

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>

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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: alignment software, data access protocol, data processing software, image analysis software, software application, 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: 20260905T132831+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 50 mentions in open access literature.

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

Squair DR, et al. (2026) ZNFX1 uses two-component ubiquitin circuitry to quarantine viral RNA. *Molecular cell*, 86(6), 1164.

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).

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).

Solís KH, et al. (2025) Multiple LPA3 Receptor Agonist Binding Sites Evidenced Under Docking and Functional Studies. *International journal of molecular sciences*, 26(9).

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.

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

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.

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

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.

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

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).

Chan J, et al. (2023) Identification and characterization of immunoglobulin tau (IgT) in Asian Seabass (*Lateolabrax niloticus*) and mucosal immune response to nervous necrosis virus. *Frontiers in immunology*, 14, 1146387.

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

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

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.

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.