

Resource Summary Report

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Database of Secondary Structure Assignments

RRID:SCR_002725

Type: Tool

Proper Citation

Database of Secondary Structure Assignments (RRID:SCR_002725)

Resource Information

URL: <http://swift.cmbi.ru.nl/gv/dssp/>

Proper Citation: Database of Secondary Structure Assignments (RRID:SCR_002725)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on February 28, 2023. Database of secondary structure assignments (and much more) for all protein entries in the Protein Data Bank (PDB) and the program that calculates DSSP entries from PDB entries. DSSP is distributed on a basis of trust and instructions are available on the site. * Precompiled executables are also available for Linux and Windows. (The Windows .exe file was compiled under Linux using Mingw32, has never seen a Windows environment and should thus be virus-free. Download the source if you want to be 100% sure.) Under Windows the DSSP output does not make it to the console, so redirect it to a file instead: dsspcmbi source.pdb destination.dssp > messages.txt * Several changes have been made to the DSSP program to solve problems with recent PDB files. These are documented in the source code. * FTP access to the DSSP files resides at the CMBI: ftp.cmbi.kun.nl/pub/molbio/data/dssp or ftp://ftp.ebi.ac.uk/pub/databases/dssp/. If you have problems downloading the DSSP files, it is likely that your FTP program is not able to handle tens of thousands of files in one directory. In this case, install a proper FTP program, for example NCFTP. However, it is recommended that you download DSSP files with the rsync command.

Abbreviations: DSSP

Resource Type: database, data or information resource, software resource

Defining Citation: [PMID:6667333](#), [PMID:21071423](#)

Keywords: amino acid sequence, hydrogen bonding, protein conformation, proteins, gold standard, bio.tools, FASEB list

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Database of Secondary Structure Assignments

Resource ID: SCR_002725

Alternate IDs: nif-0000-23901, biotools:dssp, OMICS_06247

Alternate URLs: <http://srs.ebi.ac.uk/srsbin/cgi-bin/wgetz?-page+LibInfo+-lib+DSSP>, <https://bio.tools/dssp>, <https://sources.debian.org/src/dssp/>

Old URLs: <http://www.sander.ebi.ac.uk/dssp/>

Record Creation Time: 20220129T080215+0000

Record Last Update: 20260807T042542+0000

Ratings and Alerts

No rating or validation information has been found for Database of Secondary Structure Assignments.

No alerts have been found for Database of Secondary Structure Assignments.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 59 mentions in open access literature.

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

Zatorski N, et al. (2024) Structural analysis of genomic and proteomic signatures reveal dynamic expression of intrinsically disordered regions in breast cancer. *iScience*, 27(9), 110640.

Cisneros AF, et al. (2024) Mutational biases favor complexity increases in protein interaction networks after gene duplication. *Molecular systems biology*, 20(5), 549.

Johnson NV, et al. (2024) Discovery and characterization of a pan-betacoronavirus S2-binding antibody. *Structure (London, England : 1993)*, 32(11), 1893.

Cisneros AF, et al. (2023) Epistasis between promoter activity and coding mutations shapes gene evolvability. *Science advances*, 9(5), eadd9109.

Badonyi M, et al. (2023) Buffering of genetic dominance by allele-specific protein complex assembly. *Science advances*, 9(22), eadf9845.

Alugoju P, et al. (2023) In silico molecular docking and molecular dynamic simulation of agarwood compounds with molecular targets of Alzheimer's disease???. *F1000Research*, 12, 230.

Sica MP, et al. (2022) Protocol to study the oligomeric organization of single-span transmembrane peptides using molecular dynamics simulations. STAR protocols, 3(3), 101636.

Mattox DE, et al. (2021) Comprehensive analysis of lectin-glycan interactions reveals determinants of lectin specificity. PLoS computational biology, 17(10), e1009470.

Mattenberger F, et al. (2021) Globally defining the effects of mutations in a picornavirus capsid. eLife, 10.

Tran TH, et al. (2021) KRAS interaction with RAF1 RAS-binding domain and cysteine-rich domain provides insights into RAS-mediated RAF activation. Nature communications, 12(1), 1176.

Rao RSP, et al. (2021) Evolutionary Dynamics of Indels in SARS-CoV-2 Spike Glycoprotein. Evolutionary bioinformatics online, 17, 11769343211064616.

Das D, et al. (2020) PlantPepDB: A manually curated plant peptide database. Scientific reports, 10(1), 2194.

Sobolev OV, et al. (2020) A Global Ramachandran Score Identifies Protein Structures with Unlikely Stereochemistry. Structure (London, England : 1993), 28(11), 1249.

Hansen BK, et al. (2020) Structure and Function of the Bacterial Protein Toxin Phenomycin. Structure (London, England : 1993), 28(5), 528.

Bakail M, et al. (2019) Design on a Rational Basis of High-Affinity Peptides Inhibiting the Histone Chaperone ASF1. Cell chemical biology, 26(11), 1573.

Humbert MV, et al. (2019) Characterization of two putative Dichelobacter nodosus footrot vaccine antigens identifies the first lysozyme inhibitor in the genus. Scientific reports, 9(1), 10055.

Dharmaiah S, et al. (2019) Structures of N-terminally processed KRAS provide insight into the role of N-acetylation. Scientific reports, 9(1), 10512.

Raj S, et al. (2019) Identification of lead molecules against potential drug target protein MAPK4 from L. donovani: An in-silico approach using docking, molecular dynamics and binding free energy calculation. PloS one, 14(8), e0221331.

Agip AA, et al. (2018) Cryo-EM structures of complex I from mouse heart mitochondria in two biochemically defined states. Nature structural & molecular biology, 25(7), 548.

Osborne AJ, et al. (2018) Two distinct conformations of factor H regulate discrete complement-binding functions in the fluid phase and at cell surfaces. The Journal of biological chemistry, 293(44), 17166.