

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

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: 20260821T193813+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 306 mentions in open access literature.

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

Mrnjavac N, et al. (2026) Protein folds and catalytic strategies at the origin of biological CO₂ fixation. *FEMS microbiology ecology*, 102(5).

Elrashedy A, et al. (2026) Immunoinformatics-based design of artificial chimeric proteins as universal vaccine candidates against foot-and-mouth disease virus serotypes A, O, and SAT2. *Scientific reports*, 16(1).

Chasapi MN, et al. (2026) metagRoot: a comprehensive database of protein families associated with plant root microbiomes. *Nucleic acids research*, 54(D1), D1733.

Vinod R, et al. (2026) Trainable subnetworks reveal insights into structure knowledge organization in protein language models. *PLoS computational biology*, 22(2), e1013925.

Anderson OH, et al. (2026) Flagellar glycosylation with pseudaminic acids is widespread in the genus *Clostridium*. *BMC microbiology*, 26(1).

Buschmann L, et al. (2026) Much ado about nothing: modeling amino acid replacement with predicted protein structures. *Bioinformatics (Oxford, England)*, 42(5).

Ashford P, et al. (2026) Gene duplication is associated with gene diversification and potential neofunctionalization in lung cancer evolution. *Genome research*, 36(3), 561.

Sikora M, et al. (2026) Novel Knotted Solenoid fold with order-shifted coil arrangement leads to nontrivial 31 topology. *Proceedings of the National Academy of Sciences of the United States of America*, 123(17), e2525920123.

Chaves RBR, et al. (2026) Characterization of an AsnC/Lrp-family transcriptional regulator in *Herbaspirillum rubrisubalbicans* M1: linking plant interaction, nitrogen response and PHB metabolism. *Frontiers in microbiology*, 17, 1792436.

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.

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

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.

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.

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*.

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