Resource Summary Report

Generated by Kravitz on Sep 20, 2026

MegaMotifbase

RRID:SCR_007775
Type: Tool

Proper Citation

MegaMotifbase (RRID:SCR_007775)

Resource Information

URL: http://caps.ncbs.res.in/MegaMotifbase/index.html

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Description: A database of structural motifs for protein structures related at the family and-or superfamily level. Such motifs among structurally aligned proteins are recognized by the conservation of amino acid preference and solvent inaccessibility and are examined for the conservation of other important structural features like secondary structural content, hydrogen bonding pattern and residue packing. These motifs may form the common core by maintaining a particular spatial orientation pattern when compared across different proteins belonging to the same family or superfamily. Such motifs can also be employed to design and rationalize protein engineering and folding experiments. Therefore, the MegaMotifbase can be a useful resource to gain knowledge about structure and functional relationship of proteins. Alignments are available for download.

Synonyms: MegaMotifbase

Resource Type: data or information resource, database

Keywords: protein families, protein superfamilies

Resource Name: MegaMotifbase

Resource ID: SCR_007775

Alternate IDs: nif-0000-03108

Record Creation Time: 20220129T080243+0000

Record Last Update: 20260919T195710+0000

Ratings and Alerts

No rating or validation information has been found for MegaMotifbase.

No alerts have been found for MegaMotifbase.

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 Kravitz .

Kubrycht J, et al. (2012) Virtual interactomics of proteins from biochemical standpoint. Molecular biology international, 2012, 976385.