

(19)



(11)

**EP 2 319 924 B1**

(12)

**EUROPEAN PATENT SPECIFICATION**

(45) Date of publication and mention of the grant of the patent:  
**09.03.2016 Bulletin 2016/10**

(51) Int Cl.:  
**G01N 33/68 (2006.01) C07K 14/47 (2006.01)**  
**C12N 15/09 (2006.01) C07K 16/18 (2006.01)**  
**C12Q 1/68 (2006.01) G01N 33/53 (2006.01)**  
**G01N 37/00 (2006.01)**

(21) Application number: **09806761.4**

(22) Date of filing: **14.08.2009**

(86) International application number:  
**PCT/JP2009/064363**

(87) International publication number:  
**WO 2010/018870 (18.02.2010 Gazette 2010/07)**

(54) **POLYPEPTIDE MARKER FOR DIAGNOSIS OF ARTERIOSCLEROSIS, METHOD FOR DETECTION OF ARTERIOSCLEROSIS BY USING THE MAKER OR THE LIKE, AND KIT FOR DIAGNOSIS OF ARTERIOSCLEROSIS**

POLYPEPTIDMARKER ZUR DIAGNOSE VON ARTERIOSKLEROSE, VERFAHREN FÜR DEN NACHWEIS VON ARTERIOSKLEROSE ANHAND DES MARKERS ODER DERGLEICHEN UND KIT FÜR DIE DIAGNOSE VON ARTERIOSKLEROSE

MARQUEUR POLYPEPTIDIQUE POUR LE DIAGNOSTIC DE L'ARTÉRIOSCLÉROSE, PROCÉDÉ DE DÉTECTION DE L'ARTÉRIOSCLÉROSE À L'AIDE DU MARQUEUR OU SIMILAIRE, ET TROUSSE DE DIAGNOSTIC DE L'ARTÉRIOSCLÉROSE

(84) Designated Contracting States:  
**AT BE BG CH CY CZ DE DK EE ES FI FR GB GR HR HU IE IS IT LI LT LU LV MC MK MT NL NO PL PT RO SE SI SK SM TR**

(30) Priority: **15.08.2008 JP 2008209210**

(43) Date of publication of application:  
**11.05.2011 Bulletin 2011/19**

(60) Divisional application:  
**15199553.7**

(73) Proprietors:  
 • **FUJIKURA KASEI CO., LTD.**  
**Itabashi-ku**  
**Tokyo 174-0046 (JP)**  
 • **National University Corporation Chiba University**  
**Chiba-shi**  
**Chiba 263-8522 (JP)**

(72) Inventors:  
 • **NAKAMURA Rika**  
**Saitama 3400203 (JP)**  
 • **KURODA Hideyuki**  
**Saitama 3400203 (JP)**

- **TOMIYOSHI Go**  
**Saitama 3400203 (JP)**
- **HIWASA Takaki**  
**Chiba-shi**  
**Chiba 260-8670 (JP)**
- **TAKIGUCHI Masaki**  
**Chiba-shi**  
**Chiba 260-8670 (JP)**
- **SAEKI Naokatsu**  
**Chiba-shi**  
**Chiba 260-8670 (JP)**
- **MACHIDA Toshio**  
**Chiba-shi**  
**Chiba 260-8670 (JP)**

(74) Representative: **Potter Clarkson LLP**  
**The Belgrave Centre**  
**Talbot Street**  
**Nottingham NG1 5GG (GB)**

(56) References cited:  
**WO-A2-2006/048291 WO-A2-2006/102979**  
**JP-A- 2005 168 498 JP-A- 2005 168 498**  
**JP-A- 2007 010 567 JP-A- 2007 278 907**  
**US-A1- 2004 048 286 US-A1- 2007 072 175**  
**US-A1- 2007 190 586**

Note: Within nine months of the publication of the mention of the grant of the European patent in the European Patent Bulletin, any person may give notice to the European Patent Office of opposition to that patent, in accordance with the Implementing Regulations. Notice of opposition shall not be deemed to have been filed until the opposition fee has been paid. (Art. 99(1) European Patent Convention).

**EP 2 319 924 B1**

Remarks:

The file contains technical information submitted after the application was filed and not included in this specification

**Description**

## TECHNICAL FIELD

5 **[0001]** The present invention relates to polypeptide markers for diagnosing arteriosclerosis, gene markers for diagnosing arteriosclerosis, antibodies, probes for detecting an arteriosclerosis marker gene, a DNA microarray or a DNA chip for detecting the arteriosclerosis marker genes, a method for detecting arteriosclerosis, and a kit for diagnosing arteriosclerosis.

10 **[0002]** Priority is claimed on Japanese Patent Application No. 2008-209210, filed August 15, 2008.

## BACKGROUND ART

15 **[0003]** Arteriosclerosis is a disease frequently found in aorta, coronary arteries, cerebral arteries, and carotid arteries, being a main cause of myocardial infarction and cerebral infarction. At present, the presence of atherosclerosis is said to be crucial for the ground of the onset of ischemic organ diseases such as ischemic heart disease and cerebrovascular disorder, which are top leading causes of death. Arteriosclerotic lesions are pathomorphologically characterized by: fatty streaks which are subendothelial accumulations of cholesterol ester-storing cells (foam cells); and as an advanced stage thereof, invasions of smooth muscle cells, macrophages, T cells, and the like; as well as fibrous plaques showing cellular necrosis and fat accumulation. The site with fat accumulation is structurally fragile, where plaques are ruptured, triggered by a hemodynamic force, and thereby a thrombus is rapidly formed by reactions of tissue factors and blood coagulation factors. It has been elucidated that the occurrence of thrombotic blockage by the rupture of plaques in a coronary artery is closely associated with the onset of so-called acute coronary syndromes such as acute myocardial infarction, unstable angina pectoris, and cardiac sudden death (Non-Patent Document 1)

25 **[0004]** Arteriosclerosis is gradually developed without subjective symptoms, and all of the sudden, myocardial infarction, cerebral infarction, or angina pectoris occurs. Thus, early stage detection is required. So far, ultrasonography, angiography, imaging tests with MRI (magnetic resonance imaging devices) or such a device, electrocardiography, electroencephalography, and the like have been widely carried out for the diagnosis of arteriosclerotic lesions. However, methods by means of biochemical examination have been demanded so that diagnosis of an arteriosclerotic lesion can achieve an early detection.

30 **[0005]** In the diagnosis of an arteriosclerotic lesion by means of biochemical examination, there has been known measurements of arteriosclerosis-induced lipoproteins which are associated with lipid accumulation in the vascular wall such as LDL (low density lipoprotein), lipoprotein (Lp- $\alpha$ ), remnant lipoprotein, and oxidized LDL in serum or plasma. In particular, measurement of arteriosclerosis-associated substances in blood are attracting attention in recent years. It is reported that measurement of an inflammatory substance: CRP (C-reactive protein), and measurement of the chlamydia antibody titer are useful.

35 **[0006]** As for the diagnosis method of an arteriosclerotic lesion by means of such measurement of an arteriosclerosis-induced lipoprotein, the following methods are known. For example, regarding the LDL measurement, the followings have been proposed: measurement of neutrophil, monocyte/ macrophage or like inflammatory cell-originated components such as lactoferrin, myeloperoxidase, granulocytic elastase in serum or plasma, forming a complex with the oxidized LDL existing in the serum or the plasma, by an immunological means (Patent Document 1); use of an immunoassay method with a fused polypeptide comprising the extracellular region of an oxidized LDL receptor and a part of the heavy chain constant region of an immunoglobulin (Patent Document 2); use of an anti-human aldehyde-modified  $\alpha$ 1 antitrypsin monoclonal antibody capable of specifically recognizing oxidized LDL- $\alpha$ 1 antitrypsin complex (Patent Documents 3 and 4); measurement of the degree of oxidative denaturation of LDL in plasma by an oxidizing agent comprising an azo compound such as V-70 (Patent Document 5); and the like.

45 **[0007]** Furthermore, regarding the diagnosis of an arteriosclerotic lesion by means of lipoprotein measurement, the followings have been disclosed: measurement of remnant lipoprotein (RLP) in denatured blood (Patent Document 6); diagnosis of rheumatoid or arteriosclerotic lesions through detection of the expression of the human cartilage GP39-L polypeptide gene (Patent Document 7); diagnosis of arteriosclerotic lesions through measurement of apoB100 lipoprotein in blood (Patent Document 8); measurement of human phospholipid transfer protein (PLTP) with use of a monoclonal antibody against PLTP (Patent Document 9); use of an apo lipoprotein A-I antibody as a marker for diagnosing arteriosclerosis (Patent Document 10); and the like.

50 **[0008]** In addition, regarding other means related to the diagnosis of an arteriosclerotic lesion, the followings have been proposed: diagnosis of hyperlipemia or arteriosclerotic lesions with use of an antibody against a sodium dependent bile acid transporter protein (Patent Document 11); diagnosis through measurement of the coagulation factor VII-activating protease (FSAP) as a risk factor for atherosclerosis (Patent Document 12); examination of arteriosclerosis through detection of an endothelial and smooth muscle cell-derived neuropilin-like molecule (ESDN) or the gene expression thereof (Patent Document 13); use of an anti-human hepatic triglyceride lipase antibody (Patent Document 14); diagnosis

of arteriosclerotic lesions by using the serotonin concentration in a plasma sample as a marker (Patent Documents 15 and 16); and the like.

**[0009]** Furthermore, regarding yet other means related to the diagnosis of an arteriosclerotic lesion, the followings have been proposed: diagnosis of chronic renal failure or atherosclerosis by using, as the analyte, an sMAD3 polypeptide which is an iso-form of MAD required for the signal transduction of DPP which is a TGF-family member of cytokine/growth factor (Patent Document 17); measurement of a complex of Lp- $\alpha$  and  $\alpha$ 2-macroglobulin/interleukin 6 in blood as the analyte by an immunological means using an antibody thereof (Patent Document 18); use of a monoclonal antibody against a paraoxonase (Patent Document 19); detection of arteriosclerosis through measurement of a saturated ultra long-chain fatty acid (Patent Document 20); diagnosis of atherosclerosis by using an RC-9 protein and an antibody thereof (Patent Document 21); and the like.

**[0010]** In this way, many methods have been proposed regarding the biochemical examination related to the diagnosis of an arteriosclerotic lesion. However, most of the detection markers of them are risk markers. For more radical and specific diagnosis of an arteriosclerotic lesion, an advanced development of markers capable of specifically detecting such a lesion has been demanded.

**[0011]** Therefore, Patent Document 22 has proposed, as a marker for specifically detecting an arteriosclerotic lesion, a polypeptide marker for diagnosing arteriosclerosis, a gene marker for diagnosing arteriosclerosis, an antibody specifically bindable to the polypeptide marker for diagnosing arteriosclerosis, a probe for detecting the gene marker for diagnosing arteriosclerosis, and a method for detecting an arteriosclerotic lesion.

**[0012]** WO 2006/048291 relates to arrays containing a transcriptome of a diseased tissue and methods of using the arrays for diagnosis, prognosis, screening, and identification of disease.

**[0013]** US 2007/072175 relates to a nucleotide array containing polynucleotide probes complementary to, or fragments of, Cynomolgus monkey genes, and the use of such a nucleotide array to characterize the biological effects, including the actions, targets, and toxicities, of therapeutic agents in primates.

Patent Document 1: Japanese Unexamined Patent Application, First Publication No. 2002-48790

Patent Document 2: Japanese Unexamined Patent Application, First Publication No. 2002-17353

Patent Document 3: Japanese Unexamined Patent Application, First Publication No. 2000-184885

Patent Document 4: Japanese Unexamined Patent Application, First Publication No. H10-142226

Patent Document 5: Japanese Unexamined Patent Application, First Publication No. H9-203736

Patent Document 6: Japanese Unexamined Patent Application, First Publication No. 2002-181820

Patent Document 7: Japanese Unexamined Patent Application, First Publication No. 2002-142781

Patent Document 8: Japanese Unexamined Patent Application, First Publication No. 2002-55106

Patent Document 9: Japanese Unexamined Patent Application, First Publication No. H11-346782

Patent Document 10: Japanese Unexamined Patent Application, First Publication No. H8-160042

Patent Document 11: Japanese Unexamined Patent Application, First Publication No. 2003-310281

Patent Document 12: Japanese Unexamined Patent Application, First Publication No. 2003-304873

Patent Document 13: Japanese Unexamined Patent Application, First Publication No. 2003-189872

Patent Document 14: Japanese Unexamined Patent Application, First Publication No. 2002-308900

Patent Document 15: Japanese Unexamined Patent Application, First Publication No. 2002-277461

Patent Document 16: Japanese Unexamined Patent Application, First Publication No. 2002-131313

Patent Document 17: Japanese Unexamined Patent Application, First Publication No. 2002-238589

Patent Document 18: Japanese Unexamined Patent Application, First Publication No. 2001-249128

Patent Document 19: Japanese Unexamined Patent Application, First Publication No. 2000-333674

5 Patent Document 20: Japanese Unexamined Patent Application, First Publication No. 2000-206113

Patent Document 21: Published Japanese translation No. 2000-503764 of PCT International Publication

10 Patent Document 22: Japanese Unexamined Patent Application, First Publication No. 2005-168498

Non-Patent Document 1: N. Eng. J. Med., 326, 242-250, 1992.

Non-Patent Document 2: Journal of Biological Chemistry, 272, 556, 1997.

15 **[0014]** According to the technique of Patent Document 22, an arteriosclerotic lesion can be detected with easy manipulation, and an early detection of arteriosclerosis can be expected. However, it does not satisfy an adequate level. There has been a demand for more accurate detection of an arteriosclerotic lesion with use of a greater number of polypeptide markers for diagnosing arteriosclerosis, gene markers for diagnosing arteriosclerosis, and the like. Therefore, it is an object of the present invention to provide polypeptide markers for diagnosing arteriosclerosis, gene markers for diagnosing arteriosclerosis, antibodies, probes for detecting an arteriosclerosis marker gene, a DNA microarray or a  
20 DNA chip for detecting an arteriosclerosis marker gene, a method for detecting arteriosclerosis, and a kit for diagnosing arteriosclerosis, with which an arteriosclerotic lesion can be detected with much improved accuracy.

#### DISCLOSURE OF INVENTION

25 **[0015]** The present invention is as defined in the accompanying claims.

**[0016]** The inventors of the present invention have searched for proteins which are expressed in serum of a diseased patient with an arteriosclerotic lesion so as to find out more markers for diagnosing arteriosclerosis which can specifically detect an arteriosclerotic lesion. As a result, they found out novel polypeptide markers for diagnosing arteriosclerosis which can specifically detect an arteriosclerotic lesion, which has led to the completion of the present invention.

30 **[0017]** In the specific search method, the screening was conducted in the following manner by using serum of diseased patients with arteriosclerotic lesions who had been hospitalized in a hospital or cooperative institutes with the consent of patients or their families. The obtained cDNA clone was inserted in a plasmid pBluescript II to determine the nucleotide sequence. Thereafter, it was recombined in a pGEX plasmid and transfected in *E. coli*. The protein was abundantly expressed with IPTG (isopropyl  $\beta$ -D-thiogalactoside) to thereby prepare the protein extract. Next, the protein extract  
35 was solid-phased in a 96-well plate. The antibody level in the serum was measured by the ELISA method. Using these measured values, a significance test was conducted between the arteriosclerosis patient group and the normal group. As a result, significant differences were found between the patient group and the normal group with thirteen clones serving as the marker. Furthermore, the reaction between the protein extract and a large number of patient serums was examined by the western blotting method. As a result, five clones serving as the marker newly exhibited a positive  
40 reaction with the serums of diseased patients with arteriosclerotic lesion, by which these five clones were found to be useful as specific markers for the presence of an arteriosclerotic lesion, or for an unstable plaque. Then, it became possible by utilizing the antigenicity of these clones or probes for these genes, to develop a method for detecting arteriosclerosis, and moreover to produce a diagnosis kit for use in such a detection method.

45 **[0018]** That is, the present invention includes polypeptide markers for diagnosing arteriosclerosis, gene markers for diagnosing arteriosclerosis, antibodies, probes for detecting an arteriosclerosis marker gene, a DNA microarray or a DNA chip for detecting an arteriosclerosis marker gene, a method for detecting arteriosclerosis, and a kit for diagnosing arteriosclerosis, which are described below.

50 [1] Use of a polypeptide having an amino acid sequence set forth in SEQ ID NO: 1 of the Sequence Listing, or a partial amino acid sequence thereof consisting of four or more amino acids, as a polypeptide marker for diagnosing atherosclerosis.

[2] Use of a gene represented by a nucleotide sequence that encodes the amino acid sequence of the polypeptide marker for diagnosing arteriosclerosis according to [1], or a partial amino acid sequence thereof consisting of four  
55 or more amino acids, as a gene marker for diagnosing atherosclerosis.

[3] Use of a gene having a nucleotide sequence set forth in SEQ ID NO: 2 of the Sequence Listing, or a partial nucleotide sequence thereof consisting of twelve or more nucleotides, as a gene marker for diagnosing atherosclerosis.

rosis.

[4] Use of an antibody specifically bindable to the polypeptide according to [1] for diagnosing atherosclerosis.

5 [5] Use of a probe for diagnosing arteriosclerosis, which comprises all or a part of DNA that is hybridizable with the gene according to [2] or [3] under a stringent condition.

[6] The use of a probe for diagnosing arteriosclerosis according to [5], which comprises all or a part of antisense DNA for the gene according to [3].

10 [7] Use of a DNA microarray or a DNA chip for diagnosing arteriosclerosis, wherein the probe for detecting an arteriosclerosis marker gene according to [5] and/or the probe for detecting an arteriosclerosis marker gene according to [6] is/are immobilized on a base plate.

15 [8] A method for detecting arteriosclerosis, wherein the antibody according to [4] is used to detect the expression of an arteriosclerosis marker polypeptide that is specifically bindable to the antibody, in a specimen sample.

[9] A method for detecting arteriosclerosis, wherein the polypeptide marker for diagnosing arteriosclerosis according to [1] is used to detect the expression of an antibody that is specifically bindable to the polypeptide marker for diagnosing arteriosclerosis, in specimen blood.

20 [10] A method for detecting arteriosclerosis, wherein the probe for detecting an arteriosclerosis marker gene according to [5] or [6] is used to detect the expression of a gene that is hybridizable with the probe for detecting an arteriosclerosis marker gene, in a specimen cell.

25 [11] A method for detecting arteriosclerosis, wherein a primer is constructed based on a nucleotide sequence set forth in SEQ ID NO: 2 of the Sequence Listing, and PCR is conducted with use of the primer to detect the expression of an arteriosclerosis marker gene.

30 [12] A kit for diagnosing arteriosclerosis, including at least one item selected from the group consisting of the probe for detecting an arteriosclerosis marker gene according to [5] or [6], the DNA microarray or the DNA chip for detecting an arteriosclerosis marker gene according to [7], and the antibody according to [4].

35 [13] A kit for diagnosing arteriosclerosis, including a polypeptide marker for diagnosing arteriosclerosis which comprises a polypeptide having an amino acid sequence set forth in any one of SEQ ID NO: 1 of the Sequence Listing, or a partial amino acid sequence thereof consisting of four or more amino acids.

[0019] An arteriosclerotic lesion can be detected with much higher accuracy by using the polypeptide marker for diagnosing arteriosclerosis, the gene marker for diagnosing arteriosclerosis, the antibody, the probe for detecting an arteriosclerosis marker gene, the DNA microarray or the DNA chip for detecting an arteriosclerosis marker gene, the method for detecting arteriosclerosis, and the kit for diagnosing arteriosclerosis of the present invention.

#### BRIEF DESCRIPTION OF THE DRAWINGS

45 [0020] FIG. 1 shows the results of the expression of arteriosclerosis marker genes by the western blotting method in the Examples.

#### DESCRIPTION OF EMBODIMENTS

50 [0021] The polypeptide marker for diagnosing arteriosclerosis and the gene marker for diagnosing arteriosclerosis of the present invention can be used for the detection of arteriosclerosis as they are specifically expressed in arteriosclerotic lesions. Polypeptides serving as the polypeptide marker used for diagnosing arteriosclerosis of the present invention are polypeptides having an amino acid sequence set forth in SEQ ID NO: 1 of the Sequence Listing, or a partial amino acid sequence thereof consisting of four or more amino acids.

55 [0022] Here, the term "partial amino acid sequence" refers to a sequence being a part of the amino acid sequence set forth in any one of SEQ ID NOs of the Sequence Listing mentioned above, consisting of four or more, preferably five or more, more preferably six or more, and yet more preferably seven or more amino acids.

[0023] The information on the amino acid sequence of the above-mentioned polypeptide of the present invention is

## EP 2 319 924 B1

available from the NCBI GeneBank database as of July 31st, 2008, with the accession number: XM\_001129783 (SEQ ID NO: 1). Other polypeptides disclosed herein but not mentioned by the present claims are available from the NCBI GeneBank database as of July 31st, 2008, with the accession numbers: NM\_006088 (SEQ ID NO: 3), NM\_014878 (SEQ ID NO: 5), NM\_207514 (SEQ ID NO: 7), NM\_001128847 (SEQ ID NO: 9), NM\_001017408 (SEQ ID NO: 11),  
5 NM\_015089 (SEQ ID NO: 13), NM\_133337 (SEQ ID NO: 15), NM\_022406 (SEQ ID NO: 17), NM\_001402 (SEQ ID NO: 19), NM\_005349 (SEQ ID NO: 21), NM\_005406 (SEQ ID NO: 23), NM\_016436 (SEQ ID NO: 25), NM\_032408 (SEQ ID NO: 27), and NM\_014377 (SEQ ID NO: 29).

**[0024]** In addition, the gene marker used for diagnosing arteriosclerosis of the present invention comprises a gene represented by a nucleotide sequence which encodes the above-mentioned polypeptide of SEQ ID NO: 1 having the amino acid sequence or a partial amino acid sequence thereof consisting of four or more amino acids. The gene marker for diagnosing arteriosclerosis may be a gene having a nucleotide sequence capable of expressing the above-mentioned polypeptide.

**[0025]** The gene serving as the gene marker used for diagnosing arteriosclerosis of the present invention are genes having a nucleotide sequence set forth in SEQ ID NO: 2 of the Sequence Listing, or a partial nucleotide sequence thereof consisting of twelve or more nucleotides. The information on that gene, and other nucleotide sequences disclosed herein although not mentioned by the claims (SEQ ID NOs: 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, and 36 of the Sequence Listing), (nucleotide sequence information) are respectively available from the NCBI GeneBank database, with the following accession number.

**[0026]** That is, the gene serving as the gene marker for diagnosing arteriosclerosis can be exemplified by [Clone Name: S19A3; SEQ ID NO: 2 of the Sequence Listing; Accession No. XM\_001129783; Gene Name: (PREDICTED) similar to LIM and senescent domain 1 (LOC729260); Gene Description: similar to the LIMS 1 gene. LIMS1 is an adaptor protein which contains five LIM domains, or double zinc fingers. LIMS1 may possibly play a role in integrin-mediated cell adhesion or spreading.]. Other genes disclosed herein but not mentioned by the present claims are: [Clone Name: TS27A2; SEQ ID NO: 4 of the Sequence Listing; Accession No. NM\_006088; Gene Name: tubulin, beta 2C (TUBB2C);  
25 Gene Description: a component protein of microtubules], [Clone Name: S21B1; SEQ ID NO: 6 of the Sequence Listing; Accession No. NM\_014878; Gene Name: KIAA0020 (KIAA0020); Gene Description: reportedly a minor histocompatibility antigen], [Clone Name: S25E1; SEQ ID NO: 8 of the Sequence Listing; Accession No. NM\_207514; Gene Name: differentially expressed in FDCP 8 homolog (mouse) (DEF8); Gene Description: unknown function], [Clone Name: TS12D2; SEQ ID NO: 10 of the Sequence Listing; Accession No. NM\_001128847; Gene Name: SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4 (SMARCA4); Gene Description: unknown],  
30 [Clone Name: S36C3; SEQ ID NO: 12 of the Sequence Listing; Accession No. NM\_001017408; Gene Name: golgi associated PDZ and coiled-coil motif containing (GOPC); Gene Description: bindable to Rhotekin, an effector of a low molecular weight GTP-binding protein Rho. Moreover, reportedly, the binding between Rhotekin and GOPC is regulated in a Rho dependent manner.], [Clone Name: N48B1; SEQ ID NO: 14 of the Sequence Listing; Accession No. NM\_015089;  
35 Gene Name: p53-associated parkin-like cytoplasmic protein (PARC); Gene Description: associated with transition from metaphase to anaphase during cell division, and also associated with ubiquitin-dependent protein degradation], [Clone Name: S28D1; SEQ ID NO: 16 of the Sequence Listing; Accession No. NM\_133337; Gene Name: fer-1-like 3, myoferlin (*C. elegans*) (FER1L3); Gene Description: a type II membrane protein similar to a skeletal muscle protein, dysferlin, this gene having a C2 domain is suggested to be possibly associated with regeneration and repair of cytoplasmic membrane and nuclear membrane], [Clone Name: TS27H1; SEQ ID NO: 18 of the Sequence Listing; Accession No. NM\_022406;  
40 Gene Name: X-ray repair complementing defective repair in Chinese hamster cells 4 (XRCC4); Gene Description: a protein encoded by this gene acts to complete the repair of a DNA double strand through nonhomologous end-joining and V(D)J recombination, together with DNA ligase IV and DNA-dependent protein kinase. The nonhomologous end-joining pathway is necessary for the normal development and suppression on tumors.], [Clone Name: PA105; SEQ ID  
45 NO: 20 of the Sequence Listing; Accession No. NM\_031229; Gene Name: RanBP-type and C3HC4-type zinc finger containing 1 (RBCK1); Gene Description: unknown function. Its amino acid sequence is similar to that of mouse UIP28/UbcM4 interacting protein], [Clone Name: S16D2; SEQ ID NO: 22 of the Sequence Listing; Accession No. NM\_005349; Gene Name: recombination signal binding protein for immunoglobulin kappa J region (RBPJ); Gene Description: unknown], [Clone Name: S27D3; SEQ ID NO: 24 of the Sequence Listing; Accession No. NM\_005406; Gene  
50 Name: Rho-associated, coiled-coil containing protein kinase 1 (ROCK1); Gene Description: serine/threonine kinase activated by a low molecular weight GTP-binding protein Rho, and associated not only with cell contraction but also with morphological regulation, migration, regulation of gene expression, and like physiological functions.], [Clone Name: S36E1; SEQ ID NO: 26 of the Sequence Listing; Accession No. NM\_016436; Gene Name: PHD finger protein 20 (PHF20); Gene Description: associated with DNA-dependent transcriptional regulation.], [Clone Name: S39D6; SEQ ID  
55 NO: 28 of the Sequence Listing; Accession No. NM\_032408; Gene Name: bromodomain adjacent to zinc finger domain, 1B (BAZ1B); Gene Description: a member of the bromodomain protein family involved in chromatin-dependent regulation of transcription.], [Clone Name: TS27B2; SEQ ID NO: 30 of the Sequence Listing; Accession No. NM\_014377; Gene Name: zuotin related factor 1 (ZRF1); Gene Description: a member of the M-phase phosphoprotein family, acting as a

**EP 2 319 924 B1**

molecular chaperone.], [Clone Name: PA202; SEQ ID NO: 32 of the Sequence Listing; Accession No. NM\_003692; Gene Name: transmembrane protein with EGF-like and two follistatin-like domains 1 (TMEFF1); Gene Description: reportedly inhibits nodal signaling through binding to the nodal coreceptor Cripto in *Xenopus*], [Clone Name: PA213; SEQ ID NO: 34 of the Sequence Listing; Accession No. NM\_006807; Gene Name: chromobox homolog 1 (HP1 beta homolog *Drosophila*) (CBX1); Gene Description: localized at heterochromatin sites, where it mediates gene silencing.], [Clone Name: PA234; SEQ ID NO: 36 of the Sequence Listing; Accession No. BC030642; Gene Name: PARK2 co-regulated (PACRG); Gene Description: Parkinson's disease-associated gene, and reportedly regulated by the ubiquitin-proteasome system.].

**[0027]** In addition, the term "partial nucleotide sequence" refers to a sequence being a part of the nucleotide sequence set forth in any one of SEQ ID NOs of the Sequence Listing mentioned above, consisting of twelve or more, preferably fifteen or more, more preferably eighteen or more, and yet more preferably twenty or more nucleotides (hereunder, the same definition will be applied).

**[0028]** The above-mentioned genes serving as the gene marker for diagnosing arteriosclerosis are summarized in Table 1.

[Table 1]

	Clone Name	SEQ ID NO.	Accession No	Gene Name
1	S19A3	2	XM_001129783	(PREDICTED)similar to LIM and senescent domain 1 (LOC729260)
2	TS27A2	4	NM_006088	tubulin, beta 2C (TUBB2C)
3	S21B1	6	NM_014878	KIAA0020 (KIAA0020)
4	S25E1	8	NM_207514	differentially expressed in FDCP 8 homolog (mouse) (DEF8)
5	TS12D2	10	NM_001128847	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a member 4 (SMARCA4)
6	S36C3	12	NM_001017408	golgi associated PDZ and coiled-coil motif containing (GOPC)
7	N48B1	14	NM_015089	p53-associated parkin-like cytoplasmic protein (PARC)
8	S28D1	16	NM_133337	fer-1-like 3, myoferlin ( <i>C. elegans</i> ) (FER1L3)
9	TS27H1	18	NM_022406	X-ray repair complementing defective repair in Chinese hamster cells 4 (XRCC4)
10	PA105	20	NM_031229	RanBP-type and C3HC4-type zinc finger containing 1 (RBCK1)
11	S16D2	22	NM_005349	recombination signal binding protein for immunoglobulin kappa J region (RBPJ)
12	S27D3	24	NM_005406	Rho-associated, coiled-coil containing protein kinase 1 (ROCK1)
13	S36E1	26	NM_016436	PHD finger protein 20 (PHF20)
14	S39D6	28	NM_032408	bromodomain adjacent to zinc finger domain, 1B (BAZ1B)
15	TS27B2	30	NM_014377	zuotin related factor 1 (ZRF1)
16	PA202	32	NM_003692	transmembrane protein with EGF-like and two follistatin-like domains 1 (TMEFF1)
17	PA213	34	NM_006807	chromobox homolog 1 (HP1 beta homolog <i>Drosophila</i> ) (CBX1)
18	PA234	36	BC030642	PARK2 co-regulated (PACRG)

**[0029]** The antibody of the present invention is an antibody specifically bindable to, as an antigen, a polypeptide serving as the above-mentioned polypeptide marker having an amino acid sequence set forth in SEQ ID NO: 1 of the Sequence Listing, or a partial amino acid sequence thereof consisting of four or more amino acids, for diagnosing arteriosclerosis. The antibody may be either monoclonal or polyclonal. These antibodies can be produced by a usual method using the above-mentioned polypeptide as an antigen.

**[0030]** The antibody of the present invention may be labeled with a labeling substance. As for the labeling substance,

it is possible to use an enzyme, a radioisotope, a fluorescent dye, biotin, digoxigenin, or the like. The enzyme is not specifically limited as long as it fulfills the requirements such as a large turnover number (number of revolution), stability in the antibody-binding state, and capability of rendering the substrate a specific color. For example, peroxidases for use in usual EIA (enzyme immunoassay),  $\beta$ -galactosidase, alkaline phosphatase, glucose oxidase, acetylcholine esterase, glucose-6-phosphate dehydrogenase, malate dehydrogenase, or the like can be used. In addition, it is also possible to use an enzyme inhibitory substance, a coenzyme, or the like. These enzymes can be bound to the antibody by a known method using a maleimide compound or such a crosslinking agent.

**[0031]** As for the substrate, it is possible to use a known substance according to the type of the enzyme to be used. For example, 3,3',5,5'-tetramethylbenzidine can be used as a substrate when peroxidase is used as an enzyme, while paranitrophenol can be used as a substrate when alkaline phosphatase is used as an enzyme.

**[0032]** As for the radioisotope, it is possible to use  $^{125}\text{I}$ ,  $^3\text{H}$ , or such a substance for use in usual RIA (radioimmunoassay).

**[0033]** As for the fluorescent dye, it is possible to use fluorescein isothiocyanate (FITC), tetramethylrhodamine isothiocyanate (TRITC), or such a substance for use in usual fluorescence antibody technique.

**[0034]** In addition, these labeled antibodies may be tagged with a metal such as manganese or iron. By administering such a metal-tagged antibody into the body and assaying the metal by MRI or such a means, the presence of an antigen peptide bound to this antibody (a polypeptide marker for diagnosing arteriosclerosis) can be detected.

**[0035]** In addition, the probe for detecting an arteriosclerosis marker gene of the present invention is a probe which comprises all or a part of DNA that is hybridizable with the gene serving as the gene marker for diagnosing arteriosclerosis mentioned above under a stringent condition. Here, the term "stringent condition" of the present invention can be exemplified by: hybridization in a buffer solution containing 50% formamide,  $5\times\text{SSC}$ ,  $5\times\text{Denhardt's solution}$ , 0.1M sodium dihydrogenphosphate (pH6.5), 0.5% SDS, and 100  $\mu\text{g/ml}$  denatured salmon sperm DNA, at 42°C, followed by a washing treatment in a buffer solution containing  $1\times\text{SSC}$  (0.15M NaCl and 0.015M sodium citrate) and 0.1% SDS (sodium dodecyl sulfate) at 42°C (Condition 1); or, hybridization in a buffer solution containing  $5\times\text{SSC}$ ,  $5\times\text{Denhardt's solution}$ , 0.1M sodium dihydrogenphosphate (pH6.5), 0.5% SDS, and 100  $\mu\text{g/ml}$  denatured salmon sperm DNA, at 65°C, followed by a washing treatment in a buffer solution containing  $0.1\times\text{SSC}$  and 0.1% SDS at 65°C (Condition 2). The latter (Condition 2) is more preferred. As for the factors to influence the stringency of hybridization, there are various kinds of factors other than the temperature condition mentioned above. It is possible for those skilled in the art to combine various kinds of such factors to achieve equivalent stringency to the stringency of hybridization exemplified above.

**[0036]** Moreover, the probe used for diagnosing arteriosclerosis of the present invention can be exemplified by a probe which comprises all or a part of antisense DNA for the gene having a nucleotide sequence set forth in SEQ ID NO: 2 of the Sequence Listing. That is, it is a probe which comprises DNA having a nucleotide sequence complementary to the nucleotide sequence set forth in SEQ ID NO: 2 mentioned above, or a partial nucleotide sequence thereof consisting of twelve or more nucleotides.

**[0037]** These probes for detecting an arteriosclerosis marker gene may be appropriately labeled with a fluorescent label or the like.

**[0038]** Moreover, the DNA microarray or the DNA chip for detecting an arteriosclerosis marker gene of the present invention is used for the detection of the expression of the gene used for the diagnosis of an arteriosclerotic lesion through the detection, wherein the above-mentioned probe for detecting an arteriosclerosis marker gene is immobilized on a base plate. Regarding the above-mentioned probe for detecting an arteriosclerosis marker gene to be immobilized, it is either possible to use a single kind or a plurality of kinds thereof.

**[0039]** The DNA microarray or the DNA chip can be produced by a usual method. The DNA microarray can be obtained by, for example, spotting a solution containing respective probe(s) for detecting an arteriosclerosis marker gene that has been prepared in advance on a base plate and drying this plate. In addition, the DNA chip can be obtained by, for example, synthesizing DNA having a desired nucleotide sequence on a base plate by photolithography.

**[0040]** Hereunder is a description of the method for detecting arteriosclerosis of the present invention.

**[0041]** The method for detecting arteriosclerosis of the present invention is a method in which the above-mentioned polypeptide marker having an amino acid sequence set forth in SEQ ID NO: 1 of the Sequence Listing, or a partial amino acid sequence thereof consisting of four or more amino acids, for diagnosing arteriosclerosis is used to detect the expression of an antibody (arteriosclerosis marker antibody) that is specifically bindable to the polypeptide marker for diagnosing arteriosclerosis, in a specimen blood (hereunder, referred to as the "detection method (1)"). In the specimen blood collected from a diseased patient with an arteriosclerotic lesion, the above-mentioned arteriosclerosis marker antibody is induced by the expression of the polypeptide serving as the polypeptide marker for diagnosing arteriosclerosis. So, it is possible to detect arteriosclerosis through detection of the arteriosclerosis marker antibody with use of the polypeptide marker having an amino acid sequence set forth in SEQ ID NO: 1 of the Sequence Listing, or a partial amino acid sequence thereof consisting of four or more amino acids, for diagnosing arteriosclerosis.

**[0042]** The detection method (1) can be specifically exemplified by a method in which: the solid-phased polypeptide marker for diagnosing arteriosclerosis is contacted with a serum collected from a test subject so that the marker can bind to antibodies in the serum; unbound proteins are removed; next a labeled antibody (secondary antibody) that is

specifically bindable to the antibodies in the serum is added to allow a reaction therebetween; and the signal from the labeled antibody is detected. As to the labeling substance for the abovementioned labeled antibody, it is possible to use an enzyme, a radioisotope, a fluorescent dye, biotin, digoxigenin, or the like, which has been enumerated as a substance to label the antibody of the present invention.

5 **[0043]** When an enzyme is used as a labeling substance, the amount of the antibody can be calculated by: adding a substrate which is decomposed to take a color by an enzymatic action; optically measuring the amount of the decomposed substrate to thereby obtain the enzymatic activity; converting this value into the amount of the antibody bound; and making a comparison between the converted value and a reference value. Alternatively, the amount of the antibody can also be obtained with high sensitivity by: adding a substrate which emits light by an enzymatic action; and measuring  
10 with a weak luminescence analyzer (luminometer).

**[0044]** When a radioisotope is used as a labeling substance, the amount of the antibody can be calculated by measuring the level of radiation emitted from the radioisotope with a scintillation counter or such a device. When a fluorescent dye is used as a labeling substance, the amount of the antibody can be calculated by measuring the quantity of fluorescence with a measurement device equipped with a fluorescence spectrometer or such a device.

15 **[0045]** In the detection method (1), the western blotting method can be applied. Moreover, it is also possible to isolate a conjugate of the polypeptide marker having an amino acid sequence set forth in SEQ ID NO: 1 of the Sequence Listing, or a partial amino acid sequence thereof consisting of four or more amino acids, for diagnosing arteriosclerosis, the antibody of the specimen blood, and the labeled antibody, by a known isolation method (a chromatography method, a salting-out method, an alcohol precipitation method, an enzyme method, an in-phase method, or the like), followed by  
20 the detection of the signal from the labeled antibody.

**[0046]** Moreover, in the diagnosis of arteriosclerosis by using the detection method (1), it is also possible to examine whether or not the arteriosclerosis marker antibody(antibodies) is(are) present in the specimen blood collected from a test subject so as to determine that the test subject showing the presence of one or more types of arteriosclerosis marker antibodies is a diseased patient with an arteriosclerotic lesion, or a person with a high risk of an arteriosclerotic lesion.

25 **[0047]** In addition, the method for detecting arteriosclerosis of the present invention is a method for detecting arteriosclerosis in which the above-mentioned probe for detecting an arteriosclerosis marker gene is used to detect the expression of a gene (arteriosclerosis marker gene) that is hybridizable with the probe for detecting an arteriosclerosis marker gene, in a specimen cell (hereunder, referred to as the "detection method (2)"). In the specimen cell collected from a diseased patient with an arteriosclerotic lesion, the arteriosclerosis marker gene is expressed. So, it is possible  
30 to detect arteriosclerosis through detection of the expression of the arteriosclerosis marker gene with use of the probe for detecting an arteriosclerosis marker gene.

**[0048]** The detection method (2) can be specifically exemplified by a method in which: a probe for detecting an arteriosclerosis marker gene, which has a nucleotide sequence that encodes the amino acid sequence set forth in SEQ ID NO: 1 of the sequence listing, or a partial amino acid sequence thereof consisting of four or more amino acids, or  
35 having a nucleotide sequence set forth in SEQ ID NO: 2 of the sequence listing, or a partial nucleotide sequence thereof consisting of twelve or more nucleotides, as mentioned above in a suitable length for hybridization is prepared; a fluorescence label or such a label is appropriately added thereto; this labeled probe is contacted with a sample collected from a specimen cell to perform a hybridization reaction; and the expression of the gene serving as the gene marker for diagnosing arteriosclerosis is detected.

40 **[0049]** In the detection method (2), it is possible to employ a known detection method except for using the probe for detecting an arteriosclerosis marker gene of the present invention. For example, a northern blotting method can be employed. Moreover, in the detection method (2), any one of the above-mentioned probes for detecting an arteriosclerosis marker gene can be used. It is either possible to use a single kind of probe for detecting an arteriosclerosis marker gene or a plurality of kinds of probes for detecting an arteriosclerosis marker gene.

45 **[0050]** In addition, the detection method (2) may also use a DNA microarray or a DNA chip in which the probe(s) for detecting an arteriosclerosis marker gene is/are immobilized on a base plate.

**[0051]** Furthermore, in the detection method (2), it is also possible to employ quantitative or semi-quantitative PCR (Polymerase Chain Reaction) in order to amplify the arteriosclerosis marker gene in the sample collected from the specimen cell. The PCR may be either RT-PCR (reverse transcription PCR) or real-time RT-PCR. For carrying out the  
50 PCR, a primer set including a sense primer and an antisense primer for amplifying the arteriosclerosis marker gene is used. These primers can be appropriately constructed based on a nucleotide sequence set forth in any one of SEQ ID NO: 2 of the Sequence Listing.

**[0052]** On the completion of the amplification of the arteriosclerosis marker gene by such quantitative or semi-quantitative PCR in this way, the expression of the arteriosclerosis marker gene can be detected by using this sample. By  
55 so doing, the detection sensitivity can be improved.

**[0053]** Moreover, in the diagnosis of arteriosclerosis by using the detection method (2), it is possible to detect the arteriosclerosis marker gene in a test subject and compare the result with a result of a healthy subject detected by the same method to thereby determine that the test subject showing a large detection level is a diseased patient with an

arteriosclerotic lesion, or a person with a high risk of an arteriosclerotic lesion.

**[0054]** In addition, the method for detecting arteriosclerosis of the present invention is a method in which the antibody bindable to, as an antigen, a polypeptide serving as the polypeptide marker having an amino acid sequence set forth in SEQ ID NO: 1 of the Sequence Listing, or a partial amino acid sequence thereof consisting of four or more amino acids, for diagnosing arteriosclerosis of present invention, is used to detect the expression of a polypeptide (arteriosclerosis marker polypeptide) that is specifically bindable to the antibody, in a specimen sample (hereunder, referred to as the "detection method (3)"). In the specimen sample collected from a diseased patient with an arteriosclerotic lesion, the arteriosclerosis marker polypeptide is expressed. So, it is possible to detect arteriosclerosis through detection of the arteriosclerosis marker polypeptide with use of the antibody of the present invention.

**[0055]** The detection method (3) can be executed by a known immunoassay method except for using the antibody of the present invention. The immunoassay method can be exemplified by the western blotting method, the ELISA (Enzyme-Linked Immunosorbent Assay) method, a radioimmunoassay method, or a fluorescence antibody technique.

**[0056]** The antibody for use in the detection method (3) may be either monoclonal or polyclonal.

**[0057]** When the fluorescence antibody technique is applied to the detection method (3), either a direct fluorescence antibody test or an indirect fluorescence antibody test may be used. The direct fluorescence antibody test is a method in which an antibody for use in the detection is labeled with fluorescence, and then the antibody is contacted to a sample cell as being the test sample to bind them to each other so that a cell expressing the arteriosclerosis marker polypeptide can be labeled. In addition, the indirect fluorescence antibody test is a method in which a non-labeled antibody of the present invention is contacted to a sample cell to bind them to each other, and then the antibody is further bound to a labeled secondary antibody (anti-immunoglobulin antibody) so that a cell expressing the arteriosclerosis marker polypeptide can be labeled.

**[0058]** Moreover, when detecting arteriosclerosis through detection of the expression of the arteriosclerosis marker polypeptide, it is also possible, rather than using the antibody of the present invention as mentioned above, to use TOF-MASS to directly detect the arteriosclerosis marker polypeptide, or to use a chip in which a protein that is interactive with the arteriosclerosis marker polypeptide is immobilized on a base plate.

**[0059]** Moreover, in the diagnosis of arteriosclerosis by using the detection method (3), it is possible to examine whether or not the arteriosclerosis marker polypeptide(s) is(are) present in the specimen sample collected from a test subject so as to determine that the test subject showing the presence of one or more types of arteriosclerosis marker polypeptides is a diseased patient with an arteriosclerotic lesion, or a person with a high risk of an arteriosclerotic lesion.

**[0060]** The probe for detecting an arteriosclerosis marker gene for use in the detection of an arteriosclerotic lesion of the present invention, the DNA microarray or the DNA chip for detecting an arteriosclerosis marker gene in which the probe for detecting an arteriosclerosis marker gene is immobilized, and the antibody for detecting the arteriosclerosis marker polypeptide of the present invention can be prepared as a product of a kit for diagnosing arteriosclerosis which comprises at least one of these items and with which arteriosclerosis can be detected and diagnosed as mentioned above.

**[0061]** In addition, the polypeptide marker for diagnosing arteriosclerosis of the present invention can also be prepared as a product of a kit for diagnosing arteriosclerosis with which arteriosclerosis can be detected and diagnosed as mentioned above.

**[0062]** When the polypeptide marker for diagnosing arteriosclerosis, the gene marker for diagnosing arteriosclerosis, the antibody, and the probe for detecting an arteriosclerosis marker gene of the present invention described above are jointly used with those of the Patent Document 22, arteriosclerosis can be detected with much higher accuracy.

#### Examples

**[0063]** Hereunder is a detailed description of the present invention with reference to Examples. However, the present invention is not to be limited by the following description.

#### Production Example

(Preparation of samples)

#### **[0064]**

(1) The subjects were patients with carotid artery stenoses who had visited our hospital or cooperative institutes. The reference (control) healthy subjects were selected from outpatients so that both groups had matched gender and age ( $\pm 5$  years). When they were visiting as outpatients or hospitalized in the neurosurgery department; 1) their families were explained that this study was to be conducted for research purposes and that cooperation with the study was not compulsory, and informed consents were obtained from them; 2) questions about the family history, the past history, the life style such as drinking and smoking habits, and the work style were asked; 3) blood was

collected and separated into serum and corpuscle components and cryopreserved; and furthermore, 4) the clinical seriousness, the therapeutic process, the findings of the blood examination and the like were recorded on the basis of the medical record of the doctor. The patient blood as the analyte was separated into serum and cryopreserved at -80°C until the study was started. The antibodies and the medical records were used after encryption and anonymization.

(2) Regarding the target of screening with serum, commercial  $\lambda$ ZAP II phage vectors (STRATAGENE) recombined with a human microvascular endothelium-derived cDNA library were used.

(Expression cloning method)

**[0065]**

(3) The screening by the expression cloning method was conducted with reference to the method of St John, T et. al. (Science, 231, 845-850, 1986).

1) The above-mentioned phage vector of (2) was infected into *E. coli* (XL1-Blue) and cultured on a NZY agar medium ( $\Phi$ 15 cm dish).

2) After confirming the emergence of plaques, an IPTG-treated nitrocellulose membrane was placed on the medium, and the phage-derived protein was expressed and transferred to the nitrocellulose membrane.

3) The patient serum which had been diluted 2000-fold with 1% BSA/PBS and the nitrocellulose membrane were incubated overnight to cause a reaction between the expression proteins and the antibodies in the serum (serum IgG).

4) After washing, the alkaline phosphatase-labeled goat anti-human IgG antibody as a secondary antibody was reacted with the nitrocellulose membrane.

5) Serum IgG-recognizing clones were identified by using NBT (nitroblue tetrazolium) and BCIP (5-bromo-4-chloro-3-indolyl-phosphate) as a coloring reagent.

6) The positive clones were subjected to secondary and tertiary screening (in  $\Phi$ 10 cm dish) and false positive clones were removed.

7) The selected phage was converted to pBlueScript with the ExAssist helper phage system (Stratagene, La Jolla, CA).

8) The plasmid was purified with use of the Plasmid Miniprep kit (Sigma).

9) The nucleotide sequences of the obtained clones were determined by a

sequencer, and were subjected to a homology search using published databases. By so doing, the genes were identified and these clones were used as candidate antigen proteins.

(ELISA method)

**[0066]**

(4) ELISA method as secondary screening

1) The pBluescript including the insert of the candidate antigen protein was recombined into a protein expression and purification vector pGEX-4T (Amersham Bioscience). From the obtained nucleotide sequence information, restriction enzymes suitable for the recombination from pBluescript to pGEX-4T were selected, and treatments were done with restriction enzymes such as BamH I, Sal I, Not I, EcoR I, Xho I, and Sma I.

2) After agarose gel electrophoresis, the band of interest was cut out by using the purification kit GeneElute Minus EtBr Spin Columns (SIGMA), and the restriction enzyme digested insert and the pGEX-4T were recovered.

3) The insert and the pGEX-4T were ligated with the Ligation-Convenience Kit (Nippongene) to thereby produce a plasmid containing the insert.

4) When there was no restriction enzyme suitable for some clones, the inserts thereof were produced by PCR. Primers having a restriction enzyme recognition site were produced in advance, and RNA extracted from aneurysmal tissue was used as a template to conduct reverse transcription PCR. Thereby, cDNA was produced. Another PCR was conducted to obtain the total length of the insert. Thereafter, the same treatment was carried out using the restriction enzymes and the ligation kit.

5) The obtained recombinant pGEX-4T was used to transform *E. coli* competent cell BL21 (Nippongene) modified for eukaryotic protein expression.

6) This product was cultured in an ampicillin-containing LB medium, and the expression of the insert DNA-

## EP 2 319 924 B1

derived protein was induced with IPTG.

7) *E. coli* was recovered through centrifugal separation and ruptured by sonication to separate into a soluble fraction and an insoluble fraction.

8) If the target protein was in the insoluble fraction, this was solubilized by using urea.

9) The antigen protein was purified with the glutathione-Sepharose (Amersham Pharmacia).

10) The antigen protein was injected in a 96-well ELISA plate at a concentration of 10 µg/ml, stored at 4°C overnight, and solid-phased.

11) After washing with PBS and blocking with a PBS solution containing 10% fetal bovine serum, patient serum and control serum (serum of healthy subject) were diluted 2000-fold and reacted with the solid-phased protein.

12) After washing with PBS, HRP-labeled goat anti-human IgG antibody was added.

13) A color was developed by adding a substrate, and the absorption at OD 490 nm was measured using a plate reader.

(Western blotting method)

(5) Secondary screening by western blotting method

### [0067]

1) *E. coli* (SOLR, JM109, BL21) transformed with the pBluescript or the pGEX-4T including the insert of the candidate antigen protein obtained from the above, was cultured with 2 ml of LB ampicillin (50 µg/ml) overnight.

2) This was transferred to 20 ml of LB ampicillin and cultured for one hour, and was then added with IPTG to give a final concentration of 1 mM. The resultant sample with IPTG and a control sample (without the addition of IPTG) were cultured for another 3 hours.

3) The culture liquid was centrifuged, and *E. coli* was recovered therefrom. This was dissolved with a SDS sample buffer for use as a sample of the western method.

4) This sample was electrophoresed on a 10% polyacrylamide gel, and the protein was transferred to a nitrocellulose membrane using a blotting apparatus.

5) This was blocked with 1% skim milk and then was added with a 2000-fold diluted patient serum as a primary antibody, followed by overnight incubation.

6) After washing with PBST (20 mM Tris-HCl (pH 7.6), 50 mM NaCl, 0.1% Tween-20), 30,000-fold diluted HRP-labeled goat anti-human IgG antibody was added and allowed to react for 20 minutes.

7) After washing with PBST, a luminescent reagent Immobilon Western (MILLIPORE) was used to effect light emission.

8) The membrane was exposed to a film and developed.

9) The band which became detectable depending on the IPTG treatment was assumed to be of an antigen protein.

Verification of the gene marker for diagnosing arteriosclerosis by sequencing

[0068] The nucleotide sequences of the genes (gene markers for diagnosing arteriosclerosis) of the detected clones were determined by sequencing. The thus determined nucleotide sequences were cross-checked with nucleotide sequences in published gene databases. As a result, the genes of the obtained clones had consistent nucleotide sequences with those of the genes that encode the polypeptides for diagnosing arteriosclerosis mentioned above.

Example 1

Measurement of the antibody titer by ELISA method

[0069] Using the experimental protocol of the Production Example mentioned above, the antibody levels of the thirteen out of the eighteen types of the detected arteriosclerosis diagnostic marker candidates were measured by ELISA, and the presence of the serum antibodies was confirmed. The results of the measurement are shown in Table 2.

[Table 2]

Clone name	Patient (P)			Healthy subject (N)	
	Average	Standard deviation	p value (two-sided)	Average	Standard deviation
S19A3	0.386	0.00912	0.0000	0.272	0.0624

EP 2 319 924 B1

(continued)

Clone name	Patient (P)			Healthy subject (N)	
	Average	Standard deviation	p value (two-sided)	Average	Standard deviation
TS27A2	0.306	0.1246	0.0011	0.229	0.0909
S21B1	0.206	0.1271	0.0078	0.146	0.0779
S25E1	0.346	0.3338	0.0145	0.210	0.1515
TS12D2	0.318	0.1959	0.0227	0.242	0.1019
S36C3	0.050	0.0407	0.0281	0.035	0.0207
N48B1	0.211	0.1109	0.0472	0.165	0.1065
S28D1	0.493	0.2525	0.0642	0.400	0.2251
TS27H1	0.093	0.0827	0.0645	0.067	0.0393
PA105	0.256	0.1414	0.0000	0.1417	0.0891
PA202	0.289	0.1546	0.0097	0.2157	0.1054
PA213	0.440	0.2052	0.0002	0.2955	0.1368
PA234	0.150	0.1001	0.0131	0.1046	0.0705

Example 2

Verification of the expression of arteriosclerosis marker genes by western blotting method

**[0070]** The five types of clones of the candidate gene markers identified by the expression cloning method, that is, those unused in Example 1, were verified for the expression of the arteriosclerosis marker gene in arteriosclerosis patients by the western blotting method. The detection results thereof are shown in FIG. 1 (positive signal in western blots is indicated by the arrow in the figure.). FIG. 1(a) shows the results of Clone Name: S16D2 (SEQ ID NO: 22 of the Sequence Listing), FIG. 1(b) shows the results of Clone Name: S27D3 (SEQ ID NO: 24 of the Sequence Listing), FIG. 1(c) shows the results of Clone Name: S36E1 (SEQ ID NO: 26 of the Sequence Listing), FIG. 1(d) shows the results of Clone Name: S39D6 (SEQ ID NO: 28 of the Sequence Listing), and FIG. 1(e) shows the results of Clone Name: TS27B2 (SEQ ID NO: 30 of the Sequence Listing).

**[0071]** As shown in Table 2, with the thirteen types of candidate gene markers for diagnosing arteriosclerosis obtained from the screening of this Example, the measurement by the ELISA method showed a difference between the antibody titer of patients and the antibody titer of healthy subject serums. Furthermore, with eleven types of candidate gene markers, a significant difference was found.

**[0072]** In addition, as shown in FIG. 1, with five types of candidate gene markers obtained from the screening of this Example, positive signals for the specific reaction were confirmed by the western blotting method.

INDUSTRIAL APPLICABILITY

**[0073]** According to the polypeptide markers for diagnosing arteriosclerosis, the gene markers for diagnosing arteriosclerosis, the antibodies, the probes for detecting the arteriosclerosis marker genes, the DNA microarray or the DNA chip for detecting the arteriosclerosis marker genes, the method for detecting arteriosclerosis, and the kit for diagnosing arteriosclerosis of the present invention, arteriosclerosis can be readily detected with high accuracy. These can be favorably used for the early stage diagnosis of arteriosclerosis.

**[0074]** Sequence Listing

SEQUENCE LISTING

**[0075]**

<110> Fujikura Kasei Co., LTD National University Corporation Chiba University

<120> POLYPEPTIDE MARKER FOR DIAGNOSIS OF ARTERIOSCLEROSIS, METHOD FOR DETECTION OF

EP 2 319 924 B1

ARTERIOSCLEROSIS BY USING THE MAKER OR THE LIKE, AND KIT FOR DIAGNOSIS OF ARTERIOSCLEROSIS

<130> SHIBE/P48247EP

5

<140> EP 09806761.4

<141> 2009-08-14

<150> JP 2008-209210

10

<151> 2008-08-15

<160> 36

<210> 1

15

<211> 568

<212> PRT

<213> Homo sapiens

<400> 1

20

```

Met Glu Ser Phe Leu Leu Asp Asp Ile Ser Ser Val Ile Gln Asn Lys
 1           5           10           15
Gly Ile Glu Arg Ile Ile Ser Pro Met Ile Val Gln Leu Cys His Leu
 20           25           30           35
Leu Ile Ser Met Glu Arg Lys Glu Val Glu Asn Glu Val Phe Ala Ser
 35           40           45
Leu Glu Lys Met Ala Glu Glu Leu Ala Lys Ala Cys Glu Asp Phe Val
 50           55
Gln Val Val Lys Ser Ser Gly Asn Thr Glu Ala Val Ser Val Ser Pro
 65           70           75           80
Val Ile Val Asn Ala Ala Leu Val Phe Gln Lys Ala Val Val Val Trp
 85           90           95
Val Phe Lys Ser Glu Lys His Gly Ile Val Asp Glu Val Leu Trp Gln
 100          105          110
Ile Cys Lys Ala Arg Val Asp Ile Ser Phe Ser Trp Arg Leu Thr Arg
 115          120          125
Leu Thr Cys Val Gly Thr Val Gly Val Thr Leu Ala Gly Lys Gln Gly
 130          135          140
Gly Leu Asp Ile Val Ser Pro Gly Ser Val Ser Cys His Ser His Pro
 145          150          155          160
Cys Ala Gln Ser Ser Gln Ala Pro Thr Met Ala Phe Ser Gly Arg Ala
 165          170          175
Arg Pro Cys Ile Ile Pro Glu Asn Glu Glu Ile Pro Arg Ala Ala Leu
 180          185          190
Asn Thr Val His Glu Ala Asn Gly Thr Glu Asp Glu Arg Ala Val Ser
 195          200          205
Lys Leu Gln Arg Arg His Ser Asp Val Lys Val Tyr Lys Glu Phe Cys
 210          215          220
Asp Phe Tyr Ala Lys Phe Asn Met Ala Asn Ala Leu Ala Ser Ala Thr

```

55



EP 2 319 924 B1

<212> DNA  
 <213> Homo sapiens

<400> 2

5  
 atggagtcctt tcctcttggg tgacatcagc tctgtgatac agaacaaagg cattgagaga 60  
 atcatctcac caatgatcgt tcagctttgc catctgctca tctcaatgga gaggaaagaa 120  
 10 gtggagaatg aagtatttgc ctcggtggag aagatggctg aggaattggc gaaagcttgt 180  
 gaagacttcg tgcaagttgt caaaagttca ggcaacacgg aagctgtgtc tgtttctcct 240  
 gtcattgtaa atgcagccct ggtctttcaa aaagctgtgg ttgtgtgggt ctttaagagt 300  
 15 gaaaagcacg gcattgttga tgaagtcttg tggcaaata gcaaggcacg tgtggatatt 360  
 tctttctctt ggaggcttac aaggctgacg tgcgtgggaa cagtgggagt gaccctggct 420  
 gggaagcagg gaggcctgga tattgtttct cctggctctg tgcctgcca ttctcatccc 480  
 20 tgtgctcaga gctctcaagc acccacgatg gccttctcag gccgagcgcg cccctgcatt 540  
 atcccagaga acgaagaaat cccccgagca gcccttaaca ctgtccacga ggccaatggg 600  
 accgaggacg agagggctgt ttccaaactg cagcgcaggc acagtgacgt gaaagtctac 660  
 25 aaggagtctt gtgactttta tgcgaaattc aacatggcca acgccctggc cagcgcctact 720  
 tgcgagcgt gcaagggcgg ctttgcgccc gctgagacga tcgtgaacag taatggggag 780  
 ctgtaccatg agcagtgttt cgtgtgcgct cagtgttcc agcagttccc agaaggactc 840  
 30 ttctatgagt ttgaaggaag aaagtactgt gaacatgact ttcagatgct ctttgcccct 900  
 tgctgtcatc agtgtggtga attcatcatt ggccgagtta tcaaagccat gaataacagc 960  
 tggcatccgg agtgttccg ctgtgacctc tgccaggaag ttctggcaga tctcgggttt 1020  
 35 gtcaagaatg ctgggagaca cctgtgtcgc ccctgtcata atcgtgagaa agccagaggc 1080  
 cttgggaaat acatctgcca gaaatgccat gctatcatcg atgagcagcc tctgatattc 1140  
 aagaacgacc cctaccatcc agaccatttc aactgcgcca actgcgggaa ggatctgact 1200  
 40 gccgatgcac aggagctgaa aggggagcta tactgcctgc catgccatga taaaatgggg 1260  
 gtccccatct gtggcgcttg ccgacggccc atcgaagggc gtgtggtgaa cgccatgggc 1320  
 aagcagtggc atgtggagca ttttgtttgt gccaaagtgtg agaaaccctt tcttggacat 1380  
 45 cgccattatg agaggaaagg cctggcgtat tgtgaaactc actataacca gctatattgg 1440  
 gatgtttgct tccactgcaa tcgtgttata gaaggtgatg tggctctctgc tcttaataag 1500  
 gcctggtgcg tgaactgctt tgccctgttct acctgcaaca ctaaattaac actcaaggat 1560  
 50 aagtttgttg aaattgacct aaagccagtc tgcaaacact gttatgagaa aatgccagaa 1620  
 gaatttaaga ggcgacttgc caaacgggag agagaagcaa aggataagga caagcagaaa 1680  
 aagaaaaagc cagtctgttt attgtaa 1700

55  
 <210> 3  
 <211> 445  
 <212> PRT

<213> Homo sapiens

<400> 3

5

10

15

20

25

30

35

40

45

50

55

EP 2 319 924 B1

1 Met Arg Glu Ile Val His Leu Gln Ala Gly Gln Cys Gly Asn Gln Ile  
 5 Gly Ala Lys Phe Trp Glu Val Ile Ser Asp Glu His Gly Ile Asp Pro  
 10 Thr Gly Thr Tyr His Gly Asp Ser Asp Leu Gln Leu Glu Arg Ile Asn  
 15 Val Tyr Tyr Asn Glu Ala Thr Gly Gly Lys Tyr Val Pro Arg Ala Val  
 20 Leu Val Asp Leu Glu Pro Gly Thr Met Asp Ser Val Arg Ser Gly Pro  
 25 Phe Gly Gln Ile Phe Arg Pro Asp Asn Phe Val Phe Gly Gln Ser Gly  
 30 Ala Gly Asn Asn Trp Ala Lys Gly His Tyr Thr Glu Gly Ala Glu Leu  
 35 Val Asp Ser Val Leu Asp Val Val Arg Lys Glu Ala Glu Ser Cys Asp  
 40 Cys Leu Gln Gly Phe Gln Leu Thr His Ser Leu Gly Gly Gly Thr Gly  
 45 Ser Gly Met Gly Thr Leu Leu Ile Ser Lys Ile Arg Glu Glu Tyr Pro  
 50 Asp Arg Ile Met Asn Thr Phe Ser Val Val Pro Ser Pro Lys Val Ser  
 55 Asp Thr Val Val Glu Pro Tyr Asn Ala Thr Leu Ser Val His Gln Leu  
 60 Val Glu Asn Thr Asp Glu Thr Tyr Cys Ile Asp Asn Glu Ala Leu Tyr  
 65 Asp Ile Cys Phe Arg Thr Leu Lys Leu Thr Thr Pro Thr Tyr Gly Asp  
 70 Leu Asn His Leu Val Ser Ala Thr Met Ser Gly Val Thr Thr Cys Leu  
 75 Arg Phe Pro Gly Gln Leu Asn Ala Asp Leu Arg Lys Leu Ala Val Asn  
 80 Met Val Pro Phe Pro Arg Leu His Phe Phe Met Pro Gly Phe Ala Pro  
 85 Leu Thr Ser Arg Gly Ser Gln Gln Tyr Arg Ala Leu Thr Val Pro Glu  
 90 Leu Thr Gln Gln Met Phe Asp Ala Lys Asn Met Met Ala Ala Cys Asp  
 95 Pro Arg His Gly Arg Tyr Leu Thr Val Ala Ala Val Phe Arg Gly Arg  
 100 Met Ser Met Lys Glu Val Asp Glu Gln Met Leu Asn Val Gln Asn Lys  
 105 Asn Ser Ser Tyr Phe Val Glu Trp Ile Pro Asn Asn Val Lys Thr Ala  
 110 Val Cys Asp Ile Pro Pro Arg Gly Leu Lys Met Ser Ala Thr Phe Ile  
 115

EP 2 319 924 B1

Gly Asn Ser Thr Ala Ile Gln Glu Leu Phe Lys Arg Ile Ser Glu Gln  
370 375 380  
5 Phe Thr Ala Met Phe Arg Arg Lys Ala Phe Leu His Trp Tyr Thr Gly  
385 390 395 400  
Glu Gly Met Asp Glu Met Glu Phe Thr Glu Ala Glu Ser Asn Met Asn  
405 410 415  
10 Asp Leu Val Ser Glu Tyr Gln Gln Tyr Gln Asp Ala Thr Ala Glu Glu  
420 425 430  
Glu Gly Glu Phe Glu Glu Glu Ala Glu Glu Glu Val Ala  
435 440 445

15 <210> 4  
<211> 1338  
<212> DNA  
<213> Homo sapiens

20 <400> 4

25

30

35

40

45

50

55

EP 2 319 924 B1

atgagggaaa tcgtgcactt gcaggccggg cagtgcggca accaaatcgg cgccaagttt 60  
 tgggaggtga tcagcgatga gcacggcatc gacccacgg gcacctacca cggggacagc 120  
 5 gacctgcagc tggaacgcat caacgtgtac tacaatgagg ccaccggcgg caagtacgtg 180  
 ccccgcgccg tgctcgtgga tctggagccc ggcaccatgg actccgtgcg ctcggggccc 240  
 ttcgggcaga tcttccggcc ggacaacttc gttttcggtc agagtgggtc tgggaacaac 300  
 10 tgggccaagg ggcactacac agaaggcgcg gagctgggtg actcgggtgct ggatggtgtg 360  
 agaaaggagg ctgagagctg tgactgcctg cagggtttcc agctgaccca ctccctgggt 420  
 ggggggactg ggtctgggat ggggtaccctc ctcatcagca agatccggga ggagtacca 480  
 15 gacaggatca tgaacacggt tagtgtggtg ccttcgcca aagtgtcaga cacagtgggtg 540  
 gagccctaca acgccaccct ctcagtccac cagctcgtag aaaacacaga cgagacctac 600  
 tgcatgata acgaagctct ctacgacatt tgcttcagaa ccctaaagct gaccacgccc 660  
 20 acctatggtg acctgaacca cctggtgtct gctaccatga gtggggtcac cacctgcctg 720  
 cgcttcccag gccagctcaa tgctgacctg cggaagctgg ctgtgaacat ggtcccgttt 780  
 ccccggtgc acttcttcat gcccggcttt gcccactga ccagccgggg cagccagcag 840  
 25 taccgggctg tgaccgtgcc cgagctcacc cagcagatgt ttgatgcaa gaacatgatg 900  
 gctgcctgcg acccccgcca tggccgctac ctgacgggtg ccgccgtgtt caggggcccgc 960  
 atgtccatga aggaggtgga tgagcaaatg cttaatgtcc aaaacaaaaa cagcagctat 1020  
 30 tttgttgagt ggatcccaa caatgtgaaa acggctgtct gtgacatccc acctcggggg 1080  
 ctaaaaatgt ccgccacctt cattggcaac agcacggcca tccaggagct gttcaagcgc 1140  
 atctccgagc agttcacggc catgttccgg cgcaaggcct tcctgactg gtacacgggc 1200  
 35 gagggcatgg acgagatgga gttcaccgag gccgagagca acatgaatga cctggtgtcc 1260  
 gagtaccagc agtaccagga tgccacagcc gaggaggagg gcgagttcga ggaggaggct 1320  
 gaggaggagg tggcctag 1338

40

<210> 5  
 <211> 648  
 <212> PRT  
 <213> Homo sapiens

45

<400> 5

50

55

EP 2 319 924 B1

1 Met Glu Val Lys Gly Lys Lys Gln Phe Thr Gly Lys Ser Thr Lys Thr  
 5 Ala Gln Glu Lys Asn Arg Phe His Lys Asn Ser Asp Ser Gly Ser Ser  
 Lys Thr Phe Pro Thr Arg Lys Val Ala Lys Glu Gly Gly Pro Lys Val  
 10 Thr Ser Arg Asn Phe Glu Lys Ser Ile Thr Lys Leu Gly Lys Lys Gly  
 Val Lys Gln Phe Lys Asn Lys Gln Gln Gly Asp Lys Ser Pro Lys Asn  
 15 Lys Phe Gln Pro Ala Asn Lys Phe Asn Lys Lys Arg Lys Phe Gln Pro  
 Asp Gly Arg Ser Asp Glu Ser Ala Ala Lys Lys Pro Lys Trp Asp Asp  
 20 Phe Lys Lys Lys Lys Lys Glu Leu Lys Gln Ser Arg Gln Leu Ser Asp  
 Lys Thr Asn Tyr Asp Ile Val Val Arg Ala Lys Gln Met Trp Glu Ile  
 25 Leu Arg Arg Lys Asp Cys Asp Lys Glu Lys Arg Val Lys Leu Met Ser  
 Asp Leu Gln Lys Leu Ile Gln Gly Lys Ile Lys Thr Ile Ala Phe Ala  
 30 His Asp Ser Thr Arg Val Ile Gln Cys Tyr Ile Gln Tyr Gly Asn Glu  
 Glu Gln Arg Lys Gln Ala Phe Glu Glu Leu Arg Asp Asp Leu Val Glu  
 35 Leu Ser Lys Ala Lys Tyr Ser Arg Asn Ile Val Lys Lys Phe Leu Met  
 Tyr Gly Ser Lys Pro Gln Ile Ala Glu Ile Ile Arg Ser Phe Lys Gly  
 40 His Val Arg Lys Met Leu Arg His Ala Glu Ala Ser Ala Ile Val Glu  
 Tyr Ala Tyr Asn Asp Lys Ala Ile Leu Glu Gln Arg Asn Met Leu Thr  
 45 Glu Glu Leu Tyr Gly Asn Thr Phe Gln Leu Tyr Lys Ser Ala Asp His  
 Arg Thr Leu Asp Lys Val Leu Glu Val Gln Pro Glu Lys Leu Glu Leu  
 50 Ile Met Asp Glu Met Lys Gln Ile Leu Thr Pro Met Ala Gln Lys Glu  
 305 310 315 320

55

EP 2 319 924 B1

Ala Val Ile Lys His Ser Leu Val His Lys Val Phe Leu Asp Phe Phe  
 325 330 335  
 5 Thr Tyr Ala Pro Pro Lys Leu Arg Ser Glu Met Ile Glu Ala Ile Arg  
 340 345 350  
 Glu Ala Val Val Tyr Leu Ala His Thr His Asp Gly Ala Arg Val Ala  
 355 360 365  
 10 Met His Cys Leu Trp His Gly Thr Pro Lys Asp Arg Lys Val Ile Val  
 370 375 380  
 Lys Thr Met Lys Thr Tyr Val Glu Lys Val Ala Asn Gly Gln Tyr Ser  
 385 390 395 400  
 15 His Leu Val Leu Leu Ala Ala Phe Asp Cys Ile Asp Asp Thr Lys Leu  
 405 410 415  
 Val Lys Gln Ile Ile Ile Ser Glu Ile Ile Ser Ser Leu Pro Ser Ile  
 420 425 430 435  
 20 Val Asn Asp Lys Tyr Gly Arg Lys Val Leu Leu Tyr Leu Leu Ser Pro  
 435 440 445  
 Arg Asp Pro Ala His Thr Val Arg Glu Ile Ile Glu Val Leu Gln Lys  
 450 455 460 465  
 25 Gly Asp Gly Asn Ala His Ser Lys Lys Asp Thr Glu Val Arg Arg Arg  
 465 470 475 480  
 Glu Leu Leu Glu Ser Ile Ser Pro Ala Leu Leu Ser Tyr Leu Gln Glu  
 485 490 495  
 30 His Ala Gln Glu Val Val Leu Asp Lys Ser Ala Cys Val Leu Val Ser  
 500 505 510  
 Asp Ile Leu Gly Ser Ala Thr Gly Asp Val Gln Pro Thr Met Asn Ala  
 515 520 525  
 35 Ile Ala Ser Leu Ala Ala Thr Gly Leu His Pro Gly Gly Lys Asp Gly  
 530 535 540  
 Glu Leu His Ile Ala Glu His Pro Ala Gly His Leu Val Leu Lys Trp  
 545 550 555 560  
 40 Leu Ile Glu Gln Asp Lys Lys Met Lys Glu Asn Gly Arg Glu Gly Cys  
 565 570 575  
 Phe Ala Lys Thr Leu Val Glu His Val Gly Met Lys Asn Leu Lys Ser  
 580 585 590  
 45 Trp Ala Ser Val Asn Arg Gly Ala Ile Ile Leu Ser Ser Leu Leu Gln  
 595 600 605  
 Ser Cys Asp Leu Glu Val Ala Asn Lys Val Lys Ala Ala Leu Lys Ser  
 610 615 620  
 50 Leu Ile Pro Thr Leu Glu Lys Thr Lys Ser Thr Ser Lys Gly Ile Glu  
 625 630 635 640  
 Ile Leu Leu Glu Lys Leu Ser Thr  
 645

55 <210> 6  
 <211> 1947  
 <212> DNA  
 <213> Homo sapiens

EP 2 319 924 B1

<400> 6

	atggaagtta aagggaaaaa gcaattcaca ggaaagagta caaagacagc acaagaaaaa	60
5	aacagatttc ataaaaatag tgattctggt tcttcaaaga catttccaac aaggaaagtt	120
	gctaaagaag gtggacctaa agtcacatct aggaactttg agaaaagtat cacaaaactt	180
	gggaaaaaagg gtgtaaagca gttcaagaat aagcagcaag gggacaaatc accaaagaac	240
10	aaattccagc cggcaaataa attcaacaag aagagaaaat tccagccaga tggtagaagc	300
	gatgaatcag cagccaagaa gcccaaattg gatgacttca aaaagaagaa gaaagaactg	360
	aagcaaagca gacaactcag tgataaaacc aactatgaca ttgttgttcg ggcaaagcag	420
15	atgtgggaga ttttaagaag aaaagactgt gacaaagaaa aaagagtaaa gttaatgagt	480
	gatttgcaga agttgattca agggaaaatt aaaactattg catttgcaca cgattcaact	540
	cgtgtgatcc agtgttacat tcagtatggt aatgaagaac agagaaaaca ggcttttgaa	600
20	gaattgagcag atgatttggt tgagttaagt aaagccaaat attcgagaaa tattgttaag	660
	aaatttctca tgtatggaag taaaccacag attgcagaga taatcagaag ttttaaaggc	720
	cacgtgagga agatgctgcg gcatgchgaa gcatcagcca tcgtggagta cgatacaat	780
25	gacaaagcca ttttggagca gaggaacatg ctgacggaag agctctatgg gaacacattt	840
	cagctttaca agtcagcaga tcaccgaact ctggacaaag tgtagaggt acagccagaa	900
	aaattagaac ttattatgga tgaaatgaaa cagattctaa ctccaatggc caaaaggaa	960
30	gctgtgatta agcactcatt ggtgcataaa gtattcttgg acttttttac ctatgcaccc	1020
	cccaaactca gatcagaaat gattgaagcc atccgcgaag cggtggtcta cctggcacac	1080
	acacacgatg gcgccagagt ggccatgcac tgcctgtggc atggcacgcc caaggacagg	1140
35	aaagtgattg tgaaaacaat gaagacttat gttgaaaagg tggctaattg ccaatactcc	1200
	catttggttt tactggcggc atttgattgt attgatgata ctaagcttgt gaagcagata	1260
	atcatatcag aaattatcag ttcattgcct agcatagtaa atgacaaata tggaaggaag	1320
40	gtcctattgt acttactaag ccccagagat cctgcacata cagtacgaga aatcattgaa	1380
	gttctgcaaa aaggagatgg aatgacacac agtaagaaag atacagaggt ccgcagacgg	1440
	gagctcctag aatccatttc tccagcttg ttaagctacc tgcaagaaca cgccaagaa	1500
45	gtggtgctag ataagtctgc gtgtgtggtg gtgtctgaca ttctgggatc tgccactgga	1560
	gacgttcagc ctaccatgaa tgccatcgcc agcttggcag caacaggact gcatcctggt	1620
	ggcaaggacg gagagcttca cattgcagaa catcctgcag gacatctagt tctgaagtgg	1680
50	ttaatagagc aagataaaaa gatgaaagaa aatgggagag aaggttgttt tgcaaaaaca	1740
	cttgtagagc atgttggtat gaagaacctg aagtcctggg ctagtgtaaa tcgaggtgcc	1800
	attattcttt ctagcctcct ccagagttgt gacctggaag ttgcaaaaa agtcaaagct	1860
55	gcactgaaaa gcttgattcc tacattggaa aaaacaaaa gcaccagcaa aggaatagaa	1920
	attctacttg aaaaactgag cacatag	1947

**EP 2 319 924 B1**

<210> 7  
<211> 512  
<212> PRT  
<213> Homo sapiens

5

<400> 7

10

15

20

25

30

35

40

45

50

55

EP 2 319 924 B1

Met Ala Ile Leu Ser Leu Arg Ala Pro Gly Pro Trp Gln Ala Met Gln  
 1 5 10 15  
 Val Trp Ala Asp Arg Thr Leu Leu Thr Pro His Thr Gly Val Thr Ser  
 5 20 25 30  
 Gln Val Leu Gly Val Ala Ala Ala Val Met Thr Pro Leu Pro Gly Gly  
 35 40 45  
 His Ala Ala Gly Arg Thr Arg Glu Ala Arg Trp Asp Ala Met Glu Tyr  
 10 50 55 60  
 Asp Glu Lys Leu Ala Arg Phe Arg Gln Ala His Leu Asn Pro Phe Asn  
 65 70 75 80  
 Lys Gln Ser Gly Pro Arg Gln His Glu Gln Gly Pro Gly Glu Glu Val  
 15 85 90 95  
 Pro Asp Val Thr Pro Glu Glu Ala Leu Pro Glu Leu Pro Pro Gly Glu  
 100 105 110  
 Pro Glu Phe Arg Cys Pro Glu Arg Val Met Asp Leu Gly Leu Ser Glu  
 115 120 125  
 Asp His Phe Ser Arg Pro Val Gly Leu Phe Leu Ala Ser Asp Val Gln  
 130 135 140  
 Gln Leu Arg Gln Ala Ile Glu Glu Cys Lys Gln Val Ile Leu Glu Leu  
 145 150 155 160  
 Pro Glu Gln Ser Glu Lys Gln Lys Asp Ala Val Val Arg Leu Ile His  
 165 170 175  
 Leu Arg Leu Lys Leu Gln Glu Leu Lys Asp Pro Asn Glu Asp Glu Pro  
 180 185 190  
 Asn Ile Arg Val Leu Leu Glu His Arg Phe Tyr Lys Glu Lys Ser Lys  
 195 200 205  
 Ser Val Lys Gln Thr Cys Asp Lys Cys Asn Thr Ile Ile Trp Gly Leu  
 210 215 220  
 Ile Gln Thr Trp Tyr Thr Cys Thr Gly Cys Tyr Tyr Arg Cys His Ser  
 225 230 235 240  
 Lys Cys Leu Asn Leu Ile Ser Lys Pro Cys Val Ser Ser Lys Val Ser  
 245 250 255  
 His Gln Ala Glu Tyr Glu Leu Asn Ile Cys Pro Glu Thr Gly Leu Asp  
 260 265 270  
 Ser Gln Asp Tyr Arg Cys Ala Glu Cys Arg Ala Pro Ile Ser Leu Arg  
 275 280 285  
 Gly Val Pro Ser Glu Ala Arg Gln Cys Asp Tyr Thr Gly Gln Tyr Tyr  
 290 295 300  
 Cys Ser His Cys His Trp Asn Asp Leu Ala Val Ile Pro Ala Arg Val  
 305 310 315 320  
 Val His Asn Trp Asp Phe Glu Pro Arg Lys Val Ser Arg Cys Ser Met  
 325 330 335

55

EP 2 319 924 B1

Arg Tyr Leu Ala Leu Met Val Ser Arg Pro Val Leu Arg Leu Arg Glu  
 340 345 350  
 5 Ile Asn Pro Leu Leu Phe Ser Tyr Val Glu Glu Leu Val Glu Ile Arg  
 355 360 365  
 Lys Leu Arg Gln Asp Ile Leu Leu Met Lys Pro Tyr Phe Ile Thr Cys  
 370 37  
 10 Arg Glu Ala Met Glu Ala Arg Leu Leu Leu Gln Leu Gln Asp Arg Gln  
 385 390 395 400  
 His Phe Val Glu Asn Asp Glu Met Tyr Ser Val Gln Asp Leu Leu Asp  
 405 410 415  
 15 Val His Ala Gly Arg Leu Gly Cys Ser Leu Thr Glu Ile His Thr Leu  
 420 425 430  
 Phe Ala Lys His Ile Lys Leu Asp Cys Glu Arg Cys Gln Ala Lys Gly  
 435 440 445  
 20 Phe Val Cys Glu Leu Cys Arg Glu Gly Asp Val Leu Phe Pro Phe Asp  
 450 455 460  
 Ser His Thr Ser Val Cys Ala Asp Cys Ser Ala Val Phe His Arg Asp  
 465 470 475 480  
 25 Cys Tyr Tyr Asp Asn Ser Thr Thr Cys Pro Lys Cys Ala Arg Leu Ser  
 485 490 495  
 Leu Arg Lys Gln Ser Leu Phe Gln Glu Pro Gly Pro Asp Val Glu Ala  
 500 505 510

30 <210> 8  
 <211> 1539  
 <212> DNA  
 <213> Homo sapiens

35 <400> 8

40

45

50

55

EP 2 319 924 B1

5      gaatggccat cctgtccctg cgagcccctg ggccctggca ggcgatgcag gtatgggcag      60  
       acaggacgct gttgactccg cacaccggcg tgactttctca ggttctcggg gtggcagctg      120  
       cagtgatgac accgcttcct ggtggtcacg ccgcgggcag gacgcgggag gccagggtgg      180  
       atgctatgga atatgatgag aagctggccc gtttccggca ggcccacctc aacccttca      240  
       acaagcagtc tgggccgaga cagcatgagc agggccctgg ggaggaggtc ccggacgtca      300  
 10     ctcctgaaga ggccctgcct gagctgcccc ctggggagcc ggaattccgc tgccctgaac      360  
       gCGTgatgga tctcggcctg tctgaggacc acttctcccg ccctgtgggt ctgttctctg      420  
       cctctgacgt ccagcagctg cggcaggcga tcgaggagtg caagcagggtg attctggagc      480  
 15     tgcccagca gtcggagaag cagaaggatg ccgtggtgcg actcatccac ctccggctga      540  
       agctccagga gctgaaggac cccaatgagg atgagccaaa catccgagtg ctcttgagc      600  
       accgctttta caaggagaag agcaagagcg tcaagcagac ctgtgacaag tgtaacacca      660  
 20     tcatctgggg gctcattcag acctggtaca cctgcacagg gtgttattac cgctgtcaca      720  
       gtaagtgctt gaacctcatc tccaagccct gtgtgagctc caaagtcagc caccaagctg      780  
       aatacgaact gaacatctgc cctgagacag ggctggacag ccaggattac cgctgtgccg      840  
 25     agtgccgggc gcccatctct ctgcggggtg tgcccagtga ggccaggcag tgcgactaca      900  
       ccggccagta ctactgcagc cactgccact ggaacgacct ggctgtgatc cctgcacgcg      960  
 30     ttgtacacaa ctgggacttt gagcctcgaa aggtttctcg ctgcagcatg cgctacctgg      1020  
       cgctgatggt gtctcggccc gtactcaggc tccgggagat caaccctctg ctgttcagct      1080  
       acgtggagga gctggtggag attcgcaagc tgcgccagga catcctgctc atgaagccgt      1140  
 35     acttcatcac ctgcagggag gccatggagg ctcgtctgct gctgcagctc caggatcggc      1200  
       agcattttgt ggagaacgac gagatgtact ctgtccagga cctcctggac gtgcatgccg      1260  
       gccgcctggg ctgctcgtc accgagatcc acacgtctt cgccaagcac atcaagctgg      1320  
 40     actgcgagcg gtgccaggcc aagggtctcg tgtgtgagct ctgcagagag ggcgacgtgc      1380  
       tgttcccgtt cgacagccac acgtctgtgt ggcgccactg ctccgcggtc ttccacaggg      1440  
       actgctacta cgacaactcc accactgtc ccaagtgtgc ccggctcagc ctgaggaagc      1500  
 45     agtcgctctt ccaggagcca ggtcccgatg tggaggcct                              1539

<210> 9

<211> 1614

<212> PRT

50     <213> Homo sapiens

<400> 9

55

EP 2 319 924 B1

1 Met Ser Thr Pro Asp Pro Pro Leu Gly Gly Thr Pro Arg Pro Gly Pro  
 5 Ser Pro Gly Pro Gly Pro Ser Pro Gly Ala Met Leu Gly Pro Ser Pro  
 Gly Pro Ser Pro Gly Ser Ala His Ser Met Met Gly Pro Ser Pro Gly  
 10 Pro Pro Ser Ala Gly His Pro Ile Pro Thr Gln Gly Pro Gly Gly Tyr  
 Pro Gln Asp Asn Met His Gln Met His Lys Pro Met Glu Ser Met His  
 15 Glu Lys Gly Met Ser Asp Asp Pro Arg Tyr Asn Gln Met Lys Gly Met  
 Gly Met Arg Ser Gly Gly His Ala Gly Met Gly Pro Pro Pro Ser Pro  
 20 Met Asp Gln His Ser Gln Gly Tyr Pro Ser Pro Leu Gly Gly Ser Glu  
 His Ala Ser Ser Pro Val Pro Ala Ser Gly Pro Ser Ser Gly Pro Gln  
 25 Met Ser Ser Gly Pro Gly Gly Ala Pro Leu Asp Gly Ala Asp Pro Gln  
 Ala Leu Gly Gln Gln Asn Arg Gly Pro Thr Pro Phe Asn Gln Asn Gln  
 30 Leu His Gln Leu Arg Ala Gln Ile Met Ala Tyr Lys Met Leu Ala Arg  
 35  
 40  
 45  
 50  
 55

EP 2 319 924 B1

Gly Gln Pro Leu Pro Asp His Leu Gln Met Ala Val Gln Gly Lys Arg  
 195 200 205  
 5 Pro Met Pro Gly Met Gln Gln Gln Met Pro Thr Leu Pro Pro Pro Ser  
 210 215  
 Val Ser Ala Thr Gly Pro Gly Pro Gly Pro Gly Pro Gly Pro Gly Pro  
 225 230 235 240  
 10 Gly Pro Gly Pro Ala Pro Pro Asn Tyr Ser Arg Pro His Gly Met Gly  
 245 250 255  
 Gly Pro Asn Met Pro Pro Pro Gly Pro Ser Gly Val Pro Pro Gly Met  
 260 265 270  
 15 Pro Gly Gln Pro Pro Gly Gly Pro Pro Lys Pro Trp Pro Glu Gly Pro  
 275 280 285  
 Met Ala Asn Ala Ala Ala Pro Thr Ser Thr Pro Gln Lys Leu Ile Pro  
 290 295 300  
 20 Pro Gln Pro Thr Gly Arg Pro Ser Pro Ala Pro Pro Ala Val Pro Pro  
 305 310 315 320  
 Ala Ala Ser Pro Val Met Pro Pro Gln Thr Gln Ser Pro Gly Gln Pro  
 325 330 335  
 25 Ala Gln Pro Ala Pro Met Val Pro Leu His Gln Lys Gln Ser Arg Ile  
 340 345 350  
 Thr Pro Ile Gln Lys Pro Arg Gly Leu Asp Pro Val Glu Ile Leu Gln  
 355 360 365  
 30 Glu Arg Glu Tyr Arg Leu Gln Ala Arg Ile Ala His Arg Ile Gln Glu  
 370 375 380  
 Leu Glu Asn Leu Pro Gly Ser Leu Ala Gly Asp Leu Arg Thr Lys Ala  
 385 390 395 400  
 35 Thr Ile Glu Leu Lys Ala Leu Arg Leu Leu Asn Phe Gln Arg Gln Leu  
 405 410 415  
 Arg Gln Glu Val Val Val Cys Met Arg Arg Asp Thr Ala Leu Glu Thr  
 420 425 430  
 40 Ala Leu Asn Ala Lys Ala Tyr Lys Arg Ser Lys Arg Gln Ser Leu Arg  
 435 440 445  
 Glu Ala Arg Ile Thr Glu Lys Leu Glu Lys Gln Gln Lys Ile Glu Gln  
 450 455 460  
 45 Glu Arg Lys Arg Arg Gln Lys His Gln Glu Tyr Leu Asn Ser Ile Leu  
 465 470 475 480  
 Gln His Ala Lys Asp Phe Lys Glu Tyr His Arg Ser Val Thr Gly Lys  
 485 490 495  
 50 Ile Gln Lys Leu Thr Lys Ala Val Ala Thr Tyr His Ala Asn Thr Glu  
 500 505 510  
 Arg Glu Gln Lys Lys Glu Asn Glu Arg Ile Glu Lys Glu Arg Met Arg  
 515 520 525  
 55 Arg Leu Met Ala Glu Asp Glu Glu Gly Tyr Arg Lys Leu Ile Asp Gln  
 530 535 540  
 Lys Lys Asp Lys Arg Leu Ala Tyr Leu Leu Gln Gln Thr Asp Glu Tyr  
 545 550 555 560

EP 2 319 924 B1

Val Ala Asn Leu Thr Glu Leu Val Arg Gln His Lys Ala Ala Gln Val  
 565 570 575  
 Ala Lys Glu Lys Lys Lys Lys Lys Lys Lys Lys Lys Ala Glu Asn Ala  
 580 585 590  
 Glu Gly Gln Thr Pro Ala Ile Gly Pro Asp Gly Glu Pro Leu Asp Glu  
 595 600 605  
 Thr Ser Gln Met Ser Asp Leu Pro Val Lys Val Ile His Val Glu Ser  
 610 615 620  
 Gly Lys Ile Leu Thr Gly Thr Asp Ala Pro Lys Ala Gly Gln Leu Glu  
 625 630 635 640  
 Ala Trp Leu Glu Met Asn Pro Gly Tyr Glu Val Ala Pro Arg Ser Asp  
 645 650 655  
 Ser Glu Glu Ser Gly Ser Glu Glu Glu Glu Glu Glu Glu Glu Glu  
 660 665 670  
 Gln Pro Gln Ala Ala Gln Pro Pro Thr Leu Pro Val Glu Glu Lys Lys  
 675 680 685  
 Lys Ile Pro Asp Pro Asp Ser Asp Asp Val Ser Glu Val Asp Ala Arg  
 690 695 700  
 His Ile Ile Glu Asn Ala Lys Gln Asp Val Asp Asp Glu Tyr Gly Val  
 705 710 715 720  
 Ser Gln Ala Leu Ala Arg Gly Leu Gln Ser Tyr Tyr Ala Val Ala His  
 725 730 735  
 Ala Val Thr Glu Arg Val Asp Lys Gln Ser Ala Leu Met Val Asn Gly  
 740 745 750  
 Val Leu Lys Gln Tyr Gln Ile Lys Gly Leu Glu Trp Leu Val Ser Leu  
 755 760 765  
 Tyr Asn Asn Asn Leu Asn Gly Ile Leu Ala Asp Glu Met Gly Leu Gly  
 770 775 780  
 Lys Thr Ile Gln Thr Ile Ala Leu Ile Thr Tyr Leu Met Glu His Lys  
 785 790 795 800  
 Arg Ile Asn Gly Pro Phe Leu Ile Ile Val Pro Leu Ser Thr Leu Ser  
 805 810 815  
 Asn Trp Ala Tyr Glu Phe Asp Lys Trp Ala Pro Ser Val Val Lys Val  
 820 825 830  
 Ser Tyr Lys Gly Ser Pro Ala Ala Arg Arg Ala Phe Val Pro Gln Leu  
 835 840 845  
 Arg Ser Gly Lys Phe Asn Val Leu Leu Thr Thr Tyr Glu Tyr Ile Ile  
 850 855 860  
 Lys Asp Lys His Ile Leu Ala Lys Ile Arg Trp Lys Tyr Met Ile Val  
 865 870 875 880  
 Asp Glu Gly His Arg Met Lys Asn His His Cys Lys Leu Thr Gln Val  
 885 890 895  
 Leu Asn Thr His Tyr Val Ala Pro Arg Arg Leu Leu Leu Thr Gly Thr  
 900 905 910  
 Pro Leu Gln Asn Lys Leu Pro Glu Leu Trp Ala Leu Leu Asn Phe Leu  
 915 920 925

EP 2 319 924 B1

Leu Pro Thr Ile Phe Lys Ser Cys Ser Thr Phe Glu Gln Trp Phe Asn  
 930 935 940  
 Ala Pro Phe Ala Met Thr Gly Glu Lys Val Asp Leu Asn Glu Glu Glu  
 5 945 950 955  
 Thr Ile Leu Ile Ile Arg Arg Leu His Lys Val Leu Arg Pro Phe Leu  
 965 970 975  
 Leu Arg Arg Leu Lys Lys Glu Val Glu Ala Gln Leu Pro Glu Lys Val  
 10 980 985 990  
 Glu Tyr Val Ile Lys Cys Asp Met Ser Ala Leu Gln Arg Val Leu Tyr  
 995 1000 1005  
 Arg His Met Gln Ala Lys Gly Val Leu Leu Thr Asp Gly Ser Glu Lys  
 15 1010 1015 1020  
 Asp Lys Lys Gly Lys Gly Gly Thr Lys Thr Leu Met Asn Thr Ile Met  
 1025 1030 1035 1040  
 Gln Leu Arg Lys Ile Cys Asn His Pro Tyr Met Phe Gln His Ile Glu  
 20 1045 1050 1055  
 Glu Ser Phe Ser Glu His Leu Gly Phe Thr Gly Gly Ile Val Gln Gly  
 1060 1065 1070  
 Leu Asp Leu Tyr Arg Ala Ser Gly Lys Phe Glu Leu Leu Asp Arg Ile  
 25 1075 1080 1085  
 Leu Pro Lys Leu Arg Ala Thr Asn His Lys Val Leu Leu Phe Cys Gln  
 1090 1095 1100  
 Met Thr Ser Leu Met Thr Ile Met Glu Asp Tyr Phe Ala Tyr Arg Gly  
 30 1105 1110 1115 1120  
 Phe Lys Tyr Leu Arg Leu Asp Gly Thr Thr Lys Ala Glu Asp Arg Gly  
 1125 1130 1135  
 Met Leu Leu Lys Thr Phe Asn Glu Pro Gly Ser Glu Tyr Phe Ile Phe  
 35 1140 1145 1150  
 Leu Leu Ser Thr Arg Ala Gly Gly Leu Gly Leu Asn Leu Gln Ser Ala  
 1155 1160 1165  
 Asp Thr Val Ile Ile Phe Asp Ser Asp Trp Asn Pro His Gln Asp Leu  
 40 1170 1175 1180  
 Gln Ala Gln Asp Arg Ala His Arg Ile Gly Gln Gln Asn Glu Val Arg  
 1185 1190 1200  
 Val Leu Arg Leu Cys Thr Val Asn Ser Val Glu Glu Lys Ile Leu Ala  
 45 1205 1210 1215  
 Ala Ala Lys Tyr Lys Leu Asn Val Asp Gln Lys Val Ile Gln Ala Gly  
 1220 1225 1230  
 Met Phe Asp Gln Lys Ser Ser Ser His Glu Arg Arg Ala Phe Leu Gln  
 50 1235 1240 1245  
 Ala Ile Leu Glu His Glu Glu Gln Asp Glu Glu Glu Asp Glu Val Pro  
 1250 1255 1260  
 Asp Asp Glu Thr Val Asn Gln Met Ile Ala Arg His Glu Glu Glu Phe  
 55 1265 1270 1275 1280  
 Asp Leu Phe Met Arg Met Asp Leu Asp Arg Arg Arg Glu Glu Ala Arg  
 1285 1290 1295

EP 2 319 924 B1

Asn Pro Lys Arg Lys Pro Arg Leu Met Glu Glu Asp Glu Leu Pro Ser  
 1300 1305 1310

5 Trp Ile Ile Lys Asp Asp Ala Glu Val Glu Arg Leu Thr Cys Glu Glu  
 1315 1320 1325

Glu Glu Glu Lys Met Phe Gly Arg Gly Ser Arg His Arg Lys Glu Val  
 1330 1335 1340

10 Asp Tyr Ser Asp Ser Leu Thr Glu Lys Gln Trp Leu Lys Ala Ile Glu  
 1345 1350 1355 1360

Glu Gly Thr Leu Glu Glu Ile Glu Glu Glu Val Arg Gln Lys Lys Ser  
 1365 1370 1375

15 Ser Arg Lys Arg Lys Arg Asp Ser Asp Ala Gly Ser Ser Thr Pro Thr  
 1380 1385 1390

Thr Ser Thr Arg Ser Arg Asp Lys Asp Asp Glu Ser Lys Lys Gln Lys  
 1395 1400 1405

20 Lys Arg Gly Arg Pro Pro Ala Glu Lys Leu Ser Pro Asn Pro Pro Asn  
 1410 1415 1420

Leu Thr Lys Lys Met Lys Lys Ile Val Asp Ala Val Ile Lys Tyr Lys  
 1425 1430 1435 1440

25 Asp Ser Ser Ser Gly Arg Gln Leu Ser Glu Val Phe Ile Gln Leu Pro  
 1445 1450 1455

Ser Arg Lys Glu Leu Pro Glu Tyr Tyr Glu Leu Ile Arg Lys Pro Val  
 1460 1465 1470

30 Asp Phe Lys Lys Ile Lys Glu Arg Ile Arg Asn His Lys Tyr Arg Ser  
 1475 1480 1485

Leu Asn Asp Leu Glu Lys Asp Val Met Leu Leu Cys Gln Asn Ala Gln  
 1490 1495 1500

35 Thr Phe Asn Leu Glu Gly Ser Leu Ile Tyr Glu Asp Ser Ile Val Leu  
 1505 1510 1515 1520

Gln Ser Val Phe Thr Ser Val Arg Gln Lys Ile Glu Lys Glu Asp Asp  
 1525 1530 1535

40 Ser Glu Gly Glu Glu Ser Glu Glu Glu Glu Glu Gly Glu Glu Glu Gly  
 1540 1545 1550

Ser Glu Ser Glu Ser Arg Ser Val Lys Val Lys Ile Lys Leu Gly Arg  
 1555 1560 1565

45 Lys Glu Lys Ala Gln Asp Arg Leu Lys Gly Gly Arg Arg Arg Pro Ser  
 1570 1575 1580

Arg Gly Ser Arg Ala Lys Pro Val Val Ser Asp Asp Asp Ser Glu Glu  
 1585 1590 1595 1600

50 Glu Gln Glu Glu Asp Arg Ser Gly Ser Gly Ser Glu Glu Asp  
 1605 1610

<210> 10  
 <211> 4845  
 <212> DNA  
 <213> Homo sapiens

<400> 10

EP 2 319 924 B1

atgtccactc cagaccacc cctgggcgga actcctcggc caggtccttc cccgggcctt 60

5

10

15

20

25

30

35

40

45

50

55

EP 2 319 924 B1

5 ggccttccc ctggagccat gctgggccct agcccgggtc cctcgccggg ctccgccac 120  
 agcatgatgg ggcccagccc agggccgccc tcagcaggac accccatccc caccagggg 180  
 10 cctggagggg accctcagga caacatgcac cagatgcaca agcccatgga gtccatgcat 240  
 gagaagggca tgtcggacga cccgcgctac aaccagatga aaggaatggg gatgcggtca 300  
 gggggccatg ctgggatggg gccccgccc agcccatgg accagcactc ccaaggttac 360  
 15 ccctcggccc tgggtggctc tgagcatgcc tctagtccag ttccagccag tggcccgtct 420  
 tcggggcccc agatgtcttc cgggccagga ggtgccccgc tggatggtgc tgacccccag 480  
 gccttggggc agcagaaccg gggcccaacc ccatttaacc agaaccagct gcaccagctc 540  
 20 agagctcaga tcatggccta caagatgctg gccagggggc agcccctccc cgaccacctg 600  
 cagatggcgg tgcagggcaa gcggccgatg cccgggatgc agcagcagat gccaacgcta 660  
 cctccaccct cgggtgccgc aacaggacc ggccttgcc ctggccctgg ccccggcccg 720  
 25 ggtcccggcc cggcacctcc aaattacagc aggcctcatg gtatgggagg gcccaacatg 780  
 cctccccag gaccctcggg cgtgcccccc gggatgccag gccagcctcc tggagggcct 840  
 cccaagccct ggctgaagg acccatggcg aatgctgctg ccccccacgag caccctcag 900  
 30 aagctgattc cccgcagcc aacgggccc ccttcccccg cgccccctgc cgtcccacc 960  
 gccgcctcgc ccgtgatgcc accgcagacc cagtcccccg ggcagccggc ccagcccgcg 1020  
 cccatgggtgc cactgcacca gaagcagagc cgcatacccc ccatccagaa gccgcggggc 1080  
 35 ctcgaccctg tggagatcct gcaggagcgc gagtacaggc tgcaggctcg catcgcacac 1140  
 cgaattcagg aacttgaaaa ccttcccggg tccctggccg gggatttgcg aaccaaagcg 1200  
 accattgagc tcaaggccct caggctgctg aacttccaga ggcagctcgc ccaggaggtg 1260  
 40 gtggtgtgca tgcggagggg cacagcgtg gagacagccc tcaatgctaa ggcctacaag 1320  
 cgcagcaagc gccagtcctt gcgagggcc cgcatacctg agaagctgga gaagcagcag 1380  
 aagatcgagc aggagcga ggcggcgag aagcaccagg aatacctcaa tagcattctc 1440  
 45 cagcatgcca aggatttcaa ggaatatcac agatccgtca caggcaaaat ccagaagctg 1500  
 accaaggcag tggccacgta ccatgccaac acggagcggg agcagaagaa agagaacgag 1560  
 cggatcgaga aggagcgc atgctggaag atgaggaggg gtaccgcaag 1620  
 50 ctcatcgacc agaagaagga caagcgcctg gcctacctt tgcagcagac agacgagtac 1680  
 gtggctaacc tcacggagct ggtgcccag cacaaggctg cccaggctgc caaggagaaa 1740  
 aagaagaaaa agaaaaagaa gaaggcagaa aatgcagaag gacagacgcc tgccattggg 1800  
 55 ccggatggcg agcctctgga cgagaccagc cagatgagcg acctcccggg gaaggatgatc 1860  
 cacgtggaga gtgggaagat cctcacaggc acagatgccc ccaagccgg gcagctggag 1920  
 gcctggctcg agatgaacc ggggtatgaa gtagctccga ggtctgatag tgaagaaagt 1980  
 60 ggctcagaag aagaggaaga ggaggaggag gaagagcagc cgcaggcagc acagcctccc 2040  
 accctgcccg tggaggagaa gaagaagatt ccagatccag acagcagatga cgtctctgag 2100

EP 2 319 924 B1

gtggacgCGC ggcacatcat tgagaatgcc aagcaagatg tcgatgatga atatggcgtg 2160  
 tcccaggccc ttgcacgtgg cctgcagtcc tactatgccg tggcccatgc tgtcactgag 2220  
 5 agagtggaca agcagtcagc gcttatggtc aatgggtgcc tcaaacagta ccagatcaaa 2280  
 ggtttggagt ggctgggtgc cctgtacaac aacaacctga acggcatcct ggccgacgag 2340  
 atgggcctgg ggaagaccat ccagaccatc gcgctcatca cgtacctcat ggagcacaaa 2400  
 10 cgcacatcaatg ggcccttccct catcatcgtg cctctctcaa cgctgtccaa ctgggcgtac 2460  
 gagtttgaca agtgggcccc ctccgtgggtg aagggtgtctt acaagggatc cccagcagca 2520  
 agacgggcct ttgtcccca gctccggagt ggaagttca acgtcttgct gacgacgtac 2580  
 15 gagtacatca tcaaagacaa gcacatcctc gccaaagatcc gttggaagta catgattgtg 2640  
 gacgaaggtc accgcatgaa gaaccaccac tgcaagctga cgcaggtgct caacacgcac 2700  
 tatgtggcac cccgccgcct gctgctgacg ggcacaccgc tgcagaacaa gcttcccagag 2760  
 ctctgggCGC tgctcaactt cctgctgccc accatcttca agagctgcag caccttcgag 2820  
 20 cagtggttta acgcaccctt tgccatgacc ggggaaaagg tggacctgaa tgaggaggaa 2880  
 accattctca tcatccggcg tctccacaaa gtgctgcggc cttcttgct ccgacgactc 2940  
 aagaaggaag tcgaggcca gttgcccga aagggtggagt acgtcatcaa gtgcgacatg 3000  
 25 tctgcgctgc agcgagtgt ctaccgccac atgcaggcca agggcgtgct gctgactgat 3060  
 ggctccgaga aggacaagaa gggcaaaggc ggcaccaaga ccctgatgaa caccatcatg 3120  
 cagctgcgga agatctgcaa ccaccctac atgttccagc acatcgagga gtccttttcc 3180  
 30 gagcacttgg ggttcaactg cggcattgtc caagggtggtg acctgtaccg agcctcgggt 3240  
 aaatttgagc ttcttgatag aattcttccc aaactccgag caaccaacca caaagtgtgtg 3300  
 ctgttctgcc aatgacctc cctcatgacc atcatggaag attactttgc gtatcgcggc 3360  
 35 tttaaatacc tcaggcttga tggaaaccag aaggcggagg accggggcat gctgctgaaa 3420  
 accttcaacg agcccggctc tgagtacttc atcttctgct tcagcaccgg ggctgggggg 3480  
 ctcggcctga acctccagtc ggcagacact gtgatcattt ttgacagcga ctggaatcct 3540  
 40 caccaggacc tgcaagcgca ggaccgagcc caccgcatcg ggcagcagaa cgagggtcgt 3600  
 gtgctccgcc tctgcaccgt caacagcgtg gaggagaaga tcctagctgc agccaagtac 3660  
 aagctcaacg tggaccagaa ggtgatccag gccggcatgt tcgaccagaa gtcctccagc 3720  
 45 catgagcggc gcgccttccct gcaggccatc ctggagcacg aggagcagga tgaggaggaa 3780  
 gacgaggtgc ccgacgacga gaccgtcaac cagatgatcg cccggcacga ggaggagttt 3840  
 gatctgttca tgcgcatgga cctggaccgc aggcgcgagg aggcccgcaa cccaagcgg 3900  
 50 aagccgcgcc tcatggagga ggacgagctc ccctcgtgga tcatcaagga cgacgcggag 3960  
 gtggagcggc tgacctgtga ggaggaggag gagaagatgt tcggccgtgg ctcccgccac 4020  
 cgcaaggagg tggactacag cgactcactg acggagaagc agtggctcaa ggccatcgag 4080  
 55 gagggcacgc tggaggagat cgaagaggag gtccggcaga agaaatcatc acggaagcgc 4140  
 aagcgagaca gcgacgccgg ctctccacc cggaccacca gcaccgcag ccgcgacaag 4200

EP 2 319 924 B1

gacgacgaga gcaagaagca gaagaagcgc gggcggccgc ctgccgagaa actctcccct 4260  
 aacccaccca acctcaccaa gaagatgaag aagattgtgg atgccgtgat caagtacaag 4320  
 5 gacagcagca gtggacgtca gctcagcgag gtcttcatcc agctgccctc gcgaaaggag 4380  
 ctgcccgagt actacgagct catccgcaag cccgtggact tcaagaagat aaaggagcgc 4440  
 attcgaacc acaagtaccg cagcctcaac gacctagaga aggacgtcat gtcctgtgac 4500  
 10 cagaacgcac agaccttcaa cctggagggc tccctgatct atgaagactc catcgtcttg 4560  
 cagtcggtct tcaccagcgt gcggcagaaa atcgagaagg aggatgacag tgaaggcgag 4620  
 gagagtgagg aggaggaaga gggcgaggag gaaggctccg aatccgaatc tcggtccgctc 4680  
 15 aaagtgaaga tcaagcttgg ccggaaggag aaggcacagg accggctgaa gggcggccgg 4740  
 cggcggccga gccgagggtc ccgagccaag ccggtcgtga gtgacgatga cagtgaggag 4800  
 gaacaagagg aggaccgctc aggaagtggc agcgaagaag actga 4845

20

<210> 11  
 <211> 454  
 <212> PRT  
 <213> Homo sapiens

25

<400> 11

30

35

40

45

50

55

EP 2 319 924 B1

	Met	Ser	Ala	Gly	Gly	Pro	Cys	Pro	Ala	Ala	Ala	Gly	Gly	Gly	Pro	Gly
	1				5					10					15	
5	Gly	Ala	Ser	Cys	Ser	Val	Gly	Ala	Pro	Gly	Gly	Val	Ser	Met	Phe	Arg
				20					25					30		
	Trp	Leu	Glu	Val	Leu	Glu	Lys	Glu	Phe	Asp	Lys	Ala	Phe	Val	Asp	Val
			35					40					45			
10	Asp	Leu	Leu	Leu	Gly	Glu	Ile	Asp	Pro	Asp	Gln	Ala	Asp	Ile	Thr	Tyr
	50						55					60				
	Glu	Gly	Arg	Gln	Lys	Met	Thr	Ser	Leu	Ser	Ser	Cys	Phe	Ala	Gln	Leu
	65					70					75					80
15	Cys	His	Lys	Ala	Gln	Ser	Val	Ser	Gln	Ile	Asn	His	Lys	Leu	Glu	Ala
					85					90					95	
	Gln	Leu	Val	Asp	Leu	Lys	Ser	Glu	Leu	Thr	Glu	Thr	Gln	Ala	Glu	Lys
				100					105					110		
20	Val	Val	Leu	Glu	Lys	Glu	Val	His	Asp	Gln	Leu	Leu	Gln	Leu	His	Ser
			115					120					125			
	Ile	Gln	Leu	Gln	Leu	His	Ala	Lys	Thr	Gly	Gln	Ser	Ala	Asp	Ser	Gly
		130					135					140				
25	Thr	Ile	Lys	Ala	Lys	Leu	Glu	Arg	Glu	Leu	Glu	Ala	Asn	Lys	Lys	Glu
	145					150					155					160
	Lys	Met	Lys	Glu	Ala	Gln	Leu	Glu	Ala	Glu	Val	Lys	Leu	Leu	Arg	Lys
					165					170					175	
30	Glu	Asn	Glu	Ala	Leu	Arg	Arg	His	Ile	Ala	Val	Leu	Gln	Ala	Glu	Val
				180					185					190		
	Tyr	Gly	Ala	Arg	Leu	Ala	Ala	Lys	Tyr	Leu	Asp	Lys	Glu	Leu	Ala	Gly
			195					200					205			

35  
40  
45  
50  
55

EP 2 319 924 B1

Arg Val Gln Gln Ile Gln Leu Leu Gly Arg Asp Met Lys Gly Pro Ala  
 210 215 220  
 5 His Asp Lys Leu Trp Asn Gln Leu Glu Ala Glu Ile His Leu His Arg  
 225 230 235 240  
 His Lys Thr Val Ile Arg Ala Cys Arg Gly Arg Asn Asp Leu Lys Arg  
 245 250 255  
 10 Pro Met Gln Ala Pro Pro Gly His Asp Gln Asp Ser Leu Lys Lys Ser  
 260 265 270  
 Gln Gly Val Gly Pro Ile Arg Lys Val Leu Leu Leu Lys Glu Asp His  
 275 280 285  
 15 Glu Gly Leu Gly Ile Ser Ile Thr Gly Gly Lys Glu His Gly Val Pro  
 290 295 300  
 Ile Leu Ile Ser Glu Ile His Pro Gly Gln Pro Ala Asp Arg Cys Gly  
 305 310 315 320  
 20 Gly Leu His Val Gly Asp Ala Ile Leu Ala Val Asn Gly Val Asn Leu  
 325 330 335  
 Arg Asp Thr Lys His Lys Glu Ala Val Thr Ile Leu Ser Gln Gln Arg  
 340 345 350  
 25 Gly Glu Ile Glu Phe Glu Val Val Tyr Val Ala Pro Glu Val Asp Ser  
 355 360 365  
 Asp Asp Glu Asn Val Glu Tyr Glu Asp Glu Ser Gly His Arg Tyr Arg  
 370 375 380  
 30 Leu Tyr Leu Asp Glu Leu Glu Gly Gly Gly Asn Pro Gly Ala Ser Cys  
 385 390 395 400  
 Lys Asp Thr Ser Gly Glu Ile Lys Val Leu Gln Gly Phe Asn Lys Lys  
 405 410 415  
 35 Ala Val Thr Asp Thr His Glu Asn Gly Asp Leu Gly Thr Ala Ser Glu  
 420 425 430 435  
 Thr Pro Leu Asp Asp Gly Ala Ser Lys Leu Asp Asp Leu His Thr Leu  
 435 440 445  
 40 Tyr His Lys Lys Ser Tyr  
 450

<210> 12

<211> 1365

<212> DNA

45 <213> Homo sapiens

<400> 12

50 ccatgtcggc gggcgggtcca tgcccagcag cagccggagg gggcccaggg ggcgcctcct 60  
 gctccgtggg ggcccctggc ggggtatcca tgttccggtg gctggagggtg ctggagaagg 120  
 agttcgacaa agcttttgtg gatgtggatc tgctcctggg agagatcgat ccagaccaag 180  
 55 cggacatcac ttatgagggg cgacagaaga tgaccagcct gagctcctgc tttgcacagc 240  
 tttgccacaa agcccagtct gtgtctcaaa tcaaccacaa gctggaggca cagttggtgg 300  
 atctgaaatc tgaactgaca gaaaccaag cagagaaagt tgttttggag aaagaagtac 360

EP 2 319 924 B1

atgatcagct tttacagctg cactctattc agctgcagct tcatgctaaa actggtcaaa 420  
 gtgctgactc tgggtaccatt aaggcaaaat tggaaagaga gcttgaggca aacaaaaaag 480  
 5 aaaaaatgaa agaagcaciaa cttgaagctg aagtgaaatt gttgagaaaa gagaatgaag 540  
 cccttcgtag acatatagct gttctccagg ctgaagtata tggggcgaga ctagctgcca 600  
 agtacttgga taaggaactg gcaggaaggg tccaacagat acaattgcta ggacgagata 660  
 10 tgaagggacc tgctcatgat aagctttgga accaattaga agctgaaata catttgcatc 720  
 gtcacaaaac tgtgatccga gcctgcagag gacgtaatga cttgaaacga ccaatgcaag 780  
 caccaccagg ccatgatcaa gattccctaa agaaaagcca aggtggtggt ccaattagaa 840  
 15 aagttctcct ccttaaggaa gatcatgaag gccttggcat ttcaattaca ggtgggaaag 900  
 aacatggtgt tccaatcctc atctctgaga tccatccggg gcaacctgct gatagatgcg 960  
 gagggctgca cgttggggat gctatthttg cagtcaacgg agttaaccta agggacacia 1020  
 20 agcataaaga agctgtaact attctthtctc agcagagagg agagattgaa tttgaagtag 1080  
 tttatgtggc tcctgaagtg gattctgatg atgaaaacgt agagtatgaa gatgagagtg 1140  
 gacatcgтта ccgthttgtac cttgatgagt tagaaggagg tggtaaccct ggtgctagtt 1200  
 25 gcaaagacac aagtggggaa atcaaagtat tacaaggatt taataagaag gcagtaactg 1260  
 acacacatga aaatggagac ctgggactg caagtgaaac tccgctagat gacggtgctt 1320  
 caaaattaga tgatctgcac actctgtatc ataaaaaatc ttatt 1365

30

<210> 13  
 <211> 2517  
 <212> PRT  
 <213> Homo sapiens

35

<400> 13

40

45

50

55

EP 2 319 924 B1

Met Val Gly Glu Arg His Ala Gly Asp Leu Met Val Pro Leu Gly Pro  
 1 5 10 15  
 Arg Leu Gln Ala Tyr Pro Glu Glu Leu Ile Arg Gln Arg Pro Gly His  
 5 20 25 30  
 Asp Gly His Pro Glu Tyr Leu Ile Arg Trp Ser Val Leu Lys Cys Gly  
 35 40 45  
 Glu Val Gly Lys Val Gly Val Glu Glu Gly Lys Ala Glu His Ile Leu  
 10 50 55 60  
 Met Trp Leu Ser Ala Pro Glu Val Tyr Ala Asn Cys Pro Gly Leu Leu  
 65 70 75 80  
 Gly Glu Arg Ala Leu Ser Lys Gly Leu Gln His Glu Pro Ala Gly Val  
 15 85 90 95  
 Ser Gly Ser Phe Pro Arg Asp Pro Gly Gly Leu Asp Glu Val Ala Met  
 100 105 110  
 Gly Glu Met Glu Ala Asp Val Gln Ala Leu Val Arg Arg Ala Ala Arg  
 20 115 120 125  
 Gln Leu Ala Glu Ser Gly Thr Pro Ser Leu Thr Ala Ala Val Leu His  
 130 135 140

25

30

35

40

45

50

55

EP 2 319 924 B1

Thr 145 Ile His Val Leu 150 Ser Ala Tyr Ala Ser Ile 155 Gly Pro Leu Thr Gly 160  
 Val Phe Arg Glu Thr 165 Gly Ala Leu Asp Leu 170 Leu Met His Met Leu 175 Cys  
 5  
 Asn Pro Glu Pro 180 Gln Ile Arg Arg Ser 185 Ala Gly Lys Met Leu 190 Gln Ala  
 Leu Ala Ala 195 His Asp Ala Gly Ser 200 Arg Ala His Val Leu 205 Leu Ser Leu  
 10  
 Ser Gln Gln Asp Gly Ile 210 Glu Gln His Met Asp Phe 220 Asp Ser Arg Tyr  
 Thr 225 Leu Leu Glu Leu Phe 230 Ala Glu Thr Thr Ser 235 Ser Glu Glu His Cys 240  
 15  
 Met Ala Phe Glu Gly 245 Ile His Leu Pro Gln 250 Ile Pro Gly Lys Leu 255 Leu  
 Phe Ser Leu Val 260 Lys Arg Tyr Leu Cys 265 Val Thr Ser Leu Leu Asp Gln  
 20  
 Leu Asn Ser 275 Ser Pro Glu Leu Gly 280 Ala Gly Asp Gln Ser 285 Ser Pro Cys  
 Ala Thr Arg Glu Lys Ser Arg 295 Gly Gln Arg Glu Leu 300 Glu Phe Ser Met  
 25  
 Ala Val Gly Asn Leu Ile 310 Ser Glu Leu Val Arg 315 Ser Met Gly Trp Ala 320  
 Arg Asn Leu Ser Glu 325 Gln Gly Met Ser Pro 330 Pro Arg Pro Thr Arg Ser 335  
 30  
 Ile Phe Gln Pro Tyr Ile Ser Gly Pro 345 Ser Leu Leu Leu Pro Thr Ile 350  
 Val Thr Thr Pro Arg Arg Gln Gly 360 Trp Val Phe Arg Gln Arg Ser Glu 365  
 35  
 Phe Ser Ser Arg Ser Gly Tyr 375 Gly Glu Tyr Val Gln Gln Thr Leu Gln 380  
 Pro Gly Met Arg Val Arg 390 Met Leu Asp Asp Tyr 395 Glu Glu Ile Ser Ala 400  
 40  
 Gly Asp Glu Gly Glu 405 Phe Arg Gln Ser Asn 410 Asn Gly Ile Pro Pro Val 415  
 Gln Val Phe Trp Gln Ser Thr Gly Arg 425 Thr Tyr Trp Val His Trp His 430  
 45  
 Met Leu Glu Ile Leu Gly Pro Glu 440 Glu Ala Thr Glu Asp 445 Lys Ala Ser  
 Ala Ala Val Glu Lys Gly Ala 455 Gly Ala Thr Val Leu Gly Thr Ala Phe 460  
 50  
 Pro Ser Trp Asp Trp Asn 470 Pro Met Asp Gly Leu 475 Tyr Pro Leu Pro Tyr 480  
 Leu Gln Pro Glu Pro 485 Gln Lys Asn Glu Arg 490 Val Gly Tyr Leu Thr Gln 495  
 55  
 Ala Glu Trp Trp 500 Glu Leu Leu Phe Phe 505 Ile Lys Lys Leu Asp 510 Leu Cys

EP 2 319 924 B1

5  
 10  
 15  
 20  
 25  
 30  
 35  
 40  
 45  
 50  
 55

Glu Gln Gln Pro Ile Phe Gln Asn Leu Trp Lys Asn Leu Asp Glu Thr  
 515 520 525  
 Leu Gly Glu Lys Ala Leu Gly Glu Ile Ser Val Ser Val Glu Met Ala  
 530 535 540  
 Glu Ser Leu Leu Gln Val Leu Ser Ser Arg Phe Glu Gly Ser Thr Leu  
 545 550 555  
 Asn Asp Leu Leu Asn Ser Gln Ile Tyr Thr Lys Tyr Gly Leu Leu Ser  
 565 570 575  
 Asn Glu Pro Ser Ser Ser Ser Thr Ser Arg Asn His Ser Cys Thr Pro  
 580 585 590  
 Asp Pro Glu Glu Glu Ser Lys Ser Glu Ala Ser Phe Ser Glu Glu Glu  
 595 600 605  
 Thr Glu Ser Leu Lys Ala Lys Ala Glu Ala Pro Lys Thr Glu Ala Glu  
 610 615 620  
 Pro Thr Lys Thr Arg Thr Glu Thr Pro Met Ala Gln Ser Asp Ser Gln  
 625 630 635  
 Leu Phe Asn Gln Leu Leu Val Thr Glu Gly Met Thr Leu Pro Thr Glu  
 645 650  
 Met Lys Glu Ala Ala Ser Glu Met Ala Arg Ala Leu Arg Gly Pro Gly  
 660 665 670  
 Pro Arg Ser Ser Leu Asp Gln His Val Ala Ala Val Val Ala Thr Val  
 675 680 685  
 Gln Ile Ser Ser Leu Asp Thr Asn Leu Gln Leu Ser Gly Leu Ser Ala  
 690 695 700  
 Leu Ser Gln Ala Val Glu Glu Val Thr Glu Arg Asp His Pro Leu Val  
 705 710 715  
 Arg Pro Asp Arg Ser Leu Arg Glu Lys Leu Val Lys Met Leu Val Glu  
 725 730 735  
 Leu Leu Thr Asn Gln Val Gly Glu Lys Met Val Val Val Gln Ala Leu  
 740 745 750  
 Arg Leu Leu Tyr Leu Leu Met Thr Lys His Glu Trp Arg Pro Leu Phe  
 755 760 765  
 Ala Arg Glu Gly Gly Ile Tyr Ala Val Leu Val Cys Met Gln Glu Tyr  
 770 775 780  
 Lys Thr Ser Val Leu Val Gln Gln Ala Gly Leu Ala Ala Leu Lys Met  
 785 790 795 800  
 Leu Ala Val Ala Ser Ser Ser Glu Ile Pro Thr Phe Val Thr Gly Arg  
 805 810 815  
 Asp Ser Ile His Ser Leu Phe Asp Ala Gln Met Thr Arg Glu Ile Phe  
 820 825 830  
 Ala Ser Ile Asp Ser Ala Thr Arg Pro Gly Ser Glu Ser Leu Leu Leu  
 835 840 845  
 Thr Val Pro Ala Ala Val Ile Leu Met Leu Asn Thr Glu Gly Cys Ser  
 850 855 860  
 Ser Ala Ala Arg Asn Gly Leu Leu Leu Leu Asn Leu Leu Leu Cys Asn  
 865 870 875 880

EP 2 319 924 B1

His His Thr Leu Gly Asp Gln Ile Ile Thr Gln Glu Leu Arg Asp Thr  
 885 890 895  
 5 Leu Phe Arg His Ser Gly Ile Ala Pro Arg Thr Glu Pro Met Pro Thr  
 900 905 910  
 Thr Arg Thr Ile Leu Met Met Leu Leu Asn Arg Tyr Ser Glu Pro Pro  
 915 920 925  
 10 Gly Ser Pro Glu Arg Ala Ala Leu Glu Thr Pro Ile Ile Gln Gly Gln  
 930 935 940  
 Asp Gly Ser Pro Glu Leu Leu Ile Arg Ser Leu Val Gly Gly Pro Ser  
 945 950 955 960  
 15 Ala Glu Leu Leu Leu Asp Leu Glu Arg Val Leu Cys Arg Glu Gly Ser  
 965 970 975  
 Pro Gly Gly Ala Val Arg Pro Leu Leu Lys Arg Leu Gln Gln Glu Thr  
 980 985 990  
 20 Gln Pro Phe Leu Leu Leu Leu Arg Thr Leu Asp Ala Pro Gly Pro Asn  
 995 1000 1005  
 Lys Thr Leu Leu Leu Ser Val Leu Arg Val Ile Thr Arg Leu Leu Asp  
 1010 1015 1020  
 25 Phe Pro Glu Ala Met Val Leu Pro Trp His Glu Val Leu Glu Pro Cys  
 1025 1030 1035 1040  
 Leu Asn Cys Leu Ser Gly Pro Ser Ser Asp Ser Glu Ile Val Gln Glu  
 1045 1050 1055  
 30 Leu Thr Cys Phe Leu His Arg Leu Ala Ser Met His Lys Asp Tyr Ala  
 1060 1065 1070  
 Val Val Leu Cys Cys Leu Gly Ala Lys Glu Ile Leu Ser Lys Val Leu  
 1075 1080 1085  
 35 Asp Lys His Ser Ala Gln Leu Leu Leu Gly Cys Glu Leu Arg Asp Leu  
 1090 1095 1100  
 Val Thr Glu Cys Glu Lys Tyr Ala Gln Leu Tyr Ser Asn Leu Thr Ser  
 1105 1110 1115 1120  
 40 Ser Ile Leu Ala Gly Cys Ile Gln Met Val Leu Gly Gln Ile Glu Asp  
 1125 1130 1135  
 His Arg Arg Thr His Gln Pro Ile Asn Ile Pro Phe Phe Asp Val Phe  
 1140 1145 1150  
 45 Leu Arg His Leu Cys Gln Gly Ser Ser Val Glu Val Lys Glu Asp Lys  
 1155 1160 1165  
 Cys Trp Glu Lys Val Glu Val Ser Ser Asn Pro His Arg Ala Ser Lys  
 1170 1175 1180  
 50 Leu Thr Asp His Asn Pro Lys Thr Tyr Trp Glu Ser Asn Gly Ser Thr  
 1185 1190 1195 1200  
 Gly Ser His Tyr Ile Thr Leu His Met His Arg Gly Val Leu Val Arg  
 1205 1210 1215  
 55 Gln Leu Thr Leu Leu Val Ala Ser Glu Asp Ser Ser Tyr Met Pro Ala  
 1220 1225 1230  
 Arg Val Val Val Phe Gly Gly Asp Ser Thr Ser Cys Ile Gly Thr Glu  
 1235 1240 1245

EP 2 319 924 B1

Leu Asn Thr Val Asn Val Met Pro Ser Ala Ser Arg Val Ile Leu Leu  
 1250 1255 1260  
 5  
 Glu Asn Leu Asn Arg Phe Trp Pro Ile Ile Gln Ile Arg Ile Lys Arg  
 1265 1270 1275 1280  
 Cys Gln Gln Gly Gly Ile Asp Thr Arg Val Arg Gly Val Glu Val Leu  
 1285 1290 1295  
 10  
 Gly Pro Lys Pro Thr Phe Trp Pro Leu Phe Arg Glu Gln Leu Cys Arg  
 1300 1305 1310  
 Arg Thr Cys Leu Phe Tyr Thr Ile Arg Ala Gln Ala Trp Ser Arg Asp  
 1315 1320 1325  
 15  
 Ile Ala Glu Asp His Arg Arg Leu Leu Gln Leu Cys Pro Arg Leu Asn  
 1330 1335 1340  
 Arg Val Leu Arg His Glu Gln Asn Phe Ala Asp Arg Phe Leu Pro Asp  
 1345 1350 1355 1360  
 20  
 Asp Glu Ala Ala Gln Ala Leu Gly Lys Thr Cys Trp Glu Ala Leu Val  
 1365 1370 1375  
 Ser Pro Leu Val Gln Asn Ile Thr Ser Pro Asp Ala Glu Gly Val Ser  
 1380 1385 1390  
 25  
 Ala Leu Gly Trp Leu Leu Asp Gln Tyr Leu Glu Gln Arg Glu Thr Ser  
 1395 1400 1405  
 Arg Asn Pro Leu Ser Arg Ala Ala Ser Phe Ala Ser Arg Val Arg Arg  
 1410 1415 1420  
 30  
 Leu Cys His Leu Leu Val His Val Glu Pro Pro Pro Gly Pro Ser Pro  
 1425 1430 1435 1440  
 Glu Pro Ser Thr Arg Pro Phe Ser Lys Asn Ser Lys Gly Arg Asp Arg  
 1445 1450 1455  
 35  
 Ser Pro Ala Pro Ser Pro Val Leu Pro Ser Ser Ser Leu Arg Asn Ile  
 1460 1465 1470  
 Thr Gln Cys Trp Leu Ser Val Val Gln Glu Gln Val Ser Arg Phe Leu  
 1475 1480 1485  
 40  
 Ala Ala Ala Trp Arg Ala Pro Asp Phe Val Pro Arg Tyr Cys Lys Leu  
 1490 1495 1500  
 Tyr Glu His Leu Gln Arg Ala Gly Ser Glu Leu Phe Gly Pro Arg Ala  
 1505 1510 1515 1520  
 45  
 Ala Phe Met Leu Ala Leu Arg Ser Gly Phe Ser Gly Ala Leu Leu Gln  
 1525 1530 1535  
 Gln Ser Phe Leu Thr Ala Ala His Met Ser Glu Gln Phe Ala Arg Tyr  
 1540 1545 1550  
 50  
 Ile Asp Gln Gln Ile Gln Gly Gly Leu Ile Gly Gly Ala Pro Gly Val  
 1555 1560 1565  
 Glu Met Leu Gly Gln Leu Gln Arg His Leu Glu Pro Ile Met Val Leu  
 1570 1575 1580  
 55  
 Ser Gly Leu Glu Leu Ala Thr Thr Phe Glu His Phe Tyr Gln His Tyr  
 1585 1590 1595 1600  
 Met Ala Asp Arg Leu Leu Ser Phe Gly Ser Ser Trp Leu Glu Gly Ala  
 1605 1610 1615

EP 2 319 924 B1

Val Leu Glu Gln Ile Gly Leu Cys Phe Pro Asn Arg Leu Pro Gln Leu  
 1620 1625 1630  
 5 Met Leu Gln Ser Leu Ser Thr Ser Glu Glu Leu Gln Arg Gln Phe His  
 1635 1640 1645  
 Leu Phe Gln Leu Gln Arg Leu Asp Lys Leu Phe Leu Glu Gln Glu Asp  
 1650 1655 1660  
 10 Glu Glu Glu Lys Arg Leu Glu Glu Glu Glu Glu Glu Glu Glu Glu  
 1665 1670 1675 1680  
 Glu Ala Glu Lys Glu Leu Phe Ile Glu Asp Pro Ser Pro Ala Ile Ser  
 1685 1690 1695  
 15 Ile Leu Val Leu Ser Pro Arg Cys Trp Pro Val Ser Pro Leu Cys Tyr  
 1700 1705 1710  
 Leu Tyr His Pro Arg Lys Cys Leu Pro Thr Glu Phe Cys Asp Ala Leu  
 1715 1720 1725  
 20 Asp Arg Phe Ser Ser Phe Tyr Ser Gln Ser Gln Asn His Pro Val Leu  
 1730 1735 1740  
 Asp Met Gly Pro His Arg Arg Leu Gln Trp Thr Trp Leu Gly Arg Ala  
 1745 1750 1755 1760  
 25 Glu Leu Gln Phe Gly Lys Gln Ile Leu His Val Ser Thr Val Gln Met  
 1765 1770 1775  
 Trp Leu Leu Leu Lys Phe Asn Gln Thr Glu Glu Val Ser Val Glu Thr  
 1780 1785 1790  
 30 Leu Leu Lys Asp Ser Asp Leu Ser Pro Glu Leu Leu Leu Gln Ala Leu  
 1795 1800 1805  
 Val Pro Leu Thr Ser Gly Asn Gly Pro Leu Thr Leu His Glu Gly Gln  
 1810 1815 1820  
 35 Asp Phe Pro His Gly Gly Val Leu Arg Leu His Glu Pro Gly Pro Gln  
 1825 1830 1835 1840  
 Arg Ser Gly Glu Ala Leu Trp Leu Ile Pro Pro Gln Ala Tyr Leu Asn  
 1845 1850 1855  
 40 Val Glu Lys Asp Glu Gly Arg Thr Leu Glu Gln Lys Arg Asn Leu Leu  
 1860 1865 1870  
 Ser Cys Leu Leu Val Arg Ile Leu Lys Ala His Gly Glu Lys Gly Leu  
 1875 1880 1885  
 45 His Ile Asp Gln Leu Val Cys Leu Val Leu Glu Ala Trp Gln Lys Gly  
 1890 1895 1900  
 Pro Asn Pro Pro Gly Thr Leu Gly His Thr Val Ala Gly Gly Val Ala  
 1905 1910 1915 1920  
 50 Cys Thr Ser Thr Asp Val Leu Ser Cys Ile Leu His Leu Leu Gly Gln  
 1925 1930 1935  
 Gly Tyr Val Lys Arg Arg Asp Asp Arg Pro Gln Ile Leu Met Tyr Ala  
 1940 1945 1950  
 55 Ala Pro Glu Pro Met Gly Pro Cys Arg Gly Gln Ala Asp Val Pro Phe  
 1955 1960 1965  
 Cys Gly Ser Gln Ser Glu Thr Ser Lys Pro Ser Pro Glu Ala Val Ala  
 1970 1975 1980

EP 2 319 924 B1

Thr Leu Ala Ser Leu Gln Leu Pro Ala Gly Arg Thr Met Ser Pro Gln  
 1985 1990 1995 2000  
 5  
 Glu Val Glu Gly Leu Met Lys Gln Thr Val Arg Gln Val Gln Glu Thr  
 2005 2010 2015  
 Leu Asn Leu Glu Pro Asp Val Ala Gln His Leu Leu Ala His Ser His  
 2020 2025 2030  
 10  
 Trp Gly Ala Glu Gln Leu Leu Gln Ser Tyr Ser Glu Asp Pro Glu Pro  
 2035 2040 2045  
 Leu Leu Leu Ala Ala Gly Leu Cys Val His Gln Ala Gln Ala Val Pro  
 2050 2055 2060  
 15  
 Val Arg Pro Asp His Cys Pro Val Cys Val Ser Pro Leu Gly Cys Asp  
 2065 2070 2075 2080  
 Asp Asp Leu Pro Ser Leu Cys Cys Met His Tyr Cys Cys Lys Ser Cys  
 2085 2090 2095  
 20  
 Trp Asn Glu Tyr Leu Thr Thr Arg Ile Glu Gln Asn Leu Val Leu Asn  
 2100 2105 2110  
 Cys Thr Cys Pro Ile Ala Asp Cys Pro Ala Gln Pro Thr Gly Ala Phe  
 2115  
 25  
 Ile Arg Ala Ile Val Ser Ser Pro Glu Val Ile Ser Lys Tyr Glu Lys  
 2130 2135 2140  
 Ala Leu Leu Arg Gly Tyr Val Glu Ser Cys Ser Asn Leu Thr Trp Cys  
 2145 2150 2155 2160  
 30  
 Thr Asn Pro Gln Gly Cys Asp Arg Ile Leu Cys Arg Gln Gly Leu Gly  
 2165 2170 2175  
 Cys Gly Thr Thr Cys Ser Lys Cys Gly Trp Ala Ser Cys Phe Asn Cys  
 2180 2185 2190  
 35  
 Ser Phe Pro Glu Ala His Tyr Pro Ala Ser Cys Gly His Met Ser Gln  
 2195 2200 2205  
 Trp Val Asp Asp Gly Gly Tyr Tyr Asp Gly Met Ser Val Glu Ala Gln  
 2210 2215 2220  
 40  
 Ser Lys His Leu Ala Lys Leu Ile Ser Lys Arg Cys Pro Ser Cys Gln  
 2225 2230 2235 2240  
 Ala Pro Ile Glu Lys Asn Glu Gly Cys Leu His Met Thr Cys Ala Lys  
 2245 2250 2255  
 45  
 Cys Asn His Gly Phe Cys Trp Arg Cys Leu Lys Ser Trp Lys Pro Asn  
 2260 2265 2270  
 His Lys Asp Tyr Tyr Asn Cys Ser Ala Met Val Ser Lys Ala Ala Arg  
 2275 2280 2285  
 50  
 Gln Glu Lys Arg Phe Gln Asp Tyr Asn Glu Arg Cys Thr Phe His His  
 2290 2295 2300  
 Gln Ala Arg Glu Phe Ala Val Asn Leu Arg Asn Arg Val Ser Ala Ile  
 2305 2310 2315  
 55  
 His Glu Val Pro Pro Pro Arg Ser Phe Thr Phe Leu Asn Asp Ala Cys  
 2325 2330 2335  
 Gln Gly Leu Glu Gln Ala Arg Lys Val Leu Ala Tyr Ala Cys Val Tyr  
 2340 2345 2350

EP 2 319 924 B1

Ser Phe Tyr Ser Gln Asp Ala Glu Tyr Met Asp Val Val Glu Gln Gln  
 2355 2360 2365  
 5 Thr Glu Asn Leu Glu Leu His Thr Asn Ala Leu Gln Ile Leu Leu Glu  
 2370 2375 2380  
 Glu Thr Leu Leu Arg Cys Arg Asp Leu Ala Ser Ser Leu Arg Leu Leu  
 2385 2390 2395 2400  
 10 Arg Ala Asp Cys Leu Ser Thr Gly Met Glu Leu Leu Arg Arg Ile Gln  
 2405 2410 2415  
 Glu Arg Leu Leu Ala Ile Leu Gln His Ser Ala Gln Asp Phe Arg Val  
 2420 2425 2430  
 15 Gly Leu Gln Ser Pro Ser Val Glu Ala Trp Glu Ala Lys Gly Pro Asn  
 2435 2440 2445  
 Met Pro Gly Ser Gln Pro Gln Ala Ser Ser Gly Pro Glu Ala Glu Glu  
 2450 2455 2460  
 20 Glu Glu Glu Asp Asp Glu Asp Asp Val Pro Glu Trp Gln Gln Asp Glu  
 2465 2470 2475 2480  
 Phe Asp Glu Glu Leu Asp Asn Asp Ser Phe Ser Tyr Asp Glu Ser Glu  
 2485 2490 2495  
 25 Asn Leu Asp Gln Glu Thr Phe Phe Phe Gly Asp Glu Glu Glu Asp Glu  
 2500 2505 2510  
 Asp Glu Ala Tyr Asp  
 2515

30 <210> 14  
 <211> 7554  
 <212> DNA  
 <213> Homo sapiens

35 <400> 14

40

45

50

55

EP 2 319 924 B1

	atggtggggg aacggcatgc tggggacctc atggtgccct tagggcctcg gctgcaggca	60
	tatcctgaag aactcattcg acagaggcct gggcatgacg ggcatcctga atacctgac	120
5	cgatggagtg tcctgaagtg tggggaagtg ggcaaagtgg gtgtggaaga aggcaaagca	180
	gagcacatcc tcatgtggct gtcggctcct gaggtctacg ccaactgccc tgggctgtta	240
	ggtgagcggg cactatctaa gggacttcag cacgaaccag ctgggggttc aggaagcttt	300
10	cctcgagatc caggaggcct ggatgaagtg gcaatgggag agatggaggc tgatgttcag	360
	gcgctggtac gcagggcggc caggcagctg gcagaaagtg ggacccaag cctcacggcc	420
	gctgtgcttc acaccatcca cgtgctcagt gcctacgcca gcatcgggcc cctcactggt	480
15	gtcttcaggg agacaggagc cctggacctg ctcatgcaca tgttatgcaa tcctgagcct	540
	cagatccgcc ggagtgcagg caaatgctg caggctctgg cagcccacga tgctgggagt	600
	cgggctcacg tccttctatc actgagccag caagatggca tcgagcagca catggatfff	660
20	gacagtcgct atacattgct ggagctgttt gcagaaacca catcctctga agaactgc	720
	atggcctttg agggcattca tctgcctcag atcccaggaa agctgctfff ctcctgggtg	780
25	aagcgctacc tttgtgtcac gtcctcctg gatcagctga atagcagtcc agagctggga	840

25

30

35

40

45

50

55

EP 2 319 924 B1

gctggagacc aaagctcccc atgtgccaca agagagaaaa gccggggaca gcggggaactg 900  
 gagttcagca tggctgtggg caacctcatc tctgagcttg tgcggagcat gggctgggcc 960  
 5 cggaacctca gcgaacaggg catgtcacct ccccgccaa cccggtccat ctttcagccc 1020  
 tacatttcag gccccagcct tttactcccc accattgtca ccacccccag aagacaaggg 1080  
 tgggtcttcc gccagcgctc tgaattctcc agccgtagtg gctatggaga atatgtgcag 1140  
 10 cagacactcc agccagggat gcgagtgcgg atgctggatg attatgagga gatcagtgct 1200  
 ggggacgagg gcgagttccg gcagagcaac aacggcattc cccctgtgca ggttttctgg 1260  
 cagtcgacag gccgcactta ctgggtgcac tggcacatgc tggagatcct gggccctgag 1320  
 15 gaagccactg aggataaggc ttcagcagct gtggagaagg gggcaggggc tactgtgttg 1380  
 ggcacagcat ttccctcctg ggactggaat cctatggatg ggctgtacc tttgccgtac 1440  
 ctccagcccc aacctcagaa gaatgagaga gtgggatatc tgaccaggc tgaatggtg 1500  
 20 gagctgcttt tctttatcaa aaagtggac ttgtgtgagc agcagccaat tttccagaat 1560  
 ctttgaaga acctggatga gaccctgggt gaaaaggccc taggtgagat ctctgtgtcc 1620  
 gtggaaatgg ccgagagtct gctgcagggt ctcagtagtc gatttgaggg cagcactctc 1680  
 25 aatgacctgc tcaactccca gatctacacc aagtatggc tgctgtctaa tgaaccaagc 1740  
 agctcgtcta cttcacgaaa tcactcctgt accccagatc cagaagagga gtccaagtcg 1800  
 gaggccagct tctcagagga agagactgag tccctcaaag caaaggccga ggcccctaag 1860  
 acagaggccg agcccaccaa gacaaggacc gagaccccca tggcacagag tgattctcag 1920  
 30 ctgtttaacc agcttctggt gactgagggg atgaccctgc cactgagat gaaggaggca 1980  
 gccagtgaaa tggccagagc cttgccccgt cccggctctc gcagctccct ggatcagcat 2040  
 gtggcagcgg tcgtggccac tgtgcagata tccagcttg acacaaacct gcagctttca 2100  
 35 gggctctctg ccctctctca ggctgtggag gaggtcactg agcgggacca ccctctggtc 2160  
 cgtcctgaca gatcgtgag agagaagcta gtgaagatgc tgggtggagct gctgaccaac 2220  
 caggtgggag agaagatggt ggtcgtgcag gccctgcgcc tcctttacctg ctcatgacc 2280  
 40 aagcacgagt ggcggccgct ctttgccagg gaggggtggca tctatgctgt gctggtctgc 2340  
 atgcaagaat ataagacttc tgtcttgggt cagcaggctg ggctggcggc actgaagatg 2400  
 ctggccgctc ccagctctc ggagatcccc acttttgta ctggccgaga ttctatccac 2460  
 45 tctttgtttg atgctcagat gaccagagag atcttcgcca gcatcgaact agccacacgc 2520  
 ccgggctctg agagcctgct cctcactgtc cctgcagccg tgatcctgat gctgaatact 2580  
 gaggggtgct cttctgcagc gagaaatggc ttactcctgc tcaacctact tttgtgcaac 2640  
 50 caccacactc tgggagacca gattataacc caagagctga gagacacggt gtttaggcac 2700  
 tcagggatag caccaagaac agaacctatg cctaccacac gcaccatcct catgatgctt 2760  
 ctcaatcgct actcagagcc gccgggcagc cctgagcgtg cagcactaga gacccccatc 2820  
 55 atccagggtc aggatgggtc ccctgagcta ctgattcgat ccctggttg gggcccatct 2880  
 gcagaactac tcctggactt ggagcgtgtg ctgtgccgtg agggcagccc cggaggtgcc 2940

EP 2 319 924 B1

gtgaggcccc tcctcaagcg cctccagcag gagaccagc ctttctcct gttgctgcg 3000  
 actctggatg ctccggggcc caacaagact ctgctgctgt ctgtgctgag ggtcataacc 3060  
 5 cgactgctgg atttcctga ggcaatggc ctcccctggc acgaggtctt ggagccctgc 3120  
 ctcaactgcc tgagtggccc tagcagtgc tccgagattg ttcaggagct gacctgcttc 3180  
 ctacatcgcc tggcctcgat gcataaggac tatgctgtgg tgctctgctg cctgggagca 3240  
 10 aaagagatcc tctccaaagt cctggacaag cactcagctc agctgctgct gggctgtgag 3300  
 cttcgggacc tggtgacaga gtgtgagaag tacgcacagc tctatagcaa cctcacctcc 3360  
 agcatcctgg ccggctgcat tcagatgggtg ctgggccaga tcgaagacca cagacgaacc 3420  
 15 caccaacca tcaatatccc cttctttgat gtgttcctca ggcattctctg ccagggctcc 3480  
 agtgtggaag tgaaggagga caagtgctgg gagaagggtg aggtgtcctc caaccgcac 3540  
 cgagccagca agctgacgga ccacaacccc aagacctact gggagtcaa cggcagcacc 3600  
 20 ggctcccact acatcacct gcacatgcac cgtgggtgtc ttgttaggca gctcactttg 3660  
 ctggtggcca gtgaggactc aagctacatg ccagccaggg tgggtggtt tgggggtgac 3720  
 agcaccagct gcatcggcac tgagctcaac acggtgaatg tgatgccctc tgccagccgg 3780  
 25 gtgatcctct tggagaacct gaaccgcttc tggcccatca tccagatccg cataaagcgc 3840  
 tgccagcagg gcggcattga caccgggtt cgggggtgtg aggtcctggg ccctaagccc 3900  
 acattctggc cactgttccg ggagcagctg tgtcgcgaa catgtctctt ctacacaatt 3960  
 30 cgggcacaag cctggagccg ggacatagca gaggaccacc ggcgcctcct ccagctctgt 4020  
 cccagactga acagggtttt gcgccacgag cagaattttg ctgaccgctt cctccctgat 4080  
 gatgaggccg cccaggcact gggcaagacc tgctgggagg ccctggtcag ccccctgggtg 4140  
 35 cagaacatca cctctcccga tgcggaaggc gtgagtgccc tgggatggct gctggatcag 4200  
 tacttagaac agagagagac ctctcggaac cccttgagtc gagcagcgtc ctttgcttct 4260  
 cgagttcgtc gcctttgcca cttgctgggtg catgtggaac ctctcctgg gccttctcct 4320  
 40 gagccatcca ctcggccctt cagcaagaac agcaagggtc gggaccggag cccggcgcct 4380  
 tcgccagtgc ttccaagcag cagcctgagg aacataaccc agtgctggct gagcgtgggtg 4440  
 caggagcagg tcagcagatt cctggctgca gcttgagggg ccccagactt tgtgcctcgt 4500  
 45 tactgtaaac tctatgagca cttgcagaga gcaggctccg agctgtttgg gcctcgggca 4560  
 gccttcatgc tggctctgcg cagtggcttc tctggcgcct tgctgcagca gtccttctc 4620  
 actgctgctc acatgagtga gcagtttgcc aggtacattg accaacagat ccaggggtggc 4680  
 50 ctgattgggtg gagcccctgg agtggaaatg ctggggcagc ttcagcggca cctggaaccc 4740  
 attatggtcc tttctggtct ggaactggcc acaacttttg agcacttcta tcagcattat 4800  
 atggcggacc gtctcctgag ctttggttcg agctggctgg agggggctgt gctagagcag 4860  
 55 attggcctct gttttcccaa ccgcctccca cagctgatgc tgacagcct gagcacctct 4920  
 gaggagctgc agcggcagtt ccacctctc cagctccagc ggctcgacaa gttgttcttg 4980

EP 2 319 924 B1

gagcaggaag atgaggagga aaagagacta gaggaagagg aggaggaaga ggaggaagag 5040  
 gaagctgaga aagaattatt tatcgaagat ccaagtccag ccatttctat actggtcctg 5100  
 5 tcaccacgct gctggcccgt ctccccactc tgctacctgt accatcccag aaagtgcctt 5160  
 cccacagaat tctgtgatgc ccttgaccgt ttctccagtt tctacagcca gagtcagaac 5220  
 catccagtcc tggacatggg accacatcgg cgactgcagt ggacgtggct gggccgggct 5280  
 10 gagctgcagt ttgggaagca gatactgcat gtgtccaccg tgcagatgtg gctgctgctg 5340  
 aaattcaatc agacagagga ggtgtcagta gagaccttgc tgaaggattc tgacctctcc 5400  
 ccagagctgc tgctccaggc actcgtgcc ctcacctcag ggaatggccc tttgaccctg 5460  
 15 catgagggcc aggactttcc acacgggggt gtgctgcggc ttcattgagcc tgggccccag 5520  
 cgcagtgggg aggccctgtg gctgatacct ccccaggcat acctgaacgt agagaaggat 5580  
 gaaggccgaa ccctggaaca gaagaggaat ctcttgagct gtcttcttgt tcgtattctc 5640  
 20 aaagcccatg gggaaaaggg cctccacatt gatcagctgg tttgtctggt gctggaggcc 5700  
 tggcagaagg gtccaaatcc tcttgaacc ctgggccaca ctgttgctgg ggggtgtggc 5760  
 tgtaccagta cagatgtcct ctcttgcac ctgcacctct taggccaggg ctacgtgaaa 5820  
 cggcgtgatg accggcccca gatcctgatg tatgccgctc cagagcccat ggggcccctg 5880  
 25 cggggtcagg cagatgtccc tttctgtggc agccagagcg aaacctcaa gccagccca 5940  
 gaagctgtgg ctaccctggc atctctacag ctgcctgcag gccgcacat gagccccag 6000  
 gaagtagaag ggttgatgaa gcagacggtg cgtcaggtgc aggagacgt gaacttagag 6060  
 30 ccagatgtcg ctacgacact tttggctcat tcccactggg gcgctgaaca gctgctgcag 6120  
 agctacagtg aggaccctga gccactgctg ctggcagctg ggctgtgcgt acaccaggct 6180  
 caggctgtac ccgtacggcc tgaccactgc cccgtctgtg tgagccccct ggggtgtgac 6240  
 35 gacgacctgc cctctctctg ctgcatgcac tattgctgta agtcttgctg gaatgagtac 6300  
 ctgacaactc ggatcgagca gaaccttgtt ttgaattgca cctgccccat tgccgactgc 6360  
 cccgcccagc ccaccggagc cttcattcgt gccatcgtct cctcgccaga ggtcatctcc 6420  
 40 aagtatgaga aggcgctcct gcgtggctat gtggagagct gctccaacct gacctggtgc 6480  
 accaaccacc agggctgcga ccgcatcctg tgccgccagg gcctgggctg tgggaccacc 6540  
 tgctccaagt gtggctgggc ctcttgcttc aactgtagct tcctgaggc aactaccct 6600  
 45 gctagctgtg gccatatgtc tcagtgggtc gacgacggtg gctactatga cggcatgagc 6660  
 gtggaggcgc agagcaagca cctggccaag ctcatctcca agcgctgtcc cagctgtcag 6720  
 gctcccatcg agaagaacga ggggtgcctg cacatgacct gtgccaaatg taaccatgga 6780  
 50 ttctgctggc gctgcctcaa gtcctggaag ccaaatcaca aagactatta caactgctct 6840  
 gccatggtaa gcaaggcagc tcgccaggag aagcggtttc aggactataa tgagaggtgc 6900  
 actttccatc accaggcgcg ggagtttgct gtgaacttgc ggaaccgggt gtctgccatc 6960  
 55 catgaagtgc ccccgccag atccttcacc ttctcaatg atgcctgccca gggactggag 7020  
 caggctcggg aggtgctggc ctacgcctgc gtgtacagct tctacagcca ggacgcagag 7080

EP 2 319 924 B1

tacatggatg tggaggagca gcagacagag aacctggagc tgcacaccaa tgcctgcag 7140  
atcctcctgg aggaaaccct gctgcggtgc agagacctgg cctcctccct gcgcctcctg 7200  
5 cgggccgact gcctcagcac gggcatggag ctgctccggc ggatccagga gaggctgctt 7260  
gccatcctgc agcattctgc ccaggatttc cgggttggtc ttcagagtcc atcagtagag 7320  
gcctgggagg caaaaggacc caacatgcct ggcagtcagc cccaggcctc ctcaggcca 7380  
10 gaggcagaag aggaggagga agacgatgag gatgatgtgc ccgagtggca gcaggatgag 7440  
tttgatgagg agctggacaa tgacagcttc tcctacgatg agtctgagaa cctggaccaa 7500  
gagactttct tctttggtga tgaggaagag gatgaagatg aggcctatga ctga 7554

15

<210> 15  
<211> 2048  
<212> PRT  
<213> Homo sapiens

20

<400> 15

25

30

35

40

45

50

55

EP 2 319 924 B1

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

40

45

50

55

EP 2 319 924 B1

Phe Asp Glu Leu Phe Phe Tyr Asn Val Asn Met Thr Pro Ser Glu Leu  
 245 250 255  
 5 Met Asp Glu Ile Ile Ser Ile Arg Val Tyr Asn Ser His Ser Leu Arg  
 260 265 270  
 Ala Asp Cys Leu Met Gly Glu Phe Lys Ile Asp Val Gly Phe Val Tyr  
 275 280 285  
 10 Asp Glu Pro Gly His Ala Val Met Arg Lys Trp Leu Leu Asn Asp  
 290 295 300  
 Pro Glu Asp Thr Ser Ser Gly Ser Lys Gly Tyr Met Lys Val Ser Met  
 305 310 315 320  
 15 Phe Val Leu Gly Thr Gly Asp Glu Pro Pro Pro Glu Arg Arg Asp Arg  
 325 330 335  
 Asp Asn Asp Ser Asp Asp Val Glu Ser Asn Leu Leu Leu Pro Ala Gly  
 340 345 350  
 20 Ile Ala Leu Arg Trp Val Thr Phe Leu Leu Lys Ile Tyr Arg Ala Glu  
 355 360 365  
 Asp Ile Pro Gln Met Asp Asp Ala Phe Ser Gln Thr Val Lys Glu Ile  
 370 375 380  
 25 Phe Gly Gly Asn Ala Asp Lys Lys Asn Leu Val Asp Pro Phe Val Glu  
 385 390 395 400  
 Val Ser Phe Ala Gly Lys Lys Val Cys Thr Asn Ile Ile Glu Lys Asn  
 405 410 415  
 30 Ala Asn Pro Glu Trp Asn Gln Val Val Asn Leu Gln Ile Lys Phe Pro  
 420 425 430  
 Ser Val Cys Glu Lys Ile Lys Leu Thr Ile Tyr Asp Trp Asp Arg Leu  
 435 440 445  
 35 Thr Lys Asn Asp Val Val Gly Thr Thr Tyr Leu His Leu Ser Lys Ile  
 450 455 460  
 Ala Ala Ser Gly Gly Glu Val Glu Val Asn Thr Gly Glu Thr Glu Val  
 465 470 475 480  
 40 Gly Phe Val Pro Thr Phe Gly Pro Cys Tyr Leu Asn Leu Tyr Gly Ser  
 485 490 495  
 Pro Arg Glu Tyr Thr Gly Phe Pro Asp Pro Tyr Asp Glu Leu Asn Thr  
 500 505 510  
 45 Gly Lys Gly Glu Gly Val Ala Tyr Arg Gly Arg Ile Leu Val Glu Leu  
 515 520 525  
 Ala Thr Phe Leu Glu Lys Thr Pro Pro Asp Lys Lys Leu Glu Pro Ile  
 530 535 540  
 50 Ser Asn Asp Asp Leu Leu Val Val Glu Lys Tyr Gln Arg Arg Arg Lys  
 545 550 555 560  
 Tyr Ser Leu Ser Ala Val Phe His Ser Ala Thr Met Leu Gln Asp Val  
 565 570 575  
 55 Gly Glu Ala Ile Gln Phe Glu Val Ser Ile Gly Asn Tyr Gly Asn Lys  
 580 585 590  
 Phe Asp Thr Thr Cys Lys Pro Leu Ala Ser Thr Thr Gln Tyr Ser Arg  
 595 600 605

EP 2 319 924 B1

Ala Val Phe Asp Gly Asn Tyr Tyr Tyr Tyr Leu Pro Trp Ala His Thr  
610 615 620

5 Lys Pro Val Val Thr Leu Thr Ser Tyr Trp Glu Asp Ile Ser His Arg  
625 630 635 640

Leu Asp Ala Val Asn Thr Leu Leu Ala Met Ala Glu Arg Leu Gln Thr  
645 650 655

10 Asn Ile Glu Ala Leu Lys Ser Gly Ile Gln Gly Lys Ile Pro Ala Asn  
660 665 670

Gln Leu Ala Glu Leu Trp Leu Lys Leu Ile Asp Glu Val Ile Glu Asp  
675 680 685

15 Thr Arg Tyr Thr Leu Pro Leu Thr Glu Gly Lys Ala Asn Val Thr Val  
690 695 700

Leu Asp Thr Gln Ile Arg Lys Leu Arg Ser Arg Ser Leu Ser Gln Ile  
705 710 715 720

20 His Glu Ala Ala Val Arg MET Arg Ser Glu Ala Thr Asp Val Lys Ser  
725 730 735

Thr Leu Ala Glu Ile Glu Asp Trp Leu Asp Lys Leu Met Gln Leu Thr  
740 745 750

25 Glu Glu Pro Gln Asn Ser Met Pro Asp Ile Ile Ile Trp Met Ile Arg  
755 760 765

Gly Glu Lys Arg Leu Ala Tyr Ala Arg Ile Pro Ala His Gln Val Leu  
770 775 780

30 Tyr Ser Thr Ser Gly Glu Asn Ala Ser Gly Lys Tyr Cys Gly Lys Thr  
785 790 795 800

Gln Thr Ile Phe Leu Lys Tyr Pro Gln Glu Lys Asn Asn Gly Pro Lys  
805 810 815

35 Val Pro Val Glu Leu Arg Val Asn Ile Trp Leu Gly Leu Ser Ala Val  
820 825 830

Glu Lys Lys Phe Asn Ser Phe Ala Glu Gly Thr Phe Thr Val Phe Ala  
835 840 845

40 Glu Met Tyr Glu Asn Gln Ala Leu Met Phe Gly Lys Trp Gly Thr Ser  
850 855 860

Gly Leu Val Gly Arg His Lys Phe Ser Asp Val Thr Gly Lys Ile Lys  
865 870 875 880

45 Leu Lys Arg Glu Phe Phe Leu Pro Pro Lys Gly Trp Glu Trp Glu Gly  
885 890 895

Glu Trp Ile Val Asp Pro Glu Arg Ser Leu Leu Thr Glu Ala Asp Ala  
900 905 910

50 Gly His Thr Glu Phe Thr Asp Glu Val Tyr Gln Asn Glu Ser Arg Tyr  
915 920 925

Pro Gly Gly Asp Trp Lys Pro Ala Glu Asp Thr Tyr Thr Asp Ala Asn  
930 935 940

55 Gly Asp Lys Ala Ala Ser Pro Ser Glu Leu Thr Cys Pro Pro Gly Trp  
945 950 955 960

Glu Trp Glu Asp Asp Ala Trp Ser Tyr Asp Ile Asn Arg Ala Val Asp  
965 970 975

EP 2 319 924 B1

Glu Lys Gly Trp Glu Tyr Gly Ile Thr Ile Pro Pro Asp His Lys Pro  
 980 985 990  
 Lys Ser Trp Val Ala Ala Glu Lys Met Tyr His Thr His Arg Arg Arg  
 5 995 1000 1005  
 Arg Leu Val Arg Lys Arg Lys Lys Asp Leu Thr Gln Thr Ala Ser Ser  
 1010 1015 1020  
 Thr Ala Arg Ala Met Glu Glu Leu Gln Asp Gln Glu Gly Trp Glu Tyr  
 1025 1030 1035 1040  
 Ala Ser Leu Ile Gly Trp Lys Phe His Trp Lys Gln Arg Ser Ser Asp  
 1045 1050 1055  
 Thr Phe Arg Arg Arg Arg Trp Arg Arg Lys Met Ala Pro Ser Glu Thr  
 15 1060 1065 1070  
 His Gly Ala Ala Ala Ile Phe Lys Leu Glu Gly Ala Leu Gly Ala Asp  
 1075 1080 1085  
 Thr Thr Glu Asp Gly Asp Glu Lys Ser Leu Glu Lys Gln Lys His Ser  
 20 1090 1095 1100  
 Ala Thr Thr Val Phe Gly Ala Asn Thr Pro Ile Val Ser Cys Asn Phe  
 1105 1110 1115 1120  
 Asp Arg Val Tyr Ile Tyr His Leu Arg Cys Tyr Val Tyr Gln Ala Arg  
 25 1125 1130 1135  
 Asn Leu Leu Ala Leu Asp Lys Asp Ser Phe Ser Asp Pro Tyr Ala His  
 1140 1145 1150  
 Ile Cys Phe Leu His Arg Ser Lys Thr Thr Glu Ile Ile His Ser Thr  
 30 1155 1160 1165  
 Leu Asn Pro Thr Trp Asp Gln Thr Ile Ile Phe Asp Glu Val Glu Ile  
 1170 1175 1180  
 Tyr Gly Glu Pro Gln Thr Val Leu Gln Asn Pro Pro Lys Val Ile Met  
 35 1185 1190 1195 1200  
 Glu Leu Phe Asp Asn Asp Gln Val Gly Lys Asp Glu Phe Leu Gly Arg  
 1205 1210 1215  
 Ser Ile Phe Ser Pro Val Val Lys Leu Asn Ser Glu Met Asp Ile Thr  
 40 1220 1225 1230  
 Pro Lys Leu Leu Trp His Pro Val Met Asn Gly Asp Lys Ala Cys Gly  
 1235 1240 1245  
 Asp Val Leu Val Thr Ala Glu Leu Ile Leu Arg Gly Lys Asp Gly Ser  
 45 1250 1255 1260  
 Asn Leu Pro Ile Leu Pro Pro Gln Arg Ala Pro Asn Leu Tyr Met Val  
 1265 1270 1275 1280  
 Pro Gln Gly Ile Arg Pro Val Val Gln Leu Thr Ala Ile Glu Ile Leu  
 50 1285 1290 1295  
 Ala Trp Gly Leu Arg Asn Met Lys Asn Phe Gln Met Ala Ser Ile Thr  
 1300 1305 1310  
 Ser Pro Ser Leu Val Val Glu Cys Gly Gly Glu Arg Val Glu Ser Val  
 1315 1320 1325  
 Val Ile Lys Asn Leu Lys Lys Thr Pro Asn Phe Pro Ser Ser Val Leu  
 55 1330 1335 1340

EP 2 319 924 B1

Phe Met Lys Val Phe Leu Pro Lys Glu Glu Leu Tyr Met Pro Pro Leu  
 1345 1350 1355 1360  
 Val Ile Lys Val Ile Asp His Arg Gln Phe Gly Arg Lys Pro Val Val  
 5 1365 1370 1375  
 Gly Gln Cys Thr Ile Glu Arg Leu Asp Arg Phe Arg Cys Asp Pro Tyr  
 1380 1385 1390  
 Ala Gly Lys Glu Asp Ile Val Pro Gln Leu Lys Ala Ser Leu Leu Ser  
 10 1395 1400 1405  
 Ala Pro Pro Cys Arg Asp Ile Val Ile Glu Met Glu Asp Thr Lys Pro  
 1410 1415 1420  
 Leu Leu Ala Ser Lys Leu Thr Glu Lys Glu Glu Glu Ile Val Asp Trp  
 15 1425 1430 1435 1440  
 Trp Ser Lys Phe Tyr Ala Ser Ser Gly Glu His Glu Lys Cys Gly Gln  
 1445 1450 1455  
 Tyr Ile Gln Lys Gly Tyr Ser Lys Leu Lys Ile Tyr Asn Cys Glu Leu  
 20 1460 1465 1470  
 Glu Asn Val Ala Glu Phe Glu Gly Leu Thr Asp Phe Ser Asp Thr Phe  
 1475 1480 1485  
 Lys Leu Tyr Arg Gly Lys Ser Asp Glu Asn Glu Asp Pro Ser Val Val  
 25 1490 1495 1500  
 Gly Glu Phe Lys Gly Ser Phe Arg Ile Tyr Pro Leu Pro Asp Asp Pro  
 1505 1510 1515 1520  
 Ser Val Pro Ala Pro Pro Arg Gln Phe Arg Glu Leu Pro Asp Ser Val  
 30 1525 1530 1535  
 Pro Gln Glu Cys Thr Val Arg Ile Tyr Ile Val Arg Gly Leu Glu Leu  
 1540 1545 1550  
 Gln Pro Gln Asp Asn Asn Gly Leu Cys Asp Pro Tyr Ile Lys Ile Thr  
 35 1555 1560 1565  
 Leu Gly Lys Lys Val Ile Glu Asp Arg Asp His Tyr Ile Pro Asn Thr  
 1570 1575 1580  
 Leu Asn Pro Val Phe Gly Arg Met Tyr Glu Leu Ser Cys Tyr Leu Pro  
 40 1585 1590 1595 1600  
 Gln Glu Lys Asp Leu Lys Ile Ser Val Tyr Asp Tyr Asp Thr Phe Thr  
 1605 1610 1615  
 Arg Asp Glu Lys Val Gly Glu Thr Ile Ile Asp Leu Glu Asn Arg Phe  
 45 1620 1625 1630  
 Leu Ser Arg Phe Gly Ser His Cys Gly Ile Pro Glu Glu Tyr Cys Val  
 1635 1640 1645  
 Ser Gly Val Asn Thr Trp Arg Asp Gln Leu Arg Pro Thr Gln Leu Leu  
 50 1650 1655 1660  
 Gln Asn Val Ala Arg Phe Lys Gly Phe Pro Gln Pro Ile Leu Ser Glu  
 1665 1670 1675 1680  
 Asp Gly Ser Arg Ile Arg Tyr Gly Gly Arg Asp Tyr Ser Leu Asp Glu  
 55 1685 1690 1695  
 Phe Glu Ala Asn Lys Ile Leu His Gln His Leu Gly Ala Pro Glu Glu  
 1700 1705 1710

EP 2 319 924 B1

Arg Leu Ala Leu His Ile Leu Arg Thr Gln Gly Leu Val Pro Glu His  
 1715 1720 1725  
 Val Glu Thr Arg Thr Leu His Ser Thr Phe Gln Pro Asn Ile Ser Gln  
 5 1730 1735 1740  
 Gly Lys Leu Gln Met Trp Val Asp Val Phe Pro Lys Ser Leu Gly Pro  
 1745 1750 1755 1760  
 Pro Gly Pro Pro Phe Asn Ile Thr Pro Arg Lys Ala Lys Lys Tyr Tyr  
 10 1765 1770 1775  
 Leu Arg Val Ile Ile Trp Asn Thr Lys Asp Val Ile Leu Asp Glu Lys  
 1780 1785 1790  
 Ser Ile Thr Gly Glu Glu Met Ser Asp Ile Tyr Val Lys Gly Trp Ile  
 15 1795 1800 1805  
 Pro Gly Asn Glu Glu Asn Lys Gln Lys Thr Asp Val His Tyr Arg Ser  
 1810 1815 1820  
 Leu Asp Gly Glu Gly Asn Phe Asn Trp Arg Phe Val Phe Pro Phe Asp  
 20 1825 1830 1835 1840  
 Tyr Leu Pro Ala Glu Gln Leu Cys Ile Val Ala Lys Lys Glu His Phe  
 1845 1850 1855  
 Trp Ser Ile Asp Gln Thr Glu Phe Arg Ile Pro Pro Arg Leu Ile Ile  
 25 1860 1865 1870  
 Gln Ile Trp Asp Asn Asp Lys Phe Ser Leu Asp Asp Tyr Leu Gly Phe  
 1875 1880 1885  
 Leu Glu Leu Asp Leu Arg His Thr Ile Ile Pro Ala Lys Ser Pro Glu  
 30 1890 1895 1900  
 Lys Cys Arg Leu Asp Met Ile Pro Asp Leu Lys Ala Met Asn Pro Leu  
 1905 1910 1915 1920  
 Lys Ala Lys Thr Ala Ser Leu Phe Glu Gln Lys Ser Met Lys Gly Trp  
 35 1925 1930 1935  
 Trp Pro Cys Tyr Ala Glu Lys Asp Gly Ala Arg Val Met Ala Gly Lys  
 1940 1945 1950  
 Val Glu Met Thr Leu Glu Ile Leu Asn Glu Lys Glu Ala Asp Glu Arg  
 40 1955 1960 1965  
 Pro Ala Gly Lys Gly Arg Asp Glu Pro Asn Met Asn Pro Lys Leu Asp  
 1970 1975 1980  
 Leu Pro Asn Arg Pro Glu Thr Ser Phe Leu Trp Phe Thr Asn Pro Cys  
 45 1985 1990 1995 2000  
 Lys Thr Met Lys Phe Ile Val Trp Arg Arg Phe Lys Trp Val Ile Ile  
 2005 2010 2015  
 Gly Leu Leu Phe Leu Leu Ile Leu Leu Leu Phe Val Ala Val Leu Leu  
 50 2020 2025 2030  
 Tyr Ser Leu Pro Asn Tyr Leu Ser Met Lys Ile Val Lys Pro Asn Val  
 2035 2040 2045

55 <210> 16  
 <211> 6147  
 <212> DNA  
 <213> Homo sapiens

## EP 2 319 924 B1

&lt;400&gt; 16

5 catgctgcga gtgattgtgg aatctgccag caatatccct aaaacgaaat ttggcaagcc 60  
 ggatcctatt gtttctgtca tttttaagga tgagaaaaag aaaacaaaga aagttgataa 120  
 tgaattgaac cctgtctgga atgagat ttt ggagtttgac ttgaggggta taccactgga 180  
 10 cttttcatct tcccttggga ttattgtgaa agat ttttgag acaattggac aaaataaatt 240  
 aattggcacg gcgactgtag ccctgaagga cctgactggt gaccagagca gatccctgcc 300  
 gtacaagctg atctccctgc taaatgaaaa agggcaagat actggggcca ccattgactt 360  
 ggtgatcggc tatgatccgc cttctgctcc acatccaaat gacctgagcg ggcccagcgt 420  
 15 gccaggcatg ggaggagatg gggaagaaga tgaaggtgat gaagacaggt tggacaatgc 480  
 agtcaggggc cctgggcca aggggccagt tgggacggtg tcggaagctc agcttgctcg 540  
 gaggctcacc aaagtaaaga acagccggcg gatgctgtca aataagccac aggacttcca 600  
 20 gatccgcgtc cgagtgattg agggccgaca gttaagtggg aacaacataa ggctgtggt 660  
 caaagttcac gtctgtggcc agacacaccg aacaagaatc aagagaggaa acaacccttt 720  
 ttttgatgag ttgttttct acaatgtcaa catgaccct tctgaattga tggatgagat 780  
 25 catcagcatc cgggtttata attctcactc tctgcgggca gattgtctga tgggggaatt 840  
 taagattgat gttggatttg tttatgatga acctggccat gctgtcatga gaaagtggct 900  
 tcttctcaat gacccggaag ataccagttc aggttctaaa ggttatatga aagtcagcat 960  
 30 gtttgtcctg ggaaccggag atgagcctcc tcctgagaga cgagatcgtg ataatgacag 1020  
 tgatgatgtg gagagtaatt tgttactccc tgctggcatt gccctccggt gggtgacctt 1080  
 cttgctgaaa atctaccgag ctgaggacat cccccagatg gatgatgcct tctcacagac 1140  
 35 agtaaaggaa atat tggag gcaatgcaga taagaaaaat ctcgtggatc cttttgtaga 1200  
 agtttcctt gctggaaaaa aggtttgtac aacataatt gagaaaaatg caaacccaga 1260  
 gtggaatcag gtcgtcaatc ttcagatcaa gtttccttca gtgtgtgaaa aaataaaaact 1320  
 40 aacaatatat gactgggacc gtcttactaa aatgatgta gttggaacaa catatctaca 1380  
 cctctctaaa attgctgcct ctggtgggga agtggaagta aacacaggag aacagaggt 1440  
 aggctttggt ccaacgtttg gacctgtta cctgaatctt tatggaagcc ccaggagta 1500  
 45 cacgggattc ccagaccct atgatgagct gaatactgga aagggggaag gagttgccta 1560  
 cagaggcagg atcttggttg aattagccac ttttcttgag aagacaccac cagataaaaa 1620  
 gcttgagccc atttcaaag atgacctgct ggttggtgag aaataaccagc gaaggcggaa 1680  
 50 gtacagcctg tctgccgtgt ttcattcagc caccatggtg caagatggtg gtgaggccat 1740  
 tcagtttgaa gtcagcattg ggaactatgg caacaagttt gacaccacct gtaagccttt 1800  
 ggcatcaaca actcagtaca gccgtgctgt atttgatggc aactactatt attacttgcc 1860  
 55 ttgggcccac accaagccag ttgttacct gacttcatac tgggaggata ttagtcatcg 1920  
 cctggatgcg gtgaacactc tcctagctat ggcagaacgg ctgcaaacaa atatagaagc 1980

EP 2 319 924 B1

tctaaaatca gggatacaag gtaaaattcc tgcaaaccag ctggctgaat tgtggctgaa 2040  
 gctgatagat gaagttatag aagacacgag atacacgttg cctctcacag aaggaaaagc 2100  
 5 caacgtcaca gttctcgata ctccagatccg aaagctgcgg tccaggtctc tctcccaaat 2160  
 acatgaggcg gctgtgagga tgaggtcgga agccacagat gtgaagtcca cactggcaga 2220  
 aattgaggac tggcttgata aattaatgca gctgactgaa gagccacaga acagcatgcc 2280  
 10 tgacatcatc atctggatga tccggggaga gaagagactg gcctatgcac gaattcccgc 2340  
 acatcaggtc ttgtactcca ccagtgggta gaatgcatct ggaaaatact gtgggaaaac 2400  
 ccaaaccatc tttctgaagt atccacagga gaaaaacaac gggccaaagg tgcctgtgga 2460  
 gttgcgagtg aacatctggc taggcttaag tgctgtggag aagaagttta acagcttcgc 2520  
 15 agaaggaact ttcaccgtct ttgctgaaat gtatgaaaat caagctctca tgtttgaaa 2580  
 atggggact tctggattag taggacgtca taagttttct gatgtcacag gaaaaataaa 2640  
 actcaagagg gaattttttc tgcctccaaa aggctgggaa tgggaaggag agtgatagat 2700  
 20 tgatcctgaa agaagcttgc tgactgaggc agatgcaggt cacacggagt tcaactgatga 2760  
 agtctatcag aacgagagcc gctaccccgg gggcgactgg aagccggccg aggacaccta 2820  
 cacggatgag aacggcgata aagcagcatc acccagcgag ttgacttgct ctccaggttg 2880  
 25 ggaatgggaa gatgatgcat ggtccttatga cataaatcga gcggtggatg agaaaggctg 2940  
 ggaatatgga atcaccattc ctccctgatca taagcccaaa tcctgggttg cagcagagaa 3000  
 aatgtaccac actcatagac ggcgaaggct ggtccgaaaa cgcaagaaag atttaacaca 3060  
 30 gactgcttca agcaccgcaa gggccatgga ggaattgcaa gaccaagagg gctgggaata 3120  
 tgcttctcta attggctgga aatttctactg gaaacaacgt agttcagata ccttccgccg 3180  
 cagacgctgg aggagaaaaa tggctccttc agaaacacat ggtgcagctg ccatctttaa 3240  
 35 acttgaaggc gcccttgggg cagacactac cgaagatggg gatgagaaga gcctggagaa 3300  
 acagaagcac agtgccacca ctgtgttcgg agcaaacc cccattgttt cctgcaattt 3360  
 tgacagagtc tacatctacc atctgcgctg ctatgtctat caagccagaa acctcttggc 3420  
 40 tttagataag gatagctttt cagatccata tgctcatatc tgtttctctc atcggagcaa 3480  
 aaccactgag atcatccatt caaccctgaa tcccacgtgg gaccaaaca ttatattcga 3540  
 tgaagttgaa atctatgggg aaccccaaac agttctacag aatccacca aagttatcat 3600  
 45 ggaacttttt gacaatgacc aagtgggcaa agatgaattt ttaggacgaa gcattttctc 3660  
 tcctgtggtg aaactgaact cagaaatgga catcacacc aaacttctct ggcacccagt 3720  
 aatgaatgga gacaaagcct gcggggatgt tcttgaact gcagagctga ttctgagggg 3780  
 50 caaggatggc tccaaccttc ccattcttcc ccctcaaagg gcgccaaatc tatacatggc 3840  
 cccccagggg atcaggcctg tggctcagct cactgccatt gagattctag cttggggctt 3900  
 aagaaatag aaaaacttcc agatggcttc taccacatcc cccagtcttg ttgtggagtg 3960  
 55 tggaggagaa aggggtggaat cgggtggtgat caaaaacctt aagaagacac ccaactttcc 4020  
 aagttctggt ctcttcatga aagtgttctt gcccaaggag gaattgtaca tgccccact 4080

EP 2 319 924 B1

ggtgatcaag gtcacgacc acaggcagtt tgggcggaag cctgtcgtcg gccagtgcac 4140  
 catcgagcgc ctggaccgct ttcgctgtga cccttatgca gggaaagagg acatcgtccc 4200  
 5 acagctcaaa gcctcccttc tgtctgcccc accatgccgg gacatcgta tcgaaatgga 4260  
 agacaccaaa ccattactgg cttctaagct gacagaaaag gaggaagaaa tcgtggactg 4320  
 gtggagtaaa ttttatgctt cctcagggga acatgaaaaa tgcggacagt atattcagaa 4380  
 10 aggctattcc aagctcaaga tatataattg tgaactagaa aatgtagcag aatttgaggg 4440  
 cctgacagac ttctcagata cgttcaagtt gtaccgaggc aagtcggatg aaaatgaaga 4500  
 tccttctgtg gttggagagt ttaagggctc ctttcggatc taccctctgc cggatgaccc 4560  
 15 cagcgtgcc a gcccctcca gacagtttcg ggaattacct gacagcgtcc cacaggaatg 4620  
 cacggtagg atttacattg ttcgaggctt agagctccag cccaggaca acaatggcct 4680  
 gtgtgaccct tacataaaaa taacactggg caaaaaagtc attgaagacc gagatcacta 4740  
 20 cattccaac actctcaacc cagtctttgg caggatgtac gaactgagct gctacttacc 4800  
 tcaagaaaaa gacctgaaaa tttctgtcta tgattatgac acctttacc gggatgaaaa 4860  
 agtaggagaa acaattattg atctggaaaa ccgattcctt tcccgctttg ggtcccactg 4920  
 25 cggcatacca gaggagtact gtgtttctgg agtcaatacc tggcgagatc aactgagacc 4980  
 aacacagctg cttcaaaatg tcgccagatt caaaggcttc ccacaacca tcctttccga 5040  
 agatgggagt agaatcagat atggaggacg agactacagc ttggatgaat ttgaagccaa 5100  
 30 caaaatcctg caccagcacc tcggggcccc tgaagagcgg cttgctcttc acatcctcag 5160  
 gactcagggg ctggtccctg agcacgtgga aacaaggact ttgcacagca ccttcagacc 5220  
 caacatttcc cagggaaaaac ttcagatgtg ggtggatggt tcccccaaga gtttggggcc 5280  
 35 accaggccct ctttcaaca tcacaccccg gaaagccaag aaatactacc tgcgtgtgat 5340  
 catctggaac accaaggacg ttatcttggg cgagaaaagc atcacaggag aggaaatgag 5400  
 tgacatctac gtcaaaggct ggattcctgg caatgaagaa aacaaacaga aacagatgt 5460  
 40 ccattacaga tctttggatg gtgaagggaa ttttaactgg cgatttgttt tcccgtttga 5520  
 ctaccttcca gccgaacaac tctgtatcgt tgcgaaaaaa gagcatttct ggagtattga 5580  
 ccaaacggaa tttcgaatcc caccaggct gatcattcag atatgggaca atgacaagtt 5640  
 45 ttctctggat gactacttgg gtttcctaga acttgacttg cgtcacacga tcattcctgc 5700  
 aaaatcacca gagaaatgca ggttgacat gattccggac ctcaaagcca tgaaccccct 5760  
 taaagccaag acagcctccc tctttgagca gaagtccatg aaaggatggt ggccatgcta 5820  
 50 cgcagagaaa gatggcggcc gcgtaatggc tgggaaagtg gagatgacat tggaaatcct 5880  
 caacgagaag gaggccgacg agaggccagc cgggaagggg cgggacgaac ccaacatgaa 5940  
 cccaagctg gacttaccaa atcgaccaga aacctccttc ctctggttca ccaacccatg 6000  
 55 caagaccatg aagttcatcg tgtggcggcc ctttaagtgg gtcacatcg gcttgctgtt 6060  
 cctgcttatc ctgctgctct tcgtggccgt gctcctctac tctttgccga actatattgtc 6120

aatgaagatt gtaaagccaa atgtgta

6147

5 <210> 17  
<211> 336  
<212> PRT  
<213> Homo sapiens

10 <400> 17

15

20

25

30

35

40

45

50

55

EP 2 319 924 B1

1 Met Glu Arg Lys Ile Ser Arg Ile His Leu Val Ser Glu Pro Ser Ile  
 5 Thr His Phe Leu Gln Val Ser Trp Glu Lys Thr Leu Glu Ser Gly Phe  
 Val Ile Thr Leu Thr Asp Gly His Ser Ala Trp Thr Gly Thr Val Ser  
 10 Glu Ser Glu Ile Ser Gln Glu Ala Asp Asp Met Ala Met Glu Lys Gly  
 Lys Tyr Val Gly Glu Leu Arg Lys Ala Leu Leu Ser Gly Ala Gly Pro  
 15 Ala Asp Val Tyr Thr Phe Asn Phe Ser Lys Glu Ser Cys Tyr Phe Phe  
 Phe Glu Lys Asn Leu Lys Asp Val Ser Phe Arg Leu Gly Ser Phe Asn  
 20 Leu Glu Lys Val Glu Asn Pro Ala Glu Val Ile Arg Glu Leu Ile Cys  
 Tyr Cys Leu Asp Thr Ile Ala Glu Asn Gln Ala Lys Asn Glu His Leu  
 25 Gln Lys Glu Asn Glu Arg Leu Leu Arg Asp Trp Asn Asp Val Gln Gly  
 Arg Phe Glu Lys Cys Val Ser Ala Lys Glu Ala Leu Glu Thr Asp Leu  
 30 Tyr Lys Arg Phe Ile Leu Val Leu Asn Glu Lys Lys Thr Lys Ile Arg  
 Ser Leu His Asn Lys Leu Leu Asn Ala Ala Gln Glu Arg Glu Lys Asp  
 35 Ile Lys Gln Glu Gly Glu Thr Ala Ile Cys Ser Glu Met Thr Ala Asp  
 Arg Asp Pro Val Tyr Asp Glu Ser Thr Asp Glu Glu Ser Glu Asn Gln  
 40 Thr Asp Leu Ser Gly Leu Ala Ser Ala Ala Val Ser Lys Asp Asp Ser  
 Ile Ile Ser Ser Leu Asp Val Thr Asp Ile Ala Pro Ser Arg Lys Arg  
 45 Arg Gln Arg Met Gln Arg Asn Leu Gly Thr Glu Pro Lys Met Ala Pro  
 Gln Glu Asn Gln Leu Gln Glu Lys Glu Asn Ser Arg Pro Asp Ser Ser  
 50 Leu Pro Glu Thr Ser Lys Lys Glu His Ile Ser Ala Glu Asn Met Ser  
 305 Leu Glu Thr Leu Arg Asn Ser Ser Pro Glu Asp Leu Phe Asp Glu Ile  
 55 325 330 335

<210> 18  
 <211> 1011  
 <212> DNA

EP 2 319 924 B1

<213> Homo sapiens

<400> 18

5           aatggagaga aaaataagca gaatccacct tgtttctgaa cccagtataa ctcattttct       60  
           acaagtatct tgggagaaaa cactggaatc tggttttggtt attacactta ctgatgggtca     120  
 10       ttcagcatgg actgggacag tttctgaatc agagatttcc caagaagctg atgacatggc     180  
           aatggaaaaa gggaaatatg ttggtgaact gagaaaaagca ttgttgtcag gagcaggacc     240  
           agctgatgta tacacgttta atttttctaa agagtcttgt tatttcttct ttgagaaaaa     300  
 15       cctgaaagat gtctcattca gacttggttc cttcaaccta gagaaagttg aaaaccagc     360  
           tgaagtcatt agagaactta tttgttattg cttggacacc attgcagaaa atcaagccaa     420  
           aaatgagcac ctgcagaaaag aaaatgaaag gcttctgaga gattggaatg atgttcaagg     480  
 20       acgatttgaa aaatgtgtga gtgctaagga agctttggag actgatcttt ataagcggtt     540  
           tattctggtg ttgaatgaga agaaaacaaa aatcagaagt ttgcataata aattatataa     600  
           tgcagctcaa gaacgagaaa aggacatcaa acaagaaggg gaaactgcaa tctgttctga     660  
 25       aatgactgct gaccgagatc cagtctatga tgagagtact gatgaggaaa gtgaaaacca     720  
           aactgatctc tctgggttgg cttcagctgc tgtaagtaaa gatgattcca ttatttcaag     780  
           tcttgatgtc actgatattg caccaagtag aaaaaggaga cagcgaatgc aaagaaatct     840  
 30       tgggacagaa cctaaaatgg ctctcagga gaatcagctt caagaaaagg aaaattctag     900  
           gcctgattct tctactacctg agacgtcgaa aaaggagcac atctcagctg aaaacatgtc     960  
           tttagaaact ctgagaaaca gcagcccaga agacctcttt gatgagattt a           1011

35       <210> 19  
           <211> 510  
           <212> PRT  
           <213> Homo sapiens

40       <400> 19

          Met Asp Glu Lys Thr Lys Lys Ala Glu Glu Met Ala Leu Ser Leu Thr  
           1                   5                   10                   15  
 45       Arg Ala Val Ala Gly Gly Asp Glu Gln Val Ala Met Lys Cys Ala Ile  
                   20                   25                   30  
           Trp Leu Ala Glu Gln Arg Val Pro Leu Ser Val Gln Leu Lys Pro Glu  
                   35                   40                   45  
 50       Val Ser Pro Thr Gln Asp Ile Arg Leu Trp Val Ser Val Glu Asp Ala  
                   50                   55                   60  
           Gln Met His Thr Val Thr Ile Trp Leu Thr Val Arg Pro Asp Met Thr  
                   65                   70                   75                   80

55

EP 2 319 924 B1

Val Ala Ser Leu Lys Asp Met Val Phe Leu Asp Tyr Gly Phe Pro Pro  
 85 90 95  
 Val Leu Gln Gln Trp Val Ile Gly Gln Arg Leu Ala Arg Asp Gln Glu  
 5 100 105 110  
 Thr Leu His Ser His Gly Val Arg Gln Asn Gly Asp Ser Ala Tyr Leu  
 115 120 125  
 Tyr Leu Leu Ser Ala Arg Asn Thr Ser Leu Asn Pro Gln Glu Leu Gln  
 10 130 135 140  
 Arg Glu Arg Gln Leu Arg Met Leu Glu Asp Leu Gly Phe Lys Asp Leu  
 145 150 155 160  
 Thr Leu Gln Pro Arg Gly Pro Leu Glu Pro Gly Pro Pro Lys Pro Gly  
 15 165 170 175  
 Val Pro Gln Glu Pro Gly Arg Gly Gln Pro Asp Ala Val Pro Glu Pro  
 180 185 190  
 Pro Pro Val Gly Trp Gln Cys Pro Gly Cys Thr Phe Ile Asn Lys Pro  
 195 200 205  
 Thr Arg Pro Gly Cys Glu Met Cys Cys Arg Ala Arg Pro Glu Ala Tyr  
 210 215 220  
 Gln Val Pro Ala Ser Tyr Gln Pro Asp Glu Glu Glu Arg Ala Arg Leu  
 225 230 235 240  
 Ala Gly Glu Glu Glu Ala Leu Arg Gln Tyr Gln Gln Arg Lys Gln Gln  
 245 250 255  
 Gln Gln Glu Gly Asn Tyr Leu Gln His Val Gln Leu Asp Gln Arg Ser  
 260 265 270  
 Leu Val Leu Asn Thr Glu Pro Ala Glu Cys Pro Val Cys Tyr Ser Val  
 275 280 285  
 Leu Ala Pro Gly Glu Ala Val Val Leu Arg Glu Cys Leu His Thr Phe  
 290 295 300  
 Cys Arg Glu Cys Leu Gln Gly Thr Ile Arg Asn Ser Gln Glu Ala Glu  
 305 310 315 320  
 Val Ser Cys Pro Phe Ile Asp Asn Thr Tyr Ser Cys Ser Gly Lys Leu  
 325 330 335  
 Leu Glu Arg Glu Ile Lys Ala Leu Leu Thr Pro Glu Asp Tyr Gln Arg  
 340 345 350  
 Phe Leu Asp Leu Gly Ile Ser Ile Ala Glu Asn Arg Ser Ala Phe Ser  
 355 360 365  
 Tyr His Cys Lys Thr Pro Asp Cys Lys Gly Trp Cys Phe Phe Glu Asp  
 370 375 380  
 Asp Val Asn Glu Phe Thr Cys Pro Val Cys Phe His Val Asn Cys Leu  
 385 390 395 400  
 Leu Cys Lys Ala Ile His Glu Gln Met Asn Cys Lys Glu Tyr Gln Glu  
 405 410 415  
 Asp Leu Ala Leu Arg Ala Gln Asn Asp Val Ala Ala Arg Gln Thr Thr  
 420 425 430  
 Glu Met Leu Lys Val Met Leu Gln Gln Gly Glu Ala Met Arg Cys Pro  
 435 440 445

EP 2 319 924 B1

5 Gln Cys Gln Ile Val Val Gln Lys Lys Asp Gly Cys Asp Trp Ile Arg  
450 455 460  
Cys Thr Val Cys His Thr Glu Ile Cys Trp Val Thr Lys Gly Pro Arg  
465 470 475 480  
Trp Gly Pro Gly Gly Pro Gly Asp Thr Ser Gly Gly Cys Arg Cys Arg  
485 490 495  
10 Val Asn Gly Ile Pro Cys His Pro Ser Cys Gln Asn Cys His  
500 505 510

<210> 20

<211> 1533

<212> DNA

15 <213> Homo sapiens

<400> 20

20

25

30

35

40

45

50

55

EP 2 319 924 B1

atggacgaga agaccaagaa agcagaggaa atggccctga gcctcacccg agcagtggcg 60  
 ggcggggatg aacaggtggc aatgaagtgt gccatctggc tggcagagca acgggtgccc 120  
 5 ctgagtgtgc aactgaagcc tgaggtctcc ccaacgcagg acatcaggct gtgggtgagc 180  
 gtggaggatg ctcagatgca caccgtcacc atctggctca cagtgcgccc tgatatgaca 240  
 gtggcgtctc tcaaggacat ggtttttctg gactatggct tcccaccagt cttgcagcag 300  
 10 tgggtgattg ggcagcggct ggcacgagac caggagaccc tgcactccca tggggtgcgg 360  
 cagaatgggg acagtgccta cctctatctg ctgtcagccc gcaacacctc cctcaacct 420  
 caggagctgc agcgggagcg gcagctgcgg atgctggaag atctgggctt caaggacctc 480  
 15 acgctgcagc cgcggggccc tctggagcca ggcccccaa agcccggggt cccccaggaa 540  
 cccggacggg ggcagccaga tgcagtgcct gagccccac cgggtgggctg gcagtgcccc 600  
 ggggtgcacct tcatcaaaa gccacgcgg cctggctgtg agatgtgctg ccgggcgctg 660  
 20 cccgaggcct accaggtccc cgcctcatac cagcccgcagc aggaggagcg agcgcgcctg 720  
 gcgggagagg aggaggcgct gcgtcagtac cagcagcgga agcagcagca gcaggagggg 780  
 aactacctgc agcacgtcca gctggaccag aggagcctgg tgctgaacac ggagcccgcc 840  
 25 gagtgcctcg tgtgctactc ggtgctggcg cccggcgagg ccgtgggtgct gcgtgagtgt 900  
 ctgcacacct tctgcaggga gtgcctgcag ggcaccatcc gcaacagcca ggaggcggag 960  
 gtctcttgcc ccttcattga caacacctac tcgtgctcgg gcaagctgct ggagagggag 1020  
 30 atcaaggcgc tctgacccc tgaggattac cagcgatttc tagacctggg catctccatt 1080  
 gctgaaaacc gcagtgcctt cagctacat tgcaagaccc cagattgcaa gggatgggtgc 1140  
 ttctttgagg atgatgtcaa tgagttcacc tgccctgtgt gttccacgt caactgcctg 1200  
 35 ctctgcaagg ccatccatga gcagatgaac tgcaaggagt atcaggagga cctggccctg 1260  
 cgggctcaga acgatgtggc tgcccggcag acgacagaga tgctgaaggat gatgctgcag 1320  
 cagggcgagg ccatgcgctg cccccagtgc cagatcgtgg tacagaagaa ggacggctgc 1380  
 40 gactggatcc gctgcaccgt ctgccacacc gagatctgct gggtcaccaa gggcccacgc 1440  
 tggggccctg gggggccagg agacaccagc gggggctgcc gctgcagggt aaatgggatt 1500  
 45 ccttgccacc caagctgtca gaactgccac tga 1533

<210> 21

<211> 500

<212> PRT

50 <213> Homo sapiens

<400> 21

55

EP 2 319 924 B1

1 Met Asp His Thr Glu Gly Ser Pro Ala Glu Glu Pro Pro Ala His Ala  
 5 Pro Ser Pro Gly Lys Phe Gly Glu Arg Pro Pro Pro Lys Arg Leu Thr  
 Arg Glu Ala Met Arg Asn Tyr Leu Lys Glu Arg Gly Asp Gln Thr Val  
 10 Leu Ile Leu His Ala Lys Val Ala Gln Lys Ser Tyr Gly Asn Glu Lys  
 Arg Phe Phe Cys Pro Pro Pro Cys Val Tyr Leu Met Gly Ser Gly Trp  
 15 Lys Lys Lys Lys Glu Gln Met Glu Arg Asp Gly Cys Ser Glu Gln Glu  
 Ser Gln Pro Cys Ala Phe Ile Gly Ile Gly Asn Ser Asp Gln Glu Met  
 20 Gln Gln Leu Asn Leu Glu Gly Lys Asn Tyr Cys Thr Ala Lys Thr Leu  
 Tyr Ile Ser Asp Ser Asp Lys Arg Lys His Phe Met Leu Ser Val Lys  
 25 Met Phe Tyr Gly Asn Ser Asp Asp Ile Gly Val Phe Leu Ser Lys Arg  
 Ile Lys Val Ile Ser Lys Pro Ser Lys Lys Lys Gln Ser Leu Lys Asn  
 30 Ala Asp Leu Cys Ile Ala Ser Gly Thr Lys Val Ala Leu Phe Asn Arg  
 Leu Arg Ser Gln Thr Val Ser Thr Arg Tyr Leu His Val Glu Gly Gly  
 35 Asn Phe His Ala Ser Ser Gln Gln Trp Gly Ala Phe Phe Ile His Leu  
 Leu Asp Asp Asp Glu Ser Glu Gly Glu Glu Phe Thr Val Arg Asp Gly  
 40 Tyr Ile His Tyr Gly Gln Thr Val Lys Leu Val Cys Ser Val Thr Gly  
 Met Ala Leu Pro Arg Leu Ile Ile Arg Lys Val Asp Lys Gln Thr Ala  
 45 Leu Leu Asp Ala Asp Asp Pro Val Ser Gln Leu His Lys Cys Ala Phe  
 Tyr Leu Lys Asp Thr Glu Arg Met Tyr Leu Cys Leu Ser Gln Glu Arg  
 50 Ile Ile Gln Phe Gln Ala Thr Pro Cys Pro Lys Glu Pro Asn Lys Glu  
 55

EP 2 319 924 B1

	305				310					315				320		
	Met	Ile	Asn	Asp	Gly 325	Ala	Ser	Trp	Thr	Ile 330	Ile	Ser	Thr	Asp	Lys	Ala
5																
	Glu	Tyr	Thr	Phe 340	Tyr	Glu	Gly	Met	Gly 345	Pro	Val	Leu	Ala	Pro	Val	Thr
10																
	Pro	Val	Pro 355	Val	Val	Glu	Ser	Leu 360	Gln	Leu	Asn	Gly	Gly 365	Gly	Asp	Val
15																
	Ala	Met 370	Leu	Glu	Leu	Thr	Gly 375	Gln	Asn	Phe	Thr	Pro 380	Asn	Leu	Arg	Val
20																
	Trp	Phe	Gly	Asp	Val	Glu	Ala	Glu	Thr	Met	Tyr 395	Arg	Cys	Gly	Glu	Ser
25																
	Met	Leu	Cys	Val	Val 405	Pro	Asp	Ile	Ser	Ala 410	Phe	Arg	Glu	Gly	Trp	Arg
30																
	Trp	Val	Arg	Gln 420	Pro	Val	Gln	Val	Pro 425	Val	Thr	Leu	Val	Arg 430	Asn	Asp
35																
	Gly	Ile	Ile 435	Tyr	Ser	Thr	Ser	Leu 440	Thr	Phe	Thr	Tyr	Thr 445	Pro	Glu	Pro
40																
	Gly	Pro 450	Arg	Pro	His	Cys	Ser 455	Ala	Ala	Gly	Ala	Ile 460	Leu	Arg	Ala	Asn
45																
	Ser	Ser	Gln	Val	Pro	Pro 470	Asn	Glu	Ser	Asn	Thr 475	Asn	Ser	Glu	Gly	Ser
50																
	Tyr	Thr	Asn	Ala	Ser 485	Thr	Asn	Ser	Thr	Ser 490	Val	Thr	Ser	Ser	Thr 495	Ala
55																
	Thr	Val	Val	Ser 500												

<210> 22  
 <211> 1503  
 <212> DNA  
 <213> Homo sapiens

<400> 22

EP 2 319 924 B1

ccatggacca cacggagggc tcgcccgcgg aggagccgcc tgcgcatgct ccatcgcttg 60  
 ggaaatattg tgagcggcct ccacctaacc gacttactag ggaagctatg cgaaattatt 120  
 5 taaaagagcg aggggatcaa acagtactta ttcttcatgc aaaagttgca cagaagtcac 180  
 atggaaatga aaaaagggtt ttttgcccac ctcttctgtg atatcttatg ggcagtggat 240  
 ggaagaaaaa aaaagaacaa atggaacgcg atggttgttc tgaacaagag tctcaaccgt 300  
 10 gtgcatttat tgggatagga aatagtgacc aagaaatgca gcagctaac ttggaaggaa 360  
 agaactattg cacagccaaa acattgtata tatctgactc agacaagcga aagcacttca 420  
 tgttctctgt aaagatgttc tatggcaaca gtgatgacat tgggtgtgtc ctgagcaagc 480  
 15 ggataaaagt catctccaaa cttccaaaa agaagcagtc attgaaaaat gctgacttat 540  
 gcattgcctc aggaacaaag gtggctctgt ttaatcgact acgatcccag acagttagta 600  
 ccagatactt gcatgtagaa ggaggtaatt ttcattgccag ttcacagcag tggggagcct 660  
 20 tttttattca tctcttggat gatgatgaat cagaaggaga agaattcaca gtccgagatg 720  
  
 gctacatcca ttatggacaa acagtcaaac ttgtgtgctc agttactggc atggcactcc 780  
 25 caagattgat aattaggaaa gttgataagc agaccgcatt attggatgca gatgatcctg 840  
 tgtcacaact ccataaatgt gcattttacc ttaaggatac agaaagaatg tatttgtgcc 900  
 tttctcaaga aagaataatt caatttcagg ccaactccatg tccaaaagaa ccaataaag 960  
 30 agatgataaa tgatggcgct tcctggacaa tcattagcac agataaggca gagtatacat 1020  
 tttatgaggg aatgggccct gtccttgccc cagtcactcc tgtgcctgtg gtagagagcc 1080  
 ttcagttgaa tggcgggtgg gacgtagcaa tgcttgaact tacaggacag aatttcactc 1140  
 35 caaatttacg agtgtgggtt ggggatgtag aagctgaaac tatgtacagg tgtggagaga 1200  
 gtatgctctg tgctgtccca gacatttctg cattccgaga aggttgagaga tgggtccggc 1260  
 aaccagtcca ggttccagta actttggctc gaaatgatgg aatcatttat tccaccagcc 1320  
 40 ttacctttac ctacacacca gaaccagggc cgcgccaca ttgcagtgca gcaggagcaa 1380  
 tccttcgagc caattcaagc caggtgcccc ctaacgaatc aaacacaaac agcgagggaa 1440  
 gttacacaaa cgccagcaca aattcaacca gtgtcacatc atctacagcc acagtggat 1500  
 45 cct 1503

<210> 23

<211> 1354

<212> PRT

50 <213> Homo sapiens

<400> 23

55

EP 2 319 924 B1

	Met	Ser	Thr	Gly	Asp	Ser	Phe	Glu	Thr	Arg	Phe	Glu	Lys	Met	Asp	Asn
	1				5					10					15	
5	Leu	Leu	Arg	Asp	Pro	Lys	Ser	Glu	Val	Asn	Ser	Asp	Cys	Leu	Leu	Asp
				20					25					30		
	Gly	Leu	Asp	Ala	Leu	Val	Tyr	Asp	Leu	Asp	Phe	Pro	Ala	Leu	Arg	Lys
			35					40					45			
10	Asn	Lys	Asn	Ile	Asp	Asn	Phe	Leu	Ser	Arg	Tyr	Lys	Asp	Thr	Ile	Asn
		50					55					60				
	Lys	Ile	Arg	Asp	Leu	Arg	Met	Lys	Ala	Glu	Asp	Tyr	Glu	Val	Val	Lys
	65					70					75					80
15	Val	Ile	Gly	Arg	Gly	Ala	Phe	Gly	Glu	Val	Gln	Leu	Val	Arg	His	Lys
					85						90				95	
	Ser	Thr	Arg	Lys	Val	Tyr	Ala	Met	Lys	Leu	Leu	Ser	Lys	Phe	Glu	Met
				100					105					110		
20	Ile	Lys	Arg	Ser	Asp	Ser	Ala	Phe	Phe	Trp	Glu	Glu	Arg	Asp	Ile	Met
			115					120					125			
	Ala	Phe	Ala	Asn	Ser	Pro	Trp	Val	Val	Gln	Leu	Phe	Tyr	Ala	Phe	Gln
		130					135					140				
25	Asp	Asp	Arg	Tyr	Leu	Tyr	Met	Val	Met	Glu	Tyr	Met	Pro	Gly	Gly	Asp
	145					150					155					160
	Leu	Val	Asn	Leu	Met	Ser	Asn	Tyr	Asp	Val	Pro	Glu	Lys	Trp	Ala	Arg
				165						170					175	
30																
35																
40																
45																
50																
55																

EP 2 319 924 B1

Phe Tyr Thr Ala Glu Val Val Leu Ala Leu Asp Ala Ile His Ser Met  
 180 185 190  
 5 Gly Phe Ile His Arg Asp Val Lys Pro Asp Asn Met Leu Leu Asp Lys  
 195 200 205  
 Ser Gly His Leu Lys Leu Ala Asp Phe Gly Thr Cys Met Lys Met Asn  
 210 215 220  
 10 Lys Glu Gly Met Val Arg Cys Asp Thr Ala Val Gly Thr Pro Asp Tyr  
 225 230 235 240  
 Ile Ser Pro Glu Val Leu Lys Ser Gln Gly Gly Asp Gly Tyr Tyr Gly  
 245 250 255  
 15 Arg Glu Cys Asp Trp Trp Ser Val Gly Val Phe Leu Tyr Glu Met Leu  
 260 265 270  
 Val Gly Asp Thr Pro Phe Tyr Ala Asp Ser Leu Val Gly Thr Tyr Ser  
 275 280 285  
 20 Lys Ile Met Asn His Lys Asn Ser Leu Thr Phe Pro Asp Asp Asn Asp  
 290 295 300  
 Ile Ser Lys Glu Ala Lys Asn Leu Ile Cys Ala Phe Leu Thr Asp Arg  
 305 310 315 320  
 25 Glu Val Arg Leu Gly Arg Asn Gly Val Glu Glu Ile Lys Arg His Leu  
 325 330 335  
 Phe Phe Lys Asn Asp Gln Trp Ala Trp Glu Thr Leu Arg Asp Thr Val  
 340 345 350  
 30 Ala Pro Val Val Pro Asp Leu Ser Ser Asp Ile Asp Thr Ser Asn Phe  
 355 360 365  
 Asp Asp Leu Glu Glu Asp Lys Gly Glu Glu Glu Thr Phe Pro Ile Pro  
 370 375 380  
 35 Lys Ala Phe Val Gly Asn Gln Leu Pro Phe Val Gly Phe Thr Tyr Tyr  
 385 390 395 400  
 Ser Asn Arg Arg Tyr Leu Ser Ser Ala Asn Pro Asn Asp Asn Arg Thr  
 405 410 415  
 40 Ser Ser Asn Ala Asp Lys Ser Leu Gln Glu Ser Leu Gln Lys Thr Ile  
 420 425 430  
 Tyr Lys Leu Glu Glu Gln Leu His Asn Glu Met Gln Leu Lys Asp Glu  
 435 440 445  
 45 Met Glu Gln Lys Cys Arg Thr Ser Asn Ile Lys Leu Asp Lys Ile Met  
 450 455 460  
 Lys Glu Leu Asp Glu Glu Gly Asn Gln Arg Arg Asn Leu Glu Ser Thr  
 465 470 475 480  
 50 Val Ser Gln Ile Glu Lys Glu Lys Met Leu Leu Gln His Arg Ile Asn  
 485 490 495  
 Glu Tyr Gln Arg Lys Ala Glu Gln Glu Asn Glu Lys Arg Arg Asn Val  
 500 505 510  
 55 Glu Asn Glu Val Ser Thr Leu Lys Asp Gln Leu Glu Asp Leu Lys Lys  
 515 520 525  
 Val Ser Gln Asn Ser Gln Leu Ala Asn Glu Lys Leu Ser Gln Leu Gln  
 530 535 540

EP 2 319 924 B1

Lys Gln Leu Glu Glu Ala Asn Asp Leu Leu Arg Thr Glu Ser Asp Thr  
 545 550 555 560  
 Ala Val Arg Leu Arg Lys Ser His Thr Glu Met Ser Lys Ser Ile Ser  
 565 570 575  
 Gln Leu Glu Ser Leu Asn Arg Glu Leu Gln Glu Arg Asn Arg Ile Leu  
 580 585 590  
 Glu Asn Ser Lys Ser Gln Thr Asp Lys Asp Tyr Tyr Gln Leu Gln Ala  
 595 600 605  
 Ile Leu Glu Ala Glu Arg Arg Asp Arg Gly His Asp Ser Glu Met Ile  
 610 615 620  
 Gly Asp Leu Gln Ala Arg Ile Thr Ser Leu Gln Glu Glu Val Lys His  
 625 630 635 640  
 Leu Lys His Asn Leu Glu Lys Val Glu Gly Glu Arg Lys Glu Ala Gln  
 645 650 655  
 Asp Met Leu Asn His Ser Glu Lys Glu Lys Asn Asn Leu Glu Ile Asp  
 660 665 670  
 Leu Asn Tyr Lys Leu Lys Ser Leu Gln Gln Arg Leu Glu Gln Glu Val  
 675 680 685  
 Asn Glu His Lys Val Thr Lys Ala Arg Leu Thr Asp Lys His Gln Ser  
 690 695 700  
 Ile Glu Glu Ala Lys Ser Val Ala Met Cys Glu Met Glu Lys Lys Leu  
 705 710 715 720  
 Lys Glu Glu Arg Glu Ala Arg Glu Lys Ala Glu Asn Arg Val Val Gln  
 725 730 735  
 Ile Glu Lys Gln Cys Ser Met Leu Asp Val Asp Leu Lys Gln Ser Gln  
 740 745 750  
 Gln Lys Leu Glu His Leu Thr Gly Asn Lys Glu Arg Met Glu Asp Glu  
 755 760 765  
 Val Lys Asn Leu Thr Leu Gln Leu Glu Gln Glu Ser Asn Lys Arg Leu  
 770 775 780  
 Leu Leu Gln Asn Glu Leu Lys Thr Gln Ala Phe Glu Ala Asp Asn Leu  
 785 790 795 800  
 Lys Gly Leu Glu Lys Gln Met Lys Gln Glu Ile Asn Thr Leu Leu Glu  
 805 810 815  
 Ala Lys Arg Leu Leu Glu Phe Glu Leu Ala Gln Leu Thr Lys Gln Tyr  
 820 825 830  
 Arg Gly Asn Glu Gly Gln Met Arg Glu Leu Gln Asp Gln Leu Glu Ala  
 835 840 845  
 Glu Gln Tyr Phe Ser Thr Leu Tyr Lys Thr Gln Val Lys Glu Leu Lys  
 850 855 860  
 Glu Glu Ile Glu Glu Lys Asn Arg Glu Asn Leu Lys Lys Ile Gln Glu  
 865 870 875 880  
 Leu Gln Asn Glu Lys Glu Thr Leu Ala Thr Gln Leu Asp Leu Ala Glu  
 885 890 895  
 Thr Lys Ala Glu Ser Glu Gln Leu Ala Arg Gly Leu Leu Glu Glu Gln  
 900 905 910

EP 2 319 924 B1

Tyr Phe Glu Leu Thr Gln Glu Ser Lys Lys Ala Ala Ser Arg Asn Arg  
 915 920 925  
 5 Gln Glu Ile Thr Asp Lys Asp His Thr Val Ser Arg Leu Glu Glu Ala  
 930 935 940  
 Asn Ser Met Leu Thr Lys Asp Ile Glu Ile Leu Arg Arg Glu Asn Glu  
 945 950 955 960  
 10 Glu Leu Thr Glu Lys Met Lys Lys Ala Glu Glu Glu Tyr Lys Leu Glu  
 965 970 975  
 Lys Glu Glu Glu Ile Ser Asn Leu Lys Ala Ala Phe Glu Lys Asn Ile  
 980 985 990  
 15 Asn Thr Glu Arg Thr Leu Lys Thr Gln Ala Val Asn Lys Leu Ala Glu  
 995 1000 1005  
 Ile Met Asn Arg Lys Asp Phe Lys Ile Asp Arg Lys Lys Ala Asn Thr  
 1010 1015 1020  
 20 Gln Asp Leu Arg Lys Lys Glu Lys Glu Asn Arg Lys Leu Gln Leu Glu  
 1025 1030 1035 1040  
 Leu Asn Gln Glu Arg Glu Lys Phe Asn Gln Met Val Val Lys His Gln  
 1045 1050 1055  
 25 Lys Glu Leu Asn Asp Met Gln Ala Gln Leu Val Glu Glu Cys Ala His  
 1060 1065 1070  
 Arg Asn Glu Leu Gln Met Gln Leu Ala Ser Lys Glu Ser Asp Ile Glu  
 1075 1080 1085  
 30 Gln Leu Arg Ala Lys Leu Leu Asp Leu Ser Asp Ser Thr Ser Val Ala  
 1090 1095 1100  
 Ser Phe Pro Ser Ala Asp Glu Thr Asp Gly Asn Leu Pro Glu Ser Arg  
 1105 1110 1115 1120  
 35 Ile Glu Gly Trp Leu Ser Val Pro Asn Arg Gly Asn Ile Lys Arg Tyr  
 1125 1130 1135  
 Gly Trp Lys Lys Gln Tyr Val Val Val Ser Ser Lys Lys Ile Leu Phe  
 1140 1145 1150  
 40 Tyr Asn Asp Glu Gln Asp Lys Glu Gln Ser Asn Pro Ser Met Val Leu  
 1155 1160 1165  
 Asp Ile Asp Lys Leu Phe His Val Arg Pro Val Thr Gln Gly Asp Val  
 1170 1175 1180  
 45 Tyr Arg Ala Glu Thr Glu Glu Ile Pro Lys Ile Phe Gln Ile Leu Tyr  
 1185 1190 1195 1200  
 Ala Asn Glu Gly Glu Cys Arg Lys Asp Val Glu Met Glu Pro Val Gln  
 1205 1210 1215  
 50 Gln Ala Glu Lys Thr Asn Phe Gln Asn His Lys Gly His Glu Phe Ile  
 1220 1225 1230  
 Pro Thr Leu Tyr His Phe Pro Ala Asn Cys Asp Ala Cys Ala Lys Pro  
 1235 1240 1245  
 55 Leu Trp His Val Phe Lys Pro Pro Pro Ala Leu Glu Cys Arg Arg Cys  
 1250 1255 1260  
 His Val Lys Cys His Arg Asp His Leu Asp Lys Lys Glu Asp Leu Ile  
 1265 1270 1275 1280

EP 2 319 924 B1

Cys Pro Cys Lys Val Ser Tyr Asp Val Thr Ser Ala Arg Asp Met Leu  
1285 1290 1295  
5 Leu Leu Ala Cys Ser Gln Asp Glu Gln Lys Lys Trp Val Thr His Leu  
1300 1305  
Val Lys Lys Ile Pro Lys Asn Pro Pro Ser Gly Phe Val Arg Ala Ser  
1315 1320 1325  
10 Pro Arg Thr Leu Ser Thr Arg Ser Thr Ala Asn Gln Ser Phe Arg Lys  
1330 1335 1340  
Val Val Lys Asn Thr Ser Gly Lys Thr Ser  
1345 1350

15 <210> 24  
<211> 4065  
<212> DNA  
<213> Homo sapiens

20 <400> 24

25

30

35

40

45

50

55

EP 2 319 924 B1

acatgtcgac tggggacagt tttgagactc gatttgaaaa aatggacaac ctgctgcggg 60  
 atcccaaatc ggaagtgaat tcggattggt tgctggatgg attggatgct ttggtatatg 120  
 5 atttgattt tcctgcctta agaaaaaaca aaaatattga caacttttta agcagatata 180  
 aagacacaat aaataaaatc agagatttac gaatgaaagc tgaagattat gaagtagtga 240  
 aggtgattgg tagaggtgca tttggagaag ttcaattggt aaggcataaa tccaccagga 300  
 10 aggtatatgc tatgaagctt ctcagcaaat ttgaaatgat aaagagatct gattctgctt 360  
 ttttctggga agaaagggac atcatggctt ttgccaacag tccttgggtt gttcagcttt 420  
 tttatgcatt ccaagatgat cgttatctct acatggtgat ggaatacatg cctggtggag 480  
 15 atcttgtaaa cttaatgagc aactatgatg tgcctgaaaa atgggcacga ttctatactg 540  
 cagaagtagt tcttgcattg gatgcaatcc attccatggg ttttattcac agagatgtga 600  
 agcctgataa catgctgctg gataaatctg gacatttgaa gttagcagat tttggtactt 660  
 20 gtatgaagat gaataaggaa ggcatggtac gatgtgatac agcggttgga acacctgatt 720  
 atatttcccc tgaagtatta aaatcccaag gtggtgatgg ttattatgga agagaatgtg 780  
 actggtggtc ggttggggta tttttatacg aaatgcttgt aggtgataca cttttttatg 840  
 25 cagattcttt ggttggaaact tacagtaaaa ttatgaacca taaaaattca cttacctttc 900  
 ctgatgataa tgacatatca aaagaagcaa aaaaccttat ttgtgccttc cttactgaca 960  
 ggggaagtgag gttagggcga aatggtgtag aagaaatcaa acgacatctc ttcttcaaaa 1020  
 30 atgaccagtg ggcttgggaa acgctccgag aactgtagc accagttgta cccgatttaa 1080  
 gtagtgacat tgatactagt aattttgatg acttgggaaga agataaagga gaggaagaaa 1140  
 cattccctat tcctaaagct ttcgttggca atcaactacc tttttagga tttacatatt 1200  
 35 atagcaatcg tagatactta tcttcagcaa atcctaataga taacagaact agctccaatg 1260  
 cagataaaaag cttgcaggaa agtttgcaaa aaacaatcta taagctggaa gaacagctgc 1320  
 ataataaat gcagttaaaa gatgaaatgg agcagaagtg cagaacctca aacataaaac 1380  
 40

45

50

55

EP 2 319 924 B1

tagacaagat aatgaaagaa ttggatgaag agggaaatca aagaagaaat ctagaatcta 1440  
 cagtgtctca gattgagaag gagaaaatgt tgctacagca tagaattaat gagtacccaaa 1500  
 5 gaaaagctga acaggaaaat gagaagagaa gaaatgtaga aaatgaagtt tctacattaa 1560  
 aggatcagtt ggaagactta aagaaagtca gtcagaattc acagcttgct aatgagaagc 1620  
 tgtcccagtt acaaaagcag ctagaagaag ccaatgactt acttaggaca gaatcggaca 1680  
 10 cagctgtaag attgaggaag agtcacacag agatgagcaa gtcaattagt cagttagagt 1740  
 ccctgaacag agagttgcaa gagagaaatc gaattttaga gaattctaag tcacaaacag 1800  
 acaaagatta ttaccagctg caagctatat tagaagctga acgaagagac agaggctatg 1860  
 15 attctgagat gattggagac cttcaagctc gaattacatc tttacaagag gaggtgaagc 1920  
 atctcaaaca taatctcgaa aaagtggaag gagaaagaaa agaggctcaa gacatgctta 1980  
 atcactcaga aaaggaaaag aataatntag agatagattt aaactacaaa cttaaactcat 2040  
 20 tacaacaacg gttagaacaa gaggtaaagt aacacaaagt aaccaaagct cgtttaactg 2100  
 acaaacatca atctattgaa gaggcaaagt ctgtggcaat gtgtgagatg gaaaaaaagc 2160  
 tgaaagaaga aagagaagct cgagagaagg ctgaaaatcg ggttgttcag attgagaaac 2220  
 25 agtgttccat gctagacgtt gatctgaagc aatctcagca gaaactagaa catttgactg 2280  
 gaaataaaga aaggatggag gatgaagtta agaactaac cctgcaactg gagcaggaat 2340  
 caaataagcg gctgttgta caaatgaat tgaagactca agcatttgag gcagacaatt 2400  
 30 taaaaggttt agaaaagcag atgaaacagg aaataaatac tttattggaa gcaaagagat 2460  
 tattagaatt tgagttagct cagcttacga aacagtatag aggaaatgaa ggacagatgc 2520  
 gggagctaca agatcagctt gaagctgagc aatattttctc gacactttat aaaaccagg 2580  
 35 taaaggaact taaagaagaa attgaagaaa aaaacagaga aaatttaag aaaatacagg 2640  
 aactacaaaa tgaaaaagaa actcttgcta ctcagttgga tctagcagaa acaaaaagctg 2700  
 agtctgagca gttggcgcga ggccttctgg aagaacagta ttttgaattg acgcaagaaa 2760  
 40 gcaagaaagc tgcttcaaga aatagacaag agattacaga taaagatcac actgttagtc 2820  
 ggcttgaaga agcaaacagc atgctaacca aagatattga aatattaaga agagagaatg 2880  
 aagagctaac agagaaaatg aagaaggcag aggaagaata taaactggag aaggaggagg 2940  
 45 agatcagtaa tcttaaggct gcctttgaaa agaataatcaa cactgaacga acccttaaaa 3000  
 cacaggctgt taacaaattg gcagaaataa tgaatcgaaa agattttaaa attgatagaa 3060  
 agaaagctaa tacacaagat ttgagaaaga aagaaaagga aaatcgaaag ctgcaactgg 3120  
 50 aactcaacca agaaagagag aaattcaacc agatggtagt gaaacatcag aaggaactga 3180  
 atgacatgca agcgaattg gtagaagaat gtgcacatag gaatgagctt cagatgcagt 3240  
 tggccagcaa agagagtgat attgagcaat tgcgtgctaa acttttggac ctctcggatt 3300  
 55 ctacaagtgt tgctagtttt cctagtgctg atgaaactga tggtaacctc ccagagtcaa 3360  
 gaattgaagg ttggctttca gtaccaata gaggaatat caaacgatat ggctggaaga 3420

EP 2 319 924 B1

aacagtatgt tgtggtaagc agcaaaaaaa ttttgttcta taatgacgaa caagataagg 3480  
 agcaatccaa tccatctatg gtattggaca tagataaact gtttcacgtt agacctgtaa 3540  
 5 cccaaggaga tgtgtataga gctgaaactg aagaaattcc taaaatattc cagatactat 3600  
 atgcaaatga aggtgaatgt agaaaagatg tagagatgga accagtacaa caagctgaaa 3660  
 aaactaattt ccaaaatcac aaaggccatg agttttattcc tacactctac cactttcctg 3720  
 10 ccaattgtga tgcctgtgcc aaacctctct ggcattgtttt taagccaccc cctgccctag 3780  
 agtgtcgaag atgccatggt aagtgccaca gagatcactt agataagaaa gaggacttaa 3840  
 tttgtccatg taaagtaagt tatgatgtaa catcagcaag agatatgctg ctgttagcat 3900  
 15 gttctcagga tgaacaaaaa aatgggtaa ctcathtagt aaagaaaatc cctaagaatc 3960  
 caccatctgg ttttgttcgt gcttcccctc gaacgctttc tacaagatcc actgcaaatc 4020  
 agtctttccg gaaagtggtc aaaaatacat ctggaaaaac tagtt 4065

20

<210> 25  
 <211> 1012  
 <212> PRT  
 <213> Homo sapiens

25

<400> 25

30

35

40

45

50

55

EP 2 319 924 B1

Met Thr Lys His Pro Pro Asn Arg Arg Gly Ile Ser Phe Glu Val Gly  
 1 5 10 15  
 Ala Gln Leu Glu Ala Arg Asp Arg Leu Lys Asn Trp Tyr Pro Ala His  
 5 20 25 30  
 Ile Glu Asp Ile Asp Tyr Glu Glu Gly Lys Val Leu Ile His Phe Lys  
 35 40 45  
 Arg Trp Asn His Arg Tyr Asp Glu Trp Phe Cys Trp Asp Ser Pro Tyr  
 10 50 55 60  
 Leu Arg Pro Leu Glu Lys Ile Gln Leu Arg Lys Glu Gly Leu His Glu  
 65 70 75 80  
 Glu Asp Gly Ser Ser Glu Phe Gln Ile Asn Glu Gln Val Leu Ala Cys  
 15 85 90 95  
 Trp Ser Asp Cys Arg Phe Tyr Pro Ala Lys Val Thr Ala Val Asn Lys  
 100 105 110  
 Asp Gly Thr Tyr Thr Val Lys Phe Tyr Asp Gly Val Val Gln Thr Val  
 115 120 125  
 Lys His Ile His Val Lys Ala Phe Ser Lys Asp Gln Asn Ile Val Gly  
 130 135 140  
 Asn Ala Arg Pro Lys Glu Thr Asp His Lys Ser Leu Ser Ser Ser Pro  
 145 150 155 160  
 Asp Lys Arg Glu Lys Phe Lys Glu Gln Arg Lys Ala Thr Val Asn Val  
 165 170 175  
 Lys Lys Asp Lys Glu Asp Lys Pro Leu Lys Thr Glu Lys Arg Pro Lys  
 180 185 190  
 Gln Pro Asp Lys Glu Gly Lys Leu Ile Cys Ser Glu Lys Gly Lys Val  
 195 200 205

35

40

45

50

55

EP 2 319 924 B1

Ser Glu Lys Ser Leu Pro Lys Asn Glu Lys Glu Asp Lys Glu Asn Ile  
 210 215 220  
 Ser Glu Asn Asp Arg Glu Tyr Ser Gly Asp Ala Gln Val Asp Lys Lys  
 5 225 230 235 240  
 Pro Glu Asn Asp Ile Val Lys Ser Pro Gln Glu Asn Leu Arg Glu Pro  
 245 250 255  
 Lys Arg Lys Arg Gly Arg Pro Pro Ser Ile Ala Pro Thr Ala Val Asp  
 10 260 265 270  
 Ser Asn Ser Gln Thr Leu Gln Pro Ile Thr Leu Glu Leu Arg Arg Arg  
 275 280 285  
 Lys Ile Ser Lys Gly Cys Glu Val Pro Leu Lys Arg Pro Arg Leu Asp  
 15 290 295 300  
 Lys Asn Ser Ser Gln Glu Lys Ser Lys Asn Tyr Ser Glu Asn Thr Asp  
 305 310 315 320  
 Lys Asp Leu Ser Arg Arg Arg Ser Ser Arg Leu Ser Thr Asn Gly Thr  
 20 325 330 335  
 His Glu Ile Leu Asp Pro Asp Leu Val Val Ser Asp Leu Val Asp Thr  
 340 345 350  
 Asp Pro Leu Gln Asp Thr Leu Ser Ser Thr Lys Glu Ser Glu Glu Gly  
 25 355 360 365  
 Gln Leu Lys Ser Ala Leu Glu Ala Gly Gln Val Ser Ser Ala Leu Thr  
 370 375 380  
 Cys His Ser Phe Gly Asp Gly Ser Gly Ala Ala Gly Leu Glu Leu Asn  
 30 385 390 395 400  
 Cys Pro Ser Met Gly Glu Asn Thr Met Lys Thr Glu Pro Thr Ser Pro  
 405 410 415  
 Leu Val Glu Leu Gln Glu Ile Ser Thr Val Glu Val Thr Asn Thr Phe  
 35 420 425 430  
 Lys Lys Thr Asp Asp Phe Gly Ser Ser Asn Ala Pro Ala Val Asp Leu  
 435 440 445  
 Asp His Lys Phe Arg Cys Lys Val Val Asp Cys Leu Lys Phe Phe Arg  
 40 450 455 460  
 Lys Ala Lys Leu Leu His Tyr His Met Lys Tyr Phe His Gly Met Glu  
 465 470 475 480  
 Lys Ser Leu Glu Pro Glu Glu Ser Pro Gly Lys Arg His Val Gln Thr  
 45 485 490 495  
 Arg Gly Pro Ser Ala Ser Asp Lys Pro Ser Gln Glu Thr Leu Thr Arg  
 500 505 510  
 Lys Arg Val Ser Ala Ser Ser Pro Thr Thr Lys Asp Lys Glu Lys Asn  
 515 520 525  
 Lys Glu Lys Lys Phe Lys Glu Phe Val Arg Val Lys Pro Lys Lys Lys  
 530 535 540  
 Lys Lys Lys Lys Lys Lys Thr Lys Pro Glu Cys Pro Cys Ser Glu Glu  
 545 550 555 560  
 Ile Ser Asp Thr Ser Gln Glu Pro Ser Pro Pro Lys Ala Phe Ala Val  
 565 570 575

EP 2 319 924 B1

Thr Arg Cys Gly Ser Ser His Lys Pro Gly Val His Met Ser Pro Gln  
 580 585 590  
 5 Leu His Gly Pro Glu Ser Gly His His Lys Gly Lys Val Lys Ala Leu  
 595 600 605  
 Glu Glu Asp Asn Leu Ser Glu Ser Ser Ser Glu Ser Phe Leu Trp Ser  
 610 615 620  
 10 Asp Asp Glu Tyr Gly Gln Asp Val Asp Val Thr Thr Asn Pro Asp Glu  
 625 630 635 640  
 Glu Leu Asp Gly Asp Asp Arg Tyr Asp Phe Glu Val Val Arg Cys Ile  
 645 650 655  
 15 Cys Glu Val Gln Glu Glu Asn Asp Phe Met Ile Gln Cys Glu Glu Cys  
 660 665 670  
 Gln Cys Trp Gln His Gly Val Cys Met Gly Leu Leu Glu Glu Asn Val  
 675 680 685  
 20 Pro Glu Lys Tyr Thr Cys Tyr Val Cys Gln Asp Pro Pro Gly Gln Arg  
 690 695 700  
 Pro Gly Phe Lys Tyr Trp Tyr Asp Lys Glu Trp Leu Ser Arg Gly His  
 705 710 715 720  
 25 Met His Gly Leu Ala Phe Leu Glu Glu Asn Tyr Ser His Gln Asn Ala  
 725 730 735  
 Lys Lys Ile Val Ala Thr His Gln Leu Leu Gly Asp Val Gln Arg Val  
 740 745 750  
 30 Ile Glu Val Leu His Gly Leu Gln Leu Lys Met Ser Ile Leu Gln Ser  
 755 760 765  
 Arg Glu His Pro Asp Leu Pro Leu Trp Cys Gln Pro Trp Lys Gln His  
 770 775 780  
 35 Ser Gly Glu Gly Arg Ser His Phe Arg Asn Ile Pro Val Thr Asp Thr  
 785 790 795 800  
 Arg Ser Lys Glu Glu Ala Pro Ser Tyr Arg Thr Leu Asn Gly Ala Val  
 805 810 815  
 40 Glu Lys Pro Arg Pro Leu Ala Leu Pro Leu Pro Arg Ser Val Glu Glu  
 820 825 830  
 Ser Tyr Ile Thr Ser Glu His Cys Tyr Gln Lys Pro Arg Ala Tyr Tyr  
 835 840 845  
 45 Pro Ala Val Glu Gln Lys Leu Val Val Glu Thr Arg Gly Ser Ala Leu  
 850 855 860  
 Asp Asp Ala Val Asn Pro Leu His Glu Asn Gly Asp Asp Ser Leu Ser  
 865 870 875 880  
 50 Pro Arg Leu Gly Trp Pro Leu Asp Gln Asp Arg Ser Lys Gly Asp Ser  
 885 890 895  
 Asp Pro Lys Pro Gly Ser Pro Lys Val Lys Glu Tyr Val Ser Lys Lys  
 900 905 910  
 55 Ala Leu Pro Glu Glu Ala Pro Ala Arg Lys Leu Leu Asp Arg Gly Gly  
 915 920 925  
 Glu Gly Leu Leu Ser Ser Gln His Gln Trp Gln Phe Asn Leu Leu Thr  
 930 935 940

EP 2 319 924 B1

His Val Glu Ser Leu Gln Asp Glu Val Thr His Arg MET Asp Ser Ile  
 945 950 955 960  
 5 Glu Lys Glu Leu Asp Val Leu Glu Ser Trp Leu Asp Tyr Thr Gly Glu  
 965 970 975  
 Leu Glu Pro Pro Glu Pro Leu Ala Arg Leu Pro Gln Leu Lys His Cys  
 980 985 990  
 10 Ile Lys Gln Leu Leu Met Asp Leu Gly Lys Val Gln Gln Ile Ala Leu  
 995 1000 1005  
 Cys Cys Ser Thr  
 1010

15 <210> 26  
 <211> 3039  
 <212> DNA  
 <213> Homo sapiens

20 <400> 26

25

30

35

40

45

50

55

EP 2 319 924 B1

atgacaaagc atccacctaa cagacgagga atcagctttg aagtgggagc ccagttggaa 60  
 gcccgggacc gtttaaaaaa ctggtatcca gctcacatag aagacattga ctacgaggaa 120  
 5 ggaaaagtac tcatccattt caagcgttgg aaccatcgtt atgatgagtg gttctgctgg 180  
 gacagtcctt atttacgccc tttagagaaa atacagctga ggaaagaggg cttgcatgaa 240  
 gaggatggat cttctgaatt tcaataaat gagcaggtcc ttgcttgctg gtctgattgt 300  
 10 cgtttttacc cggccaaagt cactgctggt aacaaggatg gtacttacac tgtgaaattt 360  
 tatgatggag tagttcagac tgtcaaacat attcatgtca aagctttttc caaagatcag 420  
 aatattgtgg gtaatgctag gcctaaagaa acagatcaca aaagtctttc atcatctcct 480  
 15 gataaacgag agaagtttaa agaacagaga aaagcaacag tgaatgtgaa gaaagacaaa 540  
 gaagataaac ccttaaagac agaaaagcga cccaagcagc ctgataaaga aggaaagtta 600  
 atctgttctg aaaaggggaa agtgtcagag aaaagtcttc ccaagaacga gaaggaagac 660  
 20 aaggaaaaca tttccgaaaa tgacagagag tattctggag atgcccaagt ggataagaaa 720  
 cctgaaaatg acattgtgaa gagtccacaa gaaaacttga gggaaaccaa aagaaaacga 780  
 ggcagacccc cttccatagc tcctactgct gtggattcaa actctcaaac tttgcaacca 840  
 25 ataacattgg aactgagaag aaggaaaata tcaaaaggat gtgaagtccc attaaaacgt 900  
 cctcggcttg acaaaaattc atcccaggaa aagtcaaaaa actactcggg aaacactgac 960  
 aaagacttat cgaggagacg ttctccagg ctgtccacta atgggaccca tgagatccta 1020  
 30 gatcctgact tggttgtatc agatttggtt gatacggatc ctttgcaaga cacgttgtct 1080  
 agtaccaagg aatctgaaga aggtcagttg aagtctgctt tggaaactgg ccaggtctca 1140  
 tctgactga cttgccactc ctttggggat ggatccgggg ctgcaggctt ggagttgaac 1200  
 35 tgcccatcaa tgggagaaaa cacgatgaaa acagaaccga cttctcccct tgtggaatta 1260  
 caagagattt cgactgtgga agtaacaaat acttttaaga aaacagatga ttttgggtca 1320  
 tctaatgcac cagctgtcga cctagacat aagtttagat gcaaagttgt ggactgttta 1380  
 40

45

50

55

EP 2 319 924 B1

aaatTTTTCC gcaaagccaa actgTTgcac tatcacatga agtatttcca tggaatggag 1440  
 aagtCactgg agccagaaga gagcccggga aagaggcatg tccaaaccag gggcccttca 1500  
 5 gcttcagaca agcccagcca ggagaccctg accaggaagc ggttctctgc cagttcccca 1560  
 actacaaaag acaaggaaaa gaataaagag aagaaattca aggagtttgt gagagtgaag 1620  
 ccaaagaaga aaaagaaaaa gaaaaagaaa accaaacctg aatgcccctg cagtgaggag 1680  
 10 atcagtgaca cctcccagga accttctcca cccaaggcat ttgctgttac caggtgtggg 1740  
 tcctcacaca agccaggggt ccatatgagc cgcagcttc atggcccaga atctggacac 1800  
 cacaaagga aagtgaagc attggaggag gataatttga gtgagtcctc ttctgagagc 1860  
 15 tttctctgga gtgatgatga gtatggccaa gatgtggatg tgaccaccaa cccagatgag 1920  
 gaacttgatg gggatgaccg ctatgacttc gaggtggtcc gctgcatctg tgaggtccag 1980  
 gaggaaaatg acttcatgat tcagtgtgaa gagtgccagt gctggcagca tggggtctgc 2040  
 20 atgggattac tggaagaaaa tgtgcccagag aaatacacct gttatgtttg ccaagaccct 2100  
 ccaggtcaga ggcctggctt caagtactgg tatgacaagg agtggctgag caggggacat 2160  
 atgcatggcc tggcatttct agaagagaac tactcccatc agaatgcca gaagatcgtg 2220  
 25 gccaccacc agcttcttgg tgatgtgcag agagtgattg aggttctgca tggcctgcag 2280  
 ctcaagatga gcatcttgca aagccgggag catcctgatc tgccgctgtg gtgccagcct 2340  
 tggaacagc actcagggga ggggagatct catttcagaa acatccctgt cactgacacc 2400  
 30 aggagcaagg aggaagctcc aagctataga actttgaacg gggcagtgga gaagcccagg 2460  
 cccctggccc tgcccctgcc gcgttctgtg gaggaatcct atatcaccag tgagcattgc 2520  
 taccagaagc cccgcgccta ttaccctgcc gtggagcaga agctggtggt ggagacgagg 2580  
 35 ggctctgccc tcgacgatgc ggtcaacccc ctccatgaga acggcgatga ttccctttcc 2640  
 ccgcgcctgg gctggcctct agaccaagac aggagcaagg gggacagtga ccccaaacc 2700  
 ggctcccaa aggtgaagga atatgtctcc aaaaaggccc taccagaaga agcccctgct 2760  
 40 cggaagctgc tggacagagg tggagagggg ctgctgagct cccagcacca gtggcagttt 2820  
 aacctgctga cccatgtgga atctcttcag gatgaagtta cgcacaggat ggactccatt 2880  
 gagaaggagt tggatgtggt ggagagctgg ctggactaca ctggggaact ggagcccct 2940  
 45 gagccgctgg ccaggcttcc gcagctcaag cattgtatca agcagctgct gatggacctg 3000  
 ggcaaggtgc agcagatcgc cctctgctgc tcaacatga 3039

<210> 27  
 50 <211> 1483  
 <212> PRT  
 <213> Homo sapiens

<400> 27  
 55

EP 2 319 924 B1

Met Ala Pro Leu Leu Gly Arg Lys Pro Phe Pro Leu Val Lys Pro Leu  
1 5 10 15  
5 Pro Gly Glu Glu Pro Leu Phe Thr Ile Pro His Thr Gln Glu Ala Phe  
20 25 30

10

15

20

25

30

35

40

45

50

55

EP 2 319 924 B1

Arg Thr Arg Glu Glu Tyr Glu Ala Arg Leu Glu Arg Tyr Ser Glu Arg  
 35 40 45  
 Ile Trp Thr Cys Lys Ser Thr Gly Ser Ser Gln Leu Thr His Lys Glu  
 5 50 55 60  
 Ala Trp Glu Glu Glu Gln Glu Val Ala Glu Leu Leu Lys Glu Glu Phe  
 65 70 75 80  
 Pro Ala Trp Tyr Glu Lys Leu Val Leu Glu Met Val His His Asn Thr  
 10 85 90 95  
 Ala Ser Leu Glu Lys Leu Val Asp Thr Ala Trp Leu Glu Ile Met Thr  
 100 105 110  
 Lys Tyr Ala Val Gly Glu Glu Cys Asp Phe Glu Val Gly Lys Glu Lys  
 15 115 120 125  
 Met Leu Lys Val Lys Ile Val Lys Ile His Pro Leu Glu Lys Val Asp  
 130 135 140  
 Glu Glu Ala Thr Glu Lys Lys Ser Asp Gly Ala Cys Asp Ser Pro Ser  
 145 150 155 160  
 Ser Asp Lys Glu Asn Ser Ser Gln Ile Ala Gln Asp His Gln Lys Lys  
 165 170 175  
 Glu Thr Val Val Lys Glu Asp Glu Gly Arg Arg Glu Ser Ile Asn Asp  
 180 185 190  
 Arg Ala Arg Arg Ser Pro Arg Lys Leu Pro Thr Ser Leu Lys Lys Gly  
 195 200 205  
 Glu Arg Lys Trp Ala Pro Pro Lys Phe Leu Pro His Lys Tyr Asp Val  
 210 215 220  
 Lys Leu Gln Asn Glu Asp Lys Ile Ile Ser Asn Val Pro Ala Asp Ser  
 225 230 235 240  
 Leu Ile Arg Thr Glu Arg Pro Pro Asn Lys Glu Ile Val Arg Tyr Phe  
 245 250 255  
 Ile Arg His Asn Ala Leu Arg Ala Gly Thr Gly Glu Asn Ala Pro Trp  
 260 265 270  
 Val Val Glu Asp Glu Leu Val Lys Lys Tyr Ser Leu Pro Ser Lys Phe  
 275 280 285  
 Ser Asp Phe Leu Leu Asp Pro Tyr Lys Tyr Met Thr Leu Asn Pro Ser  
 290 295 300  
 Thr Lys Arg Lys Asn Thr Gly Ser Pro Asp Arg Lys Pro Ser Lys Lys  
 305 310 315 320  
 Ser Lys Thr Asp Asn Ser Ser Leu Ser Ser Pro Leu Asn Pro Lys Leu  
 325 330 335  
 Trp Cys His Val His Leu Lys Lys Ser Leu Ser Gly Ser Pro Leu Lys  
 340 345 350  
 Val Lys Asn Ser Lys Asn Ser Lys Ser Pro Glu Glu His Leu Glu Glu  
 355 360 365  
 Met Met Lys Met Met Ser Pro Asn Lys Leu His Thr Asn Phe His Ile  
 370 375 380  
 Pro Lys Lys Gly Pro Pro Ala Lys Lys Pro Gly Lys His Ser Asp Lys  
 385 390 395 400

EP 2 319 924 B1

Pro Leu Lys Ala Lys Gly Arg Ser Lys Gly Ile Leu Asn Gly Gln Lys  
 405 410 415  
 Ser Thr Gly Asn Ser Lys Ser Pro Lys Lys Gly Leu Lys Thr Pro Lys  
 5 420 425 430  
 Thr Lys Met Lys Gln Met Thr Leu Leu Asp Met Ala Lys Gly Thr Gln  
 435 440 445  
 Lys Met Thr Arg Ala Pro Arg Asn Ser Gly Gly Thr Pro Arg Thr Ser  
 10 450 455 460  
 Ser Lys Pro His Lys His Leu Pro Pro Ala Ala Leu His Leu Ile Ala  
 465 470 475 480  
 Tyr Tyr Lys Glu Asn Lys Asp Arg Glu Asp Lys Arg Ser Ala Leu Ser  
 15 485 490 495  
 Cys Val Ile Ser Lys Thr Ala Arg Leu Leu Ser Ser Glu Asp Arg Ala  
 500 505 510  
 Arg Leu Pro Glu Glu Leu Arg Ser Leu Val Gln Lys Arg Tyr Glu Leu  
 20 515 520 525  
 Leu Glu His Lys Lys Arg Trp Ala Ser Met Ser Glu Glu Gln Arg Lys  
 530 535 540  
 Glu Tyr Leu Lys Lys Lys Arg Glu Glu Leu Lys Lys Lys Leu Lys Glu  
 25 545 550 555 560  
 Lys Ala Lys Glu Arg Arg Glu Lys Glu Met Leu Glu Arg Leu Glu Lys  
 565 570 575  
 Gln Lys Arg Tyr Glu Asp Gln Glu Leu Thr Gly Lys Asn Leu Pro Ala  
 30 580 585 590  
 Phe Arg Leu Val Asp Thr Pro Glu Gly Leu Pro Asn Thr Leu Phe Gly  
 595 600 605  
 Asp Val Ala Met Val Val Glu Phe Leu Ser Cys Tyr Ser Gly Leu Leu  
 35 610 615 620  
 Leu Pro Asp Ala Gln Tyr Pro Ile Thr Ala Val Ser Leu Met Glu Ala  
 625 630 635 640  
 Leu Ser Ala Asp Lys Gly Gly Phe Leu Tyr Leu Asn Arg Val Leu Val  
 40 645 650 655  
 Ile Leu Leu Gln Thr Leu Leu Gln Asp Glu Ile Ala Glu Asp Tyr Gly  
 660 665 670  
 Glu Leu Gly Met Lys Leu Ser Glu Ile Pro Leu Thr Leu His Ser Val  
 45 675 680 685  
 Ser Glu Leu Val Arg Leu Cys Leu Arg Arg Ser Asp Val Gln Glu Glu  
 690 695 700  
 Ser Glu Gly Ser Asp Thr Asp Asp Asn Lys Asp Ser Ala Ala Phe Glu  
 50 705 710 715 720  
 Asp Asn Glu Val Gln Asp Glu Phe Leu Glu Lys Leu Glu Thr Ser Glu  
 725 730 735  
 Phe Phe Glu Leu Thr Ser Glu Glu Lys Leu Gln Ile Leu Thr Ala Leu  
 740 745 750  
 Cys His Arg Ile Leu Met Thr Tyr Ser Val Gln Asp His Met Glu Thr  
 55 755 760 765

EP 2 319 924 B1

Arg Gln Gln Met Ser Ala Glu Leu Trp Lys Glu Arg Leu Ala Val Leu  
 770 775 780  
 Lys Glu Glu Asn Asp Lys Lys Arg Ala Glu Lys Gln Lys Arg Lys Glu  
 785 790 795  
 Met Glu Ala Lys Asn Lys Glu Asn Gly Lys Val Glu Asn Gly Leu Gly  
 805 810 815  
 Lys Thr Asp Arg Lys Lys Glu Ile Val Lys Phe Glu Pro Gln Val Asp  
 820 825 830  
 Thr Glu Ala Glu Asp Met Ile Ser Ala Val Lys Ser Arg Arg Leu Leu  
 835 840 845  
 Ala Ile Gln Ala Lys Lys Glu Arg Glu Ile Gln Glu Arg Glu Met Lys  
 850 855 860  
 Val Lys Leu Glu Arg Gln Ala Glu Glu Glu Arg Ile Arg Lys His Lys  
 865 870 875 880  
 Ala Ala Ala Glu Lys Ala Phe Gln Glu Gly Ile Ala Lys Ala Lys Leu  
 885 890 895  
 Val Met Arg Arg Thr Pro Ile Gly Thr Asp Arg Asn His Asn Arg Tyr  
 900 905 910  
 Trp Leu Phe Ser Asp Glu Val Pro Gly Leu Phe Ile Glu Lys Gly Trp  
 915 920 925  
 Val His Asp Ser Ile Asp Tyr Arg Phe Asn His His Cys Lys Asp His  
 930 935 940  
 Thr Val Ser Gly Asp Glu Asp Tyr Cys Pro Arg Ser Lys Lys Ala Asn  
 945 950 955 960  
 Leu Gly Lys Asn Ala Ser Met Asn Thr Gln His Gly Thr Ala Thr Glu  
 965 970 975  
 Val Ala Val Glu Thr Thr Thr Pro Lys Gln Gly Gln Asn Leu Trp Phe  
 980 985 990  
 Leu Cys Asp Ser Gln Lys Glu Leu Asp Glu Leu Leu Asn Cys Leu His  
 995 1000 1005  
 Pro Gln Gly Ile Arg Glu Ser Gln Leu Lys Glu Arg Leu Glu Lys Arg  
 1010 1015 1020  
 Tyr Gln Asp Ile Ile His Ser Ile His Leu Ala Arg Lys Pro Asn Leu  
 1025 1030 1035 1040  
 Gly Leu Lys Ser Cys Asp Gly Asn Gln Glu Leu Leu Asn Phe Leu Arg  
 1045 1050 1055  
 Ser Asp Leu Ile Glu Val Ala Thr Arg Leu Gln Lys Gly Gly Leu Gly  
 1060 1065 1070  
 Tyr Val Glu Glu Thr Ser Glu Phe Glu Ala Arg Val Ile Ser Leu Glu  
 1075 1080 1085  
 Lys Leu Lys Asp Phe Gly Glu Cys Val Ile Ala Leu Gln Ala Ser Val  
 1090 1095 1100  
 Ile Lys Lys Phe Leu Gln Gly Phe Met Ala Pro Lys Gln Lys Arg Arg  
 1105 1110 1115 1120  
 Lys Leu Gln Ser Glu Asp Ser Ala Lys Thr Glu Glu Val Asp Glu Glu  
 1125 1130 1135

EP 2 319 924 B1

Lys Lys Met Val Glu Glu Ala Lys Val Ala Ser Ala Leu Glu Lys Trp  
 1140 1145 1150  
 Lys Thr Ala Ile Arg Glu Ala Gln Thr Phe Ser Arg Met His Val Leu  
 5 1155 1160 1165  
 Leu Gly Met Leu Asp Ala Cys Ile Lys Trp Asp Met Ser Ala Glu Asn  
 1170 1175 1180  
 Ala Arg Cys Lys Val Cys Arg Lys Lys Gly Glu Asp Asp Lys Leu Ile  
 10 1185 1190 1195 1200  
 Leu Cys Asp Glu Cys Asn Lys Ala Phe His Leu Phe Cys Leu Arg Pro  
 1205 1210 1215  
 Ala Leu Tyr Glu Val Pro Asp Gly Glu Trp Gln Cys Pro Ala Cys Gln  
 15 1220 1225 1230  
 Pro Ala Thr Ala Arg Arg Asn Ser Arg Gly Arg Asn Tyr Thr Glu Glu  
 1235 1240 1245  
 Ser Ala Ser Glu Asp Ser Glu Asp Asp Glu Ser Asp Glu Glu Glu  
 20 1250 1255 1260  
 Glu Glu Glu Glu Glu Glu Glu Glu Asp Tyr Glu Val Ala Gly Leu  
 1265 1270 1275 1280  
 Arg Leu Arg Pro Arg Lys Thr Ile Arg Gly Lys His Ser Val Ile Pro  
 25 1285 1290 1295  
 Pro Ala Ala Arg Ser Gly Arg Arg Pro Gly Lys Lys Pro His Ser Thr  
 1300 1305 1310  
 Arg Arg Ser Gln Pro Lys Ala Pro Pro Val Asp Asp Ala Glu Val Asp  
 30 1315 1320 1325  
 Glu Leu Val Leu Gln Thr Lys Arg Ser Ser Arg Arg Gln Ser Leu Glu  
 1330 1335 1340  
 Leu Gln Lys Cys Glu Glu Ile Leu His Lys Ile Val Lys Tyr Arg Phe  
 35 1345 1350 1355 1360  
 Ser Trp Pro Phe Arg Glu Pro Val Thr Arg Asp Glu Ala Glu Asp Tyr  
 1365 1370 1375  
 Tyr Asp Val Ile Thr His Pro Met Asp Phe Gln Thr Val Gln Asn Lys  
 40 1380 1385 1390  
 Cys Ser Cys Gly Ser Tyr Arg Ser Val Gln Glu Phe Leu Thr Asp Met  
 1395 1400 1405  
 Lys Gln Val Phe Thr Asn Ala Glu Val Tyr Asn Cys Arg Gly Ser His  
 45 1410 1415 1420  
 Val Leu Ser Cys Met Val Lys Thr Glu Gln Cys Leu Val Ala Leu Leu  
 1425 1430 1435 1440  
 His Lys His Leu Pro Gly His Pro Tyr Val Arg Arg Lys Arg Lys Lys  
 50 1445 1450 1455  
 Phe Pro Asp Arg Leu Ala Glu Asp Glu Gly Asp Ser Glu Pro Glu Ala  
 1460 1465 1470  
 Val Gly Gln Ser Arg Gly Arg Arg Gln Lys Lys  
 55 1475 1480

<210> 28

<211> 4452

**EP 2 319 924 B1**

<212> DNA  
<213> Homo sapiens

<400> 28

5

10

15

20

25

30

35

40

45

50

55

EP 2 319 924 B1

atggcgccgc tcctgggccg caagcccttc ccgctggtga agccgttgcc cggagaggag 60  
 ccgctcttca ccatcccgca cactcaggag gccttccgca cccgggaaga gtatgaagcc 120  
 5 cgcttgaaa ggtacagtga gcgcatttgg acgtgcaaga gtactggaag cagtcagcta 180  
 acacacaagg aagcctggga ggaagaacag gaagttgctg agcttttgaa ggaggagttt 240  
 cctgcctggt atgagaagct tgttctggaa atggttcacc ataacacagc ctccttagag 300  
 10 aagttagtag atactgcttg gttggagatc atgaccaa atgctgtggg agaagagtgt 360  
 gacttcgagg ttgggaagga gaaaatgctc aagggtgaaga ttgtgaagat tcatcctttg 420  
 gagaaagtgg atgaagaggc cactgagaag aaatctgatg gtgcctgtga ttctccatca 480  
 15 agtgacaaag agaactccag tcagattgct caggaccatc agaagaagga gacagttgtg 540  
 aaagaggatg aaggaaggag agagagtatt aatgacagag cacgtagatc gccacgaaaa 600  
 cttcctactt cattaaaaaa aggagaaagg aaatgggctc ctccaaaatt tctgcctcac 660  
 20 aaatatgatg tgaaactaca aaatgaagat aagatcatca gtaacgtgcc agcagacagc 720  
 ttgattcgta cagagcgccc accaaataag gagatagttc gatactttat acggcataat 780  
 gcattacgag ctggtactgg tgaaaatgca ccttgggctg tagaagatga attggtgaag 840  
 25 aaatactctc tgcccagcaa gttcagtgac tttttacttg atccatacaa gtatatgact 900  
 ctcaaccctt ctactaagag gaagaatact ggatccccag acaggaagcc ctcaaagaaa 960  
 tccaagacag acaactcttc tcttagttca ccactaaatc ctaagttatg gtgtcacgta 1020  
 30 cacttgaaga agtcattgag tggctcgcca ctcaaagtga agaactcaaa gaattccaaa 1080  
 tctcctgaag aacatctaga agaaatgatg aagatgatgt cgcccaataa gctgcacact 1140  
 aactttcaca ttcctaaaaa aggcccacct gccaaagaaac caggaagca cagtgacaag 1200  
 35 cctttgaagg caaagggcag aagcaaaggc atcctgaatg gacagaaatc cacagggat 1260  
 tccaaatctc ccaaaaaagg actgaagact cctaaaacca aaatgaagca gatgactttg 1320  
 ttggatatgg ccaaaggcac gcagaagatg acacgagccc cacggaattc tgggggtaca 1380  
 40 cctaggacct ctagtaaacc tcataaacat ctgcctctg cagccctaca cctcattgca 1440  
 tactacaaag aaaacaaaga caggaggagc aagaggagcg ccctgtcctg tgttatctcc 1500  
 aaaacagctc gtcttctctc tagtgaagat agagctcgtc tcccagaaga attgcaagat 1560  
 45 cttgttcaaa aacgctatga acttctagag cacaaaaaga ggtgggcttc tatgtctgaa 1620  
 gaacaacgga aagaatattt gaaaaagaaa cgggaggagc tgaaaaagaa gttgaaggaa 1680  
 aaagccaaag aacgaagaga gaaagaaatg cttgagagat tagaaaaaca gaagcggat 1740  
 50 gaggaccaag agttaactgg caaaaacctt ccagcattca gattggtgga taccctgaa 1800  
 gggctgcca acacgctggt tggggatgtg gccatggtgg tggaattctt gagctgttat 1860  
 tctgggctac ttttaccaga tgctcagtat cctattactg ctgtgtccct tatggaagcc 1920  
 55

EP 2 319 924 B1

ttgagtgcag ataaggggtg ctttttatac cttaacaggg tgttggtcat cctcttacag 1980  
 accctcctac aagatgagat agcagaagac tatggtgaat tgggaatgaa gctgtcggaa 2040  
 5 atccccttga ctctgcattc tgtttcagag ctggtgcggc tctgcttgcg cagatctgat 2100  
 gttcaggagg aaagcgaggg ctcacacaca gatgacaata aagattcagc tgcatttgag 2160  
 gataatgagg tacaagatga gttcctagaa aagctggaga cctctgaatt ttttgagctg 2220  
 10 acgtcagagg agaagctaca gatcttgaca gcactgtgcc accggatcct catgacatac 2280  
 tcagtgaag accacatgga gaccagacag cagatgtctg cagagttgtg gaaggaacgg 2340  
 cttgctgtgt tgaaggaaga aatgataag aagagagcag agaaacagaa acggaaagaa 2400  
 15 atggaagcca aaaataaaga aatggaaaa gttgagaatg ggtaggcaa aactgatagg 2460  
 aaaaaagaaa ttgtgaagtt tgagcccaa gtagatacag aagctgaaga catgattagt 2520  
 gctgtgaaga gcagaagggt gcttgccatt caagctaaga aggaacggga aatccaggaa 2580  
 20 agagaaatga aagtgaact ggaacgcaa gctgaagaag aacgaatacg gaagcacaaa 2640  
 gcagctgctg agaaagcttt ccaggaaggg attgccaagg ccaaactagt catgcgcagg 2700  
 actcctattg gcacagatcg aaaccataat agatactggc tcttctcaga tgaagttcca 2760  
 25 ggattattca ttgaaaaagg ctgggtacat gacagcattg actaccgatt caaccatcac 2820  
 tgcaaagacc acacagtctc tggatgatgag gattactgtc ctcgcagtaa gaaagcaaac 2880  
 ttaggtaaaa atgcaagcat gaacacacaa catggaacag caacagaagt tgctgtagag 2940  
 30 acaaccacac ccaaacaagg acagaaccta tggtttttat gtgatagtca aaaggagctg 3000  
 gatgagttgc taaactgtct tcaccctcag ggaataagag aaagtcaact taaagagaga 3060  
 ctagagaaga ggtaccagga cattattcac tctattcatc tagcacggaa gccaaatttg 3120  
 35 ggtctaaaat cttgtgatgg caaccaggag cttttaaact tccttcgtag tgatctcatt 3180  
 gaagttgcaa caaggttaca aaaaggagga cttggatatg tggaagaaac atcagaatth 3240  
 gaagcccggg tcatthcatt agagaaattg aaggattttg gtgagtgtgt gattgccctt 3300  
 40 caggccagtg tcataaagaa atthctcaa ggcttcatgg ctccaagca aaagagaaga 3360  
 aaactccaaa gtgaagattc agcaaaaact gaggaagtgg atgaagagaa gaaaatggta 3420  
 gaggaagcaa aggttgcattc tgactggag aatggaaga cagcaatccg ggaagctcag 3480  
 45 actthctcca ggatgcacgt gctgcttggg atgcttgatg cctgtatcaa gtgggatatg 3540  
 tccgcagaaa atgctaggtg caaagthtgt cgaaagaaag gtgaggatga caaattgatc 3600  
 thgtgtgatg agtgaataa agcctthcac ctgthttgtc tgaggccggc cctctatgaa 3660  
 50 gtaccagatg gtgagtggca gtgcccagct tgccagcccg ctactgccag gcgcaactcc 3720  
 cgtggcagga actatactga agagtctgct tctgaggaca gtgaagatga tgagagtgat 3780  
 gaagaggagg aggaggaaga agaggaggag gaggaagaag attatgaggt ggctggthtg 3840  
 55 cgattgagac ctcgaaagac catccggggc aagcacagcg tcatcccccc tgcagcaagg 3900  
 tcaggccggc gcccggttaa gaagccacac tctaccagga ggtctcagcc caaggcacca 3960

EP 2 319 924 B1

cctgtggatg atgctgaggt ggatgagctg gtgcttcaga ccaagcggag ctcccggagg 4020  
caaagcctgg agctgcagaa gtgtgaagag atcctccaca agatcgtgaa gtaccgcttc 4080  
5 agctggccct tcagggagcc tgtgaccaga gatgaggccg aggactacta tgatgtgatc 4140  
acgcacccca tggactttca gacagtgcag aacaaatgtt cctgtgggag ctaccgctct 4200  
gtgcaggagt ttcttactga catgaagcaa gtgtttacca atgctgaggt ttacaactgc 4260  
10 cgtggcagcc atgtgctaag ctgcatggtg aagacagaac agtgtctagt ggctctgttg 4320  
cataaacacc ttcttgcca cccatatgtc cgcaggaagc gcaagaagtt tcctgatagg 4380  
cttgctgaag atgaagggga cagtgcagca gaggccgttg gacagtccag gggacgaaga 4440  
15 cagaagaagt ag 4452

<210> 29

<211> 621

<212> PRT

20 <213> Homo sapiens

<400> 29

25

30

35

40

45

50

55

EP 2 319 924 B1

Met Leu Leu Leu Pro Ser Ala Ala Asp Gly Arg Gly Thr Ala Ile Thr  
1 5 10 15

His Ala Leu Thr Ser Ala Ser Thr Leu Cys Gln Val Glu Pro Val Gly  
5 20 25 30

Arg Trp Phe Glu Ala Phe Val Lys Arg Arg Asn Arg Asn Ala Ser Ala  
35 40 45

Ser Phe Gln Glu Leu Glu Asp Lys Lys Glu Leu Ser Glu Glu Ser Glu  
10 50 55 60

Asp Glu Glu Leu Gln Leu Glu Glu Phe Pro Met Leu Lys Thr Leu Asp  
65 70 75 80

Pro Lys Asp Trp Lys Asn Gln Asp His Tyr Ala Val Leu Gly Leu Gly  
15 85 90 95

His Val Arg Tyr Lys Ala Thr Gln Arg Gln Ile Lys Ala Ala His Lys  
100 105 110

Ala Met Val Leu Lys His His Pro Asp Lys Arg Lys Ala Ala Gly Glu  
20 115 120 125

Pro Ile Lys Glu Gly Asp Asn Asp Tyr Phe Thr Cys Ile Thr Lys Ala  
130 135 140

Tyr Glu Met Leu Ser Asp Pro Val Lys Arg Arg Ala Phe Asn Ser Val  
25 145 150 155 160

Asp Pro Thr Phe Asp Asn Ser Val Pro Ser Lys Ser Glu Ala Lys Asp  
165 170 175

Asn Phe Phe Glu Val Phe Thr Pro Val Phe Glu Arg Asn Ser Arg Trp  
30 180 185 190

Ser Asn Lys Lys Asn Val Pro Lys Leu Gly Asp Met Asn Ser Ser Phe  
195 200 205

Glu Asp Val Asp Ile Phe Tyr Ser Phe Trp Tyr Asn Phe Asp Ser Trp  
35 210 215 220

Arg Glu Phe Ser Tyr Leu Asp Glu Glu Glu Lys Glu Lys Ala Glu Cys



EP 2 319 924 B1

595 600 605  
Ala Gln Glu Gln Val Leu Asn Ala Ser Arg Ala Lys Lys  
610 615 620

5

<210> 30  
<211> 1866  
<212> DNA  
<213> Homo sapiens

10

<400> 30

15

20

25

30

35

40

45

50

55

EP 2 319 924 B1

	tc	atg	tctgccaagc	gccgcggacg	gccggggcac	cgccatcacc	cacgctctga	60
	cct	ctgcctc	tacactctgt	caagttgaac	ctgtggaag	atggtttgaa	gcttttgta	120
5	ag	aggagaaa	cagaaatgct	tctgcctctt	ttcaggaact	ggaggataag	aaagagttat	180
	cc	gaggaatc	agaagatgaa	gaattgcagt	tggaagagtt	tcccatgctg	aaaacacttg	240
	at	cccaaaga	ctggaagaac	caagatcatt	atgcagttct	tggacttggc	catgtgagat	300
10	aca	aggctac	acagagacag	atcaaagcag	ctcataaagc	aatggtttta	aaacatcacc	360
	cag	acaaacg	gaaagcagct	ggtgaaccaa	taaaagaagg	agataatgac	tacttcactt	420
	gc	ataactaa	agcttatgaa	atgttatctg	atccagtgaa	aagacgagca	tttaacagtg	480
15	tag	atcctac	ttttgataac	tcagttcctt	ctaaaagtga	agcaaaggat	aatttcttcg	540
	aag	tgtttac	cccagtgttt	gaaaggaatt	ccagatggtc	aaataaaaaa	aatgttccta	600
	aac	ttggtgga	tatgaattca	tcatttgaag	atgtagatat	atthttattct	ttctggtata	660
20	at	tttgattc	ttggagagaa	ttttcttatt	tagatgaaga	agaaaaagaa	aaagcagaat	720
	gt	cgtgatga	gaggagatgg	attgaaaagc	agaacagagc	aacaagagca	caaagaaaaa	780
	aag	aagaaat	gaacagaata	agaacattag	ttgacaatgc	atacagctgt	gatccaagga	840
25	ta	aaaaagtt	caaggaagaa	gaaaaagcca	agaaagaagc	agaaaagaaa	gcaaaagcag	900
	aag	ctaaacg	gaaggagcaa	gaagctaaag	aaaaacaaag	acaagctgaa	ttagaagctg	960
	ct	cggttagc	taaggagaaa	gaagaggagg	aagtcagaca	gcaagcattg	ctggcaaaga	1020
30	agg	aaaaaaga	tatccagaaa	aaagccatta	agaaggaaag	gcaaaaactt	cgaaactcat	1080
	gca	agacctg	gaatcattht	tctgataatg	aggcagagcg	ggttaaaatg	atggaagaag	1140
	tg	aaaaaact	ttgtgatcgg	cttgaactgg	caagcttaca	gtgcttgaat	gaaacactca	1200
35	cat	catgcac	aaaagaagta	ggaaaggctg	ctttggaaaa	acagatagaa	gaaataaatg	1260
	ag	caaatcag	aaaagagaaa	gaggaagctg	aggctcgtat	gcgacaagca	tctaagaaca	1320
	cag	agaaatc	aactggtgga	ggtggaaatg	gaagtaaaaa	ttggtcagaa	gatgatctac	1380
40	aatt	actaat	taaagctgtg	aatctgttcc	ctgctggaac	aaattcaaga	tgggaagtta	1440
	tt	gctaatta	catgaacata	cattcttctt	ctggagtcaa	aagaactgcc	aaagatgtta	1500
	tt	ggcaaagc	aaagagtctc	caaaaacttg	accctcatca	aaaagatgac	ataaataaaa	1560
45	agg	catttga	taagttcaaa	aaagaacatg	gagtggtacc	tcaagcagac	aacgcaacgc	1620
	ct	tcaaacg	atthgaaggt	ccatatacag	acttcacccc	ttggacaaca	gaagaacaga	1680
50	ag	cttttgga	acaagctttg	aaaacatacc	cagtaaatac	acctgaaaga	tgggaaaaaa	1740
	tag	cagaagc	ggtgcctggc	aggacaaaga	aggactgcat	gaaacgatac	aaggaacttg	1800
	tc	gagatggt	aaaagcaaag	aaagctgctc	aagaacaagt	gctgaatgca	agtagagcca	1860
55	ag	aaat						1866

<210> 31  
<211> 380

EP 2 319 924 B1

<212> PRT  
 <213> Homo sapiens

<400> 31

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

55

EP 2 319 924 B1

Glu Phe Ile Tyr Ser Thr Gln Lys Ala Ser Cys Arg Cys Glu Ser Gly  
 290 295 300  
 Tyr Thr Gly Gln His Cys Glu Lys Thr Asp Phe Ser Ile Leu Tyr Val  
 5 305 310 315 320  
 Val Pro Ser Arg Gln Lys Leu Thr His Val Leu Ile Ala Ala Ile Ile  
 325 330 335  
 Gly Ala Val Gln Ile Ala Ile Ile Val Ala Ile Val Met Cys Ile Thr  
 10 340 345 350  
 Arg Lys Cys Pro Lys Asn Asn Arg Gly Arg Arg Gln Lys Gln Asn Leu  
 355 360 365  
 Gly His Phe Thr Ser Asp Thr Ser Ser Arg Met Val  
 15 370 375 380

<210> 32

<211> 1143

<212> DNA

20 <213> Homo sapiens

<400> 32

atgggCGCCg cagccgctga ggcgccgctc cggctgcctg ccgcgcctcc gctcgccttc 60  
 tgctgctaca cgctcggtgct tctgctcttc gccttctctc tgcccgggag ccgcgcgtcc 120  
 aaccagcccc cgggtggtgg cggcggcagc ggcggggact gtcccggcgg caaaggcaag 180  
 agcatcaact gctcagaatt aaatgtgagg gagtctgacg taagagtttg tgatgagtca 240  
 tcatgtaa atggaggagt ctgtaaagaa gatggagatg gtttgaaatg tgcatgccaa 300  
 tttcagtgcc atacaaatta tattcctgtc tgtggatcaa atggggacac ttatcaaaat 360  
 gaatgctttc tcagaagggc tgcttgtaag caccagaaag agataacagt aatagcaaga 420  
 ggaccatgct actctgataa tggatctgga tctggagaag gagaagagga agggctcaggg 480  
 gcagaagttc acagaaaaca ctccaagtgt ggaccctgca aatataaagc tgagtgtgat 540  
 gaagatgcag aaaatgttgg gtgtgtatgt aatatagatt gcagtggata cagttttaat 600  
 cctgtgtgtg cttctgatgg gagttcctat aacaatccct gttttgttcg agaagcatct 660  
 tgtataaagc aagaacaaat tgatataagg catcttggtc attgcacaga tacagatgac 720  
 actagtttgt tgggaaagaa agatgatgga ctacaatatc gaccagatgt gaaagatgct 780  
 agtgatcaaa gagaagatgt ttatattgga aaccacatgc cttgccctga aaacctcaat 840  
 ggttactgca tccatggaaa atgtgaattc atctattcta ctcagaaggc ttctttaga 900  
 tgtgaatctg gctacactgg acagcactgt gaaaagacag acttttagtat tctctatgta 960  
 gtgccaagta ggcaaaagct cactcatggt cttattgcag caattattgg agctgtacag 1020  
 attgccatca tagtagcaat tgtaatgtgc ataacaagaa aatgccccaa aaacaataga 1080  
 ggacgtcgac agaagcaaaa cctaggtcat tttacttcag atacgtcatc cagaatgggt 1140  
 55 taa 1143

<210> 33

EP 2 319 924 B1

<211> 185  
 <212> PRT  
 <213> Homo sapiens

5 <400> 33

Met Gly Lys Lys Gln Asn Lys Lys Lys Val Glu Glu Val Leu Glu Glu  
 1 5 10 15  
 Glu Glu Glu Glu Tyr Val Val Glu Lys Val Leu Asp Arg Arg Val Val  
 20 25 30  
 Lys Gly Lys Val Glu Tyr Leu Leu Lys Trp Lys Gly Phe Ser Asp Glu  
 35 40 45  
 Asp Asn Thr Trp Glu Pro Glu Glu Asn Leu Asp Cys Pro Asp Leu Ile  
 50 55 60  
 Ala Glu Phe Leu Gln Ser Gln Lys Thr Ala His Glu Thr Asp Lys Ser  
 65 70 75 80  
 Glu Gly Gly Lys Arg Lys Ala Asp Ser Asp Ser Glu Asp Lys Gly Glu  
 85 90 95  
 Glu Ser Lys Pro Lys Lys Lys Lys Glu Glu Ser Glu Lys Pro Arg Gly  
 100 105 110  
 Phe Ala Arg Gly Leu Glu Pro Glu Arg Ile Ile Gly Ala Thr Asp Ser  
 115 120 125  
 Ser Gly Glu Leu Met Phe Leu Met Lys Trp Lys Asn Ser Asp Glu Ala  
 130 135 140  
 Asp Leu Val Pro Ala Lys Glu Ala Asn Val Lys Cys Pro Gln Val Val  
 145 150 155 160  
 Ile Ser Phe Tyr Glu Glu Arg Leu Thr Trp His Ser Tyr Pro Ser Glu  
 165 170 175  
 Asp Asp Asp Lys Lys Asp Asp Lys Asn  
 180 185

<210> 34  
 <211> 558  
 <212> DNA  
 <213> Homo sapiens

40 <400> 34

45

50

55

EP 2 319 924 B1

	atggggaaaa aacaaaacaa gaagaaagtg gaggaggtgc tagaagagga ggaagaggaa	60
	tatgtggtgg aaaaagttct cgaccgtcga gtggtaaagg gcaaagtgga gtacctccta	120
5	aagtggaagg gattctcaga tgaggacaac acatgggagc cagaagagaa cctggattgc	180
	cccgacctca ttgctgagtt tctgcagtca cagaaaacag cacatgagac agataaatca	240
	gagggaggca agcgcaaagc tgattctgat tctgaagata agggagagga gagcaaacca	300
10	aagaagaaga aagaagagtc agaaaagcca cgaggctttg ctcgaggttt ggagccggag	360
	cggattattg gagctacaga ctccagtgga gagctcatgt tcctgatgaa atggaaaaac	420
	tctgatgagg ctgacctggt ccctgccaaag gaagccaatg tcaagtgcc acaggttgtc	480
15	atataccttct atgaggaaag gctgacgtgg cattcctacc cctcggagga tgatgacaaa	540
	aaagatgaca agaactaa	558

20 <210> 35  
 <211> 257  
 <212> PRT  
 <213> Homo sapiens

25 <400> 35

30

35

40

45

50

55

EP 2 319 924 B1

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

Asn

<210> 36  
 <211> 774  
 <212> DNA  
 <213> Homo sapiens

<400> 36

atggtggcag aaaaagagac cctgagctta aacaaatgcc cagacaagat gccgaagagg 60

55

	accaagctgc tggcacaaca gccgctcccg gtgcaccagc ctcaactctct ggtttctgag	120
	ggtttcacag tcaaagccat gatgaaaaac tcagtcgtga gaggccctcc agctgcaggg	180
5	gcattttaaag aaagaccaac caagcccaca gcatttcgaa aattctatga gcgaggtgac	240
	ttcccaattg cccttgagca tgattcgaaa ggaaacaaaa tcgcctggaa ggtagaaatt	300
	gagaagctgg attaccatca ttatctgcct ctgttttttg atgggctttg tgaaatgaca	360
10	tttccctatg agttttttgc tcggcaagga atccacgaca tgctggaaca cggtgggaac	420
	aagatcctac ctgtccttcc acagctcatt atcccagataa aaaatgcctt gaacctccga	480
	aaccgacagg tcatctgtgt cactctcaag gtcctccagc atctggttgt gtcagctgag	540
15	atggtgggca agaccttggg gccttattac cgtcaaatacc tccctgtcct gaacatcttt	600
	aagaatatga atgtgaactc cggagacggc attgactaca gccagcagaa gagggagaac	660
	attggggact tgatccagga gacactggag gccttcgagc gctacggagg agaaaatgcc	720
20	tttatcaaca ttaagtacgt ggtccaacc tacgagtctt gcttgctaaa ctaa	774

### Claims

- 25 1. Use of a polypeptide having an amino acid sequence set forth in SEQ ID NO 1 of the Sequence Listing, or a partial amino acid sequence thereof consisting of four or more amino acids, as a polypeptide marker for diagnosing arteriosclerosis.
- 30 2. Use of a polynucleotide represented by a nucleotide sequence that encodes the amino acid sequence according to claim 1, or a partial amino acid sequence thereof consisting of four or more amino acids, as a polynucleotide marker for diagnosing arteriosclerosis.
- 35 3. Use of a polynucleotide having a nucleotide sequence set forth in SEQ ID NO 2 of the Sequence Listing, or a partial nucleotide sequence thereof consisting of twelve or more nucleotides, as a gene expression marker for diagnosing arteriosclerosis.
- 40 4. Use of an antibody specifically bindable to the polypeptide according to claim 1 for diagnosing arteriosclerosis.
5. Use of a probe for diagnosing arteriosclerosis, which comprises all or a part of DNA that is hybridizable with the nucleotide sequence according to either one of claim 2 and claim 3 under a stringent condition.
- 45 6. The use of a probe for diagnosing arteriosclerosis according to claim 5, which comprises all or a part of antisense DNA for the polynucleotide according to claim 3.
7. Use of a DNA microarray or a DNA chip for diagnosing arteriosclerosis, wherein the probe for detecting an arteriosclerosis marker expression gene according to claim 5 and/or the probe for detecting an arteriosclerosis marker expression gene according to claim 6 is/are immobilized on a base plate.
- 50 8. A method for detecting arteriosclerosis, wherein the antibody according to claim 4 is used to detect the expression of the arteriosclerosis marker polypeptide of SEQ ID NO 1 that is specifically bindable to the antibody, in a specimen sample.
- 55 9. A method for detecting arteriosclerosis, wherein the polypeptide marker of SEQ ID NO 1 used for diagnosing arteriosclerosis according to claim 1 is used to detect the expression of an arteriosclerosis marker antibody that is specifically bindable to the polypeptide marker for diagnosing arteriosclerosis, in a specimen blood.
10. A method for detecting arteriosclerosis, wherein the probe for detecting the arteriosclerosis polynucleotide marker according to either one of claim 5 and claim 6 is used to detect the expression of an arteriosclerosis marker poly-

nucleotide that is hybridizable with the probe for detecting the expression of the arteriosclerosis marker gene, in a specimen cell.

- 5 11. A method for detecting arteriosclerosis, wherein a primer is constructed based on a nucleotide sequence set forth in SEQ ID NO 2 of the Sequence Listing, and PCR is conducted with use of the primer to detect the expression of the arteriosclerosis marker gene encoding the polypeptide of SEQ ID NO 1.
- 10 12. Use of a kit for diagnosing arteriosclerosis, including at least one item selected from the group consisting of the probe for detecting the expression of the arteriosclerosis marker gene according to either one of claim 5 and claim 6, the DNA microarray or the DNA chip for detecting the expression of the arteriosclerosis marker gene according to claim 7, and the antibody according to claim 4.
- 15 13. Use of a kit for diagnosing arteriosclerosis, including a polypeptide marker for diagnosing arteriosclerosis which comprises a polypeptide having an amino acid sequence set forth in SEQ ID NO 1 of the Sequence Listing, or a partial amino acid sequence thereof consisting of four or more amino acids.

### Patentansprüche

- 20 1. Gebrauch eines Polypeptids mit einer in SEQ ID NO 1 des Sequenzprotokolls angegebenen Aminosäuresequenz oder einer teilweisen Aminosäuresequenz davon, bestehend aus vier oder mehr Aminosäuren, als ein Polypeptidmarker zum Diagnostizieren von Arteriosklerose.
- 25 2. Gebrauch eines Polynukleotids, repräsentiert durch eine Nukleotidsequenz, die für die Aminosäuresequenz nach Anspruch 1 oder für eine teilweise Aminosäuresequenz davon, bestehend aus vier oder mehr Aminosäuren, codiert, als ein Polynukleotidmarker zum Diagnostizieren von Arteriosklerose.
- 30 3. Gebrauch eines Polynukleotids mit einer in SEQ ID NO 2 des Sequenzprotokolls angegebenen Nukleotidsequenz oder einer teilweisen Nukleotidsequenz davon, bestehend aus zwölf oder mehr Nukleotiden, als ein Genexpressionsmarker zum Diagnostizieren von Arteriosklerose.
- 35 4. Gebrauch eines Antikörpers, der spezifisch an das Polypeptid nach Anspruch 1 binden kann, zum Diagnostizieren von Arteriosklerose.
- 40 5. Gebrauch einer Sonde zum Diagnostizieren von Arteriosklerose, welche die gesamte DNA, die unter einer stringenten Bedingung mit der Nukleotidsequenz nach Anspruch 2 oder 3 hybridisiert werden kann, oder einen Teil davon umfasst.
- 45 6. Gebrauch einer Sonde zum Diagnostizieren von Arteriosklerose nach Anspruch 5, umfassend die gesamte Antisense-DNA für das Polynukleotid nach Anspruch 3 oder einen Teil davon.
- 50 7. Gebrauch eines DNA-Microarrays oder eines DNA-Chips zum Diagnostizieren von Arteriosklerose, wobei die Sonde zum Erkennen eines Arteriosklerosemarker-Expressionsgens nach Anspruch 5 und/oder die Sonde zum Erkennen eines Arteriosklerosemarker-Expressionsgens nach Anspruch 6 auf einer Grundplatte befestigt ist/sind.
- 55 8. Verfahren zum Erkennen von Arteriosklerose, wobei der Antikörper nach Anspruch 4 verwendet wird, um die Expressierung des Arteriosklerosemarker-Polypeptids nach SEQ ID NO 1, das spezifisch an den Antikörper binden kann, in einer Probe zu erkennen.
9. Verfahren zum Erkennen von Arteriosklerose, wobei der Polypeptid marker von SEQ ID NO 1 zum Diagnostizieren von Arteriosklerose nach Anspruch 1 eingesetzt wird, um die Expressierung eines Arteriosklerosemarker-Antikörpers, der spezifisch an den Polypeptidmarker zum Diagnostizieren von Arteriosklerose bindet, in einem Probenblut zu erkennen.
10. Verfahren zum Erkennen von Arteriosklerose, wobei die Sonde zum Erkennen des Arteriosklerose-Polynukleotidmarkers nach Anspruch 5 oder 6 eingesetzt wird, um die Expressierung eines Arteriosklerosemarker-Polynukleotids, das zum Erkennen der Expressierung des Arteriosklerosemarkergens mit der Sonde hybridisiert werden kann, in einer Probenzelle zu erkennen.

## EP 2 319 924 B1

11. Verfahren zum Erkennen von Arteriosklerose, wobei ein Primer auf der Grundlage einer in SEQ ID NO 2 des Sequenzprotokolls angegebenen Nukleotidsequenz erzeugt wird und PCR unter Verwendung des Primers durchgeführt wird, um die Exprimierung des Arteriosklerosemarkergens zu erkennen, das für das Polypeptid nach SEQ ID NO 1 codiert.

5

12. Gebrauch eines Kits zum Diagnostizieren von Arteriosklerose, wenigstens ein Objekt enthaltend, ausgewählt aus der Gruppe bestehend aus der Sonde zum Erkennen der Exprimierung des Arteriosklerosemarkergens nach Anspruch 5 oder 6, dem DNA-Microarray oder dem DNA-Chip zum Erkennen der Exprimierung des Arteriosklerosemarkergens nach Anspruch 7 und dem Antikörper nach Anspruch 4.

10

13. Gebrauch eines Kits zum Diagnostizieren von Arteriosklerose, einschließlich eines Polypeptidmarkers zum Diagnostizieren von Arteriosklerose, welcher Folgendes umfasst:

15

ein Polypeptid mit einer in SEQ ID NO 1 des Sequenzprotokolls angegebenen Aminosäuresequenz oder einer teilweisen Aminosäuresequenz davon, bestehend aus vier oder mehr Aminosäuren.

### Revendications

20 1. Utilisation d'un polypeptide ayant une séquence d'acides aminés décrite dans SEQ ID n° 1 du listage de séquences, ou une séquence d'acides aminés partielle de celle-ci constituée de quatre acides aminés ou plus, en tant que marqueur polypeptidique pour le diagnostic de l'artériosclérose.

25 2. Utilisation d'un polynucléotide représenté par une séquence nucléotidique qui code pour la séquence d'acides aminés selon la revendication 1, ou une séquence d'acides aminés partielle de celle-ci constituée de quatre acides aminés ou plus, en tant que marqueur polynucléotidique pour le diagnostic de l'artériosclérose.

30 3. Utilisation d'un polynucléotide ayant une séquence nucléotidique décrite dans SEQ ID n° 2 du listage de séquences, ou une séquence nucléotidique partielle de celle-ci constituée de douze nucléotides ou plus, en tant que marqueur d'expression génétique pour le diagnostic de l'artériosclérose.

4. Utilisation d'un anticorps pouvant être spécifiquement lié au polypeptide selon la revendication 1 pour le diagnostic de l'artériosclérose.

35 5. Utilisation d'une sonde pour le diagnostic de l'artériosclérose, qui comprend la totalité ou une partie de l'ADN qui peut être hybridé avec la séquence nucléotidique selon l'une quelconque des revendications 2 ou 3 sous une condition stringente.

40 6. Utilisation d'une sonde pour le diagnostic de l'artériosclérose selon la revendication 5, qui comprend la totalité ou une partie de l'ADN antisens pour le polynucléotide selon la revendication 3.

45 7. Utilisation d'un micro-réseau à ADN ou d'une puce à ADN pour le diagnostic de l'artériosclérose, dans laquelle la sonde permettant de détecter un marqueur d'expression génétique de l'artériosclérose selon la revendication 5 et/ou la sonde permettant de détecter un marqueur d'expression génétique de l'artériosclérose selon la revendication 6 est/sont immobilisée(s) sur une plaque de base.

50 8. Procédé de détection de l'artériosclérose, dans lequel l'anticorps selon la revendication 4 est utilisé pour détecter l'expression du polypeptide marqueur de l'artériosclérose de SEQ ID n° 1 qui peut être spécifiquement lié à l'anticorps, dans un échantillon d'essai.

55 9. Procédé de détection de l'artériosclérose, dans lequel le marqueur polypeptidique de SEQ ID n° 1 utilisé pour le diagnostic de l'artériosclérose selon la revendication 1 est utilisé pour détecter l'expression d'un anticorps marqueur de l'artériosclérose qui peut être spécifiquement lié au marqueur polypeptidique pour le diagnostic de l'artériosclérose, dans un échantillon de sang.

10. Procédé de détection de l'artériosclérose, dans lequel la sonde permettant de détecter le marqueur polynucléotidique de l'artériosclérose selon l'une quelconque des revendications 5 ou 6 est utilisée pour détecter l'expression d'un polynucléotide marqueur de l'artériosclérose qui peut être hybridé avec la sonde permettant de détecter l'expression

## EP 2 319 924 B1

du gène marqueur de l'artériosclérose, dans une cellule d'essai.

- 5
11. Procédé de détection de l'artéri osclérose, dans lequel une amorce est construite d'après l'ensemble de séquences nucléotidiques décrit dans SEQ ID n° 2 du listage de séquences, et la PCR est effectuée en utilisant l'amorce pour détecter l'expression du gène marqueur de l'artériosclérose codant pour le polypeptide de SEQ ID n° 1.
- 10
12. Utilisation d'un kit de diagnostic de l'artériosclérose comprenant au moins un élément choisi dans le groupe constitué par la sonde permettant de détecter l'expression du gène marqueur de l'artériosclérose selon l'une quelconque des revendications 5 ou 6, le micro-réseau à ADN ou la puce à ADN permettant de détecter l'expression du gène marqueur de l'artériosclérose selon la revendication 7 et l'anticorps selon la revendication 4.
- 15
13. Utilisation d'un kit de diagnostic de l'artériosclérose comprenant un marqueur polypeptidique pour le diagnostic de l'artériosclérose qui comprend un polypeptide ayant un ensemble de séquences d'acides aminés décrit dans SEQ ID n° 1 du listage de séquences, ou une séquence d'acides aminés partielle de celle-ci constituée de quatre acides aminés ou plus.

20

25

30

35

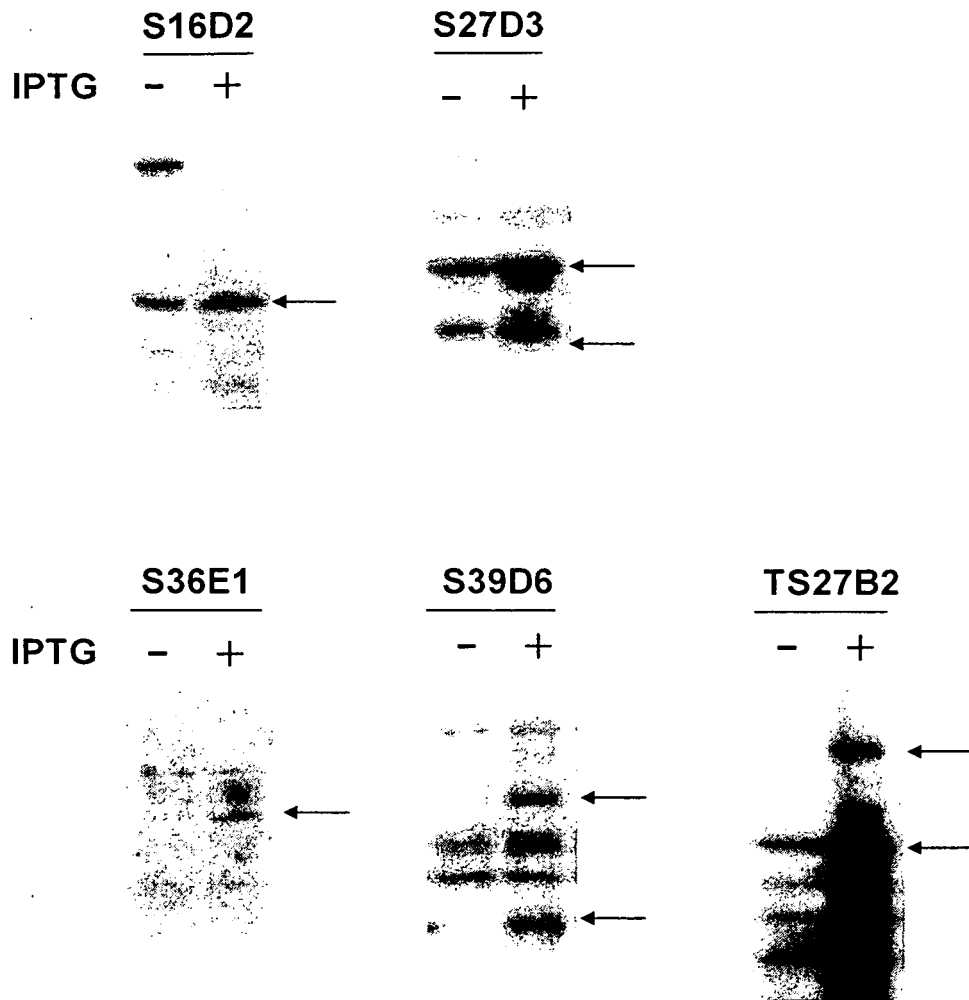
40

45

50

55

FIG. 1



**REFERENCES CITED IN THE DESCRIPTION**

*This list of references cited by the applicant is for the reader's convenience only. It does not form part of the European patent document. Even though great care has been taken in compiling the references, errors or omissions cannot be excluded and the EPO disclaims all liability in this regard.*

**Patent documents cited in the description**

- JP 2008209210 A [0002] [0075]
- WO 2006048291 A [0012]
- US 2007072175 A [0013]
- JP 2002048790 A [0013]
- JP 2002017353 A [0013]
- JP 2000184885 A [0013]
- JP H10142226 A [0013]
- JP H9203736 A [0013]
- JP 2002181820 A [0013]
- JP 2002142781 A [0013]
- JP 2002055106 A [0013]
- JP H11346782 A [0013]
- JP H8160042 A [0013]
- JP 2003310281 A [0013]
- JP 2003304873 A [0013]
- JP 2003189872 A [0013]
- JP 2002308900 A [0013]
- JP 2002277461 A [0013]
- JP 2002131313 A [0013]
- JP 2002238589 A [0013]
- JP 2001249128 A [0013]
- JP 2000333674 A [0013]
- JP 2000206113 A [0013]
- JP 2005168498 A [0013]
- EP 09806761 A [0075]

**Non-patent literature cited in the description**

- *N. Eng. J. Med.*, 1992, vol. 326, 242-250 [0013]
- *Journal of Biological Chemistry*, 1997, vol. 272, 556 [0013]
- **ST JOHN, T.** *Science*, 1986, vol. 231, 845-850 [0065]

专利名称(译)	用于诊断动脉硬化的多肽标记物，使用该制造者等检测动脉硬化的方法，以及用于诊断动脉硬化的试剂盒		
公开(公告)号	<a href="#">EP2319924B1</a>	公开(公告)日	2016-03-09
申请号	EP2009806761	申请日	2009-08-14
[标]申请(专利权)人(译)	藤仓化成株式会社		
申请(专利权)人(译)	FUJIKURA KASEI CO., LTD. 国立大学法人千叶大学		
当前申请(专利权)人(译)	FUJIKURA KASEI CO., LTD. 国立大学法人千叶大学		
[标]发明人	NAKAMURA RIKA KURODA HIDEYUKI TOMIYOSHI GO HIWASA TAKAKI TAKIGUCHI MASAKI SAEKI NAOKATSU MACHIDA TOSHIO		
发明人	NAKAMURA RIKA KURODA HIDEYUKI TOMIYOSHI GO HIWASA TAKAKI TAKIGUCHI MASAKI SAEKI NAOKATSU MACHIDA TOSHIO		
IPC分类号	G01N33/68 C07K14/47 C12N15/09 C07K16/18 C12Q1/68 G01N33/53 G01N37/00		
CPC分类号	C07K14/47 C12Q1/6883 C12Q2600/158 G01N33/6893 G01N2800/323 G01N33/5302		
代理机构(译)	POTTER CLARKSON LLP		
优先权	2008209210 2008-08-15 JP		
其他公开文献	EP2319924A1 EP2319924A4		
外部链接	<a href="#">Espacenet</a>		

#### 摘要(译)

公开了用于诊断动脉硬化的多肽标记物;用于诊断动脉硬化的基因标记物;抗体;用于检测动脉硬化标志物基因的探针;用于检测动脉硬化标记基因的DNA微阵列或DNA芯片;一种检测动脉硬化的方法;和用于诊断动脉硬化的试剂盒;可以检测到动脉硬化病变，并且准确性大大提高。具体公开了：用于诊断动脉硬化的多肽标记物，其包含具有SEQ ID NO：1,3,5,7,9,11,13,15,17,19中任一所示氨基酸序列的多肽，序列表中的21,23,25,27,29,31,33和35，或其部分氨基酸序列;编码氨基酸序列的基因;用于检测基因的探针;DNA微阵列或包含该探针的DNA芯片;可与多肽结合的抗体作为抗原;包括上述任何一项的试剂盒;以及通过使用上述任一项检测动脉硬化的方法。

Met Glu Ser Phe Leu Leu Asp Asp Ile Ser Ser Val Ile Gln Asn Lys  
 1 5 10 15  
 Gly Ile Glu Arg Ile Ile Ser Pro Met Ile Val Gln Leu Cys His Leu  
 20 25 30  
 Leu Ile Ser Met Glu Arg Lys Glu Val Glu Asn Glu Phe Ala Ser  
 35 40 45  
 Leu Glu Lys Met Ala Glu Glu Leu Ala Lys Ala Cys Glu Asp Phe Val  
 50 55 60  
 Gln Val Val Lys Ser Ser Gly Asn Thr Glu Ala Val Ser Val Ser Pro  
 65 70 75 80  
 Val Ile Val Asn Ala Ala Leu Val Phe Gln Lys Ala Val Val Val Trp  
 85 90 95  
 Val Phe Lys Ser Glu Lys His Gly Ile Val Asp Glu Val Leu Trp Gln  
 100 105 110  
 Ile Cys Lys Ala Arg Val Asp Ile Ser Phe Ser Trp Arg Leu Thr Arg  
 115 120 125  
 Leu Thr Cys Val Gly Thr Val Gly Val Thr Leu Ala Gly Lys Gln Gly  
 130 135 140  
 Gly Leu Asp Ile Val Ser Pro Gly Ser Val Ser Cys His Ser His Pro  
 145 150 155 160  
 Cys Ala Gln Ser Ser Gln Ala Pro Thr Met Ala Phe Ser Gly Arg Ala  
 165 170 175  
 Arg Pro Cys Ile Ile Pro Glu Asn Glu Glu Ile Pro Arg Ala Ala Leu  
 180 185 190  
 Asn Thr Val His Glu Ala Asn Gly Thr Glu Asp Glu Arg Ala Val Ser  
 195 200 205  
 Lys Leu Gln Arg Arg His Ser Asp Val Lys Val Tyr Lys Glu Phe Cys  
 210 215 220  
 Asp Phe Tyr Ala Lys Phe Asn Met Ala Asn Ala Leu Ala Ser Ala Thr