi, stones); and tumors of the kidney including, but not
5 limited to, benign tumors, such as renal papillary adenoma, renal fibroma or hamartoma (renomedullary interstitial cell tumor), angiomyolipoma, and oncocytoma, and malignant tumors, including renal cell carcinoma (hypernephroma, adenocarcinoma of kidney), which includes urothelial carcinomas of renal pelvis.

Disorders of the breast include, but are not limited to, disorders of development;
10 inflammations, including but not limited to, acute mastitis, periductal mastitis, periductal mastitis (recurrent subareolar abscess, squamous metaplasia of lactiferous ducts), mammary duct ectasia, fat necrosis, granulomatous mastitis, and pathologies associated with silicone breast implants; fibrocystic changes; proliferative breast disease including, but not limited to, epithelial hyperplasia, sclerosing adenosis, and small duct papillomas;
15 tumors including, but not limited to, stromal tumors such as fibroadenoma, phyllodes tumor, and sarcomas, and epithelial tumors such as large duct papilloma; carcinoma of the breast including in situ (noninvasive) carcinoma that includes ductal carcinoma in situ (including Paget's disease) and lobular carcinoma in situ, and invasive (infiltrating) carcinoma including, but not limited to, invasive ductal carcinoma, no special type,
20 invasive lobular carcinoma, medullary carcinoma, colloid (mucinous) carcinoma, tubular carcinoma, and invasive papillary carcinoma, and miscellaneous malignant neoplasms.

Disorders in the male breast include, but are not limited to, gynecomastia and carcinoma.

Disorders involving the testis and epididymis include, but are not limited to,
25 congenital anomalies such as cryptorchidism, regressive changes such as atrophy, inflammations such as nonspecific epididymitis and orchitis, granulomatous (autoimmune) orchitis, and specific inflammations including, but not limited to, gonorrhea, mumps, tuberculosis, and syphilis, vascular disturbances including torsion, testicular tumors including germ cell tumors that include, but are not limited to,
30 seminoma, spermatocytic seminoma, embryonal carcinoma, yolk sac tumor choriocarcinoma, teratoma, and mixed tumors, tumor of sex cord-gonadal stroma including, but not limited to, leydig (interstitial) cell tumors and sertoli cell tumors (androblastoma), and testicular lymphoma, and miscellaneous lesions of tunica

vaginalis.

Disorders involving the prostate include, but are not limited to, inflammations, benign enlargement, for example, nodular hyperplasia (benign prostatic hypertrophy or hyperplasia), and tumors such as carcinoma.

- 5 Disorders involving the thyroid include, but are not limited to, hyperthyroidism; hypothyroidism including, but not limited to, cretinism and myxedema; thyroiditis including, but not limited to, hashimoto thyroiditis, subacute (granulomatous) thyroiditis, and subacute lymphocytic (painless) thyroiditis; Graves disease; diffuse and multinodular goiter including, but not limited to, diffuse nontoxic (simple) goiter and
- 10 multinodular goiter; neoplasms of the thyroid including, but not limited to, adenomas, other benign tumors, and carcinomas, which include, but are not limited to, papillary carcinoma, follicular carcinoma, medullary carcinoma, and anaplastic carcinoma; and congenital anomalies.

- Disorders involving the skeletal muscle include tumors such as
- 15 rhabdomyosarcoma.

- Disorders involving the pancreas include those of the exocrine pancreas such as congenital anomalies, including but not limited to, ectopic pancreas; pancreatitis, including but not limited to, acute pancreatitis; cysts, including but not limited to, pseudocysts; tumors, including but not limited to, cystic tumors and carcinoma of the
- 20 pancreas; and disorders of the endocrine pancreas such as, diabetes mellitus; islet cell tumors, including but not limited to, insulinomas, gastrinomas, and other rare islet cell tumors.

- Disorders involving the small intestine include the malabsorption syndromes such as, celiac sprue, tropical sprue (postinfectious sprue), whipple disease,
- 25 disaccharidase (lactase) deficiency, abetalipoproteinemia, and tumors of the small intestine including adenomas and adenocarcinoma.

- Disorders related to reduced platelet number, thrombocytopenia, include idiopathic thrombocytopenic purpura, including acute idiopathic thrombocytopenic purpura, drug-induced thrombocytopenia, HIV-associated thrombocytopenia, and
- 30 thrombotic microangiopathies: thrombotic thrombocytopenic purpura and hemolytic-uremic syndrome.

Disorders involving precursor T-cell neoplasms include precursor T lymphoblastic leukemia/lymphoma. Disorders involving peripheral T-cell and natural

killer cell neoplasms include T-cell chronic lymphocytic leukemia, large granular lymphocytic leukemia, mycosis fungoides and Sézary syndrome, peripheral T-cell lymphoma, unspecified, angioimmunoblastic T-cell lymphoma, angiocentric lymphoma (NK/T-cell lymphoma^{4a}), intestinal T-cell lymphoma, adult T-cell leukemia/lymphoma, and anaplastic large cell lymphoma.

Disorders involving the ovary include, for example, polycystic ovarian disease, Stein-leventhal syndrome, Pseudomyxoma peritonei and stromal hyperthecosis; ovarian tumors such as, tumors of coelomic epithelium, serous tumors, mucinous tumors, endometrioid tumors, clear cell adenocarcinoma, cystadenofibroma, brenner tumor, surface epithelial tumors; germ cell tumors such as mature (benign) teratomas, monodermal teratomas, immature malignant teratomas, dysgerminoma, endodermal sinus tumor, choriocarcinoma; sex cord-stomal tumors such as, granulosa-theca cell tumors, thecoma-fibromas, androblastomas, hill cell tumors, and gonadoblastoma; and metastatic tumors such as Krukenberg tumors.

Bone-forming cells include the osteoprogenitor cells, osteoblasts, and osteocytes. The disorders of the bone are complex because they may have an impact on the skeleton during any of its stages of development. Hence, the disorders may have variable manifestations and may involve one, multiple or all bones of the body. Such disorders include, congenital malformations, achondroplasia and thanatophoric dwarfism, diseases associated with abnormal matix such as type 1 collagen disease, osteoporosis, paget disease, rickets, osteomalacia, high-turnover osteodystrophy, low-turnover of aplastic disease, osteonecrosis, pyogenic osteomyelitis, tuberculous osteomyelitis, osteoma, osteoid osteoma, osteoblastoma, osteosarcoma, osteochondroma, chondromas, chondroblastoma, chondromyxoid fibroma, chondrosarcoma, fibrous cortical defects, fibrous dysplasia, fibrosarcoma, malignant fibrous histiocytooma, ewing sarcoma, primitive neuroectodermal tumor, giant cell tumor, and metastatic tumors.

The lipase polypeptides are thus useful for treating a lipase-associated disorder characterized by aberrant expression or activity of a lipase. The polypeptides can also be useful for treating a disorder characterized by excessive amounts of lipoproteins, triglycerides or cholesterol. In one embodiment, the method involves administering an agent (e.g., an agent identified by a screening assay described herein), or combination of agents that modulates (e.g., upregulates or downregulates) expression

or activity of the protein. In another embodiment, the method involves administering the lipase as therapy to compensate for reduced or aberrant expression or activity of the protein.

5 Methods for treatment include but are not limited to the use of soluble lipase or fragments of the lipase protein that compete for substrates including those disclosed herein. These lipases or fragments can have a higher affinity for the target so as to provide effective competition.

10 Stimulation of activity is desirable in situations in which the protein is abnormally downregulated and/or in which increased activity is likely to have a beneficial effect, such as virally-infected cells. Likewise, inhibition of activity is desirable in situations in which the protein is abnormally upregulated and/or in which decreased activity is likely to have a beneficial effect. In one example of such a situation, a subject has a disorder characterized by aberrant metabolism of lipids resulting in altered lipoprotein concentrations, energy homeostasis, atherosclerosis,
15 body weight, and body weight parameters.

In yet another aspect of the invention, the proteins of the invention can be used as "bait proteins" in a two-hybrid assay or three-hybrid assay (see, e.g., U.S. Patent No. 5,283,317; Zervos *et al.* (1993) *Cell* 72:223-232; Madura *et al.* (1993) *J. Biol. Chem.* 268:12046-12054; Bartel *et al.* (1993) *Biotechniques* 14:920-924; Iwabuchi *et al.* (1993) *Oncogene* 8:1693-1696; and Brent WO 94/10300), to identify other
20 proteins (captured proteins) which bind to or interact with the proteins of the invention and modulate their activity.

The lipase polypeptides also are useful to provide a target for diagnosing a disease or predisposition to disease mediated by the lipase, including, but not limited to,
25 diseases involving tissues in which the lipase are expressed as disclosed herein. Accordingly, methods are provided for detecting the presence, or levels of, the lipase in a cell, tissue, or organism. The method involves contacting a biological sample with a compound capable of interacting with the lipase such that the interaction can be detected.

The polypeptides are also useful for treating a disorder characterized by
30 reduced amounts of these components. Thus, increasing or decreasing the activity of the lipase is beneficial to treatment. The polypeptides are also useful to provide a target for diagnosing a disease characterized by excessive substrate or reduced levels of substrate. Accordingly, where substrate is excessive, use of the lipase polypeptides

can provide a diagnostic assay. Furthermore, for example, lipases having reduced activity can be used to diagnose conditions in which reduced substrate is responsible for the disorder.

One agent for detecting lipase is an antibody capable of selectively binding to the lipase polypeptide. A biological sample includes tissues, cells and biological fluids isolated from a subject, as well as tissues, cells and fluids present within a subject.

The lipase also provides a target for diagnosing active disease, or predisposition to disease, in a patient having a variant lipase. Thus, lipase can be isolated from a biological sample and assayed for the presence of a genetic mutation that results in an aberrant protein. This includes amino acid substitution, deletion, insertion, rearrangement, (as the result of aberrant splicing events), and inappropriate post-translational modification. Analytic methods include altered electrophoretic mobility, altered tryptic peptide digest, altered lipase activity in cell-based or cell-free assay, alteration in binding to or hydrolysis of lipids, binding to activator proteins, cell surface receptors, apoproteins, lipoproteins, proteoglycans, heparin, or antibody-binding pattern, altered isoelectric point, direct amino acid sequencing, and any other of the known assay techniques useful for detecting mutations in a protein in general or in a lipase specifically, including assays discussed herein.

In vitro techniques for detection of lipase include enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitations and immunofluorescence. Alternatively, the protein can be detected *in vivo* in a subject by introducing into the subject a labeled anti-lipase antibody. For example, the antibody can be labeled with a radioactive marker whose presence and location in a subject can be detected by standard imaging techniques. Particularly useful are methods, which detect the allelic variant of the lipase expressed in a subject, and methods, which detect fragments of the lipase in a sample.

The lipase polypeptides are also useful in pharmacogenomic analysis. Pharmacogenomics deal with clinically significant hereditary variations in the response to drugs due to altered drug disposition and abnormal action in affected persons. See, e.g., Eichelbaum, M. (1996) *Clin. Exp. Pharmacol. Physiol.* 23(10-11):983-985, and Linder, M.W. (1997) *Clin. Chem.* 43(2):254-266. The clinical outcomes of these variations result in severe toxicity of therapeutic drugs in certain individuals or therapeutic failure of drugs in certain individuals as a result of individual variation in

metabolism. Thus, the genotype of the individual can determine the way a therapeutic compound acts on the body or the way the body metabolizes the compound. Further, the activity of drug metabolizing enzymes affects both the intensity and duration of drug action. Thus, the pharmacogenomics of the individual permit the selection of effective compounds and effective dosages of such compounds for prophylactic or therapeutic treatment based on the individual's genotype. The discovery of genetic polymorphisms in some drug metabolizing enzymes has explained why some patients do not obtain the expected drug effects, show an exaggerated drug effect, or experience serious toxicity from standard drug dosages. Polymorphisms can be expressed in the phenotype of the extensive metabolizer and the phenotype of the poor metabolizer. Accordingly, genetic polymorphism may lead to allelic protein variants of the lipase in which one or more of the lipase functions in one population is different from those in another population. The polypeptides thus allow a target to ascertain a genetic predisposition that can affect treatment modality. Thus, in a lipase-based treatment, polymorphism may give rise to catalytic regions that are more or less active. Accordingly, dosage would necessarily be modified to maximize the therapeutic effect within a given population containing the polymorphism. As an alternative to genotyping, specific polymorphic polypeptides could be identified.

The lipase polypeptides are also useful for monitoring therapeutic effects during clinical trials and other treatment. Thus, the therapeutic effectiveness of an agent that is designed to increase or decrease gene expression, protein levels or lipase activity can be monitored over the course of treatment using the lipase polypeptides as an end-point target. The monitoring can be, for example, as follows: (i) obtaining a pre-administration sample from a subject prior to administration of the agent; (ii) detecting the level of expression or activity of the protein in the pre-administration sample; (iii) obtaining one or more post-administration samples from the subject; (iv) detecting the level of expression or activity of the protein in the post-administration samples; (v) comparing the level of expression or activity of the protein in the pre-administration sample with the protein in the post-administration sample or samples; and (vi) increasing or decreasing the administration of the agent to the subject accordingly.

Antibodies

The invention also provides antibodies that selectively bind to the lipase and its variants and fragments. An antibody is considered to selectively bind, even if it also binds to other proteins that are not substantially homologous with the lipase. These other proteins share homology with a fragment or domain of the lipase polypeptide. This conservation in specific regions gives rise to antibodies that bind to both proteins by virtue of the homologous sequence. In this case, it would be understood that antibody binding to the lipase is still selective.

To generate antibodies, an isolated lipase polypeptide is used as an immunogen to generate antibodies using standard techniques for polyclonal and monoclonal antibody preparation. Either the full-length protein or antigenic peptide fragment can be used. Regions having a high antigenicity index are shown in Figure 2.

Antibodies are preferably prepared from these regions or from discrete fragments in these regions. However, antibodies can be prepared from any region of the peptide as described herein. A preferred fragment produces an antibody that diminishes or completely prevents substrate hydrolysis or binding. Antibodies can be developed against the entire lipase protein or domains of the lipase as described herein. Antibodies can also be developed against specific functional sites as disclosed herein.

The antigenic peptide can comprise a contiguous sequence of at least 13, 14, 15, or 30 amino acid residues. In one embodiment, fragments correspond to regions that are located on the surface of the protein, e.g., hydrophilic regions. These fragments are not to be construed, however, as encompassing any fragments, which may be disclosed prior to the invention.

Antibodies can be polyclonal or monoclonal. An intact antibody, or a fragment thereof (e.g. Fab or F(ab')₂) can be used.

Detection can be facilitated by coupling (i.e., physically linking) the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, β -galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl

chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include ^{125}I , ^{131}I , ^{35}S or ^3H .

- 5 An appropriate immunogenic preparation can be derived from native, recombinantly expressed, or chemically synthesized peptides.

Antibody Uses

- 10 The antibodies can be used to isolate a lipase by standard techniques, such as affinity chromatography or immunoprecipitation. The antibodies can facilitate the purification of the natural lipase from cells and recombinantly produced lipase expressed in host cells.

The antibodies are useful to detect the presence of lipase in cells or tissues to determine the pattern of expression of the lipase among various tissues in an organism and over the course of normal development.

- 15 The antibodies can be used to detect lipase *in situ*, *in vitro*, or in a cell lysate or supernatant in order to evaluate the abundance and pattern of expression.

The antibodies can be used to assess abnormal tissue distribution or abnormal expression during development.

- 20 Antibody detection of circulating fragments of the full length lipase can be used to identify lipase turnover.

- 25 Further, the antibodies can be used to assess lipase expression in disease states such as in active stages of the disease or in an individual with a predisposition toward disease related to lipid metabolism. When a disorder is caused by an inappropriate tissue distribution, developmental expression, or level of expression of the lipase protein, the antibody can be prepared against the normal lipase protein. If a disorder is characterized by a specific mutation in the lipase, antibodies specific for this mutant protein can be used to assay for the presence of the specific mutant lipase polypeptides. However, intracellularly-made antibodies ("intrabodies") are also encompassed, which would recognize intracellular lipase-peptide regions.

- 30 The antibodies can also be used to assess normal and aberrant subcellular localization of cells in the various tissues in an organism. Antibodies can be developed against the whole lipase or portions of the lipase.

One method of delivering a chemotherapeutic agent to a vertebrate cancer cell which is abnormally expressing a lipase molecule involves contacting the cell with an antibody or biologically active antibody fragments where the antibody or antibody fragments specifically bind to a polypeptide encoded by the nucleotide sequence shown in SEQ ID NO:1 or other nucleotide sequences that differ from SEQ ID NO:1 in codon sequence due to the degeneracy of the genetic code.

The diagnostic uses can be applied, not only in genetic testing, but also in monitoring a treatment modality. Accordingly, where treatment is ultimately aimed at correcting lipase expression level or the presence of aberrant lipase proteins and aberrant tissue distribution or developmental expression, antibodies directed against the lipase or relevant fragments can be used to monitor therapeutic efficacy.

Antibodies accordingly can be used diagnostically to monitor protein levels in tissue as part of a clinical testing procedure, e.g., to, for example, determine the efficacy of a given treatment regimen.

Additionally, antibodies are useful in pharmacogenomic analysis. Thus, antibodies prepared against polymorphic lipases can be used to identify individuals that require modified treatment modalities.

The antibodies are also useful as diagnostic tools as an immunological marker for aberrant lipase analyzed by electrophoretic mobility, isoelectric point, tryptic peptide digest, and other physical assays known to those in the art.

The antibodies are also useful for tissue typing. Thus, where a specific lipase has been correlated with expression in a specific tissue, antibodies that are specific for this lipase can be used to identify a tissue type.

The antibodies are also useful in forensic identification. Accordingly, where an individual has been correlated with a specific genetic polymorphism resulting in a specific polymorphic protein, an antibody specific for the polymorphic protein can be used as an aid in identification.

The antibodies are also useful for inhibiting the various lipase functions as described herein.

These uses can also be applied in a therapeutic context in which treatment involves inhibiting lipase function. Antibodies can be prepared against specific fragments containing sites required for function or against intact lipase associated with a cell.

Completely human antibodies are particularly desirable for therapeutic treatment of human patients. For an overview of this technology for producing human antibodies, see Lonberg *et al.* (1995) *Int. Rev. Immunol.* 13:65-93. For a detailed discussion of this technology for producing human antibodies and human monoclonal antibodies and protocols for producing such antibodies, e.g., U.S. Patent 5,625,126; 5 U.S. Patent 5,633,425; U.S. Patent 5,569,825; U.S. Patent 5,661,016; and U.S. Patent 5,545,806.

The invention also encompasses kits for using antibodies to detect the presence of a lipase protein in a biological sample. The kit can comprise antibodies such as a 10 labeled or labelable antibody and a compound or agent for detecting lipase in a biological sample; means for determining the amount of lipase in the sample; and means for comparing the amount of lipase in the sample with a standard. The compound or agent can be packaged in a suitable container. The kit can further comprise instructions for using the kit to detect lipase.

15

Polynucleotides

The nucleotide sequence in SEQ ID NO:2 was obtained by sequencing the deposited human cDNA. Accordingly, the sequence of the deposited clone is controlling as to any discrepancies between the two and any reference to the sequence of SEQ ID 20 NO:2 includes reference to the sequence of the deposited cDNA.

The specifically disclosed cDNA comprises the coding region and 5' and 3' untranslated sequences in SEQ ID NO:2.

The invention provides isolated polynucleotides encoding the novel lipase. The term "lipase polynucleotide" or "lipase nucleic acid" refers to the sequence shown in 25 SEQ ID NO:2 or in the deposited cDNA. The term "lipase polynucleotide" or "lipase nucleic acid" further includes variants and fragments of the lipase polynucleotide.

An "isolated" lipase nucleic acid is one that is separated from other nucleic acid present in the natural source of the lipase nucleic acid. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the lipase nucleic acid (i.e., sequences 30 located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. However, there can be some flanking nucleotide sequences, for example up to about 5KB. The important point is that the lipase nucleic acid is isolated from flanking sequences such that it can be subjected to the specific

manipulations described herein, such as recombinant expression, preparation of probes and primers, and other uses specific to the lipase nucleic acid sequences.

Moreover, an "isolated" nucleic acid molecule, such as a cDNA or RNA molecule, can be substantially free of other cellular material, or culture medium when
5 produced by recombinant techniques, or chemical precursors or other chemicals when chemically synthesized. However, the nucleic acid molecule can be fused to other coding or regulatory sequences and still be considered isolated.

In some instances, the isolated material will form part of a composition (for example, a crude extract containing other substances), buffer system or reagent mix.
10 In other circumstances, the material may be purified to essential homogeneity, for example as determined by PAGE or column chromatography such as HPLC. Preferably, an isolated nucleic acid comprises at least about 50, 80 or 90 % (on a molar basis) of all macromolecular species present.

For example, recombinant DNA molecules contained in a vector are considered
15 isolated. Further examples of isolated DNA molecules include recombinant DNA molecules maintained in heterologous host cells or purified (partially or substantially) DNA molecules in solution. Isolated RNA molecules include *in vivo* or *in vitro* RNA transcripts of the isolated DNA molecules of the present invention. Isolated nucleic acid molecules according to the present invention further include such molecules produced
20 synthetically.

In some instances, the isolated material will form part of a composition (or example, a crude extract containing other substances), buffer system or reagent mix. In other circumstances, the material may be purified to essential homogeneity, for example as determined by PAGE or column chromatography such as HPLC. Preferably, an
25 isolated nucleic acid comprises at least about 50, 80 or 90% (on a molar basis) of all macromolecular species present.

The lipase polynucleotides can encode the mature protein plus additional amino or carboxyterminal amino acids, or amino acids interior to the mature polypeptide (when the mature form has more than one polypeptide chain, for instance). Such sequences
30 may play a role in processing of a protein from precursor to a mature form, facilitate protein trafficking, prolong or shorten protein half-life or facilitate manipulation of a protein for assay or production, among other things. As generally is the case *in situ*, the

additional amino acids may be processed away from the mature protein by cellular enzymes.

The lipase polynucleotides include, but are not limited to, the sequence encoding the mature polypeptide alone, the sequence encoding the mature polypeptide and
5 additional coding sequences, such as a leader or secretory sequence (e.g., a pre-pro or pro-protein sequence), the sequence encoding the mature polypeptide, with or without the additional coding sequences, plus additional non-coding sequences, for example introns and non-coding 5' and 3' sequences such as transcribed but non-translated sequences that play a role in transcription, mRNA processing (including splicing and
10 polyadenylation signals), ribosome binding and stability of mRNA. In addition, the polynucleotide may be fused to a marker sequence encoding, for example, a peptide that facilitates purification.

Lipase polynucleotides can be in the form of RNA, such as mRNA, or in the form DNA, including cDNA and genomic DNA obtained by cloning or produced by
15 chemical synthetic techniques or by a combination thereof. The nucleic acid, especially DNA, can be double-stranded or single-stranded. Single-stranded nucleic acid can be the coding strand (sense strand) or the non-coding strand (anti-sense strand).

Lipase nucleic acid can comprise the nucleotide sequence shown in SEQ ID NO:2, corresponding to human cDNA.

20 In one embodiment, the lipase nucleic acid comprises only the coding region.

The invention further provides variant lipase polynucleotides, and fragments thereof, that differ from the nucleotide sequence shown in SEQ ID NO:2 due to degeneracy of the genetic code and thus encode the same protein as that encoded by the nucleotide sequence shown in SEQ ID NO:2.

25 The invention also provides lipase nucleic acid molecules encoding the variant polypeptides described herein. Such polynucleotides may be naturally occurring, such as allelic variants (same locus), homologs (different locus), and orthologs (different organism), or may be constructed by recombinant DNA methods or by chemical synthesis. Such non-naturally occurring variants may be made by mutagenesis
30 techniques, including those applied to polynucleotides, cells, or organisms. Accordingly, as discussed above, the variants can contain nucleotide substitutions, deletions, inversions and insertions.

Typically, variants have a substantial identity with a nucleic acid molecule of SEQ ID NO:2 and the complements thereof. Variation can occur in either or both the coding and non-coding regions. The variations can produce both conservative and non-conservative amino acid substitutions.

5 Orthologs, homologs, and allelic variants can be identified using methods well known in the art. These variants comprise a nucleotide sequence encoding a lipase that is at least about 60-65%, 65-70%, typically at least about 70-75%, more typically at least about 80-85%, and most typically at least about 90-95% or more homologous to the nucleotide sequence shown in SEQ ID NO:2. Such nucleic acid molecules can readily
10 be identified as being able to hybridize under stringent conditions, to the nucleotide sequence shown in SEQ ID NO:2 or a fragment of the sequence. It is understood that stringent hybridization does not indicate substantial homology where it is due to general homology, such as poly A sequences, or sequences common to all or most proteins or all lipase enzymes. Moreover, it is understood that variants do not include any of the
15 nucleic acid sequences that may have been disclosed prior to the invention.

As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences encoding a polypeptide at least about 60-65% homologous to each other typically remain hybridized to each other. The conditions can be such that sequences at least about 65%,
20 at least about 70%, at least about 75%, at least about 80%, at least about 90%, at least about 95% or more identical to each other remain hybridized to one another. Such stringent conditions are known to those skilled in the art and can be found in *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6, incorporated by reference. One example of stringent hybridization conditions are
25 hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2 X SSC, 0.1% SDS at 50-65°C. In another non-limiting example, nucleic acid molecules are allowed to hybridize in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more low stringency washes in 0.2X SSC/0.1% SDS at room temperature, or by one or more moderate
30 stringency washes in 0.2X SSC/0.1% SDS at 42°C, or washed in 0.2X SSC/0.1% SDS at 65°C for high stringency. In one embodiment, an isolated nucleic acid molecule that hybridizes under stringent conditions to the sequence of SEQ ID NO:1 corresponds to a naturally-occurring nucleic acid molecule. As used herein, a "naturally-occurring"

nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (e.g., encodes a natural protein).

As understood by those of ordinary skill, the exact conditions can be determined empirically and depend on ionic strength, temperature and the concentration of destabilizing agents such as formamide or denaturing agents such as SDS. Other factors considered in determining the desired hybridization conditions include the length of the nucleic acid sequences, base composition, percent mismatch between the hybridizing sequences and the frequency of occurrence of subsets of the sequences within other non-identical sequences. Thus, equivalent conditions can be determined by varying one or more of these parameters while maintaining a similar degree of identity or similarity between the two nucleic acid molecules.

The present invention also provides isolated nucleic acids that contain a single or double stranded fragment or portion that hybridizes under stringent conditions to the nucleotide sequence of SEQ ID NO:2 or the complement of SEQ ID NO:2. In one embodiment, the nucleic acid consists of a portion of the nucleotide sequence of SEQ ID NO:2 or the complement of SEQ ID NO:2.

It is understood that isolated fragments include any contiguous sequence not disclosed prior to the invention as well as sequences that are substantially the same and which are not disclosed. Accordingly, if a fragment is disclosed prior to the present invention, that fragment is not intended to be encompassed by the invention. When a sequence is not disclosed prior to the present invention, an isolated nucleic acid fragment is at least about 5, preferably at least about 10, 15, 18, 20, 23 or 25 nucleotides, and can be 30, 40, 50, 100, 200, 500 or more nucleotides in length.

For example, nucleotide sequences 1 to about 1874 and about 2252 to about 2446 and sequences from about 2252 to 2264 are not disclosed prior to the invention. The nucleotide sequence from about 282-428 encompasses fragments greater than 15, 18, 20, 23 or 25 nucleotides; the nucleotide sequence from about 531 to about 912 encompasses fragments greater than 17, 20, 25, or 30 nucleotides; the nucleotide sequences from about 2264 to 2446 encompasses fragments greater than 20, 23, 25, or 30 nucleotides. Longer fragments, for example, 30 or more nucleotides in length, which encode antigenic proteins or polypeptides described herein are useful.

Furthermore, the invention provides polynucleotides that comprise a fragment of the full-length lipase polynucleotides. The fragment can be single or double-stranded

and can comprise DNA or RNA. The fragment can be derived from either the coding or the non-coding sequence.

In another embodiment an isolated lipase nucleic acid encodes the entire coding region. Other fragments include nucleotide sequences encoding the amino acid
5 fragments described herein.

Thus, lipase nucleic acid fragments further include sequences corresponding to the domains described herein, subregions also described, and specific functional sites. Lipase nucleic acid fragments also include combinations of the domains, segments, and other functional sites described above. A person of ordinary skill in the art would be
10 aware of the many permutations that are possible.

Where the location of the domains or sites have been predicted by computer analysis, one of ordinary skill would appreciate that the amino acid residues constituting these domains can vary depending on the criteria used to define the domains.

However, it is understood that a lipase fragment includes any nucleic acid
15 sequence that does not include the entire gene.

The invention also provides lipase nucleic acid fragments that encode epitope bearing regions of the lipase proteins described herein.

Nucleic acid fragments, according to the present invention, are not to be construed as encompassing those fragments that may have been disclosed prior to the
20 invention.

Polynucleotide Uses

The nucleotide sequences of the present invention can be used as a "query sequence" to perform a search against public databases, for example, to identify other
25 family members or related sequences. Such searches can be performed using the NBLAST and XBLAST programs (version 2.0) of Altschul *et al.* (1990) *J. Mol. Biol.* 215:403-10. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to the proteins of the invention. To obtain gapped alignments for comparison purposes,
30 Gapped BLAST can be utilized as described in Altschul *et al.* (1997) *Nucleic Acids Res.* 25(17):3389-3402. When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used. See <http://www.ncbi.nlm.nih.gov>.

The nucleic acid fragments of the invention provide probes or primers in assays such as those described below. "Probes" are oligonucleotides that hybridize in a base-specific manner to a complementary strand of nucleic acid. Such probes include polypeptide nucleic acids, as described in Nielsen *et al.* (1991) *Science* 254:1497-1500. Typically, a probe comprises a region of nucleotide sequence that hybridizes under highly stringent conditions to at least about 15, typically about 20-25, and more typically about 40, 50 or 75 consecutive nucleotides of the nucleic acid sequence shown in SEQ ID NO:2 and the complements thereof. More typically, the probe further comprises a label, e.g., radioisotope, fluorescent compound, enzyme, or enzyme co-factor.

As used herein, the term "primer" refers to a single-stranded oligonucleotide which acts as a point of initiation of template-directed DNA synthesis using well-known methods (e.g., PCR, LCR) including, but not limited to those described herein. The appropriate length of the primer depends on the particular use, but typically ranges from about 15 to 30 nucleotides. The term "primer site" refers to the area of the target DNA to which a primer hybridizes. The term "primer pair" refers to a set of primers including a 5' (upstream) primer that hybridizes with the 5' end of the nucleic acid sequence to be amplified and a 3' (downstream) primer that hybridizes with the complement of the sequence to be amplified.

The lipase polynucleotides are thus useful for probes, primers, and in biological assays.

Where the polynucleotides are used to assess lipase properties or functions, such as in the assays described herein, all or less than all of the entire cDNA can be useful. Assays specifically directed to lipase functions, such as assessing agonist or antagonist activity, encompass the use of known fragments. Further, diagnostic methods for assessing lipase function can also be practiced with any fragment, including those fragments that may have been known prior to the invention. Similarly, in methods involving treatment of lipase dysfunction, all fragments are encompassed including those, which may have been known in the art.

The lipase polynucleotides are useful as a hybridization probe for cDNA and genomic DNA to isolate a full-length cDNA and genomic clones encoding the polypeptide described in SEQ ID NO:1 and to isolate cDNA and genomic clones that correspond to variants producing the same polypeptide shown in SEQ ID NO:1 or the

other variants described herein. Variants can be isolated from the same tissue and organism from which the polypeptides shown in SEQ ID NO:1 were isolated, different tissues from the same organism, or from different organisms. This method is useful for isolating genes and cDNA that are developmentally-controlled and therefore may be expressed in the same tissue or different tissues at different points in the development of an organism.

The probe can correspond to any sequence along the entire length of the gene encoding the lipase. Accordingly, it could be derived from 5' noncoding regions, the coding region, and 3' noncoding regions.

10 The nucleic acid probe can be, for example, the full-length cDNA of SEQ ID NO:2 or a fragment thereof that is sufficient to specifically hybridize under stringent conditions to mRNA or DNA.

Fragments of the polynucleotides described herein are also useful to synthesize larger fragments or full-length polynucleotides described herein. For example, a fragment can be hybridized to any portion of an mRNA and a larger or full-length cDNA can be produced.

The fragments are also useful to synthesize antisense molecules of desired length and sequence.

Antisense nucleic acids of the invention can be designed using the nucleotide sequence of SEQ ID NO:2, and constructed using chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (e.g., an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, e.g., phosphorothioate derivatives and acridine substituted nucleotides can be used. Examples of modified nucleotides which can be used to generate the antisense nucleic acid include 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-

methyllaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (i.e., RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest).

Additionally, the nucleic acid molecules of the invention can be modified at the base moiety, sugar moiety or phosphate backbone to improve, e.g., the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup *et al.* (1996) *Bioorganic & Medicinal Chemistry* 4:5). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, e.g., DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described in Hyrup *et al.* (1996), *supra*; Perry-O'Keefe *et al.* (1996) *Proc. Natl. Acad. Sci. USA* 93:14670. PNAs can be further modified, e.g., to enhance their stability, specificity or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996), *supra*, Finn *et al.* (1996) *Nucleic Acids Res.* 24(17):3357-63, Mag *et al.* (1989) *Nucleic Acids Res.* 17:5973, and Peterser *et al.* (1975) *Bioorganic Med. Chem. Lett.* 5:1119.

The nucleic acid molecules and fragments of the invention can also include other appended groups such as peptides (e.g., for targeting host cell lipases *in vivo*), or agents facilitating transport across the cell membrane (see, e.g., Letsinger *et al.* (1989) *Proc. Natl. Acad. Sci. USA* 86:6553-6556; Lemaitre *et al.* (1987) *Proc. Natl. Acad.*

Sci. USA 84:648-652; PCT Publication No. WO 88/0918) or the blood brain barrier (see, e.g., PCT Publication No. WO 89/10134). In addition, oligonucleotides can be modified with hybridization-triggered cleavage agents (see, e.g., Krol *et al.* (1988) *Bio-Techniques* 6:958-976) or intercalating agents (see, e.g., Zon (1988) *Pharm Res.* 5:539-549).

The lipase polynucleotides are also useful as primers for PCR to amplify any given region of a lipase polynucleotide.

The lipase polynucleotides are also useful for constructing recombinant vectors. Such vectors include expression vectors that express a portion of, or all of, the lipase polypeptides. Vectors also include insertion vectors, used to integrate into another polynucleotide sequence, such as into the cellular genome, to alter *in situ* expression of lipase genes and gene products. For example, an endogenous lipase coding sequence can be replaced via homologous recombination with all or part of the coding region containing one or more specifically introduced mutations.

The lipase polynucleotides are also useful for expressing antigenic portions of the lipase proteins.

The lipase polynucleotides are also useful as probes for determining the chromosomal positions of the lipase polynucleotides by means of *in situ* hybridization methods, such as FISH. (For a review of this technique, see Verma *et al.* (1988) *Human Chromosomes: A Manual of Basic Techniques* (Pergamon Press, New York), and PCR mapping of somatic cell hybrids. The mapping of the sequences to chromosomes is an important first step in correlating these sequences with genes associated with disease.

Reagents for chromosome mapping can be used individually to mark a single chromosome or a single site on that chromosome, or panels of reagents can be used for marking multiple sites and/or multiple chromosomes. Reagents corresponding to noncoding regions of the genes actually are preferred for mapping purposes. Coding sequences are more likely to be conserved within gene families, thus increasing the chance of cross hybridizations during chromosomal mapping.

Once a sequence has been mapped to a precise chromosomal location, the physical position of the sequence on the chromosome can be correlated with genetic map data. (Such data are found, for example, in V. McKusick, *Mendelian Inheritance in Man*, available on-line through Johns Hopkins University Welch Medical Library). The relationship between a gene and a disease mapped to the same chromosomal region, can

then be identified through linkage analysis (co-inheritance of physically adjacent genes), described in, for example, Egeland *et al.* ((1987) *Nature* 325:783-787).

Moreover, differences in the DNA sequences between individuals affected and unaffected with a disease associated with a specified gene, can be determined. If a
5 mutation is observed in some or all of the affected individuals but not in any unaffected individuals, then the mutation is likely to be the causative agent of the particular disease. Comparison of affected and unaffected individuals generally involves first looking for structural alterations in the chromosomes, such as deletions or translocations, that are visible from chromosome spreads, or detectable using PCR based on that DNA
10 sequence. Ultimately, complete sequencing of genes from several individuals can be performed to confirm the presence of a mutation and to distinguish mutations from polymorphisms.

The lipase polynucleotide probes are also useful to determine patterns of the presence of the gene encoding the lipase and their variants with respect to tissue
15 distribution, for example, whether gene duplication has occurred and whether the duplication occurs in all or only a subset of tissues. The genes can be naturally occurring or can have been introduced into a cell, tissue, or organism exogenously.

The lipase polynucleotides are also useful for designing ribozymes corresponding to all, or a part, of the mRNA produced from genes encoding the
20 polynucleotides described herein.

The lipase polynucleotides are also useful for constructing host cells expressing a part, or all, of the lipase polynucleotides and polypeptides.

The lipase polynucleotides are also useful for constructing transgenic animals expressing all, or a part, of the lipase polynucleotides and polypeptides.

25 The lipase polynucleotides are also useful for making vectors that express part, or all, of the lipase polypeptides.

The lipase polynucleotides are also useful as hybridization probes for determining the level of lipase nucleic acid expression. Accordingly, the probes can be used to detect the presence of, or to determine levels of, lipase nucleic acid in cells,
30 tissues, and in organisms. The nucleic acid whose level is determined can be DNA or RNA. Accordingly, probes corresponding to the polypeptides described herein can be used to assess gene copy number in a given cell, tissue, or organism. This is particularly relevant in cases in which there has been an amplification of the lipase genes.

Alternatively, the probe can be used in an *in situ* hybridization context to assess the position of extra copies of the lipase genes, as on extrachromosomal elements or as integrated into chromosomes in which the lipase gene is not normally found, for example as a homogeneously staining region.

5 These uses are relevant for diagnosis of disorders involving an increase or decrease in lipase expression relative to normal, such as a developmental or a metabolic disorder. Tissues and/or cells in which the lipases are expressed and disorders in which the lipase expression is relevant, include but are not limited to, those disclosed herein above.

10 Thus, the present invention provides a method for identifying a disease or disorder associated with aberrant expression or activity of lipase nucleic acid, in which a test sample is obtained from a subject and nucleic acid (e.g., mRNA, genomic DNA) is detected, wherein the presence of the nucleic acid is diagnostic for a subject having or at risk of developing a disease or disorder associated with aberrant
15 expression or activity of the nucleic acid.

One aspect of the invention relates to diagnostic assays for determining nucleic acid expression as well as activity in the context of a biological sample (e.g., blood, serum, cells, tissue) to determine whether an individual has a disease or disorder, or is at risk of developing a disease or disorder, associated with aberrant
20 nucleic acid expression or activity. Such assays can be used for prognostic or predictive purpose to thereby prophylactically treat an individual prior to the onset of a disorder characterized by or associated with expression or activity of the nucleic acid molecules.

In vitro techniques for detection of mRNA include Northern hybridizations and
25 *in situ* hybridizations. *In vitro* techniques for detecting DNA includes Southern hybridizations and *in situ* hybridization.

Probes can be used as a part of a diagnostic test kit for identifying cells or tissues that express the lipase, such as by measuring the level of a lipase-encoding nucleic acid in a sample of cells from a subject e.g., mRNA or genomic DNA, or determining if the
30 lipase gene has been mutated.

Nucleic acid expression assays are useful for drug screening to identify compounds that modulate lipase nucleic acid expression (e.g., antisense, polypeptides, peptidomimetics, small molecules or other drugs). A cell is contacted with a candidate

compound and the expression of mRNA determined. The level of expression of the mRNA in the presence of the candidate compound is compared to the level of expression of the mRNA in the absence of the candidate compound. The candidate compound can then be identified as a modulator of nucleic acid expression based on this comparison and be used, for example to treat a disorder characterized by aberrant nucleic acid expression. The modulator can bind to the nucleic acid or indirectly modulate expression, such as by interacting with other cellular components that affect nucleic acid expression.

Modulatory methods can be performed *in vitro* (e.g., by culturing the cell with the agent) or, alternatively, *in vivo* (e.g., by administering the agent to a subject) in patients or in transgenic animals.

The invention thus provides a method for identifying a compound that can be used to treat a disorder associated with nucleic acid expression of the lipase gene. The method typically includes assaying the ability of the compound to modulate the expression of the lipase nucleic acid and thus identifying a compound that can be used to treat a disorder characterized by undesired lipase nucleic acid expression.

The assays can be performed in cell-based and cell-free systems. Cell-based assays include cells naturally expressing the lipase nucleic acid or recombinant cells genetically engineered to express specific nucleic acid sequences.

Alternatively, candidate compounds can be assayed *in vivo* in patients or in transgenic animals.

The assay for lipase nucleic acid expression can involve direct assay of nucleic acid levels, such as mRNA levels, or on collateral compounds involved in the pathway. Further, the expression of genes that are up- or down-regulated in response to the lipase activity can also be assayed. In this embodiment the regulatory regions of these genes can be operably linked to a reporter gene such as luciferase.

Thus, modulators of lipase gene expression can be identified in a method wherein a cell is contacted with a candidate compound and the expression of mRNA determined. The level of expression of lipase mRNA in the presence of the candidate compound is compared to the level of expression of lipase mRNA in the absence of the candidate compound. The candidate compound can then be identified as a modulator of nucleic acid expression based on this comparison and be used, for example to treat a disorder characterized by aberrant nucleic acid expression. When expression of mRNA

is statistically significantly greater in the presence of the candidate compound than in its absence, the candidate compound is identified as a stimulator of nucleic acid expression. When nucleic acid expression is statistically significantly less in the presence of the candidate compound than in its absence, the candidate compound is identified as an inhibitor of nucleic acid expression.

Accordingly, the invention provides methods of treatment, with the nucleic acid as a target, using a compound identified through drug screening as a gene modulator to modulate lipase nucleic acid expression. Modulation includes both up-regulation (i.e. activation or agonization) or down-regulation (suppression or antagonization) or effects on nucleic acid activity (e.g. when nucleic acid is mutated or improperly modified). Treatment includes disorders characterized by aberrant expression or activity of the nucleic acid. In addition, disorders that are influenced by the lipase may also be treated. Examples of such disorders are disclosed herein.

Alternatively, a modulator for lipase nucleic acid expression can be a small molecule or drug identified using the screening assays described herein as long as the drug or small molecule inhibits the lipase nucleic acid expression.

The lipase polynucleotides are also useful for monitoring the effectiveness of modulating compounds on the expression or activity of the lipase gene in clinical trials or in a treatment regimen. Thus, the gene expression pattern can serve as a barometer for the continuing effectiveness of treatment with the compound, particularly with compounds to which a patient can develop resistance. The gene expression pattern can also serve as a marker indicative of a physiological response of the affected cells to the compound. Accordingly, such monitoring would allow either increased administration of the compound or the administration of alternative compounds to which the patient has not become resistant. Similarly, if the level of nucleic acid expression falls below a desirable level, administration of the compound could be commensurately decreased.

Monitoring can be, for example, as follows: (i) obtaining a pre-administration sample from a subject prior to administration of the agent; (ii) detecting the level of expression of a specified mRNA or genomic DNA of the invention in the pre-administration sample; (iii) obtaining one or more post-administration samples from the subject; (iv) detecting the level of expression or activity of the mRNA or genomic DNA in the post-administration samples; (v) comparing the level of expression or activity of the mRNA or genomic DNA in the pre-administration sample with the

mRNA or genomic DNA in the post-administration sample or samples; and (vi) increasing or decreasing the administration of the agent to the subject accordingly.

The lipase polynucleotides are also useful in diagnostic assays for qualitative changes in lipase nucleic acid, and particularly in qualitative changes that lead to pathology. The polynucleotides can be used to detect mutations in lipase genes and gene expression products such as mRNA. The polynucleotides can be used as hybridization probes to detect naturally-occurring genetic mutations in the lipase gene and thereby to determine whether a subject with the mutation is at risk for a disorder caused by the mutation. Mutations include deletion, addition, or substitution of one or more nucleotides in the gene, chromosomal rearrangement, such as inversion or transposition, modification of genomic DNA, such as aberrant methylation patterns or changes in gene copy number, such as amplification. Detection of a mutated form of the lipase gene associated with a dysfunction provides a diagnostic tool for an active disease or susceptibility to disease when the disease results from overexpression, underexpression, or altered expression of a lipase.

Mutations in the lipase gene can be detected at the nucleic acid level by a variety of techniques. Genomic DNA can be analyzed directly or can be amplified by using PCR prior to analysis. RNA or cDNA can be used in the same way.

In certain embodiments, detection of the mutation involves the use of a probe/primer in a polymerase chain reaction (PCR) (see, e.g. U.S. Patent Nos. 4,683,195 and 4,683,202), such as anchor PCR or RACE PCR, or, alternatively, in a ligation chain reaction (LCR) (see, e.g., Landegran *et al.* (1988) *Science* 241:1077-1080; and Nakazawa *et al.* (1994) *PNAS* 91:360-364), the latter of which can be particularly useful for detecting point mutations in the gene (see Abravaya *et al.* (1995) *Nucleic Acids Res.* 23:675-682). This method can include the steps of collecting a sample of cells from a patient, isolating nucleic acid (e.g., genomic, mRNA or both) from the cells of the sample, contacting the nucleic acid sample with one or more primers which specifically hybridize to a gene under conditions such that hybridization and amplification of the gene (if present) occurs, and detecting the presence or absence of an amplification product, or detecting the size of the amplification product and comparing the length to a control sample. Deletions and insertions can be detected by a change in size of the amplified product compared to the normal genotype. Point mutations can be identified by hybridizing amplified DNA to normal RNA or antisense DNA sequences.

It is anticipated that PCR and/or LCR may be desirable to use as a preliminary amplification step in conjunction with any of the techniques used for detecting mutations described herein.

Alternative amplification methods include: self sustained sequence replication (Guatelli *et al.* (1990) *Proc. Natl. Acad. Sci. USA* 87:1874-1878), transcriptional amplification system (Kwoh *et al.* (1989) *Proc. Natl. Acad. Sci. USA* 86:1173-1177), Q-Beta Replicase (Lizardi *et al.* (1988) *Bio/Technology* 6:1197), or any other nucleic acid amplification method, followed by the detection of the amplified molecules using techniques well-known to those of skill in the art. These detection schemes are especially useful for the detection of nucleic acid molecules if such molecules are present in very low numbers.

Alternatively, mutations in a lipase gene can be directly identified, for example, by alterations in restriction enzyme digestion patterns determined by gel electrophoresis.

Further, sequence-specific ribozymes (U.S. Patent No. 5,498,531) can be used to score for the presence of specific mutations by development or loss of a ribozyme cleavage site.

Perfectly matched sequences can be distinguished from mismatched sequences by nuclease cleavage digestion assays or by differences in melting temperature.

Sequence changes at specific locations can also be assessed by nuclease protection assays such as RNase and S1 protection or the chemical cleavage method.

Furthermore, sequence differences between a mutant lipase gene and a wild-type gene can be determined by direct DNA sequencing. A variety of automated sequencing procedures can be utilized when performing the diagnostic assays ((1995) *Biotechniques* 19:448), including sequencing by mass spectrometry (see, e.g., PCT International Publication No. WO 94/16101; Cohen *et al.* (1996) *Adv. Chromatogr.* 36:127-162; and Griffin *et al.* (1993) *Appl. Biochem. Biotechnol.* 38:147-159).

Other methods for detecting mutations in the gene include methods in which protection from cleavage agents is used to detect mismatched bases in RNA/RNA or RNA/DNA duplexes (Myers *et al.* (1985) *Science* 230:1242); Cotton *et al.* (1988) *PNAS* 85:4397; Saleeba *et al.* (1992) *Meth. Enzymol.* 217:286-295), electrophoretic mobility of mutant and wild type nucleic acid is compared (Orita *et al.* (1989) *PNAS* 86:2766; Cotton *et al.* (1993) *Mutat. Res.* 285:125-144; and Hayashi *et al.* (1992) *Genet. Anal. Tech. Appl.* 9:73-79), and movement of mutant or wild-type fragments in

polyacrylamide gels containing a gradient of denaturant is assayed using denaturing gradient gel electrophoresis (Myers *et al.* (1985) *Nature* 313:495). The sensitivity of the assay may be enhanced by using RNA (rather than DNA), in which the secondary structure is more sensitive to a change in sequence. In one embodiment, the subject method utilizes heteroduplex analysis to separate double stranded heteroduplex molecules on the basis of changes in electrophoretic mobility (Keen *et al.* (1991) *Trends Genet.* 7:5). Examples of other techniques for detecting point mutations include, selective oligonucleotide hybridization, selective amplification, and selective primer extension.

10 In other embodiments, genetic mutations can be identified by hybridizing a sample and control nucleic acids, e.g., DNA or RNA, to high density arrays containing hundreds or thousands of oligonucleotide probes (Cronin *et al.* (1996) *Human Mutation* 7:244-255; Kozal *et al.* (1996) *Nature Medicine* 2:753-759). For example, genetic mutations can be identified in two dimensional arrays containing
15 light-generated DNA probes as described in Cronin *et al. supra*. Briefly, a first hybridization array of probes can be used to scan through long stretches of DNA in a sample and control to identify base changes between the sequences by making linear arrays of sequential overlapping probes. This step allows the identification of point mutations. This step is followed by a second hybridization array that allows the
20 characterization of specific mutations by using smaller, specialized probe arrays complementary to all variants or mutations detected. Each mutation array is composed of parallel probe sets, one complementary to the wild-type gene and the other complementary to the mutant gene.

The lipase polynucleotides are also useful for testing an individual for a genotype
25 that while not necessarily causing the disease, nevertheless affects the treatment modality. Thus, the polynucleotides can be used to study the relationship between an individual's genotype and the individual's response to a compound used for treatment (pharmacogenomic relationship). Accordingly, the lipase polynucleotides described herein can be used to assess the mutation content of the gene in an individual in order to
30 select an appropriate compound or dosage regimen for treatment.

Thus polynucleotides displaying genetic variations that affect treatment provide a diagnostic target that can be used to tailor treatment in an individual. Accordingly, the

production of recombinant cells and animals containing these polymorphisms allow effective clinical design of treatment compounds and dosage regimens.

The methods can involve obtaining a control biological sample from a control subject, contacting the control sample with a compound or agent capable of detecting mRNA, or genomic DNA, such that the presence of mRNA or genomic DNA is
5 detected in the biological sample, and comparing the presence of mRNA or genomic DNA in the control sample with the presence of mRNA or genomic DNA in the test sample.

The lipase polynucleotides are also useful for chromosome identification when
10 the sequence is identified with an individual chromosome and to a particular location on the chromosome. First, the DNA sequence is matched to the chromosome by *in situ* or other chromosome-specific hybridization. Sequences can also be correlated to specific chromosomes by preparing PCR primers that can be used for PCR screening of somatic cell hybrids containing individual chromosomes from the desired species. Only hybrids
15 containing the chromosome containing the gene homologous to the primer will yield an amplified fragment. Sublocalization can be achieved using chromosomal fragments. Other strategies include prescreening with labeled flow-sorted chromosomes and preselection by hybridization to chromosome-specific libraries. Further mapping strategies include fluorescence *in situ* hybridization, which allows hybridization with
20 probes shorter than those traditionally used. Reagents for chromosome mapping can be used individually to mark a single chromosome or a single site on the chromosome, or panels of reagents can be used for marking multiple sites and/or multiple chromosomes. Reagents corresponding to noncoding regions of the genes actually are preferred for mapping purposes. Coding sequences are more likely to be conserved within gene
25 families, thus increasing the chance of cross hybridizations during chromosomal mapping.

The lipase polynucleotides can also be used to identify individuals based on small biological samples. This can be done for example using restriction fragment-length polymorphism (RFLP) to identify an individual. Thus, the polynucleotides
30 described herein are useful as DNA markers for RFLP (See U.S. Patent No. 5,272,057).

Furthermore, the lipase sequence can be used to provide an alternative technique, which determines the actual DNA sequence of selected fragments in the genome of an individual. Thus, the lipase sequences described herein can be used to prepare two PCR

primers from the 5' and 3' ends of the sequences. These primers can then be used to amplify DNA from an individual for subsequent sequencing.

Panels of corresponding DNA sequences from individuals prepared in this manner can provide unique individual identifications, as each individual will have a unique set of such DNA sequences. It is estimated that allelic variation in humans occurs with a frequency of about once per each 500 bases. Allelic variation occurs to some degree in the coding regions of these sequences, and to a greater degree in the noncoding regions. The lipase sequences can be used to obtain such identification sequences from individuals and from tissue. The sequences represent unique fragments of the human genome. Each of the sequences described herein can, to some degree, be used as a standard against which DNA from an individual can be compared for identification purposes.

If a panel of reagents from the sequences is used to generate a unique identification database for an individual, those same reagents can later be used to identify tissue from that individual. Using the unique identification database, positive identification of the individual, living or dead, can be made from extremely small tissue samples.

The lipase polynucleotides can also be used in forensic identification procedures. PCR technology can be used to amplify DNA sequences taken from very small biological samples, such as a single hair follicle, body fluids (e.g. blood, saliva, or semen). The amplified sequence can then be compared to a standard allowing identification of the origin of the sample.

The lipase polynucleotides can thus be used to provide polynucleotide reagents, e.g., PCR primers, targeted to specific loci in the human genome, which can enhance the reliability of DNA-based forensic identifications by, for example, providing another "identification marker" (i.e. another DNA sequence that is unique to a particular individual). As described above, actual base sequence information can be used for identification as an accurate alternative to patterns formed by restriction enzyme generated fragments. Sequences targeted to the noncoding region are particularly useful since greater polymorphism occurs in the noncoding regions, making it easier to differentiate individuals using this technique.

The lipase polynucleotides can further be used to provide polynucleotide reagents, e.g., labeled or labelable probes which can be used in, for example, an *in situ*

hybridization technique, to identify a specific tissue. This is useful in cases in which a forensic pathologist is presented with a tissue of unknown origin. Panels of lipase probes can be used to identify tissue by species and/or by organ type.

In a similar fashion, these primers and probes can be used to screen tissue culture for contamination (i.e. screen for the presence of a mixture of different types of cells in a culture).

Alternatively, the lipase polynucleotides can be used directly to block transcription or translation of lipase gene sequences by means of antisense or ribozyme constructs. Thus, in a disorder characterized by abnormally high or undesirable lipase gene expression, nucleic acids can be directly used for treatment.

The lipase polynucleotides are thus useful as antisense constructs to control lipase gene expression in cells, tissues, and organisms. A DNA antisense polynucleotide is designed to be complementary to a region of the gene involved in transcription, preventing transcription and hence production of lipase protein. An antisense RNA or DNA polynucleotide would hybridize to the mRNA and thus block translation of mRNA into lipase protein.

Examples of antisense molecules useful to inhibit nucleic acid expression include antisense molecules complementary to a fragment of the 5' untranslated region of SEQ ID NO:2 which also includes the start codon and antisense molecules which are complementary to a fragment of the 3' untranslated region of SEQ ID NO:2.

Alternatively, a class of antisense molecules can be used to inactivate mRNA in order to decrease expression of lipase nucleic acid. Accordingly, these molecules can treat a disorder characterized by abnormal or undesired lipase nucleic acid expression. This technique involves cleavage by means of ribozymes containing nucleotide sequences complementary to one or more regions in the mRNA that attenuate the ability of the mRNA to be translated. Possible regions include coding regions and particularly coding regions corresponding to the catalytic and other functional activities of the lipase protein.

The lipase polynucleotides also provide vectors for gene therapy in patients containing cells that are aberrant in lipase gene expression. Thus, recombinant cells, which include the patient's cells that have been engineered *ex vivo* and returned to the patient, are introduced into an individual where the cells produce the desired lipase protein to treat the individual.

The invention also encompasses kits for detecting the presence of a lipase nucleic acid in a biological sample. For example, the kit can comprise reagents such as a labeled or labelable nucleic acid or agent capable of detecting lipase nucleic acid in a biological sample; means for determining the amount of lipase nucleic acid in the sample; and means for comparing the amount of lipase nucleic acid in the sample with a standard. The compound or agent can be packaged in a suitable container. The kit can further comprise instructions for using the kit to detect lipase mRNA or DNA.

Computer Readable Means

10 The nucleotide or amino acid sequences of the invention are also provided in a variety of mediums to facilitate use thereof. As used herein, "provided" refers to a manufacture, other than an isolated nucleic acid or amino acid molecule, which contains a nucleotide or amino acid sequence of the present invention. Such a manufacture provides the nucleotide or amino acid sequences, or a subset thereof
15 (e.g., a subset of open reading frames (ORFs)) in a form which allows a skilled artisan to examine the manufacture using means not directly applicable to examining the nucleotide or amino acid sequences, or a subset thereof, as they exists in nature or in purified form.

 In one application of this embodiment, a nucleotide or amino acid sequence of
20 the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium that can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM;
25 and hybrids of these categories such as magnetic/optical storage media. The skilled artisan will readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide or amino acid sequence of the present invention.

 As used herein, "recorded" refers to a process for storing information on
30 computer readable medium. The skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate manufactures comprising the nucleotide or amino acid sequence information of the present invention.

A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide or amino acid sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition,
5 a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as
10 DB2, Sybase, Oracle, or the like. The skilled artisan can readily adapt any number of dataprocessor structuring formats (e.g., text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing the nucleotide or amino acid sequences of the invention in
15 computer readable form, the skilled artisan can routinely access the sequence information for a variety of purposes. For example, one skilled in the art can use the nucleotide or amino acid sequences of the invention in computer readable form to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or
20 regions of the sequences of the invention which match a particular target sequence or target motif.

As used herein, a "target sequence" can be any DNA or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be
25 present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 100 amino acids or from about 30 to 300 nucleotide residues. However, it is well recognized that commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

30 As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein

target motifs include, but are not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

Computer software is publicly available which allows a skilled artisan to
5 access sequence information provided in a computer readable medium for analysis and comparison to other sequences. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, MacPattern (EMBL),
10 BLASTN and BLASTX (NCBIA).

For example, software which implements the BLAST (Altschul *et al.* (1990) *J. Mol. Biol.* 215:403-410) and BLAZE (Brutlag *et al.* (1993) *Comp. Chem.* 17:203-207) search algorithms on a Sybase system can be used to identify open reading frames (ORFs) of the sequences of the invention which contain homology to ORFs or
15 proteins from other libraries. Such ORFs are protein encoding fragments and are useful in producing commercially important proteins such as enzymes used in various reactions and in the production of commercially useful metabolites.

Vectors/Host Cells

20 The invention also provides vectors containing the lipase polynucleotides. The term "vector" refers to a vehicle, preferably a nucleic acid molecule that can transport the lipase polynucleotides. When the vector is a nucleic acid molecule, the lipase polynucleotides are covalently linked to the vector nucleic acid. With this aspect of the invention, the vector includes a plasmid, single or double stranded phage, a single or
25 double stranded RNA or DNA viral vector, or artificial chromosome, such as a BAC, PAC, YAC, OR MAC.

A vector can be maintained in the host cell as an extrachromosomal element where it replicates and produces additional copies of the lipase polynucleotides. Alternatively, the vector may integrate into the host cell genome and produce additional
30 copies of the lipase polynucleotides when the host cell replicates.

The invention provides vectors for the maintenance (cloning vectors) or vectors for expression (expression vectors) of the lipase polynucleotides. The vectors can function in procaryotic or eukaryotic cells or in both (shuttle vectors).

Expression vectors contain cis-acting regulatory regions that are operably linked in the vector to the lipase polynucleotides such that transcription of the polynucleotides is allowed in a host cell. The polynucleotides can be introduced into the host cell with a separate polynucleotide capable of affecting transcription. Thus, the second
5 polynucleotide may provide a trans-acting factor interacting with the cis-regulatory control region to allow transcription of the lipase polynucleotides from the vector. Alternatively, a trans-acting factor may be supplied by the host cell. Finally, a trans-acting factor can be produced from the vector itself.

It is understood, however, that in some embodiments, transcription and/or
10 translation of the lipase polynucleotides can occur in a cell-free system.

The regulatory sequence to which the polynucleotides described herein can be operably linked include promoters for directing mRNA transcription. These include, but are not limited to, the left promoter from bacteriophage λ , the lac, TRP, and TAC promoters from *E. coli*, the early and late promoters from SV40, the CMV immediate
15 early promoter, the adenovirus early and late promoters, and retrovirus long-terminal repeats.

In addition to control regions that promote transcription, expression vectors may also include regions that modulate transcription, such as repressor binding sites and enhancers. Examples include the SV40 enhancer, the cytomegalovirus immediate early
20 enhancer, polyoma enhancer, adenovirus enhancers, and retrovirus LTR enhancers.

In addition to containing sites for transcription initiation and control, expression vectors can also contain sequences necessary for transcription termination and, in the transcribed region a ribosome binding site for translation. Other regulatory control elements for expression include initiation and termination codons as well as
25 polyadenylation signals. The person of ordinary skill in the art would be aware of the numerous regulatory sequences that are useful in expression vectors. Such regulatory sequences are described, for example, in Sambrook *et al.* (1989) *Molecular Cloning: A Laboratory Manual 2nd. ed.*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY).

30 A variety of expression vectors can be used to express a lipase polynucleotide. Such vectors include chromosomal, episomal, and virus-derived vectors, for example vectors derived from bacterial plasmids, from bacteriophage, from yeast episomes, from yeast chromosomal elements, including yeast artificial chromosomes, from viruses such

as baculoviruses, papovaviruses such as SV40, Vaccinia viruses, adenoviruses, poxviruses, pseudorabies viruses, and retroviruses. Vectors may also be derived from combinations of these sources such as those derived from plasmid and bacteriophage genetic elements, e.g. cosmids and phagemids. Appropriate cloning and expression
5 vectors for prokaryotic and eukaryotic hosts are described in Sambrook *et al.* (1989) *Molecular Cloning: A Laboratory Manual 2nd. ed.*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY.

The regulatory sequence may provide constitutive expression in one or more host cells (i.e. tissue specific) or may provide for inducible expression in one or more cell
10 types such as by temperature, nutrient additive, or exogenous factor such as a hormone or other ligand. A variety of vectors providing for constitutive and inducible expression in prokaryotic and eukaryotic hosts are well known to those of ordinary skill in the art.

The lipase polynucleotides can be inserted into the vector nucleic acid by well-known methodology. Generally, the DNA sequence that will ultimately be expressed is
15 joined to an expression vector by cleaving the DNA sequence and the expression vector with one or more restriction enzymes and then ligating the fragments together. Procedures for restriction enzyme digestion and ligation are well known to those of ordinary skill in the art.

The vector containing the appropriate polynucleotide can be introduced into an
20 appropriate host cell for propagation or expression using well-known techniques. Bacterial cells include, but are not limited to, *E. coli*, *Streptomyces*, and *Salmonella typhimurium*. Eukaryotic cells include, but are not limited to, yeast, insect cells such as *Drosophila*, animal cells such as COS and CHO cells, and plant cells.

As described herein, it may be desirable to express the polypeptide as a fusion
25 protein. Accordingly, the invention provides fusion vectors that allow for the production of the lipase polypeptides. Fusion vectors can increase the expression of a recombinant protein, increase the solubility of the recombinant protein, and aid in the purification of the protein by acting for example as a ligand for affinity purification. A proteolytic cleavage site may be introduced at the junction of the fusion moiety so that the desired
30 polypeptide can ultimately be separated from the fusion moiety. Proteolytic enzymes include, but are not limited to, factor Xa, thrombin, and enterokinase. Typical fusion expression vectors include pGEX (Smith *et al.* (1988) *Gene* 67:31-40), pMAL (New England Biolabs, Beverly, MA) and pRIT5 (Pharmacia, Piscataway, NJ) which fuse

glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein. Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amann *et al.* (1988) *Gene* 69:301-315) and pET 11d (Studier *et al.* (1990) *Gene Expression Technology: Methods in Enzymology* 185:60-89).

5 Recombinant protein expression can be maximized in a host bacteria by providing a genetic background wherein the host cell has an impaired capacity to proteolytically cleave the recombinant protein. (Gottesman, S. (1990) *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California 119-128). Alternatively, the sequence of the polynucleotide of interest can be altered to
10 provide preferential codon usage for a specific host cell, for example *E. coli*. (Wada *et al.* (1992) *Nucleic Acids Res.* 20:2111-2118).

 The lipase polynucleotides can also be expressed by expression vectors that are operative in yeast. Examples of vectors for expression in yeast e.g., *S. cerevisiae* include pYepSec1 (Baldari *et al.* (1987) *EMBO J.* 6:229-234), pMFa (Kurjan *et al.* (1982) *Cell*
15 30:933-943), pJRY88 (Schultz *et al.* (1987) *Gene* 54:113-123), and pYES2 (Invitrogen Corporation, San Diego, CA).

 The lipase polynucleotides can also be expressed in insect cells using, for example, baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (e.g., Sf 9 cells) include the pAc series (Smith *et al.*
20 (1983) *Mol. Cell Biol.* 3:2156-2165) and the pVL series (Lucklow *et al.* (1989) *Virology* 170:31-39).

 In certain embodiments of the invention, the polynucleotides described herein are expressed in mammalian cells using mammalian expression vectors. Examples of mammalian expression vectors include pCDM8 (Seed, B. (1987) *Nature* 329:840) and
25 pMT2PC (Kaufman *et al.* (1987) *EMBO J.* 6:187-195).

 The expression vectors listed herein are provided by way of example only of the well-known vectors available to those of ordinary skill in the art that would be useful to express the lipase polynucleotides. The person of ordinary skill in the art would be aware of other vectors suitable for maintenance propagation or expression of the
30 polynucleotides described herein. These are found for example in Sambrook *et al.* (1989) *Molecular Cloning: A Laboratory Manual 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY.*

The invention also encompasses vectors in which the nucleic acid sequences described herein are cloned into the vector in reverse orientation, but operably linked to a regulatory sequence that permits transcription of antisense RNA. Thus, an antisense transcript can be produced to all, or to a portion, of the polynucleotide sequences described herein, including both coding and non-coding regions. Expression of this antisense RNA is subject to each of the parameters described above in relation to expression of the sense RNA (regulatory sequences, constitutive or inducible expression, tissue-specific expression).

The invention also relates to recombinant host cells containing the vectors described herein. Host cells therefore include prokaryotic cells, lower eukaryotic cells such as yeast, other eukaryotic cells such as insect cells, and higher eukaryotic cells such as mammalian cells.

The recombinant host cells are prepared by introducing the vector constructs described herein into the cells by techniques readily available to the person of ordinary skill in the art. These include, but are not limited to, calcium phosphate transfection, DEAE-dextran-mediated transfection, cationic lipid-mediated transfection, electroporation, transduction, infection, lipofection, and other techniques such as those found in Sambrook *et al.* (*Molecular Cloning: A Laboratory Manual*, 2d ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY).

Host cells can contain more than one vector. Thus, different nucleotide sequences can be introduced on different vectors of the same cell. Similarly, the lipase polynucleotides can be introduced either alone or with other polynucleotides that are not related to the lipase polynucleotides such as those providing trans-acting factors for expression vectors. When more than one vector is introduced into a cell, the vectors can be introduced independently, co-introduced or joined to the lipase polynucleotide vector.

In the case of bacteriophage and viral vectors, these can be introduced into cells as packaged or encapsulated virus by standard procedures for infection and transduction. Viral vectors can be replication-competent or replication-defective. In the case in which viral replication is defective, replication will occur in host cells providing functions that complement the defects.

Vectors generally include selectable markers that enable the selection of the subpopulation of cells that contain the recombinant vector constructs. The marker can

be contained in the same vector that contains the polynucleotides described herein or may be on a separate vector. Markers include tetracycline or ampicillin-resistance genes for prokaryotic host cells and dihydrofolate reductase or neomycin resistance for eukaryotic host cells. However, any marker that provides selection for a phenotypic trait
5 will be effective.

While the mature proteins can be produced in bacteria, yeast, mammalian cells, and other cells under the control of the appropriate regulatory sequences, cell-free transcription and translation systems can also be used to produce these proteins using RNA derived from the DNA constructs described herein.

10 Where secretion of the polypeptide is desired, appropriate secretion signals are incorporated into the vector. The signal sequence can be endogenous to the lipase polypeptides or heterologous to these polypeptides.

Where the polypeptide is not secreted into the medium, the protein can be isolated from the host cell by standard disruption procedures, including freeze thaw,
15 sonication, mechanical disruption, use of lysing agents and the like. The polypeptide can then be recovered and purified by well-known purification methods including ammonium sulfate precipitation, acid extraction, anion or cationic exchange chromatography, phosphocellulose chromatography, hydrophobic-interaction chromatography, affinity chromatography, hydroxylapatite chromatography, lectin
20 chromatography, or high performance liquid chromatography.

It is also understood that depending upon the host cell in recombinant production of the polypeptides described herein, the polypeptides can have various glycosylation patterns, depending upon the cell, or maybe non-glycosylated as when produced in bacteria. In addition, the polypeptides may include an initial modified methionine in
25 some cases as a result of a host-mediated process.

Uses of Vectors and Host Cells

It is understood that "host cells" and "recombinant host cells" refer not only to the particular subject cell but also to the progeny or potential progeny of such a cell.
30 Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

The host cells expressing the polypeptides described herein, and particularly recombinant host cells, have a variety of uses. First, the cells are useful for producing lipase proteins or polypeptides that can be further purified to produce desired amounts of lipase protein or fragments. Thus, host cells containing expression vectors are useful for polypeptide production.

Host cells are also useful for conducting cell-based assays involving the lipase or lipase fragments. Thus, a recombinant host cell expressing a native lipase is useful to assay for compounds that stimulate or inhibit lipase function. This includes disappearance of substrate (triglycerides, phospholipids, lipoproteins), appearance of end product (fatty acids), and the various other molecular functions described herein that include, but are not limited to, substrate recognition, substrate binding, subunit association, and interaction with other cellular components. Modulation of gene expression can occur at the level of transcription or translation.

Host cells are also useful for identifying lipase mutants in which these functions are affected. If the mutants naturally occur and give rise to a pathology, host cells containing the mutations are useful to assay compounds that have a desired effect on the mutant lipase (for example, stimulating or inhibiting function) which may not be indicated by their effect on the native lipase.

Recombinant host cells are also useful for expressing the chimeric polypeptides described herein to assess compounds that activate or suppress activation or alter specific function by means of a heterologous domain, segment, site, and the like, as disclosed herein.

Further, mutant lipase can be designed in which one or more of the various functions is engineered to be increased or decreased, for example, substrate binding activity or the catalytic activity of the lipase, and used to augment or replace lipase proteins in an individual. Thus, host cells can provide a therapeutic benefit by replacing an aberrant lipase or providing an aberrant lipase that provides a therapeutic result. In one embodiment, the cells provide lipase that are abnormally active.

In another embodiment, the cells provide lipase that are abnormally inactive. These lipases can compete with endogenous lipase polypeptides in the individual.

In another embodiment, cells expressing lipase that cannot be activated, are introduced into an individual in order to compete with endogenous lipases for its various substrates. For example, in the case in which excessive lipase or analog is part of a

treatment modality, it may be necessary to inactivate this molecule at a specific point in treatment. Providing cells that compete for the molecule, but which cannot be affected by lipase activation would be beneficial.

Homologously recombinant host cells can also be produced that allow the *in situ* alteration of endogenous lipase polynucleotide sequences in a host cell genome. The host cell includes, but is not limited to, a stable cell line, cell *in vivo*, or cloned microorganism. This technology is more fully described in WO 93/09222, WO 91/12650, WO 91/06667, U.S. 5,272,071, and U.S. 5,641,670. Briefly, specific polynucleotide sequences corresponding to the lipase polynucleotides or sequences proximal or distal to a lipase gene are allowed to integrate into a host cell genome by homologous recombination where expression of the gene can be affected. In one embodiment, regulatory sequences are introduced that either increase or decrease expression of an endogenous sequence. Accordingly, a lipase can be produced in a cell not normally producing it. Alternatively, increased expression of lipase can be effected in a cell normally producing the protein at a specific level. Further, expression can be decreased or eliminated by introducing a specific regulatory sequence. The regulatory sequence can be heterologous to the lipase protein sequence or can be a homologous sequence with a desired mutation that affects expression. Alternatively, the entire gene can be deleted. The regulatory sequence can be specific to the host cell or capable of functioning in more than one cell type. Still further, specific mutations can be introduced into any desired region of the gene to produce mutant lipase proteins. Such mutations could be introduced, for example, into specific functional regions such as the triglyceride or phospholipid binding site.

In one embodiment, the host cell can be a fertilized oocyte or embryonic stem cell that can be used to produce a transgenic animal containing the altered lipase gene. Alternatively, the host cell can be a stem cell or other early tissue precursor that gives rise to a specific subset of cells and can be used to produce transgenic tissues in an animal. See also Thomas *et al.*, *Cell* 51:503 (1987) for a description of homologous recombination vectors. The vector is introduced into an embryonic stem cell line (e.g., by electroporation) and cells in which the introduced gene has homologously recombined with the endogenous lipase gene is selected (see e.g., Li, E. *et al.* (1992) *Cell* 69:915). The selected cells are then injected into a blastocyst of an animal (e.g., a mouse) to form aggregation chimeras (see e.g., Bradley, A. in *Teratocarcinomas and*

Embryonic Stem Cells: A Practical Approach, E.J. Robertson, ed. (IRL, Oxford, 1987) pp. 113-152). A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term. Progeny harboring the homologously recombined DNA in their germ cells can be used to breed animals in which all cells of the animal contain the homologously recombined DNA by germline transmission of the transgene. Methods for constructing homologous recombination vectors and homologous recombinant animals are described further in Bradley, A. (1991) *Current Opinion in Biotechnology* 2:823-829 and in PCT International Publication Nos. WO 90/11354; WO 91/01140; and WO 93/04169.

10 The genetically engineered host cells can be used to produce non-human transgenic animals. A transgenic animal is preferably a mammal, for example a rodent, such as a rat or mouse, in which one or more of the cells of the animal include a transgene. A transgene is exogenous DNA which is integrated into the genome of a cell from which a transgenic animal develops and which remains in the genome of the mature animal in one or more cell types or tissues of the transgenic animal. These animals are useful for studying the function of a lipase protein and identifying and evaluating modulators of lipase protein activity.

Other examples of transgenic animals include non-human primates, sheep, dogs, cows, goats, chickens, and amphibians.

20 In one embodiment, a host cell is a fertilized oocyte or an embryonic stem cell into which a lipase polynucleotide sequences have been introduced.

A transgenic animal can be produced by introducing nucleic acid into the male pronuclei of a fertilized oocyte, e.g., by microinjection, retroviral infection, and allowing the oocyte to develop in a pseudopregnant female foster animal. Any of the lipase nucleotide sequences can be introduced as a transgene into the genome of a non-human animal, such as a mouse.

25 Any of the regulatory or other sequences useful in expression vectors can form part of the transgenic sequence. This includes intronic sequences and polyadenylation signals, if not already included. A tissue-specific regulatory sequence(s) can be operably linked to the transgene to direct expression of the lipase protein to particular cells.

30 Methods for generating transgenic animals via embryo manipulation and microinjection, particularly animals such as mice, have become conventional in the art and are described, for example, in U.S. Patent Nos. 4,736,866 and 4,870,009, both by

Leder *et al.*, U.S. Patent No. 4,873,191 by Wagner *et al.* and in Hogan, B., *Manipulating the Mouse Embryo*, (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1986). Similar methods are used for production of other transgenic animals. A transgenic founder animal can be identified based upon the presence of the transgene in its genome and/or expression of transgenic mRNA in tissues or cells of the animals. A transgenic founder animal can then be used to breed additional animals carrying the transgene. Moreover, transgenic animals carrying a transgene can further be bred to other transgenic animals carrying other transgenes. A transgenic animal also includes animals in which the entire animal or tissues in the animal have been produced using the homologously recombinant host cells described herein.

In another embodiment, transgenic non-human animals can be produced which contain selected systems, which allow for regulated expression of the transgene. One example of such a system is the *cre/loxP* recombinase system of bacteriophage P1. For a description of the *cre/loxP* recombinase system, see, e.g., Lakso *et al.* (1992) *PNAS* 89:6232-6236. Another example of a recombinase system is the FLP recombinase system of *S. cerevisiae* (O'Gorman *et al.* (1991) *Science* 251:1351-1355. If a *cre/loxP* recombinase system is used to regulate expression of the transgene, animals containing transgenes encoding both the *Cre* recombinase and a selected protein is required. Such animals can be provided through the construction of "double" transgenic animals, e.g., by mating two transgenic animals, one containing a transgene encoding a selected protein and the other containing a transgene encoding a recombinase.

Clones of the non-human transgenic animals described herein can also be produced according to the methods described in Wilmut *et al.* (1997) *Nature* 385:810-813 and PCT International Publication Nos. WO 97/07668 and WO 97/07669. In brief, a cell, e.g., a somatic cell, from the transgenic animal can be isolated and induced to exit the growth cycle and enter G₀ phase. The quiescent cell can then be fused, e.g., through the use of electrical pulses, to an enucleated oocyte from an animal of the same species from which the quiescent cell is isolated. The reconstructed oocyte is then cultured such that it develops to morula or blastocyst and then transferred to a pseudopregnant female foster animal. The offspring born of this female foster animal will be a clone of the animal from which the cell, e.g., the somatic cell, is isolated.

Transgenic animals containing recombinant cells that express the polypeptides described herein are useful to conduct the assays described herein in an *in vivo* context.

Accordingly, the various physiological factors that are present *in vivo* and that could affect, for example, binding, activation, and protein turnover, may not be evident from *in vitro* cell-free or cell-based assays. Accordingly, it is useful to provide non-human transgenic animals to assay *in vivo* lipase function, including substrate interaction, the effect of specific mutant on lipase function and substrate interaction, and the effect of chimeric lipases. It is also possible to assess the effect of null mutations, that is mutations that substantially or completely eliminate one or more lipase functions.

In general, methods for producing transgenic animals include introducing a nucleic acid sequence according to the present invention, the nucleic acid sequence capable of expressing the lipase in a transgenic animal, into a cell in culture or *in vivo*. When introduced *in vivo*, the nucleic acid is introduced into an intact organism such that one or more cell types and, accordingly, one or more tissue types, express the nucleic acid encoding the lipase. Alternatively, the nucleic acid can be introduced into virtually all cells in an organism by transfecting a cell in culture, such as an embryonic stem cell, as described herein for the production of transgenic animals, and this cell can be used to produce an entire transgenic organism. As described, in a further embodiment, the host cell can be a fertilized oocyte. Such cells are then allowed to develop in a female foster animal to produce the transgenic organism.

20 Pharmaceutical Compositions

The lipase nucleic acid molecules, protein modulators of the protein, and antibodies (also referred to herein as "active compounds") can be incorporated into pharmaceutical compositions suitable for administration to a subject, e.g., a human. Such compositions typically comprise the nucleic acid molecule, protein, modulator, or antibody and a pharmaceutically acceptable carrier.

The term "administer" is used in its broadest sense and includes any method of introducing the compositions of the present invention into a subject. This includes producing polypeptides or polynucleotides *in vivo* as by transcription or translation, *in vivo*, of polynucleotides that have been exogenously introduced into a subject. Thus, polypeptides or nucleic acids produced in the subject from the exogenous compositions are encompassed in the term "administer."

As used herein the language "pharmaceutically acceptable carrier" is intended to include any and all solvents, dispersion media, coatings, antibacterial and antifungal

agents, isotonic and absorption delaying agents, and the like, compatible with pharmaceutical administration. The use of such media and agents for pharmaceutically active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active compound, such media can be used in the

5 compositions of the invention. Supplementary active compounds can also be incorporated into the compositions. A pharmaceutical composition of the invention is formulated to be compatible with its intended route of administration. Examples of routes of administration include parenteral, e.g., intravenous, intradermal, subcutaneous, oral (e.g., inhalation), transdermal (topical), transmucosal, and rectal administration.

10 Solutions or suspensions used for parenteral, intradermal, or subcutaneous application can include the following components: a sterile diluent such as water for injection, saline solution, fixed oils, polyethylene glycols, glycerine, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as

15 ethylenediaminetetraacetic acid; buffers such as acetates, citrates or phosphates and agents for the adjustment of tonicity such as sodium chloride or dextrose. pH can be adjusted with acids or bases, such as hydrochloric acid or sodium hydroxide. The parenteral preparation can be enclosed in ampules, disposable syringes or multiple dose vials made of glass or plastic.

20 Pharmaceutical compositions suitable for injectable use include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion. For intravenous administration, suitable carriers include physiological saline, bacteriostatic water, Cremophor EL™ (BASF, Parsippany, NJ) or phosphate buffered saline (PBS). In all

25 cases, the composition must be sterile and should be fluid to the extent that easy syringability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid

30 polyethylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. Prevention of the action of microorganisms can be achieved by various antibacterial and

antifungal agents, for example, parabens, chlorobutanol, phenol, ascorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars, polyalcohols such as mannitol, sorbitol, sodium chloride in the composition. Prolonged absorption of the injectable compositions can be brought about
5 by including in the composition an agent which delays absorption, for example, aluminum monostearate and gelatin.

Sterile injectable solutions can be prepared by incorporating the active compound (e.g., a lipase protein or anti-lipase antibody) in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as
10 required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle which contains a basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, the preferred methods of preparation are vacuum drying and freeze-drying which yields a powder of
15 the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

Oral compositions generally include an inert diluent or an edible carrier. They can be enclosed in gelatin capsules or compressed into tablets. For oral administration, the agent can be contained in enteric forms to survive the stomach or further coated or
20 mixed to be released in a particular region of the GI tract by known methods. For the purpose of oral therapeutic administration, the active compound can be incorporated with excipients and used in the form of tablets, troches, or capsules. Oral compositions can also be prepared using a fluid carrier for use as a mouthwash, wherein the compound in the fluid carrier is applied orally and swished and expectorated or swallowed.

25 Pharmaceutically compatible binding agents, and/or adjuvant materials can be included as part of the composition. The tablets, pills, capsules, troches and the like can contain any of the following ingredients, or compounds of a similar nature: a binder such as microcrystalline cellulose, gum tragacanth or gelatin; an excipient such as starch or lactose, a disintegrating agent such as alginic acid, Primogel, or corn starch; a lubricant
30 such as magnesium stearate or Sterotes; a glidant such as colloidal silicon dioxide; a sweetening agent such as sucrose or saccharin; or a flavoring agent such as peppermint, methyl salicylate, or orange flavoring.

For administration by inhalation, the compounds are delivered in the form of an aerosol spray from pressured container or dispenser, which contains a suitable propellant, e.g., a gas such as carbon dioxide, or a nebulizer.

Systemic administration can also be by transmucosal or transdermal means. For
5 transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art, and include, for example, for transmucosal administration, detergents, bile salts, and fusidic acid derivatives. Transmucosal administration can be accomplished through the use of nasal sprays or suppositories. For transdermal administration, the active
10 compounds are formulated into ointments, salves, gels, or creams as generally known in the art.

The compounds can also be prepared in the form of suppositories (e.g., with conventional suppository bases such as cocoa butter and other glycerides) or retention enemas for rectal delivery.

15 In one embodiment, the active compounds are prepared with carriers that will protect the compound against rapid elimination from the body, such as a controlled release formulation, including implants and microencapsulated delivery systems. Biodegradable, biocompatible polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid.
20 Methods for preparation of such formulations will be apparent to those skilled in the art. The materials can also be obtained commercially from Alza Corporation and Nova Pharmaceuticals, Inc. Liposomal suspensions (including liposomes targeted to infected cells with monoclonal antibodies to viral antigens) can also be used as pharmaceutically acceptable carriers. These can be prepared according to methods known to those skilled
25 in the art, for example, as described in U.S. Patent No. 4,522,811.

It is especially advantageous to formulate oral or parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. "Dosage unit form" as used herein refers to physically discrete units suited as unitary dosages for the subject to be treated; each unit containing a predetermined quantity of active compound
30 calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier. The specification for the dosage unit forms of the invention are dictated by and directly dependent on the unique characteristics of the active compound

and the particular therapeutic effect to be achieved, and the limitations inherent in the art of compounding such an active compound for the treatment of individuals.

The nucleic acid molecules of the invention can be inserted into vectors and used as gene therapy vectors. Gene therapy vectors can be delivered to a subject by, for
5 example, intravenous injection, local administration (U.S. 5,328,470) or by stereotactic injection (see e.g., Chen *et al.* (1994) *PNAS* 91:3054-3057). The pharmaceutical preparation of the gene therapy vector can include the gene therapy vector in an acceptable diluent, or can comprise a slow release matrix in which the gene delivery vehicle is imbedded. Alternatively, where the complete gene delivery vector can be
10 produced intact from recombinant cells, e.g. retroviral vectors, the pharmaceutical preparation can include one or more cells which produce the gene delivery system.

The pharmaceutical compositions can be included in a container, pack, or dispenser together with instructions for administration.

As defined herein, a therapeutically effective amount of protein or polypeptide
15 (i.e., an effective dosage) ranges from about 0.001 to 30 mg/kg body weight, preferably about 0.01 to 25 mg/kg body weight, more preferably about 0.1 to 20 mg/kg body weight, and even more preferably about 1 to 10 mg/kg, 2 to 9 mg/kg, 3 to 8 mg/kg, 4 to 7 mg/kg, or 5 to 6 mg/kg body weight.

The skilled artisan will appreciate that certain factors may influence the
20 dosage required to effectively treat a subject, including but not limited to the severity of the disease or disorder, previous treatments, the general health and/or age of the subject, and other diseases present. Moreover, treatment of a subject with a therapeutically effective amount of a protein, polypeptide, or antibody can include a single treatment or, preferably, can include a series of treatments. In a preferred
25 example, a subject is treated with antibody, protein, or polypeptide in the range of between about 0.1 to 20 mg/kg body weight, one time per week for between about 1 to 10 weeks, preferably between 2 to 8 weeks, more preferably between about 3 to 7 weeks, and even more preferably for about 4, 5, or 6 weeks. It will also be appreciated that the effective dosage of antibody, protein, or polypeptide used for
30 treatment may increase or decrease over the course of a particular treatment. Changes in dosage may result and become apparent from the results of diagnostic assays as described herein.

The present invention encompasses agents which modulate expression or activity. An agent may, for example, be a small molecule. For example, such small molecules include, but are not limited to, peptides, peptidomimetics, amino acids, amino acid analogs, polynucleotides, polynucleotide analogs, nucleotides, nucleotide
5 analogs, organic or inorganic compounds (i.e., including heteroorganic and organometallic compounds) having a molecular weight less than about 10,000 grams per mole, organic or inorganic compounds having a molecular weight less than about 5,000 grams per mole, organic or inorganic compounds having a molecular weight less than about 1,000 grams per mole, organic or inorganic compounds having a
10 molecular weight less than about 500 grams per mole, and salts, esters, and other pharmaceutically acceptable forms of such compounds.

It is understood that appropriate doses of small molecule agents depends upon a number of factors within the purview of the ordinarily skilled physician, veterinarian, or researcher. The dose(s) of the small molecule will vary, for example,
15 depending upon the identity, size, and condition of the subject or sample being treated, further depending upon the route by which the composition is to be administered, if applicable, and the effect which the practitioner desires the small molecule to have upon the nucleic acid or polypeptide of the invention. Exemplary doses include milligram or microgram amounts of the small molecule per kilogram of
20 subject or sample weight (e.g., about 1 microgram per kilogram to about 500 milligrams per kilogram, about 100 micrograms per kilogram to about 5 milligrams per kilogram, or about 1 microgram per kilogram to about 50 micrograms per kilogram. It is furthermore understood that appropriate doses of a small molecule depend upon the potency of the small molecule with respect to the expression or
25 activity to be modulated. Such appropriate doses may be determined using the assays described herein. When one or more of these small molecules is to be administered to an animal (e.g., a human) in order to modulate expression or activity of a polypeptide or nucleic acid of the invention, a physician, veterinarian, or researcher may, for example, prescribe a relatively low dose at first, subsequently increasing the dose
30 until an appropriate response is obtained. In addition, it is understood that the specific dose level for any particular animal subject will depend upon a variety of factors including the activity of the specific compound employed, the age, body weight, general health, gender, and diet of the subject, the time of administration, the route of

administration, the rate of excretion, any drug combination, and the degree of expression or activity to be modulated.

This invention may be embodied in many different forms and should not be construed as limited to the embodiments set forth herein; rather, these embodiments are provided so that this disclosure will fully convey the invention to those skilled in the art. Many modifications and other embodiments of the invention will come to mind in one skilled in the art to which this invention pertains having the benefit of the teachings presented in the foregoing description. Although specific terms are employed, they are used as in the art unless otherwise indicated.

EXPERIMENTAL

Example 1: 18892 Expression Analysis

Total RNA was prepared from various human tissues by single step extraction method using RNA STAT-60 according to the manufacturer's instructions (Tel Test, Inc.). Each RNA preparation was treated with DNaseI (Ambion) at 37°C for 1 hour. DNaseI treatment was determined to be complete if the sample required at least 38 PCR amplification cycles to reach a threshold level of fluorescence using β -2 microglobulin as an internal amplicon reference. The integrity of the RNA samples following DNaseI treatment was confirmed by agarose gel electrophoresis and ethidium bromide staining.

After phenol extraction, cDNA was prepared from the sample using the SuperScriptTM Choice System following the manufacturer's instructions (GibcoBRL). A negative control of RNA without reverse transcriptase was mock reverse transcribed for each RNA sample.

Expression of the novel 18892 lipase gene sequence was measured by TaqMan⁷ quantitative PCR (Perkin Elmer Applied Biosystems) in cDNA prepared from the following normal human tissues: ovary, liver, breast, lung, colon, kidney, prostate.

Probes were designed based on the 18892 sequence. The 18892 sequence probe was labeled using FAM (6-carboxyfluorescein), and the β -2 microglobulin reference was labeled with a different fluorescent dye, VIC. The differential labeling of the target kinase-like sequence and internal reference gene thus enabled measurement in the same well. Forward and reverse primers and probes for both the β -2 microglobulin and the target 18892 sequence were added to the TaqMan Universal PCR Master Mix

(PE Applied Biosystems). Although the final concentration of primer and probe could vary, each was internally consistent within a given experiment. A typical experiment contained 200 nM of forward and reverse primers plus 100 nM probe for β -2 microglobulin and 600 nM forward and reverse primers plus 200 nM probe for the target 18892 sequence. TaqMan matrix experiments were carried out on an ABI PRISM 7700 Sequence Detection System (PE Applied Biosystems). The thermal cycler conditions were as follows: hold for 2 min at 50°C and 10 min at 95°C, followed by two-step PCR for 40 cycles of 95°C for 15 sec followed by 60°C for 1 min.

- 10 The following method was used to quantitatively calculate 18892 expression in the various tissues relative to β -2 microglobulin expression in the same tissue. The threshold cycle (Ct) value is defined as the cycle at which a statistically significant increase in fluorescence is detected. A lower Ct value is indicative of a higher mRNA concentration. The Ct value of the 18892 sequence is normalized by subtracting the
- 15 Ct value of the β -2 microglobulin gene to obtain a Δ Ct value using the following formula: Δ Ct = Ct₁₈₈₉₂ - Ct _{β -2 microglobulin}. Expression is then calibrated against a cDNA sample showing a comparatively low level of expression of the 18892 sequence. The Δ Ct value for the calibrator sample is then subtracted from Δ Ct for each tissue sample according to the following formula: $\Delta\Delta$ Ct = Δ Ct_{sample} - Δ Ct_{calibrator}. Relative expression
- 20 is then calculated using the arithmetic formula given by $2^{-\Delta\Delta$ Ct}. Expression of the target 18892 sequence in each of the tissues tested was then graphically represented in the different figures included herein.

INDICATIONS RELATING TO DEPOSITED MICROORGANISM
OR OTHER BIOLOGICAL MATERIAL

(PCT Rule 13bis)

A. The indications made below relate to the deposited microorganism or other biological material referred to in the description on page 4, line 30	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet ☐	
Name of depository institution American Type Culture Collection	
Address of depository institution (including postal code and country) 10801 University Blvd. Manassas, VA 20110-2209 US	
Date of deposit 12 May 2000 (12.05.00)	Accession Number PTA-1870
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet ☐	
Page 8, line 28; Page 9, line 3; Page 90, lines 8, 12, 18 and 20; Page 91, lines 2, 8, 19 and 20.	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indicators are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	

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Authorized officer	

THAT WHICH IS CLAIMED:

1. An isolated polypeptide having an amino acid sequence selected from the
5 group consisting of:
 - (a) The amino acid sequence shown in SEQ ID NO:1;
 - (b) The amino acid sequence encoded by the cDNA contained in ATCC
Deposit No. PTA-1870;
 - (c) The amino acid sequence of an allelic variant of the amino acid sequence
10 shown in SEQ ID NO:1;
 - (d) The amino acid sequence of an allelic variant of the amino acid sequence
encoded by the cDNA contained in ATCC Deposit No. PTA-1870
 - (e) The amino acid sequence of a sequence variant of the amino acid
sequence shown in SEQ ID NO:1, wherein the sequence variant is encoded by a nucleic
15 acid molecule hybridizing to the nucleic acid molecule shown in SEQ ID NO:2 under
stringent conditions;
 - (f) The amino acid sequence of a sequence variant of the amino acid
sequence encoded by the cDNA clone contained in ATCC Deposit No. PTA-1870,
wherein the sequence variant is encoded by a nucleic acid molecule hybridizing under
20 stringent conditions to the cDNA contained in ATCC Deposit No. PTA-1870;
 - (g) The amino acid sequence of a fragment of the amino acid sequence
shown in SEQ ID NO:1, or wherein the fragment is greater than 13 amino acids;
 - (h) The amino acid sequence of a variant of the amino acid sequence shown
in SEQ ID NO:1, wherein said variant encodes the mature polypeptide;
 - 25 (i) The amino acid sequence of an epitope bearing region of any one of the
polypeptides of (a)-(h).
2. An isolated antibody that selectively binds to a polypeptide of claim 1,
(a)-(i).
30
3. An isolated nucleic acid molecule having a nucleotide sequence selected
from the group consisting of:
 - (a) The nucleotide sequence shown in SEQ ID NO:2;

- (b) The nucleotide sequence in the cDNA contained in ATCC Deposit No. PTA-1870;
- (c) A nucleotide sequence encoding the amino acid sequence shown in SEQ ID NO:1;
- 5 (d) A nucleotide sequence encoding the mature amino acid sequence of SEQ ID NO:1;
- (e) A nucleotide sequence encoding the amino acid sequence encoded by the cDNA contained in ATCC Deposit No. PTA-1870; and
- (f) A nucleotide sequence complementary to any of the nucleotide
10 sequences in (a), (b), (c), (d) or (e).
4. An isolated nucleic acid molecule having a nucleotide sequence selected from the group consisting of:
- (a) A nucleotide sequence encoding an amino acid sequence of a sequence
15 variant of the amino acid sequence shown in SEQ ID NO:1 that hybridizes to the nucleotide sequence shown in SEQ ID NO:2 under stringent conditions;
- (b) A nucleotide sequence encoding the amino acid sequence of a sequence variant of the amino acid sequence encoded by the cDNA contained in ATCC Deposit No. PTA-1870 the nucleic acid sequence of the sequence variant hybridizing to the
20 cDNA contained in ATCC Deposit No. PTA-1870 under stringent conditions; and
- (c) A nucleotide sequence complementary to either of the nucleotide sequences in (a) or (b).
5. A nucleic acid vector comprising the nucleic acid sequences in either of
25 claims 3 or 4.
6. A host cell containing the vector of claim 5.
7. A method for producing any of the polypeptides in claim 1 comprising
30 introducing a nucleotide sequence encoding any of the polypeptide sequences in (a)-(i) into a host cell, and culturing the host cell under conditions in which the proteins are expressed from the nucleic acid.

8. A method for detecting the presence of any of the polypeptides in claim 1 in a sample, said method comprising contacting said sample with an agent that specifically allows detection of the presence of the polypeptide in the sample and then detecting the presence of the polypeptide.

5

9. The method of claim 8, wherein said agent is capable of selective physical association with said polypeptide.

10. The method of claim 9, wherein said agent binds to said polypeptide.

10

11. The method of claim 10, wherein said agent is an antibody.

12. The method of claim 10, wherein said agent is selected from the group comprising triglycerides, phospholipids, heparin, cell surface receptors, or apoproteins.

15

13. A kit comprising reagents used for the method of claim 8, wherein the reagents comprise an agent that specifically binds to said polypeptide.

14. A method for detecting the presence of any of the nucleic acid sequences in either of claims 3 or 4 in a sample, the method comprising contacting the sample with an oligonucleotide that hybridizes to the nucleic acid sequences under stringent conditions and determining whether the oligonucleotide binds to the nucleic acid sequence in the sample.

20

15. The method of claim 14, wherein the nucleic acid, whose presence is detected, is mRNA.

25

16. A kit comprising reagents used for the method of claim 14, wherein the reagents comprise a compound that hybridizes under stringent conditions to any of the nucleic acid molecules.

30

17. The method of claim 16 wherein a fragment of the polypeptide is contacted.

18. A method for identifying an agent that binds to any of the polypeptides in claim 1, said method comprising contacting the polypeptide with an agent that binds to the polypeptide and assaying the complex formed with the agent bound to the
5 polypeptide.

19. A method for identifying an agent that modulates the level or activity of any of the polypeptides in claim 1 in a cell, the method comprising contacting the agent with a cell capable of expressing said polypeptide such that said polypeptide
10 level or activity can be modulated in said cell by said agent and measuring said polypeptide level or activity.

20. A method for identifying an agent that interacts with any of the polypeptides in claim 1 in a cell, the method comprising contacting said agent with a
15 cell capable of allowing an interaction between said polypeptide and said agent such that said polypeptide can interact with said agent and measuring the interaction.

21. A method of screening a cell to identify an agent that modulates the level or activity of any of the polypeptides in claim 1 in said cell, said method
20 comprising contacting said agent with a cell capable of expressing said polypeptide such that said polypeptide level or activity can be modulated in said cell by said agent and measuring said polypeptide level or activity.

22. A method of screening a cell to identify an agent that interacts with
25 any of the polypeptides in claim 1, said method comprising contacting said agent with a cell capable of allowing an interaction between said polypeptide and said agent such that said polypeptide can interact with said agent and measuring the interaction.

23. A method for modulating the activity of any of the polypeptides in
30 claim 1, the method comprising contacting any of the polypeptides of claim 1 with an agent under conditions that allow the agent to modulate the activity of the polypeptide.

24. The method of claim 23 wherein said modulation is in a subject having or predisposed to atherosclerosis, obesity, hypertriacylglycerolaemia or chylomicronemia syndrome.

5 25. A pharmaceutical composition containing any of the polypeptides of claim 1 in a pharmaceutically acceptable carrier.

26. A pharmaceutical composition containing any of the nucleic acid molecules of claims 3 or 4 in a pharmaceutically acceptable carrier.

10

27. A non-human transgenic animal wherein one or more cells of said animal contains any of the nucleic acid sequences of claims 3 or 4.

28. A method for producing a transgenic animal according to claim 27,
15 said method comprising introducing any of the nucleic acid sequences of claims 3 or 4 into a cell, wherein said cell is present in said animal or gives rise to said animal.

29. An agent identified by the methods of claims 18-22.

20 30. A method for treating cancer in a patient, comprising introducing into the vicinity of the cancer in the patient an expression vector comprising the nucleotide sequence of SEQ ID NO:2.

25 31. The method of claim 30, wherein said cancer is located in ovarian tissue.

32. A method of delivering a chemotherapeutic agent to a vertebrate cancer cell which is abnormally expressing a lipase molecule, wherein said method comprises contacting the cell with a polypeptide comprising the amino acid sequence of SEQ ID NO:1.

30

33. The method of claim 32, wherein said cancer cell is in the ovary.

34. A method of treating a pre-neoplastic or neoplastic disease characterized by abnormal expression of a lipase molecule in a patient comprising administering to said patient a therapeutically effective amount of a composition comprising a polypeptide wherein said polypeptide is encoded by a nucleotide sequence of SEQ ID NO:2 and other nucleotide sequences that differ from SEQ ID NO:2 in codon sequence due to the degeneracy of the genetic code.

35. A vector combination for use in ovarian cancer treatment, comprising an expression vector comprising a promoter operably linked to a heterologous nucleotide sequence encoding a polypeptide of SEQ ID NO:1 and fragments thereof.

36. A method of delivering a chemotherapeutic agent to a vertebrate cancer cell which is abnormally expressing a lipase molecule said method comprising contacting the cell with an antibody or biologically active antibody fragments, which antibody or antibody fragments specifically bind to a polypeptide encoded by a nucleotide sequence of SEQ ID NO:2 or other nucleotide sequences that differ from SEQ ID NO:2 in codon sequence due to the degeneracy of the genetic code.

GCAAGAGAAAATGCCACAGTGGAAACTCTTAAGGCTCTGGGAGTAAATCATCTTGTGAAATGTGACACACGATCTCTC 74
 M L R F Y L F I S L L C L S R S D 17
 CAGTTTCCAT ATG TTG AGA TTC TAC TTA TTC ATC AGT TTG TTG TGC TTG TCA AGA TCA GAC 51
 A E E T C P S F T R L S F H S A V V G T 37
 GCA GAA GAA ACA TGT CCT TCA TTC ACC AGG CTG AGC TTT CAC AGT GCA GTG GTT GGT ACG 111
 G L N V R L M L Y T R K N L T C A Q T I 57
 GGA CTA AAT GTG AGG CTG ATG CTC TAC ACA AGG AAA AAC CTG ACC TGC GCA CAA ACC ATC 171
 N S S A F G N L N V T K K T T F I V H G 77
 AAC TCC TCA GCT TTT GGG AAC TTG AAT GTG ACC AAG AAA ACC ACC TTC ATT GTC CAT GGA 231
 F R P T G S P E V W M D D L V K G L L S 97
 TTC AGG CCA ACA GGC TCC CCT CCT GTT TGG ATG GAT GAC TTA GTA AAG GGT TTG CTC TCT 291
 V E D M N V V V V D W N R G A T T L I Y 117
 GTT GAA GAC ATG AAC GTA GTT GTT GTT GAT TGG AAT CGA GGA GCT ACA ACT TTA ATA TAT 351
 T H A S S K T R K V A M V L K E F I D Q 137
 ACC CAT GGC TCT AGT AAG ACC AGA AAA GTA GCC ATG GTC TTG AAG GAA TTT ATT GAC CAG 411
 M L A E G A S L D D I Y M I G V S L G A 157
 ATG TTG GCA GAA GGA GCT TCT CTT GAT GAC ATT TAC ATG ATC GGA GTA AGT CTA GGA GCC 471
 H I S G F V G E M Y D G W L G R I T G L 177
 CAC ATA TCT GGG TTT GTT GGA GAG ATG TAC GAT GGA TGG CTG GGG AGA ATT ACA GGC CTC 531
 D P A G P L F N G K P H Q D R L D P S D 197
 GAC CCT GCA GGC CCT TTA TTC AAC GGG AAA CCT CAC CAA GAC AGA TTA GAT CCC AGT GAT 591
 A Q F V D V I H S D T D A L G Y K E P L 217
 GCG CAG TTT GTT GAT GTT ATC CAT TCC GAC ACT GAT GCA CTG GGC TAC AAG GAG CCA TTA 651
 G N I D F Y P N G G L D Q P G C P K T I 237
 GGA AAC ATA GAC TTC TAC CCA AAT GGA GGA TTG GAT CAA OCT GGC TGC CCC AAA ACA ATA 711
 L G G F Q Y F K C D H Q R S V Y L Y L S 257
 TTG GGA GGA TTT CAG TAT TTT AAA TGT GAC CAC CAG AGG TCT GTA TAC CTG TAC CTG TCT 771
 S L R E S C T I T A Y P C D S Y Q D Y R 277
 TCC CTG AGA GAG AGC TGC ACC ATC ACT GCG TAT CCC TGT GAC TCC TAC CAG GAT TAT AGG 831
 N G K C V S C G T S Q K E S C P L L G Y 297
 AAT GGC AAG TGT GTC AGC TGC GGC ACG TCA CAA AAA GAG TCC TGT CCC CTT CTG GGC TAT 891
 Y A D N W K D H L R G K D P P M T K A F 317
 TAT GCT GAT AAT TGG AAA GAC CAT CTA AGG GGG AAA GAT OCT CCA ATG ACG AAG GCA TTC 951
 F D T A E E S P F C M Y H Y F V D I I T 337
 TTT GAC ACA GCT GAG GAG AGC CCA TTC TGC ATG TAT CAT TAC TTT GTG GAT ATT ATA ACA 1011
 W N K N V R R G D I T I K L R D K A G N 357
 TGG AAC AAG AAT GTA AGA AGA GGG GAC ATT ACC ATC AAA TTG AGA GAC AAA GCT GGA AAC 1071
 T T E S K I N H E P T T F Q K Y H Q V S 377
 ACC ACA GAA TCC AAA ATC AAT CAT GAA CCC ACC ACA TTT CAG AAA TAT CAC CAA GTG AGT 1131

FIGURE 1A

U	U	A	A	E	N	U	U	U	A	V	A	A	I	S	U	A	E	S	33'	
CTA	CTT	GCA	AGA	TTT	AAT	CAA	GAT	CTG	GAT	AAA	GTG	GCT	GCA	ATT	TCC	TTG	ATG	TTC	TCT	1191
T	G	S	L	I	G	P	R	Y	K	L	R	I	L	R	M	K	L	R	S	417
ACA	GGA	TCT	CTA	ATA	GGC	CCA	AGG	TAC	AAG	CTC	AGG	ATT	CTC	CGA	ATG	AAG	TTA	AGG	TCC	1251
L	A	H	P	E	R	P	Q	L	C	R	Y	D	L	V	L	M	E	N	V	437
CTT	GCC	CAT	COG	GAG	AGG	CCT	CAG	CTG	TGT	CGG	TAT	GAT	CTT	GTC	CTG	ATG	GAA	AAC	GTT	1311
E	T	V	F	Q	P	I	L	C	P	E	L	Q	L	*						452
GAA	ACA	GTC	TTC	CAA	CCT	ATT	CTT	TGC	CCA	GAG	TTG	CAG	TTG	TAA						1356

CTGTTGCCAGGACACATGGCCATAAATAATAGAAAGAAAGCTACAACACAGGCTGTTTGAAAGCTTCACCTCACCTTT
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 CCTTGTGATTATAAAACGATCCTGGGAAGGAGCCCTAACTAGGGCAAGTCAGAAATAGCCAGGCTCGCAGCAGCCGAG
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FIGURE 1B

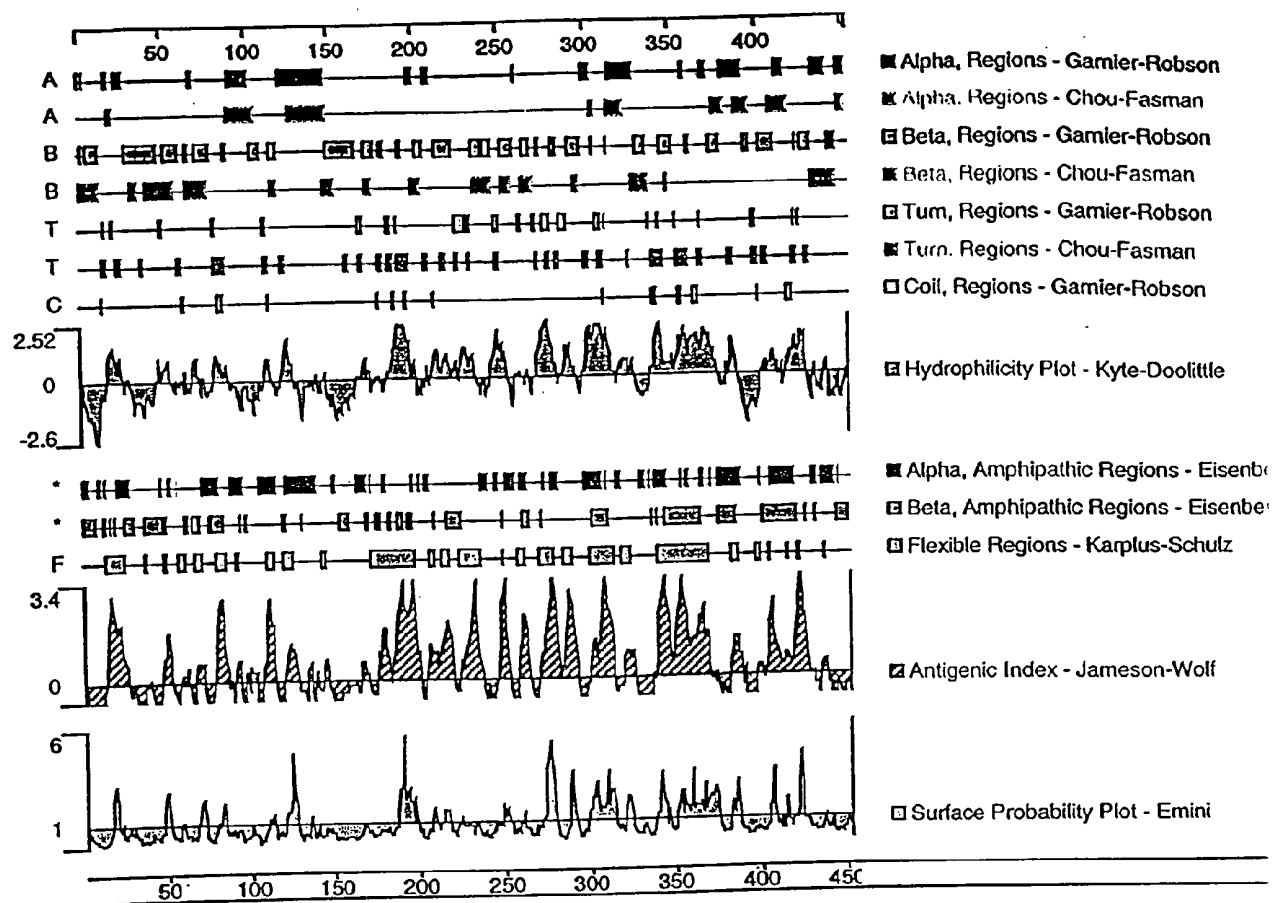
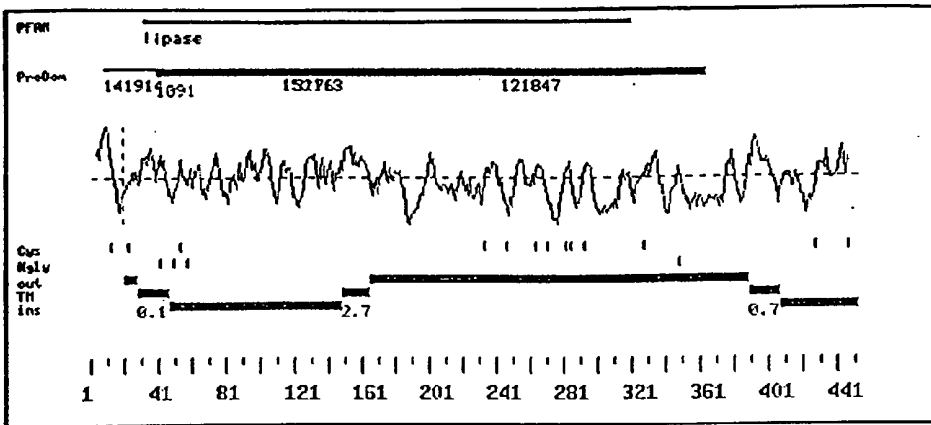


Figure 2

[Back to original CT](#)

Analysis of 18892 (451 aa)



Signal Peptide Predictions for 18892

Method	Predict	Score	Mat@
SignalP (eukaryote)	YES		19

Note: amino-terminal 70aa used for signal peptide prediction

Transmembrane Segments Predicted by MEMSAT

Start	End	Orient	Score
28	46	out->ins	0.1
148	164	ins->out	2.7
389	406	out->ins	0.7

Transmembrane segments for presumed mature peptide

Start	End	Orient	Score
10	28	out->ins	0.1
130	146	ins->out	2.7
371	388	out->ins	0.7

Figure 3

Query: 50 NLTC 53
 Query: 58 MSSA 61
 Query: 66 NVTK 69
 Query: 357 NTTE 360

>PS00004|PDOC00004|CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.

Query: 69 KKTT 72

>PS00005|PDOC00005|PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.

Query: 47 TRK 49
 Query: 68 TKK 70
 Query: 121 SSK 123
 Query: 124 TRK 126
 Query: 258 SLR 260
 Query: 287 SQK 289
 Query: 348 TIK 350

>PS00006|PDOC00006|CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.

Query: 14 SRSD 17
 Query: 97 SVED 100
 Query: 144 SLDD 147
 Query: 175 TGLD 178
 Query: 206 SDTD 209
 Query: 258 SLRE 261
 Query: 272 SYQD 275
 Query: 287 SQKE 290
 Query: 320 TAEK 323

>PS00008|PDOC00008|MYRISTYL N-myristoylation site.

Query: 36 GTGLNV 41
 Query: 152 GVSLGA 157
 Query: 176 GLDPAG 181
 Query: 232 GCPKTI 237

>PS00016|PDOC00016|RGD Cell attachment sequence.

Query: 344 -RGD 346

>PS00029|PDOC00029|LEUCINE_ZIPPER Leucine zipper pattern.

Query: 394 LMFSTGSLIGPRYKLRILRMKL 415

Figure 4

```

A LOCAL ALIGNMENT / SEQUENCE ANALYSIS REPORT
-----
Searching for complete domains
hmmfam - search a single seq against HMM database
HMMER 2.1.1 (Dec 1998)
Copyright (C) 1992-1998 Washington University School of Medicine
HMMER is freely distributed under the GNU General Public License (GPL).
-----
HMM file: /prod/ddm/seqanal/PFAM/pfam4.2/Pfam
Sequence file: /usr/ns-home/docs/seqanal/orfanal/oa-script.17055.seq
-----
Query: 18892

Scores for sequence family classification (score includes all domains):
Model Description Score E-value N
-----
lipase Lipase 262.8 4.5e-75 1

Parsed for domains:
Model Domain seq-f seq-t hmm-f hmm-t score E-value
-----
lipase 1/1 31 319 .. 1 328 {} 262.8 4.5e-75

Alignments of top-scoring domains:
lipase: domain 1 of 1, from 31 to 319: score 262.8, E = 4.5e-75
      *->gpkfkddevtieirflllytnenvknatqkLiqayppqrirksnfntr
      ++ + ++r++lyt +n t+ ++ + + + n n ++
18892 31 HSA--VVGITGLNVLMLYTRKNL---TCAQT---INSSAFGNLNVTK 69

      ktrfIiHGftdkgeeEswlskmckaLfqvekvsgnvIvVDWlggaitnEy
      kt fI+HGf+ +g+ + w +++k L++ve+ nv+vVDW +ga+t
18892 70 KTTFIVHGFRPTGSPPVWMDLVKGLLSVEDM--NVVVVDWNRGATT--- 114

      aLKyifYpqaVlNvrVVGaeIAklqeLeeelnvspenvHLIGHSLGAHV
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18892 115 ----LIYTHASSKTRKVMVLKEFIDQML--AEGASLDDIYMGVSLGAHI 159

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18892 206 S--DTDA----LGYKEPLGNIDFYFNGG-LDQPGCPKTIIL----- 238

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18892 239 -GGFYQYFKCDHQRSVYLYLSSLRSC-----TITAYPCDSYQDYRNGKC 281

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Figure 5

Transcriptional Profiling Data
from Five Different Patients

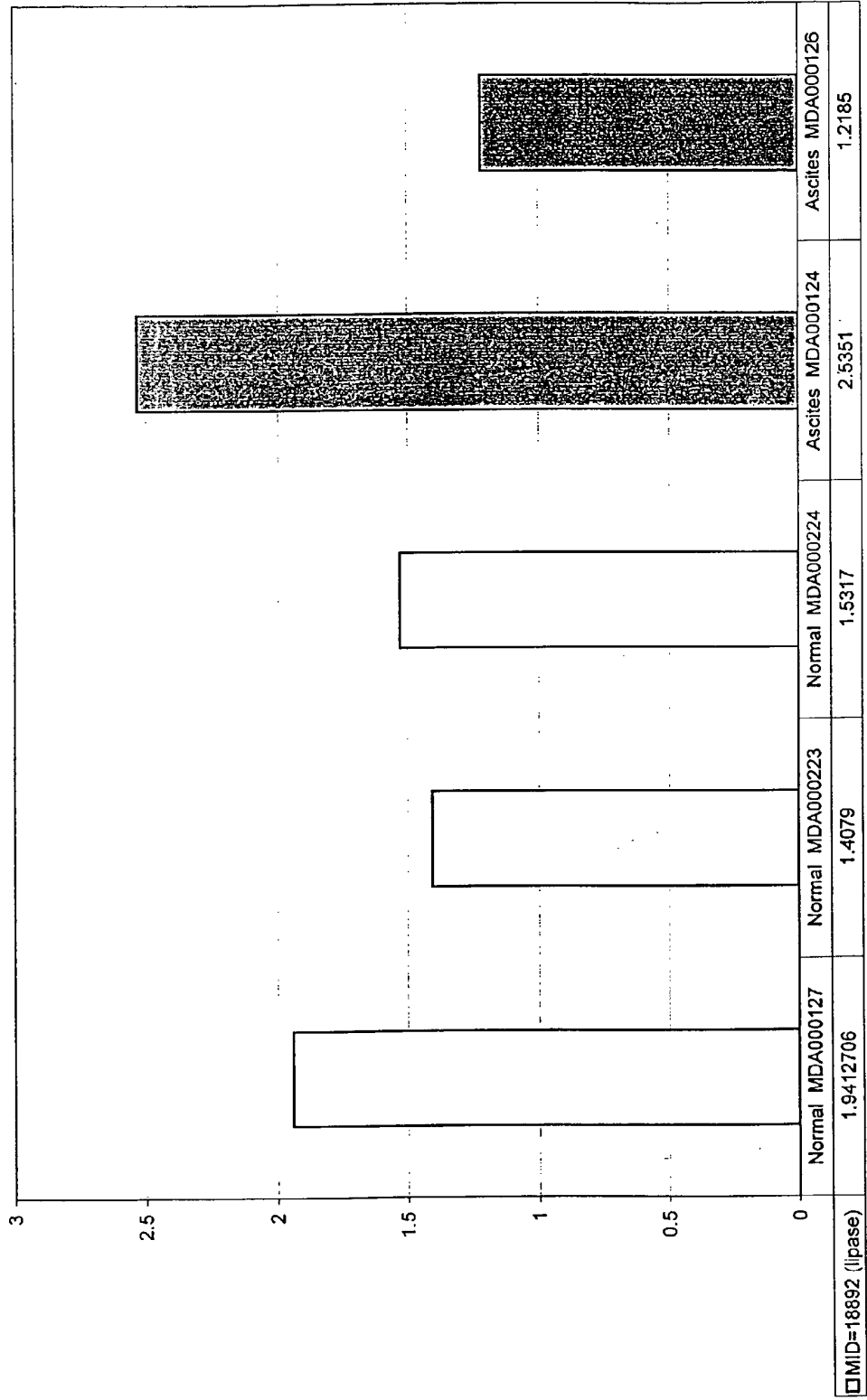


Figure 6

Transcriptional Profiling Data in
Normal and Diseased Patients

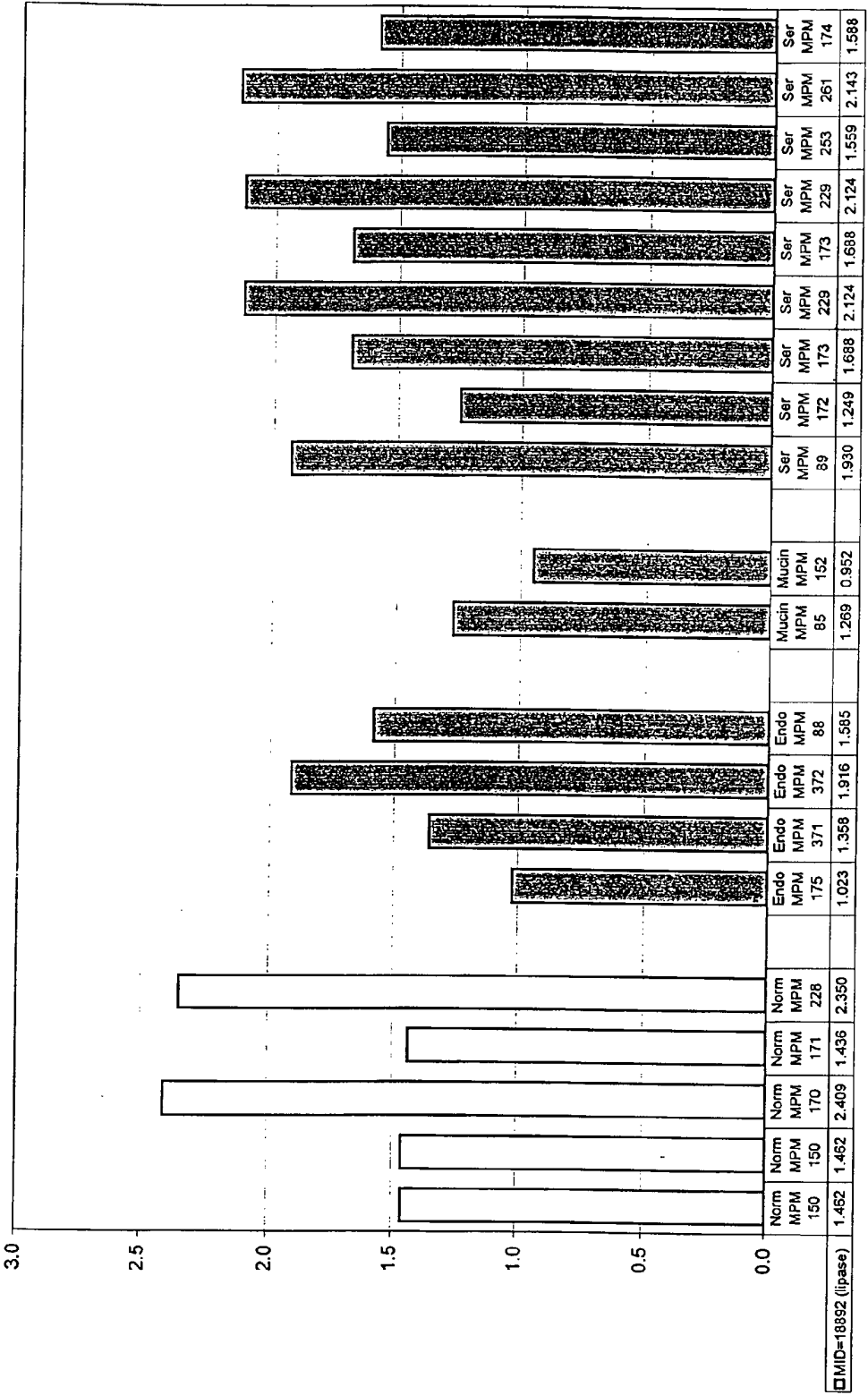


Figure 7

Phase 1.1.3 expression of 18892



Figure 8

18892 Expression in Clinical Tissues

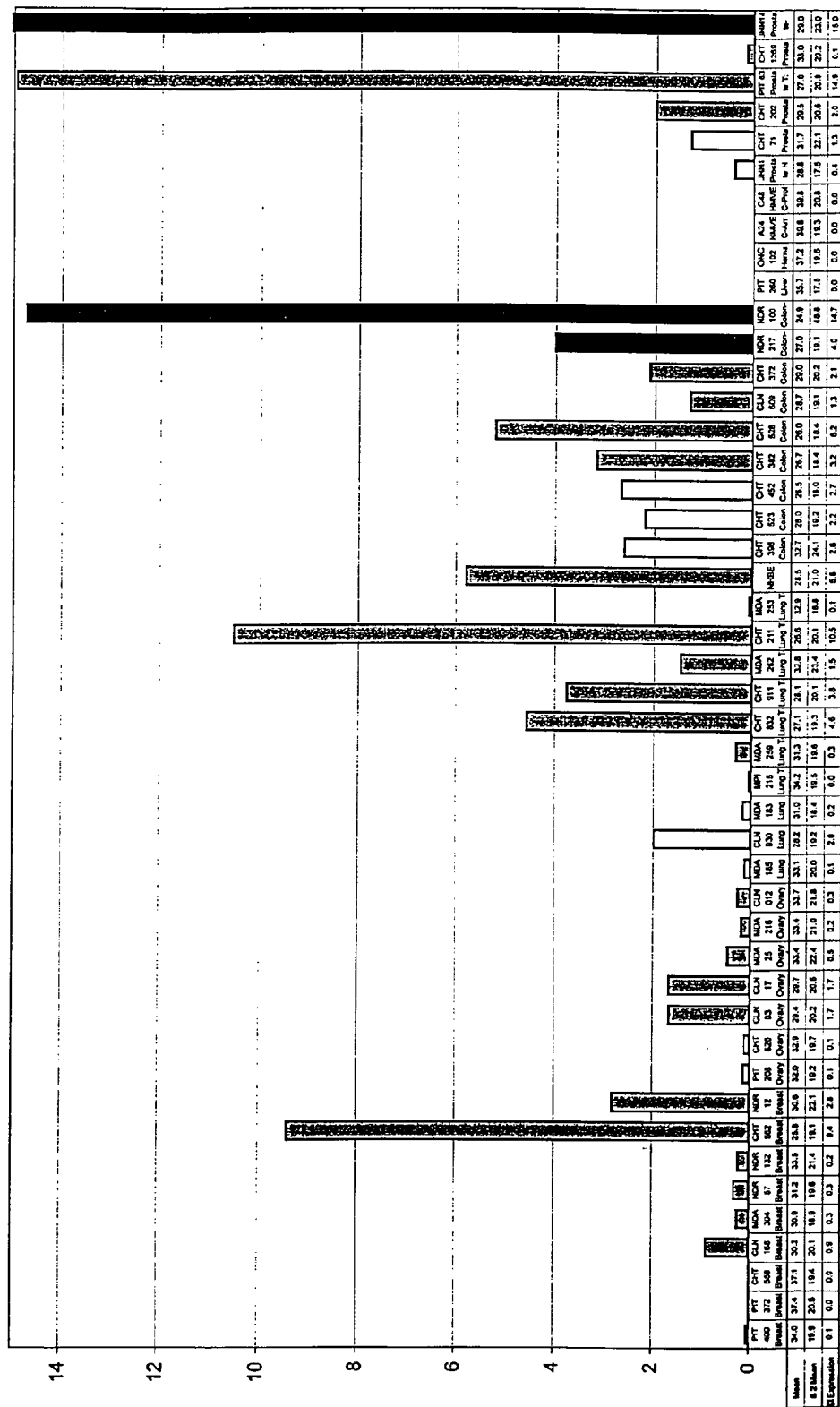


Figure 9

18992 Expression in Oncology Phase II Plate

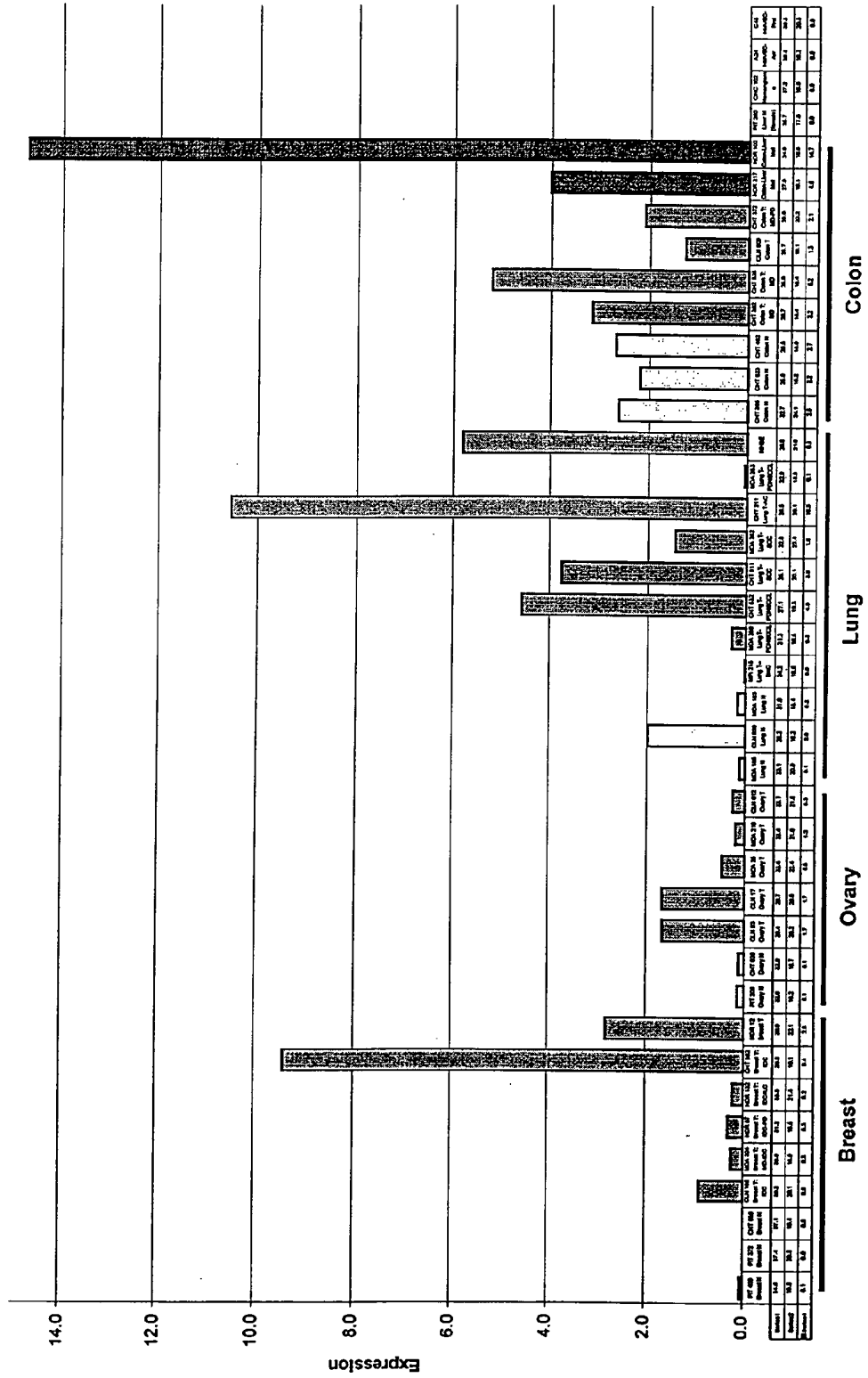


Figure 10

18892 Vessel/Liver Panel



Figure 12

SEQUENCE LISTING

<110> Kapellar-Libermann, Rosana

<120> 18892, A NOVEL HUMAN LIPASE

<130> 5800-66-1

<160> 3

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 2446

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (90)...(1445)

<400> 1

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                               Met Leu Arg Phe Tyr Leu Phe Ile
                               1                               5

agt ttg ttg tgc ttg tca aga tca gac gca gaa gaa aca tgt cct tca      161
Ser Leu Leu Cys Leu Ser Arg Ser Asp Ala Glu Glu Thr Cys Pro Ser
   10                               15                               20

ttc acc agg ctg agc ttt cac agt gca gtg gtt ggt acg gga cta aat      209
Phe Thr Arg Leu Ser Phe His Ser Ala Val Val Gly Thr Gly Leu Asn
   25                               30                               35                               40

gtg agg ctg atg ctc tac aca agg aaa aac ctg acc tgc gca caa acc      257
Val Arg Leu Met Leu Tyr Thr Arg Lys Asn Leu Thr Cys Ala Gln Thr
                               45                               50                               55

atc aac tcc tca gct ttt ggg aac ttg aat gtg acc aag aaa acc acc      305
Ile Asn Ser Ser Ala Phe Gly Asn Leu Asn Val Thr Lys Lys Thr Thr
                               60                               65                               70

ttc att gtc cat gga ttc agg cca aca ggc tcc cct cct gtt tgg atg      353
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                               75                               80                               85

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   90                               95                               100

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  105                               110                               115                               120

tct agt aag acc aga aaa gta gcc atg gtc ttg aag gaa ttt att gac      497
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                               125                               130                               135

cag atg ttg gca gaa gga gct tct ctt gat gac att tac atg atc gga      545
Gln Met Leu Ala Glu Gly Ala Ser Leu Asp Asp Ile Tyr Met Ile Gly
                               140                               145                               150

gta agt cta gga gcc cac ata tct ggg ttt gtt gga gag atg tac gat      593
Val Ser Leu Gly Ala His Ile Ser Gly Phe Val Gly Glu Met Tyr Asp
   155                               160                               165

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tat tat gct gat aat tgg aaa gac cat cta agg ggg aaa gat cct cca Tyr Tyr Ala Asp Asn Trp Lys Asp His Leu Arg Gly Lys Asp Pro Pro 300 305 310	1025
atg acg aag gca ttc ttt gac aca gct gag gag agc cca ttc tgc atg Met Thr Lys Ala Phe Phe Asp Thr Ala Glu Glu Ser Pro Phe Cys Met 315 320 325	1073
tat cat tac ttt gtg gat att ata aca tgg aac aag aat gta aga aga Tyr His Tyr Phe Val Asp Ile Ile Thr Trp Asn Lys Asn Val Arg Arg 330 335 340	1121
ggg gac att acc atc aaa ttg aga gac aaa gct gga aac acc aca gaa Gly Asp Ile Thr Ile Lys Leu Arg Asp Lys Ala Gly Asn Thr Thr Glu 345 350 355 360	1169
tcc aaa atc aat cat gaa ccc acc aca ttt cag aaa tat cac caa gtg Ser Lys Ile Asn His Glu Pro Thr Thr Phe Gln Lys Tyr His Gln Val 365 370 375	1217
agt cta ctt gca aga ttt aat caa gat ctg gat aaa gtg gct gca att Ser Leu Leu Ala Arg Phe Asn Gln Asp Leu Asp Lys Val Ala Ala Ile 380 385 390	1265
tcc ttg atg ttc tct aca gga tct cta ata ggc cca agg tac aag ctc Ser Leu Met Phe Ser Thr Gly Ser Leu Ile Gly Pro Arg Tyr Lys Leu 395 400 405	1313
agg att ctc cga atg aag tta agg tcc ctt gcc cat ccg gag agg cct Arg Ile Leu Arg Met Lys Leu Arg Ser Leu Ala His Pro Glu Arg Pro 410 415 420	1361
cag ctg tgt cgg tat gat ctt gtc ctg atg gaa aac gtt gaa aca gtc Gln Leu Cys Arg Tyr Asp Leu Val Leu Met Glu Asn Val Glu Thr Val 425 430 435 440	1409

ttc caa cct att ctt tgc cca gag ttg cag ttg taa ctgttgccag 1455
 Phe Gln Pro Ile Leu Cys Pro Glu Leu Gln Leu *
 445 450

gacacatggc cataaataat agaaagaaag ctacaaccac aggctgtttg aaagcttcac 1515
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 <211> 451
 <212> PRT
 <213> Homo sapiens

<400> 2
 Met Leu Arg Phe Tyr Leu Phe Ile Ser Leu Leu Cys Leu Ser Arg Ser
 1 5 10 15
 Asp Ala Glu Glu Thr Cys Pro Ser Phe Thr Arg Leu Ser Phe His Ser
 20 25 30
 Ala Val Val Gly Thr Gly Leu Asn Val Arg Leu Met Leu Tyr Thr Arg
 35 40 45
 Lys Asn Leu Thr Cys Ala Gln Thr Ile Asn Ser Ser Ala Phe Gly Asn
 50 55 60
 Leu Asn Val Thr Lys Lys Thr Thr Phe Ile Val His Gly Phe Arg Pro
 65 70 75 80
 Thr Gly Ser Pro Pro Val Trp Met Asp Asp Leu Val Lys Gly Leu Leu
 85 90 95
 Ser Val Glu Asp Met Asn Val Val Val Asp Trp Asn Arg Gly Ala
 100 105 110
 Thr Thr Leu Ile Tyr Thr His Ala Ser Ser Lys Thr Arg Lys Val Ala
 115 120 125
 Met Val Leu Lys Glu Phe Ile Asp Gln Met Leu Ala Glu Gly Ala Ser
 130 135 140
 Leu Asp Asp Ile Tyr Met Ile Gly Val Ser Leu Gly Ala His Ile Ser
 145 150 155 160
 Gly Phe Val Gly Glu Met Tyr Asp Gly Trp Leu Gly Arg Ile Thr Gly
 165 170 175
 Leu Asp Pro Ala Gly Pro Leu Phe Asn Gly Lys Pro His Gln Asp Arg
 180 185 190
 Leu Asp Pro Ser Asp Ala Gln Phe Val Asp Val Ile His Ser Asp Thr
 195 200 205
 Asp Ala Leu Gly Tyr Lys Glu Pro Leu Gly Asn Ile Asp Phe Tyr Pro
 210 215 220
 Asn Gly Gly Leu Asp Gln Pro Gly Cys Pro Lys Thr Ile Leu Gly Gly
 225 230 235 240
 Phe Gln Tyr Phe Lys Cys Asp His Gln Arg Ser Val Tyr Leu Tyr Leu
 245 250 255
 Ser Ser Leu Arg Glu Ser Cys Thr Ile Thr Ala Tyr Pro Cys Asp Ser
 260 265 270
 Tyr Gln Asp Tyr Arg Asn Gly Lys Cys Val Ser Cys Gly Thr Ser Gln
 275 280 285
 Lys Glu Ser Cys Pro Leu Leu Gly Tyr Tyr Ala Asp Asn Trp Lys Asp
 290 295 300
 His Leu Arg Gly Lys Asp Pro Pro Met Thr Lys Ala Phe Phe Asp Thr

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305              310              315              320
Ala Glu Glu Ser Pro Phe Cys Met Tyr His Tyr Phe Val Asp Ile Ile
              325              330              335
Thr Trp Asn Lys Asn Val Arg Arg Gly Asp Ile Thr Ile Lys Leu Arg
              340              345              350
Asp Lys Ala Gly Asn Thr Thr Glu Ser Lys Ile Asn His Glu Pro Thr
              355              360              365
Thr Phe Gln Lys Tyr His Gln Val Ser Leu Leu Ala Arg Phe Asn Gln
              370              375              380
Asp Leu Asp Lys Val Ala Ala Ile Ser Leu Met Phe Ser Thr Gly Ser
385              390              395              400
Leu Ile Gly Pro Arg Tyr Lys Leu Arg Ile Leu Arg Met Lys Leu Arg
              405              410              415
Ser Leu Ala His Pro Glu Arg Pro Gln Leu Cys Arg Tyr Asp Leu Val
              420              425              430
Leu Met Glu Asn Val Glu Thr Val Phe Gln Pro Ile Leu Cys Pro Glu
              435              440              445
Leu Gln Leu
450

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<210> 3
<211> 329
<212> PRT
<213> Homo sapiens

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Leu Tyr Thr Asn Glu Asn Val Lys Asn Ala Thr Gln Leu Ile Gln Ala
              20              25              30
Tyr Pro Gln Arg Ile Arg Lys Ser Asn Phe Asn Thr Ser Arg Lys Thr
              35              40              45
Arg Phe Ile Ile His Gly Phe Thr Asp Lys Gly Glu Glu Glu Ser Trp
50              55              60
Leu Ser Lys Met Cys Lys Ala Leu Phe Gln Val Glu Lys Val Ser Gly
65              70              75              80
Asn Val Ile Val Val Asp Trp Leu Gly Gly Ala Ile Thr Asn Glu Tyr
              85              90              95
Ala Leu Lys Tyr Ile Phe Tyr Pro Gln Ala Val Leu Asn Val Arg Val
              100              105              110
Val Gly Ala Glu Ile Ala Lys Leu Gln Glu Leu Glu Glu Glu Leu
              115              120              125
Asn Val Ser Pro Glu Asn Val His Leu Ile Gly His Ser Leu Gly Ala
130              135              140
His Val Ala Gly Ala Ala Gly Arg Arg Phe Lys Gly Lys Thr Lys His
145              150              155              160
Lys Leu Gly Arg Ile Thr Gly Leu Asp Pro Ala Gly Pro Tyr Phe Lys
              165              170              175
Gly Thr Glu Glu Leu Thr Arg Leu Asp Pro Gly Asp Ala Glu Phe Val
180              185              190
Asp Ala Ile His Thr Asp Phe Ser Pro Ile Gly Pro Gly Leu Gly Met
195              200              205
Gly Thr Ser Gln Arg Val Gly His Val Asp Arg Tyr Pro Asn Gly Gly
210              215              220
Ser Ser Glu Gln Pro Gly Cys Gln Lys Ile Val Leu Ala Gln Ile Arg
225              230              235              240
Ala Thr Arg Gly Ile Trp Glu Tyr Phe Ala Glu Ser Val Arg Cys Gly
              245              250              255
His Glu Arg Ser Val Lys Tyr Tyr Ala Asp Ser Ile Leu Asn Glu Tyr
260              265              270
Lys Asn Asn Asp Gly Pro Gly Ser Arg Ala Tyr Met Cys Ile Ser Tyr
275              280              285
Asp Ala Phe Leu Glu Gly Asp Cys Leu Leu Cys Val Asn Lys Lys Cys
290              295              300
Pro Lys Met Gly Ser Tyr Pro Asp Gln Lys Gln Lys Lys Thr His Gly
305              310              315              320
Val His Gln Thr Phe Lys Leu Glu Glu
              325

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