Method of Screening for a Carnitine Transporter Agonist or Antagonist and its Uses

The present invention is directed to a method of screening for a carnitine transporter agonist or for a carnitine transporter antagonist, to a kit for carrying out the method for screening for a carnitine transporter agonist or for a carnitine transporter antagonist, to a method for the manufacture of a medicament for the treatment of a carnitine transporter deficiency, to methods of diagnosis of a carnitine transporter deficiency, to the use of a protein for the manufacture of an antibody reacting with a carnitine transporter, to an oligonucleotide and to methods of treatment of a carnitine transporter deficiency.

Carnitine deficiency in humans leads to a variety of severe symptoms (Rodriguez P.R. et al, 1988, Eur. J. Pediatr., 148, 193-197). Among the most severe symptoms are cardiomyopathia, cronical amyasthenia and coma, which are caused by hypoglycaemia, or by failure of ketogenesis upon fasting, which are consequences of low serum levels of carnitine in the tissues, in particular in the liver, the kidneys, the heart, in muscles and in the intestine.

The symptoms of carnitine deficiency have been assumed to be a consequence of a deficiency of carnitine transport in the kidneys and in the intestine (Rodriguez P.R. et al, 1988). Disturbance of the carnitine transport system in the kidneys and in the intestine may lead to disturbances in the transport and in the degradation of fatty acids, which leads to a variety of severe symptoms, in particular to progressive amyasthenia, which can be diagnosed through a lipidmyopathy and a low muscular carnitine level, and to cardiomyopathia and respiratory disturbance, hypotension, respiratory insufficiency, hypoglycemia, hepatomegaly, liver failure, arrhythmia, loss of consciousness, hypertrophic or dilatative cardiomyopathia, cot death, coma, liver function disturbance, rhabdomyolysis, peripheral neuropathy, retinopathy, hepatopathy, congenital dysmorphism with midfacial hypoplasia, renal cysts, dystonia, neonatal cardiomyopathia, microcephaly, dysmorphism. Systemic carnitine deficiency is a hereditary disease and its symptoms often occur already in new borns and in small children.

So far, only a mechanism contributing to a rare autosomal recessive form of hereditary carnitine deficiency is known, wherein mutations in the carnitine transporter hOCTN2 contribute to a reduced carnitine level (Nezu J.I. et al. 1999, Nature Genet 21:91-94). hOCTN2, whose amino acid sequence is available in the NCBI database under the accession number NP_003051, corresponding to SEQ ID NO: 12 herein, is however not synthesized in a tissue-specific way in the intestine or in the kidneys, but it is synthesized ubiquitously in the human body. Thus, the major mechanisms mediating carnitine uptake from the diet and carnitine homeostasis in the kidneys by recovery of carnitine from the renal filtrate (Rodriguez P.R. et al, 1988) are still unknown.

In addition, OCTN2 is not sufficient to mediate carnitine uptake in the intestine and in the kidneys, since it has been detected only on the luminal side of the intestinal and kidney epithelium, but not on the distal side where carnitine needs to be transported to the blood vessels (Lahjouji K et al. 2002, Biochim Biophys Acta 1558: 82-93). Intriguingly, there are reports about patients suffering from systemic carnitine deficiency which can only be treated by intravenous administration of carnitine, but not by dietary carnitine administration (Rodriguez P.R. et al. 1988, Eur. J. Pediatr. 148: 193-197).

Hence, a deficiency of hOCTN2 is not a suitable marker for the majority of carnitine deficiency syndromes.

Further, the protein CT2, whose amino acid sequence is available under the accession number NP_149116 in the NCBI database (National Center for Biotechnology Information USA), corresponding to SEQ ID NO: 14 herein, is a human carnitine transporter formed in testes only. Hence, its deficiency could not account for the symptoms of systemic caritine deficiency.

WO 2001077174 discloses a protein corresponding to SEQ ID NO: 1 herein, however, no information about a function of the protein as a carnitine transporter has been provided. An amino acid sequence available under the accession number XM_291120 in the NCBI database, corresponding to SEQ ID NO: 10 herein, comprises the entire

amino acid sequence of SEQ ID NO: 1 and an additional sequence comprising 39 amino acids (corresponding to amino acids 297 to 335 in SEQ ID NO: 10) between amino acids 296 and 297 of SEQ ID NO: 1 and is therefore a splice variant of SEQ ID NO: 1. U.S. 5,559,021 discloses the rat protein AAW07635 (rB21a) which shares 47 % amino acid sequence identity with SEQ ID NO: 1 herein, however, no information about a function of the protein as a carnitine transporter has been provided. A human sequence corresponding to AAW07635 can be found in the NCBI database under the Accession Number AJ276207, which shares 46 % amino acid sequence identity to SEQ ID NO: 1 herein, however, it has been supposed to be a neurotransmitter transporter. CN 1287170 discloses the protein AAG64193, which shares 47 % amino acid sequence identity with SEQ ID NO: 1 herein, however it has been supposed to be a human nerve mass-transferring protein. EP 881290 discloses the AAW73376 protein, namely human HPDDV78, which shares 46 % amino acid sequence identity with SEQ ID NO: 1 herein, however it has been supposed to be a neurotransmitter transporter. The mouse and the rat amino acid sequences SEQ ID NO: 2 and SEQ ID NO: 3 comprised herein form part of sequences available in public data bases, which however have not been annotated and have not been supposed to comprise a carnitine transporter.

From the above, no tissue-specifically synthesized carnitine transporter of the intestine or of the kidneys and hence no enzyme whose deficiency could account for the majority of carnitine deficiency syndromes known.

Therefore, there are at present no diagnostic ways to detect the majority of carnitine deficiency syndromes at the level of the carnitine transporter, but the detection of the relevant enzymes has to be awaited. Further, there are at present no therapeutic ways for the treatment of systemic carnitine deficiency at the level of the relevant disturbed enzymatic activity. At present the only available therapeutic way is the administration of carnitine, which has often the problem of a reduced or even missing uptake of carnitine from the intestine.

In view of the above there is a need to provide new ways to diagnose and treat carnitine deficiency. Therefore, it is an object of the present invention to provide new

ways for the diagnosis of carnitine deficiency. A further object of the present invention refers to new therapeutic ways to treat carnitine deficiency. Still further objects of the present invention refer to new ways for the diagnosis of diseases associated with carnitine deficiency and to new therapeutic ways to treat diseases associated with carnitine deficiency.

SUMMARY OF INVENTION

In a first aspect, there is provided a method of screening for a carnitine transporter agonist or antagonist, wherein the method comprises the steps of:

(a) providing a carnitine transporter,

(b) providing a test compound,

(c) measuring the activity of the carnitine transporter,

wherein the carnitine transporter comprises the amino acid sequence SEQ ID NO: 1 or the carnitine transporter is encoded by a nucleic acid molecule comprising SEQ ID NO: 4 or SEQ ID NO: 15.

In a second aspect, there is provided a kit for carrying out the method according to the first aspect, comprising:

(a) a lipid membrane comprising a carnitine transporter,

(b) a detectable substrate for the carnitine transporter.

In a third aspect, there is provided a method of diagnosis of a carnitine transporter deficiency, wherein the method comprises determining the amount of a carnitine transporter comprising the amino acid sequence SEQ ID NO: 1 in a tissue sample.

The present invention provides favorable uses of a carnitine transporter which is formed in a tissue-specific way in the intestine and kidneys, in particular of humans, mice and rats. The human carnitine transporter detected in the invention comprises the amino acid sequence SEQ ID NO: 1, the closely related murine carnitine transporter comprises the amino acid sequence SEQ ID NO: 2, and the closely related rat

carnitine transporter comprises the amino acid sequence SEQ ID NO: 3. The invention refers in particular to methods for the development of drugs which influence the activity of carnitine transporters and to related test kits, to methods for the manufacture of medicaments for the treatment of carnitine deficiency, to the manufacture of antibodies against carnitine transporters, to diagnostic methods for carnitine deficiency, to oligonucleotides for detecting nucleic acids coding for carnitine transporters, and to therapeutic methods for the treatment of carnitine deficiency.

A first preferred embodiment of the present invention refers to a method of screening for a carnitine transporter agonist or antagonist, wherein the method comprises the steps of: (a) providing a carnitine transporter, (b) providing a test compound, and (c) measuring the activity of the carnitine transporter.

Preferably, the method of screening for a carnitine transporter agonist or antagonist involves (a) providing a cell, tissue sample or organism comprising a nucleic acid molecule coding for a carnitine transporter, (b) providing a test compound to said cell, tissue sample or organism, and (c) measuring the activity of the carnitine transporter. Preferably, measuring the activity of the carnitine transporter involves determining the expression of the nucleic acid molecule coding for the carnitine transporter, and/or providing a substrate for the carnitine transporter to said cell, tissue sample or organism and measuring the transport of the substrate by the carnitine transporter

across a lipid membrane of said cell, tissue sample or organism. Determining of the expression of the nucleic acid molecule coding for the carnitine transporter preferably involves determining the transcriptional activity of the nucleic acid molecule and/or determining the amount of the carnitine transporter protein.

Alternatively, the method of screening for a carnitine transporter agonist or antagonist preferably involves (a) providing a carnitine transporter comprised in a lipid membrane separating two volumes comprising an aqueous medium, (b) providing a test compound to at least one of said volumes, and (c) measuring the activity of the carnitine transporter, wherein measuring the activity of the carnitine transporter involves providing a substrate for the carnitine transporter to at least one of said volumes and measuring the transport of the substrate across said lipid membrane.

The test compound is preferably tested for an agonist or antagonist activity on the carnitine transporter. Preferably, a multitude of test compounds are screened for a carnitine transporter agonist or antagonist. Preferably a suitable substrate for the carnitine transporter is carnitine, noradrenaline, methylphenylpyridinium, creatine or serotonin.

The activity of the carnitine transporter is preferably measured by determining the rate of transport of the substrate by the carnitine transporter. Preferably, the rate of transport of the substrate across the lipid membrane is determined. Preferably, the rate of transport of the substrate from one volume to the other is determined. Preferably, the lipid membrane separates two chambers of an experimental setting or is closed to form a membrane of a lipid vesicle or to form the plasma membrane of a living or a reconstituted cell. Preferably, the lipid membrane comprises the carnitine transporter in an orientation that allows transport of a substrate from one chamber to the other chamber or across the membrane of the lipid vesicle or across the plasma membrane. Preferably, determining the rate of transport of the substrate across the lipid membrane comprises measuring the amount of the substrate transported across the lipid membrane.

Preferably, the agonist or antagonist activity of the test compound on the activity of the carnitine transporter is determined by measuring the rate of transport of the substrate by the carnitine transporter in the presence of the test compound and comparing it to the rate of transport of the substrate by the carnitine transporter in the absence of the test compound. Preferably, the method involves control measurements, wherein transport of the substrate over the lipid membrane without the carnitine transporter is measured.

In any embodiment of the present invention, the substrate of the carnitine transporter is any substrate transported by a carnitine transporter, preferably transported by a plant or animal carnitine transporter, preferably transported by a mammalian carnitine transporter, preferably transported by a human, mouse or rat carnitine transporter, in particular by a human, mouse, or rat carnitine transporter of the kidneys or the intestine. Preferably the substrate is any substrate transported by a carnitine transporter comprising the amino acid sequence SEQ ID NO: 1, SEQ ID NO: 2, or SEQ ID NO: 3, or encoded by a nucleic acid molecule comprising SEQ ID NO: 4, or by a carnitine transporter disclosed in any embodiment of the present invention. Preferably, the substrate is carnitine, noradrenaline, methylphenylpyridinium, creatine and/or serotonin. More preferably, the substrate is carnitine.

In the embodiments of the present invention, carnitine preferably comprises L-carnitine and/or D-carnitine, preferably L-carnitine. Preferably, carnitine comprises carnitine derivatives and/or carnitine analogues. Preferably, carnitine derivatives comprise carnitine metabolites and carnitine conjugates. Preferably, carnitine metabolites comprise physiological carnitine metabolites which are formed by chemical alteration of L-carnitine or D-carnitine in vivo, such as acetylcarnitine. Preferably, carnitine conjugates comprise L-carnitine, D-carnitine or a carnitine analogue which is coupled to an effector molecule. Preferably, the effector molecule is a chemical compound that shall be cotransported over a lipid membrane together with carnitine by a carnitine transporter. Preferably, the effector molecule is a drug. Preferably, the coupling is any chemical bond, preferably a covalent bond, ionic bond or Van-der-Vaals bond. Preferably, a carnitine analogue is a chemical compound which possesses an

analogous chemical structure to carnitine which allows its transport by a carnitine transporter.

The method of the invention of screening for a carnitine transporter agonist or antagonist preferably involves testing of a test compound for an agonist action enhancing the activity of a carnitine transporter. In alternative, it involves testing of a test compound for an antagonist action inhibiting the activity of a carnitine transporter. Preferably, the method of the invention of screening for a carnitine transporter agonist or antagonist is adapted to the screening of a large number of test compounds, wherein the testing of an individual test compound requires a short time, and preferably the testing of an individual test compound is economical and requires small amounts of reagents, in particular of the test compound.

A test compound tested in the method of the invention of screening for a carnitine transporter agonist or antagonist is preferably a small molecule, preferably a candidate for an effector compound binding to a protein or to an enzyme cofactor. Preferably the test compound is a candidate for an effector compound which can bind to a protein comprising the amino acid sequence SEQ ID NO: 1, SEQ ID NO: 2, or SEQ ID NO: 3 or to any carnitine transporter disclosed in an embodiment of the present invention.

Preferably, a test compound is a candidate for an effector compound which can bind to a protein or to an enzyme cofactor, wherein said protein or enzyme cofactor binds to or is a candidate for a compound binding to a protein comprising the amino acid sequence SEQ ID NO: 1, SEQ ID NO: 2, or SEQ ID NO: 3, or to any carnitine transporter disclosed in an embodiment of the present invention.

Preferably, a test compound is a candidate for an effector compound which can bind to a transcription factor or to a translation factor, preferably wherein the transcription factor or the translation factor increases or decreases the synthesis of a protein comprising the amino acid sequence SEQ ID NO: 1, SEQ ID NO: 2, or SEQ ID NO: 3

or increases or decreases the synthesis of any carnitine transporter disclosed in an embodiment of the present invention.

Preferably, a test compound is a candidate for an effector compound which can directly or indirectly increase or decrease the synthesis or the activity of a transcription factor or of a translation factor, preferably wherein the transcription factor or the translation factor increases or decreases the synthesis of a protein comprising the amino acid sequence SEQ ID NO: 1, SEQ ID NO: 2, or SEQ ID NO: 3 or increases or decreases the synthesis of any carnitine transporter disclosed in an embodiment of the present invention.

Preferably the test compound is any chemical compound, such as a naturally occurring compound, or a chemically synthesized compound that is identical or similar to a naturally occurring compound, or any chemically synthesized compound that does not occur in nature.

A naturally occurring compound is preferably a compound that can be detected in or isolated from a multicellular or single cell organism, in particular a compound that can be detected in or isolated from an animal, a plant, a fungus, a yeast, bacterium, or any other cell-containing organism or in a virus. A chemically synthesized compound that does not occur in nature is preferably synthesized by combinatorial chemistry. Preferably, it comprises a lead structure derived from a naturally occurring compound, preferably from a candidate for an effector molecule which can bind to a protein or to an enzyme cofactor.

Preferably, a carnitine transporter agonist or antagonist identified according to the invention or used in an embodiment of the invention enhances, or inhibits respectively, the activity of a kidney or intestinal carnitine transporter of an individual, preferably of a healthy individual. Preferably the carnitine transporter agonist enhances the activity of a carnitine transporter of an individual suffering from a carnitine transporter deficiency. Preferably, the carnitine transporter agonist enhances the activity of a carnitine transporter in an individual having a reduced amount of a carnitine transporter.

Preferably, the carnitine transporter agonist or antagonist enhances, or decreases respectively, the activity of a genetic variant of a carnitine transporter in an individual. Preferably, the carnitine transporter agonist enhances the activity of a genetic variant of the carnitine transporter associated with carnitine deficiency. Preferably, the carnitine transporter antagonist decreases the activity of a carnitine transporter, preferably of a kidney or intestinal carnitine transporter, in an individual having an increased activity or an increased amount of a carnitine transporter. Preferably, the activity of a carnitine transporter as mentioned herein refers to the transport rate of the carnitine transporter for a substrate, to the amount of the carnitine transporter, and/or to the strength of expression of a nucleic acid molecule coding for the carnitine transporter.

Preferably, the carnitine transporter provided in the method of the invention of screening for a carnitine transporter agonist or antagonist can also be used in any other embodiment of the present invention. The carnitine transporter is preferably a plant or animal carnitine transporter, preferably a mammalian carnitine transporter, preferably a human, mouse, or rat carnitine transporter, preferably a kidney or intestinal carnitine transporter, preferably an intestinal carnitine transporter.

Preferably, the carnitine transporter comprises the amino acid sequence SEQ ID NO: 1, SEQ ID NO: 2, or SEQ ID NO: 3 of the invention. Preferably, the carnitine transporter is a high affinity carnitine transporter produced in the kidneys and in the intestine of a healthy individual. Preferably, the carnitine transporter comprises the amino acid sequence SEQ ID NO: 1 of the high affinity carnitine transporter of the human kidneys and intestine. Preferably, the carnitine transporter comprises the amino acid sequence SEQ ID NO: 10, a functional splice variant of SEQ ID NO: 1 which comprises an additional sequence comprising 39 amino acids (corresponding to amino acids 297 to 335 in SEQ ID NO: 10) between the amino acids 296 and 297 of SEQ ID NO: 1.

Preferably, the carnitine transporter is the orthologous mouse or rat high affinity carnitine transporter produced in the kidneys and in the intestine of healthy animals. Preferably, the carnitine transporter comprises the amino acid sequence SEQ ID NO: 2

or SEQ ID NO: 3, respectively, of the mouse or rat kidney and intestinal high affinity carnitine transporter.

Preferably, the carnitine transporter is a related carnitine transporter comprising a related amino acid sequences to SEQ ID NO: 1, SEQ ID NO: 2, or SEQ ID NO: 3. Preferably, the carnitine transporter comprises a related amino acid sequence to SEQ ID NO: 1. Preferably, the carnitine transporter comprises a related amino acid sequence to SEQ ID NO: 10.

Preferably, the related carnitine transporter comprises an amino acid sequence comprising at least 30 % sequence identity to at least one of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, or SEQ ID NO: 10 and at least 10 %, preferably at least 30 %, more preferably at least 50 %, still more preferably at least 70 % of the substrate transport activity for at least one substrate, preferably for carnitine, preferably for L-carnitine, of the carnitine transporter comprising the amino acid sequence SEQ ID NO: 1 or SEQ ID NO: 10, preferably SEQ ID NO: 1.

Preferably, the related carnitine transporter comprises the amino acid sequence of the rat protein AAW07635 (rB21a), available under the accession number AJ276207, of the protein AAG64193 disclosed in CN 1287170, or of the protein AAW73376, namely human HPDDV78 disclosed in EP 881290.

Preferably, the related carnitine transporter comprises an amino acid sequence comprising at least 60 % sequence identity to at least one of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, or SEQ ID NO: 10 and at least 10 %, preferably at least 30 %, more preferably at least 50 %, more preferably at least 70 %, still more preferably at least 80 % or at least 90 % of the substrate transport activity for at least one substrate, preferably for carnitine, preferably for L-carnitine, of the carnitine transporter comprising the amino acid sequence SEQ ID NO: 1 or SEQ ID NO: 10, preferably SEQ ID NO: 1.

Preferably, the carnitine transporter comprises an amino acid sequence comprising at least 85 %, preferably at least 86 %, preferably at least 86,5 % sequence identity to at least one of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, or SEQ ID NO: 10, and at least 10 %, preferably at least 30 %, more preferably at least 50 %, more preferably at least 70 %, still more preferably at least 80 % or at least 90 % of the substrate transport activity for at least one substrate, preferably for carnitine, preferably for L-carnitine, of the carnitine transporter comprising the amino acid sequence SEQ ID NO: 1 or SEQ ID NO: 10, preferably SEQ ID NO: 1.

Preferably, the carnitine transporter comprises at least 95 %, preferably at least 95,4 % sequence identity to at least one of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, or SEQ ID NO: 10, and at least 10 %, preferably at least 30 %, more preferably at least 50 %, more preferably at least 70 %, still more preferably at least 80 % or at least 90 % of the substrate transport activity for at least one substrate, preferably for carnitine, preferably for L-carnitine, of the carnitine transporter comprising the amino acid sequence SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, or SEQ ID NO: 10.

Preferably, the amino acid sequence of the carnitine transporter differs from the amino acid sequence according to SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, or SEQ ID NO: 10 by so-called conservative amino acid substitutions which are known to the skilled person and are supposed to have little or no influence on the activity of a protein and hence on the activity of the carnitine transporter. Preferably, the carnitine transporter differs from SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, and/or SEQ ID NO: 10 by amino acid substitutions which are supposed to have little or no influence on the activity of the carnitine transporter by the skilled person who considers the amino acid sequence alignment between SEQ ID NO: 1, SEQ ID NO: 2, and SEQ ID NO: 3, disclosed herein in Fig. 3 below.

Preferably, the carnitine transporter used in any embodiment of the present invention is encoded by a nucleic acid molecule coding for a human carnitine transporter produced in the kidneys and/or in the intestine. Preferably, the nucleic acid-molecule is tissue-specifically expressed in the kidneys and/or in the intestine. Preferably, the

nucleic acid molecule codes for the human or the mouse or rat carnitine transporter comprising the amino acid sequence SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, or SEQ ID NO: 10.

Preferably, the nucleic acid molecule comprises SEQ ID NO: 4, which codes for the human kidney and intestinal carnitine transporter comprising the amino acid sequence SEQ ID NO: 1. Preferably, the nucleic acid molecule comprises SEQ ID NO: 5, which codes for the orthologous murine kidney and intestinal carnitine transporter comprising the amino acid sequence SEQ ID NO: 2. Preferably, the nucleic acid molecule comprises SEQ ID NO: 8, which codes for the orthologous rat kidney and intestinal carnitine transporter comprising the amino acid sequence SEQ ID NO: 3.

Preferably, the nucleic acid molecule comprises SEQ ID NO: 9, which is a functional splice variant of SEQ ID NO: 4, coding for the amino acid sequence SEQ ID NO: 10. SEQ ID NO: 9 comprises an additional sequence comprising 117 nucleotides (corresponding to nucleotides 888 to 1004 in SEQ ID NO: 9) which are inserted between nucleotides 887 and 888 of SEQ ID NO: 4.

Preferably, the carnitine transporter is encoded by the mRNA comprising SEQ ID NO: 15 for the human kidney and intestinal carnitine transporter. SEQ ID NO: 15 comprises the open reading frame according to SEQ ID NO: 4 and additional non-translated 5' and 3' flanking sequences. The present invention provides for the first time the complete mRNA comprising SEQ ID NO: 15, which codes for the carnitine transporter comprising the amino acid sequence SEQ ID NO: 1. SEQ ID NO: 15 comprises the open reading frame according to SEQ ID NO: 4 which codes for SEQ ID NO: 1, the 5' flanking region comprising nucleotides 1 to 45 of SEQ ID NO: 15, and the 3' flanking region comprising nucleotides 1951 to 5175 of SEQ ID NO: 15.

Preferably, the carnitine transporter is encoded by a nucleic acid molecule which is detectable by a skilled person who uses routine experiments to detect carnitine transporters which are encoded by nucleic acid molecules comprising similar sequences to SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 8, SEQ ID NO: 9, or SEQ ID

NO: 15. Preferably, the carnitine transporter is encoded by a nucleic acid sequence which is similar to SEQ ID NO: 4. Preferably, the nucleic acid molecule is similar to SEQ ID NO: 9. Preferably, the nucleic acid molecule is similar to SEQ ID NO: 15.

Preferably, the nucleic acid molecule coding for the carnitine transporter is detectable by routine experiments for the detection of nucleic acid molecules comprising a known sequence. Preferably, the nucleic acid molecule coding for the carnitine transporter is detectable by routine experiments for the detection of nucleic acid molecules comprising a sequence similar to a known sequence, preferably related to a known nucleic acid sequence, preferably homologous to a known nucleic acid sequence.

Preferably, the carnitine transporter is encoded by a nucleic acid sequence which is similar to a nucleic acid molecules coding for the amino acid sequence SEQ ID NO: 1, SEQ ID NO: 2, or SEQ ID NO: 3.

Preferably, a nucleic acid molecule is similar to a nucleic acid molecule coding for a carnitine transporter of any embodiment of the present invention, if it comprises a sequence having a detectable degree of sequence homology which is readily appreciated by the skilled person, preferably having a detectable degree of sequence identity. Preferably, a nucleic acid molecule is similar to a nucleic acid molecule coding for a carnitine transporter of any embodiment of the invention if it codes for a protein comprising an amino acid sequence having a detectable degree of sequence homology as readily appreciated by the skilled person, preferably having a detectable degree of sequence identity, to the carnitine transporter usable in the invention. Preferably, sequence identities and sequence homologies between nucleic acid molecules can be detected without undue burden in hybridization experiments, wherein complementary base pairing is allowed under stringent or under non-stringent conditions.

Preferably, a nucleic acid molecule is similar to a nucleic acid molecule coding for a carnitine transporter of an embodiment of the invention if it hybridizes to a nucleic acid molecule comprising SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 8, or SEQ ID NO: 9,

SEQ ID NO: 15, or to a complementary sequence thereof or if it hybridizes to a fragment thereof or to a complementary sequence thereof comprising at least 18 nucleotides, preferably at least 25 nucleotides, preferably at least 50 nucleotides. Preferably, non-stringent conditions are used, more preferably stringent conditions are used. The similarity of nucleic acid molecules coding for the amino acid sequences SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, or SEQ ID NO: 10 is determined in an analogous way.

Preferably, a nucleic acid molecule coding for a carnitine transporter according to an embodiment of the invention is detectable by the skilled person who uses for the detection the 5' flanking region of SEQ ID NO: 15 or the 3' flanking region of SEQ ID NO: 15, preferably the 3' flanking region. Preferably a fragment of the 3' region of SEQ ID NO: 15 is used, preferably comprising at least 18 nucleotides, preferably at least 25 nucleotides, preferably at least 50 nucleotides. Preferably, non-stringent conditions are used, more preferably stringent conditions are used. Preferably the detection involves a hybridization assay or a PCR analysis, either of which bases on the well-known concept of complementary base pairing.

Non-stringent conditions and stringent conditions of hybridization are known to the skilled person. Preferably, non-stringent conditions comprise 3x SSC, 0,5 % Sodium N-lauryl sarcosine and 60 °C. Preferably, stringent conditions comprise 1x SSC, 0,1 % Sodium dodecylsulfate (SDS) and 65 °C. Preferably 20x SSC comprises 3M NaCl, 0,3M tri-Sodium citrate, pH 7,0.

In the method of the invention of screening for a carnitine transporter agonist or antagonist which involves providing a carnitine transporter comprised in a lipid membrane, the carnitine transporter is preferably comprised in a cellular membrane, preferably in an inner mitochondrial membrane or in a plasma membrane. Suitable membrane lipids are either naturally occurring membrane lipids of cellular membranes, and/or membrane-forming lipids which are not known in nature but which are known to the chemist.

Preferably, the lipid membrane comprises lipids forming a membrane, which can comprise the carnitine transporter. Such lipids are known to the skilled person. Preferably the lipids can be used to form a liposome. Preferably, the lipids are components of or are derived from a cellular membrane, preferably a plasma membrane or an inner mitochondrial membrane. Preferably, the lipids are identical or have a similar chemical structure as lipids of biological membranes and are capable of forming a lipid bilayer or a lipid monolayer having two hydrophilic surfaces in an aqueous medium.

Preferably, the lipid membrane comprising the carnitine transporter separates two volumes comprising aqueous media. Preferably the two volumes are two buffer tanks of an experimental setting.

The lipid membrane comprising the carnitine transporter comprises preferably a reconstituted cellular membrane. The reconstituted cellular membrane is preferably derived from a living cell. The methods of forming a reconstituted cellular membrane are known to the skilled person.

Preferably the carnitine transporter is comprised in a lipid vesicle membrane. Preferably a lipid vesicle comprises a liposome or a closed reconstituted cellular membrane. The liposome or the reconstituted cellular membrane is formed by any suitable method. Preferably, the liposome or reconstituted membrane vesicle is formed by exposing a mixture comprising at least one type of membrane lipid and the carnitine transporter to ultrasonic waves or by leading the mixture through a small-diameter outlet, in particular a syringe, into a buffer solution. Preferably, the reconstituted cell is made by opening a living cell, providing the carnitine transporter and resealing the plasma membrane. During the opening and resealing of the cell components of the cytoplasm may or may not be lost, and consequently the reconstituted plasma membrane comprising the carnitine transporter may belong to a living cell or be a so-called membrane ghost.

In a preferred embodiment, the carnitine transporter is comprised in the plasma membrane of a test cell. Preferably, the test cell expresses a nucleic acid molecule coding for a carnitine transporter, preferably a plant or animal carnitine transporter, preferably a mammalian, preferably a mouse or rat carnitine transporter, preferably a human carnitine transporter, preferably a kidney or intestinal carnitine transporter, preferably a human, mouse, or rat kidney or intestinal carnitine transporter.

Preferably the test cell expresses a nucleic acid molecule coding for a carnitine transporter comprising the amino acid sequence SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 10, the rat protein AAW07635 (rB21a), available under the accession number AJ276207, the protein AAG64193 disclosed in CN 1287170, or the protein AAW73376, namely human HPDDV78 disclosed in EP 881290, preferably the test cell expresses a nucleic acid coding for SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, or SEQ ID NO: 10, preferably SEQ ID NO: 1 or SEQ ID NO: 10, preferably SEQ ID NO: 1. Preferably, the test cell expresses a nucleic acid molecule comprising SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 8, SEQ ID NO: 9, or SEQ ID NO: 15, preferably SEQ ID NO: 4, SEQ ID NO: 9 or SEQ ID NO: 15, preferably SEQ ID NO: 4 or SEQ ID NO: 15. Preferably, the test cell comprises any of said nucleic acid molecules operably linked to a transcriptional activator sequence, preferably SEQ ID NO: 4, SEQ ID NO: 9, or SEQ ID NO: 15, preferably SEQ ID NO: 4 or SEQ ID NO: 15 operably linked to a transcriptional activator sequence. Preferably, the test cell comprises a translatable RNA molecule comprising a sequence corresponding to SEQ ID NO: 4, SEQ ID NO: 9, or SEQ ID NO: 15, preferably SEQ ID NO: 4 or SEQ ID NO: 15. Preferably, the test cell comprises a microinjected cRNA molecule comprising a sequence corresponding to SEQ ID NO: 4, SEQ ID NO: 9 or SEQ ID NO: 15, preferably SEQ ID NO: 4 or SEQ ID NO: 15.

Preferably, the test cell comprises a functional carnitine transporter in its plasma membrane. Preferably, the carnitine transporter transports a substrate selected from carnitine, noradrenaline, methylphenylpyridinium, creatine, and/or serotonin across the plasma membrane. Preferably, the carnitine transporter transports the substrate into the test cell. Preferably, the test cell is a bacterial or a eukaryotic cell, in particular a

yeast cell. Preferably, the test cell belongs to a primary cell line or to a permanent cell line. Preferably, the test cell is a Xenopus laevis oocyte. Preferably, the Xenopus laevis oocyte comprises an injected cRNA comprising SEQ ID NO: 4, SEQ ID NO: 9 or SEQ ID NO: 15, preferably SEQ ID NO: 4 or SEQ ID NO: 15.

Preferably, a detectable substrate for the carnitine transporter is used. Preferably the detectable substrate allows its detection inside in the test cell. Preferably, the detectable substrate allows for the quantification of small amounts of the detectable substrate which are accumulated inside the test cell.

The method of the invention of screening of test compounds for agonist or antagonist activity of a carnitine transporter preferably comprises measuring the amount of a detectable substrate which is transported by the carnitine transporter across a lipid membrane, in particular across a plasma membrane into a test cell, wherein the amount of the substrate transported across a lipid membrane is indicative of the activity of the carnitine transporter.

Preferably, the detectable carnitine transporter substrate is a radioactively labeled substrate, a streptavidin-labeled or biotinylated substrate, or a substrate reacting with an antibody.

Preferably, the test compounds screened for having an agonist or an antagonist activity on the carnitine transporter are provided in the form of a chemical compound library. According to the invention, the term "chemical compound library" refers to a plurality of chemical compounds that have been assembled from any of multiple sources, including chemically synthesized molecules and natural products, or that have been generated by combinatorial chemistry techniques.

Preferably, the method of the invention for screening for a carnitine transporter agonist or antagonist is automated, preferably it is carried out in a robotics system.

A second preferred embodiment of the invention refers to a kit for carrying out the method of the invention of screening for a carnitine transporter agonist or antagonist comprising a lipid membrane, which comprises a carnitine transporter, and a detectable substrate for the carnitine transporter. The kit of the invention preferably allows the screening of test compounds comprised in a group of test compounds, in particular in a chemical compound library.

Preferably, the carnitine transporter provided in the kit of the invention is a human, mouse, or rat carnitine transporter. Preferably the carnitine transporter comprises the amino acid sequence SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 10, the rat protein AAW07635 (rB21a), available under the accession number AJ276207, the protein AAG64193 disclosed in CN 1287170, or the protein AAW73376, namely human HPDDV78 disclosed in EP 881290, preferably SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, or SEQ ID NO: 10, preferably SEQ ID NO: 1 or SEQ ID NO: 10, preferably SEQ ID NO: 1. Preferably, the carnitine transporter is encoded by a nucleic acid molecule comprising SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 9, SEQ ID NO: 15, preferably SEQ ID NO: 4 or SEQ ID NO: 15, or by a nucleic acid coding for at least one of said proteins. Preferably, the lipid membrane separates two volumes of an experimental setting, in particular two buffer tanks, or is closed to form a lipid vesicle, or to form the plasma membrane of a living or a reconstituted cell. Preferably, the carnitine transporter is comprised in a lipid vesicle membrane. Preferably, the carnitine transporter is comprised in the plasma membrane of a test cell.

Preferably, the kit of the invention comprises a detectable substrate for the carnitine transporter, in particular a radioactive, streptavidin-labeled or biotinylated substrate, or a substrate detectable with an antibody. Preferably, the kit comprises an antibody reacting with the substrate. Preferably, the substrate is carnitine, noradrenaline, methylphenylpyridinium, creatine, and/or serotonin. Preferably, the substrate is carnitine.

In any embodiment of the present invention, the expression "antibody" comprises any monoclonal antibody, antiserum, in particular polyvalent antiserum, antiserum fraction,

antibody fragment, recombinantly produced antibody or antibody fragment, comprising the reactivity with its antigen indicated herein.

Preferably, the kit of the invention comprises any component or feature of the method of the invention for screening of a carnitine transporter agonist or antagonist.

A third preferred embodiment of the invention refers to a method for the manufacture of a medicament for the treatment of a carnitine transporter deficiency, wherein the method comprises the steps of: (a) identifying an agonist of a carnitine transporter using the method of the invention of screening for an agonist or antagonist of a carnitine transporter, (b) providing a sufficient amount of the agonist, and (c) formulating the agonist with one or more pharmaceutically acceptable carriers or auxillary substances.

Preferably, the method refers to the manufacture of a medicament for the treatment of a carnitine transporter deficiency of the kidney or intestinal carnitine transporter. Preferably, the method refers to the manufacture of a medicament for the treatment of systemic carnitine deficiency.

Preferably, the method refers to the manufacture of a medicament for the treatment of a deficiency of carnitine, noradrenaline, methylphenylpyridinium, creatine, and/or serotonin transport. Preferably, the method refers to the manufacture of a medicament for the treatment of any deficiency of a substrate transported by a human or animal carnitine transporter of the invention comprising the amino acid sequence SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 10, the rat protein AAW07635 (rB21a), available under the accession number AJ276207, the protein AAG64193 disclosed in CN 1287170, or the protein AAW73376, namely human HPDDV78 disclosed in EP 881290, preferably SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, or SEQ ID NO: 10, preferably SEQ ID NO: 1 or SEQ ID NO: 10, preferably SEQ ID NO: 1 or encoded by a nucleic acid molecule comprising SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 9, SEQ ID NO: 15, preferably SEQ ID NO: 4 or SEQ ID NO: 15, or by a nucleic acid coding for at least one of said proteins. Preferably, the method refers to the manufacture of a

medicament for the treatment of any deficiency of a substrate transported by any carnitine transporter having a similar amino acid sequence to the carnitine transporter of the invention, which is detectable as disclosed herein or which is detectable by the skilled person basing on the disclosure herein without undue experimental burden.

Preferably, any aspect of the method of the invention of screening for a carnitine transporter agonist refers also to the step of identifying an agonist of a carnitine transporter of the method of the invention for the manufacture of a medicament for the treatment of a carnitine transporter deficiency.

In the method for the manufacture of a medicament, a sufficient amount of the agonist is preferably a therapeutically effective amount, preferably a therapeutically effective amount of a unit dose of administration of the medicament. Preferably, the a therapeutically effective amount is therapeutically sufficient for the treatment of a carnitine transporter deficiency caused by a decreased amount of a functional carnitine transporter in a patient, or caused by a variant of a carnitine transporter having a decreased activity in a patient.

The specific therapeutically effective dose level for any particular patient will depend upon a variety of factors including the activity of the identified carnitine transporter agonist, the dosage form, the age, body weight and sex of the patient, the duration of the treatment and like factors well known in the medical arts. Preferably, the unit dose is therapeutically sufficient for the treatment of an adult, a child, a small child, a new born, or for the treatment of an unborn child during pregnancy.

The total daily dose of the carnitine transporter agonist of the invention administered to a human or other mammal in single or in divided doses can be in amounts, for example, from about 0.01 to about 50 mg/kg body weight or more preferably from about 0.1 to about 25 mg/kg body weight. Single dose compositions may contain such amounts or submultiples thereof to make up the daily dose. In general, treatment regimens according to the present invention comprise administration to a patient in

need of such treatment from about 10 mg to about 1000 mg of the carnitine transporter agonist of the present invention per day in single or multiple doses.

Preferably, a combination of more than one carnitine transporter agonist is used for the manufacture of the medicament. Still preferably, the medicament comprises in addition carnitine. Preferably, the amount of carnitine comprised in a unit dose medicament is adjusted to the activity of the carnitine transporter mediated by the carnitine transporter agonist comprised in the unit dose medicament.

For the production of the medicament the carnitine transporter agonist of the present invention is preferably formulated with one or more pharmaceutically acceptable additives or auxiliary substances, such as physiological buffer solution, e.g. sodium chloride solution, demineralized water, stabilizers, such as protease or nuclease inhibitors, preferably aprotinin, ε-aminocaproic acid or pepstatin A or sequestering agents such as EDTA, gel formulations, such as white vaseline, low-viscosity paraffin and/or yellow wax, etc. depending on the kind of administration.

Suitable further additives are, for example, detergents, such as, for example, Triton X-100 or sodium deoxycholate, but also polyols, such as, for example, polyethylene glycol or glycerol, sugars, such as, for example, sucrose or glucose, zwitterionic compounds, such as, for example, amino acids such as glycine or in particular taurine or betaine and/or a protein, such as, for example, bovine or human serum albumin. Detergents, polyols and/or zwitterionic compounds are preferred.

The physiological buffer solution preferably has a pH of approx. 6.0-8.0, especially a pH of approx. 6.8-7.8, in particular a pH of approx. 7.4, and/or an osmolarity of approx. 200-400 milliosmol/liter, preferably of approx. 290-310 milliosmol/liter. The pH of the pharmaceutical composition is in general adjusted using a suitable organic or inorganic buffer, such as, for example, preferably using a phosphate buffer, tris buffer (tris(hydroxymethyl)aminomethane), HEPES buffer ([4-(2-hydroxyethyl)piperazino]ethanesulphonic acid) or MOPS buffer (3-morpholino-1-propanesulphonic acid). The choice of the respective buffer in general depends on

the desired buffer molarity. Phosphate buffer is suitable, for example, for injection and infusion solutions.

The pharmaceutical composition can be administered in a conventional manner, e.g. by means of oral dosage forms, such as, for example, tablets or capsules, by means of the mucous membranes, for example the nose or the oral cavity, in the form of dispositories implanted under the skin, by means of injections, infusions or gels which contain the pharmaceutical compositions according to the invention. It is further possible to administer the pharmaceutical composition topically and locally, if appropriate, in the form of liposome complexes. Furthermore, the treatment can be carried out by means of a transdermal therapeutic system (TTS), which makes possible a temporally controlled release of the pharmaceutical compositions. TTS are known for example, from EP 0 944 398 A1, EP 0 916 336 A1, EP 0 889 723 A1 or EP 0 852 493 A1.

Injection solutions are in general used if only relatively small amounts of a solution or suspension, for example about 1 to about 20 ml, are to be administered to the body. Infusion solutions are in general used if a larger amount of a solution or suspension, for example one or more litres, are to be administered. Since, in contrast to the infusion solution, only a few millilitres are administered in the case of injection solutions, small differences from the pH and from the osmotic pressure of the blood or the tissue fluid in the injection do not make themselves noticeable or only make themselves noticeable to an insignificant extent with respect to pain sensation. Dilution of the formulation according to the invention before use is therefore in general not necessary. In the case of the administration of relatively large amounts, however, the formulation according to the invention should be diluted briefly before administration to such an extent that an at least approximately isotonic solution is obtained. An example of an isotonic solution is a 0.9% strength sodium chloride solution. In the case of infusion, the dilution can be carried out, for example, using sterile water while the administration can be carried out, for example, via a so-called bypass.

The pharmaceutical composition can be manufactured for oral, nasal, rectal, parenteral, vaginal, topic or vaginal administration. Parental administration includes subcutaneous, intracutaneous, intramuscular, intravenous or intraperitoneal administration.

In addition, the invention also refers to agonists and antagonists of a carnitine transporter, which are identifiable using the method of the invention of screening for an agonist or antagonist of a carnitine transporter.

A fourth preferred embodiment of the invention refers to a method of diagnosis of a carnitine transporter deficiency in an animal, preferably in a human patient. Preferably, the method comprises determining the amount of a carnitine transporter comprising the amino acid sequence SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 10, the rat protein AAW07635 (rB21a), available under the accession number AJ276207, the protein AAG64193 disclosed in CN 1287170, or the protein AAW73376, namely human HPDDV78 disclosed in EP 881290, preferably comprising SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, or SEQ ID NO: 10, preferably SEQ ID NO: 1 or SEQ ID NO: 10, preferably SEQ ID NO: 1, in a tissue sample obtained from the animal or human patient.

Preferably, an antibody reacting with the carnitine transporter is used in the method of diagnosis. Preferably, an antibody of the invention is used. Preferably, the absence or the presence of a protein reacting with the antibody is determined and is indicative of the absence or the presence of the carnitine transporter in the tissue sample.

In a preferred embodiment, an antibody reacting with a variant of the carnitine transporter associated with the carnitine transporter deficiency is used. The diagnostic method of the invention, wherein the amount of a carnitine transporter or a variant thereof is determined using an antibody, involves any immunological method of the art or which will become available in the future, wherein an antibody is used for determining the amount of its antigen.

Preferably, the invention refers to the use of an ELISA assay known in the art for determining the absence or presence of the carnitine transporter or its variant in the tissue sample. Preferably, the ELISA assays is used to determine the relative amount of the carnitine transporter in the tissue sample obtained from the patient as compared to a healthy individual. Preferably, the invention refers to the use of a Western analysis known in the art, wherein the amount and in addition the size of the carnitine transporter or its variant in the tissue sample can be determined.

In a preferred embodiment, the method of diagnosis is an in vitro diagnostic method which is executed using a tissue sample which has been obtained from an animal or human patient prior to the method of diagnosis of the invention.

In a further preferred embodiment, the method of diagnosis involves an additional initial step, wherein a tissue sample is obtained from an animal or human patient. Preferably, the method of diagnosis comprises at least one step which is executed within the animal or human patient's body.

A fifth preferred embodiment of the invention refers to the use of a protein comprising the amino acid sequence SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 10, the rat protein AAW07635 (rB21a), available under the accession number AJ276207, the protein AAG64193 disclosed in CN 1287170, or the protein AAW73376, namely human HPDDV78 disclosed in EP 881290, preferably SEQ ID NO: 1 or SEQ ID NO: 10, preferably SEQ ID NO: 1, or a fragment thereof for the manufacture of an antibody reacting with a carnitine transporter comprising the amino acid sequence SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 10, the rat protein AAW07635 (rB21a), available under the accession number AJ276207, the protein AAG64193 disclosed in CN 1287170, or the protein AAW73376, namely human HPDDV78 disclosed in EP 881290, respectively, preferably SEQ ID NO: 1 or SEQ ID NO: 10, preferably SEQ ID NO: 1. Preferably, a variant of the carnitine transporter associated with a carnitine transporter deficiency is used.

The manufacture of an antibody of the invention refers to any method for the manufacture of an antibody which is available in the art, or which will become available in the future. The manufacture of an antibody of the invention refers to any meaning of the expression "antibody" mentioned herein.

Preferably, a variant of a carnitine transporter associated with a carnitine deficiency in an animal or a human patient is used for the manufacture of the antibody. A variant of a carnitine transporter associated with a carnitine deficiency is preferably a carnitine transporter comprised in a tissue sample of an animal or preferably of a human patient suffering from a carnitine deficiency, preferably systemic carnitine deficiency. The variant of the carnitine transporter is preferably comprised in a tissue sample from the kidneys or from the intestine.

A sixth preferred embodiment of the invention refers to a method of determining a variant of a carnitine transporter associated with a carnitine transporter deficiency, wherein the method comprises the steps of: (a) determining a nucleic acid sequence coding for a variant of SEQ ID NO: 1, SEQ ID NO: 2, or SEQ ID NO: 3, SEQ ID NO: 10, the rat protein AAW07635 (rB21a), available under the accession number AJ276207, the protein AAG64193 disclosed in CN 1287170, or the protein AAW73376, namely human HPDDV78 disclosed in EP 881290, preferably SEQ ID NO: 1 or SEQ ID NO: 10, preferably SEQ ID NO: 1 associated with said carnitine transporter deficiency, and (b) deducing the amino acid sequence of said variant of said carnitine transporter.

The nucleic acid sequence is preferably determined using an animal tissue sample or a human tissue sample comprising the variant of the carnitine transporter. Preferably, the nucleic acid sequence of a nucleic acid molecule comprised in the tissue sample is determined. Preferably the nucleic acid sequence corresponds to SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 8, or SEQ ID NO: 15, preferably SEQ ID NO: 4 or SEQ ID NO: 15, or codes for a variant of the carnitine transporter comprising the amino acid sequence SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 10, the rat protein AAW07635 (rB21a), available under the accession number AJ276207, the

protein AAG64193 disclosed in CN 1287170, or the protein AAW73376, namely human HPDDV78 disclosed in EP 881290, preferably SEQ ID NO: 1 or SEQ ID NO: 10, preferably SEQ ID NO: 1, preferably SEQ ID NO: 1 or SEQ ID NO: 10, preferably SEQ ID NO: 1.

The determination of the nucleic acid sequence is preferably executed using any of the methods of the art for determining nucleic acid sequences, in particular using a DNA sequencing protocol, or any method for determining nucleic acid sequences which will become available in the future.

The deduction of the amino acid sequence of the carnitine transporter variant from the nucleic acid sequence coding for the carnitine transporter variant is preferably executed using the unambiguous so-called genetic code known in the art, which assigns an individual amino acid to any nucleotide base triplet in an open reading frame of a nucleotide sequence coding for a protein.

A seventh preferred embodiment of the invention refers to a method of diagnosis of a carnitine transporter deficiency, wherein the method comprises a step of determining the amount of a nucleic acid molecule coding for a carnitine transporter comprising the amino acid sequence SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 10, the rat protein AAW07635 (rB21a), available under the accession number AJ276207, the protein AAG64193 disclosed in CN 1287170, or the protein AAW73376, namely human HPDDV78 disclosed in EP 881290, preferably SEQ ID NO: 1 or SEQ ID NO: 10, preferably SEQ ID NO: 1, preferably SEQ ID NO: 1 or SEQ ID NO: 10, preferably SEQ ID NO: 1 in a tissue sample. Preferably, the amount of a nucleic acid comprising SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 8, or SEQ ID NO: 15, preferably SEQ ID NO: 4 or SEQ ID NO: 15, is determined.

Preferably, the amount of a DNA molecule is determined. Preferably, the amount of a RNA molecule is determined. Preferably, the amount of a DNA molecule comprising SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 8, or SEQ ID NO: 15, preferably SEQ ID NO: 4 or SEQ ID NO: 15, or the amount of a corresponding RNA molecule is

determined. Preferably, the amount of a DNA molecule coding for the amino acid sequence SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 10, the rat protein AAW07635 (rB21a), available under the accession number AJ276207, the protein AAG64193 disclosed in CN 1287170, or the protein AAW73376, namely human HPDDV78 disclosed in EP 881290, preferably SEQ ID NO: 1 or SEQ ID NO: 10, preferably SEQ ID NO: 1, preferably SEQ ID NO: 1 or SEQ ID NO: 10, preferably SEQ ID NO: 1, or the amount of a corresponding RNA molecule is determined.

Preferably, the method of diagnosis involves the use of any method known in the art or which shall become available in the future for determining the amount of a nucleic acid molecule comprising a known sequence or having a detectable similarity to a known nucleic acid sequence. Preferably, the method of diagnosis comprises a step of complementary base pairing between the nucleic acid molecule coding for the carnitine transporter and a complementary nucleic acid probe of the invention.

Preferably, a nucleic acid probe of the invention comprises a nucleic acid molecule comprising a complementary sequence to the nucleic acid molecule coding for the carnitine transporter. Preferably, the nucleic acid probe comprises a complementary sequence to SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 8, or SEQ ID NO: 15, preferably SEQ ID NO: 4 or SEQ ID NO: 15. Preferably, the nucleic acid probe hybridizes to the nucleic acid molecule coding for the carnitine transporter under non-stringent conditions, preferably under stringent conditions. Preferably, the nucleic acid probe comprises an oligonucleotide comprising at least 18 nucleotides.

Preferably, the nucleic acid probe of the invention hybridizes to a variant of the nucleic acid molecule coding for a variant of the carnitine transporter associated with the carnitine transporter deficiency. Preferably, the variant of the nucleic acid molecule comprises a variant of SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 8, or SEQ ID NO: 15, preferably SEQ ID NO: 4 or SEQ ID NO: 15.

Preferably, complementary base pairing does not only refer to base pairing between a nucleic acid molecule coding for a carnitine transporter and a nucleic acid probe

comprising a complementary sequence, but also refers to base pairing between a variant of the nucleic acid molecule and the nucleic acid probe, wherein the nucleic acid probe is only in part complementary to the variant of the nucleic acid molecule. Preferably, complementary base pairing allows for the detection of any nucleic acid molecule coding for a variant of a carnitine transporter with a detectable similarity to a nucleic acid molecule coding for a carnitine transporter of a healthy individual.

Preferably, any embodiment of the invention that refers to nucleic acid molecules or to carnitine transporters encoded by nucleic acid molecules or to any variant thereof, in particular any variant associated with a carnitine transporter deficiency, or any orthologous or homologous variant thereof, refers also to nucleic acid molecules comprising similar sequences, in particular as described herein. Preferably, similar sequences hybridize in complementary base pairing. Preferably similar sequences hybridize under non-stringent conditions, preferably under stringent conditions.

Preferably, the method of diagnosis involves hybridization methods of the art for nucleic acid molecules, in particular a Southern Hybridization method of the art for the detection of a DNA molecule coding for a carnitine transporter in a tissue sample, or a Northern Hybridization method of the art for the detection of a RNA molecule coding for a carnitine transporter in a tissue sample. Preferably, the nucleic acid probe of the invention hybridizing with the DNA molecule or the RNA molecule in the tissue sample is a component of a DNA chip. Preferably, the method of diagnosis comprises a step of extraction of the DNA molecule or the RNA molecule from the tissue sample, which is executed prior to the hybridization with the nucleic acid probe of the invention.

Preferably, the method of diagnosis involves a step of amplification of a nucleic acid molecule coding for a carnitine transporter comprised in a tissue sample. Preferably, the method involves a polymerase chain reaction (PCR) known in the art for the amplification of the nucleic acid molecule. Preferably, a DNA molecule comprised in the tissue sample is amplified. Alternatively, an RNA molecule comprised in the tissue sample is amplified after an additional initial step of reverse transcribing the RNA molecule into a DNA molecule.

An eighth preferred embodiment of the invention refers to an oligonucleotide comprising SEQ ID NO: 6 or comprising the complementary sequence to SEQ ID NO: 7. Advantageously, the oligonucleotides of the invention allow to isolate the gene for a human high affinity carnitine transporter of the kidneys and the intestine.

Preferably, the oligonucleotide comprising SEQ ID NO: 6 or the complementary sequence to SEQ ID NO: 7 is used in the method of the invention of diagnosis of a carnitine transporter deficiency. Preferably, said oligonucleotide is used as a primer in a polymerase chain reaction (PCR). Preferably, said oligonucleotide is used as a component of a DNA array.

A ninth preferred embodiment of the present invention refers to a method of determining a variant of a nucleic acid molecule coding for a variant of a carnitine transporter associated with a carnitine transporter deficiency, wherein the method comprises the steps of: (a) isolating a nucleic acid molecule coding for the variant of the carnitine transporter from a tissue sample using the method of diagnosis of a carnitine transporter deficiency according to the seventh preferred embodiment of the invention, and (b) determining the nucleic acid sequence of said nucleic acid molecule.

A tenth preferred embodiment of the invention refers to a method of treatment of a carnitine transporter deficiency, wherein the method comprises introducing a nucleic acid molecule coding for a carnitine transporter comprising the amino acid sequence SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 10, the rat protein AAW07635 (rB21a), available under the accession number AJ276207, the protein AAG64193 disclosed in CN 1287170, or the protein AAW73376, namely human HPDDV78 disclosed in EP 881290, preferably SEQ ID NO: 1 or SEQ ID NO: 10, preferably SEQ ID NO: 1, into a cell. Preferably, a DNA molecule comprising SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 8, or SEQ ID NO: 15, preferably SEQ ID NO: 4 or SEQ ID NO: 15, is introduced into the cell. Preferably, said DNA sequence comprises a transcriptional promoter sequence which is operably linked to SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 8, or SEQ ID NO: 15, preferably SEQ ID NO: 4 or SEQ ID NO: 15.

A eleventh preferred embodiment of the invention refers to a method of treatment of a carnitine transporter deficiency, wherein the method comprises enhancing the transcriptional activity of a nucleic acid molecule coding for a carnitine transporter comprising the amino acid sequence SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 10, the rat protein AAW07635 (rB21a), available under the accession number AJ276207, the protein AAG64193 disclosed in CN 1287170, or the protein AAW73376, namely human HPDDV78 disclosed in EP 881290, preferably SEQ ID NO: 1 or SEQ ID NO: 10, preferably SEQ ID NO: 1, in a cell. Preferably, the transcriptional activity of a cellular gene comprising SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 8, or SEQ ID NO: 15, preferably SEQ ID NO: 4 or SEQ ID NO: 15, is enhanced.

In the methods of treatment of a carnitine transporter deficiency of the invention the cell wherein a nucleic acid molecule is introduced or wherein the transcriptional activity of a nucleic acid molecule coding for a carnitine transporter is enhanced, preferably is a kidney cell, an intestine cell, a intestine cell, a liver cell, a heart cell, and/or a muscle cell.

Preferably, the methods of treatment of a carnitine transporter deficiency of the invention refer to the treatment of a deficiency of carnitine, noradrenaline, methylphenylpyridinium, creatine, and/or serotonin transport, or of any substrate accepted by the proteins comprising the amino acid sequence SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 10, the rat protein AAW07635 (rB21a), available under the accession number AJ276207, the protein AAG64193 disclosed in CN 1287170, or the protein AAW73376, namely human HPDDV78 disclosed in EP 881290, preferably SEQ ID NO: 1 or SEQ ID NO: 10, preferably SEQ ID NO: 1. Preferably, they refer to the treatment of systemic deficiency of carnitine.

Preferably, the methods of treatment of a carnitine transporter deficiency of the invention are in vitro methods, wherein cells are treated in vitro. Preferably, the cells were isolated from a patient previously to the steps of the methods of treatment of the invention.

Further preferred embodiments of the methods of treatment of the invention refer to the introduction of a nucleic acid molecule coding for a carnitine transporter according to SEQ ID NO. 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 10, the rat protein AAW07635 (rB21a), available under the accession number AJ276207, the protein AAG64193 disclosed in CN 1287170, or the protein AAW73376, namely human HPDDV78 disclosed in EP 881290, preferably SEQ ID NO: 1 or SEQ ID NO: 10, preferably SEQ ID NO: 1, into a cell comprised in the human body, preferably in the kidneys or the intestine. In alternative, a cell is first manipulated in vitro and subsequently transferred into the human body.

Preferably, the cells used in the methods of treatment of the invention are obtained from the kidneys or from the intestine, in particular from the intestine.

The nucleic acid molecules comprising SEQ ID NO. 4, SEQ ID NO: 5, SEQ ID NO: 8, or SEQ ID NO: 15, preferably SEQ ID NO: 4 or SEQ ID NO: 15, can be introduced into test cells of the screening method of the invention or into human cells used in the methods of treatment of the invention in naked form, in the form of gene transfer vectors or complexed with liposomes or gold particles.

Examples of gene transfer vectors are viral vectors, for example adenoviral vectors or retroviral vectors (Lindemann et al. (1997), Mol. Med., 3, 466-76; Springer et al. (1988) Mol. Cell., 2, 549-58). Complexes with liposomes usually achieve a very high efficiency of transfection, in particular of skin cells (Alexander and Akhurst, 1995, Hum. Mol. Genet. 4:2279-85). In lipofection, small, unilamellar vesicles composed of cationic lipids are prepared by ultrasonicating the liposome suspension. The DNA is bound ionically on the surface of the liposomes in a ratio which is such that a positive net charge remains and all the plasmid DNA is complexed by the liposomes. In addition to the DOTMA (1,2-dioleyloxypropyl-3-trimethylammonium bromide) and DOPE (dioleoylphosphatidylethanolamine) lipid mixtures employed by Felgner, P. L. et al. (1987), Proc. Natl. Acad. Sci USA, 84, 7413 - 7414, a large number of lipid formulations have by now been synthesized and tested for their efficiency in transfecting a variety of cell lines (Behr et al. (1989) Proc. Natl. Acad. Sci. USA, 86, 6982-6986; Gao and

Huang (1991), Biochim. Biophys. Acta, 1189, 195-203; Felgner et al. (1994) J. Biol. Chem., 269, 2550-2561). Examples of the lipid formulations are DOTAP N-[1-(2,3-dioleoyloxy)propyl]-N,N,N-trimethylammonium methyl sulphate or DOGS (dioctadecylamidoglycylspermine).

Auxiliary substances which increase the transfer of nucleic acids into the cell can, for example, be proteins or peptides which are bound to the DNA or synthetic peptide-DNA molecules which enable the nucleic acid to be transported into the nucleus of the cell (Schwartz et al. (1999) Gene Therapy 6:282; Brandén et al. (1999) Nature Biotech., 17, 784). Auxiliary substances also include molecules which enable nucleic acids to be released into the cytoplasm of the cell (Planck et al. (1994) J. Biol. Chem., 269, 12918; Kichler et al. (1997) Bioconj. Chem., 8, 213) or, for example liposomes (Uhlmann and Peyman (1990), supra).

Another, particularly suitable form can be obtained by applying the above-described nucleic acids to gold particles and firing these particles into tissue or cells using what is termed a "gene gun" (Wang et al. (1999) J. Invest. Dermatol. 112: 775-81, Tuting et al. (1998) J. Invest. Dermatol. 111: 183-8).

In the following figures, sequences and examples, some preferred embodiments of the invention are described in more detail with reference to the figures 1 and 2 and in the examples. Yet, no limitation of the invention is intended by the details of the preferred embodiments. In contrast, the invention pertains to any embodiment which comprises details which are not explicitly mentioned in the embodiments herein, but which the skilled person finds without undue effort.

Description of the Figures:

Figure 1 shows a histogram illustrating the activity of the carnitine transporter involved in the methods of the invention with different substrates. Figure 1 shows an example of a determination of the activity of the carnitine transporter comprising the amino acid sequence SEQ ID NO: 1 with the substrates L-carnitine (column 1), noradrenaline (column 2), methylphenylpyridinium (column 3), and serotonin (column 4). In Figure 1, the left columns (1) to (4) indicate the transport rate in pmol $hour^{-1}$ $oocyte^{-1}$ of the carnitine transporter for the respective substrate. The right columns (1) to (4) indicate the transport rate of suitable controls not comprising the carnitine transporter.

The carnitine transporters comprising the amino acid sequence SEQ ID NO: 2 or SEQ ID NO: 3 possess comparable activities as shown for the carnitine transporter comprising the amino acid sequence SEQ ID NO: 1 in Figure 1. The carnitine transporters comprising SEQ ID NO: 1, SEQ ID NO: 2 or SEQ ID NO: 3 transport in addition creatine.

Figure 1 shows the results obtained with Xenopus laevis oocytes injected with a cRNA comprising SEQ ID NO: 4 and with the radioactively labeled substrates L-carnitine (column 1), noradrenaline (column 2), methylphenylpyridinium (column 3), and serotonin (column 4). The controls, which are depicted at the right half of each column comprise control experiments carried through for each substrate with Xenopus laevis injected with water instead of the cRNA.

Figure 2 shows a diagram illustrating the kinetics of the carnitine transporter involved in the methods of the invention. Figure 2 shows an example of a determination of the kinetics of the carnitine transporter comprising the amino acid sequence SEQ ID NO: 1 with the substrate L-carnitine. The carnitine transporter shows comparable kinetics with the substrates noradrenaline, methylphenylpyridinium, serotonin, and creatine. The carnitine transporter comprising the amino acid sequence SEQ ID NO: 2 or SEQ ID NO: 3 shows comparable kinetics as in Figure 2. In Figure2, the x-axis of the

diagram indicates the carnitine concentration in µmol litre^{-1} and the y-axis indicates the transport rate in pmol hour^{-1} oocyte^{-1} of the carnitine transporter.

As shown in Figure 2, determinations of the concentration dependency of the L-carnitine transport by the carnitine transporter show a saturation of the carnitine transport which can be adapted via Michaelis-Menten kinetics. In the example illustrated in Figure 2, a K_M-value of 15 µM is obtained. Thus, the carnitine transporter used in the methods of the invention, in particular the carnitine transporter comprising the amino acid sequence SEQ ID NO: 1, SEQ ID NO: 2, or SEQ ID NO:3, or encoded by SEQ ID NO: 4 is a high affinity carnitine transporter, such as has been described for the carnitine transport in the kidneys and the intestine (Lahjouji K, Malo C, Mitchell GA, Qureshi IA, 2002, Biochim Biophys Acta, 1558, 82-93).

Figure 3 shows an amino acid sequence alignment comprising the closely related murine, rat and human kidney and intestinal carnitine transporters comprising SEQ ID NO: 2 with SEQ ID NO: 3, and SEQ ID NO: 1, respectively, each of which comprises 634 amino acids. Corresponding amino acid positions of the individual carnitine transporters are arranged below each other in figure 3, and amino acid substitutions occurring at a given positions either in one sequence or at a given position in all three sequences are marked, in order to allow for the observation of so-called conserved regions in the related proteins and for the observation of more variable regions.

It can readily be taken from the sequence identities in figure 3 that all three proteins are closely related, yet the mouse and rat proteins are more closely related to each other than to the human carnitine transporter. Further, the skilled person takes without undue burden from figure 3 that the relatedness of the shown sequences goes beyond sequence identities and comprises so-called conserved amino acid substitutions at corresponding positions in the sequences. As is well-known in the art, conserved amino acid substitutions comprise substitutions of an amino acid at a given sequence position to a functionally similar amino acid, wherein the function of an amino acid is related to the chemical properties of its side group, in particular to the electrical charge,

acid property or base property, hydrophilicity, hydrophobicity, sulfur-content, aromatic property, or size, in particular small size, of its side group.

In addition, the skilled person takes from figure 3 without undue burden a variety of sequence motives comprising an arbitrary number of amino acids, which are characteristic for a group comprising either two or three of SEQ ID NO: 1, SEQ ID NO: 2, and/or SEQ ID NO: 3, or which are characteristic for an individual carnitine transporter, preferably for SEQ ID NO: 1. Preferably, a characteristic sequence motif comprises at least one, preferably a group of amino acids comprising at least two, amino acids which do less frequently occur in proteins. The skilled person is used to identify characteristic sequence motifs comprising unusual amino acids with undue burden.

Further, the skilled person considers the additional information about amino acid substitutions between similar amino acids and between closely similar amino acids provided in figures 4, 5, and 6 herein, showing amino acid sequence alignments between SEQ ID NO: 1 and SEQ ID NO: 2, between SEQ ID NO: 1 and SEQ ID NO: 3, and respectively, between SEQ ID NO: 2 and SEQ ID NO: 3.

Preferably, a carnitine transporter used in any embodiment of the present invention is a carnitine transporter which comprises an amino acid sequence motif which is either characteristic for all three carnitine transporters comprising the amino acid SEQ ID NO: 1, SEQ ID NO: 2, or SEQ ID NO: 3, or which is characteristic for an arbitrary group comprising two of said carnitine transporters, or which is characteristic for a single of said carnitine transporter, preferably for SEQ ID NO: 1. Preferably, the carnitine transporter comprises an amino acid motif which can be identified without undue burden due to its similarity to a sequence motif which is either characteristic for all three carnitine transporters shown in figure 3, or which is characteristic for an arbitrary group comprising two carnitine transporters, or which is characteristic for a single carnitine transporter, preferably for SEQ ID NO: 1.

Figure 4 shows an amino acid sequence alignment comprising the closely related human and murine kidney and intestinal carnitine transporters comprising SEQ ID NO: 1 and SEQ ID NO: 2, respectively, which share 86,9 % amino acid sequence identity. Identical amino acids are indicated by a bar, similar amino acids which are functionally similar are indicated by a single dot, closely similar amino acids which are almost functionally and/or structurally identical are indicated by a double dot.

Figure 5 shows an amino acid sequence alignment comprising the closely related human and rat kidney and intestinal carnitine transporters comprising SEQ ID NO: 1 and SEQ ID NO: 3, respectively, which share 86,7 % amino acid sequence identity. Identical amino acids are indicated by a bar, similar amino acids which are functionally similar are indicated by a single dot, closely similar amino acids which are almost functionally and/or structurally identical are indicated by a double dot.

Figure 6 shows an amino acid alignment comprising the closely related murine and rat kidney and intestinal carnitine transporters comprising SEQ ID NO: 2 and SEQ ID NO: 3, respectively, which share 95,4 % amino acid sequence identity. Identical amino acids are indicated by a bar, similar amino acids which are functionally similar are indicated by a single dot, closely similar amino acids which are almost functionally and/or structurally identical are indicated by a double dot.

Figure 7 shows an amino acid sequence alignment comprising SEQ ID NO: 1 and SEQ ID NO: 10. SEQ ID NO: 1 comprises the amino acid sequence of the human kidney and intestinal carnitine transporter, whereas SEQ ID NO: 10 comprises the amino acid sequence of a functional splice variant of SEQ ID NO: 1. SEQ ID NO: 10 comprises the complete and identical amino acid sequence of SEQ ID NO: 1 and an additional amino acid sequence comprising 39 amino acids (corresponding to amino acids 297 to 335 of SEQ ID NO: 10), which are inserted at the position corresponding to a position between amino acids 296 and 297 in SEQ ID NO: 1.

Figure 8 shows a nucleic acid sequence alignment comprising SEQ ID NO: 4 and SEQ ID NO: 9. SEQ ID NO: 4 codes for the amino acid sequence of the human kidney and

intestinal carnitine transporter according to SEQ ID NO: 1, whereas SEQ ID NO: 9 codes for the amino acid sequence of a functional splice variant of SEQ ID NO: 1, namely for the amino acid sequence according to SEQ ID NO: 10. SEQ ID NO: 9 comprises the complete and identical nucleic acid sequence of SEQ ID NO: 4 and an additional nucleic acid sequence comprising 117 nucleotides (corresponding to nucleotides 888 to 1004 of SEQ ID NO: 9), which are inserted at the position corresponding to a position between nucleotides 887 and 888 in SEQ ID NO: 4.

Figure 9 shows SEQ ID NO. 5.

Figure 10 shows SEQ IDs NO.6 and 7.

Figure 11 shows SEQ ID NO.8.

Figure 12 shows SEQ ID NO. 11 (NM_003060).

Figure 13 shows SEQ ID NO: 12 (NP_003051).

Figure 14 shows SEQ ID NO: 13 (NM_0033125).

Figure 15 shows SEQ ID NO: 14 (NP_149116).

Figure 16 shows SEQ ID NO: 15.

Description of the Sequences:

SEQ ID NO: 1 comprises the amino acid sequence of the human kidney and intestinal carnitine transporter.

SEQ ID NO: 2 comprises the amino acid sequence of the mouse kidney and intestinal carnitine transporter, which is orthologous to SEQ ID NO: 1.

SEQ ID NO: 3 comprises the amino acid sequence of the rat kidney and intestinal carnitine transporter, which is orthologous to SEQ ID NO. 1.

SEQ ID NO: 4 comprises the open reading frame DNA sequence coding for the human kidney and intestinal carnitine transporter comprising the amino acid sequence SEQ ID NO: 1.

SEQ ID NO: 5 comprises the open reading frame DNA sequence coding for the mouse kidney and intestinal carnitine transporter comprising the amino acid sequence SEQ ID NO: 2.

SEQ ID NO: 6 shows the oligonucleotide of the invention from the start of SEQ ID NO:4, which has been used for cloning SEQ ID NO: 4 (forward cloning primer).

SEQ ID NO: 7 shows the oligonucleotide of the invention downstream from the end of SEQ ID NO: 4, which has been used as a reverse primer for the cloning of SEQ ID NO: 4.

SEQ ID NO: 8 comprises the open reading frame DNA sequence coding for the rat kidney and intestinal carnitine transporter comprising the amino acid sequence SEQ ID NO: 3.

SEQ ID NO: 9 comprises SEQ ID NO: 4 and an additional sequence comprising 117 nucleotides inserted between nucleotides 887 and 888 of SEQ ID NO: 4. SEQ ID NO: 9 is available at the NCBI database (National Center for Biotechnology Information U.S.A.) under the accession number XM_291120.

SEQ ID NO: 10 comprises the amino acid sequence encoded by SEQ ID NO: 9, comprising SEQ ID NO: 1 and an additional sequence comprising 39 amino acids

inserted between the amino acids 296 and 297 of SEQ ID NO: 9. SEQ ID NO: 10 is available at the NCBI database under the accession number XP_291120.

SEQ ID NO: 11 comprises the DNA sequence coding for the human carnitine transporter OCTN2, which is ubiquitously expressed within the human body. SEQ ID NO: 11 is available at the NCBI database under the accession number NM_003060.

SEQ ID NO: 12 comprises the amino acid sequence encoded by SEQ ID NO. 11, which is available at the NCBI database under the accession number NP_003051.

SEQ ID NO: 13 comprises the DNA sequence coding for the human carnitine transporter CT", which is expressed in human testes only. SEQ ID NO: 13 is available at the NCBI database under the accession number NM_0033125.

SEQ ID NO: 14 comprises the amino acid sequence encoded by SEQ ID NO: 13, which is available at the NCBI database under the accession number NP_149116.

SEQ ID NO: 15 comprises the DNA sequence corresponding to the mRNA for the human kidney and intestinal carnitine transporter, comprising SEQ ID NO: 4, an additional 5'-flanking sequence and an additional 3'-flanking sequence.

Description of the Examples:

Identification and Cloning of the Gene of the Kidney and Intestinal Carntine Transporter

Surprisingly, it has been found that a nucleic acid molecule comprising SEQ ID NO: 4 is strongly expressed in the human kidneys and in the human intestine in a tissue-specific way. SEQ ID NO: 4 codes for a carnitine transporter comprising the amino acid sequence SEQ ID NO: 1.

A DNA molecule comprising SEQ ID NO: 4 was amplified in a polymerase chain reaction (PCR) using a cDNA from the human kidney as template and oligonucleotide primers comprising SEQ ID NO: 6 and the complementary sequence to SEQ ID NO: 7, which were derived from a DNA sequence publicly available in a data base under the Accession number AK09054.

Transport Measurements using Oocytes

The transport measurements of radioactively labeled compounds were executed using Xenopus laevis oocytes in the so-called "tracer flux method", wherein the transport rate of substrates across the oocyte membrane into the cytosol is determined.

Injection of Oocytes of the Clawed Frog Xenopus laevis

A Xenopus laevis oocyte was injected with a cRNA molecule comprising SEQ ID NO: 4.

The oocytes which were to be injected were aligned in a Sylgard groove. The injection was carried through using glass capillaries made from borosilicate (Hildenberg, Malsfeld; inner diameter: 0.5 mm; outer diameter 1.0 mm), which had been finely stretched within an incandescent spiral-wound filament. For sucking in and pressing out sample solutions a microinjection pump obtained from the company Drummond was used. A capillary was filled without air bubbles with mineral oil (Sigma 400-5 heavy white oil, □ = 0.88 g/ml) and mounted to a micropump provided with a manipulator.

The still fused tip of the injection capillary was carefully broken open using forceps, in order to allow for the pumping out of the oil and the sucking in of the desired volume of RNA. The sucking in of the RNA into the injection capillary was carried through under a film of sterile mineral oil, in order to avoid an increase of the concentration of the RNA and its degradation by contaminations. The injection capillary was placed on the surface of the oocyte with an angle of 90 ° and punched into the oocyte under slight pressure. The tip should not penetrate into the cytoplasm deeper than 100-200 µm. The volume of the injectates never exceeded 50 nl (approximately 5 % of the oocyte

volume of about 0.9 µl). The injection capillary was left within the oocyte for 5-10 seconds after the application of the desired volume, in order to allow for pressure compensation and to avoid leaking out of the injectate through the open punching channel.

An additional provision in order to avoid the leaking out was the "preshrinking" of the oocytes for at least 10 minutes prior to the injection in ORi comprising 130 instead of 10 mM NaCl, i.e. in hypertonic solution. Oocytes which might have lost a substantial amount of yolk and thus possibly a part of the injection solution, were sorted out.

Injected oocytes were kept in the culture medium ORi comprising gentamycin (50 mg/L) at 18 °C until the measurement of substrate uptake. Injured, acutely altered or later heavily damaged cells were discarded.

After 72 hours the oocyte was used for screening for a carnitine transporter agonist or antagonist.

Culture Medium ORi Solution

The standard buffer was a oocyte-Ringer solution ORi comprising 110 mM NaCl, 3 mM KCl, 2 mM $CaCl_2$, 1 mM $MgCl_2$, and 5 mM MOPS.

If required, Gentamycin was added at 50 mg/l,

Determination of the Substrate Uptake

Polysterene wells treated with oocyte homogenate were filled with 200 µl substrate solution. The oocytes were first washed two times with ORi solution, before use in the determination. 8 to 10 oocytes were used in a reaction mixture, in order to enable statistical evaluations. After the addition of the oocytes into the substrate solution the reaction mixture was softly mixed and incubated. The incubation was carried through at 22 °C for 1 hour. In order to stop the reaction, 1 ml of ice cold ORi was added.

The oocytes were washed four times in 15 ml ice cold ORi. Subsequently the oocytes were individually transferred into a 6 ml counter vial. The oocyte plasma membrane was disrupted by adding 100 µl 5 § SDS solution. The vials were slightly agitated to disrupt the plasma membrane. The plasma membrane was completely disrupted by agitation for 30 to 45 minutes. The lysates were mixed with 2 ml of a scintillation cocktail. The radioactivity of the lysates was determined in a liquid scintillation counter comprising a correction for the luminescence and an external standard. Each vial was counted for 5 minutes.

In order to determine the substrate concentration after the dropping in of the oocytes, 2 x 10 µl solution were removed from the reaction mixture, 100 µl 5 % SDS solution was added and evaluations with the counter were carried out. The obtained values were considered in the calculation of the transport rates.

Determination of the K_M-Value

For the determination of concentration-dependent substrate uptake serial dilutions of the investigated substrate were prepared and the radioactivity was distributed, such that in each reaction mixture between 10000 and 20000 cpm were counted in the supernatant. For the K_M determination the substrate uptake was measured for 1 hour. In addition, the measurement was carried through using H_2O-injected oocytes, in order to determine the background, i.e. the unspecific substrate uptake, for example mediated by diffusion or by endogenous transport proteins. The transport rates were calculated and graphically plotted against the substrate concentration and adapted mathematically according to the Michaelis-Menten equation.

Claims

1. A method of screening for a carnitine transporter agonist or antagonist, wherein the method comprises the steps of:

(a) providing a carnitine transporter,

(b) providing a test compound,

(c) measuring the activity of the carnitine transporter,

wherein the carnitine transporter comprises the amino acid sequence SEQ ID NO: 1 or the carnitine transporter is encoded by a nucleic acid molecule comprising SEQ ID NO: 4 or SEQ ID NO: 15.

2. The method according to claim 1, wherein the carnitine transporter is comprised in a lipid membrane, preferably a cellular membrane, preferably an inner mitochondrial membrane or a plasma membrane.

3. The method according to claim 2, wherein the carnitine transporter is comprised in a lipid vesicle membrane.

4. The method according to claim 2, wherein the carnitine transporter is comprised in the plasma membrane of a test cell.

5. The method according to claim 4, wherein the test cell expresses a nucleic acid molecule coding for a carnitine transporter comprising the amino acid sequence SEQ ID NO: 1or the test cell expresses a nucleic acid molecule comprising SEQ ID NO: 4or SEQ ID NO: 15.

6. The method according to claim 5, wherein the test cell comprises a DNA molecule comprising SEQ ID NO: 4or SEQ ID NO: 15, operably linked to a transcriptional activator sequence.

7. The method according to claim 5, wherein the test cell comprises a translatable RNA molecule comprising a sequence corresponding to SEQ ID NO: 4or SEQ ID NO: 15, preferably a microinjected cRNA molecule comprising a sequence corresponding to SEQ ID NO: 4or SEQ ID NO: 15.

8. The method according to at least one of claims 4 to 7, wherein the test cell comprises a functional carnitine transporter in its plasma membrane, preferably wherein the test cell is a Xenopus laevis oocyte.

9. The method according to at least one of claims 3 to 8, wherein the carnitine transporter transports a substrate selected from carnitine, noradrenaline, methylphenylpyridinium, creatine, and/or serotonin across the lipid membrane, preferably into the test cell.

10. The method according to at least one of claims 1 to 9, wherein a detectable substrate, in particular a radioactive substrate, a streptavidin-labeled or biotin-labeled substrate, or a substrate reacting with an antibody, is used, preferably wherein the amount of a substrate transported across a lipid membrane is indicative of the activity of the carnitine transporter.

11. The method according to at least one of claims 1 to 10 , wherein the amount of the carnitine transporter formed in a test cell comprising an expressible nucleic acid molecule comprising SEQ ID NO: 4or SEQ ID NO: 15or comprising an expressible nucleic acid molecule coding for a carnitine transporter comprising the amino acid sequence SEQ ID NO: 1 is indicative of the activity of the carnitine transporter.

12. The method according to at least one of claims 1 to 11, wherein a test compound is screened for an agonist or antagonist effect on the carnitine transporter, preferably wherein the test compound is provided in the form of a chemical library.

13. The method according to at least one of claims 1 to 12, wherein the method is carried out in a robotics system.

14. A kit for carrying out the method according to at least one of claims 1 to 13, comprising:

(a) a lipid membrane comprising a carnitine transporter,

(b) a detectable substrate for the carnitine transporter.

15. The kit according to claim 14, wherein the carnitine transporter is a human carnitine transporter comprising the amino acid sequence SEQ ID NO: 1 or wherein the carnitine transporter is encoded by a nucleic acid molecule comprising SEQ ID NO: 4or SEQ ID NO: 15.

16. The kit according to claim 14 or 15, wherein the carnitine transporter is comprised in a lipid vesicle membrane.

17. The kit according to claim 14 or 15, wherein the carnitine transporter is comprised in the plasma membrane of a test cell.

18. A method of diagnosis of a carnitine transporter deficiency, wherein the method comprises determining the amount of a carnitine transporter comprising the amino acid sequence SEQ ID NO: 1 in a tissue sample.

19. The method according to claim 18, wherein an antibody reacting with the carnitine transporter is used for determining the amount of the carnitine transporter.

20. The method according to claim 18 or 19, wherein an antibody reacting with a variant of the carnitine transporter associated with the carnitine transporter deficiency is used for determining the amount of the variant of the carnitine transporter.

21. A method of diagnosis of a carnitine transporter deficiency, wherein the method comprises determining the amount of a nucleic acid molecule coding for a carnitine transporter comprising the amino acid sequence SEQ ID NO: 1in a tissue sample.

22. The method according to claim 21, wherein a nucleic acid probe comprising a complementary sequence to the nucleic acid molecule coding for the carnitine transporter is used for determining the amount of the nucleic acid molecule.

23. The method according to claim 22, wherein the nucleic acid probe comprises a complementary sequence to SEQ ID NO: 4or SEQ ID NO: 15.

24. The method according to claim 22 or 23, wherein the nucleic acid probe hybridizes to the nucleic acid molecule coding for the carnitine transporter under non-stringent conditions, preferably under stringent conditions.

25. The method according to at least one of claims 22 to 24, wherein the nucleic acid probe comprises an oligonucleotid comprising at least 18 nucleotides.

26. The method according to claim 25, wherein an oligonucleotide comprising SEQ ID NO: 6 or the complementary sequence to SEQ ID NO: 7 is used for determining the amount of the nucleic acid molecule.

27. The method according to claim 25 or 26, wherein said oligonucleotide is used as a primer in a polymerase chain reaction (PCR).

28. The method according to any of claims 25, 26 or 27, wherein said oligonucleotide is used as a component of a DNA array.

29. The method according to at least one of claims 21 to 25 , 26, 27 or 28, wherein the amount of a DNA molecule is determined.

30. The method according to at least one of claims 21 to 25 or 26 to 29, wherein the amount of a RNA molecule comprising a sequence corresponding to SEQ ID NO: 4or SEQ ID NO: 15 is determined.

31. The method according to claim 30 which comprises a step of reverse transcribing the RNA molecule into a DNA molecule.

32. The method according to at least one of claims 21 to 25 or 26 to 31, wherein the nucleic acid probe hybridizes to a variant of said nucleic acid molecule coding for a variant of said carnitine transporter associated with the carnitine transporter deficiency.

33. The method according to claim 32, wherein the variant of the nucleic acid molecule comprises a variant of SEQ ID NO: 4or SEQ ID NO: 15coding for a variant of said carnitine transporter.

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Ser Leu Asp Glu Leu Glu Val Ile Glu Lys Glu Glu Ala Ser Ser Lys
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Pro Lys Trp Asp Asn Lys Ala Gln Tyr Met Leu Thr Cys Val Gly Phe
35 40 45

Cys Val Gly Leu Gly Asn Val Trp Arg Phe Pro Tyr Leu Cys Gln Ser
50 55 60

His Gly Gly Gly Ala Phe Met Ile Pro Phe Leu Ile Leu Leu Val Leu
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Glu Gly Ile Pro Leu Leu His Leu Glu Phe Ala Ile Gly Gln Arg Leu
85 90 95

Arg Lys Gly Ser Val Gly Val Trp Ser Ser Ile His Pro Ala Leu Lys
100 105 110

Gly Val Gly Ile Ala Ser Met Phe Val Ser Phe Met Val Gly Leu Tyr
115 120 125

Tyr Asn Thr Ile Ile Ala Trp Val Met Trp Tyr Phe Phe Asn Ser Phe
130 135 140

Gln Glu Pro Leu Pro Trp Ser Glu Cys Pro Leu Asn Gln Asn Gln Thr
145 150 155 160

Gly Tyr Val Glu Glu Cys Ala Lys Ser Ser Ser Val Asp Tyr Phe Trp
165 170 175

Tyr Arg Glu Thr Leu Asn Ile Ser Thr Pro Ile Ser Asp Ser Gly Ser
180 185 190

Ile Gln Trp Trp Ile Leu Leu Cys Leu Thr Cys Ala Trp Ser Val Leu
195 200 205

Tyr Val Cys Thr Ile Arg Gly Ile Glu Thr Thr Gly Lys Ala Val Tyr
210 215 220

Ile Thr Ser Thr Leu Pro Tyr Val Val Leu Thr Ile Phe Leu Ile Arg
225 230 235 240

Gly Leu Thr Leu Lys Gly Ala Thr Asn Gly Ile Val Phe Leu Phe Thr
245 250 255

Pro Asn Ile Thr Glu Leu Ser Asn Pro Asn Thr Trp Leu Asp Ala Gly
260 265 270

Ala Gln Val Tyr Tyr Ser Phe Ser Leu Ala Phe Gly Gly Leu Ile Ser
275 280 285

Phe Ser Ser Tyr Asn Ser Val His Asn Asn Cys Glu Met Asp Ser Val
290 295 300

Ile Val Ser Ile Ile Asn Gly Phe Thr Ser Val Tyr Ala Ala Thr Val
305 310 315 320

Val Tyr Ser Ile Ile Gly Phe Arg Ala Thr Glu Arg Phe Asp Asp Cys
325 330 335

Val Asn Thr Asn Ile Leu Thr Leu Ile Asn Gly Phe Asp Leu Pro Glu
340 345 350

Gly Asn Val Thr Ala Glu Asn Phe Glu Ala Tyr Gln His Trp Cys Asn
355 360 365

Ala Thr Asn Pro Glu Ala Tyr Ala Gln Leu Thr Phe Gln Thr Cys Asp
370 375 380

Ile Asn Thr Phe Leu Ser Glu Gly Val Glu Gly Thr Gly Leu Ala Phe
385 390 395 400

Ile Val Phe Thr Glu Ala Ile Thr Lys Met Pro Val Ser Pro Leu Trp
405 410 415

Ser Val Leu Phe Phe Ile Met Leu Phe Cys Leu Gly Leu Ser Ser Met
420 425 430

Phe Gly Asn Met Glu Gly Val Val Val Pro Leu Gln Asp Leu Asn Ile
435 440 445

Thr Pro Lys Lys Trp Pro Lys Glu Leu Leu Thr Gly Leu Ile Cys Leu
450 455 460

Gly Thr Tyr Leu Ile Ala Phe Ile Phe Thr Leu Asn Ser Gly Gln Tyr
465 470 475 480

Trp Leu Ser Leu Leu Asp Ser Tyr Ala Gly Ser Ile Pro Leu Leu Ile
485 490 495

Ile Ala Phe Cys Glu Met Phe Ala Val Val Tyr Val Tyr Gly Val Asp
500 505 510

Arg Phe Asn Lys Asp Ile Glu Phe Met Ile Gly His Lys Pro Asn Ile
515 520 525

Phe Trp Gln Val Thr Trp Arg Val Val Ser Pro Leu Ile Met Leu Val
530 535 540

Ile Phe Leu Phe Phe Phe Val Ile Glu Val Asn Lys Gln Leu Met Tyr
545 550 555 560

Ser Val Trp Asp Pro Asp Tyr Glu Glu Phe Pro Lys Ser Gln Lys Val
565 570 575

Pro Tyr Pro Asp Trp Val Tyr Ala Val Val Val Ile Val Ala Gly Val
580 585 590

Pro Cys Leu Thr Ile Pro Cys Phe Ala Ile Tyr Lys Leu Ile Arg Asn
595 600 605

Tyr Cys Gln Lys Ser Gly Asp Gln His Gly Leu Val Asn Ala Leu Ser
610 615 620

Thr Ala Ser Val Asn Gly Asp Leu Lys Asn
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<212> DNA

<213> Homo sapiens

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<212> DNA

<213> Homo sapiens

<400> 6
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<212> DNA

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<211> 2022
<212> DNA
<213> Homo sapiens

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35 40 45

Cys Val Gly Leu Gly Asn Val Trp Arg Phe Pro Tyr Leu Cys Gln Ser
50 55 60

His Gly Gly Gly Ala Phe Met Ile Pro Phe Leu Ile Leu Leu Val Leu
65 70 75 80

Glu Gly Ile Pro Leu Leu Tyr Leu Glu Phe Ala Ile Gly Gln Arg Leu
85 90 95

Arg Arg Gly Ser Leu Gly Val Trp Ser Ser Ile His Pro Ala Leu Lys
100 105 110

Gly Leu Gly Leu Ala Ser Met Leu Thr Ser Phe Met Val Gly Leu Tyr
115 120 125

Tyr Asn Thr Ile Ile Ser Trp Ile Met Trp Tyr Leu Phe Asn Ser Phe
130 135 140

Gln Glu Pro Leu Pro Trp Ser Asp Cys Pro Leu Asn Glu Asn Gln Thr
145 150 155 160

Gly Tyr Val Asp Glu Cys Ala Arg Ser Ser Pro Val Asp Tyr Phe Trp
165 170 175

Tyr Arg Glu Thr Leu Asn Ile Ser Thr Ser Ile Ser Asp Ser Gly Ser
180 185 190

Ile Gln Trp Trp Met Leu Leu Cys Leu Ala Cys Ala Trp Ser Val Leu
195 200 205

Tyr Met Cys Thr Ile Arg Gly Ile Glu Thr Thr Gly Lys Ala Val Tyr
210 215 220

Ile Thr Ser Thr Leu Pro Tyr Val Val Leu Thr Ile Phe Leu Ile Arg
225 230 235 240

Gly Leu Thr Leu Lys Gly Ala Thr Asn Gly Ile Val Phe Leu Phe Thr
245 250 255

Pro Asn Val Thr Glu Leu Ala Gln Pro Asp Thr Trp Leu Asp Ala Gly
260 265 270

Ala Gln Val Phe Phe Ser Phe Ser Leu Ala Phe Gly Gly Leu Ile Ser
275 280 285

Phe Ser Ser Tyr Asn Ser Val His Gly Ser Ala Ser His Ser Trp Gly
290 295 300

Trp Arg Ser Gly Arg Asp Ala Asp Ala Ala Leu Gly Cys Val Leu Thr
305 310 315 320

Trp Asp Leu Ile Ala Ser Arg His Asp Thr Gly Leu Val Cys Ser Asn
325 330 335

Asn Cys Glu Lys Asp Ser Val Ile Val Ser Ile Ile Asn Gly Phe Thr
340 345 350

Ser Val Tyr Val Ala Ile Val Val Tyr Ser Val Ile Gly Phe Arg Ala
355 360 365

Thr Gln Arg Tyr Asp Asp Cys Phe Ser Thr Asn Ile Leu Thr Leu Ile
370 375 380

Asn Gly Phe Asp Leu Pro Glu Gly Asn Val Thr Gln Glu Asn Phe Val
385 390 395 400

Asp Met Gln Gln Arg Cys Asn Ala Ser Asp Pro Ala Ala Tyr Ala Gln
405 410 415

Leu Val Phe Gln Thr Cys Asp Ile Asn Ala Phe Leu Ser Glu Ala Val
420 425 430

Glu Gly Thr Gly Leu Ala Phe Ile Val Phe Thr Glu Ala Ile Thr Lys
435 440 445

Met Pro Leu Ser Pro Leu Trp Ser Val Leu Phe Phe Ile Met Leu Phe
450 455 460

Cys Leu Gly Leu Ser Ser Met Phe Gly Asn Met Glu Gly Val Val Val
465 470 475 480

Pro Leu Gln Asp Leu Arg Val Ile Pro Pro Lys Trp Pro Lys Glu Val
485 490 495

Leu Thr Gly Leu Ile Cys Leu Gly Thr Phe Leu Ile Gly Phe Ile Phe
500 505 510

Thr Leu Asn Ser Gly Gln Tyr Trp Leu Ser Leu Leu Asp Ser Tyr Ala
515 520 525

Gly Ser Ile Pro Leu Leu Ile Ile Ala Phe Cys Glu Met Phe Ser Val
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Val Tyr Val Tyr Gly Val Asp Arg Phe Asn Lys Asp Ile Glu Phe Met
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Ile Gly His Lys Pro Asn Ile Phe Trp Gln Val Thr Trp Arg Val Val
565 570 575

Ser Pro Leu Leu Met Leu Ile Ile Phe Leu Phe Phe Phe Val Val Glu
580 585 590

Val Ser Gln Glu Leu Thr Tyr Ser Ile Trp Asp Pro Gly Tyr Glu Glu
595 600 605

Phe Pro Lys Ser Gln Lys Ile Ser Tyr Pro Asn Trp Val Tyr Val Val
610 615 620

Val Val Ile Val Ala Gly Val Pro Ser Leu Thr Ile Pro Gly Tyr Ala
625 630 635 640

Ile Tyr Lys Leu Ile Arg Asn His Cys Gln Lys Pro Gly Asp His Gln
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Gly Leu Val Ser Thr Leu Ser Thr Ala Ser Met Asn Gly Asp Leu Lys
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Tyr

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<211> 3252

<212> DNA

<213> Homo sapiens

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<213> Homo sapiens

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Arg Cys Arg Val Pro Asp Ala Ala Asn Leu Ser Ser Ala Trp Arg Asn
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Cys Arg Arg Tyr Arg Leu Ala Thr Ile Ala Asn Phe Ser Ala Leu Gly
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Leu Glu Pro Gly Arg Asp Val Asp Leu Gly Gln Leu Glu Gln Glu Ser
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Cys Leu Asp Gly Trp Glu Phe Ser Gln Asp Val Tyr Leu Ser Thr Ile

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Met Gly Met Gln Thr Gly Phe Ser Phe Leu Gln Ile Phe Ser Lys Asn
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Phe Glu Met Phe Val Val Leu Phe Val Leu Val Gly Met Gly Gln Ile
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Ser Asn Tyr Val Ala Ala Phe Val Leu Gly Thr Glu Ile Leu Gly Lys
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Ser Val Arg Ile Ile Phe Ser Thr Leu Gly Val Cys Ile Phe Tyr Ala
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Phe Gly Tyr Met Val Leu Pro Leu Phe Ala Tyr Phe Ile Arg Asp Trp
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Arg Met Leu Leu Val Ala Leu Thr Met Pro Gly Val Leu Cys Val Ala
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Leu Trp Trp Phe Ile Pro Glu Ser Pro Arg Trp Leu Ile Ser Gln Gly
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Gly Ile Val Val Pro Ser Thr Ile Phe Asp Pro Ser Glu Leu Gln Asp
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Leu Ser Ser Lys Lys Gln Gln Ser His Asn Ile Leu Asp Leu Leu Arg
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Thr Trp Asn Ile Arg Met Val Thr Ile Met Ser Ile Met Leu Trp Met
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Thr Ile Ser Val Gly Tyr Phe Gly Leu Ser Leu Asp Thr Pro Asn Leu
355 360 365

His Gly Asp Ile Phe Val Asn Cys Phe Leu Ser Ala Met Val Glu Val
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Pro Ala Tyr Val Leu Ala Trp Leu Leu Leu Gln Tyr Leu Pro Arg Arg

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Tyr Ser Met Ala Thr Ala Leu Phe Leu Gly Gly Ser Val Leu Leu Phe
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Met Gln Leu Val Pro Pro Asp Leu Tyr Tyr Leu Ala Thr Val Leu Val
420 425 430

Met Val Gly Lys Phe Gly Val Thr Ala Ala Phe Ser Met Val Tyr Val
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Tyr Thr Ala Glu Leu Tyr Pro Thr Val Val Arg Asn Met Gly Val Gly
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Val Tyr Leu Gly Ala Tyr Asp Arg Phe Leu Pro Tyr Ile Leu Met Gly
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Ser Leu Thr Ile Leu Thr Ala Ile Leu Thr Leu Phe Leu Pro Glu Ser
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Phe Gly Thr Pro Leu Pro Asp Thr Ile Asp Gln Met Leu Arg Val Lys
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<212> DNA

<213> Homo sapiens

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His His Val Cys Arg Pro Pro Gly Asn Val Ser Gln Val Val Phe His
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Asn His Ser Asn Trp Ser Leu Glu Asp Thr Gly Ala Leu Leu Ser Ser
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Gly Gln Lys Asp Tyr Val Thr Val Gln Leu Gln Asn Gly Glu Ile Trp
85 90 95

Glu Leu Ser Arg Cys Ser Arg Asn Lys Arg Glu Asn Thr Ser Ser Leu
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Gly Tyr Glu Tyr Thr Gly Ser Lys Lys Glu Phe Pro Cys Val Asp Gly
115 120 125

Tyr Ile Tyr Asp Gln Asn Thr Trp Lys Ser Thr Ala Val Thr Gln Trp
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Asn Leu Val Cys Asp Arg Lys Trp Leu Ala Met Leu Ile Gln Pro Leu
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Phe Met Phe Gly Val Leu Leu Gly Ser Val Thr Phe Gly Tyr Phe Ser
165 170 175

Asp Arg Leu Gly Arg Arg Val Val Leu Trp Ala Thr Ser Ser Ser Met
180 185 190

Phe Leu Phe Gly Ile Ala Ala Ala Phe Ala Val Asp Tyr Tyr Thr Phe
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Met Ala Ala Arg Phe Phe Leu Ala Met Val Ala Ser Gly Tyr Leu Val
210 215 220

Val Gly Phe Val Tyr Val Met Glu Phe Ile Gly Met Lys Ser Arg Thr
225 230 235 240

Trp Ala Ser Val His Leu His Ser Phe Phe Ala Val Gly Thr Leu Leu
245 250 255

Val Ala Leu Thr Gly Tyr Leu Val Arg Thr Trp Trp Leu Tyr Gln Met
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Ile Leu Ser Thr Val Thr Val Pro Phe Ile Leu Cys Cys Trp Val Leu

275 280 285

Pro Glu Thr Pro Phe Trp Leu Leu Ser Glu Gly Arg Tyr Glu Glu Ala
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Gln Lys Ile Val Asp Ile Met Ala Lys Trp Asn Arg Ala Ser Ser Cys
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Lys Leu Ser Glu Leu Leu Ser Leu Asp Leu Gln Gly Pro Val Ser Asn
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Ser Pro Thr Glu Val Gln Lys His Asn Leu Ser Tyr Leu Phe Tyr Asn
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Trp Ser Ile Thr Lys Arg Thr Leu Thr Val Trp Leu Ile Trp Phe Thr
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Gly Ser Leu Gly Phe Tyr Ser Phe Ser Leu Asn Ser Val Asn Leu Gly
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Gly Asn Glu Tyr Leu Asn Leu Phe Leu Leu Gly Val Val Glu Ile Pro
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Ala Tyr Thr Phe Val Cys Ile Ala Met Asp Lys Val Gly Arg Arg Thr
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Val Leu Ala Tyr Ser Leu Phe Cys Ser Ala Leu Ala Cys Gly Val Val
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Val Gly Lys Phe Ala Ile Gly Ala Ala Phe Gly Leu Ile Tyr Leu Tyr
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Thr Ala Glu Leu Tyr Pro Thr Ile Val Arg Ser Leu Ala Val Gly Ser
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Gly Ser Met Val Cys Arg Leu Ala Ser Ile Leu Ala Pro Phe Ser Val
485 490 495

Asp Leu Ser Ser Ile Trp Ile Phe Ile Pro Gln Leu Phe Val Gly Thr
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Met Ala Leu Leu Ser Gly Val Leu Thr Leu Lys Leu Pro Glu Thr Leu
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Gly Lys Arg Leu Ala Thr Thr Trp Glu Glu Ala Ala Lys Leu Glu Ser
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<212> DNA

<213> Homo sapiens

<400> 15

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