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(54) Title: NUCLEIC ACIDS OF THE HUMAN ABCC12 GENE, VECTORS CONTAINING SUCH NUCLEIC ACIDS AND USES THEREOF

(57) **Abrégé/Abstract:**

The present invention relates to a novel human ABCC12 gene as well as the cDNAs encoding the novel short and long of ABCC12 proteins isoforms. The invention also relates to vectors and recombinant host cells comprising such nucleic acids, nucleotide probes and primers, and means for the detection of polymorphisms and mutations in the ABCC12 gene or in the corresponding proteins isoforms produced by the allelic form of the ABCC12 gene.

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(54) Title: NUCLEIC ACIDS OF THE HUMAN ABCC12 GENE, VECTORS CONTAINING SUCH NUCLEIC ACIDS AND
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(57) Abstract: The present invention relates to a novel human ABCC12 gene as well as the cDNAs encoding the novel short and long of ABCC12 proteins isoforms. The invention also relates to vectors and recombinant host cells comprising such nucleic acids, nucleotide probes and primers, and means for the detection of polymorphisms and mutations in the ABCC12 gene or in the corresponding proteins isoforms produced by the allelic form of the ABCC12 gene.



WO 02/085943 A3

NUCLEIC ACIDS OF THE HUMAN ABCC12 GENE, VECTORS CONTAINING SUCH NUCLEIC ACIDS AND USES THEREOF

The present invention relates to a novel gene, designated ABCC12 and cDNAs encoding novel ABCC12 proteins. The invention also relates to vectors and recombinant host cells, nucleotide probes and primers, as well as means for the detection of polymorphisms in general, and mutations in particular in the ABCC12 gene or corresponding proteins produced by the allelic form of the ABCC12 gene.

The ATP-binding cassette (ABC) transporter superfamily is one of the largest gene families and encodes a functionally diverse group of membrane proteins involved in energy-dependent transport of a wide variety of substrates across membranes (Dean et al., *Curr Opin Genet Dev*, 1995, 5, 779-85). The active transporter proteins constitute a family of proteins that are extremely well conserved during evolution, from bacteria to humans (Ames and Lecar, *FASEB J.*, 1992, 6, 2660-2666). The ABC proteins are involved in extra- and intracellular membrane transport of various substrates, for example ions, amino acids, peptides, sugars, vitamins or steroid hormones. Among the 40 characterized humans members, 11 members have been described as associated with human disease, such as *inter alia* ABCA1, ABCA4 (ABCR) and ABCC7 (CFTR) which are thought to be involved in Tangier disease (Bodzioch M et al., *Nat. Genet.*, 1999, 22(4) ; 347-351; Brooks-Wilson et al., *Nat Genet*, 1999, 22(4), 336-345 ; Rust S et al., *Nat. Genet.*, 1999, 22, 352-355; Remaley A T et al.,), the Stargardt disease (Lewis R A et al., *Am. J. Hum. Genet.*, 1999, 64, 422-434), and the Cystic Fibrosis (Riordan JM et al., *Science*, 1989, 245, 1066-1073), respectively. These implications reveal the importance of the functional role of the ABC gene family and the discovery of new family gene members should provide new insights into the physiopathology of human diseases.

The prototype ABC protein binds ATP and uses the energy from ATP hydrolysis to drive the transport of various molecules across cell membranes. Most ABC functional proteins from eukaryotes encode full-transporter, each consisting of two ATP-binding domains (nucleotide binding fold, NBF) and two transmembrane (TM) domains. Most full-transporters are arranged in a TM-NBF-TM-NBF fashion (Dean et al., *Curr Opin Genet*, 1995, 5, 79-785).

Analysis of amino acids sequence alignments of the ATP-binding domains has allowed the ABC genes to be separated into sub-families (Allikmets et al., *Hum Mol Genet*,

1996, 5, 1649-1655). Currently, according to the recent HUGO classification, seven ABC gene sub-families named ABC A to G have been described in the human genome, *i.e.*, ABCA (ABC1 subfamily), ABCB (MDR/TAP subfamily), ABCC (CFTR/MRP subfamily), ABCD (ALD subfamily), ABCE (OABP subfamily), ABCF (GCN20 subfamily), and ABCG (white subfamily). For the most part these subfamilies contain genes that also display considerable conservation in the transmembrane domain sequences and have similar gene organization. However, ABC proteins transport very various substrates, and some members of different subfamilies have been shown to share more similarity in substrate recognition than do proteins within same subfamily. Five of the subfamilies are also represented in the yeast genome, indicating that these groups have been and retained early in the evolution of eukaryotes (Decottignies et al., *Nat Genet*, 1997, 137-45; Michaelis et al., 1995, Cold Spring Harbor Laboratory Press).

Several ABC transport proteins that have been identified in humans are associated with various diseases. Some multiple drug resistance phenotypes in tumor cells have been associated with the gene encoding the MDR (multi-drug resistance) protein, which also has an ABC transporter structure. Other ABC transporters have been associated with neuronal and tumor conditions (US Patent No. 5,858,719) or potentially involved in diseases caused by impairment of the homeostasis of metals (*Biochim Biophys Acta*. 1999 Dec 6;1461(2):18-404).

The human ABCC subfamily currently has ten identified members (ABCC1 to 10), seven of which are from the multidrug resistance-like (MRP) subgroup, two from the sulfonylurea receptor (SUR) subgroup, and the *CFTR* gene. MRP-like proteins are organic anion transporters; *i.e.*, they transport anionic drugs, exemplified by methotrexate (MTX), as well as neutral drugs conjugated to acidic ligands, such as glutathione (GSH), glucuronate, or sulfate, and play a role in resistance to nucleoside analogs (Cui et al., *Mol Pharmacol*, 1999, 55, 929-37; Kool et al., *Proc Natl Acad Sci*, 1999, 96, 6914-9 ; Schuetz et al., *Nat Med*, 1999, 5, 1048-51 ; Wijnholds et al., *Proc Natl Acad Sci*, 2000, 97, 7476-81). More specifically, ABCC1, ABCC2 and ABCC3 transport drugs conjugated to GSH, glucuronate, sulfate and other organic anions, such as MTX, whereas ABCC4 and ABCC5 proteins confer resistance to nucleotide analogs, including PMEA and purine base analogs. Several genetic variations in some ABCC subfamily members have been identified as associated with various human inherited diseases. For example, cystic fibrosis is caused by mutations in the ABCC7 gene or CFTR (cystic fibrosis transmembrane conductance

regulator) gene (Riordan et al., *Science*, 1989, 245, 1066-73). Another member of the ABCC subfamily, the ABCC2 gene, has been associated with the Dubin-Johnson syndrome (Wada et al., *Hum Mol Genet*, 1998, 7, 203-7). Also, mutations in the coding sequence of another gene belonging to the ABCC subfamily, the ABCC6 gene, have been recently
5 identified as responsible of the phenotype of pseudoxanthoma elasticum (Bergen et al., *Nat. Genet.*, 2000, 25, 228-31 ; Le Saux et al., *Nat Genet*, 2000, 25, 223-7), which is a genetic disorder of the connective tissue. Likewise, a receptor of sulfonylureas, ABCC8 or SUR1, appears to be involved in familial persistent hyperinsulinemic hypoglycemia of infancy (Thomas et al., *Science*, 1995, 268, 426-9).

10 Therefore, characterization of a new gene from the ABCC subfamily is likely to yield a biologically important transporter that may have a translocase activity and may play a major role in human pathologies.

The applicants have discovered and characterized a novel gene belonging to the ABCC protein sub-family, which has been designated ABCC12. Different transcripts
15 isoforms have been identified since the ABCC12 gene has two different splicing forms. Consequently, two different mRNAs ABCC12 were found to be expressed in humans. The two messengers which result of alternative splicing encode two ABCC12 proteins having 3 amino acid difference in length, one is designated the long ABCC12 protein isoform, while the other is designated the short ABCC12 protein isoform. The newly discovered gene also
20 shows considerable conservation of the amino acid sequences, particularly within the transmembrane region (TM) and the ATP-binding regions (NBD), and have a similar gene organization. In particular, this gene appears to be closely related to other ABCC subfamily members such as ABCC5, ABCC2 and ABCC3, particularly in the ATP-binding domain, and more particularly in the C-terminal ATP binding domains. The ABCC12 proteins, as
25 well as ABCC4 and ABCC5, is smaller than another well-known member of the subgroup, ABCC1 (MRP1), appearing to lack the extra N-terminal domain (Borst et al., *J Natl Cancer Inst*, 2000, 92, 1295-302), which is however not required for the transport function (Bakos et al., *J. Biol. Chem*, 1998, 273, 32167-75). Since structurally related ABC proteins often transport similar substrates across the membranes, it would be reasonable to suggest
30 that the ABCC12 proteins could share functional similarities with ABCC 4 and/or ABCC5 genes, i.e., the resistance to nucleotide analogs, such as PMEA, and purine base analogs (Schuetz et al., *Nat Med*, 1999 5, 1048-51 ; Wijnholds et al., *Proc Natl Acad Sci*, 2000, 97, 7476-81).

Furthermore, the applicants have mapped the novel gene ABCC12 in a region located in the 16q12 locus of the human chromosome 16, which is a region statistically linked with a genetic pathology designated paroxysmal kinesigenic choreoathetosis (Tomita et al., *Am J Hum Genet*, 1999, 65, 1688-97; Bennett et al., 2000). This result supports the hypothesis that ABCC12 represents a positional candidate for this disorder and thus that the ABCC12 gene may be one causing gene for the clinical phenotype of paroxysmal kinesigenic choreoathetosis.

Paroxysmal kinesigenic choreoathetosis (PKC), the most frequent type of paroxysmal dyskinesia, is a disorder characterized by recurrent, frequent attacks of involuntary movements and postures, including chorea and dystonia, induced by sudden voluntary movements, stress, or excitement (Swoboda et al., *Neurology*, 2000, 55, 224-30). The onset is in childhood or early adolescence, the frequency and severity diminish with age, and it responds to treatment with anticonvulsants. PKC occurs in familial and sporadic forms and affects more males than females. In most families, it is inherited as an autosomal dominant trait with incomplete penetrance. The gene locus has been mapped to human chromosome 16q11-12 (Tomita et al. (1999) *Am. J. Hum. Genet.* 65, 1588-1697 ; Bennett et al. (2000) *Neurology*, 54, 125-130).

An overlapping locus has been predicted to contain the gene for infantile convulsions with paroxysmal choreoathetosis (ICCA) (Lee et al., (1998) *Hum. Genet.* 103, 608-612). The Applicants have further determined expression pattern of the ABCC12 gene by PCR and by EST database mining that suggests that the ABCC12 gene is expressed in tissues such as CNS which is potentially involved in the etiology of PKC.

SUMMARY OF THE INVENTION

The present invention relates to a nucleic acid of the human ABCC12 gene, cDNAs, and protein isoforms, which are likely to be involved in the transport of organic anion transporters, such as cysteinyl leukotriene, anionic drugs, such as methotrexate, as well as neutral drugs conjugated to acidic ligands, such as glutathione (GSH), glucuronate, or sulfate, or in the pathology whose candidate chromosomal region is situated on chromosome 16, more precisely on the 16q arm and still more precisely in the 16q12 locus for paroxysmal kinesigenic choreoathetosis.

Thus, a first subject of the invention is a nucleic acid comprising a nucleotide sequence of any one of SEQ ID NOs: 1-32, or a complementary nucleotide sequence thereof.

The invention also relates to a nucleic acid comprising at least 8 consecutive nucleotides of a nucleotide sequence of a) any one of SEQ ID NOs: 1-32 or a complementary nucleotide sequence thereof.

5 The invention also relates to a nucleic acid having at least 80% nucleotide identity with a nucleic acid comprising a nucleotide sequence of any one of SEQ ID NOs: 1-32, or a complementary nucleotide sequence thereof.

The invention also relates to a nucleic acid having at least 85%, preferably 90%, more preferably 95% and still more preferably 98% nucleotide identity with a nucleic acid comprising a nucleotide sequence of any one of SEQ ID NOs: 1-32, or a complementary
10 nucleotide sequence thereof.

The invention also relates to a nucleic acid hybridizing, under high stringency conditions, with a nucleotide sequence of any one of SEQ ID NOs: 1-32, or a complementary nucleotide sequence thereof.

The invention also relates to a nucleic acid, particularly cDNA molecules, which
15 encode the short and long human ABCC12 proteins isoforms. Thus, the invention relates to nucleic acids comprising a nucleotide sequence of any one of SEQ ID NO: 1-32, or a complementary nucleotide sequence thereof.

The invention also relates to a nucleic acid comprising a nucleotide sequence as depicted in any one of SEQ ID NO: 1-32, or a complementary nucleotide sequence thereof.

20 According to the invention, a nucleic acid comprising a nucleotide sequence of SEQ ID NO: 1, which encodes a short ABCC12 polypeptide isoform of 1356 amino acids comprising the amino acid sequence of SEQ ID NO: 33.

According to the invention, a nucleic acid comprising a nucleotide sequence of SEQ ID NO: 2, which encodes a long ABCC12 polypeptide isoform of 1359 amino acids
25 comprising the amino acid sequence of SEQ ID NO: 34.

Thus, the invention also relates to a nucleic acid encoding a polypeptide comprising an amino acid sequence of SEQ ID NO: 33.

Thus, the invention also relates to a nucleic acid encoding a polypeptide comprising an amino acid sequence of SEQ ID NO: 34.

30 Thus, the invention also relates to a polypeptide comprising an amino acid sequence of SEQ ID NO: 33.

Thus, the invention also relates to a polypeptide comprising an amino acid sequence of SEQ ID NO: 34.

The invention also relates to a polypeptide comprising an amino acid sequence as depicted in SEQ ID NO: 33.

The invention also relates to a polypeptide comprising an amino acid sequence as depicted in SEQ ID NO: 34.

5 The invention also relates to a means for detecting polymorphisms in general, and mutations in particular, in the ABCC12 gene or in the corresponding proteins produced by the allelic forms of these genes.

According to another aspect, the invention also relates to the nucleotide sequences of ABCC12 gene comprising at least one biallelic polymorphism such as for example a
10 substitution, addition or deletion of one or more nucleotides.

Nucleotide probes and primers hybridizing with a nucleic acid sequence located in the region of the ABCC12 nucleic acid (genomic DNA, messenger RNA, cDNA), in particular, a nucleic acid sequence comprising any one of the mutations or polymorphisms.

The nucleotide probes or primers according to the invention comprise at least 8
15 consecutive nucleotides of a nucleic acid comprising any one of SEQ ID NOs: 1-32, or a complementary nucleotide sequence thereof.

Preferably, nucleotide probes or primers according to the invention will have a length of 10, 12, 15, 18 or 20 to 25, 35, 40, 50, 70, 80, 100, 200, 500, 1000, 1500 consecutive nucleotides of a nucleic acid according to the invention, in particular of a nucleic acid
20 comprising any one of SEQ ID NOs: 1-32, or a complementary nucleotide sequence thereof.

Alternatively, a nucleotide probe or primer according to the invention will consist of and/or comprise fragments having a length of 12, 15, 18, 20, 25, 35, 40, 50, 100, 200, 500, 1000, 1500 consecutive nucleotides of a nucleic acid according to the invention, more particularly of a nucleic acid comprising any one of SEQ ID NOs: 1-32, or a complementary
25 nucleotide sequence thereof.

The definition of a nucleotide probe or primer according to the invention therefore covers oligonucleotides which hybridize, under the high stringency hybridization conditions defined above, with a nucleic acid comprising any one of SEQ ID NOs: 1-32, or a complementary nucleotide sequence thereof.

30 The preferred probes and primers according to the invention comprise all or part of a nucleotide sequence comprising any one of SEQ ID NOs: 35-46, or a complementary nucleotide sequence thereof.

The nucleotide primers according to the invention may be used to amplify a nucleic acid according to the invention, and more particularly a nucleic acid comprising a nucleotide sequence of any one of SEQ ID NOs: 1-32, or a complementary nucleotide sequence thereof.

According to the invention, some nucleotide primers specific for an ABCC12 gene,
5 may be used to amplify a nucleic acid comprising any one of SEQ ID NOs: 1 or 2, and comprise a nucleotide sequence of any one of SEQ ID NOs:35-46, or a complementary nucleotide sequence thereof.

Another subject of the invention relates to a method of amplifying a nucleic acid according to the invention, and more particularly a nucleic acid comprising any one of SEQ
10 ID NOs: 1-32, a complementary nucleotide sequence thereof, a nucleic acid as depicted in any one of SEQ ID NOs: 1-32, or a complementary nucleotide sequence thereof, contained in a sample, said method comprising the steps of:

- a) bringing the sample in which the presence of the target nucleic acid is suspected into contact with a pair of nucleotide primers whose hybridization position is located respectively
15 on the 5' side and on the 3' side of the region of the target nucleic acid whose amplification is sought, in the presence of the reagents necessary for the amplification reaction; and
- b) detecting the amplified nucleic acids.

The present invention also relates to a method of detecting the presence of a nucleic acid comprising a nucleotide sequence of any one of SEQ ID NOs: 1-32, or a complementary
20 nucleotide sequence thereof, or a nucleic acid fragment or variant of any one of SEQ ID NOs: 1-32, or a complementary nucleotide sequence thereof in a sample, said method comprising the steps of:

- 1) bringing one or more nucleotide probes according to the invention into contact with the sample to be tested;
- 25 2) detecting the complex which may have formed between the probe(s) and the nucleic acid present in the sample.

According to a specific embodiment of the method of detection according to the invention, the oligonucleotide probes are immobilized on a support.

According to another aspect, the oligonucleotide probes comprise a detectable marker.

Another subject of the invention is a box or kit for amplifying all or part of a nucleic
30 acid comprising a) any one of SEQ ID NOs: 1-32, or a complementary nucleotide sequence thereof, or b) as depicted in any one of SEQ ID NOs: 1-32 or of a complementary nucleotide sequence thereof, said box or kit comprising:

1) a pair of nucleotide primers in accordance with the invention, whose hybridization position is located respectively on the 5' side and 3' side of the target nucleic acid whose amplification is sought; and optionally,

2) reagents necessary for an amplification reaction.

5 Such an amplification box or kit will preferably comprise at least one pair of nucleotide primers as described above.

The invention also relates to a box or kit for detecting the presence of a nucleic acid according to the invention in a sample, said box or kit comprising:

a) one or more nucleotide probes according to the invention;

10 b) appropriate reagents necessary for a hybridisation reaction.

According to a first aspect, the detection box or kit is characterized in that the nucleotide probe(s) and primer(s) are immobilized on a support.

According to a second aspect, the detection box or kit is characterized in that the nucleotide probe(s) and primer(s) comprise a detectable marker.

15 According to a specific embodiment of the detection kit described above, such a kit will comprise a plurality of oligonucleotide probes and/or primers in accordance with the invention which may be used to detect target nucleic acids of interest or alternatively to detect mutations in the coding regions or the non-coding regions of the nucleic acids according to the invention. According to preferred embodiment of the invention, the target nucleic acid
20 comprises a nucleotide sequence of any one of SEQ ID NOs: 1-32, or of a complementary nucleic acid sequence. Alternatively, the target nucleic acid is a nucleic acid fragment or variant of a nucleic acid comprising any one of SEQ ID NOs: 1-32, or of a complementary nucleotide sequence.

According to another preferred embodiment, a primer according to the invention
25 comprises, generally, all or part of any one of SEQ ID NOs: 1-32, or a complementary sequence thereof.

The invention also relates to a recombinant vector comprising a nucleic acid according to the invention. Preferably, such a recombinant vector will comprise a nucleic acid selected from the group consisting of

30 a) a nucleic acid comprising a nucleotide sequence of any one of SEQ ID NOs: 1-32, or a complementary nucleotide sequence thereof,

b) a nucleic acid comprising a nucleotide sequence as depicted in any one of SEQ ID NOs: 1-32, or a complementary nucleotide sequence thereof,

c) a nucleic acid having at least eight consecutive nucleotides of a nucleic acid comprising a nucleotide sequence of any one of SEQ ID NOs: 1-32, or a complementary nucleotide sequence thereof;

d) a nucleic acid having at least 80% nucleotide identity with a nucleic acid comprising a nucleotide sequence of any one of SEQ ID NOs: 1-32, or a complementary nucleotide sequence thereof;

e) a nucleic acid having 85%, 90%, 95%, or 98% nucleotide identity with a nucleic acid comprising a nucleotide sequence of any one of SEQ ID NOs: 1-32, or a complementary nucleotide sequence thereof;

f) a nucleic acid hybridizing, under high stringency hybridization conditions, with a nucleic acid comprising a nucleotide sequence of any one of SEQ ID NOs: 1-32, or a complementary nucleotide sequence; and

g) a nucleic acid encoding a polypeptide comprising an amino acid sequence of any one of SEQ ID NO: 33 and 34.

According to a first embodiment, a recombinant vector according to the invention is used to amplify a nucleic acid inserted therein, following transformation or transfection of a desired cellular host.

According to a second embodiment, a recombinant vector according to the invention corresponds to an expression vector comprising, in addition to a nucleic acid in accordance with the invention, a regulatory signal or nucleotide sequence that directs or controls transcription and/or translation of the nucleic acid and its encoded mRNA.

According to a preferred embodiment, a recombinant vector according to the invention will comprise in particular the following components:

(1) an element or signal for regulating the expression of the nucleic acid to be inserted, such as a promoter and/or enhancer sequence;

(2) a nucleotide coding region comprised within the nucleic acid in accordance with the invention to be inserted into such a vector, said coding region being placed in phase with the regulatory element or signal described in (1); and

(3) an appropriate nucleic acid for initiation and termination of transcription of the nucleotide coding region of the nucleic acid described in (2).

The present invention also relates to a defective recombinant virus comprising a cDNA nucleic acid encoding any one of short or long isoform of the ABCC12 polypeptide, involved in the transport of various substances, or in the pathology whose candidate chromosomal

region is situated on chromosome 16, more precisely on the 16q arm and still more precisely in the 16q12 locus for paroxysmal kinesigenic choreoathetosis.

In another preferred embodiment of the invention, the defective recombinant virus comprises a gDNA nucleic acid encoding any one of the ABCC12 polypeptides isoforms involved in paroxysmal kinesigenic choreoathetosis. Preferably, the ABCC12 polypeptides short and long isoforms comprise amino acid sequences of SEQ ID NO: 33 and 34, respectively.

In another preferred embodiment, the invention relates to a defective recombinant virus comprising a nucleic acid encoding the short or long ABCC12 polypeptide isoform under the control of a promoter chosen from RSV-LTR or the CMV early promoter.

According to a specific embodiment, a method of introducing a nucleic acid according to the invention into a host cell, in particular a host cell obtained from a mammal, *in vivo*, comprises a step during which a preparation comprising a pharmaceutically compatible vector and a "naked" nucleic acid according to the invention, placed under the control of appropriate regulatory sequences, is introduced by local injection at the level of the chosen tissue, for example a smooth muscle tissue, the "naked" nucleic acid being absorbed by the cells of this tissue.

According to a specific embodiment of the invention, a composition is provided for the *in vivo* production of any one of the ABCC12 proteins isoforms. This composition comprises a nucleic acid encoding the ABCC12 polypeptides isoforms placed under the control of appropriate regulatory sequences, in solution in a physiologically acceptable vehicle and/or excipient.

Therefore, the present invention also relates to a composition comprising a nucleic acid encoding the short or long isoform of the ABCC12 polypeptide comprising an amino acid sequence selected from SEQ ID NO: 33 or 34, wherein the nucleic acid is placed under the control of appropriate regulatory elements.

Consequently, the invention also relates to a pharmaceutical composition intended for the prevention of or treatment of a patient or subject affected by a paroxysmal kinesigenic choreoathetosis comprising a nucleic acid encoding any one of the short or long ABCC12 protein isoform, in combination with one or more physiologically compatible excipients.

Preferably, such a composition will comprise a nucleic acid comprising a nucleotide sequence of any one of SEQ ID NOs:1-32, wherein the nucleic acid is placed under the control of an appropriate regulatory element or signal.

In addition, the present invention is directed to a pharmaceutical composition intended for the prevention or treatment of a patient or a subject affected by a pathology located on the chromosome 16q12, such as the paroxysmal kinesigenic choreoathetosis, comprising a recombinant vector according to the invention, in combination with one or more
5 physiologically compatible excipients.

The invention also relates to the use of a nucleic acid according to the invention encoding the short or long ABCC12 protein isoform for the manufacture of a medicament intended for the prevention of a pathology located on the chromosome locus 16q12, or more particularly for the treatment of subjects affected by a paroxysmal kinesigenic choreoathetosis

10 The invention also relates to the use of a recombinant vector according to the invention comprising nucleic acids encoding any one of ABCC12 proteins isoforms for the manufacture of a medicament intended for the prevention of a pathology located on the chromosome locus 16q12 or more particularly for the treatment of subjects affected by a paroxysmal kinesigenic choreoathetosis.

15 The subject of the invention is therefore also a recombinant vector comprising nucleic acids according to the invention that encode any one of ABCC12 proteins or polypeptides isoforms involved in the paroxysmal kinesigenic choreoathetosis.

The invention also relates to the use of such a recombinant vector for the preparation of a pharmaceutical composition intended for the treatment and/or for the prevention of
20 diseases or conditions associated with deficiency of the ABCC12 gene and with a pathology located on the chromosome locus 16q12.

The present invention also relates to the use of cells genetically modified *ex vivo* with such a recombinant vector according to the invention, or cells producing a recombinant vector, wherein the cells are implanted in the body, to allow a prolonged and effective
25 expression *in vivo* of any biologically active ABCC12 polypeptides isoforms.

The invention also relates to the use of nucleic acids according to the invention encoding the ABCC12 proteins isoforms for the manufacture of a medicament intended for the prevention and/or the treatment of subjects affected by a paroxysmal kinesigenic choreoathetosis.

30 The invention also relates to the use of a recombinant vector according to the invention comprising nucleic acids encoding the ABCC12 polypeptides isoforms according to the invention for the manufacture of a medicament intended for the prevention and/or the treatment of subjects affected by a paroxysmal kinesigenic choreoathetosis.

The invention also relates to the use of a recombinant host cell according to the invention, comprising nucleic acids encoding the ABCC12 polypeptides isoforms according to the invention for the manufacture of a medicament intended for the prevention and/or the treatment of subjects affected by a a paroxysmal kinesigenic choreoathetosis.

5 The present invention also relates to the use of a recombinant vector according to the invention, preferably a defective recombinant virus, for the preparation of a pharmaceutical composition for the treatment and/or prevention of pathologies linked to the dysfunction of the transport of anionic drugs, such as methotrexate (MTX), neutral drugs conjugated to acidic ligands, such as GSH, glucuronate, or sulfate conjugated drugs.

10 The invention relates to the use of such a recombinant vector or defective recombinant virus for the preparation of a pharmaceutical composition intended for the treatment and/or for the prevention of a pathology located on the chromosome locus 16q12, such as PKC. Thus, the present invention also relates to a pharmaceutical composition comprising one or more recombinant vectors or defective recombinant viruses according to
15 the invention.

The present invention also relates to the use of cells genetically modified *ex vivo* with a virus according to the invention, or the use cells producing such viruses, implanted in the body, allowing a prolonged and effective expression *in vivo* of any one biologically active ABCC12 proteins.

20 The present invention shows that it is possible to incorporate a nucleic acid encoding ABCC12 polypeptides isoforms according to the invention into a viral vector, and that these vectors make it possible to effectively express a biologically active, mature polypeptide. More particularly, the invention shows that the *in vivo* expression of the isoforms of ABCC12 proteins may be obtained by direct administration of an adenovirus or by implantation of a
25 producing cell or of a cell genetically modified by an adenovirus or by a retrovirus incorporating such a nucleic acid.

In this regard, another subject of the invention relates to any mammalian cell infected with one or more defective recombinant viruses according to the invention. More particularly, the invention relates to any population of human cells infected with these viruses. These may
30 be in particular cells of blood origin (totipotent stem cells or precursors), fibroblasts, myoblasts, hepatocytes, keratinocytes, smooth muscle and endothelial cells, glial cells and the like.

Another subject of the invention relates to an implant comprising mammalian cells infected with one or more defective recombinant viruses according to the invention or cells producing recombinant viruses, and an extracellular matrix. Preferably, the implants according to the invention comprise 10^5 to 10^{10} cells. More preferably, they comprise 10^6 to 10^8 cells.

More particularly, in the implants of the invention, the extracellular matrix comprises a gelling compound and optionally, a support allowing the anchorage of the cells.

The invention also relates to a recombinant host cell comprising a nucleic acid of the invention, and more particularly, a nucleic acid comprising any one of SEQ ID NO: 1-32, or a complementary nucleotide sequence thereof.

The invention also relates to a recombinant host cell comprising a nucleic acid of the invention, and more particularly a nucleic acid comprising a nucleotide sequence as depicted in any one SEQ ID NO: 1-32, or a complementary nucleotide sequence thereof.

According to another aspect, the invention also relates to a recombinant host cell comprising a recombinant vector according to the invention. Therefore, the invention also relates to a recombinant host cell comprising a recombinant vector comprising any of the nucleic acids of the invention, and more particularly a nucleic acid comprising any one nucleotide sequence of SEQ ID NO: 1-32, or a complementary nucleotide sequence thereof.

Specifically, the invention relates to a recombinant host cell comprising a recombinant vector comprising a nucleic acid comprising any one of SEQ ID NOs: 1-32, or a complementary nucleotide sequence thereof.

The invention also relates to a recombinant host cell comprising a recombinant vector comprising a nucleic acid comprising a nucleotide sequence as depicted in any one of SEQ ID NOs: 1-32, or of a complementary nucleotide sequence thereof.

The invention also relates to a recombinant host cell comprising a recombinant vector comprising a nucleic acid encoding a polypeptide comprising any one amino acid sequence of SEQ ID NO: 33 or 34.

The invention also relates to a method for the production of a polypeptide comprising an amino acid sequence of any one of SEQ ID NOs: 33 or 34, or of a peptide fragment or a variant thereof, said method comprising the steps of:

a) inserting a nucleic acid encoding said polypeptide into an appropriate vector;

b) culturing, in an appropriate culture medium, a previously transformed host cell or transfecting a host cell with the recombinant vector of step a);

c) recovering the conditioned culture medium or lysing the host cell, for example by sonication or by osmotic shock;

5 d) separating and purifying said polypeptide from said culture medium or alternatively from the cell lysates obtained in step c); and

e) where appropriate, characterizing the recombinant polypeptide produced.

A polypeptide termed "homologous" to a polypeptide having an amino acid sequence selected from SEQ ID NO: 33 or 34 also forms part of the invention. Such a homologous
10 polypeptide comprises an amino acid sequence possessing one or more substitutions of an amino acid by an equivalent amino acid.

The ABCC12 polypeptide isoforms according to the invention, in particular 1) a polypeptide comprising an amino acid sequence of any one SEQ ID NO: 33 or 34, 2) a polypeptide fragment or variant of a polypeptide comprising an amino acid sequence of any
15 one of SEQ ID NO: 33 or 34, or 3) a polypeptide termed "homologous" to a polypeptide comprising amino acid sequence selected from SEQ ID NO: 33 or 34.

In a specific embodiment, an antibody according to the invention is directed against 1) a polypeptide comprising an amino acid sequence of any one SEQ ID NO: 33 or 34, 2) a polypeptide fragment or variant of a polypeptide comprising an amino acid sequence of
20 selected from SEQ ID NO: 33 or 34, or 3) a polypeptide termed "homologous" to a polypeptide comprising amino acid sequence selected from SEQ ID NO: 33 or 34. Such antibody is produced by using the trioma technique or the hybridoma technique described by Kozbor et al. (*Immunology Today* (1983) 4:72).

Thus, the subject of the invention is, in addition, a method of detecting the presence of
25 any one of the polypeptides according to the invention in a sample, said method comprising the steps of:

a) bringing the sample to be tested into contact with an antibody directed against 1) a polypeptide comprising an amino acid sequence of any one of SEQ ID NO: 33 or 34, 2) a polypeptide fragment or variant of a polypeptide comprising an amino acid sequence selected
30 from SEQ ID NOs: 33 or 34, 3) a polypeptide termed "homologous" to a polypeptide comprising amino acid sequence of any one of SEQ ID NO: 33 or 34, and

b) detecting the antigen/antibody complex formed.

The invention also relates to a box or kit for diagnosis or for detecting the presence of any one of polypeptide in accordance with the invention in a sample, said box comprising:

- a) an antibody directed against 1) a polypeptide comprising an amino acid sequence of SEQ ID NO: 33 or 34, 2) a polypeptide fragment or variant of a polypeptide comprising an amino acid sequence of any one of SEQ ID NOs: 33 or 34, or 3) a polypeptide "homologous" to a polypeptide comprising an amino acid sequence of SEQ ID NO: 33 or 34, and
- b) a reagent allowing the detection of the antigen/antibody complexes formed.

The invention also relates to a pharmaceutical composition comprising a nucleic acid according to the invention.

10 The invention also provides pharmaceutical compositions comprising a nucleic acid encoding any one of ABCC12 polypeptide isoforms according to the invention and pharmaceutical compositions comprising the ABCC12 polypeptides according to the invention intended for the treatment of a pathology located on the chromosome locus 16q12, such as the paroxysmal kinesigenic choreoathetosis.

15 The present invention also relates to a new therapeutic approach for the treatment of pathologies located on the chromosome locus 16q12, such as the paroxysmal kinesigenic choreoathetosis, comprising transferring and expressing *in vivo* a nucleic acid encoding the ABCC12 protein isoforms according to the invention.

20 Thus, the present invention offers a new approach for the treatment and/or prevention of pathologies located on the chromosome locus 16q12, such as the paroxysmal kinesigenic choreoathetosis in a patient or subject. Specifically, the present invention provides methods to restore or promote the deficiency of the gene causing such pathology.

25 Consequently, the invention also relates to a pharmaceutical composition intended for the prevention and/or treatment of subjects affected by, a dysfunction of the gene located on the chromosome locus 16q12, such as paroxysmal kinesigenic choreoathetosis, comprising a nucleic acid encoding the ABCC12 protein isoforms, in combination with one or more physiologically compatible vehicle and/or excipient.

30 According to a specific embodiment of the invention, a composition is provided for the *in vivo* production of any one of the ABCC12 proteins. This composition comprises a nucleic acid encoding any one of the ABCC12 polypeptides placed under the control of appropriate regulatory sequences, in solution in a physiologically compatible vehicle and/or excipient.

Therefore, the present invention also relates to a composition comprising a nucleic acid encoding a polypeptide comprising an amino acid sequence of any one of SEQ ID NO: 33 or 34, wherein the nucleic acid is placed under the control of appropriate regulatory elements.

5 Preferably, such a composition will comprise a nucleic acid comprising a nucleotide sequence of any one of SEQ ID NO: 1-32, placed under the control of appropriate regulatory elements.

The invention also relates to a pharmaceutical composition intended for the prevention of or treatment of subjects affected by a dysfunction of the transport of anionic drugs, such as
10 methotrexate (MTX), neutral drugs conjugated to acidic ligands, such as GSH, glucuronate, or sulfate conjugated drugs, comprising a recombinant vector according to the invention, in combination with one or more physiologically compatible vehicle and/or excipient.

According to another aspect, the subject of the invention is also a preventive or curative therapeutic method of treating diseases caused by a deficiency of the transport of
15 anionic drugs, such as methotrexate (MTX), neutral drugs conjugated to acidic ligands, such as GSH, glucuronate, or sulfate, such a method comprising administering to a patient a nucleic acid encoding one ABCC12 polypeptide isoform according to the invention, said nucleic acid being combined with one or more physiologically appropriate vehicles and/or excipients.

The invention relates to a pharmaceutical composition for the prevention and/or
20 treatment of a patient or subject affected by a dysfunction of the transport of anionic drugs, such as methotrexate (MTX), neutral drugs conjugated to acidic ligands, such as GSH, glucuronate, or sulfate comprising a therapeutically effective quantity of a polypeptide having an amino acid sequence selected from SEQ ID NO: 33 or 34, combined with one or more physiologically appropriate vehicles and/or excipients.

25 The invention also relates to a pharmaceutical composition for the prevention and/or treatment of PKC comprising a therapeutically effective quantity of a polypeptide having an amino acid sequence selected from SEQ ID NO: 33 or 34, combined with one or more physiologically appropriate vehicles and/or excipients.

The invention also relates to a pharmaceutical composition for the prevention and/or
30 treatment of PKC, such a method comprising administering to a patient a nucleic acid encoding any one of the ABCC12 polypeptide isoform according to the invention, said nucleic acid being combined with one or more physiologically appropriate vehicles and/or excipients.

According to a specific embodiment, a method of introducing at least a nucleic acid according to the invention into a host cell, in particular a host cell obtained from a mammal, *in vivo*, comprises a step during which a preparation comprising a pharmaceutically compatible vector and a "naked" nucleic acid according to the invention, placed under the control of appropriate regulatory sequences, is introduced by local injection at the level of the chosen tissue, for example a smooth muscle tissue, the "naked" nucleic acid being absorbed by the cells of this tissue.

According to yet another aspect, the subject of the invention is also a preventive or curative therapeutic method of treating diseases caused by a deficiency of the transport of anionic drugs, such as methotrexate (MTX), neutral drugs conjugated to acidic ligands, such as GSH, glucuronate, or sulfate, such a method comprising administering to a patient a therapeutically effective quantity of any one of the ABCC12 polypeptides isoforms according to the invention, said polypeptide being combined with one or more physiologically appropriate vehicles and/or excipients.

The invention also provides methods for screening small molecules and compounds that act on any one of the ABCC12 protein isoforms to identify agonists and antagonists of such polypeptides that can restore or promote improved the transport of anionic drugs, such as methotrexate (MTX), neutral drugs conjugated to acidic ligands, such as GSH, glucuronate, or sulfate to effectively cure and or prevent dysfunctions thereof. These methods are useful to identify small molecules and compounds for therapeutic use in the treatment of diseases due to a deficiency of the transport of anionic drugs, such as methotrexate (MTX), neutral drugs conjugated to acidic ligands, such as GSH conjugated drugs, glucuronate, or sulfate.

Therefore, the invention also relates to the use of any one of ABCC12 polypeptides isoforms or a cell expressing the ABCC12 polypeptides according to the invention, for screening active ingredients for the prevention and/or treatment of diseases resulting from a dysfunction of the transport of anionic drugs, such as methotrexate (MTX), neutral drugs conjugated to acidic ligands, such as GSH conjugated drugs, glucuronate, or sulfate.

The invention also relates to a method of screening a compound or small molecule, an agonist or antagonist of any one of ABCC12 polypeptides, said method comprising the following steps:

a) preparing a membrane vesicle comprising any one of the ABCC12 polypeptides and a lipid substrate comprising a detectable marker;

b) incubating the vesicle obtained in step a) with an agonist or antagonist candidate compound;

c) qualitatively and/or quantitatively measuring release of the lipid substrate comprising a detectable marker; and

5 d) comparing the release measurement obtained in step b) with a measurement of release of a labelled lipid substrate by a vesicle that has not been previously incubated with the agonist or antagonist candidate compound.

In a first specific embodiment, the short and long ABCC12 polypeptides isoforms comprise SEQ ID NO: 33 or 34, respectively.

10 The invention also relates to a method of screening a compound or small molecule, an agonist or antagonist of any one of ABCC12 polypeptides, said method comprising the following steps:

a) obtaining a cell, for example a cell line, that, either naturally or after transfecting the cell with any one of ABCC12 encoding nucleic acids, expressing the corresponding ABCC12
15 polypeptides;

b) incubating the cell of step a) in the presence of an anion labelled with a detectable marker;

c) washing the cell of step b) in order to remove the excess of the labelled anion which has not penetrated into these cells;

20 d) incubating the cell obtained in step c) with an agonist or antagonist candidate compound for any one of ABCC12 polypeptides;

e) measuring efflux of the labelled anion; and

f) comparing the value of efflux of the labelled anion determined in step e) with a value of efflux of a labelled anion measured with cell which has not been previously
25 incubated in the presence of the agonist or antagonist candidate compound for the ABCC12 polypeptides.

In a specific embodiment, the ABCC12 polypeptide comprises SEQ ID NO: 33 or 34.

BRIEF DESCRIPTION OF THE DRAWINGS

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Figure 1: represents the alignment of ABCC11, ABCC12 (long isoform), and ABCC5 proteins. Identical amino acids are shaded, gaps are indicated by periods. Walker A and B motifs and the ABC transporter family signature sequence

C are underlined and labelled with respective letters. Amino acid sequences were aligned with the PILEUP program in the Genetics Computer Group Package. Potential transmembrane spanning segments are given in bold type.

5

Figure 2: represents the physical map of the chromosome 16 and localization of the human ABCC12 and ABCC11 genes. Human ABCC12 and ABCC11 genes, flanked by markers D1653093 and D165409, are separated by about 200kb, and organized in a head-to-tail fashion, with their 5' ends facing the centromere. Loci for ICCA, PKC, and their overlap, are defined by brackets. ABCC11 and ABCC12 genes are indicated by gray and black arrows, respectively.

10

Figure 3: represents the expression profiling of the human ABCC12 gene by PCR on human Multiple Tissue cDNA (MTC®, Clontech). Each lane contains normalized, first-strand cDNA from 16 human tissues/cells. Lanes 1-66 thus represent cDNA from heart, brain, placenta, lung, liver, muscle, kidney, pancreas, spleen, thymus, testis, ovary, intestine, colon, leukocyte, and prostate, respectively. N represents the negative control ; M represent the marker lane (1kb Plus DNA Ladder). The following primer pairs amplified specific gene products : ABCC12 : forward 5'-GGT GAC AGA CAA GCG AGT TCA GAC AAT G-3', reverse 5'-CTT TGC TCC TCT GGG CCA GTG-3'.

15

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Figure 4: displays the splicing pattern of the ABCC12 and ABCC11 genes. Clear boxes represent exons, and vertical lines define splice sites. The exon numbers for each gene is shown both above and below the drawing. Filled boxes indicate the exons coding for ABC domains.

25

Figure 5: displays a phylogenetic relationship of genes in the ABCC subfamily. Complete protein sequences of all members of the ABCC subfamily were aligned with the CLUSTALW program. The distance measure is given in substitutions per amino acid.

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DETAILED DESCRIPTION OF THE INVENTION

GENERAL DEFINITIONS

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The present invention contemplates isolation of a human gene encoding ABCC12 polypeptide of the invention, including a full length, or naturally occurring form of ABCC12 and any antigenic fragments thereof from any animal, particularly mammalian or avian, and more particularly human source.

10 In accordance with the present invention, conventional molecular biology, microbiology, and recombinant DNA techniques within the skill of the art are used. Such techniques are fully explained in the literature (Sambrook et al., 1989. Molecular cloning a laboratory manual. 2ed. Cold Spring Harbor Laboratory, Cold spring Harbor, New York; Glover, 1985, DNA Cloning: A practical approach, volumes I and II oligonucleotide synthesis, 15 MRL Press, LTD., Oxford, U.K.; Hames and Higgins, 1985, Transcription and translation; Hames and Higgins, 1984, Animal Cell Culture; Freshney, 1986, Immobilized Cells And Enzymes, IRL Press; and Perbal, 1984, A practical guide to molecular cloning).

As used herein, the term "gene" refers to an assembly of nucleotides that encode a polypeptide, and includes cDNA and genomic DNA nucleic acids.

20 The term "isolated" for the purposes of the present invention designates a biological material (nucleic acid or protein) which has been removed from its original environment (the environment in which it is naturally present).

For example, a polynucleotide present in the natural state in a plant or an animal is not isolated. The same nucleotide separated from the adjacent nucleic acids in which it is naturally 25 inserted in the genome of the plant or animal is considered as being "isolated".

Such a polynucleotide may be included in a vector and/or such a polynucleotide may be included in a composition and remains nevertheless in the isolated state because of the fact that the vector or the composition does not constitute its natural environment.

The term "purified" does not require the material to be present in a form exhibiting 30 absolute purity, exclusive of the presence of other compounds. It is rather a relative definition.

A polynucleotide is in the "purified" state after purification of the starting material or of the natural material by at least one order of magnitude, preferably 2 or 3 and preferably 4 or 5 orders of magnitude.

For the purposes of the present description, the expression "nucleotide sequence" may be used to designate either a polynucleotide or a nucleic acid. The expression "nucleotide sequence" covers the genetic material itself and is therefore not restricted to the information relating to its sequence.

5 The terms "nucleic acid", "polynucleotide", "oligonucleotide" or "nucleotide sequence" cover RNA, DNA, or cDNA sequences or alternatively RNA/DNA hybrid sequences of more than one nucleotide, either in the single-stranded form or in the duplex, double-stranded form.

A "nucleic acid" is a polymeric compound comprised of covalently linked subunits
10 called nucleotides. Nucleic acid includes polyribonucleic acid (RNA) and polydeoxyribonucleic acid (DNA), both of which may be single-stranded or double-stranded. DNA includes cDNA, genomic DNA, synthetic DNA, and semi-synthetic DNA. The sequence of nucleotides that encodes a protein is called the sense sequence or coding sequence.

15 The term "nucleotide" designates both the natural nucleotides (A, T, G, C) as well as the modified nucleotides that comprise at least one modification such as (1) an analog of a purine, (2) an analog of a pyrimidine, or (3) an analogous sugar, examples of such modified nucleotides being described, for example, in the PCT application No. WO 95/04 064.

For the purposes of the present invention, a first polynucleotide is considered as being
20 "complementary" to a second polynucleotide when each base of the first nucleotide is paired with the complementary base of the second polynucleotide whose orientation is reversed. The complementary bases are A and T (or A and U), or C and G.

"Heterologous" DNA refers to DNA not naturally located in the cell, or in a chromosomal site of the cell. Preferably, the heterologous DNA includes a gene foreign to the
25 cell.

As used herein, the term "homologous" in all its grammatical forms and spelling variations refers to the relationship between proteins that possess a "common evolutionary origin," including proteins from superfamilies (*e.g.*, the immunoglobulin superfamily) and homologous proteins from different species (*e.g.*, myosin light chain, etc.) (Reeck et al., 1987,
30 Cell 50 :667)). Such proteins (and their encoding genes) have sequence homology, as reflected by their high degree of sequence similarity.

Accordingly, the term "sequence similarity" in all its grammatical forms refers to the degree of identity or correspondence between nucleic acid or amino acid sequences of proteins

that may or may not share a common evolutionary origin (*see* Reeck et al., *supra*). However, in common usage and in the instant application, the term "homologous," when modified with an adverb such as "highly," may refer to sequence similarity and not a common evolutionary origin.

5 In a specific embodiment, two DNA sequences are "substantially homologous" or "substantially similar" when at least about 50% (preferably at least about 75%, and more preferably at least about 90 or 95%) of the nucleotides match over the defined length of the DNA sequences. Sequences that are substantially homologous can be identified by comparing the sequences using standard software available in sequence data banks, or in a Southern
10 hybridization experiment under, for example, stringent conditions as defined for that particular system. Defining appropriate hybridization conditions is within the skill of the art. See, e.g., Maniatis et al., *supra*; Glover et al. (1985. DNA Cloning: A practical approach, volumes I and II oligonucleotide synthesis, MRL Press, Ltd, Oxford, U.K.); Hames and Higgins (1985. Transcription and Translation).

15 Similarly, in a particular embodiment, two amino acid sequences are "substantially homologous" or "substantially similar" when greater than 30% of the amino acids are identical, or greater than about 60% are similar (functionally identical). Preferably, the similar or homologous sequences are identified by alignment using, for example, the GCG (Genetics Computer Group, Program Manual for the GCG Package, *Version 7*, Madison,
20 Wisconsin) pileup program.

The "percentage identity" between two nucleotide or amino acid sequences, for the purposes of the present invention, may be determined by comparing two sequences aligned optimally, through a window for comparison.

The portion of the nucleotide or polypeptide sequence in the window for comparison
25 may thus comprise additions or deletions (for example "gaps") relative to the reference sequence (which does not comprise these additions or these deletions) so as to obtain an optimum alignment of the two sequences.

The percentage is calculated by determining the number of positions at which an identical nucleic base or an identical amino acid residue is observed for the two sequences
30 (nucleic or peptide) compared, and then by dividing the number of positions at which there is identity between the two bases or amino acid residues by the total number of positions in the window for comparison, and then multiplying the result by 100 in order to obtain the percentage sequence identity.

The optimum sequence alignment for the comparison may be achieved using a computer with the aid of known algorithms contained in the package from the company WISCONSIN GENETICS SOFTWARE PACKAGE, GENETICS COMPUTER GROUP (GCG), 575 Science Doctor , Madison, WISCONSIN.

5 By way of illustration, it will be possible to produce the percentage sequence identity with the aid of the BLAST software (versions BLAST 1.4.9 of March 1996, BLAST 2.0.4 of February 1998 and BLAST 2.0.6 of September 1998), using exclusively the default parameters (Altschul et al, 1990, . Mol. Biol., 215:403-410; Altschul et al, 1997, Nucleic Acids Res., 25:3389-3402). Blast searches for sequences similar/homologous to a reference
10 "request" sequence, with the aid of the Altschul et al. algorithm. The request sequence and the databases used may be of the peptide or nucleic types, any combination being possible.

The term "corresponding to" is used herein to refer to similar or homologous sequences, whether the exact position is identical or different from the molecule to which the similarity or homology is measured. A nucleic acid or amino acid sequence alignment may
15 include spaces. Thus, the term "corresponding to" refers to the sequence similarity, and not the numbering of the amino acid residues or nucleotide bases.

A gene encoding the ABCC12 polypeptides isoforms of the invention, whether genomic DNA or cDNA, can be isolated from any source, particularly from a human cDNA or genomic library. Methods for obtaining genes are well known in the art, as described above
20 (see, e.g., Sambrook et al., 1989, *Molecular cloning: a laboratory manual*. 2ed. Cold Spring Harbor Laboratory, Cold spring Harbor, New York).

Accordingly, any animal cell potentially can serve as the nucleic acid source for the molecular cloning of the ABCC12 gene. The DNA may be obtained by standard procedures known in the art from cloned DNA (e.g., a DNA "library"), and preferably is obtained from a
25 cDNA library prepared from tissues with high level expression of the protein and/or the transcripts, by chemical synthesis, by cDNA cloning, or by the cloning of genomic DNA, or fragments thereof, purified from the desired cell (See, for example, Sambrook et al., 1989, *Molecular cloning: a laboratory manual*. 2ed. Cold Spring Harbor Laboratory, Cold spring Harbor, New York; Glover, 1985, *DNA Cloning: A Practical Approach, Volumes I and II*
30 *Oligonucleotide Synthesis*, MRL Press, Ltd., Oxford, U.K).

Clones derived from genomic DNA may contain regulatory and intron DNA regions in addition to coding regions; clones derived from cDNAs will not contain intron sequences.

Whatever the source, the gene should be molecularly cloned into a suitable vector for propagation of the gene.

In the molecular cloning of the gene from genomic DNA, DNA fragments are generated, some of which will encode the desired gene. The DNA may be cleaved at specific sites using various restriction enzymes. Alternatively, one may use DNase in the presence of manganese to fragment the DNA, or the DNA can be physically sheared, as for example, by sonication. The linear DNA fragments can then be separated according to size by standard techniques, including but not limited to, agarose and polyacrylamide gel electrophoresis and column chromatography.

Once the DNA fragments are generated, identification of the specific DNA fragment containing the desired ABCC12 gene may be accomplished in a number of ways. For example, if an amount of a portion of the ABCC12 gene or its specific RNA, or a fragment thereof, is available and can be purified and labelled, the generated DNA fragments may be screened by nucleic acid hybridization to the labelled probe (Benton and Davis, *Science* (1977), 196:180; Grunstein et al., *Proc.Natl. Acad. Sci. U.S.A.* (1975) 72:3961). For example, a set of oligonucleotides corresponding to the partial coding sequence information obtained for the ABCC12 proteins can be prepared and used as probes for DNA encoding the ABCC12, as was done in a specific example, *infra*, or as primers for cDNA or mRNA (e.g., in combination with a poly-T primer for RT-PCR). Preferably, a fragment is selected that is highly unique to the ABCC12 nucleic acids or polypeptides of the invention. Those DNA fragments with substantial homology to the probe will hybridize. As noted above, the greater the degree of homology, the more stringent hybridization conditions can be used. In a specific embodiment, various stringency hybridization conditions are used to identify homologous ABCC12 gene.

Further selection can be carried out on the basis of the properties of the gene, *e.g.*, if the gene encodes a protein product having the isoelectric, electrophoretic, amino acid composition, or partial amino acid sequence of the ABCC12 proteins as disclosed herein. Thus, the presence of the gene may be detected by assays based on the physical, chemical, or immunological properties of its expressed product. For example, cDNA clones, or DNA clones which hybrid-select the proper mRNAs, can be selected which produce a protein that, *e.g.*, has similar or identical electrophoretic migration, isoelectric focusing or non-equilibrium pH gel electrophoresis behaviour, proteolytic digestion maps, or antigenic properties as known for ABCC12.

ABCC12 gene of the invention may also be identified by mRNA selection, *i.e.*, by nucleic acid hybridization followed by *in vitro* translation. According to this procedure, nucleotide fragments are used to isolate complementary mRNAs by hybridization. Such DNA fragments may represent available, purified ABCC12 DNA, or may be synthetic oligonucleotides designed from the partial coding sequence information. Immunoprecipitation analysis or functional assays (*e.g.*, tyrosine phosphatase activity) of the *in vitro* translation products of the products of the isolated mRNAs identifies the mRNA and, therefore, the complementary DNA fragments, that contain the desired sequences. In addition, specific mRNAs may be selected by adsorption of polysomes isolated from cells to immobilized antibodies specifically directed against any one of the ABCC12 polypeptides of the invention.

A radiolabeled ABCC12 cDNA can be synthesized using the selected mRNA (from the adsorbed polysomes) as a template. The radiolabeled mRNA or cDNA may then be used as a probe to identify homologous ABCC12 DNA fragments from among other genomic DNA fragments.

“Variant” of a nucleic acid according to the invention will be understood to mean a nucleic acid which differs by one or more bases relative to the reference polynucleotide. A variant nucleic acid may be of natural origin, such as an allelic variant which exists naturally, or it may also be a nonnatural variant obtained, for example, by mutagenic techniques.

In general, the differences between the reference (generally, wild-type) nucleic acid and the variant nucleic acid are small such that the nucleotide sequences of the reference nucleic acid and of the variant nucleic acid are very similar and, in many regions, identical. The nucleotide modifications present in a variant nucleic acid may be silent, which means that they do not alter the amino acid sequences encoded by said variant nucleic acid.

However, the changes in nucleotides in a variant nucleic acid may also result in substitutions, additions or deletions in the polypeptide encoded by the variant nucleic acid in relation to the polypeptides encoded by the reference nucleic acid. In addition, nucleotide modifications in the coding regions may produce conservative or non-conservative substitutions in the amino acid sequence of the polypeptide.

Preferably, the variant nucleic acids according to the invention encode polypeptides which substantially conserve the same function or biological activity as the polypeptide of the reference nucleic acid or alternatively the capacity to be recognized by antibodies directed against the polypeptides encoded by the initial reference nucleic acid.

Some variant nucleic acids will thus encode mutated forms of the polypeptides whose systematic study will make it possible to deduce structure-activity relationships of the proteins in question. Knowledge of these variants in relation to the disease studied is essential since it makes it possible to understand the molecular cause of the pathology.

5 "Fragment" will be understood to mean a nucleotide sequence of reduced length relative to the reference nucleic acid and comprising, over the common portion, a nucleotide sequence identical to the reference nucleic acid. Such a nucleic acid "fragment" according to the invention may be, where appropriate, included in a larger polynucleotide of which it is a constituent. Such fragments comprise, or alternatively consist of, oligonucleotides ranging in
10 length from 8, 10, 12, 15, 18, 20 to 25, 30, 40, 50, 70, 80, 100, 200, 500, 1000 or 1500 consecutive nucleotides of a nucleic acid according to the invention.

A "nucleic acid molecule" refers to the phosphate ester polymeric form of ribonucleosides (adenosine, guanosine, uridine or cytidine; "RNA molecules") or deoxyribonucleosides (deoxyadenosine, deoxyguanosine, deoxythymidine, or deoxycytidine;
15 "DNA molecules"), or any phosphoester analogs thereof, such as phosphorothioates and thioesters, in either single stranded form, or a double-stranded helix. Double stranded DNA-DNA, DNA-RNA and RNA-RNA helices are possible. The term nucleic acid molecule, and in particular DNA or RNA molecule, refers only to the primary and secondary structure of the molecule, and does not limit it to any particular tertiary forms. Thus, this term includes
20 double-stranded DNA found, *inter alia*, in linear or circular DNA molecules (*e.g.*, restriction fragments), plasmids, and chromosomes. In discussing the structure of particular double-stranded DNA molecules, sequences may be described herein according to the normal convention of giving only the sequence in the 5' to 3' direction along the nontranscribed strand of DNA (*i.e.*, the strand having a sequence homologous to the mRNA). A
25 "recombinant DNA molecule" is a DNA molecule that has undergone a molecular biological manipulation.

A nucleic acid molecule is "hybridizable" to another nucleic acid molecule, such as a cDNA, genomic DNA, or RNA, when a single stranded form of the nucleic acid molecule can anneal to the other nucleic acid molecule under the appropriate conditions of temperature and
30 solution ionic strength (*see* Sambrook et al., *supra*). The conditions of temperature and ionic strength determine the "stringency" of the hybridization. For preliminary screening for homologous nucleic acids, low stringency hybridization conditions, corresponding to a T_m of 55°, can be used, *e.g.*, 5x SSC, 0.1% SDS, 0.25% milk, and no formamide; or 30%

formamide, 5x SSC, 0.5% SDS. Moderate stringency hybridization conditions correspond to a higher T_m , e.g., 40% formamide, with 5x or 6x SCC. High stringency hybridization conditions correspond to the highest T_m , e.g., 50% formamide, 5x or 6x SCC. Hybridization requires that the two nucleic acids contain complementary sequences, although depending on the stringency of the hybridization, mismatches between bases are possible. The appropriate stringency for hybridizing nucleic acids depends on the length of the nucleic acids and the degree of complementation, variables well known in the art. The greater the degree of similarity or homology between two nucleotide sequences, the greater the value of T_m for hybrids of nucleic acids having those sequences. The relative stability (corresponding to higher T_m) of nucleic acid hybridizations decreases in the following order: RNA:RNA, DNA:RNA, DNA:DNA. For hybrids of greater than 100 nucleotides in length, equations for calculating T_m have been derived (*see* Sambrook et al., *supra*). For hybridization with shorter nucleic acids, *i.e.*, oligonucleotides, the position of mismatches becomes more important, and the length of the oligonucleotide determines its specificity (*see* Sambrook et al., *supra*). Preferably a minimum length for a hybridizable nucleic acid is at least about 10 nucleotides; preferably at least about 15 nucleotides; and more preferably the length is at least about 20 nucleotides.

In a specific embodiment, the term "standard hybridization conditions" refers to a T_m of 55°C, and utilizes conditions as set forth above. In a preferred embodiment, the T_m is 60°C; in a more preferred embodiment, the T_m is 65°C.

"High stringency hybridization conditions" for the purposes of the present invention will be understood to mean the following conditions:

1- Membrane competition and PREHYBRIDIZATION:

- Mix: 40 μ l salmon sperm DNA (10 mg/ml)
+ 40 μ l human placental DNA (10 mg/ml)
- Denature for 5 minutes at 96°C, then immerse the mixture in ice.
- Remove the 2X SSC and pour 4 ml of formamide mix in the hybridization tube containing the membranes.
- Add the mixture of the two denatured DNAs.
- Incubation at 42°C for 5 to 6 hours, with rotation.

2- Labeled probe competition:

- Add to the labeled and purified probe 10 to 50 μ l Cot I DNA, depending on the quantity of repeats.
- Denature for 7 to 10 minutes at 95°C.
- Incubate at 65°C for 2 to 5 hours.

5

3- HYBRIDIZATION:

- Remove the prehybridization mix.
- Mix 40 μ l salmon sperm DNA + 40 μ l human placental DNA; denature for 5 min at 96°C, then immerse in ice.
- 10 - Add to the hybridization tube 4 ml of formamide mix, the mixture of the two DNAs and the denatured labeled probe/Cot I DNA .
- Incubate 15 to 20 hours at 42°C, with rotation.

4- Washes and Exposure:

- 15 - One wash at room temperature in 2X SSC, to rinse.
- Twice 5 minutes at room temperature 2X SSC and 0.1% SDS at 65°C.
- Twice 15 minutes 0.1X SSC and 0.1% SDS at 65°C.
- Envelope the membranes in clear plastic wrap and expose.

The hybridization conditions described above are adapted to hybridization, under high stringency conditions, of a molecule of nucleic acid of varying length from 20 nucleotides to several hundreds of nucleotides. It goes without saying that the hybridization conditions described above may be adjusted as a function of the length of the nucleic acid whose hybridization is sought or of the type of labeling chosen, according to techniques known to one skilled in the art. Suitable hybridization conditions may, for example, be adjusted according to the teaching contained in the manual by Hames and Higgins (1985, *supra*).

As used herein, the term "oligonucleotide" refers to a nucleic acid, generally of at least 15 nucleotides, that is hybridizable to a nucleic acid according to the invention. Oligonucleotides can be labelled, *e.g.*, with ^{32} P-nucleotides or nucleotides to which a label, such as biotin, has been covalently conjugated. In one embodiment, a labeled oligonucleotide can be used as a probe to detect the presence of a nucleic acid encoding any one of the ABCC12 polypeptides of the invention. In another embodiment, oligonucleotides (one or both of which may be labelled) can be used as PCR primers, either for cloning full lengths or fragments of the ABCC12 nucleic acid, or to detect the presence of a nucleic acid encoding

the ABCC12 protein. In a further embodiment, an oligonucleotide of the invention can form a triple helix with the ABCC12 DNA molecule. Generally, oligonucleotides are prepared synthetically, preferably on a nucleic acid synthesizer. Accordingly, oligonucleotides can be prepared with non-naturally occurring phosphoester analog bonds, such as thioester bonds,
5 etc.

"Homologous recombination" refers to the insertion of a foreign DNA sequence of a vector in a chromosome. Preferably, the vector targets a specific chromosomal site for homologous recombination. For specific homologous recombination, the vector will contain sufficiently long regions of homology to sequences of the chromosome to allow
10 complementary binding and incorporation of the vector into the chromosome. Longer regions of homology, and greater degrees of sequence similarity, may increase the efficiency of homologous recombination.

A DNA "coding sequence" is a double-stranded DNA sequence which is transcribed and translated into a polypeptide in a cell *in vitro* or *in vivo* when placed under the control of
15 appropriate regulatory sequences. The boundaries of the coding sequence are determined by a start codon at the 5' (amino) terminus and a translation stop codon at the 3' (carboxyl) terminus. A coding sequence can include, but is not limited to, prokaryotic sequences, cDNA from eukaryotic mRNA, genomic DNA sequences from eukaryotic (*e.g.*, mammalian) DNA, and even synthetic DNA sequences. If the coding sequence is intended for expression in a
20 eukaryotic cell, a polyadenylation signal and transcription termination sequence will usually be located 3' to the coding sequence.

Transcriptional and translational control sequences are DNA regulatory sequences, such as promoters, enhancers, terminators, and the like, that provide for the expression of a coding sequence in a host cell. In eukaryotic cells, polyadenylation signals are control
25 sequences.

"Regulatory region" means a nucleic acid sequence which regulates the expression of a nucleic acid. A regulatory region may include sequences which are naturally responsible for expressing a particular nucleic acid (a homologous region) or may include sequences of a different origin (responsible for expressing different proteins or even synthetic proteins). In
30 particular, the sequences can be sequences of eukaryotic or viral genes or derived sequences which stimulate or repress transcription of a gene in a specific or non-specific manner and in an inducible or non-inducible manner. Regulatory regions include origins of replication, RNA

splice sites, enhancers, transcriptional termination sequences, signal sequences which direct the polypeptide into the secretory pathways of the target cell, and promoters.

A regulatory region from a "heterologous source" is a regulatory region which is not naturally associated with the expressed nucleic acid. Included among the heterologous regulatory regions are regulatory regions from a different species, regulatory regions from a different gene, hybrid regulatory sequences, and regulatory sequences which do not occur in nature, but which are designed by one having ordinary skill in the art.

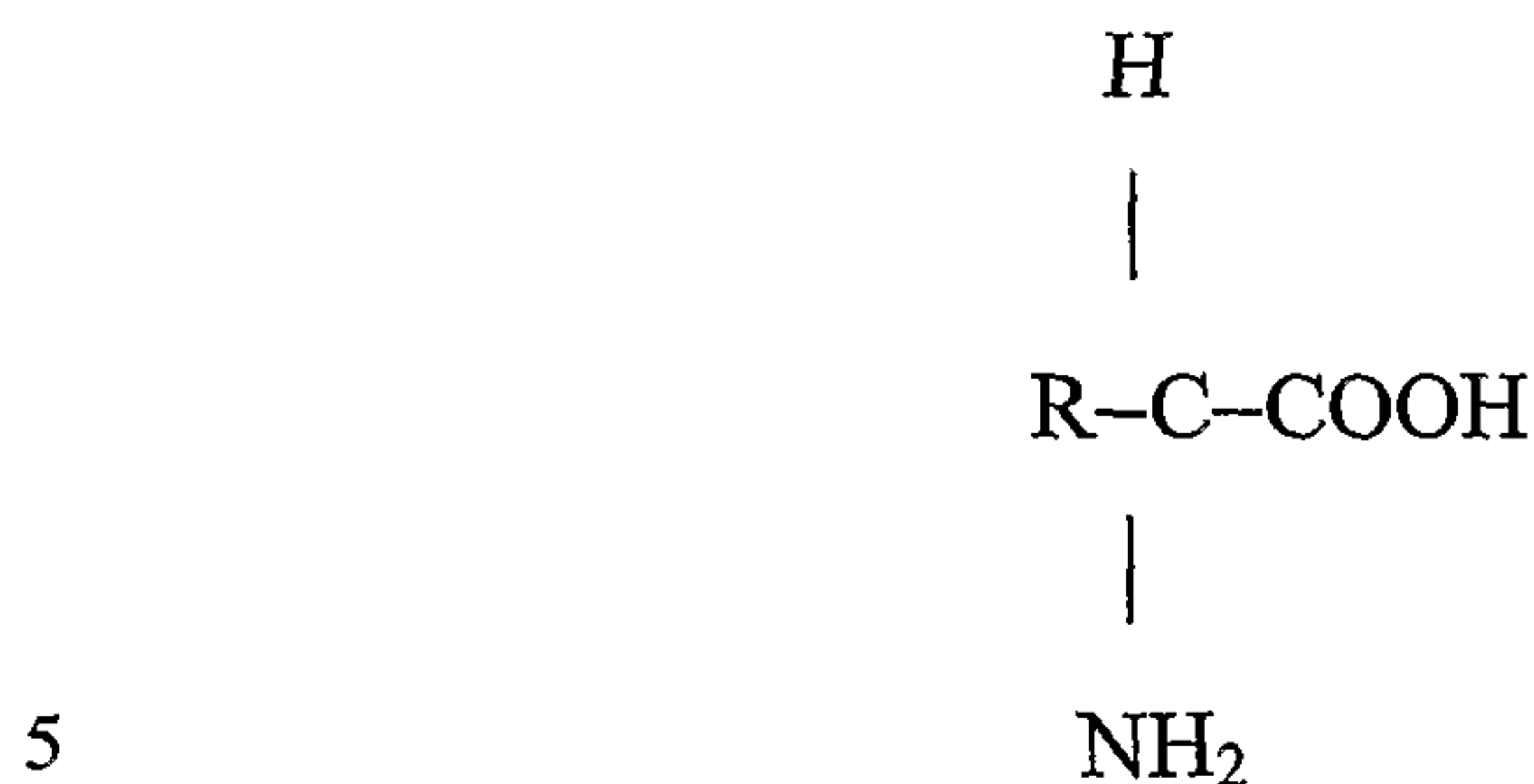
A "cassette" refers to a segment of DNA that can be inserted into a vector at specific restriction sites. The segment of DNA encodes a polypeptide of interest, and the cassette and restriction sites are designed to ensure insertion of the cassette in the proper reading frame for transcription and translation.

A "promoter sequence" is a DNA regulatory region capable of binding RNA polymerase in a cell and initiating transcription of a downstream (3' direction) coding sequence. For purposes of defining the present invention, the promoter sequence is bounded at its 3' terminus by the transcription initiation site and extends upstream (5' direction) to include the minimum number of bases or elements necessary to initiate transcription at levels detectable above background. Within the promoter sequence will be found a transcription initiation site (conveniently defined for example, by mapping with nuclease S1), as well as protein binding domains (consensus sequences) responsible for the binding of RNA polymerase.

A coding sequence is "under the control" of transcriptional and translational control sequences in a cell when RNA polymerase transcribes the coding sequence into mRNA, which is then trans-RNA spliced and translated into the protein encoded by the coding sequence.

A "signal sequence" is included at the beginning of the coding sequence of a protein to be expressed on the surface of a cell. This sequence encodes a signal peptide, N-terminal to the mature polypeptide, that directs the host cell to translocate the polypeptide. The term "translocation signal sequence" is used herein to refer to this sort of signal sequence. Translocation signal sequences can be found associated with a variety of proteins native to eukaryotes and prokaryotes, and are often functional in both types of organisms.

A "polypeptide" is a polymeric compound comprised of covalently linked amino acid residues. Amino acids have the following general structure:



Amino acids are classified into seven groups on the basis of the side chain R: (1) aliphatic side chains, (2) side chains containing a hydroxylic (OH) group, (3) side chains containing sulfur atoms, (4) side chains containing an acidic or amide group, (5) side chains containing a basic group, (6) side chains containing an aromatic ring, and (7) proline, an imino acid in which the side chain is fused to the amino group.

A "protein" is a polypeptide which plays a structural or functional role in a living cell.

The polypeptides and proteins of the invention may be glycosylated or unglycosylated.

"Homology" means similarity of sequence reflecting a common evolutionary origin.

15 Polypeptides or proteins are said to have homology, or similarity, if a substantial number of their amino acids are either (1) identical, or (2) have a chemically similar R side chain. Nucleic acids are said to have homology if a substantial number of their nucleotides are identical.

"Isolated polypeptide" or "isolated protein" is a polypeptide or protein which is substantially free of those compounds that are normally associated therewith in its natural state (e.g., other proteins or polypeptides, nucleic acids, carbohydrates, lipids). "Isolated" is not meant to exclude artificial or synthetic mixtures with other compounds, or the presence of impurities which do not interfere with biological activity, and which may be present, for example, due to incomplete purification, addition of stabilizers, or compounding into a pharmaceutically acceptable preparation.

"Fragment" of a polypeptide according to the invention will be understood to mean a polypeptide whose amino acid sequence is shorter than that of the reference polypeptide and which comprises, over the entire portion with these reference polypeptides, an identical amino acid sequence. Such fragments may, where appropriate, be included in a larger polypeptide of which they are a part. Such fragments of a polypeptide according to the invention may have a length of 5, 10, 15, 20, 30 to 40, 50, 100, 200 or 300 amino acids.

“Variant” of a polypeptide according to the invention will be understood to mean mainly a polypeptide whose amino acid sequence contains one or more substitutions, additions or deletions of at least one amino acid residue, relative to the amino acid sequence of the reference polypeptide, it being understood that the amino acid substitutions may be
5 either conservative or nonconservative.

A “variant” of a polypeptide or protein is any analogue, fragment, derivative, or mutant which is derived from a polypeptide or protein and which retains at least one biological property of the polypeptide or protein. Different variants of the polypeptide or protein may exist in nature. These variants may be allelic variations characterized by
10 differences in the nucleotide sequences of the structural gene coding for the protein, or may involve differential splicing or post-translational modification. Variants also include a related protein having substantially the same biological activity, but obtained from a different species.

The skilled artisan can produce variants having single or multiple amino acid substitutions, deletions, additions, or replacements. These variants may include, *inter alia*: (a)
15 variants in which one or more amino acid residues are substituted with conservative or non-conservative amino acids, (b) variants in which one or more amino acids are added to the polypeptide or protein, (c) variants in which one or more of the amino acids includes a substituent group, and (d) variants in which the polypeptide or protein is fused with another polypeptide such as serum albumin. The techniques for obtaining these variants, including
20 genetic (suppressions, deletions, mutations, etc.), chemical, and enzymatic techniques, are known to persons having ordinary skill in the art.

If such allelic variations, analogues, fragments, derivatives, mutants, and modifications, including alternative mRNA splicing forms and alternative post-translational modification forms result in derivatives of the polypeptide which retain any of the biological
25 properties of the polypeptide, they are intended to be included within the scope of this invention.

A “vector” is a replicon, such as plasmid, virus, phage or cosmid, to which another DNA segment may be attached so as to bring about the replication of the attached segment. A “replicon” is any genetic element (e.g., plasmid, chromosome, virus) that functions as an
30 autonomous unit of DNA replication *in vivo*, *i.e.*, capable of replication under its own control.

The present invention also relates to cloning vectors containing a gene encoding analogs and derivatives of any one of the ABCC12 polypeptides of the invention. The production and use of derivatives and analogs related to any one of the ABCC12 proteins are

within the scope of the present invention. In a specific embodiment, the derivatives or analogs are functionally active, *i.e.*, capable of exhibiting one or more functional activities associated with a wild-type ABCC12 polypeptides of the invention.

ABCC12 derivatives can be made by altering encoding nucleic acid sequences by
5 substitutions, additions or deletions that provide for functionally equivalent molecules. Preferably, derivatives are made that have enhanced or increased functional activity relative to native ABCC12. Alternatively, such derivatives may encode soluble fragments of the ABCC12 extracellular domains that have the same or greater affinity for the natural ligand of ABCC12 polypeptide of the invention. Such soluble derivatives may be potent inhibitors of
10 ligand binding to ABCC12.

Due to the degeneracy of nucleotide coding sequences, other DNA sequences which encode substantially same amino acid sequences as that of ABCC12 gene may be used in the practice of the present invention. These include but are not limited to allelic genes, homologous genes from other species, and nucleotide sequences comprising all or portions of
15 ABCC12 gene which are altered by the substitution of different codons that encode the same amino acid residue within the sequence, thus producing a silent change. Likewise, the ABCC12 derivatives of the invention include, but are not limited to those containing, as a primary amino acid sequence, all or part of the amino acid sequence of any one of the ABCC12 proteins including altered sequences in which functionally equivalent amino acid
20 residues are substituted for residues within the sequence resulting in a conservative amino acid substitution. For example, one or more amino acid residues within the sequence can be substituted by another amino acid of a similar polarity, which acts as a functional equivalent, resulting in a silent alteration. Substitutes for an amino acid within the sequence may be selected from other members of the class to which the amino acid belongs. For example, the
25 nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan and methionine. Amino acids containing aromatic ring structures are phenylalanine, tryptophan, and tyrosine. The polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine. The positively charged (basic) amino acids include arginine, lysine and histidine. The negatively charged (acidic)
30 amino acids include aspartic acid and glutamic acid. Such alterations will not be expected to affect apparent molecular weight as determined by polyacrylamide gel electrophoresis, or isoelectric point.

Particularly preferred substitutions are:

- Lys for Arg and vice versa such that a positive charge may be maintained;
- Glu for Asp and vice versa such that a negative charge may be maintained;
- Ser for Thr such that a free -OH can be maintained; and
- Gln for Asn such that a free CONH₂ can be maintained.

5 Amino acid substitutions may also be introduced to substitute an amino acid with a particularly preferable property. For example, a Cys may be introduced as a potential site for disulfide bridges with another Cys. A His may be introduced as a particularly "catalytic" site (i.e., His can act as an acid or base and is the most common amino acid in biochemical catalysis). Pro may be introduced because of its particularly planar structure, which induces
10 b-turns in the protein's structure.

The genes encoding ABCC12 derivatives and analogs of the invention can be produced by various methods known in the art. The manipulations which result in their production can occur at the gene or protein level. For example, the cloned ABCC12 sequence can be modified by any of numerous strategies known in the art (Sambrook et al., 1989,
15 *supra*). The sequence can be cleaved at appropriate sites with restriction endonuclease(s), followed by further enzymatic modification if desired, isolated, and ligated *in vitro*. Production of a gene encoding a derivative or analog of the ABCC12, should ensure that the modified gene remains within the same translational reading frame as the ABCC12 gene, uninterrupted by translational stop signals, in the region where the desired activity is encoded.

20 Additionally, the ABCC12-encoding nucleic acids can be mutated *in vitro* or *in vivo*, to create and/or destroy translation, initiation, and/or termination sequences, or to create variations in coding regions and/or form new restriction endonuclease sites or destroy pre-existing ones, to facilitate further *in vitro* modification. Preferably, such mutations enhance the functional activity of the mutated ABCC12 gene products. Any technique for mutagenesis
25 known in the art may be used, including *inter alia*, *in vitro* site-directed mutagenesis (Hutchinson et al., (1978) Biol. Chem. 253:6551; Zoller and Smith, (1984) DNA, 3:479-488; Oliphant et al., (1986) *Gene* 44:177; Hutchinson et al., (1986) *Proc. Natl. Acad. Sci. U.S.A.* 83:710; Huygen et al., (1996) *Nature Medicine*, 2(8):893-898) and use of TAB® linkers (Pharmacia). PCR techniques are preferred for site-directed mutagenesis (Higuchi, 1989,
30 "Using PCR to Engineer DNA", in *PCR Technology: Principles and Applications for DNA Amplification*, H. Erlich, ed., Stockton Press, Chapter 6, pp. 61-70).

Identified and isolated ABCC12 gene may then be inserted into an appropriate cloning vector. A large number of vector-host systems known in the art may be used. Possible vectors include, but are not limited to, plasmids or modified viruses, but the vector system must be compatible with the host cell used. Examples of vectors include, but are not limited to, *Escherichia coli*, bacteriophages such as lambda derivatives, or plasmids such as pBR322 derivatives or pUC plasmid derivatives, *e.g.*, pGEX vectors, pmal-c, pFLAG, etc. The insertion into a cloning vector can, for example, be accomplished by ligating the DNA fragment into a cloning vector which has complementary cohesive termini. However, if the complementary restriction sites used to fragment the DNA are not present in the cloning vector, the ends of the DNA molecules may be enzymatically modified. Alternatively, any site desired may be produced by ligating nucleotide sequences (linkers) onto the DNA termini; these ligated linkers may comprise specific chemically synthesized oligonucleotides encoding restriction endonuclease recognition sequences. Recombinant molecules can be introduced into host cells via transformation, transfection, infection, electroporation, etc., so that many copies of the gene sequence are generated. Preferably, the cloned gene is contained on a shuttle vector plasmid, which provides for expansion in a cloning cell, *e.g.*, *Escherichia coli*, and facile purification for subsequent insertion into an appropriate expression cell line, if such is desired. For example, a shuttle vector, which is a vector that can replicate in more than one type of organism, can be prepared for replication in both *Escherichia coli* and *Saccharomyces cerevisiae* by linking sequences from an *Escherichia coli* plasmid with sequences from the yeast 2m plasmid.

In an alternative method, the desired gene may be identified and isolated after insertion into a suitable cloning vector in a "shot gun" approach. Enrichment for the desired gene, for example, by size fractionation, can be done before insertion into the cloning vector.

The nucleotide sequence coding for the ABCC12 polypeptides or antigenic fragments, derivatives or analogs thereof, or functionally active derivatives, including chimeric proteins thereof, may be inserted into an appropriate expression vector, *i.e.*, a vector which contains the necessary elements for the transcription and translation of the inserted protein-coding sequence. Such elements are termed herein a "promoter." Thus, nucleic acid encoding the ABCC12 polypeptides of the invention are operationally associated with a promoter in an expression vector of the invention. Both cDNA and genomic sequences can be cloned and expressed under control of such regulatory sequences. An expression vector also preferably includes a replication origin.

The necessary transcriptional and translational signals can be provided on a recombinant expression vector, or they may be supplied by a native gene encoding ABCC12 and/or its flanking regions.

Potential host-vector systems include but are not limited to mammalian cell systems
5 infected with virus (*e.g.*, vaccinia virus, adenovirus, etc.); insect cell systems infected with virus (*e.g.*, baculovirus); microorganisms such as yeast containing yeast vectors; or bacteria transformed with bacteriophage, DNA, plasmid DNA, or cosmid DNA. The expression elements of vectors vary in their strengths and specificities. Depending on the host-vector system utilized, any one of a number of suitable transcription and translation elements may be
10 used.

A recombinant ABCC12 protein of the invention, or functional fragments, derivatives, chimeric constructs, or analogs thereof, may be expressed chromosomally, after integration of the coding sequence by recombination. In this regard, any of a number of amplification systems may be used to achieve high levels of stable gene expression (*See* Sambrook et al.,
15 1989, *supra*).

The cell into which the recombinant vector comprising the nucleic acid encoding any one of the ABCC12 polypeptides according to the invention is cultured in an appropriate cell culture medium under conditions that provide for expression of any one of the ABCC12 polypeptides by the cell.

20 Any of the methods previously described for the insertion of DNA fragments into a cloning vector may be used to construct expression vectors containing a gene consisting of appropriate transcriptional/translational control signals and the protein coding sequences. These methods may include *in vitro* recombinant DNA and synthetic techniques and *in vivo* recombination (genetic recombination).

25 Expression of ABCC12 polypeptides may be controlled by any promoter/enhancer element known in the art, but these regulatory elements must be functional in the host selected for expression. Promoters which may be used to control ABCC12 gene expression include, but are not limited to, the SV40 early promoter region (Benoist and Chambon, 1981 *Nature* 290:304-310), the promoter contained in the 3' long terminal repeat of Rous sarcoma virus
30 (Yamamoto, et al., 1980 *Cell* 22:787-797), the herpes thymidine kinase promoter (Wagner et al., 1981 *Proc. Natl. Acad. Sci. U.S.A.* 78:1441-1445), the regulatory sequences of the metallothionein gene (Brinster et al., 1982 *Nature* 296:39-42); prokaryotic expression vectors

such as the β -lactamase promoter (Villa-Kamaroff, et al., 1978 Proc. Natl. Acad. Sci. U.S.A. 75:3727-3731), or the *tac* promoter (DeBoer, et al., 1983 Proc. Natl. Acad. Sci. U.S.A. 80:21-25); see also "Useful proteins from recombinant bacteria" in Scientific American, 1980, 242:74-94; promoter elements from yeast or other fungi such as the Gal 4 promoter, the ADC (alcohol dehydrogenase) promoter, PGK (phosphoglycerol kinase) promoter, alkaline phosphatase promoter; and the animal transcriptional control regions, which exhibit tissue specificity and have been utilized in transgenic animals: elastase I gene control region which is active in pancreatic acinar cells (Swift et al., 1984 Cell 38:639-646; Ornitz et al., 1986 Cold Spring Harbor Symp. Quant. Biol. 50:399-409; MacDonald, 1987); insulin gene control region which is active in pancreatic beta cells (Hanahan, 1985 Nature: 315:115-122), immunoglobulin gene control region which is active in lymphoid cells (Grosschedl et al., 1984 Cell 38:647-658; Adames et al., 1985 Nature 318:533-538; Alexander et al., 1987 Mol. Cell. Biol. 7:1436-1444), mouse mammary tumor virus control region which is active in testicular, breast, lymphoid and mast cells (Leder et al., 1986 Cell 45:485-495), albumin gene control region which is active in liver (Pinkert et al., 1987 Genes and Devel. 1:268-276), alpha-fetoprotein gene control region which is active in liver (Krumlauf et al., 1985 Mol. Cell. Biol. 5:1639-1648; Hammer et al., 1987 Science 235:53-58), alpha 1-antitrypsin gene control region which is active in the liver (Kelsey et al., 1987 Genes and Devel. 1:161-171) beta-globin gene control region which is active in myeloid cells (Mogam et al., 1985 Nature 315:338-340; Kollias et al., 1986 Cell 46:89-94), myelin basic protein gene control region which is active in oligodendrocyte cells in the brain (Readhead et al., 1987 Cell 48:703-712), myosin light chain-2 gene control region which is active in skeletal muscle (Sani, 1985 Nature 314:283-286), and gonadotropic releasing hormone gene control region which is active in the hypothalamus (Mason et al., 1986 Science 234:1372-1378).

Expression vectors containing a nucleic acid encoding one of the ABCC12 polypeptides of the invention can be identified by five general approaches: (a) polymerase chain reaction (PCR) amplification of the desired plasmid DNA or specific mRNA, (b) nucleic acid hybridization, (c) presence or absence of selection marker gene functions, (d) analyses with appropriate restriction endonucleases, and (e) expression of inserted sequences. In the first approach, the nucleic acids can be amplified by PCR to provide for detection of the amplified product. In the second approach, the presence of a foreign gene inserted in an expression vector can be detected by nucleic acid hybridization using probes comprising

sequences that are homologous to an inserted marker gene. In the third approach, the recombinant vector/host system can be identified and selected based upon the presence or absence of certain "selection marker" gene functions (e.g., b-galactosidase activity, thymidine kinase activity, resistance to antibiotics, transformation phenotype, occlusion body formation in baculovirus, etc.) caused by the insertion of foreign genes in the vector. In another example, if the nucleic acid encoding any one of the ABCC12 polypeptides is inserted within the "selection marker" gene sequence of the vector, recombinants containing the ABCC12 nucleic acids can be identified by the absence of the ABCC12 gene functions. In the fourth approach, recombinant expression vectors are identified by digestion with appropriate restriction enzymes. In the fifth approach, recombinant expression vectors can be identified by assaying for the activity, biochemical, or immunological characteristics of the gene product expressed by the recombinant, provided that the expressed protein assumes a functionally active conformation.

A wide variety of host/expression vector combinations may be employed in expressing the nucleic acids of this invention. Useful expression vectors, for example, may consist of segments of chromosomal, non-chromosomal and synthetic DNA sequences. Suitable vectors include derivatives of SV40 and known bacterial plasmids, e.g., *Escherichia coli* plasmids col E1, pCR1, pBR322, pMal-C2, pET, pGEX (Smith *et al.*, 1988, Gene 67:31-40), pMB9 and their derivatives, plasmids such as RP4; phage DNAs, e.g., the numerous derivatives of phage 1, e.g., NM989, and other phage DNA, e.g., M13 and filamentous single stranded phage DNA; yeast plasmids such as the 2m plasmid or derivatives thereof; vectors useful in eukaryotic cells, such as vectors useful in insect or mammalian cells; vectors derived from combinations of plasmids and phage DNAs, such as plasmids that have been modified to employ phage DNA or other expression control sequences; and the like.

For example, in a baculovirus expression systems, both non-fusion transfer vectors, such as but not limited to pVL941 (*Bam*H1 cloning site; Summers), pVL1393 (*Bam*H1, *Sma*I, *Xba*I, *Eco*R1, *Not*I, *Xma*III, *Bgl*II, and *Pst*I cloning site; Invitrogen), pVL1392 (*Bgl*II, *Pst*I, *Not*I, *Xma*III, *Eco*RI, *Xba*I, *Sma*I, and *Bam*H1 cloning site; Summers and Invitrogen), and pBlueBacIII (*Bam*H1, *Bgl*II, *Pst*I, *Nco*I, and *Hind*III cloning site, with blue/white recombinant screening possible; Invitrogen), and fusion transfer vectors, such as but not limited to pAc700 (*Bam*H1 and *Kpn*I cloning site, in which the *Bam*H1 recognition site begins with the initiation codon; Summers), pAc701 and pAc702 (same as pAc700, with different reading frames), pAc360 (*Bam*H1 cloning site 36 base pairs downstream of a polyhedrin initiation codon;

Invitrogen(195)), and pBlueBacHisA, B, C (three different reading frames, with *Bam*H1, *Bgl*II, *Pst*I, *Nco*I, and *Hind*III cloning site, an N-terminal peptide for ProBond purification, and blue/white recombinant screening of plaques; Invitrogen (220) can be used.

Mammalian expression vectors contemplated for use in the invention include vectors
 5 with inducible promoters, such as the dihydrofolate reductase (DHFR) promoter, *e.g.*, any expression vector with a *DHFR* expression vector, or a *DHFR*/methotrexate co-amplification vector, such as pED (*Pst*I, *Sal*I, *Sba*I, *Sma*I, and *Eco*RI cloning site, with the vector expressing both the cloned gene and *DHFR*; See, Kaufman, *Current Protocols in Molecular Biology*, 16.12 (1991). Alternatively, a glutamine synthetase/methionine sulfoximine co-amplification
 10 vector, such as pEE14 (*Hind*III, *Xba*I, *Sma*I, *Sba*I, *Eco*RI, and *Bcl*I cloning site, in which the vector expresses glutamine synthase and the cloned gene; Celltech). In another embodiment, a vector that directs episomal expression under control of Epstein Barr Virus (EBV) can be used, such as pREP4 (*Bam*H1, *Sfi*I, *Xho*I, *Not*I, *Nhe*I, *Hind*III, *Nhe*I, *Pvu*II, and *Kpn*I cloning
 15 site, constitutive RSV-LTR promoter, hygromycin selectable marker; Invitrogen), pCEP4 (*Bam*H1, *Sfi*I, *Xho*I, *Not*I, *Nhe*I, *Hind*III, *Nhe*I, *Pvu*II, and *Kpn*I cloning site, constitutive hCMV immediate early gene, hygromycin selectable marker; Invitrogen), pMEP4 (*Kpn*I, *Pvu*I, *Nhe*I, *Hind*III, *Not*I, *Xho*I, *Sfi*I, *Bam*H1 cloning site, inducible methallothionein IIa gene promoter, hygromycin selectable marker: Invitrogen), pREP8 (*Bam*H1, *Xho*I, *Not*I, *Hind*III, *Nhe*I, and *Kpn*I cloning site, RSV-LTR promoter, histidinol selectable marker; Invitrogen),
 20 pREP9 (*Kpn*I, *Nhe*I, *Hind*III, *Not*I, *Xho*I, *Sfi*I, and *Bam*HI cloning site, RSV-LTR promoter, G418 selectable marker; Invitrogen), and pEBVHis (RSV-LTR promoter, hygromycin selectable marker, N-terminal peptide purifiable via ProBond resin and cleaved by enterokinase; Invitrogen). Selectable mammalian expression vectors for use in the invention include pRc/CMV (*Hind*III, *Bst*XI, *Not*I, *Sba*I, and *Apa*I cloning site, G418 selection;
 25 Invitrogen), pRc/RSV (*Hind*III, *Spe*I, *Bst*XI, *Not*I, *Xba*I cloning site, G418 selection; Invitrogen), and others. Vaccinia virus mammalian expression vectors (*see*, Kaufman, 1991, *supra*) for use according to the invention include but are not limited to pSC11 (*Sma*I cloning site, TK- and b-gal selection), pMJ601 (*Sal*I, *Sma*I, *Afl*I, *Nar*I, *Bsp*MII, *Bam*HI, *Apa*I, *Nhe*I, *Sac*II, *Kpn*I, and *Hind*III cloning site; TK- and b-gal selection), and pTKgptF1S (*Eco*RI, *Pst*I,
 30 *Sal*I, *Acc*I, *Hind*II, *Sba*I, *Bam*HI, and *Hpa* cloning site, TK or XPRT selection).

Yeast expression systems can also be used according to the invention to express the any one of the ABCC12 polypeptides. For example, the non-fusion pYES2 vector (*Xba*I, *Sph*I, *Sho*I, *Not*I, *Gst*XI, *Eco*RI, *Bst*XI, *Bam*H1, *Sac*I, *Kpn*1, and *Hind*III cloning sit;

Invitrogen) or the fusion pYESHisA, B, C (*Xba*I, *Sph*I, *Sho*I, *Not*I, *Bst*XI, *Eco*RI, *Bam*HI, *Sac*I, *Kpn*I, and *Hind*III cloning site, N-terminal peptide purified with ProBond resin and cleaved with enterokinase; Invitrogen), to mention just two, can be employed according to the invention.

5 Once a particular recombinant DNA molecule is identified and isolated, several methods known in the art may be used to propagate it. Once a suitable host system and growth conditions are established, recombinant expression vectors can be propagated and prepared in quantity. As previously explained, the expression vectors which can be used include, but are not limited to, the following vectors or their derivatives: human or animal
10 viruses such as vaccinia virus or adenovirus; insect viruses such as baculovirus; yeast vectors; bacteriophage vectors (*e.g.*, lambda), and plasmid and cosmid DNA vectors, to name but a few.

 In addition, a host cell strain may be chosen which modulates the expression of the inserted sequences, or modifies and processes the gene product in the specific fashion desired.
15 Different host cells have characteristic and specific mechanisms for the translational and post-translational processing and modification (*e.g.*, glycosylation, cleavage for example of the signal sequence) of proteins. Appropriate cell lines or host systems can be chosen to ensure the desired modification and processing of the foreign proteins expressed. For example, expression in a bacterial system can be used to produce a nonglycosylated core protein
20 product. However, the transmembrane ABCC12 proteins expressed in bacteria may not be properly folded. Expression in yeast can produce a glycosylated product. Expression in eukaryotic cells can increase the likelihood of "native" glycosylation and folding of a heterologous protein. Moreover, expression in mammalian cells can provide a tool for reconstituting, or constituting, ABCC12 activity. Furthermore, different vector/host
25 expression systems may affect processing reactions, such as proteolytic cleavages, to a different extent.

 Vectors are introduced into the desired host cells by methods known in the art, *e.g.*, transfection, electroporation, microinjection, transduction, cell fusion, DEAE dextran, calcium phosphate precipitation, lipofection (lysosome fusion), use of a gene gun, or a DNA vector
30 transporter (see, *e.g.*, Wu et al., 1992, J. Biol. Chem. 267:963-967; Wu and Wu, 1988, J. Biol. Chem. 263:14621-14624; Hartmut et al., Canadian Patent Application No. 2,012,311, filed March 15, 1990).

A cell has been "transfected" by exogenous or heterologous DNA when such DNA has been introduced inside the cell. A cell has been "transformed" by exogenous or heterologous DNA when the transfected DNA effects a phenotypic change. Preferably, the transforming DNA should be integrated (covalently linked) into chromosomal DNA making up the genome
5 of the cell.

A recombinant marker protein expressed as an integral membrane protein can be isolated and purified by standard methods. Generally, the integral membrane protein can be obtained by lysing the membrane with detergents, such as but not limited to, sodium dodecyl sulfate (SDS), Triton X-100 polyoxyethylene ester, Ipagel/nonidet P-40 (NP-40)
10 (octylphenoxy)-polyethoxyethanol, digoxin, sodium deoxycholate, and the like, including mixtures thereof. Solubilization can be enhanced by sonication of the suspension. Soluble forms of the protein can be obtained by collecting culture fluid, or solubilizing inclusion bodies, *e.g.*, by treatment with detergent, and if desired sonication or other mechanical processes, as described above. The solubilized or soluble protein can be isolated using
15 various techniques, such as polyacrylamide gel electrophoresis (PAGE), isoelectric focusing, 2-dimensional gel electrophoresis, chromatography (*e.g.*, ion exchange, affinity, immunoaffinity, and sizing column chromatography), centrifugation, differential solubility, immunoprecipitation, or by any other standard technique for the purification of proteins.

Alternatively, a nucleic acid or vector according to the invention can be introduced *in vivo* by lipofection. For the past decade, there has been increasing use of liposomes for encapsulation and transfection of nucleic acids *in vitro*. Synthetic cationic lipids designed to limit the difficulties and dangers encountered with liposome mediated transfection can be used to prepare liposomes for *in vivo* transfection of a gene encoding a marker (Felgner, et. al. (1987. PNAS 84/7413); Mackey, et al. (1988. Proc. Natl. Acad. Sci. USA 85 :8027-8031);
25 Ulmer et al. (1993. Science 259 :1745-1748). The use of cationic lipids may promote encapsulation of negatively charged nucleic acids, and also promote fusion with negatively charged cell membranes (Felgner and Ringold, (1989. Science 337:387-388)). Particularly useful lipid compounds and compositions for transfer of nucleic acids are described in International Patent Publications WO95/18863 and WO96/17823, and in U.S. Patent No.
30 5,459,127. The use of lipofection to introduce exogenous genes into the specific organs *in vivo* has certain practical advantages. Molecular targeting of liposomes to specific cells represents one area of benefit. It is clear that directing transfection to particular cell types would be particularly preferred in a tissue with cellular heterogeneity, such as pancreas, liver,

kidney, and the brain. Lipids may be chemically coupled to other molecules for the purpose of targeting [see Mackey, et. al., *supra*]. Targeted peptides, *e.g.*, hormones or neurotransmitters, and proteins such as antibodies, or non-peptide molecules could be coupled to liposomes chemically.

5 Other molecules are also useful for facilitating transfection of a nucleic acid *in vivo*, such as a cationic oligopeptide (*e.g.*, International Patent Publication WO95/21931), peptides derived from DNA binding proteins (*e.g.*, International Patent Publication WO96/25508), or a cationic polymer (*e.g.*, International Patent Publication WO95/21931).

10 It is also possible to introduce the vector *in vivo* as a naked DNA plasmid (see U.S. Patents 5,693,622, 5,589,466 and 5,580,859). Naked DNA vectors for gene therapy can be introduced into the desired host cells by methods known in the art, *e.g.*, transfection, electroporation, microinjection, transduction, cell fusion, DEAE dextran, calcium phosphate precipitation, use of a gene gun, or use of a DNA vector transporter (see, Wu et al., 1992, *supra*; Wu and Wu, 1988, *supra*; Hartmut et al., Canadian Patent Application No. 2,012,311, 15 filed March 15, 1990; Williams et al., 1991, Proc. Natl. Acad. Sci. USA 88:2726-2730). Receptor-mediated DNA delivery approaches can also be used (Curiel et al., 1992, Hum. Gene Ther. 3:147-154; Wu and Wu, 1987, J. Biol. Chem. 262:4429-4432).

“Pharmaceutically acceptable vehicle or excipient ” includes diluents and fillers which are pharmaceutically acceptable for method of administration, are sterile, and may be aqueous 20 or oleaginous suspensions formulated using suitable dispersing or wetting agents and suspending agents. The particular pharmaceutically acceptable carrier and the ratio of active compound to carrier are determined by the solubility and chemical properties of the composition, the particular mode of administration, and standard pharmaceutical practice.

Any nucleic acid, polypeptide, vector, or host cell of the invention will preferably be 25 introduced *in vivo* in a pharmaceutically acceptable vehicle or excipient. The phrase "pharmaceutically acceptable" refers to molecular entities and compositions that are physiologically tolerable and do not typically produce an allergic or similar untoward reaction, such as gastric upset, dizziness and the like, when administered to a human. Preferably, as used herein, the term "pharmaceutically acceptable" means approved by a regulatory agency 30 of the Federal or a state government or listed in the U.S. Pharmacopeia or other generally recognized pharmacopeia for use in animals, and more particularly in humans. The term "excipient" refers to a diluent, adjuvant, excipient, or vehicle with which the compound is administered. Such pharmaceutical carriers can be sterile liquids, such as water and oils,

including those of petroleum, animal, vegetable or synthetic origin, such as peanut oil, soybean oil, mineral oil, sesame oil and the like. Water or aqueous solution saline solutions and aqueous dextrose and glycerol solutions are preferably employed as excipients, particularly for injectable solutions. Suitable pharmaceutical excipients are described in

5 "Remington's Pharmaceutical Sciences" by E.W. Martin.

Naturally, the invention contemplates delivery of a vector that will express a therapeutically effective amount of the ABCC12 polypeptide for gene therapy applications. The phrase "therapeutically effective amount" is used herein to mean an amount sufficient to reduce by at least about 15 percent, preferably by at least 50 percent, more preferably by at

10 least 90 percent, and still more preferably prevent, a clinically significant deficit in the activity, function and response of the host. Alternatively, a therapeutically effective amount is sufficient to cause an improvement in a clinically significant condition in the host.

NUCLEIC ACIDS OF THE ABCC12 GENE

15 The applicants have identified a novel human ABCC-like gene, designated ABCC12. The applicants have also determined that this novel gene is located on the region of chromosome 16q12 (figure 2).

The applicants have further determined transcript sequences that correspond to the coding sequences (CDS) of the short and long ABCC12 proteins isoforms. According to the

20 invention, the ABCC12 gene comprises 29 exons and 28 introns. All exons were flanked by GT and AG dinucleotides consistent with the consensus sequences for splice junctions in eukaryotic genes (Table 1). The applicants have also identified two ABCC12 transcripts that differ by the length and sequence of exon 15 as shown in Table 1. Exon 15 of the short transcript comprises 76 nucleotides as set forth in SEQ ID No.: 17, whereas Exon 15 of the

25 long transcript has 9 additional nucleotides at the 3' end, as set forth in SEQ ID No: 32.

The short transcript of the human novel ABCC12 gene thus consists of 4273 nucleotides as set forth in SEQ ID No: 1, while the long transcript is as set forth in SEQ ID No.: 2.

30 **Table 1 : Splice sites sequences and exon sizes of ABCC12**

Exon	Size (bp)	Splice acceptor	Splice donor
1	119	Not determined	CCTGTGCAAGgtaagtcaga
2	156	ttgtctgcagGTTAGCACCC	ATGCCAAAAGgtaccaggat
3	152	ttcatcacagATTTCGAGTC	GGGCCGGTGAgcgccgcagc

4	230	ttacagacagTTCTCATTC	TGTTGGCGAGgtaagctggc
5	174	ttctttccagGTGCTCAATA	ACCCGTCCAGgtaacggcat
6	148	ttgatttcagATGTTTATGG	ACTATCCAAGgtaggacaag
7	149	tattttgcagATATAAGAAG	CGCACCCGTGgtaagagctg
8	108	tgttcttcagGCATTTAGTG	GAGAATGAAGgtataactaa
9	279	ttaatcttagAAAATTCTCA	GGTGAGAAAGgtgggtgtgt
10	72	tctctggcagGGGAAGATCT	CCTAGGACAGgtaagctgtg
11	125	gttgttccagATGCAGCTGC	ATCACCAAAGgtaatatataa
12	73	gcaccaacagGTATCAGCAC	CCTGACTGAGgtgagcgggg
13	204	ctgtccacagATTGGGGAGC	CCAGCTACAGgtgatgggac
14	135	acttctgcagTTCTTAGAGT	GCAGTTCAAGgtaactcaca
15	76 or 85	ttgtctccagGATCCTGAAC	GAAGATGCTGgtataatcgg or GGTATAATCGgttagaatcc
16	72	ctcaccctagTTTTGGCTCC	GACACAAAAGgtatttacca
17	90	gtctccacagTTCCTGAGCA	GCTTCTGGAGgttcagtata
18	104	cctcttgcagGGTACCTCCT	GGGCTCACGGgtgagtttcc
19	198	ttctccaaagATGACCTGTG	GTTTGATAAGgtagggccac
20	227	ttctccacagATCTTAAAGA	TTCTGTTACGgtaggcccat
21	138	tttcttccagCATTTTCCAC	GCATCACCTAgtgagtccca
22	157	aaaactccagTCACCTCCTC	CATCATCCAGgtaatgcctg
23	90	ttttcaacagCTGAGCGGAC	ATACATTTTCGgttaagaaatt
24	190	tcctttacagACCTGTGTTC	ACAGGTTCCGgtgaggacaa
25	160	tggttcccagGAAAGTCATC	GTACAGTAAGgtagctgttt
26	79	ttcattgcagGTACAACTTG	GAGAGACACAgtaggtctct
27	114	tgttttgtagATAATGAAAC	TAATTCAAAGgtaagaaaac
28	165	tcctccacagATCATTCTCC	AAATGGGAAGgtataggaag
29	87+3'UTR	tgactttcagGTGATTGAGT	Not determined

The applicants have characterized exonic sequences of a novel human ABCC12 gene, which are particularly useful according to the invention for the production of various means of detection of the corresponding ABCC12 gene, or nucleotide expression products in a sample.

Several exons of ABCC12 gene have been characterized by their nucleotide sequence and are identified in Tables 2 and 3. Exon 15 only differs in Tables 2 and 3. The human ABCC12 gene consists of 29 exons, having sizes which range from 72 to 279 bp. A differential splicing generates a first short isoform having an Exon of 76 nucleotides as set forth in SEQ ID No.:17, and a second long isoform having an Exon 15 of 85 nucleotides, as set forth in SEQ ID NO: 32. Of the 28 introns in the ABCC12 gene, 16 are class 0 (where the splice occurs between codons), six are class 1 (where the codon is interrupted between the first and the second nucleotide), and six are class 2 (where the splice occurs between the second and the third nucleotide of the codon).

Table 2 : Human ABCC12 exons and introns DNA (short isoform)

SEQ ID NO:	Exon or intron number	Exon start in mRNA	Exon stop in mRNA	exon start in genomic fragment	exon stop in genomic fragment	length of exon	intron start in fragment	intron stop in fragment	Length of intron
3	1	1	119	111347	111469	119	111466	113705	2240

4	2	120	275	113706	113865	156	113862	116417	2556
5	3	276	423	116418	116569	152	116566	116850	285
6	4	424	657	116851	117080	230	117085	118434	1350
7	5	658	831	118435	118608	174	118609	119395	787
8	6	832	979	119396	119543	148	119544	123935	4392
9	7	980	1128	123936	124084	149	124085	126875	2791
10	8	1129	1236	126876	126983	108	126984	129033	2050
11	9	1237	1515	129034	129312	279	129313	133486	4174
12	10	1516	1587	133487	133558	72	133559	135930	2372
13	11	1588	1712	135931	136055	125	136056	-	-
14	12	1713	1785	3997	4069	73	4070	5711	1642
15	13	1786	1989	5712	5915	204	5916	9419	3504
16	14	1990	2124	9420	9554	135	9555	9667	113
17	15	2125	2200	9668	9743	76	9744	9822	79
18	16	2201	2272	9823	9894	72	9895	12800	2906
19	17	2273	2362	12801	12890	90	12891	13904	1014
20	18	2363	2466	13905	14008	104	14009	15993	1985
21	19	2467	2664	15994	16191	198	16192	16961	770
22	20	2665	2891	16962	17188	227	17189	20320	3132
23	21	2892	3029	20321	20458	138	20459	24427	3969
24	22	3030	3186	24428	24584	157	24585	30120	5536
25	23	3187	3276	30121	30210	90	30211	32595	2385
26	24	3277	3466	32596	32785	190	32786	33244	459
27	25	3467	3626	33245	33404	160	33405	34510	1106
28	26	3627	3705	34511	34589	79	34590	35623	1034
29	27	3706	3819	35624	35737	114	35738	37256	1519
30	28	3820	3984	37257	37421	165	37422	37528	107
31	29	3985	4273	37529	37817	289	37818	-	-

Table 3 : Human ABCC12 exons and introns DNA (long isoform)

SEQ ID NO:	Exon or intron number	Exon start in mRNA	Exon stop in mRNA	exon start in genomic fragment	exon stop in genomic fragment	length of exon	intron start in fragment	intron stop in fragment	Length of intron
3	1	1	119	111347	111465	119	111466	113705	2240
4	2	120	275	113706	113861	156	113862	116417	2556
5	3	276	423	116418	116569	152	116566	116850	285
6	4	424	657	116851	117080	230	117085	118434	1350
7	5	658	831	118435	118608	174	118609	119395	787
8	6	832	979	119396	119543	148	119544	123935	4392
9	7	980	1128	123936	124084	149	124085	126875	2791
10	8	1129	1236	126876	126983	108	126984	129033	2050
11	9	1237	1515	129034	129312	279	129313	133486	4174
12	10	1516	1587	133487	133558	72	133559	135930	2372
13	11	1588	1712	135931	136055	125	136056	-	-
14	12	1713	1785	3997	4069	73	4070	5711	1642
15	13	1786	1989	5712	5915	204	5916	9419	3504
16	14	1990	2124	9420	9554	135	9555	9667	113
32	15	2125	2209	9668	9752	85	9753	9822	70

18	16	2210	2281	9823	9894	72	9895	12800	2906
19	17	2282	2371	12801	12890	90	12891	13904	1014
20	18	2372	2475	13905	14008	104	14009	15993	1985
21	19	2476	2673	15994	16191	198	16192	16961	770
22	20	2674	2900	16962	17188	227	17189	20320	3132
23	21	2901	3038	20321	20458	138	20459	24427	3969
24	22	3039	3195	24428	24584	157	24585	30120	5536
25	23	3196	3285	30121	30210	90	30211	32595	2385
26	24	3286	3475	32596	32785	190	32786	33244	459
27	25	3476	3635	33245	33404	160	33405	34510	1106
28	26	3636	3714	34511	34589	79	34590	35623	1034
29	27	3715	3828	35624	35737	114	35738	37256	1519
30	28	3829	3993	37257	37421	165	37422	37528	107
31	29	3994	4282	37529	37817	289	37818	-	-

Thus the present invention also relates to a nucleic acid comprising any one of SEQ ID NOs: 1-32, or a complementary sequence thereof.

The invention also relates to a nucleic acid comprising a nucleotide sequence as depicted in any one of SEQ ID NOs: 1-32, or a complementary nucleotide sequence thereof.

The invention also relates to a nucleic acid comprising at least 8 consecutive nucleotides of any one of SEQ ID NOs: 1-32, or a complementary nucleotide sequence.

The subject of the invention is, in addition, a nucleic acid having at least 80% nucleotide identity with a nucleic acid comprising any one of SEQ ID NOs: 1-32, or a complementary nucleotide sequence thereof.

The invention also relates to a nucleic acid having at least 85%, preferably 90%, more preferably 95% and still more preferably 98% nucleotide identity with a nucleic acid comprising any one of SEQ ID NOs: 1-32.

The invention also relates to a nucleic acid hybridizing, under high stringency conditions, with a nucleic acid comprising any one of SEQ ID NOs: 1-32, or a complementary nucleotide sequence thereof.

cDNA MOLECULE ENCODING THE SHORT AND LONG ISOFORMS OF ABCC12 PROTEINS

The applicants have further determined the cDNA sequences and the coding sequences (CDS) corresponding to the human ABCC12 gene, which encode the short and long human corresponding proteins isoforms (Example 2).

The cDNA molecule of the novel human ABCC12 gene consists of 4273 nucleotides as set forth in SEQ ID NO: 1 and contains a 4071 nucleotide coding sequence corresponding

to a 1356 amino acids (aa) ABCC12 polypeptide isoform (SEQ ID NO: 33) produced in subjects not affected by disorders of parosysmal kinesigenic choreoathetosis. The cDNA molecule of the novel human ABCC12 gene having the nucleotide sequence as set forth in SEQ ID NO: 1 comprises an open reading frame beginning from the nucleotide at position 1
5 (base A of the ATG codon for initiation of translation) to the nucleotide at position 4071 (base A of the TAA stop codon) of SEQ ID NO:1, which encodes a full length ABCC12 polypeptide of 1356 amino acids of sequence SEQ ID NO:33.

The long form of cDNA molecule of the novel human ABCC12 gene consist of 4282 nucleotides as set forth in SEQ ID No: 2 and contains a 4080 nucleotide coding sequence
10 corresponding to a 1359 amino acids (aa) ABCC12 polypeptide isoform (SEQ ID No: 34) produced in subjects not affected by disorders of paroxysmal kinesigenic choreoathetosis. The cDNA coding the long isoform of the ABCC12 protein, having the nucleotide sequence as set forth in SEQ ID No: 2, comprises an open reading frame beginning from the nucleotide 1 at position 1 (base A of the ATG codon for initiation of the translation) to the nucleotide at
15 position 4080 (base A of the TAA stop codon) of SEQ ID No: 2, which encodes the long isoform of the ABCC12 polypeptide of 1359 amino acids of sequence ID No: 34.

The present invention is thus directed to a nucleic acid comprising SEQ ID NO: 1 and 2, or a complementary nucleotide sequence thereof.

The invention also relates to a nucleic acid comprising a nucleotide sequence as
20 depicted in SEQ ID NO :1 and 2, or a complementary nucleotide sequence thereof.

The invention also relates to a nucleic acid comprising at least eight consecutive nucleotides of SEQ ID NO: 1 and 2, or a complementary nucleotide sequence thereof.

The subject of the invention is also a nucleic acid having at least 80% nucleotide identity with a nucleic acid comprising nucleotides of SEQ ID NO: 1-2, or a nucleic acid
25 having a complementary nucleotide sequence thereof .

The invention also relates to a nucleic acid having at least 85%, preferably 90%, more preferably 95% and still more preferably 98% nucleotide identity with a nucleic acid comprising a nucleotide sequence of SEQ ID NO: 1-2, or a complementary nucleotide sequence thereof .

30 Another subject of the invention is a nucleic acid hybridizing, under high stringency conditions, with a nucleic acid comprising nucleotide sequence of SEQ ID NO: 1-2, or a nucleic acid having a complementary nucleotide sequence thereof.

The invention also relates to a nucleic acid encoding a polypeptide comprising an amino acid sequence of SEQ ID NO: 33 or 34.

The invention relates to a nucleic acid encoding a polypeptide comprising an amino acid sequence as depicted in SEQ ID NO: 33 or 34.

5 The invention also relates to a polypeptide comprising amino acid sequence of SEQ ID NO: 33 or 34.

The invention also relates to a polypeptide comprising amino acid sequence as depicted in SEQ ID NO: 33 or 34.

10 The invention also relates to a polypeptide comprising an amino acid sequence having at least 80% amino acid identity with a polypeptide comprising an amino acid sequence of SEQ ID NO: 33 or 34, or a peptide fragment thereof.

The invention also relates to a polypeptide having at least 85%, preferably 90%, more preferably 95% and still more preferably 98% amino acid identity with a polypeptide comprising an amino acid sequence of SEQ ID NO: 33 or 34.

15 Preferably, a polypeptide according to the invention will have a length of 4, 5 to 10, 15, 18 or 20 to 25, 35, 40, 50, 70, 80, 100 or 200 consecutive amino acids of a polypeptide according to the invention comprising an amino acid sequence of SEQ ID NO: 33 or 34.

Topology predictions based on hydropathy profiles and comparison with other known ABC transporters, suggest that the encoded ABCC12 proteins isoforms are full
20 ABC transporters containing two ATP-binding domains (including Walker A and B domains, and signature motifs) and two transmembrane domains (Figure 1). The amino acid sequence of ABCC12 is 47% identical to the human ABCC5 protein, and 37% to human ABCC4. The ABCC12 protein, like ABCC4 and ABCC5 proteins, is smaller than another well-known member of the subgroup, ABCC1 (MRP1), appearing to lack the extra
25 N-terminal domain (Borst et al., *J Natl Cancer Inst*, 2000, 92, 1295-302), which has been shown, however, not to be required for the transport function (Bakos et al., *J. Biol. Chem.*, 1998, 273, 32167-75).

Table 4: Homology / Identity percentages between the amino acid sequences of
30 **ABCC11, ABCC5, ABCC4, ABCC1, and ABCA1 along the entire sequence**

	ABCC5	ABCC1	ABCC4	ABC-A1	ABCC12
ABCC5	100/100		49		
ABCC1	49/38	100/100			
ABCC4	49/38	52/41	100/100		
ABC-A1	-	-	-	100/100	
ABCC12	57/47	48/36	49/37	-	100/100

Alignment of the amino acid sequences of ABCC12, ABCC4, and ABCC5 genes
 5 reveals an identity ranging from 49 to 41% along the entire sequence (Table 4 and Figure 1).

Phylogenetic analysis of the ABCC subfamily proteins clearly demonstrates a close evolutionary relationship of the ABCC12 gene with the ABCC5 gene (Figure 5). In addition, the analysis of the tree suggests a recent duplication of the ABCC8 and ABCC9
 10 genes, while ABCC10 seems to be one of the first genes to separate from the common ancestor. ABCC1, ABCC2, ABCC3, and ABCC6 genes constitute a well-defined sub-cluster, while the ABCC4 and CFTR (ABCC7) genes form another reliable subset despite apparent early divergence.

15 NUCLEOTIDE PROBES AND PRIMERS

Nucleotide probes and primers hybridizing with a nucleic acid (genomic DNA, messenger RNA, cDNA) according to the invention also form part of the invention.

According to the invention, nucleic acid fragments derived from a polynucleotide comprising any one of SEQ ID NOs: 1-32 or of a complementary nucleotide sequence are
 20 useful for the detection of the presence of at least one copy of a nucleotide sequence of the ABCC12 gene or of a fragment or of a variant (containing a mutation or a polymorphism) thereof in a sample.

The nucleotide probes or primers according to the invention comprise a nucleotide sequence comprising any one of SEQ ID NOs: 1-32, or a complementary nucleotide sequence
 25 thereof.

The nucleotide probes or primers according to the invention comprise at least 8 consecutive nucleotides of a nucleic acid comprising any one of SEQ ID NOs: 1-32, or a complementary nucleotide sequence.

Preferably, nucleotide probes or primers according to the invention have a length of
 30 10, 12, 15, 18 or 20 to 25, 35, 40, 50, 70, 80, 100, 200, 500, 1000, 1500 consecutive nucleotides of a nucleic acid according to the invention, in particular of a nucleic acid comprising any one of SEQ ID NOs: 1-32, or a complementary nucleotide sequence.

Alternatively, a nucleotide probe or primer according to the invention consists of and/or comprise the fragments having a length of 12, 15, 18, 20, 25, 35, 40, 50, 100, 200, 500, 1000, 1500 consecutive nucleotides of a nucleic acid according to the invention, more particularly of a nucleic acid comprising any one of SEQ ID NOs: 1-32, or a complementary nucleotide sequence.

The definition of a nucleotide probe or primer according to the invention therefore covers oligonucleotides which hybridize, under the high stringency hybridization conditions defined above, with a nucleic acid comprising any one of SEQ ID NOs: 1-32, or a complementary nucleotide sequence.

According to a preferred embodiment, a nucleotide primer according to the invention comprises a nucleotide sequence of any one of SEQ ID NOs: 35-46 or a complementary nucleic acid sequence thereof.

Examples of primers and pairs of primers which make it possible to amplify various regions of the ABCC12 gene are presented in Table 5 below. The location of each primer of SEQ ID NOs: 35-46 within SEQ ID NO: 1 and 2, and its hybridizing region is indicated in Table 5. The abbreviation "Comp" refers to the complementary nucleic acid sequence.

Table 5: Primers for the amplification of nucleic fragments of the ABCC12 gene

SEQ ID NO:	NAME	PRIMERS	POSITION (short isoform)	POSITION (long isoform)
35	028397_A	TCCTTCGCCACATTTTCC	157-174	157-174
36	028397_B	ATTGAGCACCTCGCCAAC	comp 666-649	comp 666-649
37	028397_C	TTCTCATTACCAAATCCTCC	428-448	428-448
38	028397_D	ACATTAAACATGGCAATCACAC	comp 1157-1136	comp 1157-1136
39	028397_E	GTGTGATTGCCATGTTTAATGT	1136-1157	1136-1157
40	028397_G	GGAGTGCATTAAGAAGACGC	1929-1948	1929-1948
41	028397_H	CAGAGAGGAGGATGCCAT	comp 2643-2626	comp 2652-2635
42	028397_K	CACTGCAAGCATGGTGTTTC	2556-2574	2565-2583
43	028397_L	CTCATCGGTGTGACTCTCA	comp 3663-3645	comp 3672-3654
44	028397_O	TTTGAGAGTCACACCGATGAGAT	3643-3665	3652-3674
45	028397_P	CCCAGAACCAACCCCAAG	comp 4273-4256	comp 4282-4265
46	028397_R	GGCTCTGTGAGATGAATAGG	4104-4123	4113-4132

According to a preferred embodiment, a nucleotide primer according to the invention comprises a nucleotide sequence of any one of SEQ ID NOs: 35-46, or a complementary nucleic acid sequence thereof.

A nucleotide primer or probe according to the invention may be prepared by any suitable method well known to persons skilled in the art, including by cloning and action of

restriction enzymes or by direct chemical synthesis according to techniques such as the phosphodiester method by Narang et al. (1979, *Methods Enzymol*, 68:90-98) or by Brown et al. (1979, *Methods Enzymol*, 68:109-151), the diethylphosphoramidite method by Beaucage et al. (1981, *Tetrahedron Lett*, 22: 1859-1862) or the technique on a solid support
5 described in EU patent No. EP 0,707,592.

Each of the nucleic acids according to the invention, including the oligonucleotide probes and primers described above, may be labeled, if desired, by incorporating a marker which can be detected by spectroscopic, photochemical, biochemical, immunochemical or chemical means. For example, such markers may consist of radioactive isotopes (^{32}P , ^{33}P , ^3H ,
10 ^{35}S), fluorescent molecules (5-bromodeoxyuridine, fluorescein, acetylaminofluorene, digoxigenin) or ligands such as biotin. The labeling of the probes is preferably carried out by incorporating labeled molecules into the polynucleotides by primer extension, or alternatively by addition to the 5' or 3' ends. Examples of nonradioactive labeling of nucleic acid fragments are described in particular in French patent No. 78 109 75 or in the articles by
15 Urdea et al. (1988, *Nucleic Acids Research*, 11:4937-4957) or Sanchez-Pescador et al. (1988, *J. Clin. Microbiol.*, 26(10):1934-1938).

Preferably, the nucleotide probes and primers according to the invention may have structural characteristics of the type to allow amplification of the signal, such as the probes described by Urdea et al. (1991, *Nucleic Acids Symp Ser.*, 24:197-200) or alternatively in
20 European patent No. EP-0,225,807 (CHIRON).

The oligonucleotide probes according to the invention may be used in particular in Southern-type hybridizations with the genomic DNA or alternatively in northern-type hybridizations with the corresponding messenger RNA when the expression of the corresponding transcript is sought in a sample.

25 The probes and primers according to the invention may also be used for the detection of products of PCR amplification or alternatively for the detection of mismatches.

Nucleotide probes or primers according to the invention may be immobilized on a solid support. Such solid supports are well known to persons skilled in the art and comprise surfaces of wells of microtiter plates, polystyrene beads, magnetic beads, nitrocellulose bands
30 or microparticles such as latex particles.

Consequently, the present invention also relates to a method of detecting the presence of a nucleic acid comprising a nucleotide sequence of any one of SEQ ID NOs: 1-32, or of a complementary nucleotide sequence, or a nucleic acid fragment or variant of any one of SEQ

ID NOs: 1-32, or of a complementary nucleotide sequence in a sample, said method comprising the steps of:

1) bringing one or more nucleotide probes or primers according to the invention into contact with the sample to be tested;

5 2) detecting the complex which may have formed between the probe(s) and the nucleic acid present in the sample.

According to a specific embodiment of the method of detection according to the invention, the oligonucleotide probes and primers are immobilized on a support.

According to another aspect, the oligonucleotide probes and primers comprise a
10 detectable marker.

The invention relates, in addition, to a box or kit for detecting the presence of a nucleic acid according to the invention in a sample, said box or kit comprising:

a) one or more nucleotide probe(s) or primer(s) as described above;

b) where appropriate, the reagents necessary for the hybridization reaction.

15 According to a first aspect, the detection box or kit is characterized in that the probe(s) or primer(s) are immobilized on a support.

According to a second aspect, the detection box or kit is characterized in that the oligonucleotide probes comprise a detectable marker.

According to a specific embodiment of the detection kit described above, such a kit
20 will comprise a plurality of oligonucleotide probes and/or primers in accordance with the invention which may be used to detect a target nucleic acid of interest or alternatively to detect mutations in the coding regions or the non-coding regions of the nucleic acids according to the invention, more particularly of nucleic acids comprising any one of SEQ ID NOs: 1-30, or a complementary nucleotide sequence.

25 Thus, the probes according to the invention, immobilized on a support, may be ordered into matrices such as "DNA chips". Such ordered matrices have in particular been described in US patent No. 5,143,854, in published PCT applications WO 90/15070 and WO 92/10092.

Support matrices on which oligonucleotide probes have been immobilized at a high density are for example described in US patent No. 5,412,087 and in published PCT
30 application WO 95/11995.

The nucleotide primers according to the invention may be used to amplify any one of the nucleic acids according to the invention, and more particularly a nucleic acid comprising a nucleotide sequence of any one of SEQ ID NOs: 1-32, or of a complementary nucleotide

sequence. Alternatively, the nucleotide primers according to the invention may be used to amplify a nucleic acid fragment or variant of any one of SEQ ID NOs: 1-32, or of a complementary nucleotide sequence.

In a particular embodiment, the nucleotide primers according to the invention may be used to amplify a nucleic acid comprising any one of SEQ ID NOs: 1-32, or as depicted in any one of SEQ ID NOs: 1-32, or of a complementary nucleotide sequence.

Another subject of the invention relates to a method of amplifying a nucleic acid according to the invention, and more particularly a nucleic acid comprising a) any one of SEQ ID NOs: 1-32, or a complementary nucleotide sequence, b) as depicted in any one of SEQ ID NOs: 1-32, or of a complementary nucleotide sequence, contained in a sample, said method comprising the steps of:

a) bringing the sample in which the presence of the target nucleic acid is suspected into contact with a pair of nucleotide primers whose hybridization position is located respectively on the 5' side and on the 3' side of the region of the target nucleic acid whose amplification is sought, in the presence of the reagents necessary for the amplification reaction; and

b) detecting the amplified nucleic acids.

To carry out the amplification method as defined above, use will be preferably made of any of the nucleotide primers described above.

The subject of the invention is, in addition, a box or kit for amplifying a nucleic acid according to the invention, and more particularly a nucleic acid comprising any one of SEQ ID NOs: 1-32, or a complementary nucleotide sequence, or as depicted in any one of SEQ ID NOs: 1-32, or of a complementary nucleotide sequence, said box or kit comprising:

a) a pair of nucleotide primers in accordance with the invention, whose hybridization position is located respectively on the 5' side and 3' side of the target nucleic acid whose amplification is sought; and optionally,

b) reagents necessary for the amplification reaction.

Such an amplification box or kit will preferably comprise at least one pair of nucleotide primers as described above.

The subject of the invention is, in addition, a box or kit for amplifying all or part of a nucleic acid comprising any one of SEQ ID NOs: 1-32, or a complementary nucleotide sequence, said box or kit comprising:

1) a pair of nucleotide primers in accordance with the invention, whose hybridization position is located respectively on the 5' side and 3' side of the target nucleic acid whose amplification is sought; and optionally,

2) reagents necessary for an amplification reaction.

5 Such an amplification box or kit will preferably comprise at least one pair of nucleotide primers as described above.

The invention also relates to a box or kit for detecting the presence of a nucleic acid according to the invention in a sample, said box or kit comprising:

a) one or more nucleotide probes according to the invention;

10 b) where appropriate, reagents necessary for a hybridization reaction.

According to a first aspect, the detection box or kit is characterized in that the nucleotide probe(s) and primer(s) are immobilized on a support.

According to a second aspect, the detection box or kit is characterized in that the nucleotide probe(s) and primer(s) comprise a detectable marker.

15 According to a specific embodiment of the detection kit described above, such a kit will comprise a plurality of oligonucleotide probes and/or primers in accordance with the invention which may be used to detect target nucleic acids of interest or alternatively to detect mutations in the coding regions or the non-coding regions of the nucleic acids according to the invention. According to preferred embodiment of the invention, the target nucleic acid
20 comprises a nucleotide sequence of any one of SEQ ID NOs: 1-32, or of a complementary nucleic acid sequence. Alternatively, the target nucleic acid is a nucleic acid fragment or variant of a nucleic acid comprising any one of SEQ ID NOs: 1-32, or of a complementary nucleotide sequence.

According to the present invention, a primer according to the invention comprises,
25 generally, all or part of any one of SEQ ID NOs: 35-46, or a complementary sequence thereof.

The nucleotide primers according to the invention are particularly useful in methods of genotyping subjects and/or of genotyping populations, in particular in the context of studies of association between particular allele forms or particular forms of groups of alleles (haplotypes) in subjects and the existence of a particular phenotype (character) in these
30 subjects, for example the predisposition of these subjects to develop diseases a pathology whose candidate chromosomal region is situated on chromosome 16, more precisely on the 16q arm and still more precisely in the 16q12 locus, such as a paroxysmal kinesigenic choreoathetosis.

RECOMBINANT VECTORS

The invention also relates to a recombinant vector comprising a nucleic acid according to the invention. "Vector" for the purposes of the present invention will be understood to mean a circular or linear DNA or RNA molecule which is either in single-stranded or double-stranded form.

Preferably, such a recombinant vector will comprise a nucleic acid chosen from the following nucleic acids:

- a) a nucleic acid comprising a nucleotide sequence of any one of SEQ ID NOs: 1-32, or a complementary nucleotide sequence thereof;
- b) a nucleic acid comprising a nucleotide sequence as depicted in any one of SEQ ID NOs: 1-32, or a complementary nucleotide sequence thereof;
- c) a nucleic acid having at least eight consecutive nucleotides of a nucleic acid comprising a nucleotide sequence of any one of SEQ ID NOs: 1-32, or of a complementary nucleotide sequence thereof;
- d) a nucleic acid having at least 80% nucleotide identity with a nucleic acid comprising a nucleotide sequence of any one of SEQ ID NOs: 1-32, or a complementary nucleotide sequence thereof;
- e) a nucleic acid having 85%, 90%, 95%, or 98% nucleotide identity with a nucleic acid comprising a nucleotide sequence of any one of SEQ ID NOs: 1-32, or a complementary nucleotide sequence thereof;
- f) a nucleic acid hybridizing, under high stringency hybridization conditions, with a nucleic acid comprising a nucleotide sequence of 1) any one of SEQ ID NOs: 1-32, or a complementary nucleotide sequence thereof;
- g) a nucleic acid encoding a polypeptide comprising an amino acid sequence of SEQ ID NO: 33 or 34; and
- h) a nucleic acid encoding a polypeptide comprising amino acid sequence SEQ ID NO: 33 or 34.

According to a first embodiment, a recombinant vector according to the invention is used to amplify a nucleic acid inserted therein, following transformation or transfection of a desired cellular host.

According to a second embodiment, a recombinant vector according to the invention corresponds to an expression vector comprising, in addition to a nucleic acid in accordance

with the invention, a regulatory signal or nucleotide sequence that directs or controls transcription and/or translation of the nucleic acid and its encoded mRNA.

According to a preferred embodiment, a recombinant vector according to the invention will comprise in particular the following components:

5 (1) an element or signal for regulating the expression of the nucleic acid to be inserted, such as a promoter and/or enhancer sequence;

(2) a nucleotide coding region comprised within the nucleic acid in accordance with the invention to be inserted into such a vector, said coding region being placed in phase with the regulatory element or signal described in (1); and

10 (3) an appropriate nucleic acid for initiation and termination of transcription of the nucleotide coding region of the nucleic acid described in (2).

In addition, the recombinant vectors according to the invention may include one or more origins for replication in the cellular hosts in which their amplification or their expression is sought, markers or selectable markers.

15 By way of example, the bacterial promoters may be the LacI or LacZ promoters, the T3 or T7 bacteriophage RNA polymerase promoters, the lambda phage PR or PL promoters.

The promoters for eukaryotic cells will comprise the herpes simplex virus (HSV) virus thymidine kinase promoter or alternatively the mouse metallothionein-L promoter.

Generally, for the choice of a suitable promoter, persons skilled in the art can
20 preferably refer to the book by Sambrook et al. (1989, *Molecular cloning: a laboratory manual*. 2ed. Cold Spring Harbor Laboratory, Cold spring Harbor, New York) cited above or to the techniques described by Fuller et al. (1996, *Immunology, In: Current Protocols in Molecular Biology*, Ausubel et al.(eds.).

When the expression of the genomic sequence of any one of the ABCC12 gene will be
25 sought, use will preferably be made of the vectors capable of containing large insertion sequences. In a particular embodiment, bacteriophage vectors such as the P1 bacteriophage vectors such as the vector p158 or the vector p158/neo8 described by Sternberg (1992, *Trends Genet.*, 8:1-16; 1994, *Mamm. Genome*, 5:397-404) will be preferably used.

The preferred bacterial vectors according to the invention are for example the vectors
30 pBR322(ATCC37017) or alternatively vectors such as pAA223-3 (Pharmacia, Uppsala, Sweden), and pGEM1 (Promega Biotech, Madison, WI, UNITED STATES).

There may also be cited other commercially available vectors such as the vectors pQE70, pQE60, pQE9 (Qiagen), psiX174, pBluescript SA, pNH8A, pNH16A, pNH18A, pNH46A, pWLNEO, pSV2CAT, pOG44, pXTI, pSG (Stratagene).

They may also be vectors of the baculovirus type such as the vector pVL1392/1393
5 (PharMingen) used to transfect cells of the Sf9 line (ATCC No. CRL 1711) derived from *Spodoptera frugiperda*.

They may also be adenoviral vectors such as the human adenovirus of type 2 or 5.

A recombinant vector according to the invention may also be a retroviral vector or an adeno-associated vector (AAV). Such adeno-associated vectors are for example described by
10 Flotte et al. (1992, Am. J. Respir. Cell Mol. Biol., 7:349-356), Samulski et al. (1989, J. Virol., 63:3822-3828), or McLaughlin BA et al. (1996, Am. J. Hum. Genet., 59:561-569).

To allow the expression of a polynucleotide according to the invention, the latter must be introduced into a host cell. The introduction of a polynucleotide according to the invention into a host cell may be carried out *in vitro*, according to the techniques well known to persons
15 skilled in the art for transforming or transfecting cells, either in primer culture, or in the form of cell lines. It is also possible to carry out the introduction of a polynucleotide according to the invention *in vivo* or *ex vivo*, for the prevention or treatment of diseases linked to ABCC12 deficiencies.

To introduce a polynucleotide or vector of the invention into a host cell, a person
20 skilled in the art can preferably refer to various techniques, such as the calcium phosphate precipitation technique (Graham et al., 1973, Virology, 52:456-457 ; Chen et al., 1987, Mol. Cell. Biol., 7 : 2745-2752), DEAE Dextran (Gopal, 1985, Mol. Cell. Biol., 5:1188-1190), electroporation (Tur-Kaspa, 1996, Mol. Cell. Biol., 6:716-718 ; Potter et al., 1984, Proc Natl Acad Sci U S A., 81(22):7161-5), direct microinjection (Harland et al., 1985, J. Cell. Biol.,
25 101:1094-1095), liposomes charged with DNA (Nicolau et al., 1982, Methods Enzymol., 149:157-76; Fraley et al., 1979, Proc. Natl. Acad. Sci. USA, 76:3348-3352).

Once the polynucleotide has been introduced into the host cell, it may be stably integrated into the genome of the cell. The integration may be achieved at a precise site of the genome, by homologous recombination, or it may be randomly integrated. In some
30 embodiments, the polynucleotide may be stably maintained in the host cell in the form of an episome fragment, the episome comprising sequences allowing the retention and the replication of the latter, either independently, or in a synchronized manner with the cell cycle.

According to a specific embodiment, a method of introducing a polynucleotide according to the invention into a host cell, in particular a host cell obtained from a mammal, *in vivo*, comprises a step during which a preparation comprising a pharmaceutically compatible vector and a “naked” polynucleotide according to the invention, placed under the control of appropriate regulatory sequences, is introduced by local injection at the level of the chosen tissue, for example myocardial tissue, the “naked” polynucleotide being absorbed by the myocytes of this tissue.

Compositions for use *in vitro* and *in vivo* comprising “naked” polynucleotides are for example described in PCT Application No. WO 95/11307 (Institut Pasteur, Inserm, University of Ottawa) as well as in the articles by Tacson et al. (1996, Nature Medicine, 2(8):888-892) and Huygen et al. (1996, Nature Medicine, 2(8):893-898).

According to a specific embodiment of the invention, a composition is provided for the *in vivo* production of the ABCC12 proteins. This composition comprises a polynucleotide encoding the ABCC12 polypeptides placed under the control of appropriate regulatory sequences, in solution in a physiologically acceptable vector.

The quantity of vector which is injected into the host organism chosen varies according to the site of the injection. As a guide, there may be injected between about 0.1 and about 100 µg of polynucleotide encoding any one of the ABCC12 proteins isoforms into the body of an animal, preferably into a patient likely to develop a disease linked ABCC12 deficiency.

Consequently, the invention also relates to a pharmaceutical composition intended for the prevention of or treatment of a patient or subject affected by ABCC12 deficiency, comprising a nucleic acid encoding any one of the ABCC12 proteins isoforms, in combination with one or more physiologically compatible excipients.

Preferably, such a composition will comprise a nucleic acid comprising a nucleotide sequence of SEQ ID NO: 1 or 2, wherein the nucleic acid is placed under the control of an appropriate regulatory element or signal.

The subject of the invention is, in addition, a pharmaceutical composition intended for the prevention of or treatment of a patient or a subject affected ABCC12 deficiency, comprising a recombinant vector according to the invention, in combination with one or more physiologically compatible excipients.

The invention relates to the use of a nucleic acid according to the invention, encoding the ABCC12 protein, for the manufacture of a medicament intended for the prevention or the treatment of subjects affected by a paroxysmal kinesigenic choreoathetosis.

5 The invention also relates to the use of a recombinant vector according to the invention, comprising a nucleic acid encoding any one of the ABCC12 proteins, for the manufacture of a medicament intended for the prevention of paroxysmal kinesigenic choreoathetosis.

10 The invention further relates to the use of a nucleic acid according to the invention, encoding any one of the ABCC12 proteins, for the manufacture of a medicament intended for the prevention or the treatment of pathologies linked to the dysfunction of transport of anionic drugs, such as methotrexate (MTX), neutral drugs conjugated to acidic ligands, such as GSH, glucuronate, or sulfate.

15 The invention also relates to the use of a recombinant vector according to the invention, comprising a nucleic acid encoding any one of the ABCC12 proteins isoforms, for the manufacture of a medicament intended for the treatment of/and prevention of pathologies linked to the dysfunction of transport of anionic drugs, such as methotrexate (MTX), neutral drugs conjugated to acidic ligands, such as GSH, glucuronate, or sulfate.

20 The subject of the invention is therefore also a recombinant vector comprising a nucleic acid according to the invention that encodes any one of the ABCC12 proteins or polypeptides isoforms.

The invention also relates to the use of such a recombinant vector for the preparation of a pharmaceutical composition intended for the treatment and/or for the prevention of diseases or conditions associated with deficiency or paroxysmal kinesigenic choreoathetosis.

25 The present invention also relates to the use of cells genetically modified *ex vivo* with such a recombinant vector according to the invention, or of cells producing a recombinant vector, wherein the cells are implanted in the body, to allow a prolonged and effective expression *in vivo* of at least a biologically active ABCC12 polypeptide isoform.

Vectors useful in methods of somatic gene therapy and compositions containing such vectors.

30 The present invention also relates to a new therapeutic approach for the treatment of pathologies linked to ABCC12 deficiencies. It provides an advantageous solution to the disadvantages of the prior art, by demonstrating the possibility of treating the pathologies linked to the ABCC12 deficiency by gene therapy, by the transfer and expression *in vivo* of a

gene encoding any one of the ABCC12 proteins isoforms involved in the paroxysmal kinesigenic choreoathetosis. The invention thus offers a simple means allowing a specific and effective treatment of the 16q12 located pathologies such as, paroxysmal kinesigenic choreoathetosis.

5 Gene therapy consists in correcting a deficiency or an abnormality (mutation, aberrant expression and the like) and in bringing about the expression of a protein of therapeutic interest by introducing genetic information into the affected cell or organ. This genetic information may be introduced either *ex vivo* into a cell extracted from the organ, the modified cell then being reintroduced into the body, or directly *in vivo* into the appropriate tissue. In
10 this second case, various techniques exist, among which various transfection techniques involving complexes of DNA and DEAE-dextran (Pagano et al., *J. Virol*, 1 (1967)891), of DNA and nuclear proteins (Kaneda et al., 1989, *Science* 243:375), of DNA and lipids (Felgner et al., 1987, *PNAS* 84:7413), the use of liposomes (Fraley et al., 1980, *J.Biol.Chem.*, 255:10431), and the like. More recently, the use of viruses as vectors for the transfer of genes
15 has appeared as a promising alternative to these physical transfection techniques. In this regard, various viruses have been tested for their capacity to infect certain cell populations. In particular, the retroviruses (RSV, HMS, MMS, and the like), the HSV virus, the adeno-associated viruses and the adenoviruses.

The present invention therefore also relates to a new therapeutic approach for the
20 treatment of pathologies linked to ABCC12 deficiencies, consisting in transferring and in expressing *in vivo* genes encoding ABCC12. In a particularly preferred manner, the applicant has now found that it is possible to construct recombinant vectors comprising a nucleic acid encoding any one of the ABCC12 proteins, to administer these recombinant vectors *in vivo*, and that this administration allows a stable and effective expression of at least one of the
25 biologically active ABCC12 proteins *in vivo*, with no cytopathological effect.

Adenoviruses constitute particularly efficient vectors for the transfer and the expression of any one of the ABCC12 gene. The use of recombinant adenoviruses as vectors makes it possible to obtain sufficiently high levels of expression of this gene to produce the desired therapeutic effect. Other viral vectors such as retroviruses or adeno-associated viruses
30 (AAV) can allow a stable expression of the gene are also claimed.

The present invention is thus likely to offer a new approach for the treatment and prevention of ABCC12 deficiencies.

The subject of the invention is therefore also a defective recombinant virus comprising a nucleic acid according to the invention that encodes the ABCC12 protein or polypeptide.

The invention also relates to the use of such a defective recombinant virus for the preparation of a pharmaceutical composition which may be useful for the treatment and/or for the prevention of ABCC12 deficiencies.

The present invention also relates to the use of cells genetically modified *ex vivo* with such a defective recombinant virus according to the invention, or of cells producing a defective recombinant virus, wherein the cells are implanted in the body, to allow a prolonged and effective expression *in vivo* of the biologically active ABCC12 polypeptides.

The present invention is particularly advantageous because it is possible to induce a controlled expression, and with no harmful effect of ABCC12 in organs which are not normally involved in the expression of this protein. In particular, a significant release of the ABCC12 protein is obtained by implantation of cells producing vectors of the invention, or infected *ex vivo* with vectors of the invention.

The activity of these ABCC protein transporters produced in the context of the present invention may be of the human or animal ABCC12 type. The nucleic sequence used in the context of the present invention may be a cDNA, a genomic DNA (gDNA), an RNA (in the case of retroviruses) or a hybrid construct consisting, for example, of a cDNA into which one or more introns (gDNA) would be inserted. It may also involve synthetic or semisynthetic sequences. In a particularly advantageous manner, a cDNA or a gDNA is used. In particular, the use of a gDNA allows a better expression in human cells. To allow their incorporation into a viral vector according to the invention, these sequences are preferably modified, for example by site-directed mutagenesis, in particular for the insertion of appropriate restriction sites. The sequences described in the prior art are indeed not constructed for use according to the invention, and prior adaptations may prove necessary, in order to obtain substantial expressions. In the context of the present invention, the use of nucleic sequences encoding the human ABCC12 proteins are preferred. Moreover, it is also possible to use a construct encoding a derivative of the ABCC12 protein. A derivative of any one of the ABCC12 proteins comprises, for example, any sequence obtained by mutation, deletion and/or addition relative to the native sequence, and encoding a product retaining the lipophilic substances transport activity. These modifications may be made by techniques known to a person skilled in the art (see general molecular biological techniques below). The biological activity of the derivatives

thus obtained can then be easily determined, as indicated in particular in the examples of the measurement of the efflux of the substrate from cells. The derivatives for the purposes of the invention may also be obtained by hybridization from nucleic acid libraries, using as probe the native sequence or a fragment thereof.

5 These derivatives are in particular molecules having a higher affinity for their binding sites, molecules exhibiting greater resistance to proteases, molecules having a higher therapeutic efficacy or fewer side effects, or optionally new biological properties. The derivatives also include the modified DNA sequences allowing improved expression *in vivo*.

10 In a first embodiment, the present invention relates to a defective recombinant virus comprising a cDNA encoding the ABCC12 polypeptides isoforms. In another preferred embodiment of the invention, a defective recombinant virus comprises a genomic DNA (gDNA) encoding the ABCC12 polypeptide isoform. Preferably, the ABCC12 polypeptides isoforms comprise an amino acid sequence SEQ ID NO: 33 or 34, respectively.

15 The vectors of the invention may be prepared from various types of viruses. Preferably, vectors derived from adenoviruses, adeno-associated viruses (AAV), herpesviruses (HSV) or retroviruses are used. It is preferable to use an adenovirus, for direct administration or for the ex vivo modification of cells intended to be implanted, or a retrovirus, for the implantation of producing cells.

20 The viruses according to the invention are defective, that is to say that they are incapable of autonomously replicating in the target cell. Generally, the genome of the defective viruses used in the context of the present invention therefore lacks at least the sequences necessary for the replication of said virus in the infected cell. These regions may be either eliminated (completely or partially), or made non functional, or substituted with other sequences and in particular with the nucleic sequence encoding any one of the ABCC12
25 protein isoforms. Preferably, the defective virus retains, nevertheless, the sequences of its genome which are necessary for the encapsidation of the viral particles.

30 As regards more particularly adenoviruses, various serotypes, whose structure and properties vary somewhat, have been characterized. Among these serotypes, human adenoviruses of type 2 or 5 (Ad 2 or Ad 5) or adenoviruses of animal origin (see Application WO 94/26914) are preferably used in the context of the present invention. Among the adenoviruses of animal origin which can be used in the context of the present invention, there may be mentioned adenoviruses of canine, bovine, murine (example: Mav1, Beard et al., Virology 75 (1990) 81), ovine, porcine, avian or simian (example: SAV) origin. Preferably,

the adenovirus of animal origin is a canine adenovirus, more preferably a CAV2 adenovirus [Manhattan or A26/61 strain (ATCC VR-800) for example]. Preferably, adenoviruses of human or canine or mixed origin are used in the context of the invention. Preferably, the defective adenoviruses of the invention comprise the ITRs, a sequence allowing the encapsidation and the sequence encoding the ABCC12 proteins isoforms. Preferably, in the genome of the adenoviruses of the invention, the E1 region at least is made non functional. Still more preferably, in the genome of the adenoviruses of the invention, the E1 gene and at least one of the E2, E4 and L1-L5 genes are non functional. The viral gene considered may be made non functional by any technique known to a person skilled in the art, and in particular by total suppression, by substitution, by partial deletion or by addition of one or more bases in the gene(s) considered. Such modifications may be obtained *in vitro* (on the isolated DNA) or *in situ*, for example, by means of genetic engineering techniques, or by treatment by means of mutagenic agents. Other regions may also be modified, and in particular the E3 (WO95/02697), E2 (WO94/28938), E4 (WO94/28152, WO94/12649, WO95/02697) and L5 (WO95/02697) region. According to a preferred embodiment, the adenovirus according to the invention comprises a deletion in the E1 and E4 regions and the sequence encoding ABCC12 is inserted at the level of the inactivated E1 region. According to another preferred embodiment, it comprises a deletion in the E1 region at the level of which the E4 region and the sequence encoding the ABCC12 proteins isoforms (French Patent Application FR94 13355) are inserted.

The defective recombinant adenoviruses according to the invention may be prepared by any technique known to persons skilled in the art (Levrero et al., 1991 Gene 101; EP 185 573; and Graham, 1984, EMBO J., 3:2917). In particular, they may be prepared by homologous recombination between an adenovirus and a plasmid carrying, *inter alia*, the nucleic acid encoding any one of the ABCC12 proteins isoforms. The homologous recombination occurs after cotransfection of said adenoviruses and plasmid into an appropriate cell line. The cell line used must preferably (i) be transformable by said elements, and (ii), contain the sequences capable of complementing the part of the defective adenovirus genome, preferably in integrated form in order to avoid the risks of recombination. By way of example of a line, there may be mentioned the human embryonic kidney line 293 (Graham et al., 1977, J. Gen. Virol., 36:59), which contains in particular, integrated into its genome, the left part of the genome of an Ad5 adenovirus (12%) or lines capable of complementing the E1 and E4 functions as described in particular in Applications No. WO 94/26914 and WO95/02697.

As regards the adeno-associated viruses (AAV), they are DNA viruses of a relatively small size, which integrate into the genome of the cells which they infect, in a stable and site-specific manner. They are capable of infecting a broad spectrum of cells, without inducing any effect on cellular growth, morphology or differentiation. Moreover, they do not appear to be involved in pathologies in humans. The genome of AAVs has been cloned, sequenced and characterized. It comprises about 4700 bases, and contains at each end an inverted repeat region (ITR) of about 145 bases, serving as replication origin for the virus. The remainder of the genome is divided into 2 essential regions carrying the encapsidation functions: the left hand part of the genome, which contains the rep gene, involved in the viral replication and the expression of the viral genes; the right hand part of the genome, which contains the cap gene encoding the virus capsid proteins.

The use of vectors derived from AAVs for the transfer of genes *in vitro* and *in vivo* has been described in the literature (see in particular WO 91/18088; WO 93/09239; US 4,797,368, US5,139,941, EP 488 528). These applications describe various constructs derived from AAVs, in which the rep and/or cap genes are deleted and replaced by a gene of interest, and their use for transferring *in vitro* (on cells in culture) or *in vivo* (directly into an organism) said gene of interest. However, none of these documents either describes or suggests the use of a recombinant AAV for the transfer and expression *in vivo* or *ex vivo* one of the ABCC12 proteins, or the advantages of such a transfer. The defective recombinant AAVs according to the invention may be prepared by cotransfection, into a cell line infected with a human helper virus (for example an adenovirus), of a plasmid containing the sequence encoding the ABCC12 protein bordered by two AAV inverted repeat regions (ITR), and of a plasmid carrying the AAV encapsidation genes (rep and cap genes). The recombinant AAVs produced are then purified by conventional techniques.

As regards the herpesviruses and the retroviruses, the construction of recombinant vectors has been widely described in the literature: see in particular Breakfield et al., (1991. New Biologist, 3:203); EP 453242, EP178220, Bernstein et al. (1985); McCormick, (1985. BioTechnology, 3:689), and the like.

In particular, the retroviruses are integrating viruses, infecting dividing cells. The genome of the retroviruses essentially comprises two long terminal repeats (LTRs), an encapsidation sequence and three coding regions (gag, pol and env). In the recombinant vectors derived from retroviruses, the gag, pol and env genes are generally deleted, completely or partially, and replaced with a heterologous nucleic acid sequence of interest. These vectors

may be produced from various types of retroviruses such as in particular MoMuLV ("murine moloney leukemia virus"; also called MoMLV), MSV ("murine moloney sarcoma virus"), HaSV ("harvey sarcoma virus"); SNV ("spleen necrosis virus"); RSV ("rous sarcoma virus") or Friend's virus.

5 To construct recombinant retroviruses containing a sequence encoding any one of the ABCC12 proteins isoforms according to the invention, a plasmid containing in particular the LTRs, the encapsidation sequence and said coding sequence is generally constructed, and then used to transfect a so-called encapsidation cell line, capable of providing in trans the retroviral functions deficient in the plasmid. Generally, the encapsidation lines are therefore capable of
10 expressing the gag, pol and env genes. Such encapsidation lines have been described in the prior art, and in particular the PA317 line (US 4,861,719), the PsiCRIP line (WO 90 /02806) and the GP+envAm-12 line (WO 89/07150). Moreover, the recombinant retroviruses may contain modifications at the level of the LTRs in order to suppress the transcriptional activity, as well as extended encapsidation sequences, containing a portion of the gag gene (Bender et
15 al., 1987, J. Virol., 61:1639). The recombinant retroviruses produced are then purified by conventional techniques.

To carry out the present invention, it is preferable to use a defective recombinant adenovirus. The particularly advantageous properties of adenoviruses are preferred for the *in vivo* expression of a protein having a lipophilic substrate transport activity. The adenoviral
20 vectors according to the invention are particularly preferred for a direct administration *in vivo* of a purified suspension, or for the ex vivo transformation of cells, in particular autologous cells, in view of their implantation. Furthermore, the adenoviral vectors according to the invention exhibit, in addition, considerable advantages, such as in particular their very high infection efficiency, which makes it possible to carry out infections using small volumes of
25 viral suspension.

According to another particularly preferred embodiment of the invention, a line producing retroviral vectors containing the sequence encoding any one of the ABCC12 protein isoforms is used for implantation *in vivo*. The lines which can be used to this end are in particular the PA317 (US 4,861,719), PsiCrip (WO 90/02806) and GP+envAm-12
30 (US 5,278,056) cells modified so as to allow the production of a retrovirus containing a nucleic sequence encoding any one of the ABCC12 proteins isoforms according to the invention. For example, totipotent stem cells, precursors of blood cell lines, may be collected and isolated from a subject. These cells, when cultured, may then be transfected with the

retroviral vector containing the sequence encoding any one of the ABCC12 protein isoforms under the control of viral, nonviral or nonviral promoters specific for macrophages or under the control of its own promoter. These cells are then reintroduced into the subject. The differentiation of these cells will be responsible for blood cells expressing one of the ABCC12 protein isoforms.

Preferably, in the vectors of the invention, the sequence encoding any one of the ABCC12 proteins isoforms is placed under the control of signals allowing its expression in the infected cells. These may be expression signals which are homologous or heterologous, that is to say signals different from those which are naturally responsible for the expression of the ABCC12 proteins. They may also be in particular sequences responsible for the expression of other proteins, or synthetic sequences. In particular, they may be sequences of eukaryotic or viral genes or derived sequences, stimulating or repressing the transcription of a gene in a specific manner or otherwise and in an inducible manner or otherwise. By way of example, they may be promoter sequences derived from the genome of the cell which it is desired to infect, or from the genome of a virus, and in particular the promoters of the E1A or major late promoter (MLP) genes of adenoviruses, the cytomegalovirus (CMV) promoter, the RSV-LTR and the like. Among the eukaryotic promoters, there may also be mentioned the ubiquitous promoters (HPRT, vimentin, α -actin, tubulin and the like), the promoters of the intermediate filaments (desmin, neurofilaments, keratin, GFAP, and the like), the promoters of therapeutic genes (of the MDR, CFTR or factor VIII type, and the like), tissue-specific promoters (pyruvate kinase, villin, promoter of the fatty acid binding intestinal protein, promoter of the smooth muscle cell α -actin, promoters specific for the liver; Apo AI, Apo AII, human albumin and the like) or promoters corresponding to a stimulus (steroid hormone receptor, retinoic acid receptor and the like). In addition, these expression sequences may be modified by addition of enhancer or regulatory sequences and the like. Moreover, when the inserted gene does not contain expression sequences, it may be inserted into the genome of the defective virus downstream of such a sequence.

In a specific embodiment, the invention relates to a defective recombinant virus comprising a nucleic acid encoding any one of the ABCC12 proteins isoforms the control of a promoter chosen from RSV-LTR or the CMV early promoter.

As indicated above, the present invention also relates to any use of a virus as described above for the preparation of a pharmaceutical composition for the treatment and/or prevention of pathologies linked to the transport of lipophilic substances.

The present invention also relates to a pharmaceutical composition comprising one or
5 more defective recombinant viruses as described above. These pharmaceutical compositions may be formulated for administration by the topical, oral, parenteral, intranasal, intravenous, intramuscular, subcutaneous, intraocular or transdermal route and the like. Preferably, the pharmaceutical compositions of the invention comprises a pharmaceutically acceptable vehicle or physiologically compatible excipient for an injectable formulation, in particular for
10 an intravenous injection, such as for example into the patient's portal vein. These may relate in particular to isotonic sterile solutions or dry, in particular, freeze-dried, compositions which, upon addition depending on the case of sterilized water or physiological saline, allow the preparation of injectable solutions. Direct injection into the patient's portal vein is preferred because it makes it possible to target the infection at the level of the liver and thus to
15 concentrate the therapeutic effect at the level of this organ.

The doses of defective recombinant virus used for the injection may be adjusted as a function of various parameters, and in particular as a function of the viral vector, of the mode of administration used, of the relevant pathology or of the desired duration of treatment. In general, the recombinant adenoviruses according to the invention are formulated and
20 administered in the form of doses of between 10^4 and 10^{14} pfu/ml, and preferably 10^6 to 10^{10} pfu/ml. The term "pfu" (plaque forming unit) corresponds to the infectivity of a virus solution, and is determined by infecting an appropriate cell culture and measuring, generally after 48 hours, the number of plaques that result from infected cell lysis. The techniques for determining the pfu titer of a viral solution are well documented in the literature.

25 As regards retroviruses, the compositions according to the invention may directly contain the producing cells, with a view to their implantation.

In this regard, another subject of the invention relates to any mammalian cell infected with one or more defective recombinant viruses according to the invention. More particularly, the invention relates to any population of human cells infected with such viruses. These may
30 be in particular cells of blood origin (totipotent stem cells or precursors), fibroblasts, myoblasts, hepatocytes, keratinocytes, smooth muscle and endothelial cells, glial cells and the like.

The cells according to the invention may be derived from primary cultures. These may be collected by any technique known to persons skilled in the art and then cultured under conditions allowing their proliferation. As regards more particularly fibroblasts, these may be easily obtained from biopsies, for example according to the technique described by Ham
5 (1980). These cells may be used directly for infection with the viruses, or stored, for example by freezing, for the establishment of autologous libraries, in view of a subsequent use. The cells according to the invention may be secondary cultures, obtained for example from pre-established libraries (see for example EP 228458, EP 289034, EP 400047, EP 456640).

The cells in culture are then infected with a recombinant virus according to the
10 invention, in order to confer on them the capacity to produce a biologically active ABCC12 protein. The infection is carried out *in vitro* according to techniques known to persons skilled in the art. In particular, depending on the type of cells used and the desired number of copies of virus per cell, persons skilled in the art can adjust the multiplicity of infection and optionally the number of infectious cycles produced. It is clearly understood that these steps
15 must be carried out under appropriate conditions of sterility when the cells are intended for administration *in vivo*. The doses of recombinant virus used for the infection of the cells may be adjusted by persons skilled in the art according to the desired aim. The conditions described above for the administration *in vivo* may be applied to the infection *in vitro*. For the infection with a retrovirus, it is also possible to co-culture a cell to be infected with a cell
20 producing the recombinant retrovirus according to the invention. This makes it possible to eliminate purification of the retrovirus.

Another subject of the invention relates to an implant comprising mammalian cells infected with one or more defective recombinant viruses according to the invention or cells producing recombinant viruses, and an extracellular matrix. Preferably, the implants
25 according to the invention comprise 10^5 to 10^{10} cells. More preferably, they comprise 10^6 to 10^8 cells.

More particularly, in the implants of the invention, the extracellular matrix comprises a gelling compound and optionally a support allowing the anchorage of the cells.

For the preparation of the implants according to the invention, various types of
30 gelling agents may be used. The gelling agents are used for the inclusion of the cells in a matrix having the constitution of a gel, and for promoting the anchorage of the cells on the support, where appropriate. Various cell adhesion agents can therefore be used as gelling

agents, such as in particular collagen, gelatin, glycosaminoglycans, fibronectin, lectins and the like. Preferably, collagen is used in the context of the present invention. This may be collagen of human, bovine or murine origin. More preferably, type I collagen is used.

As indicated above, the compositions according to the invention preferably comprise
5 a support allowing the anchorage of the cells. The term anchorage designates any form of biological and/or chemical and/or physical interaction causing the adhesion and/or the attachment of the cells to the support. Moreover, the cells may either cover the support used, or penetrate inside this support, or both. It is preferable to use in the context of the invention a solid, nontoxic and/or biocompatible support. In particular, it is possible to use
10 polytetrafluoroethylene (PTFE) fibers or a support of biological origin.

The present invention thus offers a very effective means for the treatment or prevention of pathologies linked to the transport of lipophilic substances.

In addition, this treatment may be applied to both humans and any animals such as ovines, bovines, domestic animals (dogs, cats and the like), horses, fish and the like.

15

RECOMBINANT HOST CELLS

The invention relates to a recombinant host cell comprising a nucleic acid of the invention, and more particularly, a nucleic acid comprising a nucleotide sequence selected from SEQ ID NO: 1-32, or a complementary nucleotide sequence thereof.

20 The invention also relates to a recombinant host cell comprising a nucleic acid of the invention, and more particularly a nucleic acid comprising a nucleotide sequence as depicted in SEQ ID NO: 1-32, or a complementary nucleotide sequence thereof.

According to another aspect, the invention also relates to a recombinant host cell comprising a recombinant vector according to the invention. Therefore, the invention also
25 relates to a recombinant host cell comprising a recombinant vector comprising any of the nucleic acids of the invention, and more particularly a nucleic acid comprising a nucleotide sequence of selected from SEQ ID NO: 1-32, or a complementary nucleotide sequence thereof.

The invention also relates to a recombinant host cell comprising a recombinant vector
30 comprising a nucleic acid comprising a nucleotide sequence as depicted in any one of SEQ ID NOs: 1-32, or of a complementary nucleotide sequence thereof.

The preferred host cells according to the invention are for example the following:

a) prokaryotic host cells: strains of *Escherichia coli* (strain DH5- α), of *Bacillus subtilis*, of *Salmonella typhimurium*, or strains of genera such as *Pseudomonas*, *Streptomyces* and *Staphylococcus* ;

5 b) eukaryotic host cells: HeLa cells (ATCC No. CCL2), Cv 1 cells (ATCC No. CCL70), COS cells (ATCC No. CRL 1650), Sf-9 cells (ATCC No. CRL 1711), CHO cells (ATCC No. CCL-61) 3T3 cells (ATCC No. CRL-6361) or human Erythroleukemia K562 (ATCC N° CCL-243).

METHODS FOR PRODUCING ABCC12 POLYPEPTIDES ISOFORMS

10 The invention also relates to a method for the production of a polypeptide comprising an amino acid sequence SEQ ID NOs: 33 or 34, said method comprising the steps of:

a) inserting a nucleic acid encoding said polypeptide into an appropriate vector;

b) culturing, in an appropriate culture medium, a previously transformed host cell or transfecting a host cell with the recombinant vector of step a);

15 c) recovering the conditioned culture medium or lysing the host cell, for example by sonication or by osmotic shock;

d) separating and purifying said polypeptide from said culture medium or alternatively from the cell lysates obtained in step c); and

e) where appropriate, characterizing the recombinant polypeptide produced.

20 The polypeptides according to the invention may be characterized by binding to an immunoaffinity chromatography column on which the antibodies directed against this polypeptide or against a fragment or a variant thereof have been previously immobilized.

According to another aspect, a recombinant polypeptide according to the invention may be purified by passing it over an appropriate series of chromatography columns, according to methods known to persons skilled in the art and described for example in F. Ausubel et al (1989, Current Protocols in Molecular Biology, Green Publishing Associates and Wiley Interscience, N.Y).

30 A polypeptide according to the invention may also be prepared by conventional chemical synthesis techniques either in homogeneous solution or in solid phase. By way of illustration, a polypeptide according to the invention may be prepared by the technique either in homogeneous solution described by Houben Weyl (1974, Methode der Organischen

Chemie, E. Wunsch Ed., 15-I:15-II) or the solid phase synthesis technique described by Merrifield (1965, *Nature*, 207(996):522-523; 1965, *Science*, 150(693):178-185).

A polypeptide termed "homologous" to a polypeptide having an amino acid sequence selected from SEQ ID NO: 33 or 34 also forms part of the invention. Such a homologous
5 polypeptide comprises an amino acid sequence possessing one or more substitutions of an amino acid by an equivalent amino acid of SEQ ID NO: 33 or 34.

An "equivalent amino acid" according to the present invention will be understood to mean for example replacement of a residue in the L form by a residue in the D form or the replacement of a glutamic acid (E) by a pyro-glutamic acid according to techniques well
10 known to persons skilled in the art. By way of illustration, the synthesis of peptide containing at least one residue in the D form is described by Koch (1977). According to another aspect, two amino acids belonging to the same class, that is to say two uncharged polar, nonpolar, basic or acidic amino acids, are also considered as equivalent amino acids.

Polypeptides comprising at least one nonpeptide bond such as a retro-inverse bond
15 (NHCO), a carba bond (CH₂CH₂) or a ketomethylene bond (CO-CH₂) also form part of the invention.

Preferably, the polypeptides according to the invention comprising one or more additions, deletions, substitutions of at least one amino acid will retain their capacity to be recognized by antibodies directed against the nonmodified polypeptides.

20

ANTIBODIES

The ABCC12 polypeptide isoforms according to the invention, in particular 1) a polypeptide comprising an amino acid sequence of any one of SEQ ID NO: 33 or 34, 2) a polypeptide fragment or variant of a polypeptide comprising an amino acid sequence of any
25 one of SEQ ID NO: 33 or 34, or 3) a polypeptide termed "homologous" to a polypeptide comprising amino acid sequence selected from SEQ ID NO: 33 or 34, may be used for the preparation of an antibody, in particular for detecting the production of a normal or altered form of ABCC12 polypeptides in a patient.

An antibody directed against a polypeptide termed "homologous" to a polypeptide
30 having an amino acid sequence selected from SEQ ID NO: 33 or 34 also forms part of the invention. Such an antibody is directed against a homologous polypeptide comprising an amino acid sequence possessing one or more substitutions of an amino acid by an equivalent amino acid of SEQ ID NO: 33 or 34.

“Antibody” for the purposes of the present invention will be understood to mean in particular polyclonal or monoclonal antibodies or fragments (for example the F(ab)₂ and Fab fragments) or any polypeptide comprising a domain of the initial antibody recognizing the target polypeptide or polypeptide fragment according to the invention.

5 Monoclonal antibodies may be prepared from hybridomas according to the technique described by Kohler and Milstein (1975, *Nature*, 256:495-497).

According to the invention, a polypeptide produced recombinantly or by chemical synthesis, and fragments or other derivatives or analogs thereof, including fusion proteins, may be used as an immunogen to generate antibodies that recognize a polypeptide according
10 to the invention. Such antibodies include but are not limited to polyclonal, monoclonal, chimeric, single chain, Fab fragments, and an Fab expression library. The anti-ABCC5, anti-ABCC4, or anti-ABCC1 antibodies of the invention may be cross reactive, *e.g.*, they may recognize corresponding ABCC12 polypeptide from different species. Polyclonal antibodies have greater likelihood of cross reactivity. Alternatively, an antibody of the invention may be
15 specific for a single form of ABCC12. Preferably, such an antibody is specific for human ABCC12.

Various procedures known in the art may be used for the production of polyclonal antibodies to the ABCC12 polypeptide or derivative or analog thereof. For the production of antibody, various host animals can be immunized by injection with the ABCC12 polypeptide,
20 or a derivatives (*e.g.*, fragment or fusion protein) thereof, including but not limited to rabbits, mice, rats, sheep, goats, etc. In one embodiment, the ABCC12 polypeptide or a fragment thereof can be conjugated to an immunogenic carrier, *e.g.*, bovine serum albumin (BSA) or keyhole limpet hemocyanin (KLH). Various adjuvants may be used to increase the immunological response, depending on the host species, including but not limited to Freund's
25 (complete and incomplete), mineral gels such as aluminum hydroxide, surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanins, dinitrophenol, and potentially useful human adjuvants such as BCG (*bacille Calmette-Guerin*) and *Corynebacterium parvum*.

For preparation of monoclonal antibodies directed toward the ABCC12 polypeptides
30 isoforms, or a fragment, analog, or derivative thereof, any technique that provides for the production of antibody molecules by continuous cell lines in culture may be used. These include but are not limited to the hybridoma technique originally developed by Kohler and Milstein (1975, *Nature*, 256:495-497), as well as the trioma technique, the human B-cell

hybridoma technique (Kozbor et al., 1983, Immunology Today, 4:72; Cote et al. 1983, Proc. Natl. Acad. Sci. U.S.A. 80:2026-2030), and the EBV-hybridoma technique to produce human monoclonal antibodies (Cole et al., 1985, In: *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc., pp. 77-96). In an additional embodiment of the invention, monoclonal
5 antibodies can be produced in germ-free animals (WO 89/12690). In fact, according to the invention, techniques developed for the production of "chimeric antibodies" (Morrison et al., 1984, J. Bacteriol. 159:870; Neuberger et al., 1984, Nature, 312:604-608; Takeda et al., 1985, Nature 314:452-454) by splicing the genes from a mouse antibody molecule specific for the ABCC12 polypeptide together with genes from a human antibody molecule of appropriate
10 biological activity can be used; such antibodies are within the scope of this invention. Such human or humanized chimeric antibodies are preferred for use in therapy of human diseases or disorders (described *infra*), since the human or humanized antibodies are much less likely than xenogenic antibodies to induce an immune response, in particular an allergic response, themselves.

15 According to the invention, techniques described for the production of single chain antibodies (U.S. Patent Nos. 5,476,786 and 5,132,405 to Huston; U.S. Patent 4,946,778) can be adapted to produce ABCC12 polypeptide-specific single chain antibodies. An additional embodiment of the invention utilizes the techniques described for the construction of Fab expression libraries (Huse et al., 1989, Science 246:1275-1281) to allow rapid and easy
20 identification of monoclonal Fab fragments with the desired specificity for the ABCC12 polypeptide, or its derivative, or analog.

Antibody fragments which contain the idiotype of the antibody molecule can be generated by known techniques. For example, such fragments include but are not limited to: the F(ab')₂ fragment which can be produced by pepsin digestion of the antibody molecule; the
25 Fab' fragments which can be generated by reducing the disulfide bridges of the F(ab')₂ fragment, and the Fab fragments which can be generated by treating the antibody molecule with papain and a reducing agent.

In the production of antibodies, screening for the desired antibody can be accomplished by techniques known in the art, *e.g.*, radioimmunoassay, ELISA (enzyme-linked
30 immunosorbant assay), "sandwich" immunoassays, immunoradiometric assays, gel diffusion precipitin reactions, immunodiffusion assays, *in situ* immunoassays (using colloidal gold, enzyme or radioisotope labels, for example), western blots, precipitation reactions, agglutination assays (*e.g.*, gel agglutination assays, hemagglutination assays), complement

fixation assays, immunofluorescence assays, protein A assays, and immunoelectrophoresis assays, etc. In one embodiment, antibody binding is detected by detecting a label on the primary antibody. In another embodiment, the primary antibody is detected by detecting binding of a secondary antibody or reagent to the primary antibody. In a further embodiment, the secondary antibody is labelled. Many means are known in the art for detecting binding in an immunoassay and are within the scope of the present invention. For example, to select antibodies which recognize a specific epitope of the ABCC12 polypeptides, one may assay generated hybridomas for a product which binds to one ABCC12 polypeptide fragment containing such epitope. For selection of an antibody specific to one ABCC12 polypeptide from a particular species of animal, one can select on the basis of positive binding with one ABCC12 polypeptide expressed by or isolated from cells of that species of animal.

The foregoing antibodies can be used in methods known in the art relating to the localization and activity of the ABCC12 polypeptide isoforms, e.g., for Western blotting, ABCC12 polypeptide *in situ*, measuring levels thereof in appropriate physiological samples, etc. using any of the detection techniques mentioned above or known in the art.

In a specific embodiment, antibodies that agonize or antagonize the activity of one ABCC12 polypeptide can be generated. Such antibodies can be tested using the assays described *infra* for identifying ligands.

The present invention relates to an antibody directed against 1) a polypeptide comprising an amino acid sequence of the SEQ ID NO: 33 or 34, 2) a polypeptide fragment or variant of a polypeptide comprising an amino acid sequence of the SEQ ID NO: 33 or 34, or 3) a polypeptide termed "homologous" to a polypeptide comprising amino acid sequence selected from SEQ ID NO: 33 or 34, also forms part of the invention, as produced in the trioma technique or the hybridoma technique described by Kozbor et al. (1983, *Hybridoma*, 2(1):7-16).

The invention also relates to single-chain Fv antibody fragments (ScFv) as described in US patent No. 4,946,778 or by Martineau et al. (1998, *J Mol Biol*, 280(1):117-127).

The antibodies according to the invention also comprise antibody fragments obtained with the aid of phage libraries as described by Ridder et al., (1995, *Biotechnology* (NY), 13(3):255-260) or humanized antibodies as described by Reinmann et al. (1997, *AIDS Res Hum Retroviruses*, 13(11):933-943) and Leger et al., (1997, *Hum Antibodies*, 8(1):3-16).

The antibody preparations according to the invention are useful in immunological detection tests intended for the identification of the presence and/or of the quantity of antigens present in a sample.

5 An antibody according to the invention may comprise, in addition, a detectable marker which is isotopic or nonisotopic, for example fluorescent, or may be coupled to a molecule such as biotin, according to techniques well known to persons skilled in the art.

Thus, the subject of the invention is, in addition, a method of detecting the presence of a polypeptide according to the invention in a sample, said method comprising the steps of:

10 a) bringing the sample to be tested into contact with an antibody directed against 1) a polypeptide comprising an amino acid sequence of the SEQ ID NO: 33 or 34, 2) a polypeptide fragment or variant of a polypeptide comprising an amino acid sequence of the SEQ ID NO: 33 or 34, or 3) a polypeptide termed "homologous" to a polypeptide comprising amino acid sequence of SEQ ID NO: 33 or 34, and

b) detecting the antigen/antibody complex formed.

15 The invention also relates to a box or kit for diagnosis or for detecting the presence of a polypeptide in accordance with the invention in a sample, said box comprising:

20 a) an antibody directed against 1) a polypeptide comprising an amino acid sequence of SEQ ID NO:33 or 34, 2) a polypeptide fragment or variant of a polypeptide comprising an amino acid sequence of the SEQ ID NO: 33 or 34, or 3) a polypeptide termed "homologous" to a polypeptide comprising amino acid sequence of SEQ ID NO: 33 or 34, and

b) a reagent allowing the detection of the antigen/antibody complexes formed.

PHARMACEUTICAL COMPOSITIONS AND THERAPEUTIC METHODS OF TREATMENT

25 The invention also relates to pharmaceutical compositions intended for the prevention and/or treatment of a deficiency in the transport of cholesterol or inflammatory lipid substances, characterized in that they comprise a therapeutically effective quantity of a polynucleotide capable of giving rise to the production of an effective quantity of the ABCC12 functional polypeptide, in particular a polypeptide comprising an amino acid
30 sequence of SEQ ID NO: 33 or 34.

The invention also provides pharmaceutical compositions comprising a nucleic acid encoding any one of ABCC12 polypeptides isoforms according to the invention and pharmaceutical compositions comprising the ABCC12 polypeptides isoforms according to the

invention intended for the prevention and/or treatment of diseases which are mapped on the chromosome locus 16q12.

The present invention also relates to a new therapeutic approach for the treatment of pathologies linked to the transport of lipophilic substances, comprising transferring and
5 expressing *in vivo* nucleic acids encoding the ABCC12 proteins isoforms according to the invention.

Thus, the present invention offers a new approach for the treatment and/or the prevention of pathologies such as the paroxysmal kinesigenic choreoathetosis.

Consequently, the invention also relates to a pharmaceutical composition intended for
10 the prevention of or treatment of subjects affected by a dysfunction of the transport of anionic drugs, such as methotrexate (MTX), neutral drugs conjugated to acidic ligands, such as GSH conjugated drugs, glucuronate, or sulfate, comprising a nucleic acid encoding the ABCC12 proteins isoforms in combination with one or more physiologically compatible vehicle and/or excipient.

15 According to a specific embodiment of the invention, a composition is provided for the *in vivo* production any one of the ABCC12 proteins isoforms. This composition comprises a nucleic acid encoding any one of the ABCC12 polypeptides isoforms placed under the control of appropriate regulatory sequences, in solution in a physiologically acceptable vehicle and/or excipient.

20 Therefore, the present invention also relates to a composition comprising a nucleic acid encoding a polypeptide comprising an amino acid sequence of SEQ ID NO: 33 or 34, wherein the nucleic acid is placed under the control of appropriate regulatory elements.

Preferably, such a composition will comprise a nucleic acid comprising a nucleotide sequence of SEQ ID NO: 1 or 2, placed under the control of appropriate regulatory elements.

25 According to another aspect, the subject of the invention is also a preventive and/or curative therapeutic method of treating diseases caused by a deficiency in the transport of lipophilic substances, such a method comprising a step in which there is administered to a patient a nucleic acid encoding any one of the ABCC12 polypeptides isoforms according to the invention in said patient, said nucleic acid being, where appropriate, combined with one or
30 more physiologically compatible vehicles and/or excipients.

The invention also relates to a pharmaceutical composition intended for the prevention of or treatment of subjects affected by, a deficiency of the ABCC12 gene, comprising a

recombinant vector according to the invention, in combination with one or more physiologically compatible excipients.

According to a specific embodiment, a method of introducing a nucleic acid according to the invention into a host cell, in particular a host cell obtained from a mammal, *in vivo*,
5 comprises a step during which a preparation comprising a pharmaceutically compatible vector and a "naked" nucleic acid according to the invention, placed under the control of appropriate regulatory sequences, is introduced by local injection at the level of the chosen tissue, for example a smooth muscle tissue, the "naked" nucleic acid being absorbed by the cells of this tissue.

10 The invention also relates to the use of a nucleic acid according to the invention, encoding any one of the ABCC12 proteins isoforms, for the manufacture of a medicament intended for the prevention and/or treatment in various forms or more particularly for the treatment of subjects affected by a paroxysmal kinesigenic choreoathetosis.

The invention also relates to the use of a recombinant vector according to the
15 invention, comprising a nucleic acid encoding any one of the ABCC12 proteins isoforms for the manufacture of a medicament intended for the prevention and/or treatment of subjects affected by a paroxysmal kinesigenic choreoathetosis.

The invention also relates to the use of a nucleic acid according to the invention, encoding any one of the ABCC12 proteins isoforms, for the manufacture of a medicament
20 intended for the prevention and/or treatment in various forms or more particularly for the treatment of subjects affected by a deficiency in the transport of anionic drugs, such as methotrexate (MTX), neutral drugs conjugated to acidic ligands, such as GSH conjugated drugs, glucuronate, or sulfate.

The invention also relates to the use of a recombinant vector according to the
25 invention, comprising a nucleic acid encoding any one of the ABCC12 proteins isoforms, for the manufacture of a medicament intended for the prevention and/or treatment of a deficiency in the transport of anionic drugs, such as methotrexate (MTX), neutral drugs conjugated to acidic ligands, such as GSH conjugated drugs, glucuronate, or sulfate.

As indicated above, the present invention also relates to the use of a defective
30 recombinant virus according to the invention for the preparation of a pharmaceutical composition for the treatment and/or prevention of pathologies linked to the paroxysmal kinesigenic choreoathetosis.

The invention relates to the use of such a defective recombinant virus for the preparation of a pharmaceutical composition intended for the treatment and/or prevention of a deficiency associated with the transport of anionic drugs, such as methotrexate (MTX), neutral drugs conjugated to acidic ligands, such as GSH conjugated drugs, glucuronate, or sulfate.

5 Thus, the present invention also relates to a pharmaceutical composition comprising one or more defective recombinant viruses according to the invention.

The present invention also relates to the use of cells genetically modified *ex vivo* with a virus according to the invention, or of producing cells such as viruses, implanted in the body, allowing a prolonged and effective expression *in vivo* one of the biologically active

10 ABCC12 proteins isoforms.

The present invention shows that it is possible to incorporate a nucleic acid encoding any one of the ABCC12 proteins isoforms into a viral vector, and that these vectors make it possible to effectively express a biologically active, mature form. More particularly, the invention shows that the *in vivo* expression of the ABCC12 gene may be obtained by direct

15 administration of an adenovirus or by implantation of a producing cell or of a cell genetically modified by an adenovirus or by a retrovirus incorporating such a DNA.

Preferably, the pharmaceutical compositions of the invention comprise a pharmaceutically acceptable vehicle or physiologically compatible excipient for an injectable formulation, in particular for an intravenous injection, such as for example into the patient's

20 portal vein. These may relate in particular to isotonic sterile solutions or dry, in particular, freeze-dried, compositions which, upon addition depending on the case of sterilized water or physiological saline, allow the preparation of injectable solutions. Direct injection into the patient's portal vein is preferred because it makes it possible to target the infection at the level of the liver and thus to concentrate the therapeutic effect at the level of this organ.

25 A "pharmaceutically acceptable vehicle or excipient" includes diluents and fillers which are pharmaceutically acceptable for method of administration, are sterile, and may be aqueous or oleaginous suspensions formulated using suitable dispersing or wetting agents and suspending agents. The particular pharmaceutically acceptable carrier and the ratio of active compound to carrier are determined by the solubility and chemical properties of the

30 composition, the particular mode of administration, and standard pharmaceutical practice.

Any nucleic acid, polypeptide, vector, or host cell of the invention will preferably be introduced *in vivo* in a pharmaceutically acceptable vehicle or excipient. The phrase "pharmaceutically acceptable" refers to molecular entities and compositions that are

physiologically tolerable and do not typically produce an allergic or similar untoward reaction, such as gastric upset, dizziness and the like, when administered to a human. Preferably, as used herein, the term "pharmaceutically acceptable" means approved by a regulatory agency of the Federal or a state government or listed in the U.S. Pharmacopeia or other generally
5 recognized pharmacopeia for use in animals, and more particularly in humans. The term "excipient" refers to a diluent, adjuvant, excipient, or vehicle with which the compound is administered. Such pharmaceutical carriers can be sterile liquids, such as water and oils, including those of petroleum, animal, vegetable or synthetic origin, such as peanut oil, soybean oil, mineral oil, sesame oil and the like. Water or aqueous solution saline solutions
10 and aqueous dextrose and glycerol solutions are preferably employed as excipients, particularly for injectable solutions. Suitable pharmaceutical excipients are described in "Remington's Pharmaceutical Sciences" by E.W. Martin.

The pharmaceutical compositions according to the invention may be equally well administered by the oral, rectal, parenteral, intravenous, subcutaneous or intradermal route.

15 According to another aspect, the subject of the invention is also a preventive and/or curative therapeutic method of treating diseases caused by a deficiency in the transport of cholesterol or inflammatory lipid substances, comprising administering to a patient or subject a nucleic acid encoding any one of the ABCC12 proteins isoforms, said nucleic acid being combined with one or more physiologically compatible vehicles and/or excipients.

20 In another embodiment, the nucleic acid, recombinant vectors, and compositions according to the invention can be delivered in a vesicle, in particular a liposome (see Langer, 1990, *Science*, 249:1527-1533; Treat et al., 1989, *Liposomes in the Therapy of Infectious Disease and Cancer*, Lopez-Berestein and Fidler (eds.), Liss: New York, pp. 353-365; and Lopez-Berestein, 1989, In: *Liposomes in the Therapy of Infectious Disease and Cancer*,
25 Lopez-Berestein and Fidler (eds.), Liss: New York, pp. 317-327).

In a further aspect, recombinant cells that have been transformed with a nucleic acid according to the invention and that express high levels of any one of the ABCC12 proteins isoforms according to the invention can be transplanted in a subject in need of the ABCC12 polypeptide. Preferably autologous cells transformed with the ABCC12 encoding nucleic acid
30 according to the invention are transplanted to avoid rejection; alternatively, technology is available to shield non-autologous cells that produce soluble factors within a polymer matrix that prevents immune recognition and rejection.

A subject in whom administration of the nucleic acids, polypeptides, recombinant vectors, recombinant host cells, and compositions according to the invention is performed is preferably a human, but can be any animal. Thus, as can be readily appreciated by one of ordinary skill in the art, the methods and pharmaceutical compositions of the present invention are particularly suited to administration to any animal, particularly a mammal, and including, but by no means limited to, domestic animals, such as feline or canine subjects, farm animals, such as but not limited to bovine, equine, caprine, ovine, and porcine subjects, wild animals (whether in the wild or in a zoological garden), research animals, such as mice, rats, rabbits, goats, sheep, pigs, dogs, cats, etc., avian species, such as chickens, turkeys, songbirds, etc., *i.e.*, for veterinary medical use.

Preferably, a pharmaceutical composition comprising a nucleic acid, a recombinant vector, or a recombinant host cell, as defined above, will be administered to the patient or subject.

METHODS OF SCREENING AN AGONIST OR ANTAGONIST COMPOUND FOR THE ABCC12 POLYPEPTIDE

According to another aspect, the invention also relates to various methods of screening compounds or small molecules for therapeutic use which are useful in the treatment of diseases due to a deficiency in the transport of cholesterol or inflammatory lipid substances.

The invention therefore also relates to the use any one of the ABCC12 proteins isoforms, or of cells expressing the ABCC12 polypeptide, for screening active ingredients for the prevention and/or treatment of diseases resulting from a dysfunction in the ABCC12 gene. The catalytic sites and oligopeptide or immunogenic fragments any one of the ABCC12 proteins isoforms can serve for screening product libraries by a whole range of existing techniques. The polypeptide fragment used in this type of screening may be free in solution, bound to a solid support, at the cell surface or in the cell. The formation of the binding complexes between the ABCC12 polypeptides isoforms fragments and the tested agent can then be measured.

Another product screening technique which may be used in high-flux screenings giving access to products having affinity for the protein of interest is described in application WO84/03564. In this method, applied to any one of the ABCC12 proteins isoforms, various products are synthesized on a solid surface. These products react with the

corresponding ABCC12 proteins isoforms or fragment thereof and the complex is washed. The products binding any one of the ABCC12 proteins isoforms are then detected by methods known to persons skilled in the art. Non-neutralizing antibodies can also be used to capture a peptide and immobilize it on a support.

5 Another possibility is to perform a product screening method using the ABCC12 neutralizing competition antibodies, any one of the ABCC12 proteins isoforms and a product potentially binding any one of the ABCC12 proteins isoforms. In this manner, the antibodies may be used to detect the presence of a peptide having a common antigenic unit with any one of the ABCC12 proteins isoforms.

10 Of the products to be evaluated for their ability to increase activity of ABCC12, there may be mentioned in particular kinase-specific ATP homologs involved in the activation of the molecules, as well as phosphatases, which may be able to avoid the dephosphorylation resulting from said kinases. There may be mentioned in particular inhibitors of the phosphodiesterase (PDE) theophylline and 3-isobutyl-1-methylxanthine type or the
15 adenylyl cyclase forskolin activators.

Accordingly, this invention relates to the use of any method of screening products, *i.e.*, compounds, small molecules, and the like, based on the method of translocation of cholesterol or lipophilic substances between the membranes or vesicles, this being in all synthetic or cellular types, that is to say of mammals, insects, bacteria, or yeasts expressing constitutively
20 or having incorporated human ABCC12 encoding nucleic acid. To this effect, labeled lipophilic substances analogs may be used.

Furthermore, knowing that the disruption of numerous transporters have been described (van den Hazel et al., 1999, *J. Biol Chem*, 274: 1934-41), it is possible to think of using cellular mutants having a characteristic phenotype and to complement the function
25 thereof with the ABCC12 proteins isoforms and to use the whole for screening purposes.

The invention also relates to a method of screening a compound or small molecule active on the transport of a substrate, an agonist or antagonist of any one of the ABCC12 polypeptides, said method comprising the following steps:

a) preparing a membrane vesicle comprising any one of the ABCC12 proteins isoforms
30 and the substrate comprising a detectable marker;

b) incubating the vesicle obtained in step a) with an agonist or antagonist candidate compound;

c) qualitatively and/or quantitatively measuring release of the substrate comprising a detectable marker; and

d) comparing the release measurement obtained in step b) with a measurement of release of labeled substrate by a vesicle that has not been previously incubated with the
5 agonist or antagonist candidate compound.

ABCC12 polypeptides isoforms comprise an amino acid sequence of SEQ ID NO: 33 and 34.

According to a first aspect of the above screening method, the membrane vesicle is a synthetic lipid vesicle, which may be prepared according to techniques well known to a person
10 skilled in the art. According to this particular aspect, the ABCC12 proteins isoforms may be recombinant proteins.

According to a second aspect, the membrane vesicle is a vesicle of a plasma membrane derived from cells expressing at least one of ABCC12 polypeptides isoforms. These may be cells naturally expressing any one of the ABCC12 proteins isoforms or cells transfected with a
15 nucleic acid encoding at least one ABCC12 polypeptide or recombinant vector comprising a nucleic acid encoding the ABCC12 polypeptides isoforms.

According to a third aspect of the above screening method, the substrate is an anionic drug, such as the methotrexate (MTX).

According to a fourth aspect of the above screening method, the substrate is a neutral
20 drug conjugated to acidic ligands such as GSH, glucuronate, or sulfate conjugated drugs.

According to a fifth aspect, the substrate is radioactively labelled, for example with an isotope chosen from ^3H or ^{125}I .

According to a sixth aspect, the substrate is labelled with a fluorescent compound, such as NBD or pyrene.

25 According to a seventh aspect, the membrane vesicle comprising the labelled substrates and the ABCC12 polypeptides is immobilized at the surface of a solid support prior to step b).

According to a eighth aspect, the measurement of the fluorescence or of the radioactivity released by the vesicle is the direct reflection of the activity of the substrate
30 transport by any one of the ABCC12 proteins isoforms.

The invention also relates to a method of screening a compound or small molecule active on the transport of anion, an agonist or antagonist of any one of the ABCC12 proteins isoforms, said method comprising the following steps:

a) obtaining cells, for example a cell line, that, either naturally or after transfecting the cell with the ABCC12 encoding nucleic acid, expresses any one of the ABCC12 proteins isoforms;

5 b) incubating the cells of step a) in the presence of an anion labelled with a detectable marker;

c) washing the cells of step b) in order to remove the excess of the labelled anion which has not penetrated into these cells;

d) incubating the cells obtained in step c) with an agonist or antagonist candidate compound for the ABCC12 polypeptides;

10 e) measuring efflux of the labelled anion; and

f) comparing the value of efflux of the labelled anion determined in step e) with a value of the efflux of a labelled anion measured with cells that have not been previously incubated in the presence of the agonist or antagonist candidate compound of ABCC12 polypeptides.

15 In a first specific embodiment, the ABCC12 polypeptides isoforms comprise an amino acid sequence of SEQ ID NO: 33 and 34.

According to a second aspect, the cells used in the screening method described above may be cells not naturally expressing, or alternatively expressing at a low level, the ABCC12 polypeptides, said cells being transfected with a recombinant vector according to the invention
20 capable of directing the expression of a nucleic acid encoding any one of the ABCC12 proteins isoforms.

According to a third aspect, the cells may be cells having a natural deficiency in anion transport, or cells pretreated with one or more anion channel inhibitors such as VerapamilTM or tetraethylammonium.

25 According to a fourth aspect of said screening method, the anion is a radioactively labelled iodide, such as the salts $K^{125}I$ or $Na^{125}I$.

According to a fifth aspect, the measurement of efflux of the labelled anion is determined periodically over time during the experiment, thus making it possible to also establish a kinetic measurement of this efflux.

30 According to a sixth aspect, the value of efflux of the labelled anion is determined by measuring the quantity of labelled anion present at a given time in the cell culture supernatant.

According to a seventh aspect, the value of efflux of the labelled anion is determined as the proportion of radioactivity found in the cell culture supernatant relative to the total

radioactivity corresponding to the sum of the radioactivity found in the cell lysate and the radioactivity found in the cell culture supernatant.

in the presence of a compound stimulating the production of interleukine and of an agonist or antagonist candidate compound;

5 The following examples are intended to further illustrate the present invention but do not limit the invention.

EXAMPLES

EXAMPLE 1 : Search of human ABCC12 gene in genomic database

10 Searches of the GeneBank HTGS database were performed with the TBLASTN and TBLASTP programs with the known ABC transporter nucleotide and protein sequences as queries. Amino acid alignments were generated with the PILEUP program included in the Genetics Computer Group (GCG) Package. The GRAIL and GeneScan programs on Genome analysis pipeline I were utilized to predict genomic structures of the new genes.

15 The human ABCC12 transporter gene sequence was detected on the bacterial artificial chromosome (BAC) clone #AC007600 from the GenBank HTGS database. cDNA sequencing, genomic structure prediction programs, and computer searches determined the sequence and genomic structure of the new gene belonging to the ABCC subfamily.

 Primers were designed from expressed sequence tag (EST) clone sequences and
20 from predicted cDNA sequences from 5' and 3' regions of genes. ABCC12 cDNA sequence was confirmed by PCR amplification of testis or liver cDNA (Clontech). Sequencing was performed on the ABI 377 sequencer according to the manufacturer's protocols (Perkin Elmer). Positions of introns were determined by comparison between genomic (BAC AC007600) and cDNA sequences.

25

EXAMPLE 2: Radiation hybrid Mapping (Figure 2)

 The chromosomal localization of the human ABCC12 gene was determined by mapping on the GeneBridge4 radiation hybrid panel (Research Genetics), according to the manufacturer's protocol.

30 Radiation hybrid mapping placed *ABCC12* to the centromeric region of human chromosome 16, flanked by markers D16S3093 and D16S409 (Figure 2). The region encompasses 5.4 cM, or 132.5 cR, and could not be narrowed down further due to the lack of recombination and/or mapped polymorphic markers in this region. The ABCC12 gene

most likely localized on chromosome 16q12.1, since it maps closer to the 16q marker D16S409 (13.24 cR) than the 16p marker D16S3093 (119.40 cR) (Figure 2). The ABCC12 was located at the same locus, separated by about 200kb from ABCC11. ABCC11 and ABCC12 are located tandemly with their 5' ends facing towards the centromere. Two more
 5 ABCC subfamily genes, *ABCC1* and *ABCC6*, have been mapped to the short arm of the same chromosome, to 16p13.1 (Cole et al., (1992) *Science*, 258, 1650-1654 ; Allikmets et al., (1996) *Human Mol. Genet.* (1996) 5, 1649-1655. The 3' ends of *ABCC1* and *ABCC6* are only about 9 kb apart from each other so the genes face opposite directions (Cai et al., *J Mol Med*, 2000, 78, 36-46).

10 The locus for paroxysmal kinesigenic choreoathetosis (PKC) has been assigned to 16p11.2-q12.1, between markers D16S3093 and D16S416 (Tomita et al., *Am J Hum Genet*, 1999, 65, 1688-97 ; Bennett et al., 2000; Figure 2). An overlapping locus has been predicted to contain the gene for infantile convulsions with paroxysmal choreoathetosis (ICCA; Lee et al., *Hum Genet*, 1998, 103, 608-12). It was suggested that mutations in a
 15 novel ion-channel gene on chromosome 16 might be responsible for PKC and/or ICCA (Bennett et al., *Neurology*, 2000, 54, 125-30). Since another member of the ABCC subfamily, cystic fibrosis transmembrane conductance regulator (CFTR), functions as a cyclic AMP-regulated channel, and also as a regulator of other ion channels and transporters (Kleizen et al., *J Cell Biol*, 2000, 79, 544-56), it is feasible that this gene may
 20 function as ion channels (or regulators) and that mutations in these could result in a disease phenotype. Expression analysis of ABCC12 reveals that this gene is expressed in muscle and brain tissues, supporting the working hypothesis of the skeletal muscle or brain-related etiology of PKC. In summary, chromosomal localization, potential function, and expression profile make this gene a promising candidate for PKC/ICCA.

25

EXAMPLE 3: Phylogenetic Analysis (Figure 5)

Phylogenetic analyses of the ABCC subfamily proteins clearly demonstrate a relatively recent duplication of the ABCC11 and ABCC12 genes (Fig 5). The resulting neighbor-joining tree shows with maximum confidence (100-level of bootstrap support) a
 30 close evolutionary relationship of the ABCC11/ABCC12 cluster with the ABCC5 gene (Fig 5). In addition, the analysis of the tree suggests a recent duplication of the ABCC8 and ABCC9 genes, while ABCC10 seems to be one of the first genes to separate from the common ancestor. ABCC11, ABCC12, ABCC3, and ABCC6 genes constitute a well-

defined sub-cluster, while the ABCC4 and CFTR (ABCC7) genes form another reliable subset despite apparent early divergence.

EXAMPLE 4 : Cell lines.

5 The human erythroleukemia K562 cells were obtained from the American Tissue Culture Collection (Rockville MD) and were cultured in RPMI-1640 medium supplemented with 10% fetal calf serum, 2 mM 2-glutamine. The 9-(2-phosphonylmethoxyethyl)adenine (PMEA) resistant cells, K562/PMEA, were derived as described by (Hatse et al., *Mol Pharmacol*, 1996, 50, 1231-42). T-lymphoblast cell lines
10 CEM and (-)2',3'-dideoxy-3'-thiacytidine (3TC) resistant CEM-3TC cells [REFERENCES]. Cell lines, CEMss and CEM-r1, were described by (Robbins et al., *Mol Pharmacol*, 1995, 47, 391-7). CEM-r1 is highly resistant to PMEA due to an overexpression of *ABCC4* (Schuetz et al., *Nat Med*, 1999, 5, 1048-51). Total RNA from these six cell lines (three pairs of wild type and resistant cell lines) was isolated with TRIZOL (GIBCO BRL), and
15 RT-PCR performed at varying cycle numbers oligonucleotide primers as mentioned in the brief description of Figure 3, products were subcloned and verified by direct sequencing.

Reverse transcription

In a total volume of 11.5 µl, 500 ng of mRNA poly(A)+ (Clontech) mixed with 500
20 ng of oligodT are denaturated at 70°C for 10 min and then chilled on ice. After addition of 10 units of RNAsin, 10 mM DTT, 0.5 mM dNTP, Superscript first strand buffer and 200 units of Superscript II (Life Technologies), the reaction is incubated for 45 min at 42°C.

PCR

25 Each polymerase chain reaction contained 400 µM each dNTP, 2 units of *Thermus aquaticus* (Taq) DNA polymerase (Ampli Taq Gold; Perkin Elmer), 0.5 µM each primer, 2.5 mM MgCl₂, PCR buffer and 50 ng of DNA, or about 25 ng of cDNA, or 1/50th of primary PCR mixture. Reactions were carried out for 30 cycles in a Perkin Elmer 9700 thermal cycler in 96-well microtiter plates. After an initial denaturation at 94°C for 10 min, each cycle
30 consisted of: a denaturation step of 30 s (94°C), a hybridization step of 30 s (64°C for 2 cycles, 61°C for 2 cycles, 58°C for 2 cycles and 55°C for 28 cycles), and an elongation step of 1 min/kb (72°C). PCR ended with a final 72°C extension of 7 min. In case of RT-PCR,

control reactions without reverse transcriptase and reactions containing water instead of cDNA were performed for every sample.

DNA Sequencing

5 PCR products are analyzed and quantified by agarose gel electrophoresis, purified with a P100 column. Purified PCR products were sequenced using ABI Prism BigDye terminator cycle sequencing kit (Perkin Elmer Applied Biosystems). The sequence reaction mixture was purified using Microcon-100 microconcentrators (Amicon, Inc., Beverly). Sequencing reactions were resolved on an ABI 377 DNA sequencer (Perkin Elmer Applied Biosystems)
10 according to manufacturer's protocol (Applied Biosystems, Perkin Elmer).

Primers

Oligonucleotides were selected using Prime from GCG package or Oligo 4 (National Biosciences, Inc.) softwares. Primers were ordered from Life Technologies, Ltd and used
15 without further purification.

EXAMPLE 5: Expression of ABCC12 in human tissues and nucleoside -resistant cell lines

The expression pattern for the ABCC12 gene was examined by PCR on multiple
20 tissue expression arrays (Clontech) with gene specific primers resulting in about 500bp PCR fragments (Figure 3). Approximately 5000 bp mRNA species was observed by Northern blot (data not shown). The primers used in expression studies amplified the ABCC12 cDNA from exon 6 to exon 9, resulting in a 588 bp PCR fragment (Figure 3).

Systematic analysis of the tissue source of the ABCC12 ESTs from the public
25 dbEST and the proprietary Incyte LifeSeq Gold databases resulted in 18 ESTs, with the majority being derived from CNS (11). The others were from testis (3 clones), and immune system (4).

EXAMPLE 6 : Construction of the expression vector containing the complete cDNA of 30 ABCC12 in mammalian cells

The ABCC12 gene may be expressed in mammalian cells. A typical eukaryotic expression vector contains a promoter which allows the initiation of the transcription of the mRNA, a sequence encoding the protein, and the signals required for the termination of the

transcription and for the polyadenylation of the transcript. It also contains additional signals such as enhancers, the Kozak sequence and sequences necessary for the splicing of the mRNA. An effective transcription is obtained with the early and late elements of the SV40 virus promoters, the retroviral LTRs or the CMV virus early promoter. However, cellular
5 elements such as the actin promoter may also be used. Many expression vectors may be used to carry out the present invention, an example of such a vector is pcDNA3 (Invitrogen).

EXAMPLE 7 : Production of normal and mutated ABCC12 polypeptides isoforms

The normal ABCC12 polypeptide encoded by complete corresponding cDNAs whose
10 isolation is described in Example 2, or the mutated ABCC12 polypeptide whose complete cDNA may also be obtained according to the techniques described in Example 2, may be easily produced in a bacterial or insect cell expression system using the baculovirus vectors or in mammalian cells with or without the vaccinia virus vectors. All the methods are now widely described and are known to persons skilled in the art. A detailed description thereof
15 will be found for example in F. Ausubel et al. (1989, Current Protocols in Molecular Biology, Green Publishing Associates and Wiley Interscience, N.Y).

EXAMPLE 8 : Production of an antibody directed against a mutated ABCC12 polypeptide.

20 The antibodies in the present invention may be prepared by various methods (Current Protocols In Molecular Biology Volume 1 edited by Frederick M. Ausubel, Roger Brent, Robert E. Kingston, David D. Moore, J.G. Seidman, John A. Smith, Kevin Struhl - Massachusetts General Hospital Harvard Medical School, chapter 11, 1989). For example, the cells expressing a polypeptide of the present invention are injected into an animal in order to
25 induce the production of serum containing the antibodies. In one of the methods described, the proteins are prepared and purified so as to avoid contaminations. Such a preparation is then introduced into the animal with the aim of producing polyclonal antisera having a higher activity.

In the preferred method, the antibodies of the present invention are monoclonal
30 antibodies. Such monoclonal antibodies may be prepared using the hybridoma technique (Köhler et al, 1975, Nature, 256:495 ; Köhler et al, 1976, Eur. J. Immunol. 6:292; Köhler et al, 1976, Eur. J. Immunol., 6:511; Hammeling et al., 1981, Monoclonal Antibodies and T-Cell Hybridomas, Elsevier, N.Y., pp. 563-681). In general, such methods involve immunizing the

animal (preferably a mouse) with a polypeptide or better still with a cell expressing the polypeptide. These cells may be cultured in a suitable tissue culture medium. However, it is preferable to culture the cells in an Eagle medium (modified Earle) supplemented with 10% fetal bovine serum (inactivated at 56°C) and supplemented with about 10 g /l of nonessential amino acids, 1000 U/ml of penicillin and about 100 µg/ml of streptomycin.

The splenocytes of these mice are extracted and fused with a suitable myeloma cell line. However, it is preferable to use the parental myeloma cell line (SP2O) available from the ATCC. After fusion, the resulting hybridoma cells are selectively maintained in HAT medium and then cloned by limiting dilution as described by Wands et al. (1981, Gastroenterology, 80:225-232). The hybridoma cells obtained after such a selection are tested in order to identify the clones secreting antibodies capable of binding to the polypeptide.

Moreover, other antibodies capable of binding to the polypeptide may be produced according to a 2-stage procedure using anti-idiotypic antibodies such a method is based on the fact that the antibodies are themselves antigens and consequently it is possible to obtain an antibody recognizing another antibody. According to this method, the antibodies specific for the protein are used to immunize an animal, preferably a mouse. The splenocytes of this animal are then used to produce hybridoma cells, and the latter are screened in order to identify the clones which produce an antibody whose capacity to bind to the specific antibody-protein complex may be blocked by the polypeptide. These antibodies may be used to immunize an animal in order to induce the formation of antibodies specific for the protein in a large quantity.

It is preferable to use Fab and F(ab')₂ and the other fragments of the antibodies of the present invention according to the methods described here. Such fragments are typically produced by proteolytic cleavage with the aid of enzymes such as Papain (in order to produce the Fab fragments) or Pepsin (in order to produce the F(ab')₂ fragments). Otherwise, the secreted fragments recognizing the protein may be produced by applying the recombinant DNA or synthetic chemistry technology.

For the *in vivo* use of antibodies in humans, it would be preferable to use "humanized" chimeric monoclonal antibodies. Such antibodies may be produced using genetic constructs derived from hybridoma cells producing the monoclonal antibodies described above. The methods for producing the chimeric antibodies are known to persons skilled in the art (for a review, see : Morrison (1985. Science 229:1202); Oi et al., (1986, Biotechnology, 4:214); Cabilly et al., US patent No. 4,816,567; Taniguchi et al., EP 171496; Morrison et al.,

EP 173494 ; Neuberger et al., WO 8601533 ; Robinson et al., WO 8702671 ; Boulianne et al ; (1984, Nature, 312:643) ; and Neuberger et al., (1985, Nature, 314:268).

EXAMPLE 9: Identification of a causal gene for a disease linked to the chromosome locus, such as paroxysmal kinesigenic choreoathetosis by causal mutation or a transcriptional difference

Northern blot or RT-PCR analysis, according to the methods described in Example 4, using RNA specific to affected or nonaffected individuals makes it possible to detect notable variations in the level of expression of the gene studied, in particular in the absence of transcription of the gene.

EXAMPLE 10: Construction of recombinant vectors comprising a nucleic acid encoding the ABCC12 protein

Synthesis of a nucleic acid encoding the human ABCC12 protein:

Total RNA (500 ng) isolated from a human cell (for example, placental tissue, Clontech, Palo Alto, CA, USA, or THP1 cells) may be used as source for the synthesis of the cDNA of the human ABCC12 gene. Methods to reverse transcribe mRNA to cDNA are well known in the art. For example, one may use the system "Superscript one step RT-PCR (Life Technologies, Gaithersburg, MD, USA).

Oligonucleotide primers specific for ABCC12 cDNA may be used for this purpose, containing sequences as set forth in any of SEQ ID NO: 35-46. These oligonucleotide primers may be synthesized by the phosphoramidite method on a DNA synthesizer of the ABI 394 type (Applied Biosystems, Foster City, CA, USA).

Sites recognized by the restriction enzyme NotI may be incorporated into the amplified ABCC12 cDNA to flank the cDNA region desired for insertion into the recombinant vector by a second amplification step using 50 ng of human ABCC12 cDNA as template, and 0.25 μ M of the ABCC12 specific oligonucleotide primers used above containing, at their 5' end, the site recognized by the restriction enzyme NotI (5'-GCGGCCGC-3'), in the presence of 200 μ M of each of said dideoxynucleotides dATP, dCTP, dTTP and dGTP as well as the *Pyrococcus furiosus* DNA polymerase (Stratagene, Inc. La Jolla, CA, USA).

The PCR reaction may be carried out over 30 cycles each comprising a step of denaturation at 95°C for one minute, a step of renaturation at 50°C for one minute and a step

of extension at 72°C for two minutes, in a thermocycler apparatus for PCR (Cetus Perkin Elmer Norwalk, CT, USA).

Cloning of the cDNA of the human ABCC12 gene into an expression vector:

5 The human ABCC12 cDNA insert may then be cloned into the NotI restriction site of an expression vector, for example, the pCMV vector containing a cytomegalovirus (CMV) early promoter and an enhancer sequence as well as the SV40 polyadenylation signal (Beg et al., 1990, PNAS, 87:3473; Applebaum-Boden, 1996, JCI 97), in order to produce an expression vector designated pABCC12.

10 The sequence of the cloned cDNA can be confirmed by sequencing on the two strands using the reaction set "ABI Prism Big Dye Terminator Cycle Sequencing ready" (marketed by Applied Biosystems, Foster City, CA, USA) in a capillary sequencer of the ABI 310 type (Applied Biosystems, Foster City, CA, USA).

15 Construction of a recombinant adenoviral vector containing the cDNA of the human ABCC12 gene:

Modification of the expression vector pCMV- β :

The β -galactosidase cDNA of the expression vector pCMV- β (Clontech, Palo Alto, CA, USA, Gene Bank Accession No. U02451) may be deleted by digestion with the
20 restriction endonuclease NotI and replaced with a multiple cloning site containing, from the 5' end to the 3' end, the following sites: NotI, AscI, RsrII, AvrII, SwaI, and NotI, cloned at the region of the NotI restriction site. The sequence of this multiple cloning site is:

5'-CGGCCGCGGCGCGCCCCGGACCGCCTAGGATTAAATCGCGGCCCGCG-3'.

The DNA fragment between the EcoRI and SanI sites of the modified expression
25 vector pCMV may be isolated and cloned into the modified XbaI site of the shuttle vector pXCXII (McKinnon et al., 1982, Gene, 19:33; McGrory et al., 1988, Virology, 163:614).

Modification of the shuttle vector pXCXII:

A multiple cloning site comprising, from the 5' end to the 3 end the XbaI, EcoRI, SfiI,
30 PmeI, NheI, SrfI, PacI, SalI and XbaI restriction sites having the sequence:

5'CTCTAGAATTCGGCCTCCGTGGCCGTTTAAACGCTAGCGCCCGGGCTTAATTAA
GTCGACTCTAGAGC-3', may be inserted at the level of the XbaI site (nucleotide at position

3329) of the vector pXCXII (McKinnon et al., 1982, *Gene* 19:33; McGrory et al., 1988, *Virology*, 163:614).

The EcoRI-SalI DNA fragment isolated from the modified vector pCMV- β containing the CMV promoter/enhancer, the donor and acceptor splicing sites of FV40 and the polyadenylation signal of FV40 may then be cloned into the EcoRI-SalI site of the modified shuttle vector pXCX, designated pCMV-11.

Preparation of the shuttle vector pAD12-ABCA:

The human ABCC12 cDNA is obtained by an RT-PCR reaction, as described above, and cloned at the level of the NotI site into the vector pCMV-12, resulting in the obtaining of the vector pCMV-ABCC12.

Construction of the ABC1 recombinant adenovirus:

The recombinant adenovirus containing the human ABCC12 cDNA may be constructed according to the technique described by McGrory et al. (1988, *Virology*, 163:614).

Briefly, the vector pAD12-ABCA is cotransfected with the vector tGM17 according to the technique of Chen and Okayama (1987, *Mol Cell Biol.*, 7:2745-2752).

Likewise, the vector pAD12-Luciferase was constructed and cotransfected with the vector pJM17.

The recombinant adenoviruses are identified by PCR amplification and subjected to two purification cycles before a large-scale amplification in the human embryonic kidney cell line HEK 293 (American Type Culture Collection, Rockville, MD, USA).

The infected cells are collected 48 to 72 hours after their infection with the adenoviral vectors and subjected to five freeze-thaw lysing cycles.

The crude lysates are extracted with the aid of Freon (Halocarbene 113, Matheson Product, Scaucus, N.J. USA), sedimented twice in cesium chloride supplemented with 0.2% murine albumine (Sigma Chemical Co., St Louis, MO, USA) and dialysed extensively against buffer composed of 150 mM NaCl, 10 mM Hepes (pH 7.4), 5 mM KCl, 1 mM MgCl₂, and 1 mM CaCl₂.

The recombinant adenoviruses are stored at -70°C and titrated before their administration to animals or their incubation with cells in culture.

The absence of wild-type contaminating adenovirus is confirmed by screening with the aid of PCR amplification using oligonucleotide primers located in the structural portion of the deleted region.

5 Validation of the expression of the human ABCC12 cDNA:

Polyclonal antibodies specific for a human ABCC12 polypeptide may be prepared as described above in rabbits and chicks by injecting a synthetic polypeptide fragment derived from an ABCC12 protein, comprising all or part of an amino acid sequence as described in SEQ ID NO: 33 or 34. These polyclonal antibodies are used to detect and/or quantify the
10 expression of the human ABCC12 gene in cells and animal models by immunoblotting and/or immunodetection.

Expression *in vitro* of the human ABCC12 cDNA in cells:

Cells of the HEK293 line and of the COS-7 line (American Tissue Culture Collection,
15 Bethesda, MD, USA), as well as fibroblasts in primary culture derived from Tangier patients or from patients suffering from hypo-alpha-lipoproteinemia are transfected with the expression vector pCMV-ABCC12 (5-25 µg) using Lipofectamine (BRL, Gaithersburg, MD, USA) or by coprecipitation with the aid of calcium chloride (Chen et al., 1987, Mol Cell Biol., 7:2745-2752).

20 These cells may also be infected with the vector pABCC12-AdV (Index of infection, MOI=10).

The expression of human ABCC12 may be monitored by immunoblotting as well as by quantification of the efflux of cholesterol induced by apoA-1 using transfected and/or infected cells.

25

Expression *in vivo* of the ABCC12 gene in various animal models:

An appropriate volume (100 to 300 µl) of a medium containing the purified recombinant adenovirus (pABCA-AdV or pLucif-AdV) containing from 10^8 to 10^9 lysis plaque-forming units (pfu) are infused into the Saphenous vein of mice (C57BL/6, both
30 control mice and models of transgenic or knock-out mice) on day 0 of the experiment.

The evaluation of the physiological role of the ABCC12 protein in the transport of cholesterol or inflammatory lipid substances is carried out by determining the total quantity of

cholesterol or appropriate inflammatory lipid substances before (day zero) and after (days 2, 4, 7, 10, 14) the administration of the adenovirus.

Kinetic studies with the aid of radioactively labelled products are carried out on day 5 after the administration of the vectors rLucif-AdV and rABCA-AdV in order to evaluate the effect of the expression of the ABCC12 gene on the transport of cholesterol and inflammatory lipid substances.

Furthermore, *transgenic mice and rabbits overexpressing the ABCC12 gene* may be produced, in accordance with the teaching of Vaisman (1995) and Hoeg (1996) using constructs containing the human ABCC12 cDNA under the control of endogenous promoter such as ABCC12, or CMV or apoE.

The present invention is not to be limited in scope by the specific embodiments described herein. Indeed, various modifications of the invention in addition to those described herein will become apparent to those skilled in the art from the foregoing description and the accompanying figures. Such modifications are intended to fall within the scope of the appended claims.

LISTE DE SEQUENCES

<110> AVENTIS PHARMA SA
THE GOVERNMENT OF THE UNITED STATES,

<120> NUCLEIC ACIDS OF THE HUMAN ABCC12 GENE, VECTORS
CONTAINING SUCH NUCLEIC ACIDS, AND USES THEREOF

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cagcagtttt ttatgggtgg gtattattctc gtgatcttgg ctgctgtgtt tcctgctgtc 180
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Val Lys Gly Tyr Arg Gln Arg Leu Thr Val Asp Thr Leu Pro Pro Leu
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Ser Thr Tyr Asp Ser Ser Asp Thr Asn Ala Lys Arg Phe Arg Val Leu
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Trp Asp Glu Glu Val Ala Arg Val Gly Pro Glu Lys Ala Ser Leu Ser
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Ile His Gln Ile Leu Gln Gln Thr Glu Arg Thr Ser Gly Lys Val Trp
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Val Phe Phe Trp Ala Leu Ala Trp Ala Ile Asn Tyr Arg Thr Ala Ile
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Arg Leu Lys Val Ala Leu Ser Thr Leu Val Phe Glu Asn Leu Val Ser
          195          200          205
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13

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Leu	Leu	Glu	Asp	Gly	Glu	Ile	Cys	Glu	Lys	Gly	Thr	His	Lys	Glu	Leu
		675					680					685			
Met	Glu	Glu	Arg	Gly	Arg	Tyr	Ala	Lys	Leu	Ile	His	Asn	Leu	Arg	Gly
	690					695					700				
Leu	Gln	Phe	Lys	Asp	Pro	Glu	His	Leu	Tyr	Asn	Ala	Ala	Met	Val	Glu
705					710					715					720

Ala	Phe	Lys	Glu	Ser	Pro	Ala	Glu	Arg	Glu	Glu	Asp	Ala	Gly	Ile	Ile	
				725					730					735		
Val	Leu	Ala	Pro	Gly	Asn	Glu	Lys	Asp	Glu	Gly	Lys	Glu	Ser	Glu	Thr	
			740					745					750			
Gly	Ser	Glu	Phe	Val	Asp	Thr	Lys	Val	Pro	Glu	His	Gln	Leu	Ile	Gln	
		755					760					765				
Thr	Glu	Ser	Pro	Gln	Glu	Gly	Thr	Val	Thr	Trp	Lys	Thr	Tyr	His	Thr	
	770					775					780					
Tyr	Ile	Lys	Ala	Ser	Gly	Gly	Tyr	Leu	Leu	Ser	Leu	Phe	Thr	Val	Phe	
785					790					795					800	
Leu	Phe	Leu	Leu	Met	Ile	Gly	Ser	Ala	Ala	Phe	Ser	Asn	Trp	Trp	Leu	
				805					810					815		
Gly	Leu	Trp	Leu	Asp	Lys	Gly	Ser	Arg	Met	Thr	Cys	Gly	Pro	Gln	Gly	
			820					825					830			
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		835					840					845				
His	Val	Tyr	Gln	Trp	Val	Tyr	Thr	Ala	Ser	Met	Val	Phe	Met	Leu	Val	
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Phe	Gly	Val	Thr	Lys	Gly	Phe	Val	Phe	Thr	Lys	Thr	Thr	Leu	Met	Ala	
865					870					875					880	
Ser	Ser	Ser	Leu	His	Asp	Thr	Val	Phe	Asp	Lys	Ile	Leu	Lys	Ser	Pro	
				885					890					895		
Met	Ser	Phe	Phe	Asp	Thr	Thr	Pro	Thr	Gly	Arg	Leu	Met	Asn	Arg	Phe	
			900					905					910			
Ser	Lys	Asp	Met	Asp	Glu	Leu	Asp	Val	Arg	Leu	Pro	Phe	His	Ala	Glu	
		915					920					925				
Asn	Phe	Leu	Gln	Gln	Phe	Phe	Met	Val	Val	Phe	Ile	Leu	Val	Ile	Leu	
	930					935					940					
Ala	Ala	Val	Phe	Pro	Ala	Val	Leu	Leu	Val	Val	Ala	Ser	Leu	Ala	Val	
945					950					955					960	
Gly	Phe	Phe	Ile	Leu	Leu	Arg	Ile	Phe	His	Arg	Gly	Val	Gln	Glu	Leu	
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Lys	Lys	Val	Glu	Asn	Val	Ser	Arg	Ser	Pro	Trp	Phe	Thr	His	Ile	Thr	
			980					985					990			
Ser	Ser	Met	Gln	Gly	Leu	Gly	Ile	Ile	His	Ala	Tyr	Gly	Lys	Lys	Glu	
		995					1000					1005				
Ser	Cys	Ile	Thr	Tyr	His	Leu	Leu	Tyr	Phe	Asn	Cys	Ala	Leu	Arg	Trp	
	1010					1015				1020						
Phe	Ala	Leu	Arg	Met	Asp	Val	Leu	Met	Asn	Ile	Leu	Thr	Phe	Thr	Val	
1025				1030					1035						1040	
Ala	Leu	Leu	Val	Thr	Leu	Ser	Phe	Ser	Ser	Ile	Ser	Thr	Ser	Ser	Lys	
				1045				1050						1055		
Gly	Leu	Ser	Leu	Ser	Tyr	Ile	Ile	Gln	Leu	Ser	Gly	Leu	Leu	Gln	Val	
			1060					1065						1070		
Cys	Val	Arg	Thr	Gly	Thr	Glu	Thr	Gln	Ala	Lys	Phe	Thr	Ser	Val	Glu	
		1075				1080						1085				

15

Leu Leu Arg Glu Tyr Ile Ser Thr Cys Val Pro Glu Cys Thr His Pro
 1090 1095 1100
 Leu Lys Val Gly Thr Cys Pro Lys Asp Trp Pro Ser Cys Gly Glu Ile
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 Thr Phe Arg Asp Tyr Gln Met Arg Tyr Arg Asp Asn Thr Pro Leu Val
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 1140 1145 1150
 Val Gly Arg Thr Gly Ser Gly Lys Ser Ser Leu Gly Met Ala Leu Phe
 1155 1160 1165
 Arg Leu Val Glu Pro Ala Ser Gly Thr Ile Phe Ile Asp Glu Val Asp
 1170 1175 1180
 Ile Cys Ile Leu Ser Leu Glu Asp Leu Arg Thr Lys Leu Thr Val Ile
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 Pro Gln Asp Pro Val Leu Phe Val Gly Thr Val Arg Tyr Asn Leu Asp
 1205 1210 1215
 Pro Phe Glu Ser His Thr Asp Glu Met Leu Trp Gln Val Leu Glu Arg
 1220 1225 1230
 Thr Phe Met Arg Asp Thr Ile Met Lys Leu Pro Glu Lys Leu Gln Ala
 1235 1240 1245
 Glu Val Thr Glu Asn Gly Glu Asn Phe Ser Val Gly Glu Arg Gln Leu
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 Leu Cys Val Ala Arg Ala Leu Leu Arg Asn Ser Lys Ile Ile Leu Leu
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19

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23

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<400> 46

ggctctgtga gatgaatagg

20

CLAIMS

1. An isolated nucleic acid comprising any one of SEQ ID NOs: 1-32, or a complementary nucleotide sequence thereof.
- 5 2. An isolated nucleic acid comprising at least eight consecutive nucleotides of a nucleotide sequence of any one of SEQ ID NOs: 1-32, or a complementary nucleotide sequence thereof.
3. An isolated nucleic acid comprising at least 80% nucleotide identity with a nucleic acid comprising any one of SEQ ID NOs: 1-32, or a complementary nucleotide
10 sequence thereof.
4. The isolated nucleic acid according to claim 3, wherein the nucleic acid comprises an 85%, 90%, 95%, or 98% nucleotide identity with the nucleic acid comprising any one of SEQ ID NOs: 1-32, or a complementary nucleotide sequence thereof.
5. An isolated nucleic acid that hybridizes under high stringency conditions with a
15 nucleic acid comprising a) any one of SEQ ID NOs: 1-32, or a complementary nucleotide sequence thereof.
6. An isolated nucleic acid comprising a nucleotide sequence as depicted in any one of SEQ ID NOs: 1-32, or a complementary nucleotide sequence thereof.
7. A nucleotide probe or primer specific of ABCC12 gene, wherein the nucleotide
20 probe or primer comprises at least 15 consecutive nucleotides of a nucleotide sequence of any one of SEQ ID NOs: 1-32, or a complementary nucleotide sequence thereof.
8. A nucleotide probe or primer specific for an ABCC12 gene, wherein the nucleotide probe or primer comprises a nucleotide sequence of any one of SEQ ID NO: 35-46, or a complementary nucleotide sequence thereof.
- 25 9. A method of amplifying a region of the nucleic acid according to claim 1, wherein the method comprises:
 - a) contacting the nucleic acid with two nucleotide primers, wherein the first nucleotide primer hybridizes at a position 5' of the region of the nucleic acid, and the second nucleotide primer hybridizes at a position 3' of the region of the nucleic acid, in the presence of reagents
30 necessary for an amplification reaction; and
 - b) detecting the amplified nucleic acid region.

10. A method of amplifying a region of the nucleic acid according to claim 1, wherein the two nucleotide primers are selected from the group consisting of

a) a nucleotide primer comprising at least 15 consecutive nucleotides of a nucleotide sequence of any one of SEQ ID NOs: 1-32, or of a complementary nucleotide sequence,

5 b) a nucleotide primer as in any one of claims 7-9,

c) a nucleotide primer comprising a nucleotide sequence of any one of SEQ ID NOs: 35-46, or a nucleic acid having a complementary sequence thereof.

11. A kit for amplifying the nucleic acid according to claim 1, wherein the kit comprises:

10 a) two nucleotide primers whose hybridization position is located respectively 5' and 3' of the region of the nucleic acid; and optionally,

b) reagents necessary for an amplification reaction.

12. The kit according to claim 11, wherein the two nucleotide primers are selected from the group consisting of

15 a) a nucleotide primer comprising at least 15 consecutive nucleotides of a nucleotide sequence of any one of SEQ ID NOs: 1-32, or of a complementary nucleotide sequence,

b) a nucleotide primer as in any one of claims 7-9,

c) a nucleotide primer comprising a nucleotide sequence of any one of SEQ ID NOs: 35-46, or a nucleic acid having a complementary sequence thereof.

20 13. The nucleotide probe or primer according to any of claim 7-9, wherein the nucleotide probe or primer comprises a marker compound.

14. A method of detecting a nucleic acid according to claim 1, wherein the method comprises:

25 a) contacting the nucleic acid with a nucleotide probe selected from the group consisting of

1) a nucleotide probe comprising at least 15 consecutive nucleotides of a nucleotide sequence of any one of SEQ ID NOs: 1-32, or a complementary nucleotide sequence thereof,

2) a nucleotide primer as in any one of claims 7-9,

30 3) a nucleotide probe comprising a nucleotide sequence of any one of SEQ ID NOs: 35-46, or a complementary nucleotide sequence thereof, and

b) detecting a complex formed between the nucleic acid and the probe.

15. The method of claim 14, wherein the probe is immobilized on a support.

16. A kit for detecting the nucleic acid according to claim 1, wherein the kit comprises

a) a nucleotide probe selected from the group consisting of 1) a nucleotide probe comprising at least 15 consecutive nucleotides of a nucleotide sequence of any one of SEQ ID NOs: 1-32, or of a complementary nucleotide sequence, 2) a nucleotide primer as in any one of claims 7-9, 3) a nucleotide probe comprising a nucleotide sequence of any one of SEQ ID NOs: 35-46, or a complementary nucleotide sequence thereof, and optionally,

b) reagents necessary for a hybridization reaction.

17. The kit according to claim 16, wherein the probe is immobilized on a support.

18. A recombinant vector comprising the nucleic acid according claim 1.

19. The vector according to claim 18, wherein the vector is an adenovirus.

20. A recombinant host cell comprising the recombinant vector according to claim

21. A recombinant host cell comprising the nucleic acid according claim 1.

22. An isolated nucleic acid encoding a polypeptide comprising an amino acid sequence of any one of SEQ ID NO: 33 or 34.

23. A recombinant vector comprising the nucleic acid according to claim 22.

24. A recombinant host cell comprising the nucleic acid according to claim 22.

25. A recombinant host cell comprising the recombinant vector according to claim 23.

26. An isolated polypeptide selected from the group consisting of

a) a polypeptide comprising an amino acid sequence of the SEQ ID NO: 33 or 34,

b) a polypeptide fragment or variant of a polypeptide comprising an amino acid sequence of SEQ ID NO: 33 or 34, and

c) a polypeptide homologous to a polypeptide comprising amino acid sequence of SEQ ID NO: 33 or 34.

27. An antibody directed against the isolated polypeptide according to claim 26.

28. The antibody according to claim 27, wherein the antibody comprises a detectable compound.

29. A method of detecting a polypeptide, wherein the method comprises

a) contacting the polypeptide with an antibody according to claim 27; and

b) detecting an antigen/antibody complex formed between the polypeptide and the antibody.

30. A diagnostic kit for detecting a polypeptide, wherein the kit comprises

a) the antibody according to claim 27; and

b) a reagent allowing detection of an antigen/antibody complex formed between the polypeptide and the antibody.

31. A pharmaceutical composition comprising the nucleic acid according to claim 1 and a physiologically compatible excipient.

5 32. A pharmaceutical composition comprising the recombinant vector according to claim 18 and a physiologically compatible excipient.

33. Use of the nucleic acid according to claim 1 for the manufacture of a medicament intended for the prevention and/or treatment of a subject affected by paroxysmal kinesigenic choreoathetosis.

10 34. Use of a recombinant vector according to claim 21 for the manufacture of a medicament for the prevention and/or treatment of subjects affected by paroxysmal kinesigenic choreoathetosis.

35. Use of isolated ABCC12 polypeptide comprising an amino acid sequence of SEQ ID NO: 33 or 34 for the manufacture of a medicament intended for the prevention and/or
15 treatment of subjects affected by paroxysmal kinesigenic choreoathetosis.

36. A pharmaceutical composition comprising a polypeptide comprising an amino acid sequence of the SEQ ID NO: 33 or 34, and a physiologically compatible excipient.

37. Use of isolated ABCC12 polypeptide comprising an amino acid sequence of the SEQ ID NO: 33 or 34 for screening an active ingredient for the prevention or treatment of
20 paroxysmal kinesigenic choreoathetosis.

38. Use of a recombinant host cell expressing the ABCC12 polypeptide comprising an amino acid sequence of SEQ ID NO: 33 or 34 for screening an active ingredient for the prevention or treatment of paroxysmal kinesigenic choreoathetosis.

39. A method of screening an agonist or an antagonist of the ABCC12 polypeptide,
25 wherein the method comprises

a) preparing a membrane vesicle comprising at least one of the ABCC12 polypeptide and a substrate comprising a detectable marker;

b) incubating the vesicle obtained in step a) with an agonist or antagonist candidate compound;

30 c) qualitatively and/or quantitatively measuring a release of the substrate comprising the detectable marker; and

d) comparing the release of the substrate measured in step b) with a measurement of a release of a labeled substrate by a membrane vesicle that has not been previously incubated with the agonist or antagonist candidate compound.

40. A method of screening an agonist, or an antagonist of ABCC12 polypeptide,
5 wherein the method comprises

a) incubating a cell that expresses the ABCC12 polypeptide with an anion labeled with a detectable marker;

b) washing the cell of step a) whereby excess labeled anion that has not penetrated into the cell is removed;

10 c) incubating the cell obtained in step b) with an agonist or antagonist candidate compound for the ABCC12 polypeptide;

d) measuring efflux of the labeled anion from the cell; and

e) comparing the efflux of the labeled anion determined in step d) with efflux of a labeled anion measured with a cell that has not been previously incubated with the agonist or
15 antagonist candidate compound.

41. An implant comprising the recombinant host cell according to claim 24 or 25.

ABCC11	~~~~~	~~~~~MTR	KRTYWPNSS	GGLVNRGIDI	GDDMVSGLIY	KTYTLQDGEW	SOQRNPBPAP	GRAAVPFWGK	YDAARRMKIP	FRPKPREPAP	QPLDNAGLFS
ABCC12	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~MVGEGY	LTSDLDQGR	LTSDLDQGR	RRSFAR..R	YDPSIKTMIP	VRECARLAP	NPVDDAGILS
ABCC5	MKDIDIGKEY	IIPSPGYRSV	RERTSTSGTH	RDREDSKFRR	TRPLEQDAL	EHAARAGLS	LDASMSISQLR	ILDEEHKGGK	YHGLSALKH	INTSKHQ..	HPVDNAGLFS
ABCC11	YLVSWHLPPL	MIQSLRSRL	DENLPPPLSV	HUASDKNVOR	LHRLWEEBVS	RRGIEKASVL	LVMLEPQRTS	LFTDALLGTC	FCIASVLGPI	LITPKILEYS	EEOLGNVWHG
ABCC12	FAFTSWLTPV	MVKGYKHRL	TVDTLPELST	YDSSTNAKR	FRVLWDEBYA	HVGPEKASIS	HVVWKFQNR	VLMDEIVANEL	CLIMAAIGPV	ILHQILQQT	ERTSGKWVG
ABCC5	CMPTSWLSSS	ARVAHKKGEL	SMEDVWSLSK	HESSTVNCRR	LERLWQHELN	EVGEDAASLR	RVVWLFQRTS	LILSYVICMI	TQLAGFSGPA	FMVKHLLEYT	QATESNLOYS
ABCC11	VGLCPALPUS	ECVKSLSPSS	SWLIINORTAI	RPRAAVSSFA	FEKLIOQFSV	IHITSGEAIS	FFTGVDNVLE	EGVCYGPPIVL	ITCASLVICS	ISSYFIIQVE	AFIAILCYLL
ABCC12	IGLCIALPAM	EPTKVFFWAL	AWAINRYTAL	RIKVALSTLV	FENLVSTL	THISVGEVLN	ELSSBSYSLE	EAALECPHPA	TIRILMVPCA	AYAFFILGPT	ALIGISVAVI
ABCC5	LILVLGHLLP	EIVRSWSLAL	TWALNYRTGV	KLRGAILTMA	EKKILKLN	KEKSIQELIN	ICSNIDGORME	EAAVAGSLLA	GGEVVALLGM	LYNVILLGPI	GFLGSVFIH
ABCC11	VFPLAVPMTR	MAVKAQHHTS	EVSDQIRVT	SEVLTCIKLE	KMYTWKPPFA	KIHEDLRRKE	RKILHEKSLV	QSLTSTLLEF	IPHTVATAVWV	LIHTSLIKKI	TASMAFSMLA
ABCC12	FIPVQMFMAK	LNSAFERSAI	LMTDKKVQTM	NEELTCIRLI	KMYAWKESPT	NTIQDIRRE	RKILHEKAGTV	QSGNSALAPI	VSTLAIIVLTL	SCHILLIRRKI	TAPVAFSVIA
ABCC5	FYPAMPFASR	LTAYPRKRCV	AATDERVQKM	NEVLTYIKFI	KMYAWKAFS	QSVCKIREER	RRILHEKAGVF	QGTIVGVAPI	VVVTASVVVF	SVHMTLGFDL	TAAQAFTVVT
ABCC11	SLNLLRLSVF	FVPLAVKGHT	NSKSAVMRFK	KFFLOESPVF	XVOTLQDPKS	ALVFEEATES	WQ.....QI	CEGLV.....	NGAL	EL...BRNGH	ASEGMRPRD
ABCC12	MFNVMKFSLA	ILPFSIKAMA	EANVSLRRMK	KILIDKSPPS	YLTQPEDPDT	VILLANALTI	WEHEASRKSIT	PKKLO.....	NOKR	HICKKQKSEA	YSERSPPAKG
ABCC5	VFNSMTFALK	VTFPSVKSLS	EASVAVDRFK	SLFLMEVHM	IKNKPASPHI	KIEMKNATLA	WDSSHSSIQN	SEKLTPTMKK	DKRASRGKNE	KVRQLQRTSH	QAVLAEQKGH
ABCC11	AL.....G	PEHEGNS...	IGPEL	HKINIMVSKG	MMLGVCNGTG	SGKSSLSLSAI	LEEMHLLGGS	VGVQGSILAVY	PQOAWIVSCN	IRENIIIMGGA	YD.....KA
ABCC12	AT.....G	PEHQSDS...	LKSVL	HSLSFVVRKG	KILGICGNVG	SGKSSLSLAA	LGQMOLOKGV	VAVNCTLAVV	SQOAWIFHGN	VRENILFGEK	YDHORYOHTV
ABCC5	LILDSDERPS	PEHEGKHIT	LGHLRLQRTI	HSIDIEIQEG	KLVGICGSVG	SGKTSLSISAI	LGQMTLLEGS	IATSGFPAKV	ACQAWILNAT	LEDNILECKE	YDEERYNSVL
ABCC11	RTPGCACCLD	MVPTACLOLI	GERGLNLSGG	QKORISLARA	VYSDRQIYLL	DDPLSAVDAA	VGRHIFEECI	KKTLRGKTVV	LVTHQLOQYLB	FCGQIILLN	GKICENGTHS
ABCC12	RVCGLQKDL	NLPYGLFTEL	GERGLNLSGG	QKORISLARA	VYSDRQLYLL	DDPLSAVDAA	VGRHIFEECI	KKTLRGKTVV	LVTHQLOQYLB	SCDEVILLED	GEICEKGTHK
ABCC5	NSCCLRPDLA	ILPSSDLFTEL	GERGANLSGG	QKORISLARA	LXSDRSIXYI	DDPLSALDAH	VGNHIFENSAT	RKHLKSKTVL	FVTHQLOQYLV	DCDEVIFEMKE	GQITERGTHE
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ABCC12	ELMEERGRYA	KLHINLRGLO	FKDPEHLYNA	AMVEAFKESP	AEREEDAGII	VLAFGNEKDE	GKESETGSEF	VDTKVPEHQL	IQTESPQEGT	LSWRVYHHYI	QAAGGYMVSC
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ABCC12	FTVFLFLMI	GSAAFSPWML	GLMIDKGRM	FCGPQGNRTM	CEVGAVIADI	GQHVYQWVYT	ASWFMVVEG	VTKGFFVET	TLMASSSLHD	TVFEDKILKSP	MSFFDTTPTG
ABCC5	VLMALFMEIV	GSTAFSTWML	SYWIKQCSGN	TTVTRGNETS	VS.DSMKDNP	HMOYASIIYA	LSMAVMLILK	AIRGVVYVKG	TRKASTALHN	ELFRRILRSP	MKFFDTTPTG
ABCC11	RLNCFAGUL	EOLDOLRPIF	SEOFIVLSLM	VIAVILHVS	LSPYILMGA	IIMVICFYIY	MMFKKAGVF	KRELVYRSR	LFSHILNSIQ	GLSSTHVYCK	TEDPISQFKR
ABCC12	RLMNRFSKDM	DELVRLPETH	AEHLQOPFM	VVFLHVLAA	VFPVLEVVA	SLAVGFTILL	RIFHRGVQEL	KKVENVRSR	WEHTISSMQ	GLGLIHAYCK	KESCITY...
ABCC5	RIENRFSKDM	DEVVRLPFO	AEHLQONVIL	VFFCVGMIA	VFPWFLVANG	PVILFSLVH	IVSRVLIRES	KRLDNITQSE	FLSHITSSIQ	GLATHAYNK	QGEHLHRYQE
ABCC11	LTDQANNVLL	LFLSSTRMMA	LRLIEIMNLV	TLAVALFVAF	GISSTPYSFK	VMAVNIVLQI	ASSEQATARI	GLETHAQPTA	VERILLOVMKM	CVSEAPLHME	GTSCIPQGWPO
ABCC12	HLI	YFNCAIRWFA	LPMVILMNTI	HFTVALVATH	SFSSISTSSK	GLSLXYIIQI	SGILOVCVET	GHETOAKFTS	VELIREYIST	CVPECTHPLK	VGTCPEKDWES
ABCC5	LILDDNQAPFF	LETCAMRWLA	VRLDLISLAI	LTITGLMIVL	MHGQIRPAYA	GLAISXAVOI	TGLFOFTVRL	ASETEARFES	VERINHYIKI	LSLEAPARIK	NKAPSPDWPO
ABCC11	HGEIIFQDYH	MKYRDNTPTV	LHGINDLIRG	HEVVGIVGRT	GSCKSSLGMA	LFRVLVERMAG	RILIDGVDIC	SIGLEDLRSK	LSVIPODPVL	LSGTLIRPNLD	PDRRTHDQOI
ABCC12	CGEITFRDYQ	MRYRDNTPLV	LDLSINNTQS	QOTVGVIGRT	GSCKSSLGMA	LFRVLVERPAG	TAFIDEVDIC	ILSLEDLRTK	LTVIPODPVL	FVCTVRYNLD	PRESHTHEML
ABCC5	EGEVTFENAE	MRYRENPLV	LKKVSFTIKP	KEKIGIVGRT	GSCKSSLGMA	LFRINELSGG	CIKIDGVRIS	DIGLADLRSK	LSIIPQEPVL	FSGTVESNLD	PENQYTEDQI
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ABCC12	MOVLERTFMR	DTIMKLPKIL	QAEVTNGEN	FSVGERQLLC	FSVGERQLLC	FSVGERQLLC	FSVGERQLLC	FSVGERQLLC	FSVGERQLLC	FSVGERQLLC	FSVGERQLLC
ABCC5	WDALERTFMK	ECTAQLPLKI	ESEVMENGDN	FSVGERQLLC	FSVGERQLLC	FSVGERQLLC	FSVGERQLLC	FSVGERQLLC	FSVGERQLLC	FSVGERQLLC	FSVGERQLLC
ABCC11	RPEVLRKKPG	SLFAALMATA	TSSLR*~	FSVGERQLLC	FSVGERQLLC	FSVGERQLLC	FSVGERQLLC	FSVGERQLLC	FSVGERQLLC	FSVGERQLLC	FSVGERQLLC
ABCC12	KPEVIAEKPD	SAFAMLLAAE	VRL*~	FSVGERQLLC	FSVGERQLLC	FSVGERQLLC	FSVGERQLLC	FSVGERQLLC	FSVGERQLLC	FSVGERQLLC	FSVGERQLLC
ABCC5	TFSVILSND	SRYAMFAAA	ENKVAVRG*	FSVGERQLLC	FSVGERQLLC	FSVGERQLLC	FSVGERQLLC	FSVGERQLLC	FSVGERQLLC	FSVGERQLLC	FSVGERQLLC

FIGURE 1

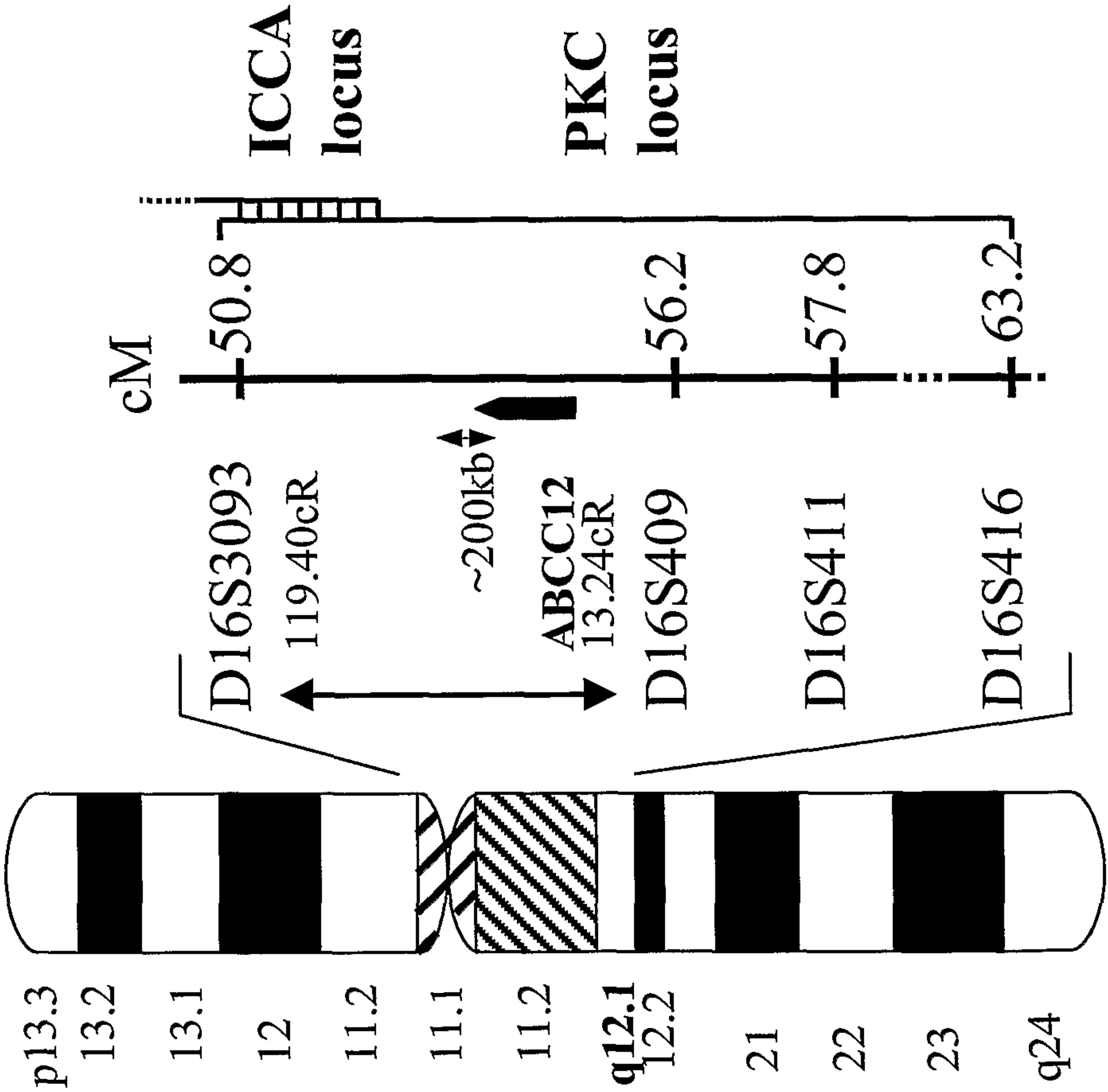


FIGURE 2

3/5



FIGURE 3

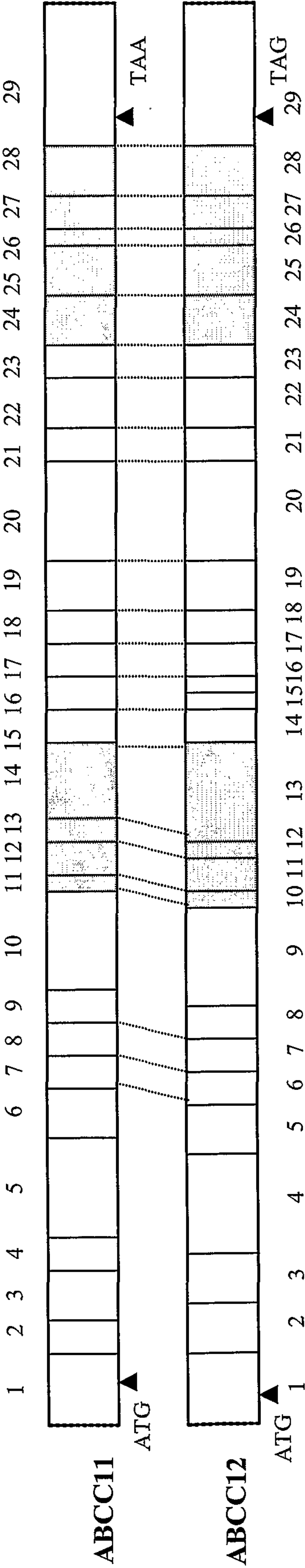


FIGURE 4

FIGURE 5

