# Resource Summary Report

Generated by Kravitz on Sep 10, 2026

## HSSP

RRID:SCR_004953
Type: Tool

### Proper Citation

HSSP (RRID:SCR_004953)

### Resource Information

**URL:** http://swift.cmbi.ru.nl/gv/hssp/

**Proper Citation:** HSSP (RRID:SCR_004953)

**Description:** HSSP (homology-derived structures of proteins) is a derived database merging structural (2-D and 3-D) and sequence information (1-D). For each protein of known 3D structure from the Protein Data Bank, the database has a file with all sequence homologues, properly aligned to the PDB protein. Homologues are very likely to have the same 3D structure as the PDB protein to which they have been aligned. As a result, the database is not only a database of sequence aligned sequence families, but it is also a database of implied secondary and tertiary structures. Likely secondary structure are carried over from the PDB protein to each homologous protein. Tertiary structure models can be built by fitting the sequence of the homologue as aligned into the 3D template of the protein of known structure. Special software is needed to construct 3D models by homology, such WHATIF by Gert Vriend or MaxSprout by Liisa Holm and Chris Sander. The command rsync can be used to obtain a local copy of the HSSP. We appreciate receiving an Email from people who do so, but there are no strings attached. Everybody can freely download the files, academia and industry alike. If your institute''s firewall doesn''t allow you to use the (preferred) rsync way of obtaining HSSP files, feel free to work with FTP. The files are in that case available from: ftp://ftp.cmbi.ru.nl//pub/molbio/data/hssp/

**Abbreviations:** HSSP

**Synonyms:** Homology-derived Secondary Structure of Proteins, homology-derived structures of proteins, HSSP - Homology derived Secondary Structure of Proteins, HSSP database, HSSP - Homology-derived Secondary Structure of Proteins, Homology derived Secondary Structure of Proteins

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

**Defining Citation:** PMID:2017436

**Keywords:** gold standard, bio.tools

**Resource Name:** HSSP

**Resource ID:** SCR_004953

**Alternate IDs:** biotools:hssp, nlx_91976

**Alternate URLs:** https://bio.tools/hssp

**Record Creation Time:** 20220129T080227+0000

**Record Last Update:** 20260905T133127+0000

## Ratings and Alerts

No rating or validation information has been found for HSSP.

No alerts have been found for HSSP.

## Data and Source Information

**Source:** SciCrunch Registry

## Usage and Citation Metrics

We found 33 mentions in open access literature.

**Listed below are recent publications.** The full list is available at Kravitz .

Kiouri DP, et al. (2025) Structure-Based Approaches for Protein-Protein Interaction Prediction Using Machine Learning and Deep Learning. Biomolecules, 15(1).

Moberg M, et al. (2025) School nurses' perceptions and experiences of delivering a universal health-promotion program targeting both children and parents in the Swedish primary school context. BMC nursing, 24(1), 1158.

Nishihara A, et al. (2024) Illuminating the coevolution of photosynthesis and Bacteria. Proceedings of the National Academy of Sciences of the United States of America, 121(25), e2322120121.

Nobu MK, et al. (2023) Unique H2-utilizing lithotrophy in serpentinite-hosted systems. The ISME journal, 17(1), 95.

Malek ME, et al. (2023) Parents' experiences of participating in the Healthy School Start Plus programme - a qualitative study. BMC public health, 23(1), 646.

Pataskar A, et al. (2022) Tryptophan depletion results in tryptophan-to-phenylalanine substitutants. Nature, 603(7902), 721.

Roder L, et al. (2022) Impact of pharmacy services on time to elexacaftor-tezacaftor-ivacaftor initiation. Journal of managed care & specialty pharmacy, 28(9), 989.

Madej M, et al. (2022) Effect of Sintering Temperature and Iron Addition on Properties and Microstructure of High Speed Steel Based Materials Produced by Spark Plasma Sintering Method. Materials (Basel, Switzerland), 15(21).

Palopoli N, et al. (2021) Intrinsically Disordered Protein Ensembles Shape Evolutionary Rates Revealing Conformational Patterns. Journal of molecular biology, 433(3), 166751.

Lara Ortiz MT, et al. (2021) Saturation Mutagenesis of the Transmembrane Region of HokC in Escherichia coli Reveals Its High Tolerance to Mutations. International journal of molecular sciences, 22(19).

Gazzarata R, et al. (2020) Healthcare Associated Infections: An Interoperable Infrastructure for Multidrug Resistant Organism Surveillance. International journal of environmental research and public health, 17(2).

Schrempf D, et al. (2020) Scalable Empirical Mixture Models That Account for Across-Site Compositional Heterogeneity. Molecular biology and evolution, 37(12), 3616.

Deng A, et al. (2020) Developing Computational Model to Predict Protein-Protein Interaction Sites Based on the XGBoost Algorithm. International journal of molecular sciences, 21(7).

Wang Y, et al. (2019) Semi-supervised prediction of protein interaction sites from unlabeled sample information. BMC bioinformatics, 20(Suppl 25), 699.

Marchetti J, et al. (2019) Ensembles from Ordered and Disordered Proteins Reveal Similar Structural Constraints during Evolution. Journal of molecular biology, 431(6), 1298.

Jendele L, et al. (2019) PrankWeb: a web server for ligand binding site prediction and visualization. Nucleic acids research, 47(W1), W345.

Latulippe K, et al. (2019) Supporting the Process of Help-Seeking by Caregivers of Functionally Dependent Older Persons Through Electronic Health: Protocol for a Multicenter Co-Design. JMIR research protocols, 8(4), e11634.

Marapaka AK, et al. (2018) Discovery, Structural and Biochemical Studies of a rare Glu/Asp Specific M1 Class Aminopeptidase from Legionella pneumophila. International journal of biological macromolecules, 120(Pt A), 1111.

Burns JA, et al. (2017) Transcriptome analysis illuminates the nature of the intracellular interaction in a vertebrate-algal symbiosis. eLife, 6.

Corral-Corral R, et al. (2017) Systematic Identification of Machine-Learning Models Aimed to Classify Critical Residues for Protein Function from Protein Structure. Molecules (Basel, Switzerland), 22(10).