

Resource Summary Report

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DMAPS - A Database of Multiple Alignments for Protein Structures

RRID:SCR_007140

Type: Tool

Proper Citation

DMAPS - A Database of Multiple Alignments for Protein Structures (RRID:SCR_007140)

Resource Information

URL: <http://bioinformatics.albany.edu/~dmaps>

Proper Citation: DMAPS - A Database of Multiple Alignments for Protein Structures (RRID:SCR_007140)

Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented September 6, 2016. DMAPS database contains pre-computed multiple structure alignments for protein chains in the Protein Data Bank (PDB). Automated structure alignments have been generated for classified protein families using CE-MC algorithm. Alignments have been built only for those families with at least three members. Currently, multiple structure alignments are available for 3050 SCOP-, 3087 CATH-, 664 ENZYME- and 1707 CE-based families. Users will be able to retrieve multiple alignments for a given PDB chain classified by one of these criteria.

Abbreviations: DMAP

Resource Type: data or information resource, database

Keywords: multiple structure alignment, protein, protein family, protein structure

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: DMAPS - A Database of Multiple Alignments for Protein Structures

Resource ID: SCR_007140

Alternate IDs: nif-0000-02755, nlx_154108, SCR_009091

Record Creation Time: 20220129T080240+0000

Record Last Update: 20260919T195124+0000

Ratings and Alerts

No rating or validation information has been found for DMAPS - A Database of Multiple Alignments for Protein Structures.

No alerts have been found for DMAPS - A Database of Multiple Alignments for Protein Structures.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.