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(54) Title: NEW NEURONAL VIABILITY FACTOR AND USE THEREOF

(57) Abstract: The present invention concerns a pharmaceutical composition comprising a pharmaceutically acceptable carrier and a compound selected in the group comprising (i) a polypeptide comprising an amino acid sequence selected in the group comprising the amino acid sequence of the long isoform in *Homo sapiens* of the RdCVF2 gene (SEQ ID NO: 10), orthologs, derivatives and fragments thereof, (ii) a polynucleotide coding for said polypeptide, (iii) a vector comprising said polynucleotide, and (iv) a host cell genetically engineered expressing said polypeptide; the use of such a composition for the manufacture of a medicament for treating and/or preventing a neurodegenerative disorder in a subject; and a method of testing a subject thought to have or be predisposed to having a neurodegenerative disorder.

NEW NEURONAL VIABILITY FACTOR AND USE THEREOF

This application claims the priority of the patent application EP07109652.3 filed June 5, 2007, which is incorporated herein by reference.

Field of the invention

The present invention relates to neurodegenerative disorders, and more particularly to a pharmaceutical composition for treating and/or preventing neurodegenerative disorders.

Background of the invention

Neurodegenerative disorders have provided a challenge for many years, in both basic research and clinical contexts.

As an example of such a neurodegenerative disorder, *retinitis pigmentosa* (RP) is a genetically heterogeneous retinal degeneration characterized by the sequential degeneration of a population of neurons corresponding to rod and cone photoreceptors. The RP first clinical signs are night blindness and narrowing of the peripheral field of vision which progressively worsens to become "tunnel-like". Eventually, the central vision is reduced to complete blindness in most cases. At a cellular level, the retinal rod photoreceptors involved in night and side visions slowly degenerate. Subsequently, the cone photoreceptors responsible for both color and high-contrast vision, visual acuity, detail perception and normal light vision are similarly affected. The retinal degeneration 1 (*rd1*) mouse is the most studied animal model for retinitis pigmentosa. It carries a recessive mutation in the rod-specific cGMP phosphodiesterase beta subunit gene leading to rod photoreceptor death through apoptosis (CARTER-DAWSON *et al., Invest. Ophthalmol. Vis. Sci.*, vol. 17(6), p:489-498, 1978 ; PORTERA-CAILLIAU *et al., Proc. Natl. Acad. Sci. U.S.A*, vol.91(3), p:974-978, 1994) followed by cone death presumably through lack of trophic support (MOHAND-SAID *et al., Proc. Natl. Acad. Sci. U.S.A*, vol.95(14), p:8357-8362, 1998).

Accordingly, the technical problem underlying the present invention is to provide novel compounds having neurotrophic activities, which compounds are

suitable for the treatment of neurodegenerative disorders such as retinitis pigmentosa for which no treatment is actually available.

The RdCVF gene, also called thioredoxin-like 6 (Txnl6) or Nucleoredoxin-like 1 (Nxnl1), encodes the Q8VC33 UniProt [6] protein, which has limited similarity to the thioredoxin superfamily and which exerts trophic activity on cone photoreceptors (LEVEILLARD *et al., Nat. Genet.* vol. 36(7), p:755-759, 2004). Thioredoxins (TXN) are usually small proteins which can be involved with pleiotropic activities such as redox control, regulation of apoptosis and cytokine activity (HOLMGREN, *Annu. Rev. Biochem.,* vol. 54, p:237-271, 1985; HOLMGREN, *J. Biol. Chem.*, vol.264(24), p:13963-13966, 1989; ARNER and HOLMGREN , *Eur. J. Biochem.*, vol.267(20), p:6102-6109, 2000). The TXN conserved active site contains two distinct cysteines (CXXC) that contribute to a thiol-oxydoreductase activity (ARNER and HOLMGREN, 2000, abovementioned; POWIS and MONTFORT, *Annu. Rev. Pharmacol. Toxicol.*, vol.41, p:261-295, 2001) catalyzes the reduction of disulfide bonds in multiple substrate proteins (HOLMGREN, *J. Biol. Chem.*, vol.254(18) , p:9113-9119, 1979; HOLMGREN, *J. Biol. Chem.*, vol.254(19), p:9627-9632, 1979). The RdCVF gene encodes two products via alternative splicing: a full length protein and a C-terminal post-transcriptionally truncated protein sharing similarities with TRX80. This latter form of human thioredoxin-1 (Txn) (PEKKARI *et al., J. Biol. Chem.*, vol.275(48), p:37474-37480, 2000; PEKKARI *et al., Blood*, vol.105(4), :1598-1605, 2005; LIU *et al., Blood*, vol.105(4):1606-1613, 2005) has no thiol-reductase activity but is involved in controlling growth of peripheral mononuclear blood cells (PEKKARI *et al.,* 2000, abovementioned; PEKKARI *et al., FEBS Lett.*, vol.539(1-3):143-148, 2003). Similar to Txn, RdCVF looks like a bifunctional gene because it encodes both a long form (RdCVF-L, 217 aa, Q8VC33) having a putative thiol-oxydoreductase activity (JEFFERY, *Trends Biochem. Sci.*, vol.24(1):8-11, 1999; JEFFERY, *Trends Genet.*, vol.19(8):415-417, 2003) and a short form (RdCVF-S, 109 aa, Q91W38) with trophic activity for cones but no redox activity.

Summary of the invention

The present invention relates to a pharmaceutical composition comprising a pharmaceutically acceptable carrier and a compound selected in the group comprising:

(i) a polypeptide comprising an amino acid sequence selected in the group comprising the amino acid sequence of the short isoform in *Homo sapiens* of the RdCVF2 gene (SEQ ID NO:1), orthologs, derivatives and fragments thereof;

(ii) a polynucleotide coding for said polypeptide;

(iii) a vector comprising said polynucleotide; and

(iv) a host cell genetically engineered expressing said polypeptide.

In another embodiment, the present invention relates to a use, for treating and/or preventing a neurodegenerative disorder, of a compound selected in the group comprising:

(i) a polypeptide comprising an amino acid sequence selected in the group comprising the amino acid sequence of the isoform in *Homo sapiens* of the RdCVF2 gene (SEQ ID NO:1), orthologs, derivatives and fragments thereof;

(ii) a polynucleotide coding for said polypeptide;

(iii) a vector comprising said polynucleotide; and

(iv) a host cell genetically engineered expressing said polypeptide.

In still another embodiment, the present invention relates to a method of preventing and/or treating a neurodegenerative disease comprising providing, to a subject displaying or predicted to display a neurodegenerative disorder, an effective amount of a composition comprising a compound selected in the group comprising:

(i) a polypeptide comprising an amino acid sequence selected in the group comprising the amino acid sequence of the short isoform in *Homo sapiens* of the RdCVF2 gene (SEQ ID NO:1), orthologs, derivatives and fragments thereof;

(ii) a polynucleotide coding for said polypeptide;

(iii) a vector comprising said polynucleotide; and

(iv) a host cell genetically engineered expressing said polypeptide.

In still another embodiment, the present invention finally relates a method of testing a subject thought to have or be predisposed to having a neurodegenerative disorder, which comprises detecting the presence of a mutation in the RdCVF2 gene and/or its associated promoter in a biological sample from said subject

Brief description of the drawings

Figure 1 shows the RdCVF and RdCVF2 gene structure conservation.

Figure 2 shows the Sequence and structure similarities of mouse RdCVF and RdCVF2 proteins with thioredoxin superfamily members.

Figure 3 shows the validation of the RdCVF2 expression in retina.

Figure 4 shows the cone viability assay in the presence of RdCVF-S and RdCVF2-S.

Detailed description

The present invention is based on the discovery of a new gene RdCVF2 as a gene paralogous to RdCVF, with the protein encoded by said gene enhancing the viability of neurons such as cone photoreceptors and olfactory neurons.

Thus, in a first aspect, the present invention provides a pharmaceutical composition comprising a pharmaceutically acceptable carrier and a compound selected in the group comprising:

(i) a polypeptide comprising an amino acid sequence selected in the group comprising the amino acid sequence of the short isoform in *Homo sapiens* of the RdCVF2 gene (SEQ ID NO:1), orthologs, derivatives and fragments thereof;

(ii) a polynucleotide coding for said polypeptide;

(iii) a vector comprising said polynucleotide; and

(iv) a host cell genetically engineered expressing said polypeptide.

As used herein, the term "polypeptide" refers to a molecular chain of amino acids enhancing the viability of neurons such as cone photoreceptors or olfactory neurons. This polypeptide, if required, can be modified *in vitro* and/or *in vivo*, for example by glycosylation, myristoylation, amidation, carboxylation or phosphorylation, and may be obtained, for example, by synthetic or recombinant techniques known in the art.

According to a preferred embodiment, the composition of the invention comprises a pharmaceutically acceptable carrier and a compound selected in the group comprising:

(i) a polypeptide comprising an amino acid sequence selected in the group comprising the amino acid sequence of the long isoform in *Homo sapiens* of the RdCVF2 gene (SEQ ID NO:10), orthologs, derivatives and fragments thereof;

(ii) a polynucleotide coding for said polypeptide;

(iii) a vector comprising said polynucleotide; and

(iv) a host cell genetically engineered expressing said polypeptide.

As used herein, the term "orthologs" refers to proteins in different species than the proteins SEQ ID NO.1 and SEQ ID NO.10 in *Homo sapiens* that evolved from a common ancestral gene by speciation. As an example of such orthologs, one can cite the proteins corresponding to RdCVF2-S in *Mus musculus* (SEQ ID NO.2), *Rattus norvegicus* (SEQ ID NO.3), *Pan troglodytes* (SEQ ID NO.4), *Bos Taurus* (SEQ ID NO.5), *Gallus gallus* (SEQ ID NO.6), *Xenopus laevis* (SEQ ID NO.7), *Tetraodon nigroviridis* (SEQ ID NO.8), and *Danio rerio* (SEQ ID NO.9).

As used herein, the term "derivatives" refers to polypeptides having a percentage of identity of at least 75% with SEQ ID NO.1, SEQ ID NO.10 or ortholog thereof, preferably of at least 85%, as an example of at least 90%, and more preferably of at least 95%.

It has to be noted that the short isoform of RdCVF2 in *Homo sapiens* has less than 40% of identity with the short isoform of RdCVF in *Homo sapiens*.

As used herein "fragments" refers to polypeptides having a length of at least 25 amino acids, preferably at least 50 amino acids, as an example at least 75 or 85 amino acids, and more preferably of at least 100 amino acids.

As used herein, "percentage of identity" between two amino acids sequences, means the percentage of identical amino-acids, between the two sequences to be compared, obtained with the best alignment of said sequences, this percentage being purely statistical and the differences between these two sequences being randomly spread over the amino acids sequences. As used herein, "best alignment" or "optimal

alignment", means the alignment for which the determined percentage of identity (see below) is the highest. Sequences comparison between two amino acids sequences are usually realized by comparing these sequences that have been previously align according to the best alignment; this comparison is realized on segments of comparison in order to identify and compared the local regions of similarity. The best sequences alignment to perform comparison can be realized, beside by a manual way, by using the global homology algorithm developed by SMITH and WATERMAN (*Ad. App. Math.*, vol.2, p:482, 1981), by using the local homology algorithm developed by NEDDLEMAN and WUNSCH (*J. Mol. Biol.*, vol.48, p:443, 1970), by using the method of similarities developed by PEARSON and LIPMAN (*Proc. Natl. Acd. Sci. USA*, vol.85, p:2444, 1988), by using computer softwares using such algorithms (GAP, BESTFIT, BLAST P, BLAST N, FASTA, TFASTA in the Wisconsin Genetics software Package, Genetics Computer Group, 575 Science Dr., Madison, WI USA), by using the MUSCLE multiple alignment algorithms (Edgar, Robert C., *Nucleic Acids Research*, vol. 32, p:1792, 2004). To get the best local alignment, one can preferably used BLAST software, with the BLOSUM 62 matrix, or the PAM 30 matrix. The identity percentage between two sequences of amino acids is determined by comparing these two sequences optimally aligned, the amino acids sequences being able to comprise additions or deletions in respect to the reference sequence in order to get the optimal alignment between these two sequences. The percentage of identity is calculated by determining the number of identical position between these two sequences, and dividing this number by the total number of compared positions, and by multiplying the result obtained by 100 to get the percentage of identity between these two sequences.

The phrase "pharmaceutically acceptable" refers to molecular entities and compositions that are physiologically tolerable and do not typically produce an allergic or similar untoward reaction, such as gastric upset, dizziness and the like, when administered to a human. Preferably, as used herein, the term "pharmaceutically acceptable" means approved by a regulatory agency of the Federal or a state government or listed in the U.S. Pharmacopeia or other generally recognized pharmacopeia for use in animals, and more particularly in humans.

The term "carrier" refers to a diluent, adjuvant, excipient, or vehicle with which the compound is administered. Such pharmaceutical carriers can be sterile liquids, such as water and oils, including those of petroleum, animal, vegetable or synthetic origin, such as peanut oil, soybean oil, mineral oil, sesame oil and the like. Water or aqueous solution saline solutions and aqueous dextrose and glycerol solutions are preferably employed as carriers, particularly for injectable solutions. Suitable pharmaceutical carriers are described in "Remington's Pharmaceutical Sciences" by E.W. Martin.

As used herein, the term "polynucleotide" refers to RNA or DNA, preferably to DNA. Said DNA may be double-stranded or single-stranded.

Preferably, the polynucleotide comprises the sequence SEQ ID NO.11.

Preferably, the polynucleotide comprises a sequence which encodes the sequence SEQ ID NO:10.

The polynucleotide of the invention may also include the coding sequence of the polypeptide defined previously, additional coding sequence such as leader sequence or a proprotein sequence, and/or additional non-coding sequence, such as introns or 5'and/or 3' UTR sequences.

As used herein, the term "vector" refers to an expression vector, and may be for example in the form of a plasmid, a viral particle, a phage, etc.

Such vectors may include bacterial plasmids, phage DNA, baculovirus, yeast plasmids, vectors derived from combinations of plasmids and phage DNA, viral DNA such as vaccinia, adenovirus, fowl pox virus, and pseudorabies. Large numbers of suitable vectors are known to those of skill in the art and are commercially available. The following vectors are provided by way of example. Bacterial: pQE70, pQE60, pQE-9 (QIAGEN), pbs, pD10, phagescript, psiX174, pbluescript SK, pbsks, pNH8A, pNH16a, pNH18A, pNH46A (STRATAGENE), ptrc99a, pKK223-3, pKK233-3, pDR540, pRIT5 (PHARMACIA). Eukaryotic: pWLNEO, pSV2CAT, pOG44, pXT1, pSG (STRATAGENE), pSVK3, pBPV, pMSG, pSVL (PHARMACIA). However, any other vector may be used as long as it is replicable and viable in the host.

The polynucleotide sequence, preferably the DNA sequence in the vector is operatively linked to an appropriate expression control sequence(s) (promoter) to direct mRNA synthesis. As representative examples of such promoters, one can mentioned prokaryotic or eukaryotic promoters such as CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. The expression vector also contains a ribosome binding site for translation initiation and a transcription vector. The vector may also include appropriate sequences for amplifying expression.

In addition, the vectors preferably contain one or more selectable marker genes to provide a phenotypic trait for selection of transformed host cells such as dihydrofolate reductase or neomycin resistance for eukaryotic cell culture, or such as tetracycline or ampicillin resistance in E. coli.

As used herein, the term "host cell genetically engineered" relates to host cells which have been transduced, transformed or transfected with the polynucleotide or with the vector described previously.

As representative examples of appropriate host cells, one can cites bacterial cells, such as E. coli, Streptomyces, Salmonella typhimurium, fungal cells such as yeast, insect cells such as Sf9, animal cells such as CHO or COS, plant cells, etc. The selection of an appropriate host is deemed to be within the scope of those skilled in the art from the teachings herein.

Preferably, said host cell is an animal cell, and most preferably a human cell.

The introduction of the polynucleotide or of the vector described previously into the host cell can be effected by method well known from one of skill in the art such as calcium phosphate transfection, DEAE-Dextran mediated transfection, or electroporation.

The composition of the invention may comprise one or more additives (e.g., stabilizers, preservatives). See, generally, *Ullmann's Encyclopedia of Industrial Chemistry, 6th Ed.* (various editors, 1989-1998, Marcel Dekker); and *Pharmaceutical Dosage Forms and Drug Delivery Systems* (ANSEL *et al.*, 1994, WILLIAMS & WILKINS).

In a further aspect, the present invention provides a use, for treating and/or preventing a neurodegenerative disorder, of a compound selected in the group comprising:

(i) a polypeptide comprising an amino acid sequence selected in the group comprising the amino acid sequence of the short isoform in *Homo sapiens* of the RdCVF2 gene (SEQ ID NO:1), orthologs, derivatives and fragments thereof;

(ii) a polynucleotide coding for said polypeptide;

(iii) a vector comprising said polynucleotide; and

(iv) a host cell genetically engineered expressing said polypeptide.

In a further aspect, the present invention provides a use, for treating and/or preventing a neurodegenerative disorder, of a compound selected in the group comprising:

(v) a polypeptide comprising an amino acid sequence selected in the group comprising the amino acid sequence of the long isoform in *Homo sapiens* of the RdCVF2 gene (SEQ ID NO:10), orthologs, derivatives and fragments thereof;

(vi) a polynucleotide coding for said polypeptide;

(vii) a vector comprising said polynucleotide; and

(viii) a host cell genetically engineered expressing said polypeptide.

Typically, the medicament may be used for the therapeutic or prophylactic treatment of a subject, said subject corresponding to a mammal, in particular to a human.

As used herein, the expression "neurodegenerative disorder" refers to a disease associated with the degeneration of neurons such as degenerative disorders of the central nervous system, preferably implying Purkinje cells degeneration, degenerative disorders of the photoreceptors, or degenerative disorders of the olfactory neurons.

As an example of degenerative disorders of the central nervous system, one can cite Alzheimer's Disease, Parkinson's Disease, and Huntington's Disease/Chorea.

As an example of degenerative disorders of the photoreceptors, one can cite cone dystrophy (e.g., retinitis pigmentosa).

As an example of degenerative disorders of olfactory neurons, one can cite anosmia.

Said polypeptide, polynucleotide, vector, and host cell are as described previously.

According to a preferred embodiment, said medicament may be used for treating and/or preventing degenerative disorders of the photoreceptors or degenerative disorders of the olfactory neurons.

There is also provided a method of preventing and/or treating a neurodegenerative disease comprising providing, to a subject displaying or predicted to display a neurodegenerative disorder, an effective amount of a composition comprising a compound selected in the group comprising:

(i) a polypeptide comprising an amino acid sequence selected in the group comprising the amino acid sequence of the short isoform in *Homo sapiens* of the RdCVF2 gene (SEQ ID NO:1), orthologs, derivatives and fragments thereof;

(ii) a polynucleotide coding for said polypeptide;

(iii) a vector comprising said polynucleotide; and

(iv) a host cell genetically engineered expressing said polypeptide.

According to the present invention, an "effective amount" of a composition is one which is sufficient to achieve a desired biological effect, in this case increasing the neuron viability. It is understood that the effective dosage will be dependent upon the age, sex, health, and weight of the recipient, kind of concurrent treatment, if any, frequency of treatment, and the nature of the effect desired. The ranges of effective doses provided below are not intended to limit the invention and represent preferred dose ranges. However, the preferred dosage can be tailored to the individual subject, as is understood and determinable by one of skill in the art, without undue experimentation.

Said polypeptide, polynucleotide, vector, and host cell are as described previously.

There is also provided a method of testing a subject thought to have or be predisposed to having a neurodegenerative disorder, which comprises the step of analyzing a biological sample from said subject for :

(i) detecting the presence of a mutation in the RdCVF2 gene and/or its associated promoter, and/or

(ii) analyzing the expression of the RdCVF2 gene.

As used herein, the term "biological sample" refers to any sample from a subject such as blood or serum.

As used herein, the expression "neurodegenerative disorder" refers to a disease associated with the degeneration of neurons such as degenerative disorders of the central nervous system, degenerative disorders of the photoreceptors, or degenerative disorders of the olfactory neurons.

Preferably, neurodegenerative disorder is a degenerative disorder of the photoreceptors such as cone dystrophy (e.g., retinitis pigmentosa).

Typical techniques for detecting a mutation in the RdCVF2 gene may include restriction fragment length polymorphism, hybridisation techniques, DNA sequencing, exonuclease reistance, microsequencing, solid phase extension using ddNTPs, extension in solution using ddNTPs, oligonucleotide assays, methods for detecting single nucleotide polymorphism such as dynamic allele-specific hybridisation, ligation chain reaction, mini-sequencing, DNA "chips", allele-specific oligonucleotide hybridisation with single or dual-labelled probes merged with PCR or with molecular beacons, and others.

Analyzing the expression of the RdCVF2 gene may be assessed by any of a wide variety of well-known methods for detecting expression of a transcribed nucleic acid or translated protein.

In a preferred embodiment, the expression of the RdCVF2 gene is assessed by analyzing the expression of mRNA transcript or mRNA precursors, such as nascent RNA, of said gene. Said analysis can be assessed by preparing mRNA/cDNA from cells in a biological sample from a subject, and hybridizing the mRNA/cDNA with a reference polynucleotide. The prepared mRNA/cDNA can be used in hybridization or amplification assays that include, but are not limited to, Southern or Northern

analyses, polymerase chain reaction analyses, such as quantitative PCR (TaqMan), and probes arrays such as GeneChip™ DNA Arrays (AFFYMETRIX).

Advantageously, the analysis of the expression level of mRNA transcribed from the RdCVF2 gene involves the process of nucleic acid amplification, e. g., by RT-PCR (the experimental embodiment set forth in U. S. Patent No. 4,683, 202), ligase chain reaction (BARANY, *Proc. Natl. Acad. Sci. USA*, vol.88, p: 189-193, 1991), self sustained sequence replication (GUATELLI *et al.*, *Proc. Natl. Acad. Sci. USA,* vol.*87, p*: 1874-1878, 1990), transcriptional amplification system (KWOH *et al.*, 1989, *Proc. Natl. Acad. Sci. USA*, vol.86, p: 1173-1177, 1989), Q-Beta Replicase (LIZARDI *et al.*, *Biol. Technology*, vol.6, p: 1197, 1988), rolling circle replication (U. S. Patent No. 5,854, 033) or any other nucleic acid amplification method, followed by the detection of the amplified molecules using techniques well known to those of skill in the art. These detection schemes are especially useful for the detection of nucleic acid molecules if such molecules are present in very low numbers. As used herein, amplification primers are defined as being a pair of nucleic acid molecules that can anneal to 5'or 3'regions of a gene (plus and minus strands, respectively, or vice-versa) and contain a short region in between. In general, amplification primers are from about 10 to 30 nucleotides in length and flank a region from about 50 to 200 nucleotides in length. Under appropriate conditions and with appropriate reagents, such primers permit the amplification of a nucleic acid molecule comprising the nucleotide sequence flanked by the primers.

In view of the present application, one of skill in the art can simply identify the sequence of the gene RdCVF2 in a subject.

As an example, the sequence of the cDNA coding for the short isoform of RdCVF2 in Homo sapiens has the sequence SEQ ID NO.11.

In another preferred embodiment, the expression of the RdCVF2 gene is assessed by analyzing the expression of the protein translated from said gene. Said analysis can be assessed using an antibody (*e.g.*, a radio-labeled, chromophore-labeled, fluorophore-labeled, or enzyme-labeled antibody), an antibody derivative (*e.g.*, an antibody conjugate with a substrate or with the protein or ligand of a protein of a protein/ligand pair (*e.g.,* biotin-streptavidin)), or an antibody fragment (*e.g.*, a

single-chain antibody, an isolated antibody hypervariable domain, *etc.*) which binds specifically to the protein translated from the RdCVF2 gene.

Said analysis can be assessed by a variety of techniques well known from one of skill in the art including, but not limited to, enzyme immunoassay (EIA), radioimmunoassay (RIA), Western blot analysis and enzyme linked immunoabsorbant assay (RIA).

Polyclonal antibodies can be prepared by immunizing a suitable animal, such as mouse, rabbit or goat, with a protein encoded by the RdCVF2 gene or a fragment thereof. The antibody titer in the immunized animal can be monitored over time by standard techniques, such as with an enzyme linked immunosorbent assay (ELISA) using immobilized polypeptide. At an appropriate time after immunization, *e.g.,* when the specific antibody titers are highest, antibody producing cells can be obtained from the animal and used to prepare monoclonal antibodies (mAb) by standard techniques, such as the hybridoma technique originally described by KOHLER and MILSTEIN (*Nature*, vol.256, p:495-497, 1975), the human B cell hybridoma technique (KOZBOR *et al.*, *Immunol.*, vol.4, p: 72, 1983), the EBV-hybridoma technique (COLE *et al., In Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss,Inc., p: 77-96, 1985) or trioma techniques. The technology for producing hybridomas is well known (see generally Current Protocols in Immunology, COLIGAN *et al.* ed. , John Wiley & Sons, New York, 1994). Hybridoma cells producing the desired monoclonal antibody are detected by screening the hybridoma culture supernatants for antibodies that bind the polypeptide of interest, e.g., using a standard ELISA assay.

The method of the invention may comprise comparing the level of expression of the RdCVF2 gene in a biological sample from a subject with the normal expression level of said gene in a control. A significantly weaker level of expression of said gene in the biological sample of a subject as compared to the normal expression level is an indication that the patient has or is predisposed to developing a neurodegenerative disorder.

The "normal" level of expression of the RdCVF2 gene is the level of expression of said gene in a biological sample of a subject not afflicted by any

neurodegenerative disorder, preferably not afflicted with retinis pigmentosa. Preferably, said normal level of expression is assessed in a control sample (*e.g.*, sample from a healthy subject, which is not afflicted by any neurodegenerative disorder) and preferably, the average expression level of said gene in several control samples.

In the following, the invention is described in more detail with reference to amino acid sequences, nucleic acid sequences and the examples. Yet, no limitation of the invention is intended by the details of the examples. Rather, the invention pertains to any embodiment which comprises details which are not explicitly mentioned in the examples herein, but which the skilled person finds without undue effort.

Examples

1) Identification of RdCVF2, a gene paralogous to RdCVF

The mouse RdCVF gene is located on chromosome 8 and contains three exons and can be transcribed in two distinct splice variants corresponding to RdCVF-L (long) and RdCVF-S (short) respectively.

The structure of both RdCVF splice variants is described in figure 1, panel a. The RdCVF-L mRNA (NM_145598, mouse chromosome 8, minus strand, from 70'033'763 to 70'027'717) is composed of three exons (1-3) of 348, 687 and 1751 bp. The RdCVF-S mRNA (BC017153, from 70'033'785 to 70'032'615) is composed of one exon (1172 bp). Coding and non-coding regions are depicted in dark grey) and light grey respectively. The genomic region surrounding the stop codon at the end of the first coding exon and the corresponding orthologous sequences in 12 other vertebrate genomes are aligned. The black triangles indicate the end of the first RdCVF-L coding exon. Conserved stop codons are colored in red. At bottom, lengths of the coding (CDS) and terminal untranslated regions (UTR) are given.

The RdCVF-L splice variant is composed of three exons, which variant codes for a protein wherein the last 109 amino acids are called the "cap".

The RdCVF-S splice variant is composed of a single exon in which the coding sequence is the same as the first exon of the long form extended by one codon followed by a stop codon (TGA) and finally a 3' untranslated region (UTR).

Consequently, the "cap" (i.e., the last 109 amino acids) of RdCVF-L are missing in RdCVF-S.

A blast search on databases enabled the identification of a paralogous gene called RdCVF2.

The structure of both RdCVF2 splice variants is described in figure 1, panel b. The RdCVF2-L mRNA (AK015847, mouse chromosome 13, plus strand, from 50'202'630 to 50'206'797) is composed of two exons (1-2) of 603 and 564 bp. The RdCVF2-S mRNA (BC016199, from 50'202'667 to 50'205'571) is composed of one exon (2904 bp). Coding and non-coding regions are depicted in dark grey) and light grey respectively. The genomic region surrounding the stop codon at the end of the first coding exon and the corresponding orthologous sequences in 12 other vertebrate genomes are aligned. The black triangles indicate the end of the first RdCVF2-L coding exon. Conserved stop codons are colored in red. At bottom, lengths of the coding (CDS) and terminal untranslated regions (UTR) are given.

This analysis enables to locate RdCVF2 gene on chromosome 13 and to demonstrate that RdCVF and RdCVF2 sequences and gene structures are highly similar between both. In fact, it appears that RdCVF2 also encodes both a thioredoxin-like protein (156 aa, SEQ ID NO.12) and a shorter form (101 aa, SEQ ID NO.2) called RdCVF2-L and RdCVF2–S respectively.

Finally, the sequence analysis has revealed that the degree of homology between RdCVF and RdCVF2 is 58.0% for the long isoforms and 53.5% for the short isoforms.

2) Conservation of RdCVF and RdCVF2 gene structure during evolution

Cone viability is related to the production of the RdCVF-S form and, by extension, to the presence of the stop codon at the end of the first exon required to obtain that isoform.

To evaluate conservation of that stop codon further, the UCSC genome browser BLAT (HINRICHS *et al., Nucleic Acids Res.*, vol.34 (Database issue):D590-598,

2006; KENT, *Genome Res.*, vol.12(4):656-664, 2002) server was used to map the mouse RdCVF and RdCVF2 genes to all the available vertebrate genomes and to extract the corresponding genomic sequences.

The results have shown that both loci were found in 13 vertebrates. All these organisms exhibited both genes except *Takifugu rubripes* and *Tetraodon nigroviridis*, in which RdCVF was duplicated at the same chromosomal location (RdCVF a and b) with an additional intron inserted into the first coding exon of this loci. It is noteworthy that the stop codon at the end of the first exon is strictly conserved in the vast majority (Figure 1, panel a and b).

Finally, this observation implies the possible existence of RdCVFs short isoforms in most vertebrates, excepting *Gallus gallus* and *Brachydanio rerio* RdCVF; *Tetraodon nigroviridis* and *Takifugu rubripes* RdCVFb.

3) Analysis of RdCVF and RdCVF2 protein sequences

In order to identify candidate RdCVF and RdCVF2 orthologous proteins, homology searches in the UniProt (WU *et al., Nucleic Acids Res.*, vol.34(Database issue), p:D187-191, 2006) and EMBL (COCHRANE *et al., Nucleic Acids Res.*, vol.34(Database issue):D10-15, 2006) public sequence databases were performed using the BLAST programs (ALTSCHUL *et al., J. Mol. Biol.*, vol.215(3):403-410, 1990 ; ALTSCHUL *et al., Nucleic Acids Res.*, vol.25(17):3389-3402, 1997).

Proteins orthologous to RdCVF(-L / 2-L) referring to the long isoforms of both RdCVF genes, were identified or predicted in vertebrates (*Rattus norvegicus*, *Homo sapiens*, *Pan troglodytes*, *Bos taurus*, *Canis familiaris*, *Gallus gallus*, *Xenopus laevis*, *Tetraodon nigroviridis*, *Brachydanio rerio*) according to protein or genome database searches.

Then, TBA (BLANCHETTE *et al., Genome Res.*, vol.14(4):708-715, 2004) and PipeAlign (PLEWNIAK *et al., Nucleic Acids Res.*, vol.31(13):3829-3832, 2003) programs were used with default parameters to generate the multiple alignments of genomic and protein sequences respectively. Protein alignment occasionally included manual adjustments in keeping with the protein secondary structure conservation.

The figure 2 (panel a) show the sequences alignment of RdCVF, RdCVF2, tryparedoxin (TRYX), nucleoredoxin (NXN) and thioredoxin (TXN). The name,

organism and accession number (in brackets) of each protein sequence are given (left). Identical (white text on black) small (A, D, G, P, S, T ; white text on green) hydrophobic (A, C, F, G, I, L, M, S, T, V, W, Y ; black text on yellow) polar (D, E, H, K, N, Q, R, S ; blue text) and charged (D, E, K, R ; white text on red) conserved residues are shown according to a conservation threshold of 85%. A consensus sequence is given below the multiple alignments in which s, h, p and c correspond to small, hydrophobic, polar and charged residues respectively. The secondary structures (β sheet and α helix) of the Crithidia fasciculata tryparedoxin I structure (1EWX) are given below the consensus sequence. The blue dashed rectangles indicate the three RdCVF(2) specific insertions. The green dashed rectangle shows the "cap" region absent in RdCVF(2)-S. The position of the human thioredoxin cleavage product (TRX80) is indicated (red triangle). Panel b displays the structure of the *Crithidia fasciculata* TRYX-I (1EWX) (left) mouse RdCVF-L (center) and mouse RdCVF2-L (right) models. Regions of TRYX-I backbone conserved in RdCVF(2)-L are colored in red. The "cap" region and the three specific insertions are depicted in green and blue respectively. The putative catalytic site ($C_{44}XXC_{47}$) is shown in yellow with a space-filling representation.

A phylogenetic analysis among the TXN superfamily established that RdCVF and RdCVF2 proteins are closely related to the TRYX and NXN members (MICOSSI *et al., Acta Crystallogr. D. Biol. Crystallogr.*, vol.58(Pt 1):21-28, 2002; KRUMME *et al., Biochemistry*, vol.42(50):14720-14728, 2003; ALPHEY *et al., J. Biol. Chem.*, vol.274(36):25613-25622, 1999; EKLUND *et al., Proteins*, vol.11(1):13-28, 1991; KUROOKA *et al., Genomics*, vol.39(3):331-339, 1997; LAUGHNER *et al., Plant Physiol.*, vol.118(3):987-996, 1998). Even distant homologs such as *Crithidia fasciculata* tryparedoxin I (O96438, TRYX-I) (ALPHEY *et al.,* 1999, abovementioned) exhibit 42.5% and 45.4% sequence similarity to mouse RdCVF(-L / 2-L) proteins. Three insertions in the multiple alignment (called 1, 2 and 3) allow one to distinguish these phylogenetic protein families (Figure 2, panel a).

Insertion 3 (residues 87-110) contains the conserved motif WLALP [W_{108}(L,V)(A,F)(L,V,I)P_{112}] and clearly discriminates the TRYX family [TRYX, NXN, RdCVF and RdCVF2] from TXN superfamily.

Insertion 2 (63-72) and two additional residues (96-97) of insertion 3 allow one to differentiate the RdCVF and RdCVF2 proteins from the rest of the TRYX family.

Finally, insertion 1 (16-21) unambiguously separates RdCVF from all the other TXN superfamily members including RdCVF2. It has to be noted that the thioredoxin active site $C_{44}XXC_{47}$ is only conserved in 44.4% (4 / 9) and 72.7% (8 / 11) of the RdCVF and RdCVF2 vertebrate proteins respectively.

4) Structural modeling of RdCVF and RdCVF2

The high sequence similarity of RdCVFs with TRYX proteins prompted us to build the RdCVF(-L / 2-L / -S / 2-S) structural models with *Crithidia fasciculata* TRYX-I crystal structure (PDB accession number: 1EWX, 1.7 Å resolution structure) (ALPHEY *et al.,* 1999, abovementioned) as a template. By analogy with human TXN and TRX80 models (PEKKARI *et al.,* 2000, abovementioned) the RdCVF(-S / 2-S) structure models were assumed to maintain the same overall folding. Structural models for mouse RdCVF and RdCVF2 (both S and L forms) using the 155 and 147 first residues respectively were constructed using the Builder homology modeling package (KOEHL and DELARUE, *J. Mol. Biol.*, vol.239(2):249-275, 1994; KOEHL and DELARUE, *Nat. Struct. Biol.*, vol.2(2):163-170, 1995; KOEHL and DELARUE, *Curr. Opin. Struct. Biol.*, vol.6(2):222-226, 1996). The final models were further refined by energy minimization, using ENCAD (LEVITT *et al., Computer Physics Comm.*, vol.91:215-231, 1995). On each model 1000 steps of conjugate gradient minimization was applied. The E_{146}(1EWX)➔P_{146}(RdCVF-L) mutation obliges the local backbone conformation in the template structure to be adapted to fit the proline. Builder samples simultaneously the conformation of the loops in the five insertions/deletions and in the E➔P mutation region, and the conformation of the side-chains, using a self consistent mean field approach. PyMOL (www.pymol.org) was used to render the final structures.

The figure 2 (panel b) show the structures of TRYX-I (1EWX) and RdCVF(-L / 2-L).

Figure 2 displays the 1EWX secondary structures (β-sheet and α-helix) below the multiple alignment (panel a) and in the TRYX-I 3D-structure (panel b).

The structure modelization shows that insertions 1, 2 and 3 correspond respectively to: an increase in size of the $\beta_{1.1}$-$\beta_{1.2}$ sheets, a one turn extension in the α_2 helix, and a larger structural region containing the TRYX-specific α_{sup}-β_{sup} and α_3 extension. The two residues (96-97) belonging to insertion 3 in the RdCVF proteins correspond to a larger constrained loop before strand β_{sup} and allow one to discriminate these proteins from TRYX members. It is worth noting that the location on the folded protein where the three insertions co-localize are on the opposite side from the putative catalytic site ($C_{44}XXC_{47}$) in RdCVFs (Figure 2, panel b).

Finally, the C-terminal region absent in RdCVF(-S / 2-S) proteins (hereafter called "cap" and depicted in green in Figure 2, panel b) is positionally fixed relative to the catalytic site. The "cap" region in TXN proteins interacts with the recycling enzyme thioredoxin reductase [7, 13] and its absence might impair the thioredoxin activity in TRX80 and RdCVF(-S / 2-S) [4, 13].

A striking feature of these structural models is the clear spatial proximity of residues from the three insertions. This coincidence points to a possibly novel interaction site in RdCVF(-L / 2-L). As expected, the backbone conformation of the refined model of RdCVF(-S / 2-S) is the same as its counterpart in the long forms, with minor modifications observed in the side-chains at the interface between the non-"cap" and "cap" regions. It should be emphasized that the absence of the "cap" yields to the emergence of a major hydrophobic patch at the RdCVF(-S / 2-S) surface. As a consequence the hydrophobic part of the accessible surface area of RdCVF proteins increases from 2394 $Å^2$ in the long form to 3157 $Å^2$ in the short form.

4) RdCVF-S, RdCVF2-S and RdCVF2-L are expressed in the retina in a rod-dependent manner

Total RNA from neural retina of 8, 15 and 35-day-old wild type (C57BL/6@N), and rd1 mutant, (C3H/He@N) mice and from olfactory epithelium (Balb/c) was purified by cesium gradient (CHIRGWIN *et al., Biochemistry*, vol.18(24):5294-5299, 1979).

Double-stranded cDNA was synthesized from 5 µg total RNA using Superscript Choice System (INVITROGEN). cDNAs were produced by random

priming and normalized according to glucose-6-phosphate dehydrogenase (GAPDH) mRNA. First strand cDNA (0.2 µl) was amplified in triplicate using 2 µM of the specific primers. Primers 5'- CATCACCAACAAAGGGCGGAAG -3' (SEQ ID NO.13) and 5'- CATTCCTCAGCAGAGAAGGGAAC -3' (SEQ ID NO.14) were used for RdCVF2-S; primers 5'-CCGTGCTATTGTTTCAGAGCCCTTAACTTTCTATC -3' (SEQ ID NO.15) and 5'- CTGACACTCCAATCGTAAAAGGCAGAAAACGC -3' (SEQ ID NO.16) were used for RdCVF2-L. Primers 5'-AAGCCGATGAGCAACTTCC-3'(SEQ ID NO.17) and 5'-TCATCTCCCAGTGGATTCTT-3' (SEQ ID NO.18) were used for rhodopsin on a lightcycler (Roche, Basel, Switzerland).

For northern blotting analysis, 2 µg of poly-A mRNA was used and the membrane was hybridized to a probe corresponding to exon 1 of the RdCVF2 gene using standard method.

The absence of DNA contamination was checked by omitting the reverse transcriptase. Results are displayed as fold difference compared to the lowest expression.

The figure 3, panel a show the results of RT-PCR on wild type and *rd1* mice retina at post-natal day 35 for the short (RdCVF2-S, 176 pb fragment) and long (RdCVF2-L, 170 pb fragment) isoforms of RdCVF2.

The figure 3, panel b shows the expression of RdCVF2 transcripts in brain, testis, normal retina (*wt*), degenerated retina (*rd1*) and in the whole mouse embryo at embryonic day 12.5 (ED12.5).

The results established that RdCVF2-S and –L are expressed in the wild-type mouse retina (Figure 3, panel a). Interestingly, RdCVF2-S and –L expression was absent in the retina of the *rd1* mouse after rod-photoreceptor degeneration. The results also show that in addition to the expression in the retina, most likely by rod photoreceptors since its expression is absent in the degenerated retina (*rd1*), a weaker expression of RdCVF2 is observed in the brain and testis. Moreover, the results have shown that an expression of the two messengers RNA corresponding to the short (RdCVF2-S) and the long (RdCVF2-L) isoforms is also detected in the olfactory

epithelium. Finally, no expression was detected in the whole mouse embryo at embryonic day 12.5.

The expression of RdCVF2-S and -L mRNA in the retina and in the olfactory epithelium was analyzed by in situ hybridization with a digoxigenin (DIG)-labeled murine antisense riboprobe.

Mouse RdCVF2-S and RdCVF2-L was amplified by PCR using the following primers: primers 5'-GTAGCTTTGTACTTTGCGGCG-3' (SEQ ID NO.19) and 5'-GTCATCAGAAAATGTATCACCTCCATAGG-3' (SEQ ID NO.20) for RdCVF2-S; primers 5'-GCCATCTCTGCGACTTATTTTTACC-3' (SEQ ID NO.21) and 5'-AATTAGTGCCACCAGCACCATC-3' (SEQ ID NO.22) for RdCVF2-L. The PCR product was cloned into PGEM easy vector (PROMEGA). Sense and antisense RdCVF2 mRNA probes generated from SP6 or T7 promoters and labeled with digoxigenin-UTP (ROCHE) were generated according to manufacturer's instruction.

After defrosting and drying at room temperature, retina and olfactory epithelium sections were post-fixed on ice for 10 min in 4% paraformaldehyde washed in PBS at room temperature for 10 min. retina sections were hybridized with sense and antisense RdCVF2 mRNA probes generated from SP6 or T7 promoters and labeled with digoxigenin-UTP. *In situ* hybridization and digoxigenin-labeled probe detection were performed as described previously (ROGER *et al., Dev. Biol.*, vol.298(2):527-539, 2006). The specificity of the staining was demonstrated by the lack of hybridization signal with the sense probe.

The figure 3, panel c shows the results of *In situ* hybridization on sections of wild-type and *rd1* mice retina with digoxigenin-labeled RdCVF2-S and L riboprobes (AS : antisens, S : sens). Original magnification: 40x.

The results show that the transcripts for RdCVF2-S and -L were detected in the photoreceptor layer. No staining was observed with the sense control probes, supporting the specificity of the RdCVF2-S and L probes. Finally, no expression was detected in the *rd1* retina after rod degeneration (result not shown). Moreover, the results have shown that the localisation of labelled cells in olfactory epithelium suggests that basal cells, immature and mature neurons strongly express RdCVF2 mRNA, and that no expression of RdCVF2 mRNA was observed at the apical

position of the cytoplasm of the supporting cells. It must be noted that a small expression of RdCVF2 mRNA was also observed during development (E12.5) specifically restrictive to the nasal development.

Finally, the expression of RdCVF2-S and of RdCVF2-L were analysed during the process of rod degeneration.

The figure 3, panel d show the expression time-courses of both RdCVF2 isoforms and rhodopsin transcripts in wild type (*wt*) and *rd1* mice at post natal day 8, 15 and 31 (PN8, PN15 and PN35).

The results established that at post-natal day 8 (PN8) before the onset of rod loss, RdCVF2-S is expressed at similar level in the wild-type and in the *rd1* retina similarly to the rod photopigment gene rhodopsin. From PN15 to PN35, the degeneration of rods (measured by the decrease in rhodopsin expression) is correlated with a decrease in RdCVF2-S expression. Consequently, these results indicate that RdCVF2-S is expressed in a rod-dependent manner.

The same results have been observed with RdCVF2-L (data not shown).

5) RdCVF2 mRNA is not only expressed in the retina and in olfactive epithelium but also in other tissues

Mouse mRNA and EST sequences associated with both RdCVF and RdCVF2 isoforms (L and S) were used to estimate the tissue specificity of each messenger. The results are presented in the following table.

Genes	isoform	mRNA and EST EMBL accession numbers	Expression location
RdCVF	L	BC021911 ; BI738445 ; CB849876 ; CK623520 ; BI731629 ; BI872244 ; BG294111 ; BI734135 ; BU505070 ; BU840744 ; BQ929742 ; BQ938066; BI73223 ; CK628091 ; BY742305 ; N539863; CO424399 ; BB277874 ; BB279867 ; CO426411	Retina, RPE, choroid and/or eye
		BF470336 ; BE983242 ; AW495183	None
	S	BC017153 ; CB849876 ; BG299078 ; BY742292	Retina and/or eye
RdCVF-2	L	CK621895 ; CK620198 ; BG288447 ; BB282056; BB279962 ; BB281743 ; BB277718 ; BB277574; BB277714 ; BI732427	Retina
		BC038905 ; BI108740	Mammary tumor, tumor and/or gross tissue
		BY715393 ; AV266697	Testis
		DT906804	Hematopoietic stem cells

		BY435086	amnion
		AI324093	Placenta
		BB552115	Oviduct
		AA261233	Foetus
		BB241367	Thymus
		AI536471	Mammary gland
		BX632214 ; BF460609 ; BX514476	
	S	BC016199 ; BG297304 ; BG297383	Retina
		BX514476	None

As reported before (LEVEILLARD *et al.,* 2004, abovementioned), the results confirmed that RdCVF-L and RdCVF-S mRNAs are specifically expressed in eye and retina as 20 / 23 and 4 / 4 sequences were found in these tissues respectively. The results show that mouse RdCVF2-L mRNA is also preferentially expressed in retina (10 / 24) but is also present in other tissue types such as tumor (2), testis (2), stem cells (2), amnion (1), placenta (1), oviduct (1), foetus (1), thymus (1), and mammary gland (1). These results confirmed the expression of RdCVF2 observed in the testis and brain (Figure 4, panel b). Finally, EST and mRNA sequences corresponding to RdCVF2-S are exclusively expressed in retina (3 / 4).

6) RdCVF2 cone viability effects

The strong similarities between RdCVF and RdCVF2 loci in terms of gene organization, conservation of sequence and rod-dependent expression led us to hypothesize that RdCVF2 protein might also be able to promote cone viability as previously reported for RdCVF-S (LEVEILLARD *et al.,* 2004, abovementioned).

RdCVF(-S / 2-S / 2-L) isoforms were cloned into the expression plasmid pcDNA3 and transfected into COS-1 cells. 48 hours after transfection, the conditioned media from the COS-transfected cells was harvested and incubated with a cone-enriched primary cell culture system from chicken embryo (60-80% of cones) (FINTZ *et al., Invest. Ophthalmol. Vis. Sci.*, vol.44(2):818-825 2003).

After seven days of incubation, a period over which these post-mitotic cells degenerate, the viability of the cells in the culture was scored using the Live/Dead assay (MOLECULAR PROBES) and a cell counting platform as previously described [4]. The viability corresponding to three independent assays is represented as fold over pcDNA3 used as negative control.

The figure 4 shows the rescue activity of RdCVF-S and RdCVF2-S when compared to that of empty vector (pcDNA3). Statistical analysis (Tuckey test) shows that the results are statistically significant ($p<0.001$).

The results show that the number of live cells in the presence of RdCVF-S is twice than the control (pcDNA3). A less pronounced, but statistically significant, increase in cone viability (1.6 fold) is observed for RdCVF2-S. These findings confirm that RdCVF2-S is also a cone viability factor similar to RdCVF-S (LEVEILLARD *et al.,* 2004, abovementioned). Importantly, no synergistic trophic effect on cones is observed when both RdCVF-S and RdCVF2-S are co-tranfected in COS-1 cells pointing to use of the same pathway by both factors (data not shown).

7) RdCVF2 OSN viability effects

Since RdCVF2 is also expressed in olfactory neurons, the possible viability activity of RdCVF2 on culture of Olfactory Sensitive Neurons (OSN) has been analysed.

Adult mice were killed by decapitation. The posterior part of the nasal septum was dissected free of the nasal cavity and immediately placed in ice-cold Dulbecco's modified Eagle's medium (DMEM) containing 50 µg/ml gentamicin (EUROBIO ; GIBCO) and 10% (v/v) fetal calf serum (EUROBIO). The cartilage of the septum was removed and the olfactory mucosa was incubated for 30 min at 37°C in a 2.4 units/ml dispase II solution (ROCHE). The olfactory epithelium was carefully separated from the underlying lamina propria under the dissection microscope and was gently triturated about 20 times to separate the cells. The resulting cell suspension was transferred to a 50 ml conical tube and the dispase was inactivated by adding 40 ml of HBSS without Calcium and magnesium. The cell suspension was centrifuged at 700 rpm for 5 min. The supernatant was aspirated and the pellet containing the cells was resuspended in a medium composed of DMEM containing insulin (10 µg/ml, SIGMA), transferin (10 µg/ml, SIGMA), selenium (10 µg/ml, SIGMA), calf foetal serum (5%), ascorbic acid (200µM,). Cells were plated at the density of cells/cm2 on 12 mm sterile glass coverslips coated with 5 µg/cm2 human collagen IV (SIGMA).

Expression vectors encoding for RdCVF(-S / 2-S/ 2-L) isoforms described previously were transfected into COS-1 cells. 48 hours after transfection, the conditioned media from the COS-transfected cells was harvested and incubated with the culture of OSN. After 4 days of culture, cells were fixed and labelled with tubulin III, and counted.

The results shown in figure 5 have established that the OSN cell viability was more important in the presence of the RdCVF2-S isoform compared to control. Protective effects were observed with RdCVF2-L.

8) RdCVF2 Purkinje cells viability effects

After decapitation of mouse at postnatal day 1-3, brains were dissected out into cold Gey's balanced salt solution containing 5 mg/ml glucose, and meninges were removed. Cerebellar parasagittal slices (350 or 250 μmthick) were cut on a McIlwain tissue chopper and transferred onto membranes of 30 mm MILLIPORE culture inserts with 0.4 μm pore size (MILLICELL; MILLIPORE, Bedford, MA). Slices were maintained in culture in six-well plates containing 1 ml or in 10 cm culture dishes containing 3 ml of medium at 35°C in an atmosphere of humidified 5% CO2. The medium was composed of 50% basal medium with Earle's salts (INVITROGEN), 25% HBSS (INVITROGEN), 25% horse serum (INVITROGEN), L-glutamine (1 mM), and 5 mg/ml glucose (Stoppini *et al., J. Neurosci. Methods.*, vol.37(2), p:173-82, 1991).

Expression vectors encoding for RdCVF(-S / 2-S / 2-L) isoforms described previously were transfected into COS-1 cells. 48 hours after transfection, the conditioned media from the COS-transfected cells was harvested and incubated with the culture of purkinje cells. After 4 days of culture, cells were fixed and counted.

9) RdCVF2 cortical neurons viability effects

Serum-free preparation of mouse cortical primary cultures was performed with mouse at postnatal day 1. After removal of meninges, entire cortices were mechanically dissociated in a phosphate buffer saline glucose solution without added divalent cations (100 mM NaCl, 3 mM KCl, 1.5 mM KH2PO4, 7.9 mM Na2HPO4, 33 mM glucose, 100 U/ml penicillin and 100 μg/ml streptomycin) and resuspended in Neurobasal-medium (GIBCO-INVITROGEN) containing 2% B27 supplement

(GIBCO), 0.5 mM glutamine, and 25 μM glutamate. Cells were then cultured onto poly-ornithine-coated coverslips to produce cultures highly enriched in neurons.

Expression vectors encoding for RdCVF(-S / 2-S / 2-L) isoforms described previously were transfected into COS-1 cells. 48 hours after transfection, the conditioned media from the COS-transfected cells was harvested and incubated with the culture of cortical neurons. After 4 days of culture, cells were fixed and counted.

Finally, the results established that a novel trophic factor for cone survival, and more generally for neuron survival has been identified. This factor defines a novel family of bifunctional proteins with potential involvement in neuroprotection and response to oxidative stress.

CLAIMS

1. A pharmaceutical composition comprising a pharmaceutically acceptable carrier and a compound selected in the group comprising:

(i) a polypeptide comprising an amino acid sequence selected in the group comprising the amino acid sequence of the long isoform in *Homo sapiens* of the RdCVF2 gene (SEQ ID NO:10), orthologs, derivatives and fragments thereof;

(ii) a polynucleotide coding for said polypeptide;

(iii)a vector comprising said polynucleotide; and

(iv)a host cell genetically engineered expressing said polypeptide.

2. The pharmaceutical composition according to claim 1, wherein the derivatives are selected in the group comprising polypeptides having a percentage of identity of at least 75% with SEQ ID NO.10 or orthologs thereof, preferably of at least 85%.

3. The pharmaceutical composition according to any one of claims 1 or 2, wherein said fragments refer to polypeptides having a length of at least 25 amino acids, preferably at least 50 amino acids.

4. The pharmaceutical composition according to any one of claims 1 to 3, wherein the polynucleotide is selected in the group comprising refers to RNA or DNA, preferably said polynucleotide is DNA.

5. The pharmaceutical composition according to claim 4, wherein said polynucleotide comprises a sequence which encodes the sequence SEQ ID NO.10.

6. The pharmaceutical composition according to any one of claims 1 to 5, wherein the vector is an expression vector selected in the group comprising plasmids, viral particles and phages.

7. The pharmaceutical composition according to any one of claims 1 to 6, wherein the host cell is selected in the group comprising bacterial cells, fungal cells, insect cells, animal cells, and plant cells, preferably said host cells is an animal cell.

8. A use, for treating and/or preventing a neurodegenerative disorder, of a compound selected in the group comprising:

(i) a polypeptide comprising an amino acid sequence selected in the group comprising the amino acid sequence of long isoform in *Homo sapiens* of the RdCVF2 gene (SEQ ID NO:10), orthologs, derivatives and fragments thereof;

(ii) a polynucleotide coding for said polypeptide;

(iii)a vector comprising said polynucleotide; and

(iv)a host cell genetically engineered expressing said polypeptide.

9. The use according to claim 8, wherein the neurodegenerative disorder is a disease associated with the degeneration of neurons selected in the group comprising degenerative disorders of the central nervous system, degenerative disorders of the photoreceptors, and degenerative disorders of the olfactory neurons.

10. The use according to claim 9, wherein the degenerative disorder of the central nervous system, is selected in the group comprising Alzheimer's Disease, Parkinson's Disease, and Huntington's Disease/Chorea.

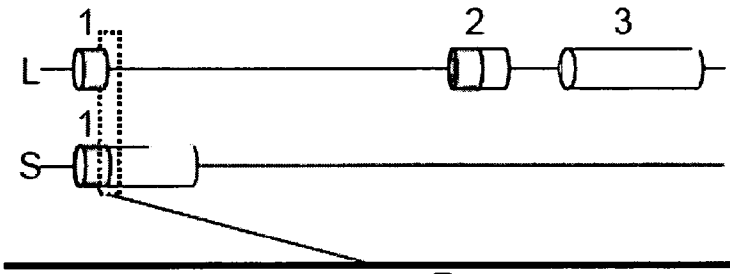
11. The use according to claim 9, wherein the degenerative disorders of the photoreceptors is selected in the group comprising cone dystrophy.

12. A method of testing a subject thought to have or be predisposed to having a neurodegenerative disorder, which comprises the step of analyzing a biological sample from said subject for :

(i) detecting the presence of a mutation in the RdCVF2 gene and/or its associated promoter, and/or

(ii) analyzing the expression of the RdCVF2 gene.

a RdCVF gene, chromosome 8 minus strand

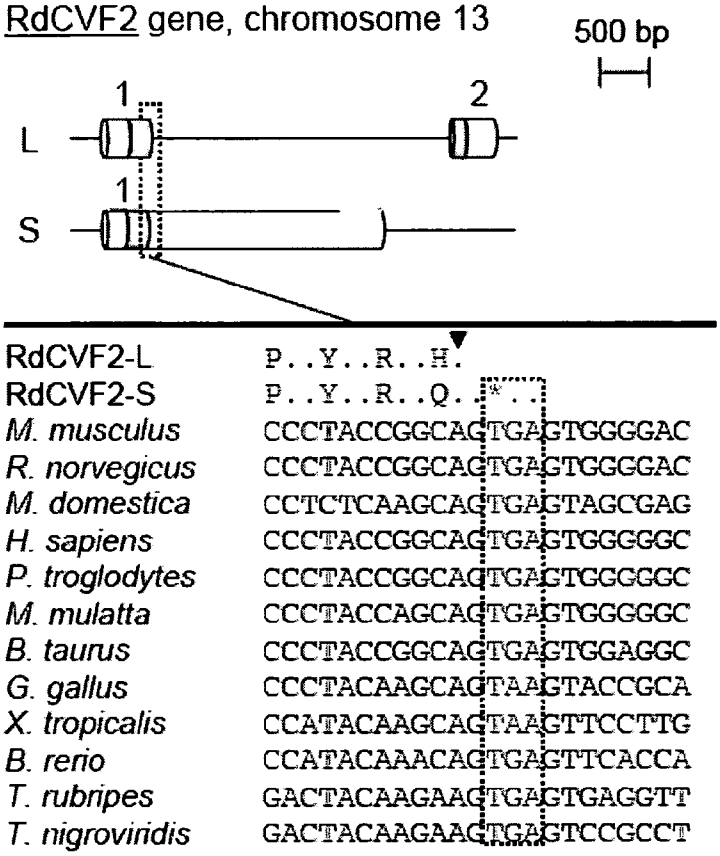


RdCVF-L	E..L..R..
RdCVF-S	E..L..R..R..*
M. musculus	GAACTGAGGAGGTGAGGCCCC
R. norvegicus	GACCTGAGGAGGTGAGGCCCC
M. domestica	GAGCTGAAAAGGTGAGCCTAC
H. sapiens	GATCTGAGGAGGTGAGGAGGG
P. troglodytes	GATCTGAGGAGGTGAGGAGGG
M. mulatta	GAACTGAGGAGGTGAGGAGGG
B. taurus	GACCTGAGGAGGTGAGACAAG
C. familiaris	GACCTGAGGAGGTGAGGTGGG
G. gallus	GACCTGAGGAGGTGG[n110]TAA
X. tropicalis	GAATTCAGGAGGTGAGATAGG
B. rerio	CCCTATAGGCAGTAC[n36]TGA
T. rubripes a	CCATACAGACAGTAGGTGGAT
T. nigroviridis a	CCATACAGACAGTAGGTGGAC
T. rubripes b	CCCTTCAGGAGGTGTGTGGTTTAG
T. nigroviridis b	CCTTTTAGGAGGTGT[n40]TGA

	L	S
5'UTR	22 bp	44 bp
CDS	654 bp	330 bp
3'UTR	2076 bp	798 bp

Figure 1a

b RdCVF2 gene, chromosome 13



	L	S
5'UTR	299 bp	264 bp
CDS	471 bp	306 bp
3'UTR	397 bp	2334 bp

Figure 1b

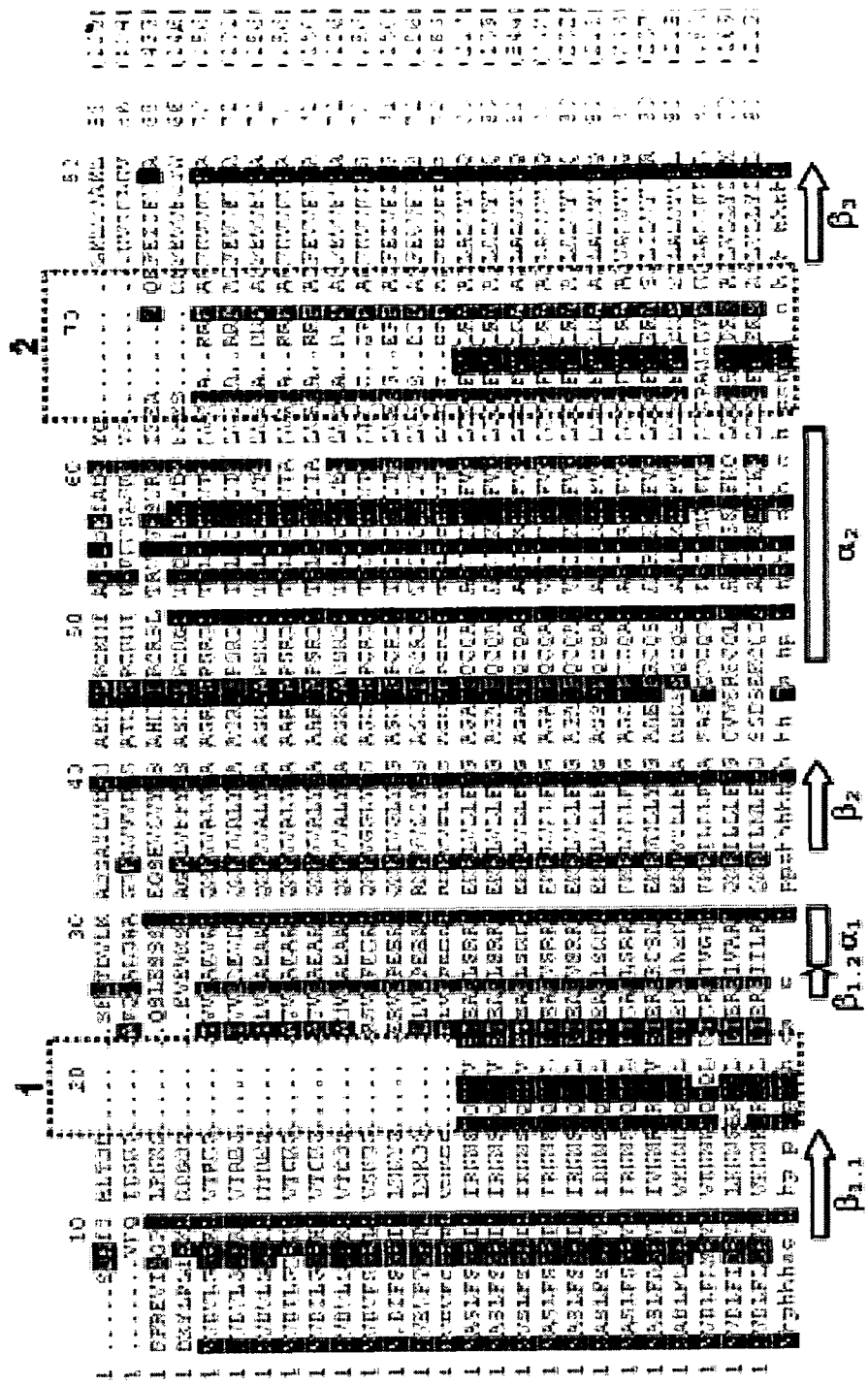


Figure 2a

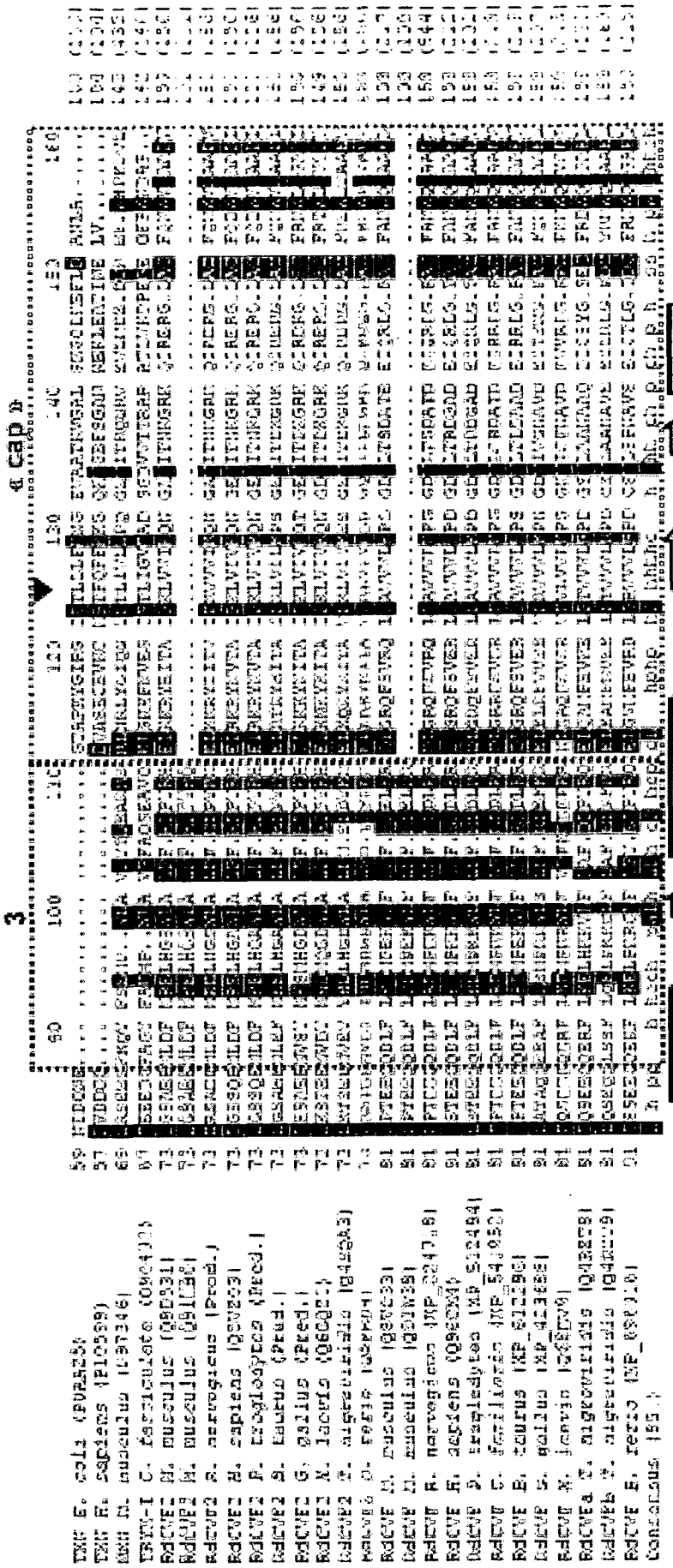


Figure 2b

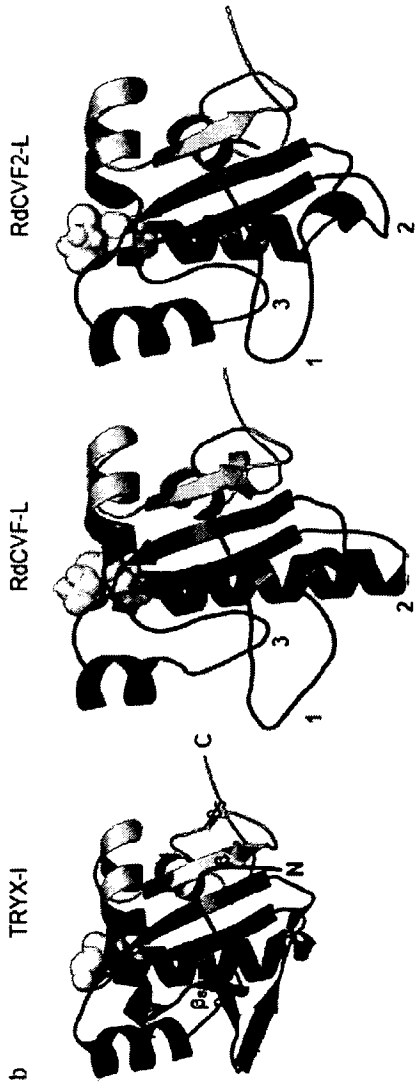


Figure 2c

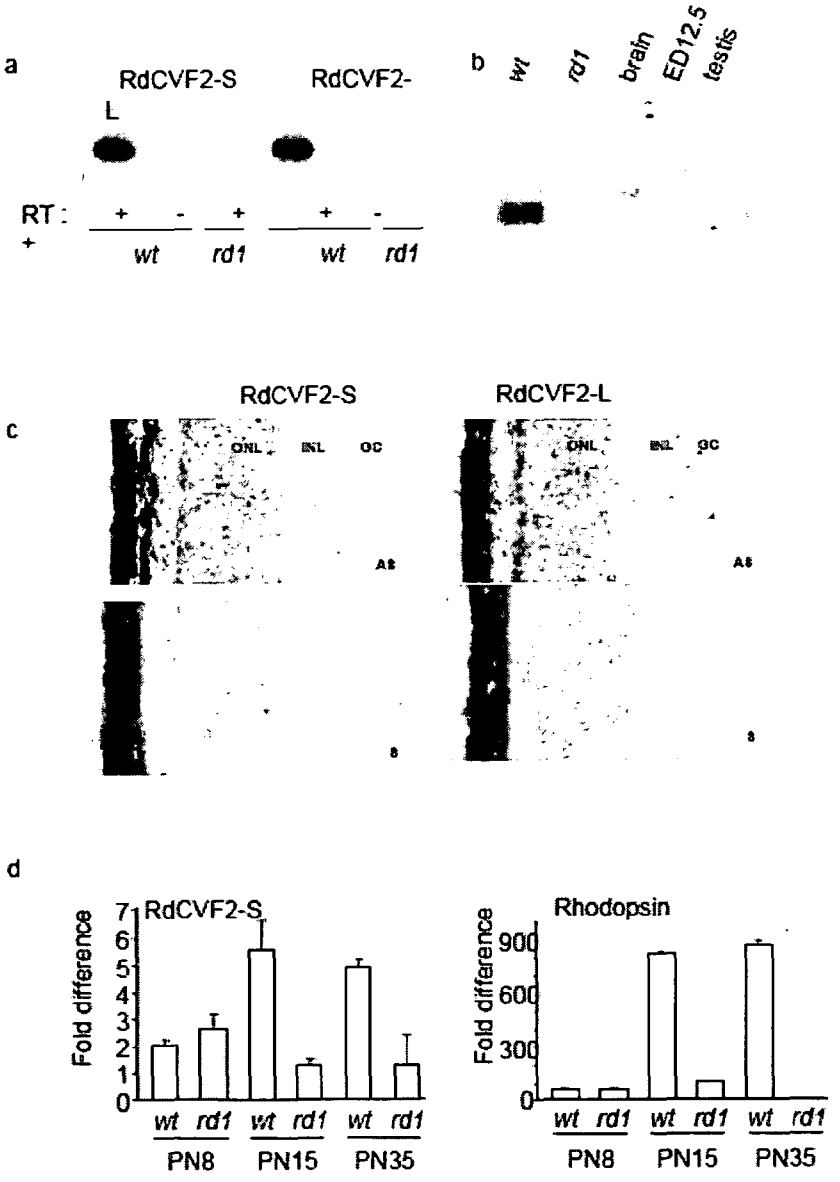

a
RdCVF2-S
RdCVF2-
L
RT :
+
+
-
+
+
-
wt
rd1
wt
rd1
b
wt
rd1
brain
ED12.5
testis
c
RdCVF2-S
RdCVF2-L
ONL
INL
GC
AS
S
d
RdCVF2-S
Fold difference
Rhodopsin
wt
rd1
PN8
PN15
PN35

Figure 3

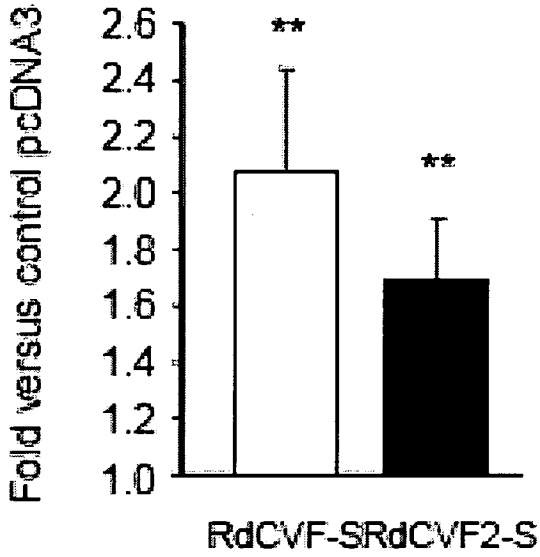


Figure 4

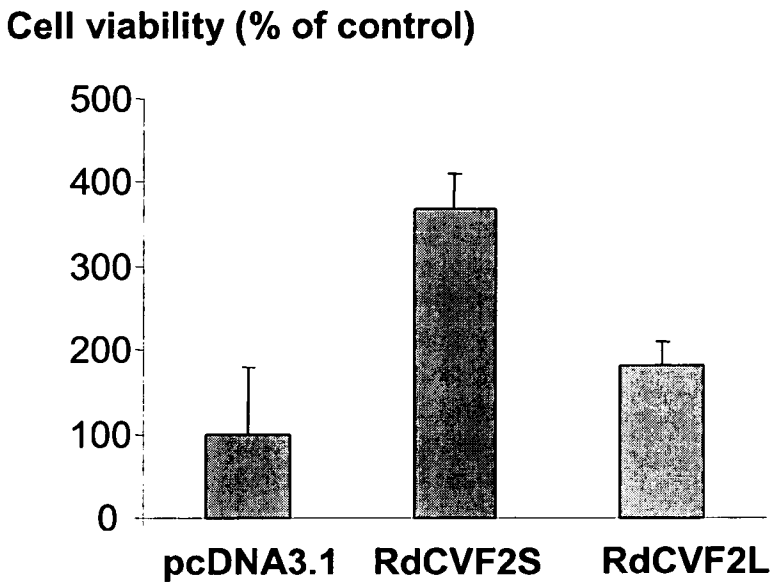


Figure 5

INTERNATIONAL SEARCH REPORT

International application No
PCT/EP2008/057031

A. CLASSIFICATION OF SUBJECT MATTER
INV. A61P25/28 G01N33/68 C12N15/85

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
A61P G01N C12N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)
EPO-Internal, Sequence Search, WPI Data, BIOSIS, PAJ

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	DATABASE GENESEQ [Online] 26 July 2001 (2001-07-26), TANG Y T ET AL: "Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries" XP002499025 retrieved from EBI Database accession no. AAM39739 abstract; sequence 2884	1-10
Y	-/--	11

[X] Further documents are listed in the continuation of Box C.

[X] See patent family annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

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"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
10 October 2008	05/11/2008

Name and mailing address of the ISA/	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL – 2280 HV Rijswijk Tel. (+31-70) 340-2040, Fax: (+31-70) 340-3016	Bobkova, Dagmar

Form PCT/ISA/210 (second sheet) (April 2005)

INTERNATIONAL SEARCH REPORT

International application No
PCT/EP2008/057031

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	-& WO 01/53312 A (HYSEQ INC [US]; TANG Y TOM [US]; LIU CHENGHUA [US]; ASUNDI VINOD [US];) 26 July 2001 (2001-07-26) abstract pages 1,2,11 page 20, lines 32,33 page 24 - page 26 page 27, line 30 pages 28,30 page 34, line 7 - line 34 page 45, line 18 - line 29	1-10
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Y		10,11

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International application No
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