Resource Summary Report

Generated by dkNET on Apr 26, 2025

MolMovDB - Database of Macromolecular Movements

RRID:SCR_007801
Type: Tool

Proper Citation

MolMovDB - Database of Macromolecular Movements (RRID:SCR_007801)

Resource Information

URL: http://molmovdb.mbb.yale.edu/molmovdb/

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Description: MolMovDB is a database that describes the motions that occur in proteins and other macromolecules, particularly using movies. Associated with it are a variety of free software tools and servers for structural analysis. The morph server enables the automatic generation of 2D and 3D animations of a plausible or semi-plausible pathway between two static conformations of a protein subunit, such as those conventionally solved by x-ray crystallography. We believe these animations and associated interpolated pathways will become a valuable research and educational tool, allowing the researcher or educator to quickly visualize the chemical transformation of a protein subunit from one conformation into another. With the server, it is easy to determine quickly whether a valid chemical pathway exists between two protein conformations, as in a protein such as calmodulin, or whether, as is the case with diphtheria toxin, the two conformations have no clearly valid chemical pathway and therefore exist most likely as the result of other processes, such as domain swapping.

Synonyms: MolMovDB

Resource Type: data or information resource, database

Funding:

Resource Name: MolMovDB - Database of Macromolecular Movements

Resource ID: SCR_007801

Alternate IDs: nif-0000-03157

Alternate URLs: http://bioinfo.mbb.yale.edu/MolMovDB/

Record Creation Time: 20220129T080243+0000

Record Last Update: 20250426T055959+0000

Ratings and Alerts

No rating or validation information has been found for MolMovDB - Database of Macromolecular Movements.

No alerts have been found for MolMovDB - Database of Macromolecular Movements.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Orellana L, et al. (2019) Large-Scale Conformational Changes and Protein Function: Breaking the in silico Barrier. Frontiers in molecular biosciences, 6, 117.

Weiss DR, et al. (2009) Can morphing methods predict intermediate structures? Journal of molecular biology, 385(2), 665.

Scott WG, et al. (2002) Visualizing the structure and mechanism of a small nucleolytic ribozyme. Methods (San Diego, Calif.), 28(3), 302.