

Resource Summary Report

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PROMALS3D

RRID:SCR_018161

Type: Tool

Proper Citation

PROMALS3D (RRID:SCR_018161)

Resource Information

URL: <http://prodata.swmed.edu/promals3d/promals3d.php>

Proper Citation: PROMALS3D (RRID:SCR_018161)

Description: Web tool as multiple sequence and structure alignment server. Automatically identifies homologs with known 3D structures for input sequences, derives structural constraints through structure based alignments and combines them with sequence constraints to construct consistency based multiple sequence alignments. Aligns sequences of multiple input structures, with output representing multiple structure based alignment refined in combination with sequence constraints.

Resource Type: data processing software, data access protocol, image analysis software, software application, alignment software, software resource, web service

Defining Citation: [DOI:10.1093/nar/gkn072](https://doi.org/10.1093/nar/gkn072)

Keywords: Structure alignment, 3D structure, sequence, protein, amino acid, homolog identification

Availability: Free, Freely available

Resource Name: PROMALS3D

Resource ID: SCR_018161

Record Creation Time: 20220129T080338+0000

Record Last Update: 20260806T054657+0000

Ratings and Alerts

No rating or validation information has been found for PROMALS3D.

No alerts have been found for PROMALS3D.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 44 mentions in open access literature.

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

de Crécy-Lagard V, et al. (2025) Limitations of current machine learning models in predicting enzymatic functions for uncharacterized proteins. *G3 (Bethesda, Md.)*, 15(10).

Jin Y, et al. (2025) Antibiotic target discovery by integrated phenotypic and activity-based profiling of electrophilic fragments. *Cell chemical biology*, 32(3), 434.

Jacquat AG, et al. (2025) The Growth, Pathogenesis, and Secondary Metabolism of *Fusarium verticillioides* Are Epigenetically Modulated by Putative Heterochromatin Protein 1 (FvHP1). *Journal of fungi (Basel, Switzerland)*, 11(6).

van Hooff JJE, et al. (2025) Repeated duplications and losses shaped SMC complex evolution from archaeal ancestors to modern eukaryotes. *Cell reports*, 44(7), 115855.

Xie J, et al. (2024) Structural basis for dimerization of a paramyxovirus polymerase complex. *Nature communications*, 15(1), 3163.

Kato K, et al. (2024) Structural basis for molecular assembly of fucoxanthin chlorophyll a/c-binding proteins in a diatom photosystem I supercomplex. *eLife*, 13.

Panmanee J, et al. (2024) A Complex Interplay Between Melatonin and ROR?: ROR? is Unlikely a Putative Receptor for Melatonin as Revealed by Biophysical Assays. *Molecular neurobiology*.

Harracksingh AN, et al. (2024) Functional characterization of optic photoreception in *Lymnaea stagnalis*. *PloS one*, 19(11), e0313407.

Licht JA, et al. (2024) They all rock: A systematic comparison of conformational movements in LeuT-fold transporters. *Structure (London, England : 1993)*, 32(9), 1528.

Shi YJ, et al. (2023) Interaction between cucumber green mottle mosaic virus MP and CP promotes virus systemic infection. *Molecular plant pathology*, 24(3), 208.

Shuoker B, et al. (2023) Sialidases and fucosidases of *Akkermansia muciniphila* are crucial for growth on mucin and nutrient sharing with mucus-associated gut bacteria. *Nature communications*, 14(1), 1833.

Filée J, et al. (2023) Bacterial origins of thymidylate metabolism in Asgard archaea and Eukarya. *Nature communications*, 14(1), 838.

Persico M, et al. (2023) Tetrasubstituted Pyrrole Derivative Mimetics of Protein-Protein Interaction Hot-Spot Residues: A Promising Class of Anticancer Agents Targeting

Melanoma Cells. *Molecules* (Basel, Switzerland), 28(10).

Hara M, et al. (2023) Centromere/kinetochore is assembled through CENP-C oligomerization. *Molecular cell*, 83(13), 2188.

Kaczmarska Z, et al. (2022) Structural basis of transposon end recognition explains central features of Tn7 transposition systems. *Molecular cell*, 82(14), 2618.

Dash A, et al. (2022) Genome-wide in silico characterization and stress induced expression analysis of BcL-2 associated athanogene (BAG) family in *Musa* spp. *Scientific reports*, 12(1), 625.

Tuerkova A, et al. (2022) Identifying Novel Inhibitors for Hepatic Organic Anion Transporting Polypeptides by Machine Learning-Based Virtual Screening. *Journal of chemical information and modeling*, 62(24), 6323.

Ghorbani A, et al. (2022) Ancestral reconstruction reveals catalytic inactivation of activation-induced cytidine deaminase concomitant with cold water adaption in the Gadiformes bony fish. *BMC biology*, 20(1), 293.

Yao L, et al. (2022) Comparing the folding landscapes of evolutionarily divergent procaspase-3. *Bioscience reports*, 42(6).

Wang F, et al. (2022) Spindle-shaped archaeal viruses evolved from rod-shaped ancestors to package a larger genome. *Cell*, 185(8), 1297.