

Resource Summary Report

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MALISAM: Manual ALIgnments of Structurally Analogous Motifs

RRID:SCR_013380

Type: Tool

Proper Citation

MALISAM: Manual ALIgnments of Structurally Analogous Motifs (RRID:SCR_013380)

Resource Information

URL: <http://prodata.swmed.edu/malisam>

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Description: MALISAM is a database of pairwise, structure-based alignments for structurally analogous motifs in proteins. Homology and analogy are two alternative scenarios to explain structural similarities among proteins. Homologs inherit similar features from their common ancestor, while analogs converge to similar structures due to a limited number of energetically favorable ways to pack secondary structural elements. Analogous pairs in this database are in three categories: a hybrid motif and a core motif, an interface motif and a core motif, an artificial protein and a natural protein. During evolution, a protein family usually preserves a common core while accumulating insertions and deletions in the periphery. A core motif is composed entirely of secondary structure elements belonging to the evolutionary core. A hybrid motif consists of both core elements and peripheral insertions that are not present in the majority of the family members. An interface motif uses secondary structural elements from two or more domains or subunits contacting along that interface.

Synonyms: MALISAM

Resource Type: data or information resource, database

Resource Name: MALISAM: Manual ALIgnments of Structurally Analogous Motifs

Resource ID: SCR_013380

Alternate IDs: nif-0000-03097

Record Creation Time: 20220129T080315+0000

Record Last Update: 20260904T000337+0000

Ratings and Alerts

No rating or validation information has been found for MALISAM: Manual ALIgnments of Structurally Analogous Motifs.

No alerts have been found for MALISAM: Manual ALIgnments of Structurally Analogous Motifs.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Hamamsy T, et al. (2024) Protein remote homology detection and structural alignment using deep learning. Nature biotechnology, 42(6), 975.

Liu W, et al. (2024) PLMSearch: Protein language model powers accurate and fast sequence search for remote homology. Nature communications, 15(1), 2775.

Kaminski K, et al. (2023) pLM-BLAST: distant homology detection based on direct comparison of sequence representations from protein language models. Bioinformatics (Oxford, England), 39(10).

Barrio-Hernandez I, et al. (2023) Clustering predicted structures at the scale of the known protein universe. Nature, 622(7983), 637.