

Resource Summary Report

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Secondary Structure Matching

RRID:SCR_008365

Type: Tool

Proper Citation

Secondary Structure Matching (RRID:SCR_008365)

Resource Information

URL: <http://www.ebi.ac.uk/msd-srv/ssm/>

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Description: Secondary Structure Matching (SSM) is an interactive service for comparing protein structures in 3D. SSM compares to other protein matching services, see results [here](#). It is used as a structure search engine in PISA service (Protein Interfaces, Surfaces and Assemblies). It queries may be launched from any web site, see instructions [here](#) and it is based on the CCP4 Coordinate Library, found [here](#). The service provides for: - pairwise comparison and 3D alignment of protein structures -multiple comparison and 3D alignment of protein structures -examination of a protein structure for similarity with the whole PDB or SCOP archives -best Ca-alignment of compared structures -download and visualization of best-superposed structures using Rasmol (Unix/Linux platforms), Rastop (MS Windows machines) and Jmol (platform-independent server-side java viewer) -linking the results to other services - PDBe Motif, OCA, SCOP, GeneCensus, FSSP, 3Dee, CATH, PDBSum, SWISS-PROT and ProtoMap. Sponsors: The project is funded by the Collaborative Computational Project Number 4 in Protein Crystallography of the Biotechnology and Biological Sciences Research Council

Synonyms: SSM

Resource Type: data or information resource, database

Keywords: alignment 3d, compare, interactive, interface, matching, multiple, pairwise, protein, secondary, structure, visualization

Resource Name: Secondary Structure Matching

Resource ID: SCR_008365

Alternate IDs: nif-0000-25563

Record Creation Time: 20220129T080247+0000

Ratings and Alerts

No rating or validation information has been found for Secondary Structure Matching.

No alerts have been found for Secondary Structure Matching.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 165 mentions in open access literature.

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

Adámková K, et al. (2025) Substrate preference, RNA binding and active site versatility of *Stenotrophomonas maltophilia* nuclease SmNuc1, explained by a structural study. The FEBS journal, 292(1), 129.

Sakurai R, et al. (2025) Culture-independent discovery of a novel thermotolerant lipase and its producer from mesophilic anaerobic digestion sludge. Applied microbiology and biotechnology, 109(1), 283.

Morais de Sousa S, et al. (2025) Functional genomics and structural insights into maize aldo-keto reductase-4 family: Stress metabolism and substrate specificity in embryos. The Journal of biological chemistry, 301(7), 110404.

Li SD, et al. (2023) Fibulin2: a negative regulator of BMSC osteogenic differentiation in infected bone fracture healing. Experimental & molecular medicine, 55(2), 443.

Bampali K, et al. (2023) GABAA receptor-mediated seizure liabilities: a mixed-methods screening approach. Cell biology and toxicology, 39(6), 2793.

Amambua-Ngwa A, et al. (2023) Chloroquine resistance evolution in *Plasmodium falciparum* is mediated by the putative amino acid transporter AAT1. Nature microbiology, 8(7), 1213.

Bitter J, et al. (2023) Enzymatic β -elimination in natural product O- and C-glycoside deglycosylation. Nature communications, 14(1), 7123.

Mao W, et al. (2023) On the role of nucleotides and lipids in the polymerization of the actin homolog MreB from a Gram-positive bacterium. eLife, 12.

Alenazi J, et al. (2022) Crystal structure of a short-chain dehydrogenase/reductase from *Burkholderia phymatum* in complex with NAD. Acta crystallographica. Section F, Structural biology communications, 78(Pt 2), 52.

Bampali K, et al. (2022) Tricyclic antipsychotics and antidepressants can inhibit γ -aminobutyric acid (GABA) receptors by two distinct mechanisms. *British journal of pharmacology*, 179(14), 3675.

Beard DK, et al. (2022) Crystal structure of a hypothetical protein from *Giardia lamblia*. *Acta crystallographica. Section F, Structural biology communications*, 78(Pt 2), 59.

Maddy J, et al. (2022) Crystal structure of an inorganic pyrophosphatase from *Chlamydia trachomatis* D/UW-3/Cx. *Acta crystallographica. Section F, Structural biology communications*, 78(Pt 3), 135.

Davidson J, et al. (2022) Crystal structure of a putative short-chain dehydrogenase/reductase from *Paraburkholderia xenovorans*. *Acta crystallographica. Section F, Structural biology communications*, 78(Pt 1), 25.

Brooks L, et al. (2022) Crystal structures of glutamyl-tRNA synthetase from *Elizabethkingia anophelis* and *E. meningosepticum*. *Acta crystallographica. Section F, Structural biology communications*, 78(Pt 8), 306.

Murad AM, et al. (2022) Structure and activity of the DHNA Coenzyme-A Thioesterase from *Staphylococcus aureus* providing insights for innovative drug development. *Scientific reports*, 12(1), 4313.

Porter I, et al. (2022) Crystal structures of FolM alternative dihydrofolate reductase 1 from *Brucella suis* and *Brucella canis*. *Acta crystallographica. Section F, Structural biology communications*, 78(Pt 1), 31.

Ramaprasad A, et al. (2022) A choline-releasing glycerophosphodiesterase essential for phosphatidylcholine biosynthesis and blood stage development in the malaria parasite. *eLife*, 11.

Snowden JS, et al. (2021) Structural insight into *Pichia pastoris* fatty acid synthase. *Scientific reports*, 11(1), 9773.

Duarte M, et al. (2021) A dual cohesin-dockerin complex binding mode in *Bacteroides cellulosolvens* contributes to the size and complexity of its cellulosome. *The Journal of biological chemistry*, 296, 100552.

Ultsch M, et al. (2021) Structures of the ApoL1 and ApoL2 N-terminal domains reveal a non-classical four-helix bundle motif. *Communications biology*, 4(1), 916.