

Resource Summary Report

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SCOP: Structural Classification of Proteins

RRID:SCR_007039

Type: Tool

Proper Citation

SCOP: Structural Classification of Proteins (RRID:SCR_007039)

Resource Information

URL: <http://scop.mrc-lmb.cam.ac.uk/scop/>

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Description: The Structural Classification of Proteins (SCOP) database is a comprehensive ordering of all proteins of known structure, according to their evolutionary and structural relationships. Protein domains in SCOP are hierarchically classified into families, superfamilies, folds and classes. The continual accumulation of sequence and structural data allows more rigorous analysis and provides important information for understanding the protein world and its evolutionary repertoire. SCOP participates in a project that aims to rationalize and integrate the data on proteins held in several sequence and structure databases. As part of this project, starting with release 1.63, we have initiated a refinement of the SCOP classification, which introduces a number of changes mostly at the levels below superfamily. The pending SCOP reclassification will be carried out gradually through a number of future releases. In addition to the expanded set of static links to external resources, available at the level of domain entries, we have started modernization of the interface capabilities of SCOP allowing more dynamic links with other databases.

Synonyms: Structural Classification of Proteins database, SCOP database

Resource Type: database, data or information resource

Defining Citation: [PMID:14681400](#)

Keywords: bio.tools, FASEB list

Resource Name: SCOP: Structural Classification of Proteins

Resource ID: SCR_007039

Alternate IDs: nlx_94704, biotools:scop

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

Record Creation Time: 20220129T080239+0000

Record Last Update: 20260819T044204+0000

Ratings and Alerts

No rating or validation information has been found for SCOP: Structural Classification of Proteins.

No alerts have been found for SCOP: Structural Classification of Proteins.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 98 mentions in open access literature.

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

Yang Y, et al. (2024) Large-scale genomic survey with deep learning-based method reveals strain-level phage specificity determinants. *GigaScience*, 13.

Germon A, et al. (2023) Protein disulfide isomerase A3 activity promotes extracellular accumulation of proteins relevant to basal breast cancer outcomes in human MDA-MB-A231 breast cancer cells. *American journal of physiology. Cell physiology*, 324(1), C113.

Sneha S, et al. (2022) In silico structural and functional characterization of *Antheraea mylitta* cocoonase. *Journal, genetic engineering & biotechnology*, 20(1), 102.

Hofbauer S, et al. (2021) Understanding molecular enzymology of porphyrin-binding ? + ? barrel proteins - One fold, multiple functions. *Biochimica et biophysica acta. Proteins and proteomics*, 1869(1), 140536.

Nishimiya D, et al. (2019) A protein scaffold, engineered SPINK2, for generation of inhibitors with high affinity and specificity against target proteases. *Scientific reports*, 9(1), 11436.

Daugavet MA, et al. (2019) Features of a novel protein, rusticalin, from the ascidian *Styela rustica* reveal ancestral horizontal gene transfer event. *Mobile DNA*, 10, 4.

Sato R, et al. (2019) Function and Role of ATP-Binding Cassette Transporters as Receptors for 3D-Cry Toxins. *Toxins*, 11(2).

Cook CE, et al. (2019) The European Bioinformatics Institute in 2018: tools, infrastructure and training. *Nucleic acids research*, 47(D1), D15.

- Manavalan B, et al. (2019) PFDB: A standardized protein folding database with temperature correction. *Scientific reports*, 9(1), 1588.
- Jin H, et al. (2019) Capsid Structure of a Freshwater Cyanophage Siphoviridae Mic1. *Structure* (London, England : 1993), 27(10), 1508.
- Moroz OV, et al. (2019) Novel Inhibitory Function of the *Rhizomucor miehei* Lipase Propeptide and Three-Dimensional Structures of Its Complexes with the Enzyme. *ACS omega*, 4(6), 9964.
- Zhao Y, et al. (2018) Comparative Analysis of Mutant Huntingtin Binding Partners in Yeast Species. *Scientific reports*, 8(1), 9554.
- Najibi SM, et al. (2017) Protein Structure Classification and Loop Modeling Using Multiple Ramachandran Distributions. *Computational and structural biotechnology journal*, 15, 243.
- Zhu H, et al. (2016) Origin of a folded repeat protein from an intrinsically disordered ancestor. *eLife*, 5.
- Abrusán G, et al. (2016) Alpha Helices Are More Robust to Mutations than Beta Strands. *PLoS computational biology*, 12(12), e1005242.
- Pérez-Lara Á, et al. (2016) PtdInsP2 and PtdSer cooperate to trap synaptotagmin-1 to the plasma membrane in the presence of calcium. *eLife*, 5.
- Sun L, et al. (2016) Prediction of complex super-secondary structure ??? motifs based on combined features. *Saudi journal of biological sciences*, 23(1), 66.
- Kazlauskas D, et al. (2016) The logic of DNA replication in double-stranded DNA viruses: insights from global analysis of viral genomes. *Nucleic acids research*, 44(10), 4551.
- Heride C, et al. (2016) The centrosomal deubiquitylase USP21 regulates Gli1 transcriptional activity and stability. *Journal of cell science*, 129(21), 4001.
- Cho YI, et al. (2015) Comparative analysis of disease-linked single nucleotide polymorphic markers from *Brassica rapa* for their applicability to *Brassica oleracea*. *PloS one*, 10(3), e0120163.