

Resource Summary Report

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GRSDB: G-Rich Sequences DataBase

RRID:SCR_007697

Type: Tool

Proper Citation

GRSDB: G-Rich Sequences DataBase (RRID:SCR_007697)

Resource Information

URL: <http://bioinformatics.ramapo.edu/GRSDB2/>

Proper Citation: GRSDB: G-Rich Sequences DataBase (RRID:SCR_007697)

Description: GRSDB2 is a second generation database of G-quadruplexes. Like its first version, GRSDB, it contains information on composition and distribution of putative Quadruplex-forming G-Rich Sequences (QGRS) mapped in the eukaryotic pre-mRNA sequences, including that are alternatively processed (alternatively spliced or alternatively polyadenylated). The data stored in the GRSDB2 is based on computational analysis of NCBI Entrez Gene entries and their corresponding annotated genomic nucleotide sequences of RefSeq/GenBank. Computations were performed with the help of an indigenously developed and previously published software program QGRS Mapper. What is new in GRSDB2: The entire database has been built with a new and much improved version of QGRS Mapper program. It contains data from a large number of eukaryotic genes from several organisms in addition to human and mouse. The data model is different than the first version in that it is centered around Entrez Gene rather than solely GenBank/RefSeq nucleotide entries. The search module has been greatly enhanced. It is possible to search the database with Entrez Gene ID, Gene Name, Gene Symbols, Aliases, relevant Accession numbers and many other parameters like numbers of poly A signals and alternatively spliced products. Complex queries can also be performed. In addition, it is now possible to search the database with Gene Ontology terms. The list of genes matching the query can be sorted. The website also allows to manipulate the list to form sets of genes and perform further computations on these sets through a "Workbench". The Gene View, Data View and Graphic View for individual database entries have been significantly enhanced with several additional computational capabilities and links. The data can now be exported into Excel for further analysis. In addition, we have added a Sequence View which displays mapped G-quadruplexes in the context of pre-mRNA sequence. GRSDB2 replaces GRSDB at, <http://bioinformatics.ramapo.edu/grsdb/index.php>

Synonyms: GRSDB, GRSDB2

Resource Type: data or information resource, database

Defining Citation: [PMID:18045785](#)

Keywords: quadruplex-forming g-rich sequences

Resource Name: GRSDB: G-Rich Sequences DataBase

Resource ID: SCR_007697

Alternate IDs: nif-0000-02930

Record Creation Time: 20220129T080243+0000

Record Last Update: 20260811T043318+0000

Ratings and Alerts

No rating or validation information has been found for GRSDB: G-Rich Sequences DataBase.

No alerts have been found for GRSDB: G-Rich Sequences DataBase.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

Listed below are recent publications. The full list is available at [RRID](#) .

Miskiewicz J, et al. (2021) How bioinformatics resources work with G4 RNAs. Briefings in bioinformatics, 22(3).