

Resource Summary Report

Generated by [dkNET](#) on Aug 5, 2026

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: 20260805T044153+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 [dkNET](#) .

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

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

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

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.

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

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

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

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

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

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*.

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.

Bell EW, et al. (2025) FakeRotLib: expedient non-canonical amino acid parameterization in Rosetta. *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.

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*.