

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: 20260729T044136+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 22 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

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.

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

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

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

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

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.

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

- 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).
- 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.
- 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.
- Wright ES, et al. (2015) DECIPHER: harnessing local sequence context to improve protein multiple sequence alignment. *BMC bioinformatics*, 16, 322.
- Bonner JE, et al. (2015) Self-efficacy and adherence to antiviral treatment for chronic hepatitis C. *Journal of clinical gastroenterology*, 49(1), 76.
- Pu L, et al. (2014) A novel cysteine-rich neurotrophic factor in *Aplysia* facilitates growth, MAPK activation, and long-term synaptic facilitation. *Learning & memory* (Cold Spring Harbor, N.Y.), 21(4), 215.
- Williams SG, et al. (2011) Using knowledge of protein structural constraints to predict the evolution of HIV-1. *Journal of molecular biology*, 410(5), 1023.