

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: database, data or information resource

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

Resource Name: CATH: Protein Structure Classification

Resource ID: SCR_007583

Alternate IDs: nif-0000-02640, r3d100012629, biotools:cath

Alternate URLs: <https://bio.tools/cath>, <https://doi.org/10.17616/R32Z1F>

Record Creation Time: 20220129T080242+0000

Record Last Update: 20260725T191148+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 291 mentions in open access literature.

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

Fierro Morales JC, et al. (2025) Reduced cell-substrate adhesion formation promotes cell migration in Dictyostelium. Molecular biology of the cell, 36(8), ar98.

Costa VA, et al. (2025) Phylogenetic Diversity and Geographic Distribution of Atlantic Salmon Calicivirus in Major Salmon Farming Regions. Journal of fish diseases, 48(6), e14107.

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

Micsonai A, et al. (2025) BeStSel: analysis site for protein CD spectra-2025 update. Nucleic acids research, 53(W1), W73.

Orr B, et al. (2025) An improved model for prediction of de novo designed proteins with diverse geometries. bioRxiv : the preprint server for biology.

Harwood G, et al. (2025) Evidence for vitellogenin DNA-binding in honey bees. Protein science : a publication of the Protein Society, 34(10), e70291.

Zhang Y, et al. (2025) Interpretable protein-DNA interactions captured by structure-sequence optimization. eLife, 14.

Erdogdu B, et al. (2025) Isoswitching drives the aging process in human brains. bioRxiv : the preprint server for biology.

Tan Y, et al. (2025) Semantical and geometrical protein encoding toward enhanced bioactivity and thermostability. eLife, 13.

Lu T, et al. (2025) Conditional Protein Structure Generation with Protpardelle-1c. bioRxiv : the preprint server for biology.

Gunther E, et al. (2025) Exploring the Structural Lexicon of the Proteome via Metric Geometry. bioRxiv : the preprint server for biology.

Kandathil SM, et al. (2025) Foldclass and Merizo-search: scalable structural similarity search for single- and multi-domain proteins using geometric learning. *Bioinformatics* (Oxford, England), 41(5).

Farag PF, et al. (2025) Prediction of secreted uncharacterized protein structures from *Beauveria bassiana* ARSEF 2860 unravels novel toxins-like families. *Scientific reports*, 15(1), 17747.

Li R, et al. (2025) Phosphoproteomic insights into the regulation of root length in rice (*Oryza sativa* L. cv. KDML 105): uncovering key events and pathways involving phosphorylated proteins. *PeerJ*, 13, e19361.

Lo WC, et al. (2025) SARST2 high-throughput and resource-efficient protein structure alignment against massive databases. *Nature communications*, 16(1), 8691.

Zhu S, et al. (2025) Multimodal diffusion for joint design of protein sequence and structure. *Protein science : a publication of the Protein Society*, 34(12), e70340.

Zheng L, et al. (2025) Multiplexed, scalable analog recording of gene regulation dynamics over weeks using intracellular protein tapes. *bioRxiv : the preprint server for biology*.

Guo X, et al. (2025) Pangenome-scale annotation of mycobacteriophages for dissecting phage-host interactions based on a sequence clustering and structural homology analysis strategy. *mSystems*, 10(8), e0050825.

Bell EW, et al. (2025) FakeRotLib: Expedient Noncanonical Amino Acid Parametrization in Rosetta. *Journal of chemical information and modeling*, 65(16), 8397.

Bell EW, et al. (2025) FakeRotLib: expedient non-canonical amino acid parameterization in Rosetta. *bioRxiv : the preprint server for biology*.