Resource Summary Report

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Molecular Modeling DataBase

RRID:SCR_010623
Type: Tool

Proper Citation

Molecular Modeling DataBase (RRID:SCR_010623)

Resource Information

URL: https://www.ncbi.nlm.nih.gov/Structure/MMDB/docs/mmdb_help.html

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Description: The Molecular Modeling DataBase (MMDB), also known as Entrez Structure, is a database of experimentally determined structures obtained from the RCSB Protein Data Bank (PDB). MMDB is developed by the Structure Group of the NCBI Computational Biology Branch. The data processing procedure at NCBI results in the addition of a number of useful features that facilitate computation on the data and link them to many other data types in the Entrez system. The structure database is considerably smaller than Entrez''s Protein or Nucleotide databases, but a large fraction of all known protein sequences have homologs in this set, and one may often learn more about a protein by examining 3-D structures of its homologs. These are accessible as Related Structures in the Links menu of Entrez Protein sequence records (illustrated example). It is then possible to align the query protein to the structure-based sequence, as shown in the illustration on this page. Additional resources can be used along with MMDB to interactively view the structures, find similar 3D structures, learn about the types of interactions and bound chemicals that have been found to exist among the similar 3D structures, and more.

Abbreviations: MMDB

Synonyms: Entrez Structure, NCBI Structure, Structure database, Structure (Molecular Modeling Database)

Resource Type: data or information resource, database

Defining Citation: PMID:17135201

Keywords: macromolecule, structure, 3d spatial image, protein structure, gold standard

Funding:

Resource Name: Molecular Modeling DataBase

Resource ID: SCR_010623

Alternate IDs: nlx_56387

Alternate URLs: http://www.ncbi.nlm.nih.gov/sites/entrez?db=structure, http://www.ncbi.nlm.nih.gov/structure

Record Creation Time: 20220129T080259+0000

Record Last Update: 20250426T060203+0000

Ratings and Alerts

No rating or validation information has been found for Molecular Modeling DataBase.

No alerts have been found for Molecular Modeling DataBase.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 16 mentions in open access literature.

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

Druce M, et al. (2016) Improving HIV proteome annotation: new features of BioAfrica HIV Proteomics Resource. Database : the journal of biological databases and curation, 2016.

Dahlmann TA, et al. (2015) Dicer-Dependent Biogenesis of Small RNAs and Evidence for MicroRNA-Like RNAs in the Penicillin Producing Fungus Penicillium chrysogenum. PloS one, 10(5), e0125989.

Schieferdecker A, et al. (2014) Denosumab mimics the natural decoy receptor osteoprotegerin by interacting with its major binding site on RANKL. Oncotarget, 5(16), 6647.

Meng L, et al. (2014) Cloning and characterization of tesk1, a novel spermatogenesis-related gene, in the tongue sole (Cynoglossus semilaevis). PloS one, 9(10), e107922.

Liew LC, et al. (2013) An RNA-seq transcriptome analysis of histone modifiers and RNA silencing genes in soybean during floral initiation process. PloS one, 8(10), e77502.

Zhang J, et al. (2013) Genome-wide analysis of the Populus Hsp90 gene family reveals differential expression patterns, localization, and heat stress responses. BMC genomics, 14, 532.

Li H, et al. (2013) Identification and expression profiles of IL-8 in bighead carp (Aristichthys nobilis) in response to microcystin-LR. Archives of environmental contamination and toxicology, 65(3), 537.

Atemnkeng VA, et al. (2013) Deoxyhypusine hydroxylase from Plasmodium vivax, the neglected human malaria parasite: molecular cloning, expression and specific inhibition by the 5-LOX inhibitor zileuton. PloS one, 8(3), e58318.

Karali D, et al. (2012) The Arabidopsis thaliana immunophilin ROF1 directly interacts with PI(3)P and PI(3,5)P2 and affects germination under osmotic stress. PloS one, 7(11), e48241.

Benning UF, et al. (2012) New aspects of Phloem-mediated long-distance lipid signaling in plants. Frontiers in plant science, 3, 53.

Bao X, et al. (2011) Non-coding nucleotides and amino acids near the active site regulate peptide deformylase expression and inhibitor susceptibility in Chlamydia trachomatis. Microbiology (Reading, England), 157(Pt 9), 2569.

Zhang F, et al. (2011) cDNA cloning and expression analysis of gustavus gene in the oriental river prawn Macrobrachium nipponense. PloS one, 6(2), e17170.

Duquesnoy RJ, et al. (2011) Humoral alloimmunity in transplantation: relevance of HLA epitope antigenicity and immunogenicity. Frontiers in immunology, 2, 59.

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

Galperin MY, et al. (2005) The Molecular Biology Database Collection: 2005 update. Nucleic acids research, 33(Database issue), D5.

Avellón A, et al. (2003) Molecular analysis of echovirus 13 isolates and aseptic meningitis, Spain. Emerging infectious diseases, 9(8), 934.