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USGENE® is the new unparalleled resource for

- Freedom-to-operate, prior-art, validity and infringement patent sequence searches
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- GETSIM for advanced similarity searching based on FASTA algorithm
- GETSEQ for simple fragment or motif sequence queries

Biosequences in USGENE®

- Peptide and nucleic acid sequences from 1982 to date
- From all relevant USPTO published applications and issued patents
- Organism name, sequence length and SEQ ID number
- Feature tables for modifications and other features
- Typically available within 7 days of publication by the USPTO

USGENE® records also contain

- Original publication title, abstract and claims
- Patent assignees and full inventor names
- Publication, application and parent case WIPO/PCT numbers and dates
- Full-text links to the USPTO

More information is available at:
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The USPTO Genetic Sequence Database, USGENE®, is produced by the SequenceBase Corporation and provided on STN as file USGENE. STN is operated by FIZ Karlsruhe and CAS worldwide and is represented in Japan by JAICI.

STN

FIZ Karlsruhe

ACCESSION NUMBER: 6825322.1 (1) cDNA (2) USGENE

TITLE: (3) Human N-methyl-D-aspartate receptor subunits, nucleic acids encoding same and uses therefor (Patent)

INVENTOR: Daggett; Lorrie P. (San Diego, CA);
Lu; Chin-Chun (San Diego, CA)
PATENT ASSIGNEE: Merck & Co Inc (Rahway NJ) (4)
PATENT INFO: US6825322 B2 20041130
APPLICATION INFO: US 2002-038937 20020104
DOCUMENT TYPE: Patent

ORGANISM: Not provided (5)
ABSTRACT:

(6) In accordance with the present invention, there are provided nucleic acids encoding human NMDA receptor protein subunits and the proteins encoded thereby. The NMDA receptor subunits of the invention comprise components of NMDA receptors that have cation-selective channels and bind glutamate and NMDA. In one aspect of the invention, the nucleic acids encode NMDAR1 and NMDAR2 subunits of human NMDA receptors. In a preferred embodiment, the invention nucleic acids encode NMDAR1, NMDAR2A, NMDAR2B, NMDAR2C and NMDAR2D subunits of human NMDA receptors. In addition to being useful for the production of NMDA receptor subunit proteins, these nucleic acids are also useful as probes, thus enabling those skilled in the art, without undue experimentation, to identify and isolate related human receptor subunits. Functional glutamate receptors can be assembled, in accordance with the present invention, from a plurality of one type of NMDA receptor subunit protein (homomeric) or from a mixture of two or more types of subunit proteins (heteromeric). In addition to disclosing novel NMDA receptor protein subunits, the present invention also comprises methods for using such receptor subunits to identify and characterize compounds which affect the function of such receptors, e.g., agonists, antagonists, and modulators of glutamate receptor function. The invention also comprises methods for determining whether unknown protein(s) are functional as NMDA receptor subunits.

CLAIMS:

(7) US6825322 B2: What is claimed:
1. An isolated and substantially pure N-methyl-D-aspartate receptor subunit comprising an amino acid sequence as set forth in SEQ ID NO:56, wherein said amino acid sequence is encoded by a DNA sequence comprising a sequence of nucleotides as set forth in SEQ ID NO. 55.
2. A substantially pure human N-methyl-D-aspartate receptor subunit comprising the sequence of amino acids set forth in SEQ ID NO: 56.
3. A method for detecting a binding partner for a receptor comprising the receptor subunit of claim 2 in a sample suspected of containing the binding partner, comprising:
(i) contacting the sample with the receptor under conditions favoring binding of the receptor to the binding partner;
(ii) determining the presence of the binding partner in the sample by detecting binding of the receptor to the binding partner.

SEQUENCE SOURCE: NUCLEIC; PSIPS; GRANTED (8)
SEQ ID NO: 1
SEQUENCE LENGTH: 4298 (9)
SEQUENCE

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        1 caagccgggc gttcggagct gtgcccggcc ccgcttcagc accgcggaca
       51 gcgccggccg cgtggggctg agcgccgagc ccccgcgcac gcttcagccc
      101 cccttccctc ggccgacgtc ccgggaccgc cgctccgggg gagacgtggc
      151 gtccgcagcc cgcggggccg ggcgagcgca ggacggcccg gaagccccgc
      201 gggggatgcg ccgagggccc cgcgttcgcg ccgcgcagag ccaggcccgc
            .
            .
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(10)

FEATURE TABLE:

Key	Location	Qualifier
CDS	262..3078	

(11)

(1) USGENE Accession Number (AN), including the sequence identity number (SEQ ID NO)

(2) Molecule Type (MTY)

(3) Original patent title

(4) Bibliographic information – Publication, application, assignee & inventor data

(5) Organism (where given) – providing the name of the organism from which the sequence is derived

(6) Original patent abstract

(7) Full patent claims

(8) Sequence source – Nucleic or Protein; PSIPS/USPTO, NCBI, etc; Granted or Application

(9) Sequence Length

(10) Patent sequence – each USGENE record is based upon a sequence

(11) Feature table - includes sequence modifications and other features, as provided by the patent applicant

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