

# Resource Summary Report

Generated by [dkNET](#) on Aug 5, 2026

## MegaMotifbase

RRID:SCR\_007775

Type: Tool

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### Proper Citation

MegaMotifbase (RRID:SCR\_007775)

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### 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:** database, data or information resource

**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:** 20260805T044156+0000

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### Ratings and Alerts

No rating or validation information has been found for MegaMotifbase.

No alerts have been found for MegaMotifbase.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 1 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [dkNET](#) .

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