

Resource Summary Report

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CATH: Protein Structure Classification

RRID:SCR_007583

Type: Tool

Proper Citation

CATH: Protein Structure Classification (RRID:SCR_007583)

Resource Information

URL: <http://www.cathdb.info/>

Proper Citation: CATH: Protein Structure Classification (RRID:SCR_007583)

Description: CATH is a hierarchical classification of protein domain structures, which clusters proteins at four major levels: Class (C), Architecture (A), Topology (T) and Homologous superfamily (H). The boundaries and assignments for each protein domain are determined using a combination of automated and manual procedures which include computational techniques, empirical and statistical evidence, literature review and expert analysis. Users can search CATH by ID/Sequence/text. They can also browse CATH from the top of the hierarchy, or download CATH data.

Synonyms: CATH

Resource Type: data or information resource, database

Keywords: architecture, class, homologous superfamily, protein cluster, protein domain structure, topology, bio.tools, FASEB list

Funding:

Resource Name: CATH: Protein Structure Classification

Resource ID: SCR_007583

Alternate IDs: nif-0000-02640, biotools:cath

Alternate URLs: <https://bio.tools/cath>

Record Creation Time: 20220129T080242+0000

Record Last Update: 20250426T055941+0000

Ratings and Alerts

No rating or validation information has been found for CATH: Protein Structure Classification.

No alerts have been found for CATH: Protein Structure Classification.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 109 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Waman VP, et al. (2025) CATH v4.4: major expansion of CATH by experimental and predicted structural data. Nucleic acids research, 53(D1), D348.

Jamasb AR, et al. (2024) Evaluating Representation Learning on the Protein Structure Universe. ArXiv.

Roterman I, et al. (2024) Model of the external force field for the protein folding process-the role of prefoldin. Frontiers in chemistry, 12, 1342434.

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

Denessiouk K, et al. (2024) The active site of the SGNH hydrolase-like fold proteins: Nucleophile-oxyanion (Nuc-Oxy) and Acid-Base zones. Current research in structural biology, 7, 100123.

Cai H, et al. (2024) Pretrainable geometric graph neural network for antibody affinity maturation. Nature communications, 15(1), 7785.

Draizen EJ, et al. (2024) Prop3D: A flexible, Python-based platform for machine learning with protein structural properties and biophysical data. BMC bioinformatics, 25(1), 11.

Waman VP, et al. (2024) Predicting human and viral protein variants affecting COVID-19 susceptibility and repurposing therapeutics. Scientific reports, 14(1), 14208.

Hamamsy T, et al. (2024) Protein remote homology detection and structural alignment using

deep learning. *Nature biotechnology*, 42(6), 975.

Soleymani F, et al. (2024) Structure-based protein and small molecule generation using EGNN and diffusion models: A comprehensive review. *Computational and structural biotechnology journal*, 23, 2779.

Olvera-Lucio FH, et al. (2024) Tandem-repeat lectins: structural and functional insights. *Glycobiology*, 34(7).

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Jacques F, et al. (2023) Roadmap to the study of gene and protein phylogeny and evolution- A practical guide. *PloS one*, 18(2), e0279597.

Nallapareddy V, et al. (2023) CATHe: detection of remote homologues for CATH superfamilies using embeddings from protein language models. *Bioinformatics (Oxford, England)*, 39(1).

Janes RW, et al. (2023) DichroPipeline: A suite of online and downloadable tools and resources for protein circular dichroism spectroscopic data analyses, interpretations, and their interoperability with other bioinformatics tools and resources. *Protein science : a publication of the Protein Society*, 32(12), e4817.

Bordin N, et al. (2023) Novel machine learning approaches revolutionize protein knowledge. *Trends in biochemical sciences*, 48(4), 345.

Wu F, et al. (2023) Improving protein structure prediction using templates and sequence embedding. *Bioinformatics (Oxford, England)*, 39(1).

Tsuchiya Y, et al. (2023) PoSSuM v.3: A Major Expansion of the PoSSuM Database for Finding Similar Binding Sites of Proteins. *Journal of chemical information and modeling*, 63(23), 7578.

Thiébaud A, et al. (2023) DrosOMA: the *Drosophila* Orthologous Matrix browser. *F1000Research*, 12, 936.

Koehler Leman J, et al. (2023) Sequence-structure-function relationships in the microbial protein universe. *Nature communications*, 14(1), 2351.