A list of Supporting Information

Appendix S2: Proof letter from NCBI for publication of DRD3 new variants

Dear GenBank Submitter:

Thank you for your submission.

Based on the data submitted to us, the scheduled release date for your submission is:

Feb 4, 2017

If this date is not correct, please let us know as soon as possible, otherwise this submission will be released on the date indicated above.

The data will become available from our different servers within a few days of release. The data are simultaneously made available to ENA in Europe and the DNA Data Bank of Japan.

Some or all of your sequences have been flagged as unverified because GenBank is unable to verify the quality of the sequence and/or annotation. Sequences flagged as unverified will not be included in NCBI BLAST databases.

Minor changes may have been made to your original submission in order to conform to database annotation conventions. In particular, please review:

- Spelling

- Citation data (page span, etc.)

- Nomenclature ('official' gene names, product labels, etc.)

- Taxonomic and source data

- Feature spans and descriptions (particularly non-coding regions)

Additional edits may have been made to your submission, including:

- Exon spans adjusted to conform to the splice donor/acceptor

 consensus sequences, GT and AG, respectively

- Strings of N's at the ends of sequences and linker past the

 polyA tail removed

- Any mRNA or ribosomal RNA sequences submitted on the minus-strand

 have been reverse-complemented

If your submission contained unpublished organism names, the scientific names have been changed to temporary names. Please notify us when the organism names are published and we will update them accordingly.

Please send any revisions, including bibliographic information (e.g., conversion from unpublished to published), biological data (e.g., new features), or sequence data to:

gb-admin@ncbi.nlm.nih.gov

Since the flatfile record is a display format only and is not an editable format of the data, do not make changes directly to a flatfile. For complete information about different methods to update a sequence record, see: https://www.ncbi.nlm.nih.gov/Genbank/update.html
An accession number has been assigned to each nucleotide sequence and was previously provided to you. Note that during the processing, we have assigned protein identifiers to any proteins within the submission. This is fielded as /protein_id.

We strongly recommend that these numbers appear in any publication which reports or discusses these data, so that readers may easily retrieve your data from our databases.

Thank you once again for your submission.

Please reply using the original subject line.

This will allow for faster processing of your correspondence.

Sincerely,

Vincent Calhoun, PhD

GenBank Direct Submission Staff

gb-admin@ncbi.nlm.nih.gov

GenBank flat file:

LOCUS   KX198702   424 bp   mRNA   linear   PRI 13-JAN-2017

DEFINITION UNVERIFIED: Homo sapiens isolate PV1 DRD3-like mRNA, partial

        sequence.

ACCESSION   KX198702

VERSION   KX198702

KEYWORDS   UNVERIFIED.

SOURCE   Homo sapiens (human)

  ORGANISM Homo sapiens

        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

        Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;

Catarrhini; Hominidae; Homo.

REFERENCE   1 (bases 1 to 424)

  AUTHORS   Pornour,M., Vaseghi,H. and Mohammad Ganji,S.

  TITLE   TNF-alpha variations in diabetes with foot ulcer related to

            dopamine receptors (DRD2 and DRD3) changes

  JOURNAL   Unpublished

REFERENCE   2 (bases 1 to 424)

  AUTHORS   Pornour,M., Vaseghi,H. and Mohammad Ganji,S.

  TITLE   Direct Submission

  JOURNAL   Submitted (05-MAY-2016) Medical Laser Research Center, ACECR,

            Aboorehian, Tehran 1315893111, Iran

COMMENT   GenBank staff is unable to verify sequence and/or annotation

            provided by the submitter.

            ##Assembly-Data-START##

            Sequencing Technology :: Sanger dideoxy sequencing

            ##Assembly-Data-END##

FEATURES   Location/Qualifiers

     source   1..424

                     /organism="Homo sapiens"

                     /mol_type="mRNA"

                     /isolate="PV1"

                     /db_xref="taxon:9606"

                     /cell_type="preipheral blood mono nuclear cells from

                     diabetes patient"

                     /country="Iran"

     misc_feature   <1..>424

                     /note="similar to DRD3; contains microsatellite insertions"

ORIGIN

        1 ggtagcactg tgcatgtgga gagtgtgtgg gtgtgggtgt gtgtgtgtgt gtgtgtgtaa

       61 gtgaatgtgc ccagatgtct gtcaaagacc ttgtgttttt ctattcttcc ttctgagagg

      121 caaagattga agaccctcga atctgatggg ctcgagattg cgggggactg cccctccgct

      181 cctatcttcc ggcccgcgaa gattctcccc cgaaagagac actgccatca tcggtttggc

      241 cctaagtcca gaggtgtaga aaatttcttt ttctgtgcgt gataaccgcg tgagaccctg

      301 ctctcacctt cccacccgag cattgcctca cgaccaaccc cccccctctt gtgtgtttct

      361 taaaaatcca tgacaagcat ggggaggcaa tctttatctc ctgccctctt ctgtttggct

      421 ttaa //

LOCUS   KX198703   430 bp   mRNA   linear   PRI 13-JAN-2017

DEFINITION UNVERIFIED: Homo sapiens isolate PVG DRD3-like mRNA, partial

            sequence.

ACCESSION   KX198703

VERSION   KX198703

KEYWORDS   UNVERIFIED.

SOURCE   Homo sapiens (human)

  ORGANISM Homo sapiens

            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

            Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;

            Catarrhini; Hominidae; Homo.

REFERENCE   1 (bases 1 to 430)

  AUTHORS   Pornour,M., Vaseghi,H. and Mohammad Ganji,S.

  TITLE   TNF-alpha variations in diabetes with foot ulcer related to

            dopamine receptors (DRD2 and DRD3) changes

  JOURNAL   Unpublished

REFERENCE   2 (bases 1 to 430)

  AUTHORS   Pornour,M., Vaseghi,H. and Mohammad Ganji,S.

  TITLE   Direct Submission

JOURNAL Submitted (05-MAY-2016) Medical Laser Research Center, ACECR,

Aboorehian, Tehran 1315893111, Iran

COMMENT   GenBank staff is unable to verify sequence and/or annotation

provided by the submitter.

##Assembly-Data-START##

Sequencing Technology :: Sanger dideoxy sequencing

##Assembly-Data-END##

FEATURES   Location/Qualifiers

source   1..430

/organism="Homo sapiens"

/mol_type="mRNA"

/isolate="PVG"

/db_xref="taxon:9606"

/cell_type="preipheral blood mono nuclear cells from

diabetes patient"

/country="Iran"

/collected_by="ACECR central lab"

misc_feature   <1..>430

/note="similar to DRD3; contains microsatellite insertions"

ORIGIN

    1 cgaaagctct gtgcatgcgg tgtgtgtgtg ggtgagcgtg tgtgtgtgtg tgtgtgtgta

   61 agtgaaagtg cccagcgtct gccaaggacc tggaaggttc cagactcctt aatgaggtaa

  121 tcttttatca ccctccactc ctgatggcat aacagcccgc ggggccctgc cagcccgctt

  181 ctcatcttcc tctccctccg ctgttctacc cagttgggaa cccctgtcct cttctgtttg

  241 gctgaagcct cttctggttg tatttaattt ccttttaagc tctactttgc cacgtgatag

  301 cactgcttta atcatttcta accagtgatt gcttcaggac agaccctggc ctgctaggtg

  361 acttcctaag catccatgac aagcatgggg aggcaatctt tatctcctgc cctcttctgt

  421 ttggctttaa