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(54) **PROTEINS HAVING EFFECTS OF CONTROLLING CELL MIGRATION AND CELL DEATH**

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(51) **Int. Cl.**
C12P 21/06 (2006.01)

(52) **U.S. Cl.** **435/69.1**; 435/6; 435/320.1; 435/325; 435/252; 435/7.1; 536/23.1

(58) **Field of Classification Search** 435/69.1, 435/7.1, 320.1, 325; 530/350
See application file for complete search history.

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(57) **ABSTRACT**

The present invention relates to proteins which have a role in controlling neuronal cell migration and cell death as well as to the DNA which encode those proteins. It is an object of the present invention to provide control of cell migration and/or cell death by providing a method for screening for promoters or inhibitors of proteins which affect the control of cell migration and/or cell death of neurons by interacting with an actin-binding protein, Filamin 1, through promoting the degradation of Filamin 1 or the DNA encoding Filamin 1. The cDNAs of S-FILIP, L-FILIP and h-FILIP cDNAs, which interact with Filamin 1, thereby negatively affecting cell migration and cell death by promoting the degradation of Filamin 1, were isolated and the full nucleotide and amino acid sequences thereof were determined.

3 Claims, 4 Drawing Sheets
(4 of 4 Drawing Sheet(s) Filed in Color)

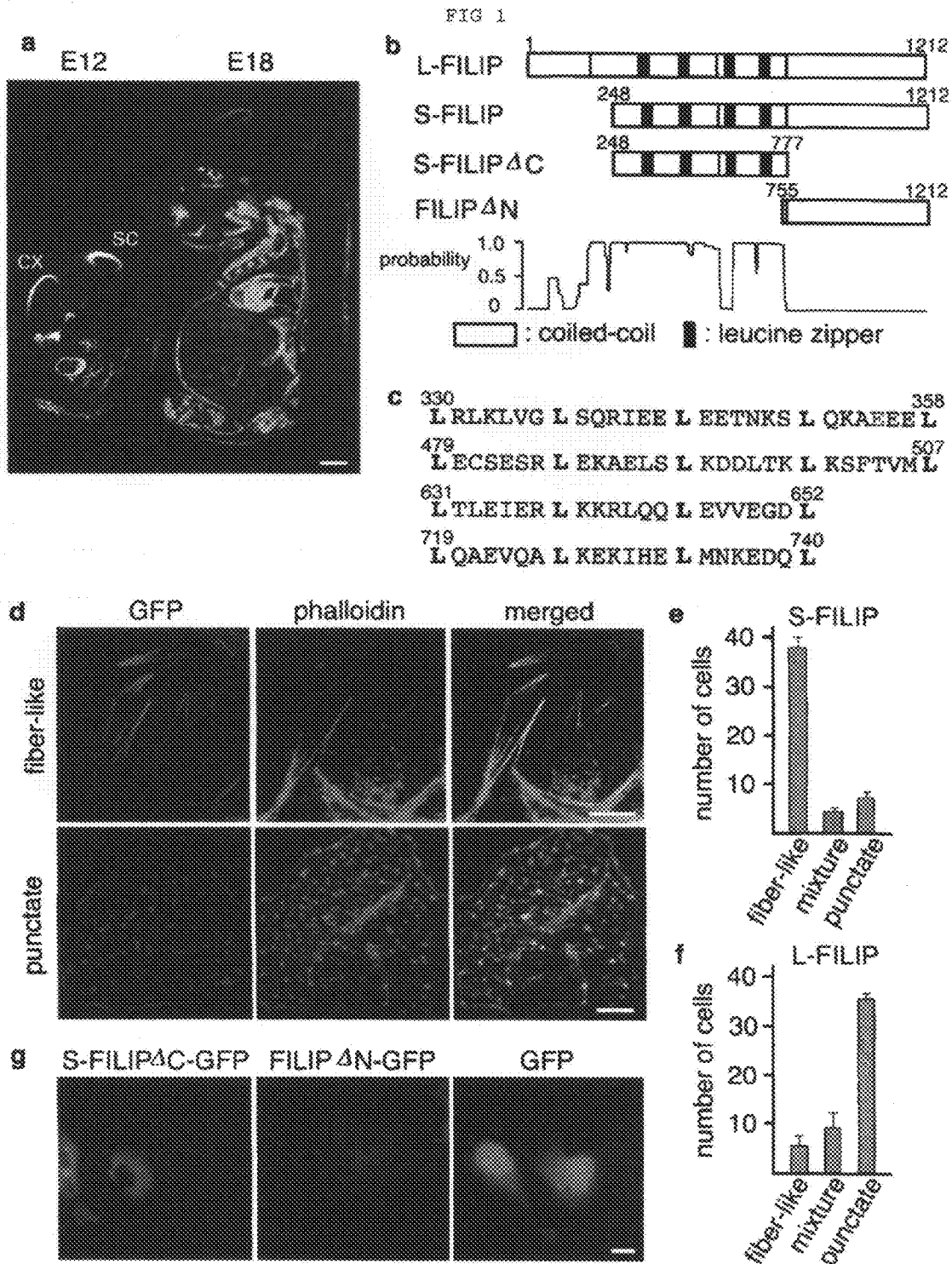


FIG 2

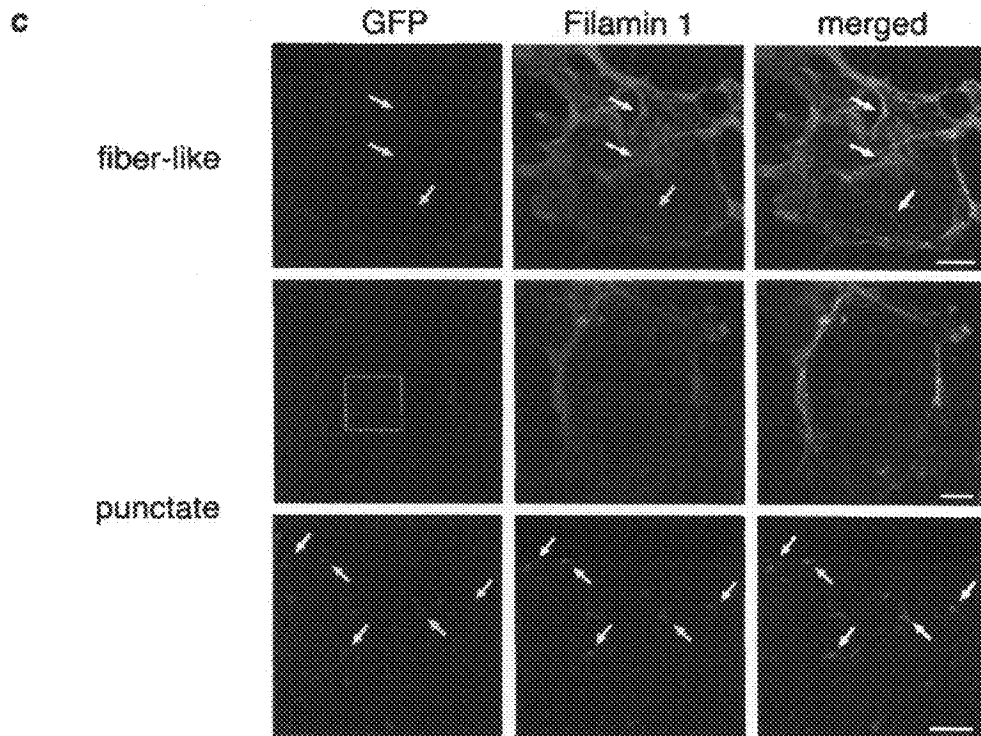
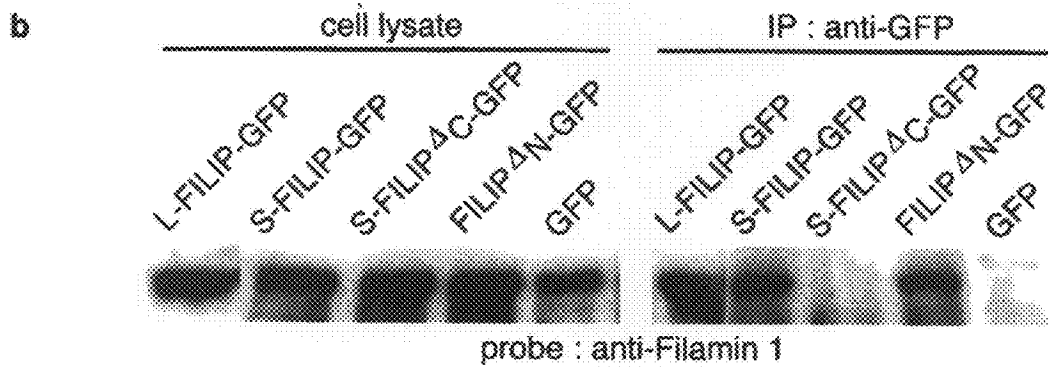
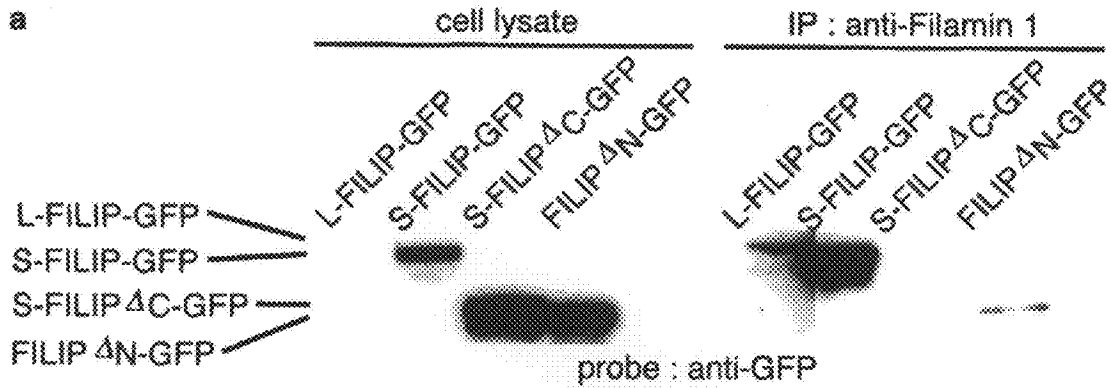


FIG 3

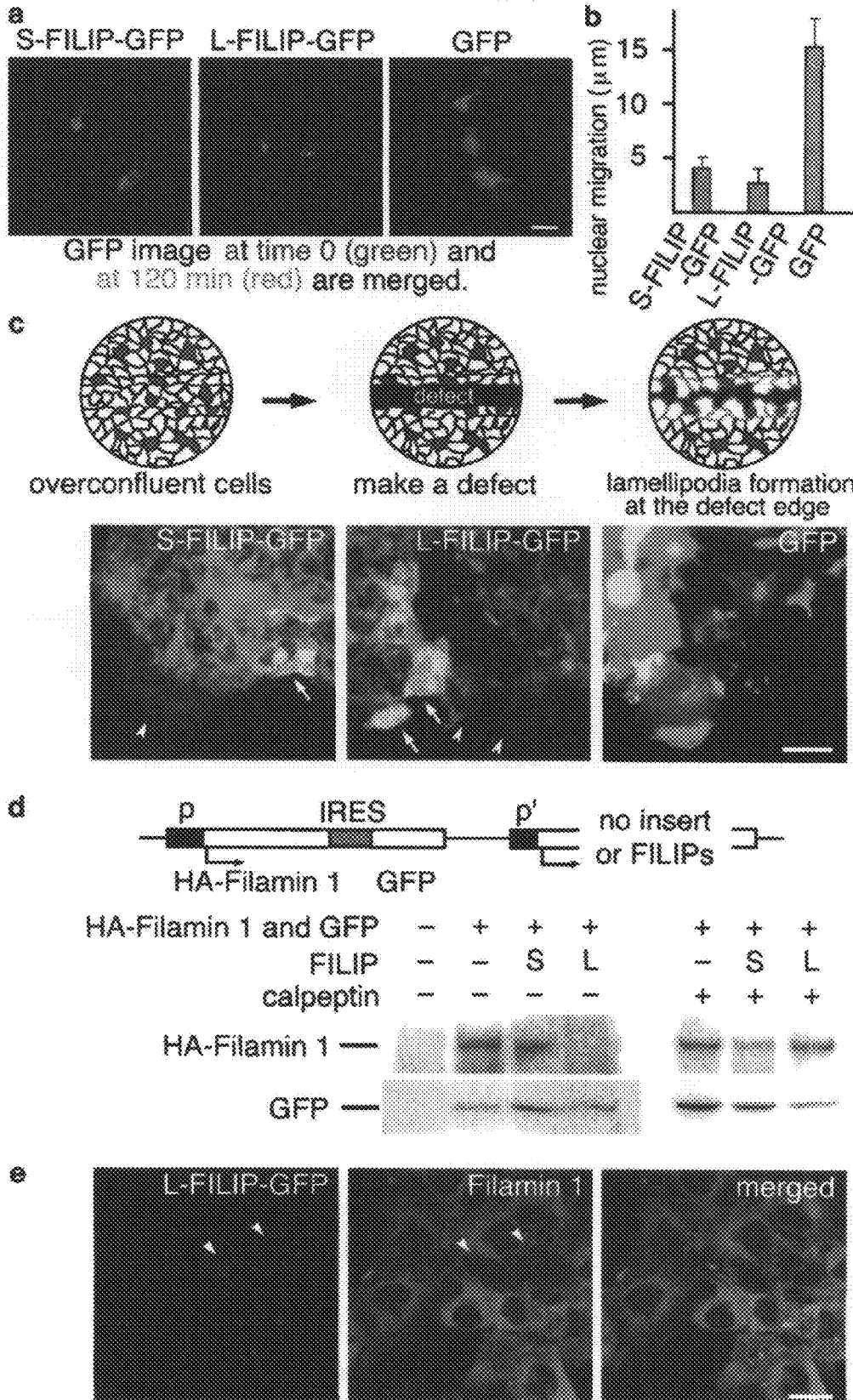
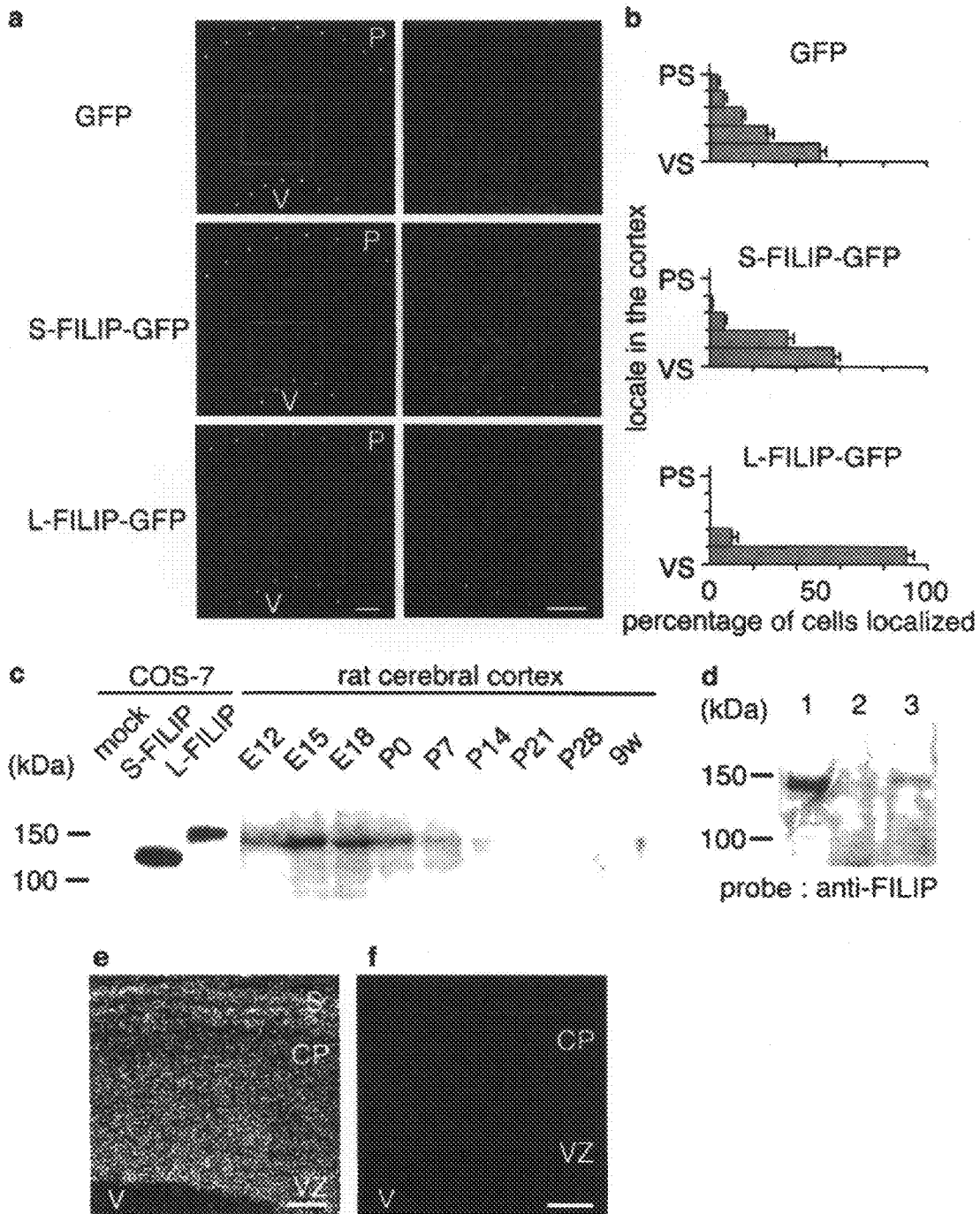


FIG 4



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**PROTEINS HAVING EFFECTS OF
CONTROLLING CELL MIGRATION AND
CELL DEATH**

CROSS REFERENCE TO RELATED
APPLICATIONS

This application is a Continuation-in-part of International Patent Application No. PCT/JP02/07676 filed Jul. 29, 2002 and published on Mar. 6, 2003 as WO 03/018804, claiming priority to Japanese application 2001-256910 filed Aug. 27, 2001. Each of the above applications, and each document cited in this text and in each of the above applications ("application cited documents") and each document cited or referenced in each of the application cited documents, and any manufacturer's specifications or instructions for any products mentioned in this text and in any document incorporated into this text, are hereby incorporated herein by reference; and, technology in each of the documents incorporated herein by reference can be used in the practice of this invention.

It is noted that in this disclosure, terms such as "comprises", "comprising", "comprising", "contains", "containing" and the like can have the meaning attributed to them in U.S. Patent law; e.g., they can mean "includes", "included", "including" and the like. Terms such as "consisting essentially of" and "consists essentially of" have the meaning attributed to them in U.S. Patent law, e.g., they allow for the inclusion of additional ingredients or steps that do not detract from the novel or basic characteristics of the invention, i.e., they exclude additional unrecited ingredients or steps that detract from novel or basic characteristics of the invention, and they exclude ingredients or steps of the prior art, such as documents in the art that are cited herein or are incorporated by reference herein, especially as it is a goal of this document to define embodiments that are patentable, e.g., novel, non-obvious, inventive, over the prior art, e.g., over documents cited herein or incorporated by reference herein. And, the terms "consists of" and "consisting of" have the meaning ascribed to them in U.S. Patent law; namely, that these terms are closed ended.

FIELD OF THE INVENTION

The present invention relates to a protein that has effects of controlling cell migration and cell death of neurons and the like, a DNA that encodes the protein, control of cell migration and/or cell death, and a method for screening a promoter or an inhibitor of the effects of controlling cell migration and/or cell death, by using the protein and the like.

BACKGROUND OF THE INVENTION

More than one hundred billion neurons exist in human brain to form complex neural circuits. Only prescribed numbers of them are formed in the adequate positions as development progresses. These neurons have very complicated shapes which never be seen in other somatic cells and extend two kinds of processes dendrite and axon from a cell body which is protoplasm including a nucleus. A dendrite comprises numerous thorn structures called spine and forms postsynaptic region that has a function for receiving information from other cells. It is known that this neuron specific shape is determined by a neuron specific actin-binding protein.

On the other hand, brain is an important organ that controls not only the action at unconsciousness level but also what is called higher-order function such as emotion, memory, learn-

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ing, and creation. However, it has not revealed yet how the regions in brain are determined and how the differentiation of brains that is specific in each region are occurred. Neuronal migration is essential for construction of brain tissue, for example in cerebral cortex, a layer structure is formed by division of neural stem cells (radial glial cell) at ventricular zone and radial migration thereof with the help of the radial processes inherited in division. Although it has been indicated that molecules such as PS-NCAM or Slit are involved in these migrations of neurons, the relation has been hardly revealed yet.

As aforementioned, radial migration of postmitotic neurons is essential for neocortical development (J. Comp. Neurol. 145, 61-83, 1972, Nat. Neurosci. 4, 143-150, 2001, Nature 409, 714-720, 2001). Neurons generated in the ventricular zone have to make at least two important decisions in order to reach their destination correctly: when to start and where to stop migration. The stop of migration is thought to be regulated by Reelin (Nature 374, 719-723, 1995, Nature 389, 730-733, 1997, Nature 389, 733-737, 1997, Neuron 24, 471-479, 1999, Neuron 24, 481-489, 1999, Cell 99, 635-647, 1999, Cell 97, 689-701, 1999, Neuron 27, 33-44, 2000), however, the molecule relating to the start of migration has been poorly understood. An exception has been reported that disruption of an actin-binding protein Filamin 1 results in a human neuronal migration disorder, periventricular nodular heterotopia, in which many neurons remain lining the ventricular surface (Neuron 16, 77-87, 1996, Neuron 21, 1315-1325, 1998).

The present invention relates to a protein of the effects of controlling cell migration and cell death of such as neurons and a DNA encoding the protein, particularly, an object of the present invention is to provide a method of controlling cell migration and/or cell death and a method of screening a promoter or an inhibitor of the effects of controlling cell migration and/or cell death with the use of proteins controlling the cell motility and cell death of neurons and the DNA encoding the proteins by interacting an actin-binding protein and promoting the degradation of the actin-binding protein.

Analysis of the cerebral cortex having disorder in layer structure is thought to provide an important clue for clarification of molecular mechanism relating to neuronal migration during the development of cerebral cortex, for instance the clarification of molecular mechanism which arrests cell migration is progressing rapidly by the study of reeler mouse. Likewise, periventricular nodular heterotopia, in which immovable neurons remain at neuroepithelial layer is thought to be another clue for solving the mechanism for starting/maintaining the migration of neurons, and abnormality of an actin-binding protein Filamin 1 has been revealed to be a cause. (Though "Filamin 1" is sometimes called "Filamin A", it is indicated "Filamin 1" in the present invention.)

Meanwhile, the inventors reported about a rat nascent stage cerebral cortex-derived cytoskeleton-associated novel protein FILIP (Filamin-interacting protein), it was predicted that the FILIP (S-FILIP) molecule comprised 965 amino acid residues in total, and revealed that it comprised coiled-coil structure including leucine zipper motifs at N-terminal-half of the molecule. Moreover, yeast two-hybrid screening or immunoprecipitation analyses revealed that the C-terminal-half of FILIP molecule is combined with an actin-binding protein, Filamin 1. Filamin 1 is an essential molecule for cell migration during cerebral cortex formation period, and it is known that mutation of Filamin 1 gene causes periventricular nodular heterotopia characterized in migration disorder of cerebral cortical neuron. This led to the possibility that FILIP (S-FILIP) controls cell migration by associating with Filamin

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1 to control those function at developing cerebral cortex. To verify this hypothesis, FILIP was expressed in a cultured cell and the aspect of cell migration was observed with time following. In consequence, migration of FILIP-expressing cell was controlled compared to the control, FILIP (S-FILIP) was indicated as a negative control factor of cell migration.

Subsequently, as the result of a keen study by the present inventors, FILIPs (L-FILIP and S-FILIP) were identified, FILIPs were found that they had functions for controlling cell motility and cell death, and the present invention was completed. That is, FILIP molecule (965 amino acid residues; S-FILIP; GenBank accession number D87257) (SEQ ID NOS: 3 and 4 in sequence listing) and L-FILIP which comprises 1212 residues, being constructed by adding 247 residues to molecule on the N terminal side (GenBank accession number AB055759) (SEQ ID NOS: 1 and 2 in the sequence listing).

Moreover, the result of a further study by the present inventor, human FILIP molecule (1213 amino acid residues; h-FILIP; -GenBank accession number AB086011) (SEQ ID NOS: 5 and 6 in the sequence listing), which is a human orthologue of mouse L-FILIP, was identified from human DNA library.

The present inventors found that when the novel protein L-FILIP or S-FILIP was introduced into cells, these molecules partially coexisted with filamentous-actin within the cells, and in the same cell, the degradation of filamentous-actin was yielded, it became smaller and shorter, the lamellipodia formation ratio from cell membrane was decreased, and the cell migration ratio was significantly decreased. They also found that L-FILIP which is a novel molecule had more significant Filamin 1 degradation promoting effect as well as it expressed more protein at cerebral cortex neuroepithelium than S-FILIP, from the result of investigation using cultured cells. These facts revealed that S-FILIP but L-FILIP mainly plays the role of controlling cell migration negatively by promoting degradation of Filamin 1 at cerebral cortex neuroepithelium.

When S-FILIP or L-FILIP and Filamin 1 were expressed in the same cell, the change in Filamin 1 was observed, and the degradation of Filamin 1 progressed by expression of FILIP was observed similarly as aforementioned. These changes were also significant at L-FILIP. When the expression of Filamin 1 at the brain of normal rats during their fatal stage was examined, expression of Filamin 1 gene was observed, while a number of cells were observed of which expression amount of Filamin 1 protein had largely decreased in cells localized in ventricular zone, where expression of FILIP gene being observed, and cell migration toward cortical plate having not yet occurred. On the other hand, reduction of the cell number was identified in the cultured cell to which novel molecule L-FILIP was introduced, and it was revealed that FILIPs were also related to the control of cell death. The present invention was completed based upon the knowledge mentioned above.

DESCRIPTION OF THE INVENTION

For the purposes of the present application, the term "DNA" is intended to include an isolated DNA molecule.

The present invention relates to: an isolated DNA that encodes a protein described in the following (a) or (b): (a) a protein that comprises an amino-acid sequence shown in SEQ ID NO: 2 in the sequence listing, and (b) a protein which comprises an amino-acid sequence wherein 1 or several amino acids are deleted, substituted or added in an amino-

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acid sequence shown in SEQ ID NO: 2 in the sequence listing, and has effects of controlling cell migration and cell death;

a DNA that comprises a base sequence shown in SEQ ID NO: 1 in the sequence listing, complementary sequence thereof, or a sequence comprising part or whole of these sequences

a DNA that hybridizes with the DNA consisting of the gene according to paragraph 0016 in stringent condition and encodes the proteins having the effects of controlling cell migration and cell death;

a DNA that encodes the protein described in the following (a) or (b): (a) a protein that comprises an amino-acid sequence shown in SEQ ID NO: 4 in sequence listing, and (b) a protein that comprises an amino-acid sequence wherein 1 or several amino acids are deleted, substituted, or added in an amino-acid sequence shown in SEQ ID NO: 4 in the sequence listing, and has effects of controlling cell migration and cell death;

a DNA that comprises the base sequence shown in SEQ ID NO: 3 in sequence listing, complementary sequence thereof, or a sequence comprising part or whole of these sequences;

and a DNA that hybridizes with the DNA consisting of the gene according to paragraph 0019 in stringent condition and encodes the protein having the effects of controlling cell migration and cell death.

The present invention also relates to: a DNA that encodes the protein described in the following (a) or (b): (a) a protein that comprises an amino-acid sequence shown in SEQ ID NO: 6 in the sequence listing, and (b) a protein that comprises an amino-acid sequence wherein 1 or several amino acids are deleted, substituted, or added in SEQ ID NO: 6 in the sequence listing, and has effects of controlling cell migration and cell death;

a DNA that comprises the base sequence shown in SEQ ID NO: 5 in the sequence listing, complementary sequence thereof, or a sequence comprising part or whole of these sequences;

a DNA that hybridizes with the DNA consisting the gene according to paragraph 0022 in stringent condition and encodes the protein having the effects of controlling cell migration and cell death;

a protein that comprises the amino-acid sequence shown in SEQ ID NO: 2 in the sequence listing;

a protein that comprises an amino-acid sequence wherein 1 or several amino acids are deleted, substituted, or added in the amino-acid sequence shown in SEQ ID NO: 2 in the sequence listing, and has effects of controlling cell migration and cell death;

a protein that comprises the amino-acid sequence shown in SEQ ID NO: 4 in the sequence listing;

a protein that comprises an amino-acid sequence wherein 1 or several amino acids are deleted, substituted, or added in the amino-acid sequence shown in SEQ ID NO: 4 in the sequence listing, and has effects of controlling cell migration and cell death;

a protein that comprises amino-acid sequence shown in SEQ ID NO: 6 in the sequence listing;

a protein that comprises an amino-acid sequence wherein 1 or several amino acids are deleted, substituted, or added in the amino-acid sequence shown in SEQ ID NO: 6 in the sequence listing, and has effects of controlling cell migration and cell death;

the protein according to paragraph 0025, 0027 or 0029, wherein control of cell migration and cell death is caused by the degradation of Filamin 1.

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The present invention further relates to: a peptide that comprises a part of the protein according to any one of paragraphs 0024 to 0029, and has effects of controlling cell migration and cell death;

the peptide according to paragraph 0031, wherein control of cell migration and cell death is caused by the degradation of Filamin 1;

a fusion protein or a fusion peptide wherein the protein according to any one of paragraphs 10 to 16, or the peptide according to paragraph 0031 or 0032 is bound to a marker protein and/or a peptide tag;

an antibody that specifically binds to the protein according to any one of paragraphs 0024 to 0029 or the peptide according to paragraph 0031 or 0032;

the antibody according to paragraph 0034, wherein the antibody is a monoclonal or a polyclonal antibody;

a recombinant protein or a recombinant peptide to which the antibody according to paragraph 20 or 0034 or 0035 specifically binds;

a host cell that comprises expression system which capable of expressing the protein according to any one of paragraphs 0024 to 0029 or the peptide according to paragraph 0031 or 0032;

a non-human animal whose a gene function encoding the protein according to any one of paragraphs 0024 to 0029 or the peptide according to paragraph 0031 or 0032 is deficient on its chromosome;

a non-human animal that over-expresses the protein according to any one of paragraphs 0024 to 0029 or the peptide according to paragraph 0031 or 0032;

and the non-human animal according to paragraph 0038 or 0039 which is a mouse or a rat.

The present invention still further relates to: a method for screening an inhibitor or a promoter of effects of controlling cell migration and/or cell death, wherein the protein according to any one of paragraphs 0024 to 0029, the peptide according to paragraph 0031 or 0032, or a cell membrane expressing the protein according to any one of paragraphs 0024 to 0029 or the peptide according to paragraph 0031 or 0032, and a test substance are used;

a method for screening an inhibitor or a promoter of effects of controlling cell migration and/or cell death, or an inhibitor or a promoter of the expression of the protein according to any one of paragraphs 0024 to 0029 or of the peptide according to paragraph 0031 or 0032, wherein a cell expressing the protein according to any one of paragraphs 0024 to 0029 or the peptide according to paragraph 0031 or 0032, and a test substance are used;

and a method for screening an inhibitor or a promoter of effects of controlling cell migration and/or cell death, or an inhibitor or a promoter of the expression of the protein to any one of paragraphs 0024 to 0029 or the peptide according to paragraph 0031 or 0032, wherein the non-human animal according to any one of paragraphs 0038 to 0040 and a test substance are used.

The present invention also relates to: the promoter of effects of controlling cell migration and cell death obtained by the method for screening according to any one of paragraphs 0041 to 0043;

the inhibitor of effects of controlling cell migration and cell death obtained by the method for screening according to any one of paragraphs 0041 to 0043;

a promoter of the expression of the protein according to any one of paragraphs 10 to 16 or of the peptide according to paragraph 0031 or 0032, being obtained by the method for screening according to any one of paragraphs 0041 to 0043;

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an inhibitor of the expression of the protein according to any one of paragraphs 0024 to 0029 or of the peptide according to paragraph 0031 or 0032, being obtained by the method for screening according to any one of paragraphs 0041 to 0043;

the inhibitor of metastasis of a cancer/a tumor, or a regulant of cell migration for transplantation treatment that includes the protein according to any one of paragraphs 0024 to 0029, the peptide according to paragraph 0031 or 0032, the recombinant protein or the recombinant peptide according to paragraph 0036, the antibody according to paragraph 0034 or 0035, the inhibitor of effects of controlling cell migration and cell death according to paragraph 0045, or the inhibitor of the expression according to paragraph 0047 as an active ingredient.

BRIEF DESCRIPTION OF THE DRAWINGS

The patent or patent application file contains at least one drawing executed in color. Copies of this patent or patent application publication with color drawing(s) will be provided by the Office upon request and payment of the necessary fee.

FIG. 1 is a photograph showing the localization of L-FILIP cDNA or S-FILIP cDNA of the present invention and the structure of FILIPs.

FIG. 2 is a photograph showing the results as to the interaction of L-FILIP or S-FILIP of the present invention with Filamin 1 that is an actin-binding protein.

FIG. 3 is a photograph showing the results of degradation of Filamin 1 by L-FILIP or S-FILIP of the present invention and reduction of cell motility thereby.

FIG. 4 is a photograph showing the results as to control of cell migration from ventricular zone by L-FILIP or S-FILIP in the formation of neocortex.

BEST MODE FOR CARRYING OUT THE INVENTION

As a protein according to the present invention, a protein that comprises an amino-acid in which one or several amino acids are deleted, substituted or added, and has effects of controlling cell migration and cell death in L-FILIP shown in SEQ ID NO: 2, S-FILIP shown in SEQ ID NO: 4, or an amino-acid sequence shown in SEQ ID NOS: 2 or 4 is exemplified. Aforementioned effects of controlling cell migration and cell death are effects of controlling cell motility and cell death. The protein can be prepared by known methods on the basis of its DNA sequence information etc., and its derivation is not limited specifically. A Peptide being an object of the present invention is not particularly limited as long as it is a peptide that consists of a part of a protein of the present invention and has effects of controlling cell migration and cell death. Aforementioned protein and peptide being an object of the present invention, and recombinant protein and peptide to which the antibody, which specifically binds to these proteins and peptides, specifically binds, may be generically called hereinafter as "the proteins/peptides of the present invention". Meanwhile, the proteins/peptides of the present invention can be prepared by known method on the basis of its DNA sequence information etc., and its derivation is not particularly limited to rat.

An antibody that "specifically binds" to a protein is one that binds to a protein, but which does not recognize and bind to other molecules in a sample, e.g., a biological sample, which naturally includes the protein.

As a DNA being an object of the present invention, any DNA can be used as long as it encodes the aforementioned protein of the present invention, for instance, a DNA encoding L-FILIP shown in SEQ ID NO: 2 in the sequence listing, a DNA encoding S-FILIP shown in SEQ ID NO: 4 in the sequence listing and a protein comprising an amino-acid in which one or several amino acids are deleted, substituted or added in SEQ ID NOS: 2 or 4 in the sequence listing, and having effects of controlling cell migration and cell death or an amino-acid sequence shown or a DNA comprising base sequence shown in SEQ ID NOS: 1 or 3 in the sequence listing, its complementary sequence, and part or whole of these sequences, are exemplified specifically. These can be prepared by known method on the basis of its DNA sequence information etc., for example, from gene library or cDNA library of human, mouse, rat, rabbit, and the like.

Also contemplated by the present invention are proteins or peptides which are at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% homologous to any of SEQ ID NOS: 2, 4 and 6.

A DNA that encodes the novel protein comprising effects of controlling cell migration and cell death can also be obtained by performing hybridization with the DNA comprising base sequence shown in SEQ ID NOS: 1 or 3 in the sequence listing, its complemented sequence, and part the whole of these sequences as a probe in stringent condition to various DNA libraries and isolating the DNA hybridizing with the probe. The DNA obtained in this manner is also within the scope of the present invention. As a hybridization condition for obtaining the DNA of the present invention, hybridization at 42° C. and rinse at 42° C. with buffer including 1×SSC and 0.1% SDS, more preferably hybridization at 65° C. and rinse at 65° C. with buffer including 0.1×SSC and 0.1% SDS is exemplified. Although, factors that influence on the stringency of hybridization include various factors other than above-mentioned temperature condition, those skills in the art can achieve stringency equivalent to the stringency of above-mentioned hybridization by combining various factors properly.

Also contemplated by the present invention are DNA sequences or fragments which are at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% homologous to any of SEQ ID NOS: 1, 3, or 5.

Sequence identity with respect to any of the sequences presented here can be determined by a simple “eyeball” comparison (i.e. a strict comparison) of any one or more of the sequences with another sequence to see if that other sequence has, for example, at least 70% sequence identity to the sequence(s).

Alternatively, relative sequence identity can also be determined by commercially available computer programs that can calculate % identity between two or more sequences using any suitable algorithm for determining identity, using for example default parameters. A typical example of such a computer program is CLUSTAL. Other computer program methods to determine identity and similarity between the two sequences include but are not limited to the GCG program package (Devereux et al 1984 Nucleic Acids Research 12: 387) and FASTA (Atschul et al 1990 J Molec Biol 403-410).

The sequence identity or percent homology for proteins and nucleic acids can also be calculated as $(N_{ref}-N_{dif})\times 100/N_{ref}$, wherein N_{dif} is the total number of non-identical residues in the two sequences when aligned and wherein N_{ref} is the number of residues in one of the sequences. Hence, the DNA sequence AGTCAGTC will have a sequence identity of 75% with the sequence AATCAATC ($N_{dif}=2$ and $N_{ref}=8$).

Percent homology may be calculated over contiguous sequences, i.e. one sequence is aligned with the other sequence and each amino acid in one sequence is directly compared with the corresponding amino acid in the other sequence, one residue at a time. This is called an “ungapped” alignment. Typically, such ungapped alignments are performed only over a relatively short number of residues.

Although this is a very simple and consistent method, it fails to take into consideration that, for example, in an otherwise identical pair of sequences, one insertion or deletion will cause the following amino acid residues to be put out of alignment, thus potentially resulting in a large reduction in % homology when a global alignment is performed. Consequently, most sequence comparison methods are designed to produce optimal alignments that take into consideration possible insertions and deletions without penalising unduly the overall homology score. This is achieved by inserting “gaps” in the sequence alignment to try to maximise local homology.

However, these more complex methods assign “gap penalties” to each gap that occurs in the alignment so that, for the same number of identical amino acids, a sequence alignment with as few gaps as possible—reflecting higher relatedness between the two compared sequences—will achieve a higher score than one with many gaps. “Affine gap costs” are typically used that charge a relatively high cost for the existence of a gap and a smaller penalty for each subsequent residue in the gap. This is the most commonly used gap scoring system. High gap penalties will of course produce optimised alignments with fewer gaps. Most alignment programs allow the gap penalties to be modified. However, it is preferred to use the default values when using such software for sequence comparisons. For example, when using the GCG Wisconsin Bestfit package the default gap penalty for amino acid sequences is -12 for a gap and -4 for each extension.

Calculation of maximum % homology therefore firstly requires the production of an optimal alignment, taking into consideration gap penalties. A suitable computer program for carrying out such an alignment is the GCG Wisconsin Bestfit package (University of Wisconsin, U.S.A.; Devereux et al., 1984, Nucleic Acids Research 12:387). Examples of other software than can perform sequence comparisons include, but are not limited to, the BLAST™ package (Ausubel et al., 1999 *ibid*—Chapter 18), FASTA (Atschul et al., 1990, J. Mol. Biol., 403-410) and the GENWORKS™ suite of comparison tools. Both BLAST™ and FASTA are available for offline and online searching (Ausubel et al., 1999 *ibid*, pages 7-58 to 7-60).

Although the final % homology can be measured in terms of identity, the alignment process itself is typically not based on an all- or -nothing pair comparison. Instead, a scaled similarity score matrix is generally used that assigns scores to each pairwise comparison based on chemical similarity or evolutionary distance. An example of such a matrix commonly used is the BLOSUM62 matrix—the default matrix for the BLAST™ suite of programs. GCG Wisconsin programs generally use either the public default values or a custom symbol comparison table if supplied. It is preferred to use the public default values for the GCG package, or in the case of other software, the default matrix, such as BLOSUM62.

Advantageously, the BLAST™ algorithm is employed, with parameters set to default values. The BLAST™ algorithm is described in detail at www.ncbi.nih.gov/BLAST/blast_help.html, which is incorporated herein by reference. The search parameters are defined as follows, can be advantageously set to the defined default parameters.

Advantageously, “substantial identity” when assessed by BLAST™ equates to sequences which match with an EXPECT value of at least about 7, preferably at least about 9 and most preferably 10 or more. The default threshold for EXPECT in BLAST™ searching is usually 10.

BLAST™ (Basic Local Alignment Search Tool) is the heuristic search algorithm employed by the programs blastp, blastn, blastx, tblastn, and tblastx; these programs ascribe significance to their findings using the statistical methods of Karlin and Altschul (Karlin and Altschul 1990, Proc. Natl. Acad. Sci. USA 87:2264-68; Karlin and Altschul, 1993, Proc. Natl. Acad. Sci. USA 90:5873-7; see www.ncbi.nih.gov/BLAST/blast_help.html) with a few enhancements. The BLAST™ programs are tailored for sequence similarity searching, for example to identify homologues to a query sequence. For a discussion of basic issues in similarity searching of sequence databases, see Altschul et al (1994) Nature Genetics 6:119-129.

The five BLAST™ programs available at www.ncbi.nlm.nih.gov perform the following tasks: blastp—compares an amino acid query sequence against a protein sequence database; blastn—compares a nucleotide query sequence against a nucleotide sequence database; blastx—compares the six-frame conceptual translation products of a nucleotide query sequence (both strands) against a protein sequence database; tblastn—compares a protein query sequence against a nucleotide sequence database dynamically translated in all six reading frames (both strands); tblastx—compares the six-frame translations of a nucleotide query sequence against the six-frame translations of a nucleotide sequence database.

BLAST™ uses the following search parameters:

HISTOGRAM—Display a histogram of scores for each search; default is yes. (See parameter H in the BLAST™ Manual).

DESCRIPTIONS—Restricts the number of short descriptions of matching sequences reported to the number specified; default limit is 100 descriptions. (See parameter V in the manual page).

EXPECT—The statistical significance threshold for reporting matches against database sequences; the default value is 10, such that 10 matches are expected to be found merely by chance, according to the stochastic model of Karlin and Altschul (1990). If the statistical significance ascribed to a match is greater than the EXPECT threshold, the match will not be reported. Lower EXPECT thresholds are more stringent, leading to fewer chance matches being reported. Fractional values are acceptable. (See parameter E in the BLAST™ Manual).

CUTOFF—Cutoff score for reporting high-scoring segment pairs. The default value is calculated from the EXPECT value (see above). HSPs are reported for a database sequence only if the statistical significance ascribed to them is at least as high as would be ascribed to a lone HSP having a score equal to the CUTOFF value. Higher CUTOFF values are more stringent, leading to fewer chance matches being reported. (See parameter S in the BLAST™ Manual). Typically, significance thresholds can be more intuitively managed using EXPECT.

ALIGNMENTS—Restricts database sequences to the number specified for which high-scoring segment pairs (HSPs) are reported; the default limit is 50. If more database

sequences than this happen to satisfy the statistical significance threshold for reporting (see EXPECT and CUTOFF below), only the matches ascribed the greatest statistical significance are reported. (See parameter B in the BLAST™ Manual).

MATRIX—Specify an alternate scoring matrix for BLASTP, BLASTX, TBLASTN and TBLASTX. The default matrix is BLOSUM62 (Henikoff & Henikoff, 1992). The valid alternative choices include: PAM40, PAM120, PAM250 and IDENTITY. No alternate scoring matrices are available for BLASTN; specifying the MATRIX directive in BLASTN requests returns an error response.

STRAND—Restrict a TBLASTN search to just the top or bottom strand of the database sequences; or restrict a BLASTN, BLASTX or TBLASTX search to just reading frames on the top or bottom strand of the query sequence.

FILTER—Mask off segments of the query sequence that have low compositional complexity, as determined by the SEG program of Wootton & Federhen (1993) Computers and Chemistry 17:149-163, or segments consisting of short-periodicity internal repeats, as determined by the XNU program of Clayerie & States (1993) Computers and Chemistry 17:191-201, or, for BLASTN, by the DUST program of Tatusov and Lipman (see www.ncbi.nlm.nih.gov). Filtering can eliminate statistically significant but biologically uninteresting reports from the BLAST™ output (e.g., hits against common acidic-, basic- or proline-rich regions), leaving the more biologically interesting regions of the query sequence available for specific matching against database sequences.

Low complexity sequence found by a filter program is substituted using the letter “N” in nucleotide sequence (e.g., “NNNNNNNNNNNNNN”) and the letter “X” in protein sequences (e.g., “XXXXXXXXXX”).

Filtering is only applied to the query sequence (or its translation products), not to database sequences. Default filtering is DUST for BLASTN, SEG for other programs.

It is not unusual for nothing at all to be masked by SEG, XNU, or both, when applied to sequences in SWISS-PROT, so filtering should not be expected to always yield an effect. Furthermore, in some cases, sequences are masked in their entirety, indicating that the statistical significance of any matches reported against the unfiltered query sequence should be suspect. NCBI-gi—Causes NCBI gi identifiers to be shown in the output, in addition to the accession and/or locus name.

Most preferably, sequence comparisons are conducted using the simple BLAST™ search algorithm provided at www.ncbi.nlm.nih.gov/BLAST. In some embodiments of the present invention, no gap penalties are used when determining sequence identity.

As a fusion protein and a fusion peptide of the present invention, any fusion protein and fusion peptide can be used as long as the proteins/peptides of the present invention is bound to marker protein and/or peptide tag. A marker protein is not particularly limited as long as it is a marker protein conventionally known, alkaline phosphatase, Fc region of antibodies, HRP, GFP, and the like are exemplified as specific examples. Further, as a peptide tag of the present invention, a peptide tag conventionally known such as HA tag, Myc tag, His tag, FLAG™ tag, and GST tag are specifically exemplified. The fusion protein can be prepared by known methods. It is useful in purification of the protein and the like having effects of controlling cell migration and cell death by utilizing affinity of Ni-NTA and His tag, in detection of protein having effects of controlling cell migration and cell death, and in quantification of antibodies directed against a protein having effects of controlling cell migration and cell

death. It is also useful as an inhibitor of cancer and tumor metastasis or a regulant of cell migration for transplantation therapy, and a reagent for research in the field concerned.

As an antibody that binds specifically to the proteins or peptides of the present invention, an immunity-specific antibody such as monoclonal antibody, polyclonal antibody, chimeric antibody, single-stranded antibody, and humanized antibody are exemplified as specific examples, where these antibodies can be prepared by known methods using the whole or a part of the above-mentioned proteins/peptides of the present invention, fusion protein, fusion peptide, and the like as an antigen, and monoclonal antibody is more preferable among them in view of specificity. The antibody such as monoclonal antibody is useful, for instance not only as an inhibitor of cancer and tumor metastasis or a regulant of cell migration for transplantation therapy, but also in clarifying the mechanism of such as cancer and tumor metastasis and cell migration of neuron and the like.

The aforementioned antibody of the present invention is produced by administering the proteins/peptides of the present invention, a fragment thereof containing epitope, or a cell expressing the protein on the surface of its membrane to an animal (preferably other than human) with the use of conventional protocol, for example, the monoclonal antibody can be prepared by an arbitrary method which brings antibodies developed by cultured materials of continuous cell line, such as hybridoma method (Nature 256, 495-497, 1975), trioma method, human B cell hybridoma method (Immunology Today 4, 72, 1983), and EBV-hybridoma method (MONOCLONAL ANTIBODIES AND CANCER THERAPY, pp. 77-96, Alan R. Liss, Inc., 1985) can be used.

A preparation method of single-stranded antibody (U.S. Pat. No. 4,946,778) can be applied in order to the preparation of single-stranded antibody against the above-mentioned proteins/peptides of the present invention. Further, a humanized antibody can be expressed by using a transgenic mouse or other mammal, a clone expressing the proteins/peptides of the present invention can be isolated/identified with the above-mentioned antibody, or the polypeptide can be purified with affinity chromatography. The antibodies against the proteins/peptides of the present invention may be used usefully as an inhibitor of cancer and tumor metastasis or a regulant of cell migration for transplantation therapy, and may also be used usefully in clarifying the mechanism of such as cancer and tumor metastasis and cell migration of neuron and the like, as aforementioned. Further, the recombinant protein or peptide to which these antibodies specifically bind are also included in the proteins/peptides of the present invention as aforementioned.

Functions of the proteins/peptides of the present invention can be analyzed by using, for example, antibodies such as the aforementioned monoclonal antibodies and the like that are labeled with fluorescent materials such as FITC (Fluorescein isothiocyanate), tetramethylrhodamine isothiocyanate, etc., radioisotopes such as ^{125}I , ^{32}P , ^{14}C , ^{35}S , ^3H , etc. or enzymes such as alkaline phosphatase, peroxidase, .beta.-galactosidase, phycoerythrin, etc. and by using fusion proteins fused with fluorescence proteins such as Green Fluorescent Protein (GFP) etc. As for immunological detection methods using the antibodies of the present invention, RIA method, ELISA method, fluorescent-antibody method, plaque method, spot method, hemagglutination, Ouchterlony method, etc. are exemplified.

The present invention also relates to a host cell comprising an expression system, which is able to express the proteins/peptides of the present invention. Introduction of a gene that encodes the proteins/peptides of the present invention into a

host cell can be performed by the method written in a number of standard laboratory manuals such as of Davis et al. (BASIC METHODS IN MOLECULAR BIOLOGY, 1986), and of Sambrook et al. (MOLECULAR CLONING: A LABORATORY MANUAL, 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989), for example, calcium phosphate transfection, DEAE-dextran-mediated transfection, transfection, microinjection, cationic lipid-mediated transfection, electroporation, transduction, scrape loading, ballistic introduction, and infection. As a host cell; bacterial procaryotic cell, such as *Escherichia coli*, *Streptomyces*, *Bacillus subtilis*, *Streptococcus*, and *Staphylococcus*; fungal cell, such as yeast and *Aspergillus*; insect cell, such as *Drosophila* S2 and *Spodoptera* Sf9; animal cell, such as L cell, CHO cell, COS cell, NIH3T3 cell, HeLa cell, C127 cell, BALB/c3T3 cell (including a mutant strain deficient in dihydrofolate reductase or thymidine kinase), BHK21 cell, HEK293 cell, and Bowes malignant melanoma cell; and plant cell can be exemplified.

As an expression system, any expression system can be used as long as it is an expression system that can express the proteins/peptides of the present invention in a host cell, an expression system derived from chromosome, episome, mammal, or virus, for example; a vector derived from bacterial plasmid, yeast plasmid, papova virus such as SV40, vaccinia virus, adenovirus, fowl poxvirus, pseudorabies virus, retrovirus; a vector derived from bacteriophage, transposon, or combination of these vectors, for example a vector derived from genetic component of plasmid and bacteriophage such as cosmid or phagemid can be exemplified as a specific examples. The expression system may not only yield expression but also include a regulatory sequence for controlling expression.

A host cell comprising the aforementioned expression system, a cell membrane of the cell, and the proteins/peptides of the present invention obtained by culture of the cell can be used for a method for screening the present invention as described below. For example, as the method for obtaining cell membrane, the method by F. Pietri-Rouxel et al. (Eur. J. Biochem., 247, 1174-1179, 1997) and the like can be used. For recovering and purifying the proteins/peptides of the present invention from cell culture, the known methods including ammonium sulfate—or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxyapatite chromatography, and lectin chromatography, preferably, high-performance liquid chromatography is used. As a column especially used for affinity chromatography, columns to which antibodies to the proteins/peptides of the present invention are bound, for instance, are used and when ordinary peptide tags are added to the proteins/peptides of the present invention mentioned above, columns to which substances having affinity with the peptide tags are bound are used in order to obtain the proteins/peptides of the present invention. The method for purifying the proteins/peptides of the present invention can also be applied for peptide synthesis.

In the present invention, a non-human animal whose gene function to encode the proteins/peptides of the present invention mentioned above is deficient on its chromosome means a non-human animal part or whole of whose gene on its chromosome encoding the proteins/peptides of the present invention is inactivated by gene mutation such as destruction, deletion, substitution, etc. do that whose function to express the proteins/peptides the present invention is lost. Further, a non-human animal which over-expresses the proteins/peptides of the present invention is specifically exemplified by a non-

human animal which produces larger amount of the proteins/peptides of the present invention than a wild-type non-human animal does. Although rodents or the like such as mice, rats, etc. are particularly exemplified for non-human animals of the present invention, the examples will not be limited to these animals only.

Homozygous non-human animals that are born according to Mendel's Law include a deficient type or the over-expressing type for the proteins/peptides of the present invention, as well as their wild-type littermates. By using the deficient type animals or the over-expressing type animals of these homozygous non-human animals together with their wild-type littermate at the same time, accurate comparative experiments can be carried out on the individual level. In performing screening of the present invention described below, it is, therefore preferable to use the wild type non-human animals, i.e. animals of the same species as or even better the littermates of, non-human animals whose gene function to encode the proteins/peptides of the present invention is deficient or over-expressing on their chromosomes with a combination of the deficient or over-expressing type animals. The method of producing a non-human animal whose function to encode the proteins/peptides of the present invention is deficient or over-expressing on its chromosome is now explained in the following with an L-FILIP knockout mouse and an L-FILIP transgenic mouse as examples.

A mouse, for instance, whose gene function to encode the L-FILIP protein is deficient on its chromosome, i.e. an L-FILIP knockout mouse is generated by the following steps. A gene encoding mouse L-FILIP, which is homologous to rat L-FILIP, is screened by using a gene fragment obtained by a method such as PCR or the like from the mouse gene library. A screened gene which encodes mouse L-FILIP is subcloned with a viral vector or the like and is then identified by DNA sequencing. The whole or part of a gene of this clone which encodes mouse L-FILIP is substituted with a pMC1 neo gene cassette or the like. A gene such as a diphtheria toxin A fragment (DT-A) gene, a herpes simplex virus thymidine kinase (HSV-tk) gene, etc. is introduced onto the 3'-end, and thus a targeting vector is constructed.

The targeting vectors thus constructed are linearized and introduced into ES cells by electroporation or the like to cause homologous recombination. Among the homologous recombinants, ES cells in which homologous recombination have occurred are selected by the use of antibiotics such as G418, ganciclovir (GANC), etc. It is preferable to confirm whether the ES cells selected are the recombinants of the interest by Southern blotting or the like. A clone of the ES cells confirmed is microinjected into a mouse blastocyst, and which blastocyst is placed back to the recipient mouse to generate a chimeric mouse. A heterozygous mouse can be obtained by intercrossing the chimeric mouse with a wild-type mouse. By further intercrossing the heterozygous mice, the L-FILIP knockout mice of the present invention can be generated. Whether the ability of expressing L-FILIP is lost in an L-FILIP knockout mouse is examined by Northern blotting upon isolating RNA from the mouse obtained by the above-described method and Western blotting or the like with which the L-FILIP expression in the mouse can be directly examined.

An L-FILIP transgenic mouse is created by following steps. A promoter such as chicken .beta.-actin, mouse neurofilament, SV40, etc. and poly (A) such as rabbit .beta.-globin SV40, etc. or introns are fused with cDNA encoding L-FILIP derived from human, mouse, rat, rabbit, etc., to construct a transgene. This transgene is microinjected into the pronuclear of mouse fertilized egg. After the obtained egg cell

is cultured, it is transplanted to the oviduct of the recipient mouse which was fed thereafter. Neonatal mice that have the aforementioned cDNA were selected from among all the mice born and thus the transgenic mice are created. Neonatal mice having the cDNA can be selected by extracting crude DNA from the mice tails or the like and then by a dot hybridization method using a gene encoding the introduced L-FILIP as a probe and by PCR method or the like using a specific primer.

The host cell that comprises: the gene or DNA which encodes the above-mentioned proteins/peptides of the present invention; the proteins/peptides of the present invention; the fusion protein of the proteins/peptides of the present invention combined with marker protein and/or peptide tag; antibodies against the proteins/peptides of the present invention; and an expression system which is able to express the proteins/peptide of the present invention is useful for an inhibitor for metastasis of a cancer or a tumor or a regulant of cell migration for transplantation treatment as described below specifically. It is also available for elucidation of mechanisms such as metastasis of a cancer or a tumor or cell migration of neuron and the like as well as control of cell migration and/or cell death, a method for screening an inhibitor or a promoter of effects of controlling cell migration and/or cell death, or a method for screening an inhibitor or a promoter for expressing the proteins/peptides of the present invention.

As the method for screening an inhibitor or a promoter for controlling cell migration and/or cell death of the present invention: a method using the above-mentioned proteins/peptides of the present invention or a cell membrane expressing the proteins/peptides of the present invention, and a test substance, a method using a cell membrane expressing the above-mentioned proteins/peptides of the present invention and a test substance, a method using non-human animal such as knockout mouse or transgenic mouse of the proteins/peptides of the present invention and a test substance, and others are exemplified. Further, a method using a cell membrane expressing the above-mentioned proteins/peptides of the present invention and a test substance, a method using non-human animal such as knockout mouse or transgenic mouse of the proteins/peptides of the present invention and a test substance, and others can be used for a method for screening an inhibitor or a promoter for expressing the proteins/peptides of the present invention.

As the method for screening that uses the above-mentioned the proteins/peptides of the present invention or a cell membrane expressing the proteins/peptides of the present invention and a test substance, a method of measuring and evaluating effects of controlling cell migration and cell death of the proteins/peptides of the present invention, by contacting the proteins/peptides or the proteins/peptides expressing on the surface of cell membrane with a test substance can be specifically exemplified. As the method for screening that uses a cell expressing the proteins/peptides of the present invention and a test substance, a method of measuring and evaluating effects of controlling cell migration and cell death of the proteins/peptides of the present invention, or the variation of expression amounts of the proteins/peptides of the present invention, by contacting a cell expressing the proteins/peptides of the present invention with a test substance can be specifically exemplified.

As the method for screening that uses non-human animal whose function of gene for encoding above-mentioned protein and peptide of the present invention is deficient on the chromosome or non-human animal which over-expresses the proteins/peptides of the present invention and a test sub-

stance, a method for measuring and evaluating the effects of controlling cell migration and cell death of the proteins/peptides of the present invention or the variation in expression amounts of the proteins/peptides of the present invention by contacting the cell or the tissue obtained from these non-human animal with a test substance in vitro, a method for measuring and evaluating the effects of controlling the cell migration and cell death of the proteins/peptides of the present invention or the variation in expression amounts of the proteins/peptides of the present invention at the cell or the tissue obtained from these non-human animal after administering a test substance in advance to the non-human animal whose function of gene for encoding the proteins/peptides of the present invention is deficient on the chromosome or non-human animal which over-expresses the proteins/peptides of the present invention, a method for measuring and evaluating effects of controlling cell migration and cell death of the proteins/peptides of the present invention or the variation in expression amounts of the proteins/peptides of the present invention at the non-human animal after administering a test substance in advance to the non-human animal whose function of gene for encoding the proteins/peptides of the present invention is deficient on the chromosome or non-human animal which over-expresses the proteins/peptides of the present invention, and etc., are specifically exemplified.

The promoter of effects of controlling cell migration and cell death or the promoter of expression of the present invention obtained from the screening method mentioned above can be used for such as treatment of patients requiring promotion of effects of controlling cell migration and cell death, or promotion of expression of the proteins/peptides of the present invention. The inhibitor of effects of controlling cell migration and cell death or the expression inhibitor of the present invention obtained from the screening method mentioned above can be used for such as treatment of patients requiring inhibition of effects of controlling cell migration and cell death, or inhibition of expression of the proteins/peptides of the present invention. The proteins/peptides of the present invention or the antibody against it can be used as an active ingredient for an inhibitor of cancer and tumor metastasis or a regulant of cell migration for transplantation therapy, and the like. It can be used missile therapy, as well.

The active ingredient(s) of a pharmaceutical composition is contemplated to exhibit excellent therapeutic activity, for example, in the treatment of cancer. Dosage regimes may be adjusted to provide the optimum therapeutic response. For example, several divided doses may be administered daily or the dose may be proportionally reduced as indicated by the exigencies of the therapeutic situation. Dosages may be administered at intervals of the course of several days, weeks, months or years.

The active compound may be administered in a convenient manner such as by the oral, intravenous (where water soluble), intramuscular, subcutaneous, intranasal, intradermal or suppository routes or implanting (e.g. using slow release molecules). The method of administration may depend on factors such as the location of the cancer or other ailment in the body which is to be treated. Depending on the route of administration, the active ingredient may be required to be coated in a material to protect said ingredients from the action of enzymes, acids and other natural conditions which may inactivate said ingredient.

In order to administer the combination by other than parenteral administration, it will be coated by, or administered with, a material to prevent its inactivation. For example, the combination may be administered in an adjuvant, co-administered with enzyme inhibitors or in liposomes. Adju-

vant is used in its broadest sense and includes any immune stimulating compound such as interferon. Adjuvants contemplated herein include resorcinols, non-ionic surfactants such as polyoxyethylene oleyl ether and n-hexadecyl polyethylene ether. Enzyme inhibitors include pancreatic trypsin.

Liposomes include water-in-oil-in-water CGF emulsions as well as conventional liposomes.

The active compound may also be administered parenterally or intraperitoneally. Dispersions can also be prepared in glycerol, liquid polyethylene glycols, and mixtures thereof and in oils. Under ordinary conditions of storage and use, these preparations contain a preservative to prevent the growth of microorganisms.

The pharmaceutical forms suitable for injectable use include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion. In all cases the form must be sterile and must be fluid to the extent that easy syringability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), suitable mixtures thereof, and vegetable oils. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants.

The prevention of the action of microorganisms can be brought about by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, sorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars or sodium chloride. Prolonged absorption of the injectable compositions can be brought about by the use in the compositions of agents delaying absorption, for example, aluminium monostearate and gelatin.

Sterile injectable solutions are prepared by incorporating the active compound in the required amount in the appropriate solvent with various of the other ingredients enumerated above, as required, followed by filtered sterilisation. Generally, dispersions are prepared by incorporating the sterilised active ingredient into a sterile vehicle which contains the basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, the preferred methods of preparation are vacuum drying and the freeze-drying technique which yield a powder of the active ingredient plus any additional desired ingredient from previously sterile-filtered solution thereof.

When the combination of polypeptides is suitably protected as described above, it may be orally administered, for example, with an inert diluent or with an assimilable edible carrier, or it may be enclosed in hard or soft shell gelatin capsules, or it may be compressed into tablets, or it may be incorporated directly with the food of the diet. For oral therapeutic administration, the active compound may be incorporated with excipients and used in the form of ingestible tablets, buccal tablets, troches, capsules, elixirs, suspensions, syrups, wafers, and the like. The amount of active compound in such therapeutically useful compositions in such that a suitable dosage will be obtained.

The tablets, troches, pills, capsules and the like may also contain the following: a binder such as gum tragacanth, acacia, corn starch or gelatin; excipients such as dicalcium phosphate; a disintegrating agent such as corn starch, potato

starch, alginic acid and the like; a lubricant such as magnesium stearate; and a sweetening agent such as sucrose, lactose or saccharin may be added or a flavouring agent such as peppermint, oil of wintergreen, or cherry flavouring. When the dosage unit form is a capsule, it may contain, in addition to materials of the above type, a liquid carrier.

Various other materials may be present as coatings or to otherwise modify the physical form of the dosage unit. For instance, tablets, pills, or capsules may be coated with shellac, sugar or both. A syrup or elixir may contain the active compound, sucrose as a sweetening agent, methyl and propylparabens as preservatives, a dye and flavouring such as cherry or orange flavour. Of course, any material used in preparing any dosage unit form should be pharmaceutically pure and substantially non-toxic in the amounts employed. In addition, the active compound may be incorporated into sustained-release preparations and formulations.

As used herein "pharmaceutically acceptable carrier and/or diluent" includes any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents and the like. The use of such media and agents for pharmaceutical active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active ingredient, use thereof in the therapeutic compositions is contemplated. Supplementary active ingredients can also be incorporated into the compositions.

It is especially advantageous to formulate parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units suited as unitary dosages for the mammalian subjects to be treated; each unit containing a predetermined quantity of active material calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier. The specification for the novel dosage unit forms are dictated by and directly dependent on (a) the unique characteristics of the active material and the particular therapeutic effect to be achieved, and (b) the limitations inherent in the art of compounding such as active material for the treatment of disease in living subjects having a diseased condition in which bodily health is impaired.

Acceptable carriers or diluents for therapeutic use are well known in the pharmaceutical art, and are described, for example, in Remington's Pharmaceutical Sciences, Mack Publishing Co. (A. R. Gennaro edit. 1985).

The principal active ingredients are compounded for convenient and effective administration in effective amounts with a suitable pharmaceutically acceptable carrier in dosage unit form. In the case of compositions containing supplementary active ingredients, the dosages are determined by reference to the usual dose and manner of administration of the said ingredients.

For example, in one aspect these therapeutic agents can be administered orally or parenterally. Pharmaceutical solid such as powders, granule, capsules, and tablets or pharmaceutical liquid such as syrup or elixir can be an oral administration agent, or can be an injection, a percutaneous preparation, suppository, or the like as a parenteral administration agent. These formulations can be produced in a usual manner by adding an auxiliary agent admitted pharmacologically and pharmaceutical technologically to active constituents. For example, components of formulation of diluents such as light silicic acid anhydride, starch, lactose, crystalline cellulose, and lactose calcium, disintegrator such as carboxy methyl cellulose and of lubricant such as magnesium stearate for oral agent and muscal administration agent, components of for-

mulation of solubilizer or auxiliary solubilizer such as saline, mannitol, and propylene glycol, and of suspension such as surface active agent for injection, and further components of formulation of solubilizer or auxiliary solubilizer of water or oil-based and of adhesive for external preparation are used as an auxiliary agent.

Applied dose can be determined properly depending on the kind of objective disease, age, gender, body weight, and symptom of patient and administration pattern.

Depending upon the need, the complex(es) may be administered at a dose of from about 0.001 to about 30 mg/kg body weight, such as from about 0.1 to about 10 mg/kg, or from about 0.1 to about 1 mg/kg body weight.

Of course, for any composition to be administered to an animal or human, and for any particular method of administration, it is preferred to determine therefore: toxicity, such as by determining the lethal dose (LD) and LD₅₀ in a suitable animal model e.g., rodent such as mouse; and, the dosage of the composition(s), concentration of components therein and timing of administering the composition(s), which elicit a suitable response. Such determinations do not require undue experimentation from the knowledge of the skilled artisan, this disclosure and the documents cited herein.

The present invention will be explained more specifically with examples below, but the scope of the present invention is not limited to these examples. In the following example, Wistar rats (Keari; SLC) which were housed with food and water ad libitum under a constant temperature and humidity were used. For the animal mentioned above, embryonic day 0 (EO) is defined as the day of confirmation of the vaginal plug and day of birth is designated as P0 (postnatal day 0). Rats of P0 to P7 were anesthetized by hypothermia, while Rats of P14 to adults including being pregnant were anesthetized by intraperitoneal injection of sodium pentobarbital at 40 mg/kg.

EXAMPLE 1

β Isolation of FILIP cDNA and Localization of FILIP

Although it has been known that Filamin 1 (ABP-280), an actin binding protein, is an essential component of the radial migratory machinery for obtaining postmitotic neocortical neurons (Neuron 21, 1315-1325, 1998), its expression in migratory and postmigratory neurons involved in the development of neocortex, in the region from the intermediate zone to the cortical plate (Neuron 21, 1315-1325, 1998), suggests that the start of migration out of the ventricular zone is possibly controlled by other system. In order to elucidate the molecules concerning controlling the start of neuronal migration, mRNA differential display, in situ hybridization histochemistry, and screening of rat cDNA library were conducted according to the method written in Mol. Brain. Res. 62, 187-195, 1998. First, genes that expressed more abundantly in the neocortices of Wistar rats on embryonic day 11 to 12 (E11 to 12) compared with Wistar rats on embryonic day 18 to 20 (E18 to 20) were isolated by mRNA differential display. Postmitotic neurons were at the stage of migrating out of the ventricular zone toward the pial surface on E12 Wistar rats, whereas most of them had already left there at around E18 to 20 by which neurogenesis was complete. The two hundred gene fragments obtained from the results above, which expressed dramatically on E12 but not so much on E18 to 20 were sequenced and 86 independent clones were obtained by excluding overlaps.

Then, further selection was performed by in situ hybridization histochemistry with a part of the full-length of rat

S-FILIP (165 nucleotides; base sequence 1289-1453) as a probe. Consequently, among 80 independent clones, one novel clone showing expression in the ventricular zone of the cortex was isolated, which was named filip (Filamin-interacting protein). In order to investigate expression of the FILIP (S-FILIP) gene, *in situ* hybridization for rats E12 and 18 was performed with its sagittal section. The results were shown in FIG. 1a. According to this, positive signal was confirmed at ventricular zone of cortex (cx) and superior colliculus (sc) in central nervous system of E12 (FIG. 1a left). The signal could not be confirmed abundantly at ventricular zone of E18, however, they were confirmed abundantly at heart, aorta, gastrointestinal tract, and diaphragm, and filip gene was found that they expressed at myocardium, skeletal muscle, and smooth muscle (FIG. 1a right). The scale bar in FIG. 1a shows 1 mm.

cDNA library derived from frontal cortex of a Wistar rat E11 was constructed and screened FILIP with the probe used at above-mentioned *in situ* hybridization selection and a MARATHON™ cDNA Amplification Kit (CLONTECH). Genetic information from the DNA database of Japan (DDBJ) was utilized in part to isolate FILIP cDNA. Consequently, two full-length FILIP cDNAs, different only in their 5'termini, with regions recognizing the aforementioned probes were obtained. Amino acid sequences were determined from the information of the two cDNA information respectively. The structure is shown in FIG. 1b. As a result, structures were confirmed to coincide with each other except S-FILIP (short form FILIP; GENBANK™ accession number D87257) lacked 247 residues at N-terminus of L-FILIP (long form FILIP; GENBANK™ accession number AB055759). The above-mentioned two proteins were confirmed to be intracellular proteins, since neither a signal sequence nor a transmembrane region was found by their hydrophobicity profiles. Though four leucine zipper motifs and coiled-coil region could be recognized in the C-terminal halves of S-FILIP (FIG. 1c), the amino acid sequence of the regions were found that they did not show similarity to any protein which had been reported so far (FIG. 1b, c).

Next, in order to investigate the cellular localization of S-FILIP (fiber-like; FIG. 1d top) and L-FILIP (punctate; FIG. 1d bottom), mammalian expression vectors including FILIPs-GFP (pEGFP-N1 (CLONTECH), pCAGGS (Invitrogen) or pBudCE4 (Invitrogen)) which was tagged with green fluorescent protein (GFP) at C-termini of FILIP were transfected to COS-7 cells which were maintained in Dulbecco's modified Eagle medium (DMEM) containing 10% fetal bovine serum (FBS) at 37° C. in 5% CO₂, FILIPs-GFP was expressed, and image analysis was performed by OLYMPUS™ IX-70 micro scope equipped with a digital cooled CCD camera (Hamamatsu Photonics) (GFP in FIG. 1d). Further, in order to investigate whether above-mentioned FILIPs were coexistent with F-actin, after aforementioned COS-7 cells were fixed with 4% paraformaldehyde/0.1 M phosphate buffer (PB) (pH 7.4) for 10 min, and permeabilized in 0.1% TRITON® X-100/phosphate buffered saline (PBS) for 3 min, F-actin was stained with rhodamine-phalloidin (1:40; Molecular Probes) (phalloidin in FIG. 1d), coexistence of S-FILIP or L-FILIP with F-actin was investigated (merged in FIG. 1d). The results are shown in FIG. 1d. The scale bar in FIG. 1d indicates 10 μm. According to this result, S-FILIP tagged with GFP was localized along actin stress filaments generally except at their ends, and that the possibility of colocalization of S-FILIP with F-actin was presumed. In contrast, L-FILIP exhibited a punctate distribution in cytoplasm, unlike the colocalization of F-actin.

Meanwhile, 50 cells expressing S-FILIP tagged with above-mentioned GFP (FIG. 1e) or L-FILIP tagged with above-mentioned GFP (FIG. 1f) were extracted in a random order respectively, and the numbers of cells in each expression distribution pattern of FILIPs-GFP were measured. The measurement was performed four times, and the obtained results were calculated as the mean value ± S.E. M. The result showed that each pattern of colocalization was heavily dependent on the type of FILIP molecule. Then, coexistence with F-actin in the region not including known actin-binding domain (N-terminus at S-FILIP) was investigated, as well. Expressions of S-FILIPAC-GFP (C-terminus-deficient S-FILIP tagged with GFP), FILIPAN (N-terminus-deficient FILIP tagged with GFP), or only GFP at COS-7 cell in the above-mentioned manner (FIG. 1g) suggested that S-FILIP coexist with F-actin (FIG. 1 center) despite the lack of existence of known actin-binding domain. This led to reveal that C-terminal halves (FILIPAN) being common to S-FILIP and L-FILIP was essential and sufficient for colocalization with F-actin. In contrast, L-FILIP showed little colocalization with F-actin, however, it exhibited a punctate distribution in cytoplasm of the most cells. Further, actin stress filaments were scarcely observed in COS-7 cells which express L-FILIP. The scale bar in FIG. 1g indicates 20 μm.

EXAMPLE 2

Interaction of FILIPs with Actin Binding Protein Filamin 1

In order to further examine the unique localization of S-FILIP associated with F-actin, and elucidate the factor that might serve as a link between both molecules, a yeast two-hybrid screen was performed using the C-terminal half of S-FILIP (bait) and the whole embryo library (prey) of mouse E11. Using MATCHMAKER™ Two-Hybrid system (CLONTECH) for a yeast two-hybrid screen, the whole embryo library derived from brain of E11 mouse preintegrated into MATCHMAKER™ library (CLONTECH) was transformed with yeast strain PJ69-2A which was transformed with pAS2-1 plasmid vector carrying cDNA that encoded the common C-terminal region of FILIPs (residues 508-965 of the deduced amino acid sequence of S-FILIP), and C-terminal half of S-FILIP were mated with the whole embryo library of E11 mouse. As a result, over 8×10⁶ clones were screened and 17 clones were selected based on three selection markers. In that way, a clone encoding Filamin 1, a protein interacting with actin filament, that interacts with F-actin into isotropic, orthogonal arrays and increases the viscosity and stiffness of the F-actin network was identified from these clones.

Next, L-FILIP-GFP, S-FILIP-GFP, a fusion protein where GFP bound to N-terminal half of S-FILIP tagged with GFP (S-FILIP.DELTA.C-GFP), a fusion protein where GFP bound to C-terminal half common to FILIPs (FILIP.DELTA.N-GFP), or cell lysates obtained from COS-7 cells expressing only GFP (protein solution solubilized in a buffer containing 20 mM TRIS™, (pH 7.5), 150 mM NaCl, 1000 U/ml DNase I, 1% NP-40, 1 mM phenylmethanesulfonyl fluoride, 5 μg/ml aprotinin, 1.5 μM pepstatin A, 2 μM leupeptin) were immunoprecipitated using either anti-GFP antibodies (CLONTECH) or anti-filamin 1 antibodies (Chemicon), and immunoprecipitated protein was detected with anti-Filamin 1 or anti-GFP antibodies as probes. The results of immunoprecipitation with anti-GFP antibodies are shown in FIG. 2a, and the results of immunoprecipitation with anti-Filamin 1 antibodies are shown in FIG. 2b. These results led to confirm the

formation of complex comprising either full-length FILIPs or S-FILIP having C-terminal half and Filamin 1.

Further, in order to perform immunocytochemistry, or examine colocalization of S-FILIP (fiber-like; FIG. 2c) or L-FILIP (punctate; FIG. 2c) with Filamin 1, S-FILIP-GFP or L-FILIP-GFP was transfected with COS-7 cell, the cells were fixed to be permeabilized, and image analysis was performed with an OLYMPUS™ IX-70 microscope equipped with a digital cooled CCD camera (Hamamatsu Photonics) in following manner as mentioned in Example 1. After above-mentioned cells were permeabilized, the expression of endogenous Filamin 1 was blocked in 10% goat serum/PBS for 20 min, incubated in the coexistence of anti-Filamin 1 antibodies (1:200; Chemicon), then incubated and stained in the coexistence of anti-mouse Ig-Cy3 (1:400; Amersham-Pharmacia). These results are shown in FIG. 2c. Arrows in the figure indicate signals of FILIPs-GFP and Filamin 1 colocalizing interactively. The scale bars in upper and middle columns of the figure indicate 10 μ m, and the scale bar in the lower column of the figure indicates 3 μ m. As a result, it was confirmed that although not all but most of Filamin 1 were coexisted with S-FILIP signals (FIG. 2c). In cells expressing L-FILIP, about half of the punctate signals were confirmed to colocalized with Filamin 1 punctate signals. Accordingly, the present inventors designated these novel molecules Filamin 1-interacting proteins, FILIPs.

EXAMPLE 3

Degradation of Filamin 1 by FILIPs and Decrease of Cell Motility by the Degradation

Since Filamin 1 is deeply involved in cell migration in various cells (Science 255, 325-327, 1992), it is probable that FILIPs control cell migration via Filamin 1. Thus, investigation was performed whether or not FILIPs affect cell migration rate by introducing FILIPs into COS-7 cells, which possessed Filamin 1 but not FILIPs. On the day after plating (approximately 1×10^4 cells per 1.88 cm² area), for analyzing the ratio of cell migration rate, COS-7 cells were transfected with expression vectors including S-FILIP-GFP (FIG. 3a left), L-FILIP-GFP (FIG. 3a center), and GFP only (FIG. 3a right). After 36 to 48 h of transfection, the cells were cultured in Dulbecco's modified Eagle medium (DMEM) containing 10% fetal bovine serum (FBS) on an IX-70 microscope equipped with an IX-IBC culturing apparatus (OLYMPUS™) under low cell density condition, image was analyzed twice at an interval of 120 min (FIG. 3a). [The images of GFP in FIG. 3a (green) were analyzed at an interval of 120 min, and then after the later ones had been converted to red color, these two images were merged.]. Further, in order to quantify cell migration in FIG. 3a, migrating distance (the mean value \pm s. e. m.) of each of the nucleus (n=20 for S-FILIP-GFP, n=19 for L-FILIP-GFP, and n=18 for GFP alone) was measured by each group at an interval of 120 min (FIG. 3b). The scale bar in FIG. 3a shows 50 μ m, in FIG. 3b, the cell migration occurred in the second image analysis was quantified by using phase-contrast image in combination. According to these results, it was confirmed that cell migration rate of the cells expressing FILIPs-GFP was reduced compared with the cells expressing GFP alone, under low cell density conditions, in which cell can migrate freely without interfering with other cells as well.

Next, in order to elucidate the effect of FILIPs on lamellipodium formation, a wound healing assay was performed. Over-confluent COS-7 cells were transfected with the expression vectors including either FILIPs-GFP or GFP. After 36 to

48 h of transfection, defects were made among cells (FIG. 3b), and after they were cultured for further 3 h, they were fixed and stained with rhodamine-phalloidin. After the staining, the defect edges among the cells were observed to confirm whether they had lamellipodia. The results are shown in FIG. 3c. Arrows in the figure show the defect edges at the S- and L-FILIP-GFP expression cells, arrowheads show the neighboring cells that express no FILIPs respectively, the scale bar indicates 50 μ m. Among the aforementioned COS-7 cells which formed defects, 50 cells were extracted at random, the cells where lamellipodium were formed at the wound edge and green GFP signals (FILIPs-GFP or GFP alone) were seen in the region were counted among them. As a result, it was confirmed that most of quiescent cells in the over-confluent state developed lamellipodia (sheet-like processes) in response to migration of neighboring cells. As shown in FIG. 3c, most cells expressing S- or L-FILIP-GFP did not form lamellipodia at the wound edge, compared with the cells that did not express FILIPs. In the cells expressing GFP (control), formation rate of lamellipodia was 68% at their wound edges, whereas formation rate of lamellipodia in the cells expressing S- and L-FILIP-GFP were only 28% and 4%, respectively. These results suggest that FILIPs suppress lamellipodium formation and cell migration, and lead to the consideration that FILIPs has inhibitory effects for the function of Filamin 1.

The molecular mechanism for the inhibitory effects of FILIPs on Filamin 1 was further examined by expressing recombinant FILIPs and recombinant Filamin 1 simultaneously in the same COS-7 cells using single expression vector including dual promoters. As shown in FIG. 3d, IRES (internal ribosomal entry site) sequence was inserted between HA-tagged Filamin 1 cDNA (HA-Filamin 1) and GFP cDNA, Filamin 1 and GFP were transcribed with CMV promoter (p), and FILIPs were integrated into expression vector for mammal cell (pBudCE4; Invitrogen) so as to be transcribed and expressed with EF-1 a promoter (p'), and transfected into COS-7 cells. Then, they were cultured in the presence or absence of 50 μ m calpeptine in addition to the conditions of example 1, and expression amount of HA-Filamin 1 and GFP were confirmed by SDS-PAGE method. Further, HA-Filamin 1 and GFP were confirmed that they were translated from the same mRNA in the cell. The relative amount of HA-Filamin 1 that expressed at COS-7 cells in the presence or absence of S-FILIP (S) or L-FILIP (L) was measured on the basis of GFP expression amount. (The relative amount of recombinant Filamin 1 and GFP was 4.7 in the absence of FILIPs and 1.8 in the presence of S-FILIP.) These results are shown in FIG. 3d. This revealed that the expression amount of Filamin 1 was decreased in the presence of FILIPs, especially of L-FILIP. It shows little HA-Filamin 1 protein exists in the presence of mRNA of HA-Filamin 1 and GFP. However, it was suggested that FILIPs induced degradation of Filamin 1, since these effects were lost in the presence of calpeptine which is a protease inhibitor.

Meanwhile, COS-7 cells expressing L-FILIP-GFP were generated in the same manner as mentioned in example 2, and immunoreactivity of them against Filamin 1 was examined. The results are shown in FIG. 3e. Arrows in the figure indicate COS-7 cells expressing L-FILIP-GFP, the scale bar in the figure indicates 25 μ m. As a result, at COS-7 cells expressing L-FILIP-GFP, especially the amount of endogenous Filamin 1 was remarkably declined compared with adjacent cells which do not express FILIP. It led to that COS-7 cells expressing L-FILIP-GFP showed low immunoreactivity against Filamin 1. It was also revealed that L-FILIP showed higher activity compared with S-FILIP in degradation of Filamin 1.

That is, because S-FILIP does not degrade Filamin 1 abundantly, although most of S-FILIPs in cells colocalize with Filamin 1 and F-actin, the punctate distribution of F-actin, which was observed in COS-7 cells expressing L-FILIP, was also observed even in a small fraction of cells expressing S-FILIP. Moreover, induction of degradation of Filamin 1 protein associated with FILIPs can be thought as one of causes which brings low immunoreactivity against Filamin 1 colocalizing with FILIPs (particularly L-FILIP) as shown in FIG. 2c.

EXAMPLE 4

Regulation of Cell Migration from Ventricular Zone by FILIPs in Developing Neocortex

Since FILIPs introduced into COS-7 cells exert inhibitory effects on cell migration as well as inducing degradation of Filamin 1, when Filamin 1 gene is mutated, postmitotic cells affected by the mutation remain in the ventricular zone, and cause malformation of human cortical. It is likely that FILIPs play a pivotal role in the control of cell migration in the developing neocortex (Neuron 16, 77-87, 1996, Neuron 21, 1315-1325, 1998). Thus, in order to examine the role of FILIPs on neuronal migration in vivo, plasmid DNA (S-FILIPs-GFP cDNA, L-FILIPs-GFP cDNA, or GFP cDNA) was administered into the lateral ventricle of E18 rat brain, then plasmid DNA were incorporated to ventricular zone cells by delivering electrical pulses with a square-pulse electroporator (BEX). The brain of E18 rat was sliced coronally into 200 μm with a microtome, and the dorsal portion of the cortex was dissected out and cultured for four days on a collagen-coated membrane (Transwell®-COL, Costar®-Corning) in a DMEM/F12 medium containing 10% FBS and N2 supplement. After cultured, the obtained cortex sections were fixed with 4% paraformaldehyde/0.1 M PB (pH 7.4) and their images were analyzed on a Zeiss S™ LSM510 laser-scanning confocal microscope (Zeiss™) (FIG. 4a). In FIG. 4a, each of the drawings in the right shows enlarged illustration of inside of the frames in each of the drawings in the left. White dots, p, and V show the edges of the section, pial surface, and lateral ventricle, respectively. Scale bars in FIG. 4a indicate 200 μm (left) and 100 μm (right). The migration rate of each cell against GFP or FILIPs-GFP was obtained by determining the quantity of cells at each site of cortex [cortex was divided equally into five section from lateral ventricle side (VS) to pial surface side (PS)] which were on the fourth day since they were cultured (FIG. 4b). The value of S-FILIP-GFP was obtained from three sections, while that of L-FILIP-GFP was obtained from five sections and the mean value were calculated as \pm s. e. m., respectively.

Consequently, in GFP-expressing cells (GFP) as control, it was confirmed that a number of labeling cells localizing in the ventricular zone was migrating out towards pial surface. These cells were spindle-shaped with leading and trailing processes oriented cortex radially (Neurosci. Res. (Suppl.) 24, S18, 2000). In contrast, cells expressing S- or L-FILIP-GFP were quite different in shape and migration rate from those of GFP-expressing cells only. These expressing cells were round, did not spread long and radially, and hardly migrated staying around neighborhood of the ventricular zone. These effects of FILIPs in ventricular zone cells were consistent with those in COS-7 cells. Fewer cells expressed L-FILIP-GFP compared with GFP or S-FILIP-GFP. The number of cells expressing L-FILIP-GFP did not show sig-

nificant difference even where they were cultured. These might be caused by the low efficiency of the transfection or translation.

Next, the ontogenetic expression profiles of L- and S-FILIPs in developing rat neocortex were analyzed by immunoblotting with anti-FILIP antibodies. The results are shown in FIG. 4c. The above-mentioned anti-FILIP antibodies (polyclonal anti-FILIP antibody) were prepared with rabbits immunized by synthesized peptide equivalent to the 892nd to 909th residues of the amino acid sequence of S-FILIP, as the method described in J. Neurochem. 75, 1-8, 2000. From this result, L-FILIP was confirmed more remarkably than S-FILIP in cortex developing process. S-FILIP and L-FILIP appear to play similar roles, however, it is apparent that L-FILIP is the major partner of Filamin 1 in the developing neocortex, since L-FILIP expresses at higher level and shows higher capacity for inducing Filamin 1 degradation. Expression of filips mRNA was low on E18, it is likely that already transcribed FILIP proteins remain in sufficient amounts.

Because filips express in ventricular zone, it is likely that FILIPs interact with Filamin 1 gene and induce the degradation in ventricular zone. Cortical solution of E12 rat [protein solution solubilized with a buffer containing 20 mM TRIS™ (pH 7.5), 150 mM NaCl, 1000 U/ml DNase I, 1% NP-40, 1 mM phenylmethanesulfonyl fluoride, 5 $\mu\text{g}/\text{ml}$ aprotinin, 1.5 μM pepstatin A, 2 μM leupeptin] were immunoprecipitated using either anti-Filamin 1 antibodies or anti-c-Myc antibodies (Santa Cruz), and protein was detected using anti-FILIP antibody as a probe. The results are shown in FIG. 4d. The results show that L-FILIP was detected from neocortex solution of E12 rat, while S-FILIP was hardly detected (line 1 in FIG. 4d). Further, since L-FILIP was coimmunoprecipitated with anti-Filamin 1 antibodies in the same solution (line 3 in FIG. 4d), it was revealed that endogenous FILIP (L-FILIP mainly) interacted with endogenous Filamin 1. However, anti-c-Myc antibodies (control) did not show any positive signal (line 2 in FIG. 4d).

It has been known that Filamin 1 protein expresses in migrating and postmigratory neurons in the intermediate zone and the cortical plate of human embryonic brain (Neuron 21, 1315-1325, 1998). Expression of Filamin 1 at rat cerebral cortex was examined with in situ hybridization histochemical study. The results are shown in FIG. 4e. In the figure, CP, S, V, and VZ indicates cortical plate, cranium, lateral ventricle, and ventricular zone, respectively. The scale bar shows 100 μm . The expression of Filamin 1 gene could be confirmed all through the developing cortex, particularly the high expression in ventricular zone was confirmed from these results. Further, expression of the above-mentioned Filamin 1 at cerebral cortex of rat was examined with immunohistochemistry. Frozen sections prepared from E16 rat cerebral cortices fixed with the Zamboni's solution [0.1 M PB (pH 7.4), 2% paraformaldehyde, 0.21% picric acid] were air-dried, permeabilized with PBS containing 0.2% TRITON® X-100, 0.5% bovine serum albumin for 30 min and incubated in the coexistence of anti-Filamin antibodies (1:40; Sigma), followed by incubation in the coexistence of anti-goat IgG antibodies bound with fluorescein (1:100; Jackson ImmunoResearch Laboratories) and stained. The results are shown in FIG. 4f. In the figure, CP, V, and VZ indicate cortical plate, lateral ventricle, and ventricular zone, respectively. The scale bar shows 100 μm . It was revealed by these results that ventricular zone cell highly expressed Filamin 1 gene, while Filamin-like immunoreactivity was lower than those observed in the intermediate zone and cortical plate. Since Filamin 1 is closely related to cell migration (Science 255, 325-7, 1992, Neuron 21, 1315-25, 1998), it is likely that

degradation of Filamin 1 in the ventricular zone through the action of FILIPs is a significant process for controlling the start of migration. The process is a unique molecular mechanism of inhibitory control over radial migration of cells out of the ventricular zone during developing cortex.

INDUSTRIAL APPLICABILITY

The proteins having effects of controlling cell migration and cell death and DNA encoding the proteins are control molecules of cytoskeletal protein. Therefore, they are applicable for an inhibitor for metastasis of a cancer or a tumor or

a regulant of cell migration for transplantation treatment as well as for controlling cell motility and cell death. They are further applicable for controlling cell motility and cell death, screening for promoters or inhibitors of effects of controlling cell migration and/or cell death, and promoters or inhibitors for expressing the proteins/peptides of the present invention, and etc. by using the aforementioned proteins having effects of controlling cell motility and cell death and DNA encoding the proteins. Furthermore, using the proteins/peptides of the present invention makes it possible to reveal the mechanisms of metastasis of a cancer or a tumor, cell migration of neuron and the like.

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1886	agc tgc agt gta gac tta aag aag aag ctc gat ggc ata gag gag ser cys ser val asp leu leu lys lys arg leu asp gln gln gln 590 595 600
1934	gta gaa agy gaa ata aac cga ggt agy tgc agy tgc aag ggg tct gag ttc val gln arg gln ile asn arg gln tyr ser cys lys gln ser gln phe 605 610 615 620
1982	acc tgc ccg gaa gac aat aag atc aga gaa cta aag ctt gaa atc gag thr cys pro gln asp asn lys ile arg gln leu thr leu gln ile gln 625 630 635
2030	aga ctc aag aaa ccg ctc cag cag tgc gag gtc gag gtc gag gtc gag gtc gag arg leu lys lys arg leu gln gln val val gln gln gln gln gln gln gln 640 645 650
2078	atg aag acc gag gac gaa tat gac cag tgc gag cag agy ttc aga acc met lys thr gln asp gln tyr asp gln leu gln gln phe arg thr 655 660 665
2126	gag cag gat aag gca aac ttc ctc cag cag ctc gag gaa atc aaa gln gln asp lys ala asn phe leu ser gln gln gln gln ile lys 670 675 680
2174	cac caa atg gcc aag cac aaa gcc ata gag aaa ggg gag gcc gtc gag agc his gln met ala lys his lys ala ile gln lys gln ala val ser 685 690 695 700
2222	cag gaa gcc gaa ctc gca cac agy ttc cgg ctc gag gag gtc aaa agt gln gln ala gln arg phe arg leu gln gln ala lys ser 705 710 715
2270	cgt gat tca cag gcc gag gtc gag gtc gag gtc ctc aag aag atc cac gag arg asp leu gln ala gln val gln ala leu lys gln lys ile his gln 720 725 730
2318	ctg atg aac aag gaa gac cag ctc cag ctc cag ctc caa gtc gac tat tgc leu met asn lys gln asp gln leu ser gln leu val asp tyr ser 735 740 745
2366	gtc ctt cag caa aga ttt atg gaa gaa gaa act aag aac aag aac atg val leu gln gln arg phe met gln gln thr lys asn lys asn met 750 755 760
2414	ggg agy gtc ctc aat ctc acc aag gag cta gag ctc tcc aag cgc gln arg gln val leu asn leu thr lys gln leu gln leu ser lys arg 765 770 775 780
2462	tac aag cga gct ctc aag ctc agc agt ggg aac ggc cga agy atg gtc gag tyr ser arg ala leu arg pro ser gln asn gln arg arg met val asp 785 790 795
2510	gtg ctt gtc gcc tcc act ggg gtc cag acc gag gtc gtc ggc gat val pro val ala ser thr gln thr gln ala val cys gln asp 800 805 810

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 Ala Ala Gln Gln Thr Pro Ala Val Phe Ile Arg Lys Ser Phe Gln
 815 820 825

gag gaa atc cac atc atg agt aat ctt cga cag gta ggc ctg aag aaa
 Gln Gln Asn His Ile Met Ser Asn Leu Arg Gln Val Gly Leu Lys Lys
 830 835 840

ccc atg gaa cgg tcc tcc gtc ctc gac agg tat ccc cca gca gca aat
 Pro Met Gln Arg Ser Ser Val Leu Asp Tyr Pro Pro Ala Ala Asn
 845 850 855 860

gag ctc acc atg agg aag ctt tgg att cct tgg atg aga aaa aga gaa
 Gln Leu Thr Met Arg Lys Ser Trp Ile Pro Trp Met Arg Lys Arg Gln
 865 870 875

aac ggt cct tcc atc ccg cag gaa ggg aac agg cca aac cag ggt
 Asn Gly Pro Ser Thr Pro Gln Gln Lys Gly Pro Arg Pro Asn Gln Gly
 880 885 890

gaa ggg cac ccc ggg gag ctg gtc cta gca cca aag cag ggc cag cc
 Ala Gly His Pro Gly Gln Leu Val Leu Ala Pro Lys Gln Gly Pro
 895 900 905

cta cac atc cgt gtg aca cca gat cat gag aac agc act gcc acc ctg
 Leu His Ile Arg Val Thr Pro Asp His Gln Asn Ser Thr Ala Thr Leu
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gag atc aca agc ccc aca cca gag gtt ttc agt acc acc gtc
 Arg Ile Thr Ser Pro Thr Ser Gln Gln Phe Ser Ser Thr Thr Val
 925 930 935 940

att cct acc tta ggc aac cag aaa cca aga ata acc att cca tca
 Ile Pro Thr Leu Gly Asn Gln Lys Pro Arg Ile Thr Ile Pro Ser
 945 950 955

ccc aat gtc atg tcc caa aag ccc aaa agt gca gat cct act ctg ggc
 Pro Asn Val Met Ser Ser Gln Lys Pro Lys Ser Ala Asp Pro Thr Leu Gly
 960 965 970

cca gaa cga gca ggc atg tcc cct gtc acc atg att act acc att tcc
 Pro Gln Arg Ala Met Ser Pro Val Thr Ile Thr Thr Ile Ser Arg Gln
 975 980 985

aaq agc ccc gaa ggt gga agc ggc ggc ttt gcc gac agc cct gca tcc
 Lys Ser Pro Gln Gly Gly Arg Ser Ala Phe Ala Asp Arg Pro Ala Ser
 990 995 1000

ccc atc caa atc atg acg gtg tca aca tct gca gct ccc act gaa atc
 Pro Ile Gln Ile Met Thr Val Ser Thr Ser Thr Ala Pro Thr Gln Ile
 1005 1010 1015 1020

gct gtc tcc cct gaa tcc cag gaa gtc cct atg gga agc act atc ctg
 Ala Val Ser Pro Gln Ser Gln Gln Val Pro Met Gly Arg Thr Ile Leu
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aaa gtc acc ccc gaa aaa cca aat gtt cca gcc ccc gtc cgg aag tac
 Lys Val Thr Pro Gln Lys Gln Thr Val Pro Ala Pro Val Arg Lys Tyr
 1040 1045 1050

aac tcc aat gct aat atc atc acc acc gaa gac aat aaa att cac att
 Asn Ser Asn Ala Asn Ile Ile Thr Thr Gln Asp Asn Lys Ile His Ile
 1055 1060 1065

caq ctg ggt tcc cag ttt aag cga tct cct ggg cct gcc gct gaa ggc
 His Leu Gly Ser Gln Phe Lys Arg Ser Pro Gly Pro Ala Ala Gln Gly
 1070 1075 1080

gtg agc cca gtt atc acc gtc cgg cct gtc aac gtc aca ggc gag aag
 Val Ser Pro Val Ile Thr Val Arg Pro Val Asn Val Thr Ala Gln Lys
 1085 1090 1095 1100

gag gtt tct tca aca ggc aca gtc ctt cgc ctt ccc agc aac cac ctg tct
 Gln Val Ser Thr Gly Thr Val Leu Arg Ser Pro Arg Asn His Leu Ser
 1105 1110 1115

tca aqa ccc ggt gta Ser Ala Ser Lys Val Thr Ser Thr Ile Thr Ile Thr Pro
 Ser Arg Pro Gly Ala Ser Lys Val Thr Ser Thr Ile Thr Ile Thr Pro
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gtc aca acg tca tcc aca cga gga acc caa tca gtg tca gga caa gat 3518
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ggg tca tct cag cgg cct acc ccc acc cgc att cct atg tca aaa ggt 3566
Gly Ser Ser Gln Arg Pro Thr Pro Thr Arg Ile Pro Met Ser Lys Gly
      1150                1155                1160

atg aaa gct gga aag cca gta gtg gca gcc tca gga gca gga aat ctg 3614
Met Lys Ala Gly Lys Pro Val Val Ala Ala Ser Gly Ala Gly Asn Leu
      1165                1170                1175                1180

acc aaa ttc cag cct cga gct gag act cag tct atg aaa ata gag ctg 3662
Thr Lys Phe Gln Pro Arg Ala Glu Thr Gln Ser Met Lys Ile Glu Leu
      1185                1190                1195

aag aaa tct gca gcc agc agc act gcc tct ctt gga ggg ggg aag ggc 3710
Lys Lys Ser Ala Ala Ser Ser Thr Ala Ser Leu Gly Gly Gly Lys Gly
      1200                1205                1210

tgagggcagt ggctaagggg gtatgttgta aggatgctac tgctgcagtg gaaacaaacc 3770

ttcctctgtg ccaacccttt ccttgtaacta ctaatttaag ttttaaataat cttgtttata 3830

aaataacat ttaatagcca tgcaccccc tccattttg tgcatctgtt tcaatgcagg 3890

ggaatagaat taattagcag aatttctgtt tgctgaatgt tctgttgaag atgttggtcc 3950

agttcagttt tacttctagc atgtggcccc attcaaggta gctcacgagt tgtgaagccc 4010

tcaatatcgt caccggagag atttgaggac cacattacat atgctcccaa aggctggctc 4070

ccaattttcc taattgtaag ccaactttaa tagactcagt tctgtgattt ttttttccaa 4130

aaaaaaaaata ttttgaataa ggacagagtt taacagttgt cattttgcac tatcaagcca 4190

tgagtttgat atatgggtta taagaaaaga atactttcag agctatcaca gggctctctaa 4250

acttttgtaa aaacaaaagc ccctaatatg acctcaggaa acaatttgaa catgaaataa 4310

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<210> SEQ ID NO 2

<211> LENGTH: 1212

<212> TYPE: PRT

<213> ORGANISM: Rattus norvegicus

<400> SEQUENCE: 2

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Ser Cys Pro Lys Ser Ser Ile Ile Ser Ser Asp Gly Gly Lys Gly Pro
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Ser Glu Asp Ala Lys Lys Asn Lys Ala Asn Arg Lys Glu Glu Asp Val
      35           40           45

Met Ala Ser Gly Thr Ile Lys Arg His Leu Lys Pro Ser Gly Glu Ser
      50           55           60

Glu Lys Lys Thr Lys Lys Ser Val Glu Leu Ser Lys Glu Asp Leu Ile
      65           70           75           80

Gln Leu Leu Ser Ile Met Glu Gly Glu Leu Gln Ala Arg Glu Asp Val
      85           90           95

Ile His Met Leu Arg Thr Glu Lys Thr Lys Pro Glu Val Leu Glu Ala
      100          105          110

His Tyr Gly Ser Ala Glu Pro Glu Lys Val Leu Arg Val Leu His Arg
      115          120          125

Asp Ala Ile Leu Ala Gln Glu Lys Ser Ile Gly Glu Asp Val Tyr Glu
      130          135          140

Lys Pro Ile Ser Glu Leu Asp Arg Leu Glu Glu Lys Gln Lys Glu Thr

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145				150						155				160	
Tyr	Arg	Arg	Met	Leu	Glu	Gln	Leu	Leu	Leu	Ala	Glu	Lys	Cys	His	Arg
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Arg	Thr	Val	Tyr	Glu	Leu	Glu	Asn	Glu	Lys	His	Lys	His	Thr	Asp	Tyr
			180					185					190		
Met	Asn	Lys	Ser	Asp	Asp	Phe	Thr	Asn	Leu	Leu	Glu	Gln	Glu	Arg	Glu
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Arg	Leu	Lys	Lys	Leu	Leu	Glu	Gln	Glu	Lys	Ala	Tyr	Gln	Ala	Arg	Lys
	210					215					220				
Glu	Lys	Glu	Asn	Ala	Lys	Arg	Leu	Asn	Lys	Leu	Arg	Asp	Glu	Leu	Val
225					230					235					240
Lys	Leu	Lys	Ser	Phe	Ala	Leu	Met	Leu	Val	Asp	Glu	Arg	Gln	Met	His
				245					250					255	
Ile	Glu	Gln	Leu	Gly	Leu	Gln	Ser	Gln	Lys	Val	Gln	Asp	Leu	Thr	Gln
			260					265					270		
Lys	Leu	Arg	Glu	Glu	Glu	Glu	Lys	Leu	Lys	Ala	Val	Thr	Tyr	Lys	Ser
		275					280					285			
Lys	Glu	Asp	Arg	Gln	Lys	Leu	Leu	Lys	Leu	Glu	Val	Asp	Phe	Glu	His
	290					295					300				
Lys	Ala	Ser	Arg	Phe	Ser	Gln	Glu	His	Glu	Glu	Met	Asn	Ala	Lys	Leu
305					310					315					320
Ala	Asn	Gln	Glu	Ser	His	Asn	Arg	Gln	Leu	Arg	Leu	Lys	Leu	Val	Gly
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Leu	Ser	Gln	Arg	Ile	Glu	Glu	Leu	Glu	Glu	Thr	Asn	Lys	Ser	Leu	Gln
			340					345					350		
Lys	Ala	Glu	Glu	Glu	Leu	Gln	Glu	Leu	Arg	Glu	Lys	Ile	Ala	Lys	Gly
		355					360					365			
Glu	Cys	Gly	Asn	Ser	Ser	Leu	Met	Ala	Glu	Val	Glu	Ser	Leu	Arg	Lys
	370					375					380				
Arg	Val	Leu	Glu	Met	Glu	Gly	Lys	Asp	Glu	Glu	Ile	Thr	Lys	Thr	Glu
385					390					395					400
Ala	Gln	Cys	Arg	Glu	Leu	Lys	Lys	Lys	Leu	Gln	Glu	Glu	Glu	His	His
				405					410						415
Ser	Lys	Glu	Leu	Arg	Leu	Glu	Val	Glu	Lys	Leu	Gln	Lys	Arg	Met	Ser
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Glu	Leu	Glu	Lys	Leu	Glu	Glu	Ala	Phe	Ser	Arg	Ser	Lys	Ser	Glu	Cys
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Thr	Gln	Leu	His	Leu	Asn	Leu	Glu	Lys	Glu	Lys	Asn	Leu	Thr	Lys	Asp
	450					455					460				
Leu	Leu	Asn	Glu	Leu	Glu	Val	Val	Lys	Ser	Arg	Val	Lys	Glu	Leu	Glu
465					470					475					480
Cys	Ser	Glu	Ser	Arg	Leu	Glu	Lys	Ala	Glu	Leu	Ser	Leu	Lys	Asp	Asp
				485					490					495	
Leu	Thr	Lys	Leu	Lys	Ser	Phe	Thr	Val	Met	Leu	Val	Asp	Glu	Arg	Lys
			500					505					510		
Asn	Met	Met	Glu	Lys	Ile	Lys	Gln	Glu	Glu	Arg	Lys	Val	Asp	Gly	Leu
		515					520						525		
Asn	Lys	Asn	Phe	Lys	Val	Glu	Gln	Gly	Lys	Val	Met	Asp	Val	Thr	Glu
	530					535					540				
Lys	Leu	Ile	Glu	Glu	Ser	Lys	Lys	Leu	Leu	Lys	Leu	Lys	Ser	Glu	Met
545					550					555					560
Glu	Glu	Lys	Glu	Tyr	Ser	Leu	Thr	Lys	Glu	Arg	Asp	Glu	Leu	Met	Gly
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Lys Leu Arg Ser Glu Glu Glu Arg Ser Cys Glu Leu Ser Cys Ser Val
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 Asp Leu Leu Lys Lys Arg Leu Asp Gly Ile Glu Glu Val Glu Arg Glu
 595 600 605
 Ile Asn Arg Gly Arg Ser Cys Lys Gly Ser Glu Phe Thr Cys Pro Glu
 610 615 620
 Asp Asn Lys Ile Arg Glu Leu Thr Leu Glu Ile Glu Arg Leu Lys Lys
 625 630 635 640
 Arg Leu Gln Gln Leu Glu Val Val Glu Gly Asp Leu Met Lys Thr Glu
 645 650 655
 Asp Glu Tyr Asp Gln Leu Glu Gln Lys Phe Arg Thr Glu Gln Asp Lys
 660 665 670
 Ala Asn Phe Leu Ser Gln Gln Leu Glu Glu Ile Lys His Gln Met Ala
 675 680 685
 Lys His Lys Ala Ile Glu Lys Gly Glu Ala Val Ser Gln Glu Ala Glu
 690 695 700
 Leu Arg His Arg Phe Arg Leu Glu Glu Ala Lys Ser Arg Asp Leu Gln
 705 710 715 720
 Ala Glu Val Gln Ala Leu Lys Glu Lys Ile His Glu Leu Met Asn Lys
 725 730 735
 Glu Asp Gln Leu Ser Gln Leu Gln Val Asp Tyr Ser Val Leu Gln Gln
 740 745 750
 Arg Phe Met Glu Glu Glu Thr Lys Asn Lys Asn Met Gly Arg Glu Val
 755 760 765
 Leu Asn Leu Thr Lys Glu Leu Glu Leu Ser Lys Arg Tyr Ser Arg Ala
 770 775 780
 Leu Arg Pro Ser Gly Asn Gly Arg Arg Met Val Asp Val Pro Val Ala
 785 790 795 800
 Ser Thr Gly Val Gln Thr Glu Ala Val Cys Gly Asp Ala Ala Glu Glu
 805 810 815
 Glu Thr Pro Ala Val Phe Ile Arg Lys Ser Phe Gln Glu Glu Asn His
 820 825 830
 Ile Met Ser Asn Leu Arg Gln Val Gly Leu Lys Lys Pro Met Glu Arg
 835 840 845
 Ser Ser Val Leu Asp Arg Tyr Pro Pro Ala Ala Asn Glu Leu Thr Met
 850 855 860
 Arg Lys Ser Trp Ile Pro Trp Met Arg Lys Arg Glu Asn Gly Pro Ser
 865 870 875 880
 Thr Pro Gln Glu Lys Gly Pro Arg Pro Asn Gln Gly Ala Gly His Pro
 885 890 895
 Gly Glu Leu Val Leu Ala Pro Lys Gln Gly Gln Pro Leu His Ile Arg
 900 905 910
 Val Thr Pro Asp His Glu Asn Ser Thr Ala Thr Leu Glu Ile Thr Ser
 915 920 925
 Pro Thr Ser Glu Glu Phe Phe Ser Ser Thr Thr Val Ile Pro Thr Leu
 930 935 940
 Gly Asn Gln Lys Pro Arg Ile Thr Ile Ile Pro Ser Pro Asn Val Met
 945 950 955 960
 Ser Gln Lys Pro Lys Ser Ala Asp Pro Thr Leu Gly Pro Glu Arg Ala
 965 970 975
 Met Ser Pro Val Thr Ile Thr Thr Ile Ser Arg Glu Lys Ser Pro Glu
 980 985 990

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Gly Gly Arg Ser Ala Phe Ala Asp Arg Pro Ala Ser Pro Ile Gln Ile
 995 1000 1005

Met Thr Val Ser Thr Ser Ala Ala Pro Thr Glu Ile Ala Val Ser Pro
 1010 1015 1020

Glu Ser Gln Glu Val Pro Met Gly Arg Thr Ile Leu Lys Val Thr Pro
 1025 1030 1035 1040

Glu Lys Gln Thr Val Pro Ala Pro Val Arg Lys Tyr Asn Ser Asn Ala
 1045 1050 1055

Asn Ile Ile Thr Thr Glu Asp Asn Lys Ile His Ile His Leu Gly Ser
 1060 1065 1070

Gln Phe Lys Arg Ser Pro Gly Pro Ala Ala Glu Gly Val Ser Pro Val
 1075 1080 1085

Ile Thr Val Arg Pro Val Asn Val Thr Ala Glu Lys Glu Val Ser Thr
 1090 1095 1100

Gly Thr Val Leu Arg Ser Pro Arg Asn His Leu Ser Ser Arg Pro Gly
 1105 1110 1115 1120

Ala Ser Lys Val Thr Ser Thr Ile Thr Ile Thr Pro Val Thr Thr Ser
 1125 1130 1135

Ser Thr Arg Gly Thr Gln Ser Val Ser Gly Gln Asp Gly Ser Ser Gln
 1140 1145 1150

Arg Pro Thr Pro Thr Arg Ile Pro Met Ser Lys Gly Met Lys Ala Gly
 1155 1160 1165

Lys Pro Val Val Ala Ala Ser Gly Ala Gly Asn Leu Thr Lys Phe Gln
 1170 1175 1180

Pro Arg Ala Glu Thr Gln Ser Met Lys Ile Glu Leu Lys Lys Ser Ala
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Ala Ser Ser Thr Ala Ser Leu Gly Gly Gly Lys Gly
 1205 1210

<210> SEQ ID NO 3
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 <212> TYPE: DNA
 <213> ORGANISM: Rattus norvegicus
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (237)..(3131)

<400> SEQUENCE: 3

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ggttgaaaaa gctccttgaa caagaaaaag cttaccaagc cgcacaagaa aaggaaaacg 180

ctaagcggct caacaaactt cgagatgagc ttgtgaagct caagtccttc gccctc atg 239
 Met
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ttg gtg gac gag agg cag atg cac atc gag caa ctg ggc ctg cag agt 287
 Leu Val Asp Glu Arg Gln Met His Ile Glu Gln Leu Gly Leu Gln Ser
 5 10 15

cag aaa gtc cag gac ctc act cag aag ctg agg gag gag gaa gaa aaa 335
 Gln Lys Val Gln Asp Leu Thr Gln Lys Leu Arg Glu Glu Glu Glu Lys
 20 25 30

ctc aaa gcg gtc act tac aaa tcc aag gaa gac cgc cag aag ctg ctc 383
 Leu Lys Ala Val Thr Tyr Lys Ser Lys Glu Asp Arg Gln Lys Leu Leu
 35 40 45

aag tta gaa gtg gac ttc gaa cac aag gcc tcg agg ttt tcc cag gag 431
 Lys Leu Glu Val Asp Phe Glu His Lys Ala Ser Arg Phe Ser Gln Glu
 50 55 60 65

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70 75 80	
caa ctt cga ctc aaa ctg gtt ggc tta tcg caa agg att gag gag ctg	527
Gln Leu Arg Leu Lys Leu Val Gly Leu Ser Gln Arg Ile Glu Glu Leu	
85 90 95	
gaa gag acc aat aaa agc ctt cag aag gca gag gaa gag ctc cag gag	575
Glu Glu Thr Asn Lys Ser Leu Gln Lys Ala Glu Glu Glu Leu Gln Glu	
100 105 110	
ctg aga gag aaa att gcc aaa ggg gaa tgt gga aac tcc agt ctc atg	623
Leu Arg Glu Lys Ile Ala Lys Gly Glu Cys Gly Asn Ser Ser Leu Met	
115 120 125	
gcg gaa gtg gag agt ctg cgc aag cgc gtg ctt gag atg gag ggc aag	671
Ala Glu Val Glu Ser Leu Arg Lys Arg Val Leu Glu Met Glu Gly Lys	
130 135 140 145	
gat gaa gag atc acg aag acc gag gcc cag tgc cgg gag ctg aag aag	719
Asp Glu Glu Ile Thr Lys Thr Glu Ala Gln Cys Arg Glu Leu Lys Lys	
150 155 160	
aag ctc caa gag gaa gaa cac cac agc aag gaa ctt aga cta gaa gtg	767
Lys Leu Gln Glu Glu Glu His His Ser Lys Glu Leu Arg Leu Glu Val	
165 170 175	
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Glu Lys Leu Gln Lys Arg Met Ser Glu Leu Glu Lys Leu Glu Glu Ala	
180 185 190	
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Phe Ser Arg Ser Lys Ser Glu Cys Thr Gln Leu His Leu Asn Leu Glu	
195 200 205	
aag gag aag aac cta acc aaa gac ctg ctg aac gag ctg gag gtg gtc	911
Lys Glu Lys Asn Leu Thr Lys Asp Leu Leu Asn Glu Leu Glu Val Val	
210 215 220 225	
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Lys Ser Arg Val Lys Glu Leu Glu Cys Ser Glu Ser Arg Leu Glu Lys	
230 235 240	
gcc gag tta agc ctc aaa gat gac ctt aca aag ctg aag tcc ttc act	1007
Ala Glu Leu Ser Leu Lys Asp Asp Leu Thr Lys Leu Lys Ser Phe Thr	
245 250 255	
gtg atg ctg gtg gat gag agg aaa aat atg atg gag aaa ata aag caa	1055
Val Met Leu Val Asp Glu Arg Lys Asn Met Met Glu Lys Ile Lys Gln	
260 265 270	
gaa gag agg aaa gtg gat ggg ttg aat aaa aac ttt aag gtg gag cag	1103
Glu Glu Arg Lys Val Asp Gly Leu Asn Lys Asn Phe Lys Val Glu Gln	
275 280 285	
gga aaa gtc atg gat gtg acg gaa aag cta atc gag gaa agc aag aag	1151
Gly Lys Val Met Asp Val Thr Glu Lys Leu Ile Glu Glu Ser Lys Lys	
290 295 300 305	
ctt tta aaa ctc aaa tct gaa atg gag gaa aag gag tac agt ctg aca	1199
Leu Leu Lys Leu Lys Ser Glu Met Glu Glu Lys Glu Tyr Ser Leu Thr	
310 315 320	
aag gag agg gat gag ctg atg ggt aaa ctg agg agc gaa gaa gaa agg	1247
Lys Glu Arg Asp Glu Leu Met Gly Lys Leu Arg Ser Glu Glu Glu Arg	
325 330 335	
tcc tgt gaa ctg agc tgc agt gta gac tta cta aag aag cgg ctt gat	1295
Ser Cys Glu Leu Ser Cys Ser Val Asp Leu Leu Lys Lys Arg Leu Asp	
340 345 350	
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Gly Ile Glu Glu Val Glu Arg Glu Ile Asn Arg Gly Arg Ser Cys Lys	
355 360 365	
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Gly Ser Glu Phe Thr Cys Pro Glu Asp Asn Lys Ile Arg Glu Leu Thr	
370 375 380 385	

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gag ggg gac ttg atg aag acc gag gac gaa tat gac cag ttg gag cag	1487
Glu Gly Asp Leu Met Lys Thr Glu Asp Glu Tyr Asp Gln Leu Glu Gln	
405 410 415	
aag ttc aga acc gag cag gat aag gca aac ttc ctc tcc cag cag ctc	1535
Lys Phe Arg Thr Glu Gln Asp Lys Ala Asn Phe Leu Ser Gln Gln Leu	
420 425 430	
gag gaa atc aaa cac caa atg gcc aag cac aaa gcc ata gag aaa ggg	1583
Glu Glu Ile Lys His Gln Met Ala Lys His Lys Ala Ile Glu Lys Gly	
435 440 445	
gag gcc gtg agc cag gaa gcc gaa ctg cga cac agg ttt cgg ctg gag	1631
Glu Ala Val Ser Gln Glu Ala Glu Leu Arg His Arg Phe Arg Leu Glu	
450 455 460 465	
gag gct aaa agt cgt gat tta cag gcc gag gtg cag gct ctc aag gag	1679
Glu Ala Lys Ser Arg Asp Leu Gln Ala Glu Val Gln Ala Leu Lys Glu	
470 475 480	
aag atc cac gag ctg atg aac aag gaa gac cag ctg tct cag ctc caa	1727
Lys Ile His Glu Leu Met Asn Lys Glu Asp Gln Leu Ser Gln Leu Gln	
485 490 495	
gtc gac tat tcg gtc ctt cag caa aga ttt atg gaa gaa gaa act aag	1775
Val Asp Tyr Ser Val Leu Gln Gln Arg Phe Met Glu Glu Glu Thr Lys	
500 505 510	
aac aag aac atg ggg agg gag gtc ctc aat ctg acc aag gag cta gag	1823
Asn Lys Asn Met Gly Arg Glu Val Leu Asn Leu Thr Lys Glu Leu Glu	
515 520 525	
ctt tcc aag cgc tac agc cga gct ctc agg ccg agt ggg aac ggc cga	1871
Leu Ser Lys Arg Tyr Ser Arg Ala Leu Arg Pro Ser Gly Asn Gly Arg	
530 535 540 545	
agg atg gtg gac gtg cct gtg gcc tcc act ggg gtg cag acc gag gcg	1919
Arg Met Val Asp Val Pro Val Ala Ser Thr Gly Val Gln Thr Glu Ala	
550 555 560	
gtg tgc ggg gat gct gcg gag gag gag acc ccg gct gtg ttc att cgc	1967
Val Cys Gly Asp Ala Ala Glu Glu Glu Thr Pro Ala Val Phe Ile Arg	
565 570 575	
aaa tcc ttc cag gag gaa aat cac atc atg agt aat ctt cga cag gta	2015
Lys Ser Phe Gln Glu Glu Asn His Ile Met Ser Asn Leu Arg Gln Val	
580 585 590	
ggc ctg aag aaa ccc atg gaa cgg tcc tcg gtc ctc gac agg tat ccc	2063
Gly Leu Lys Lys Pro Met Glu Arg Ser Ser Val Leu Asp Arg Tyr Pro	
595 600 605	
cca gca gcg aat gag ctc acc atg agg aag tct tgg att cct tgg atg	2111
Pro Ala Ala Asn Glu Leu Thr Met Arg Lys Ser Trp Ile Pro Trp Met	
610 615 620 625	
aga aaa aga gaa aac ggt cct tcc act ccg cag gag aaa ggg ccc agg	2159
Arg Lys Arg Glu Asn Gly Pro Ser Thr Pro Gln Glu Lys Gly Pro Arg	
630 635 640	
cca aac cag ggt gca ggg cac ccc ggg gag ctg gtc cta gca cca aag	2207
Pro Asn Gln Gly Ala Gly His Pro Gly Glu Leu Val Leu Ala Pro Lys	
645 650 655	
cag ggc cag ccc cta cac atc cgt gtg aca cca gat cat gag aac agc	2255
Gln Gly Gln Pro Leu His Ile Arg Val Thr Pro Asp His Glu Asn Ser	
660 665 670	
act gcc acc ctg gag atc aca agc ccc aca tct gaa gag ttt ttc tct	2303
Thr Ala Thr Leu Glu Ile Thr Ser Pro Thr Ser Glu Glu Phe Phe Ser	
675 680 685	
agt acc acc gtc att cct acc tta ggc aac cag aaa cca aga ata acc	2351
Ser Thr Thr Val Ile Pro Thr Leu Gly Asn Gln Lys Pro Arg Ile Thr	

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690	695	700	705	
att att cca tca ccc aat gtc atg tcg caa aag ccc aaa agt gca gat				2399
Ile Ile Pro Ser Pro Asn Val Met Ser Gln Lys Pro Lys Ser Ala Asp	710	715	720	
cct act ctc ggc cca gaa cga gcc atg tcc cct gtc acg att act act				2447
Pro Thr Leu Gly Pro Glu Arg Ala Met Ser Pro Val Thr Ile Thr Thr	725	730	735	
att tcc aga gag aag agc ccg gaa ggt gga agg agc gcc ttt gcc gac				2495
Ile Ser Arg Glu Lys Ser Pro Glu Gly Gly Arg Ser Ala Phe Ala Asp	740	745	750	
agg cct gca tcc ccc atc caa atc atg acg gtg tca aca tct gca gct				2543
Arg Pro Ala Ser Pro Ile Gln Ile Met Thr Val Ser Thr Ser Ala Ala	755	760	765	
ccc act gaa atc gct gtc tct cct gaa tct cag gaa gtg cct atg gga				2591
Pro Thr Glu Ile Ala Val Ser Pro Glu Ser Gln Glu Val Pro Met Gly	770	775	780	785
agg act atc ctc aaa gtc acc ccg gaa aaa caa act gtt cca gcc ccc				2639
Arg Thr Ile Leu Lys Val Thr Pro Glu Lys Gln Thr Val Pro Ala Pro	790	795	800	
gtg cgg aag tac aac tcc aat gct aat atc atc acc acg gaa gac aat				2687
Val Arg Lys Tyr Asn Ser Asn Ala Asn Ile Ile Thr Thr Glu Asp Asn	805	810	815	
aaa att cac att cac ctg ggt tct cag ttt aag cga tct cct ggg cct				2735
Lys Ile His Ile His Leu Gly Ser Gln Phe Lys Arg Ser Pro Gly Pro	820	825	830	
gcc gct gaa ggc gtg agc cca gtt atc acc gtc cgg cct gtc aac gtg				2783
Ala Ala Glu Gly Val Ser Pro Val Ile Thr Val Arg Pro Val Asn Val	835	840	845	
aca gcg gag aag gag gtt tct aca ggc aca gtc ctt cgc tct ccc agg				2831
Thr Ala Glu Lys Glu Val Ser Thr Gly Thr Val Leu Arg Ser Pro Arg	850	855	860	865
aac cac ctc tct tca aga ccc ggt gct agc aaa gtg acc agc act ata				2879
Asn His Leu Ser Ser Arg Pro Gly Ala Ser Lys Val Thr Ser Thr Ile	870	875	880	
act ata acc ccg gtc aca acg tca tcc aca cga gga acc caa tca gtg				2927
Thr Ile Thr Pro Val Thr Thr Ser Ser Thr Arg Gly Thr Gln Ser Val	885	890	895	
tca gga caa gat ggg tca tct cag cgg cct acc ccc acc cgc att cct				2975
Ser Gly Gln Asp Gly Ser Ser Gln Arg Pro Thr Pro Thr Arg Ile Pro	900	905	910	
atg tca aaa ggt atg aaa gct gga aag cca gta gtg gca gcc tca gga				3023
Met Ser Lys Gly Met Lys Ala Gly Lys Pro Val Val Ala Ala Ser Gly	915	920	925	
gca gga aat ctg acc aaa ttc cag cct cga gct gag act cag tct atg				3071
Ala Gly Asn Leu Thr Lys Phe Gln Pro Arg Ala Glu Thr Gln Ser Met	930	935	940	945
aaa ata gag ctg aag aaa tct gca gcc agc agc act gcc tct ctt gga				3119
Lys Ile Glu Leu Lys Lys Ser Ala Ala Ser Ser Thr Ala Ser Leu Gly	950	955	960	
ggg ggg aag ggc tgagggcagt ggctaagggg gtatgttgta aggatgctac				3171
Gly Gly Lys Gly	965			
tgctgcagtg gaaacaaacc ttctctgtg ccaacccttt ccttgtaacta ctaatttaag				3231
ttttaaatat cttgtttata aaataacat ttaatagcca tgcaaccccc tcccattttg				3291
tgcatctggt tcaatgcagg ggaatagaat taattagcag aatttctggt tgctgaatgt				3351
tctgttgaag atgttggtcc agttcagttt tacttotagc atgtggcccc attcaaggta				3411
gctcagcagt tgtgaagccc tcaatcgtg caccggagag atttgaggac cacattacat				3471

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atgctcccaa aggctggctc ccaattttcc taattgtaag ccaactttaa tagactcagt 3531
tctgtgattt tttttccaa aaaaaaata ttttgaaata ggacagagtt taacagttgt 3591
cattttgcac tatcaagcca tgagtttgat atatgggta taagaaaaga atactttcag 3651
agctatcaca gggctctcaa acttttggaa aaacaaaagc ccctaataatg acctcaggaa 3711
acaatttgaa catgaaataa aatggaatg aactgtggaa tcttaaaaaa aaaaaaaaaa 3771
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<210> SEQ ID NO 4

<211> LENGTH: 965

<212> TYPE: PRT

<213> ORGANISM: Rattus norvegicus

<400> SEQUENCE: 4

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

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Thr Ile Ser Arg Glu Lys Ser Pro Glu Gly Gly Arg Ser Ala Phe Ala
 740 745 750

Asp Arg Pro Ala Ser Pro Ile Gln Ile Met Thr Val Ser Thr Ser Ala
 755 760 765

Ala Pro Thr Glu Ile Ala Val Ser Pro Glu Ser Gln Glu Val Pro Met
 770 775 780

Gly Arg Thr Ile Leu Lys Val Thr Pro Glu Lys Gln Thr Val Pro Ala
 785 790 795 800

Pro Val Arg Lys Tyr Asn Ser Asn Ala Asn Ile Ile Thr Thr Glu Asp
 805 810 815

Asn Lys Ile His Ile His Leu Gly Ser Gln Phe Lys Arg Ser Pro Gly
 820 825 830

Pro Ala Ala Glu Gly Val Ser Pro Val Ile Thr Val Arg Pro Val Asn
 835 840 845

Val Thr Ala Glu Lys Glu Val Ser Thr Gly Thr Val Leu Arg Ser Pro
 850 855 860

Arg Asn His Leu Ser Ser Arg Pro Gly Ala Ser Lys Val Thr Ser Thr
 865 870 875 880

Ile Thr Ile Thr Pro Val Thr Thr Ser Ser Thr Arg Gly Thr Gln Ser
 885 890 895

Val Ser Gly Gln Asp Gly Ser Ser Gln Arg Pro Thr Pro Thr Arg Ile
 900 905 910

Pro Met Ser Lys Gly Met Lys Ala Gly Lys Pro Val Val Ala Ala Ser
 915 920 925

Gly Ala Gly Asn Leu Thr Lys Phe Gln Pro Arg Ala Glu Thr Gln Ser
 930 935 940

Met Lys Ile Glu Leu Lys Lys Ser Ala Ala Ser Ser Thr Ala Ser Leu
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Gly Gly Gly Lys Gly
 965

<210> SEQ ID NO 5
 <211> LENGTH: 4247
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (7)..(3645)

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 Met Arg Ser Arg Asn Gln Gly Gly Glu Ser Ala Ser Asp Gly
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cat atc tcc tgt ccc aag ccc tcc atc atc ggc aat gct ggt gaa aaa 96
 His Ile Ser Cys Pro Lys Pro Ser Ile Ile Gly Asn Ala Gly Glu Lys
 15 20 25 30

agt ctc tca gaa gat gca aaa aag aag aag aaa tca aat agg aag gag 144
 Ser Leu Ser Glu Asp Ala Lys Lys Lys Lys Lys Ser Asn Arg Lys Glu
 35 40 45

gat gat gtc atg gcc tca gga act gtc aaa cga cac cta aaa aca tct 192
 Asp Asp Val Met Ala Ser Gly Thr Val Lys Arg His Leu Lys Thr Ser
 50 55 60

gga gaa tgt gaa cga aaa act aag aaa tcc ctg gag tta tcc aaa gaa 240
 Gly Glu Cys Glu Arg Lys Thr Lys Lys Ser Leu Glu Leu Ser Lys Glu
 65 70 75

gac ctc atc caa cta ctc agt ata atg gaa ggg gag ttg cag gcc aga 288
 Asp Leu Ile Gln Leu Leu Ser Ile Met Glu Gly Glu Leu Gln Ala Arg

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80	85	90	
gaa gat gtg atc cac atg ctg aag aca gag aaa acc aag cct gag gtt Glu Asp Val Ile His Met Leu Lys Thr Glu Lys Thr Lys Pro Glu Val 95 100 105 110			336
ctg gag gct cat tac ggg tct gcg gag cca gag aaa gtg ctg cgg gtc Leu Glu Ala His Tyr Gly Ser Ala Glu Pro Glu Lys Val Leu Arg Val 115 120 125			384
ctg cac cga gat gcc att ctt gcc cag gag aaa tcc ata gga gaa gat Leu His Arg Asp Ala Ile Leu Ala Gln Glu Lys Ser Ile Gly Glu Asp 130 135 140			432
gtc tat gag aaa cgg att tca gag ctg gac aga ctt gag gaa aaa cag Val Tyr Glu Lys Pro Ile Ser Glu Leu Asp Arg Leu Glu Glu Lys Gln 145 150 155			480
aaa gaa acc tac cgg cgc atg cta gag cag ctg ttg ctg gcc gag aag Lys Glu Thr Tyr Arg Arg Met Leu Glu Gln Leu Leu Leu Ala Glu Lys 160 165 170			528
tgt cat agg cgc acc gta tac gag tta gag aac gag aag cat aaa cac Cys His Arg Arg Thr Val Tyr Glu Leu Glu Asn Glu Lys His Lys His 175 180 185 190			576
act gac tac atg aac aag agc gac gac ttc acc aac ctg ctg gag cag Thr Asp Tyr Met Asn Lys Ser Asp Asp Phe Thr Asn Leu Leu Glu Gln 195 200 205			624
gag cgg gag agg tta aaa aag ctc ctt gaa caa gaa aag gct tat caa Glu Arg Glu Arg Leu Lys Lys Leu Leu Glu Gln Glu Lys Ala Tyr Gln 210 215 220			672
gcc cgc aaa gaa aag gaa aat gct aaa cga ctc aat aaa cta aga gat Ala Arg Lys Glu Lys Glu Asn Ala Lys Arg Leu Asn Lys Leu Arg Asp 225 230 235			720
gag ctt gtt aaa ctc aaa tcc ttt gca ctc atg ctg gtg gat gaa aga Glu Leu Val Lys Leu Lys Ser Phe Ala Leu Met Leu Val Asp Glu Arg 240 245 250			768
caa atg cac att gaa caa ctt ggc ctg caa agc cag aaa gta cag gat Gln Met His Ile Glu Gln Leu Gly Leu Gln Ser Gln Lys Val Gln Asp 255 260 265 270			816
ctt act cag aag ctg agg gaa gaa gaa gag aag ctc aaa gcc att act Leu Thr Gln Lys Leu Arg Glu Glu Glu Lys Leu Lys Ala Ile Thr 275 280 285			864
tcc aaa tcc aaa gaa gac aga cag aaa ttg ctc aag tta gaa gtg gac Ser Lys Ser Lys Glu Asp Arg Gln Lys Leu Leu Lys Leu Glu Val Asp 290 295 300			912
ttt gaa cac aag gct tcg agg ttt tct caa gag cat gaa gag atg aac Phe Glu His Lys Ala Ser Arg Phe Ser Gln Glu His Glu Glu Met Asn 305 310 315			960
gct aaa ctg gct aat caa gag tct cac aat agg caa ctt aga ctc aag Ala Lys Leu Ala Asn Gln Glu Ser His Asn Arg Gln Leu Arg Leu Lys 320 325 330			1008
ctg gtt ggc tta acc caa aga atc gag gag cta gaa gag acc aac aaa Leu Val Gly Leu Thr Gln Arg Ile Glu Glu Leu Glu Glu Thr Asn Lys 335 340 345 350			1056
aat ctg cag aag gca gag gaa gaa ctt caa gaa tta aga gat aaa att Asn Leu Gln Lys Ala Glu Glu Glu Leu Gln Glu Leu Arg Asp Lys Ile 355 360 365			1104
gcc aaa gga gaa tgt gga aac tct agc ctc atg gca gaa gtg gaa aat Ala Lys Gly Glu Cys Gly Asn Ser Ser Leu Met Ala Glu Val Glu Asn 370 375 380			1152
ctt cga aag cgt gtg ctt gaa atg gaa ggt aaa gat gag gag atc act Leu Arg Lys Arg Val Leu Glu Met Glu Gly Lys Asp Glu Glu Ile Thr 385 390 395			1200
aaa act gaa tcc cag tgt agg gaa ttg agg aag aag ctg caa gag gaa			1248

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Lys	Thr	Glu	Ser	Gln	Cys	Arg	Glu	Leu	Arg	Lys	Lys	Leu	Gln	Glu	Glu		
	400					405					410						
gaa	cac	cat	agt	aag	gag	ctc	aga	ctt	gaa	ggt	gag	aag	cta	cag	aag	1296	
Glu	His	His	Ser	Lys	Glu	Leu	Arg	Leu	Glu	Val	Glu	Lys	Leu	Gln	Lys		
415				420					425					430			
aga	atg	tct	gaa	cta	gag	aaa	ttg	gaa	gaa	gca	ttt	agc	aag	agt	aaa	1344	
Arg	Met	Ser	Glu	Leu	Glu	Lys	Leu	Glu	Ala	Phe	Ser	Lys	Ser	Lys			
			435					440						445			
tct	gag	tgc	acc	cag	cta	cat	tta	aat	ctg	gag	aaa	gaa	aag	aac	tta	1392	
Ser	Glu	Cys	Thr	Gln	Leu	His	Leu	Asn	Leu	Glu	Lys	Glu	Lys	Asn	Leu		
		450						455						460			
acc	aaa	gac	ctg	cta	aat	gaa	ttg	gag	gtg	gtc	aag	agt	cga	ggt	aaa	1440	
Thr	Lys	Asp	Leu	Leu	Asn	Glu	Leu	Glu	Val	Val	Lys	Ser	Arg	Val	Lys		
	465					470					475						
gaa	ttg	gaa	tgt	tct	gaa	agt	aga	ttg	gaa	aag	gct	gaa	tta	agc	cta	1488	
Glu	Leu	Glu	Cys	Ser	Glu	Ser	Arg	Leu	Glu	Lys	Ala	Glu	Leu	Ser	Leu		
	480					485				490							
aaa	gat	gat	ctt	acc	aag	ttg	aag	tca	ttt	acc	gtg	atg	ctg	ggt	gat	1536	
Lys	Asp	Asp	Leu	Thr	Lys	Leu	Lys	Ser	Phe	Thr	Val	Met	Leu	Val	Asp		
495					500					505					510		
gaa	agg	aaa	aat	atg	atg	gaa	aaa	ata	aaa	caa	gaa	gag	aga	aaa	gtg	1584	
Glu	Arg	Lys	Asn	Met	Met	Glu	Lys	Ile	Lys	Gln	Glu	Glu	Arg	Lys	Val		
			515						520						525		
gat	gga	ctc	aat	aaa	aat	ttt	aag	gtg	gaa	caa	gga	aaa	ggt	atg	gat	1632	
Asp	Gly	Leu	Asn	Lys	Asn	Phe	Lys	Val	Glu	Gln	Gly	Lys	Val	Met	Asp		
			530					535						540			
gta	act	gaa	aaa	cta	att	gaa	gaa	agt	aag	aaa	ctt	tta	aaa	cta	aaa	1680	
Val	Thr	Glu	Lys	Leu	Ile	Glu	Glu	Ser	Lys	Lys	Leu	Leu	Lys	Leu	Lys		
		545						550						555			
tct	gaa	atg	gag	gaa	aaa	gta	tac	aac	ttg	aca	aga	gaa	aga	gat	gag	1728	
Ser	Glu	Met	Glu	Glu	Lys	Val	Tyr	Asn	Leu	Thr	Arg	Glu	Arg	Asp	Glu		
	560					565					570						
ttg	ata	ggc	aaa	ttg	aaa	agt	gaa	gaa	gaa	aaa	tcc	tct	gaa	tta	agc	1776	
Leu	Ile	Gly	Lys	Leu	Lys	Ser	Glu	Glu	Glu	Lys	Ser	Ser	Glu	Leu	Ser		
575					580					585					590		
tgc	agt	ggt	gac	tta	cta	aag	aag	aga	ctt	gat	ggt	ata	gag	gaa	gtg	1824	
Cys	Ser	Val	Asp	Leu	Leu	Lys	Lys	Arg	Leu	Asp	Gly	Ile	Glu	Glu	Val		
			595						600						605		
gaa	aga	gaa	ata	aca	aga	gga	agg	tca	cga	aaa	ggg	tct	gag	ctc	acc	1872	
Glu	Arg	Glu	Ile	Thr	Arg	Gly	Arg	Ser	Arg	Lys	Gly	Ser	Glu	Leu	Thr		
			610					615							620		
tgc	cgg	gaa	gat	aat	aag	att	aag	gaa	cta	aca	ctt	gaa	att	gag	aga	1920	
Cys	Pro	Glu	Asp	Asn	Lys	Ile	Lys	Glu	Leu	Thr	Leu	Glu	Ile	Glu	Arg		
		625						630						635			
ctg	aag	aaa	cgt	ctc	caa	caa	ttg	gaa	gtg	gtc	gaa	ggg	gat	ttg	atg	1968	
Leu	Lys	Lys	Arg	Leu	Gln	Gln	Leu	Glu	Val	Val	Glu	Gly	Asp	Leu	Met		
	640					645					650						
aag	aca	gaa	gat	gag	tat	gat	cag	ctg	gaa	cag	aaa	ttt	aga	act	gag	2016	
Lys	Thr	Glu	Asp	Glu	Tyr	Asp	Gln	Leu	Glu	Gln	Lys	Phe	Arg	Thr	Glu		
	655				660					665					670		
cag	gat	aag	gct	aac	ttc	ctc	tct	caa	caa	cta	gag	gag	atc	aag	cac	2064	
Gln	Asp	Lys	Ala	Asn	Phe	Leu	Ser	Gln	Gln	Leu	Glu	Glu	Ile	Lys	His		
				675						680					685		
caa	att	gcc	aag	aat	aaa	gca	ata	gag	aag	ggt	gag	ggt	gtg	agc	cag	2112	
Gln	Ile	Ala	Lys	Asn	Lys	Ala	Ile	Glu	Lys	Gly	Glu	Val	Val	Ser	Gln		
			690					695						700			
gaa	gct	gaa	ctg	aga	cac	aga	ttt	cgg	ttg	gaa	gaa	gct	aaa	agt	cga	2160	
Glu	Ala	Glu	Leu	Arg	His	Arg	Phe	Arg	Leu	Glu	Glu	Ala	Lys	Ser	Arg		
		705						710							715		

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2208	gac tta aaa gcc gaa gta caa gct ctt aaa gag aag att cac gaa tta Asp Leu Lys Ala Gln Val Gln Ala Leu Lys Ile His Gln Leu	720
2256	atg aac aaa gaa gat cag ctt cag ctc cag gta gat tat ctt gra Met Asn Lys Gln Asp Gln Leu Ser Gln Leu Val Asp Tyr Ser Val	735
2304	ctt caa caa aga ttt atg gaa gaa aat aag aac aaa aac atg ggg Leu Gln Gln Arg Phe Met Gln Gln Gln Asp Lys Asn Lys Asn Met Gly	755
2352	cag gag gtt ctc aat ctg acc aaa gag ttg gag ctt tcc aag cgc tac Gln Gln Val Leu Asn Leu Thr Lys Gln Leu Gln Leu Ser Lys Arg Tyr	770
2400	agc aga gct ctt agg ccc agt gtg aat gga arg gln gly arg arg val Ser Arg Ala Leu Arg Pro Ser Val Asn Gly Arg Arg Met Val Asp Val	785
2448	ctt grg acg tca act gga gtc caa act gat gca gtc agc ggt gaa gca Pro Val Thr Ser Thr Gly Val Gln Thr Asp Ala Val Ser Gly Gln Ala	800
2496	gca gag gaa gaa acg cca gct gta ttc ata cgg aaa tcc ttc cag gaa Ala Gln Gln Gln Thr Pro Ala Val Phe Ile Arg Lys Ser Phe Gln Gln	815
2544	gaa aat cat att atg agt aat ctt cgg cag gga ttg aag aaa ccc Gln Asn His Ile Met Ser Asn Leu Arg Gln Val Gly Leu Lys Lys Pro	835
2592	gtg gaa aga tct tct gtt cta gac agg tat cct cca gca gca aat gag Val Gln Arg Ser Ser Val Leu Asp Arg Tyr Pro Pro Ala Ala Asn Gln	850
2640	ctc act atg aga aag tct tgg att cca tgg atg aga aag agg gaa aac Leu Thr Met Arg Lys Ser Trp Ile Pro Trp Met Arg Lys Arg Gln Asn	865
2688	ggc ccc tcc atc act cag gaa ggg ccc cga aca aat tcc agt cca Gly Pro Ser Ile Thr Gln Lys Gly Pro Arg Thr Asn Ser Ser Pro	880
2736	ggg ccc cca gga gag gta gtc ctt tca cca aag cag ggc cag ccc ctg Gly His Pro Gly Gln Val Val Leu Ser Pro Lys Gln Gly Gln Pro Leu	895
2784	cat att cga gtg aca cca gac cac gag aac agc act cgc act ttg gag His Ile Arg Val Thr Pro Asp His Gln Asn Ser Thr Ala Thr Leu Gln	910
2832	ata aca agc ccc aga tct gaa gaa ttt tct agt acc act gtc att Ile Thr Ser Pro Thr Ser Gln Phe Phe Ser Ser Thr Val Ile	930
2880	ctt acc tta ggg aat cag aaa cca aga ata acc att att cca tca cca Pro Thr Leu Gly Asn Gln Lys Pro Arg Ile Thr Ile Ile Pro Ser Pro	945
2928	aac gtt atg cct caa aaa caa aaa agt gga gat act act ctt ggc cca Asn Val Met Pro Gln Lys Gln Lys Ser Gly Asp Thr Thr Leu Gly Pro	960
2976	gaa cga gcc atg tcc cca gtc aca att act aca ttt tcc aga gag aag Gln Arg Ala Met Ser Pro Val Thr Ile Thr Thr Phe Ser Arg Gln Lys	975
3024	act cca gaa agt gga aga ggc gca ttt gca gac agc agg ccc aca tcc cct Thr Pro Gln Ser Gly Arg Gly Ala Phe Ala Asp Arg Pro Thr Ser Pro	995
3072	att cag ata atg acg gtg tct aca tca gca gca gca gct gag att gca Ile Gln Ile Met Thr Val Ser Thr Ser Ala Pro Ala Gln Ile Ala	1010
3120	glt tct ccc gaa tcc cag gaa atg ccc atg gga cgg aca atc ctc aaa Val Ser Pro Gln Ser Gln Met Pro Met Gly Arg Thr Ile Leu Lys	1030

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gtc acc cca gaa aaa cag act gtt cca act cca gta cgg aaa tac aac 3168
Val Thr Pro Glu Lys Gln Thr Val Pro Thr Pro Val Arg Lys Tyr Asn
    1040                    1045                    1050

tcc aat gcc aat atc ata acc aca gag gac aat aaa att cac att cac 3216
Ser Asn Ala Asn Ile Ile Thr Thr Glu Asp Asn Lys Ile His Ile His
1055                    1060                    1065                    1070

tta ggg tct cag ttt aaa cgg tcc cct ggg act tca ggt gaa gga gtc 3264
Leu Gly Ser Gln Phe Lys Arg Ser Pro Gly Thr Ser Gly Glu Gly Val
    1075                    1080                    1085

agt cca gtt att act gtc cga cca gta aac gtg aca gcc gaa aag gag 3312
Ser Pro Val Ile Thr Val Arg Pro Val Asn Val Thr Ala Glu Lys Glu
    1090                    1095                    1100

gtt tcc acc ggc act gtc ctt cgc tct ccc agg aat cac ctc tcc tca 3360
Val Ser Thr Gly Thr Val Leu Arg Ser Pro Arg Asn His Leu Ser Ser
    1105                    1110                    1115

cgg cct ggt gca agc aaa gtg acg agc act atc acc ata aca ccg gtc 3408
Arg Pro Gly Ala Ser Lys Val Thr Ser Thr Ile Thr Ile Thr Pro Val
    1120                    1125                    1130

aca acg tca tct gct cga gga acc cag tca gtg tca gga caa gac ggg 3456
Thr Thr Ser Ser Ala Arg Gly Thr Gln Ser Val Ser Gly Gln Asp Gly
1135                    1140                    1145                    1150

tca tcc cag cgg cct aca ccc acc cgc att cct atg tca aaa ggt atg 3504
Ser Ser Gln Arg Pro Thr Pro Thr Arg Ile Pro Met Ser Lys Gly Met
    1155                    1160                    1165

aaa gca gga aag cca gta gtg gca gcc cca gga gca gga aat ctg acc 3552
Lys Ala Gly Lys Pro Val Val Ala Ala Pro Gly Ala Gly Asn Leu Thr
    1170                    1175                    1180

aaa ttc gag cct cga gct gag act cag tct atg aaa ata gag ctg aag 3600
Lys Phe Glu Pro Arg Ala Glu Thr Gln Ser Met Lys Ile Glu Leu Lys
    1185                    1190                    1195

aaa tct gca gcc agc agc acc acc tct ctc gga ggg ggg aag ggc 3645
Lys Ser Ala Ala Ser Ser Thr Thr Ser Leu Gly Gly Gly Lys Gly
    1200                    1205                    1210

tgagggcagt ggctaagggg gtatgttggt cagatgctac tgctgccgtg aaagtgaacc 3705

ttcatctggt tgtgccagtt cttacatgt actaatttaa gttttaata ttgtgtttat 3765

aaaaataacca actaataacc atttgtcttt cccattttgt gcatttgttt tgatgctggg 3825

gaacaaaatt agcaaaaacta ttgcttctgt cctagaagcc agggcgtggt ttctagtcc 3885

agttttgctt ctagcaagtg gaccocatca tagaccocatc tgagocctggt tcctcatcag 3945

ttagatgtgg ggactcaatc acacgctctt caagtccggc tcccatatct cctaattgca 4005

agccaaatct aatgtacctt gttccacaat aattttttat taaaaaatc ctattacaaa 4065

ataagacata ctttaactat tgcatttgc ctctttcaca toatgaatct gctttatgtg 4125

ctggaaaaaa catcacatag ctatcacagg gcttggacct ctaaaatctt gcaaaaaaca 4185

aaggttctaa gatgatttca ggaataatg tgaacatgta ataaatgga aatgaaatat 4245

gg 4247

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<210> SEQ ID NO 6

<211> LENGTH: 1213

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 6

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Met Arg Ser Arg Asn Gln Gly Gly Glu Ser Ala Ser Asp Gly His Ile
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Ser Cys Pro Lys Pro Ser Ile Ile Gly Asn Ala Gly Glu Lys Ser Leu

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Ser	Glu	Asp	Ala	Lys	Lys	Lys	Lys	Lys	Ser	Asn	Arg	Lys	Glu	Asp	Asp
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Val	Met	Ala	Ser	Gly	Thr	Val	Lys	Arg	His	Leu	Lys	Thr	Ser	Gly	Glu
	50					55					60				
Cys	Glu	Arg	Lys	Thr	Lys	Lys	Ser	Leu	Glu	Leu	Ser	Lys	Glu	Asp	Leu
	65					70					75				80
Ile	Gln	Leu	Leu	Ser	Ile	Met	Glu	Gly	Glu	Leu	Gln	Ala	Arg	Glu	Asp
				85					90					95	
Val	Ile	His	Met	Leu	Lys	Thr	Glu	Lys	Thr	Lys	Pro	Glu	Val	Leu	Glu
			100					105					110		
Ala	His	Tyr	Gly	Ser	Ala	Glu	Pro	Glu	Lys	Val	Leu	Arg	Val	Leu	His
		115					120					125			
Arg	Asp	Ala	Ile	Leu	Ala	Gln	Glu	Lys	Ser	Ile	Gly	Glu	Asp	Val	Tyr
	130					135					140				
Glu	Lys	Pro	Ile	Ser	Glu	Leu	Asp	Arg	Leu	Glu	Glu	Lys	Gln	Lys	Glu
	145					150					155				160
Thr	Tyr	Arg	Arg	Met	Leu	Glu	Gln	Leu	Leu	Leu	Ala	Glu	Lys	Cys	His
				165					170					175	
Arg	Arg	Thr	Val	Tyr	Glu	Leu	Glu	Asn	Glu	Lys	His	Lys	His	Thr	Asp
			180					185					190		
Tyr	Met	Asn	Lys	Ser	Asp	Asp	Phe	Thr	Asn	Leu	Leu	Glu	Gln	Glu	Arg
		195					200					205			
Glu	Arg	Leu	Lys	Lys	Leu	Leu	Glu	Gln	Glu	Lys	Ala	Tyr	Gln	Ala	Arg
	210					215					220				
Lys	Glu	Lys	Glu	Asn	Ala	Lys	Arg	Leu	Asn	Lys	Leu	Arg	Asp	Glu	Leu
	225					230					235				240
Val	Lys	Leu	Lys	Ser	Phe	Ala	Leu	Met	Leu	Val	Asp	Glu	Arg	Gln	Met
				245					250					255	
His	Ile	Glu	Gln	Leu	Gly	Leu	Gln	Ser	Gln	Lys	Val	Gln	Asp	Leu	Thr
			260					265					270		
Gln	Lys	Leu	Arg	Glu	Glu	Glu	Lys	Leu	Lys	Ala	Ile	Thr	Ser	Lys	
		275					280					285			
Ser	Lys	Glu	Asp	Arg	Gln	Lys	Leu	Leu	Lys	Leu	Glu	Val	Asp	Phe	Glu
	290					295					300				
His	Lys	Ala	Ser	Arg	Phe	Ser	Gln	Glu	His	Glu	Glu	Met	Asn	Ala	Lys
	305					310					315				320
Leu	Ala	Asn	Gln	Glu	Ser	His	Asn	Arg	Gln	Leu	Arg	Leu	Lys	Leu	Val
				325					330					335	
Gly	Leu	Thr	Gln	Arg	Ile	Glu	Glu	Leu	Glu	Glu	Thr	Asn	Lys	Asn	Leu
			340					345					350		
Gln	Lys	Ala	Glu	Glu	Glu	Leu	Gln	Glu	Leu	Arg	Asp	Lys	Ile	Ala	Lys
		355					360					365			
Gly	Glu	Cys	Gly	Asn	Ser	Ser	Leu	Met	Ala	Glu	Val	Glu	Asn	Leu	Arg
	370					375					380				
Lys	Arg	Val	Leu	Glu	Met	Glu	Gly	Lys	Asp	Glu	Glu	Ile	Thr	Lys	Thr
	385					390					395				400
Glu	Ser	Gln	Cys	Arg	Glu	Leu	Arg	Lys	Lys	Leu	Gln	Glu	Glu	Glu	His
				405					410					415	
His	Ser	Lys	Glu	Leu	Arg	Leu	Glu	Val	Glu	Lys	Leu	Gln	Lys	Arg	Met
			420					425					430		
Ser	Glu	Leu	Glu	Lys	Leu	Glu	Ala	Phe	Ser	Lys	Ser	Lys	Ser	Glu	
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Cys Thr Gln Leu His Leu Asn Leu Glu Lys Glu Lys Asn Leu Thr Lys
 450 455 460
 Asp Leu Leu Asn Glu Leu Glu Val Val Lys Ser Arg Val Lys Glu Leu
 465 470 475 480
 Glu Cys Ser Glu Ser Arg Leu Glu Lys Ala Glu Leu Ser Leu Lys Asp
 485 490 495
 Asp Leu Thr Lys Leu Lys Ser Phe Thr Val Met Leu Val Asp Glu Arg
 500 505 510
 Lys Asn Met Met Glu Lys Ile Lys Gln Glu Glu Arg Lys Val Asp Gly
 515 520 525
 Leu Asn Lys Asn Phe Lys Val Glu Gln Gly Lys Val Met Asp Val Thr
 530 535 540
 Glu Lys Leu Ile Glu Glu Ser Lys Lys Leu Leu Lys Leu Lys Ser Glu
 545 550 555 560
 Met Glu Glu Lys Val Tyr Asn Leu Thr Arg Glu Arg Asp Glu Leu Ile
 565 570 575
 Gly Lys Leu Lys Ser Glu Glu Glu Lys Ser Ser Glu Leu Ser Cys Ser
 580 585 590
 Val Asp Leu Leu Lys Lys Arg Leu Asp Gly Ile Glu Glu Val Glu Arg
 595 600 605
 Glu Ile Thr Arg Gly Arg Ser Arg Lys Gly Ser Glu Leu Thr Cys Pro
 610 615 620
 Glu Asp Asn Lys Ile Lys Glu Leu Thr Leu Glu Ile Glu Arg Leu Lys
 625 630 635 640
 Lys Arg Leu Gln Gln Leu Glu Val Val Glu Gly Asp Leu Met Lys Thr
 645 650 655
 Glu Asp Glu Tyr Asp Gln Leu Glu Gln Lys Phe Arg Thr Glu Gln Asp
 660 665 670
 Lys Ala Asn Phe Leu Ser Gln Gln Leu Glu Glu Ile Lys His Gln Ile
 675 680 685
 Ala Lys Asn Lys Ala Ile Glu Lys Gly Glu Val Val Ser Gln Glu Ala
 690 695 700
 Glu Leu Arg His Arg Phe Arg Leu Glu Glu Ala Lys Ser Arg Asp Leu
 705 710 715 720
 Lys Ala Glu Val Gln Ala Leu Lys Glu Lys Ile His Glu Leu Met Asn
 725 730 735
 Lys Glu Asp Gln Leu Ser Gln Leu Gln Val Asp Tyr Ser Val Leu Gln
 740 745 750
 Gln Arg Phe Met Glu Glu Glu Asn Lys Asn Lys Asn Met Gly Gln Glu
 755 760 765
 Val Leu Asn Leu Thr Lys Glu Leu Glu Leu Ser Lys Arg Tyr Ser Arg
 770 775 780
 Ala Leu Arg Pro Ser Val Asn Gly Arg Arg Met Val Asp Val Pro Val
 785 790 795 800
 Thr Ser Thr Gly Val Gln Thr Asp Ala Val Ser Gly Glu Ala Ala Glu
 805 810 815
 Glu Glu Thr Pro Ala Val Phe Ile Arg Lys Ser Phe Gln Glu Glu Asn
 820 825 830
 His Ile Met Ser Asn Leu Arg Gln Val Gly Leu Lys Lys Pro Val Glu
 835 840 845
 Arg Ser Ser Val Leu Asp Arg Tyr Pro Pro Ala Ala Asn Glu Leu Thr
 850 855 860

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The invention claimed is:

1. An isolated DNA molecule that comprises:
 - (a) the sequence of SEQ ID NO: 1, or
 - (b) the sequence of SEQ ID NO: 3, or
 - (c) the sequence or SEQ ID NO: 5, or
 - (d) the sequence of SEQ ID NO: 1, SEQ ID NO: 3 and SEQ ID NO: 5, or
 - (e) a sequence that hybridizes with the full complement of the sequence in (a), (b), (c) or (d) under stringent conditions, wherein the variant sequence encodes a protein

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that binds to Filamin 1 and inhibits cell migration, and wherein the stringent conditions comprise hybridization at 65° C. in a buffer containing 0.1×SSC.

2. An isolated DNA molecule that encodes a protein,
 - 5 wherein the protein comprises the amino acid sequence selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 4, and SEQ ID NO: 6.
3. An isolated host cell that comprises an expression system which expresses the protein according to claim 2.

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