Resource Summary Report

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GTOP - Genomes To Protein structures

RRID:SCR_007698
Type: Tool

Proper Citation

GTOP - Genomes To Protein structures (RRID:SCR_007698)

Resource Information

URL: http://spock.genes.nig.ac.jp/~genome/gtop.html

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Description: GTOP is a database consists of data analyses of proteins identified by various genome projects. This database mainly uses sequence homology analyses and features extensive utilization of information on three-dimensional structures. GTOP is built by the Laboratory of Gene-Product Informatics at the National Institute of Genetics. This research is supported by the Japan Science and Technology Corporation and Grants-in-Aid for Scientific Research (Genomes in category C) from the Ministry of Education, Science, Sports and Culture of Japan. We use the following methods: Prediction of 3D structure Sequence homology search of PDB, using REVERSE PSI-BLAST. Functional predictions (family classifications) Sequence homology search of Swiss-Prot, a well-annotated sequence database, with the use of BLAST. Other analytical methods We are also carrying out the following analyses: Motif Analysis(PROSITE) Family classification(Pfam) Prediction of transmembrane helix domains(SOSUI) Prediction of coiled-coil regions(Multicoil) Repetitive sequence analysis(RepAlign)

Synonyms: GTOP

Resource Type: data or information resource, database

Keywords: genome, protein, sequence homology

Funding:

Resource Name: GTOP - Genomes To Protein structures

Resource ID: SCR_007698

Alternate IDs: nif-0000-02931

Record Creation Time: 20220129T080243+0000

Record Last Update: 20250507T060517+0000

Ratings and Alerts

No rating or validation information has been found for GTOP - Genomes To Protein structures.

No alerts have been found for GTOP - Genomes To Protein structures.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 6 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Uemura E, et al. (2018) Large-scale aggregation analysis of eukaryotic proteins reveals an involvement of intrinsically disordered regions in protein folding. Scientific reports, 8(1), 678.

Homma K, et al. (2016) Codon usage is less optimized in eukaryotic gene segments encoding intrinsically disordered regions than in those encoding structural domains. Nucleic acids research, 44(21), 10051.

Tomono T, et al. (2015) Investigation of glycan evolution based on a comprehensive analysis of glycosyltransferases using phylogenetic profiling. Biophysics and physicobiology, 12, 57.

Gough CA, et al. (2012) Prediction of protein-destabilizing polymorphisms by manual curation with protein structure. PloS one, 7(11), e50445.

Mochida K, et al. (2010) Genomics and bioinformatics resources for crop improvement. Plant & cell physiology, 51(4), 497.

Malik A, et al. (2007) Databases and QSAR for cancer research. Cancer informatics, 2, 99.