

Resource Summary Report

Generated by [dkNET](#) on Aug 19, 2026

ConSurf Database

RRID:SCR_002320

Type: Tool

Proper Citation

ConSurf Database (RRID:SCR_002320)

Resource Information

URL: <http://consurfdb.tau.ac.il/>

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Description: Provides pre-calculated evolutionary conservation profiles for proteins of known structure in the PDB. Enables flexibility in setting the parameters of the calculation, and accepts optional uploads of atomic coordinates, multiple sequence alignments, and phylogenetic trees for use in the calculation of conservation profiles.

Abbreviations: ConSurfDB

Synonyms: , consurf-db, ConSurf-DataBase, ConSurf-DB, ConSurfDB, ConSurf Server Database, ConSurfDataBase, ConSurf- Data Base

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

Defining Citation: [PMID:20478830](#), [PMID:15980475](#), [PMID:12499312](#), [PMID:11243830](#)

Keywords: PDB, Protein DataBase, evolution, conservation, protein, structure, pre-calculated, profile, FASEB list

Funding: Tel Aviv University; Ramat Aviv; Israel

Availability: Free, Freely available

Resource Name: ConSurf Database

Resource ID: SCR_002320

Alternate IDs: nif-0000-21098, SCR_007609, BioTools:consurf-db, nif-0000-02685

Alternate URLs: http://bental.tau.ac.il/new_ConSurfDB/, <https://bio.tools/consurf-db>

Old URLs: <http://consurf-hssp.tau.ac.il>

Record Creation Time: 20220129T080212+0000

Record Last Update: 20260819T044053+0000

Ratings and Alerts

No rating or validation information has been found for ConSurf Database.

No alerts have been found for ConSurf Database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 318 mentions in open access literature.

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

Gopalasingam CC, et al. (2026) Structural basis of Neisseria meningitidis quinol dependent nitric oxide reductase activation by dimerization. Communications biology, 9(1).

Camarillo-Benitez S, et al. (2026) Genetic and Molecular Characterization of Treacher Collins Syndrome in Three Mexican Families. International journal of molecular sciences, 27(4).

Xing D, et al. (2026) RNA-binding protein tristetraproline inhibits Th2 cell activation and differentiation in allergic rhinitis by promoting TRIM18 mRNA decay. The Journal of biological chemistry, 302(3), 111240.

Park SK, et al. (2026) Functional dissection of SPOP at the amino acid level reveals a comprehensive functional landscape of variants during tumorigenesis. Proceedings of the National Academy of Sciences of the United States of America, 123(19), e2523210123.

Medina E, et al. (2026) Structural basis for sialoglycan recognition by the immune inhibitory receptor Siglec-10. Structure (London, England : 1993), 34(5), 768.

Hanna MG, et al. (2025) BLTP3A is associated with membranes of the late endocytic pathway and is an effector of CASK. The EMBO journal, 44(21), 6168.

Zhu R, et al. (2025) Decoding allosteric landscapes: computational methodologies for enzyme modulation and drug discovery. RSC chemical biology, 6(4), 539.

Yu K, et al. (2025) Enhanced thermostability of nattokinase by rational design of disulfide bond. Microbial cell factories, 24(1), 51.

Elasbali AM, et al. (2025) A structural genomics approach to investigate Dystrophin mutations and their impact on the molecular pathways of Duchenne muscular dystrophy. Frontiers in genetics, 16, 1517707.

Awan M, et al. (2025) Effect of Myocilin E414K Variant on the Pathogenesis of Primary Open-Angle Glaucoma. *Cureus*, 17(5), e83372.

Akçe?me B, et al. (2025) Identification of deleterious non-synonymous single nucleotide polymorphisms in the mRNA decay activator ZFP36L2. *RNA biology*, 22(1), 1.

Chakraborty C, et al. (2025) Understanding the landscape of cross-species transmission, epidemiology, phylogenetics, and antigenicity of HPAI strain A(H5N1) causing a recent outbreak in the USA. *Journal, genetic engineering & biotechnology*, 23(3), 100547.

Dzuvor CKO, et al. (2025) Rational Design of Multiclade Coronavirus Spike Immunodominant Domain Nanoparticles to Elicit Broad Antibody Responses. *Research square*.

Dzuvor CKO, et al. (2025) Rational Design of Multiclade Coronavirus Spike Immunodominant Domain Nanoparticles to Elicit Broad Antibody Responses. *bioRxiv : the preprint server for biology*.

Sang Y, et al. (2024) Improving the thermostability of *Pseudoalteromonas Porphyræ* γ -carrageenase by rational design and MD simulation. *AMB Express*, 14(1), 8.

Fatalska A, et al. (2024) Recruitment of trimeric eIF2 by phosphatase non-catalytic subunit PPP1R15B. *Molecular cell*, 84(3), 506.

López-Rodríguez VR, et al. (2024) Mutational Profile and Retinal Phenotypes of PCARE-Related Cone-Rod Dystrophies in a Mexican Cohort. *Journal of ophthalmology*, 2024, 4003914.

Heinzinger M, et al. (2024) Bilingual language model for protein sequence and structure. *NAR genomics and bioinformatics*, 6(4), lqae150.

Navratna V, et al. (2024) Structure of the human heparan- γ -glucosaminide N-acetyltransferase (HGSNAT). *eLife*, 13.

Li Y, et al. (2024) Modification of the active centre of nattokinase to enhance its thermostability using a strategy based on molecular dynamics simulation, steered dynamics simulation, and conservative prediction. *Frontiers in nutrition*, 11, 1505584.