

Resource Summary Report

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Database of Spatially Interacting Motifs in Proteins

RRID:SCR_008194

Type: Tool

Proper Citation

Database of Spatially Interacting Motifs in Proteins (RRID:SCR_008194)

Resource Information

URL: <http://caps.ncbs.res.in/imotdb/>

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Description: The interacting motif database or iMOTdb, lists interacting motifs that are identified for all structural entries in the PDB. The conserved patterns or finger prints are identified for individual structural entries and also grouped together for reporting the common motifs shared among all superfamily members. The iMOT package has been employed for identifying the motifs in the database. Realization of conserved residues that represent a protein family is crucial for clearer understanding of biological function as well as for the better recognition of additional members in sequence databases. Functionally important residues are recognized well due to their high degree of conservation in closely related sequences and are annotated in functional motif databases. Structural motifs are central to the integrity of the fold and require careful analysis for their identification. It reports the availability of a database of spatially interacting motifs in single protein structures as well as those among distantly related protein structures that belong to a superfamily. Spatial interactions amongst conserved motifs are automatically measured using sequence similarity scores and distance calculations. Interactions between pairs of conserved motifs are described in the form of pseudoenergies. iMOTdb database provides information for 854,488 motifs corresponding to 60,849 protein structural domains and 22,648 protein structural entries. Interacting motifs has been shown to assist our understanding of proteins structure and function. Information on such motifs should be of valuable in protein folding, modeling and engineering experiments. As shown in previous studies conserved spatially interacting motifs act as important constraint in pattern based remote homology search methods. The iMOT DB is provided with links to aid sequence search protocol using PHI-BLAST and SCAN MOT employing the interacting motifs. The interacting motifs representing the superfamilies of proteins are derived from structural alignments obtained from PASS2. These motifs are finger prints for a given protein family and provides useful insights regarding the structural and functional role regarding the protein. Pseudo potential evaluated between the various pairs of motifs reflects the interacting strength between the regions and highlights the thermodynamic stability of the local substructure. The database would thus provide useful insight into the understanding

of the folding, structural modeling and envisaging mutational exercise on a given polypeptide.

Synonyms: IMOTdb

Resource Type: data or information resource, database

Keywords: engineering, family, fingerprint, folding, function, functional, function, alignment, biological, conservation, homology, individual, interacting, intermolecular interactions and signaling pathways databases, modeling, motif, mutational, pattern, polypeptide, protein, pseudoenergy, sequence, stability, structural, structure, substructure, superfamily, thermodynamic

Resource Name: Database of Spatially Interacting Motifs in Proteins

Resource ID: SCR_008194

Alternate IDs: nif-0000-21218

Record Creation Time: 20220129T080246+0000

Record Last Update: 20260903T234938+0000

Ratings and Alerts

No rating or validation information has been found for Database of Spatially Interacting Motifs in Proteins.

No alerts have been found for Database of Spatially Interacting Motifs in Proteins.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.