Resource Summary Report

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HOMSTRAD - Homologous Structure Alignment Database

RRID:SCR_006544
Type: Tool

Proper Citation

HOMSTRAD - Homologous Structure Alignment Database (RRID:SCR_006544)

Resource Information

URL: http://tardis.nibio.go.jp/homstrad/

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Description: A curated database of structure-based alignments for homologous protein families. All known protein structure are clustered into homologous families (i.e., common ancestry), and the sequences of representative members of each family are aligned on the basis of their 3D structures using the programs MNYFIT, STAMP and COMPARER. These structure-based alignments are annotated with JOY and examined individually.

Abbreviations: HOMSTRAD

Synonyms: HOMologous STRucture Alignment Database

Resource Type: data or information resource, database

Defining Citation: PMID:14681395

Keywords: homologous structure, protein, protein family, protein structure, align, 3d structure, structure-based alignment

Resource Name: HOMSTRAD - Homologous Structure Alignment Database

Resource ID: SCR_006544

Alternate IDs: nif-0000-02977, OMICS_00976

Old URLs: http://www-cryst.bioc.cam.ac.uk/homstrad

Record Creation Time: 20220129T080236+0000

Record Last Update: 20260919T195658+0000

Ratings and Alerts

No rating or validation information has been found for HOMSTRAD - Homologous Structure Alignment Database.

No alerts have been found for HOMSTRAD - Homologous Structure Alignment Database.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 24 mentions in open access literature.

Listed below are recent publications. The full list is available at T1D .

Sinha K, et al. (2026) BABAPPAlign: a multiple sequence alignment engine with a learned residue-level scoring function. Bioinformatics (Oxford, England), 42(5).

Hoang M, et al. (2026) Fast, accurate construction of multiple sequence alignments from protein language embeddings. bioRxiv : the preprint server for biology.

Zhang X, et al. (2025) epLSAP-Align: a non-sequential protein structural alignment solver with entropy-regularized partial linear sum assignment problem formulation. Bioinformatics (Oxford, England), 41(6).

Spicer R, et al. (2025) Evaluating the significance of embedding-based protein sequence alignment with clustering and double dynamic programming for remote homology. Scientific reports, 15(1), 39601.

van Kempen M, et al. (2024) Fast and accurate protein structure search with Foldseek. Nature biotechnology, 42(2), 243.

Crauwels C, et al. (2024) Large-scale structure-informed multiple sequence alignment of proteins with SIMSApiper. Bioinformatics (Oxford, England), 40(5).

Park M, et al. (2023) UPP2: fast and accurate alignment of datasets with fragmentary sequences. Bioinformatics (Oxford, England), 39(1).

McWhite CD, et al. (2023) Leveraging protein language models for accurate multiple sequence alignments. Genome research, 33(7), 1145.

João M, et al. (2023) On closing the inopportune gap with consistency transformation and iterative refinement. PloS one, 18(7), e0287483.

Nand M, et al. (2020) Virtual screening of anti-HIV1 compounds against SARS-CoV-2: machine learning modeling, chemoinformatics and molecular dynamics simulation based analysis. Scientific reports, 10(1), 20397.

Marcos ML, et al. (2020) The variation among sites of protein structure divergence is shaped by mutation and scaled by selection. Current research in structural biology, 2, 156.

Martins E, et al. (2019) Newly Synthesized Oxygenated Xanthones as Potential P-Glycoprotein Activators: In Vitro, Ex Vivo, and In Silico Studies. Molecules (Basel, Switzerland), 24(4).

Joung I, et al. (2019) Non-sequential protein structure alignment by conformational space annealing and local refinement. PloS one, 14(1), e0210177.

Dijkstra M, et al. (2018) Motif-Aware PRALINE: Improving the alignment of motif regions. PLoS computational biology, 14(11), e1006547.

Karami Y, et al. (2018) DaReUS-Loop: accurate loop modeling using fragments from remote or unrelated proteins. Scientific reports, 8(1), 13673.

Pandurangan AP, et al. (2017) SDM: a server for predicting effects of mutations on protein stability. Nucleic acids research, 45(W1), W229.

Gutiérrez FI, et al. (2016) Efficient and automated large-scale detection of structural relationships in proteins with a flexible aligner. BMC bioinformatics, 17, 20.

Wright ES, et al. (2015) DECIPHER: harnessing local sequence context to improve protein multiple sequence alignment. BMC bioinformatics, 16, 322.

Sela I, et al. (2015) GUIDANCE2: accurate detection of unreliable alignment regions accounting for the uncertainty of multiple parameters. Nucleic acids research, 43(W1), W7.

Bonner JE, et al. (2015) Self-efficacy and adherence to antiviral treatment for chronic hepatitis C. Journal of clinical gastroenterology, 49(1), 76.