

Resource Summary Report

Generated by [RRID](#) on Aug 6, 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: data or information resource, service resource, database

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: 20260806T054338+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 311 mentions in open access literature.

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

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

Hanna MG, et al. (2025) BLTP3A is associated with membranes of the late endocytic pathway and is an effector of CASM. 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.

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.

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. bioRxiv : the preprint server for biology.

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

Sang Y, et al. (2024) Improving the thermostability of Pseudoalteromonas Porphyrae ?-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.

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.

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

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

Cairo LV, et al. (2024) Stress-dependent condensate formation regulated by the ubiquitin-related modifier Urm1. *Cell*, 187(17), 4656.

Gemmer M, et al. (2023) Visualization of translation and protein biogenesis at the ER membrane. *Nature*, 614(7946), 160.

Aschenbrenner D, et al. (2023) Pathogenic Interleukin-10 Receptor Alpha Variants in Humans - Balancing Natural Selection and Clinical Implications. *Journal of clinical immunology*, 43(2), 495.

Pal P, et al. (2023) Parkinson's VPS35[D620N] mutation induces LRRK2-mediated lysosomal association of RILPL1 and TMEM55B. *Science advances*, 9(50), eadj1205.

Xie MJ, et al. (2023) Constructing and interpreting a large-scale variant effect map for an ultrarare disease gene: Comprehensive prediction of the functional impact of PSAT1 genotypes. *PLoS genetics*, 19(10), e1010972.

Fereshteh S, et al. (2023) Defeating a superbug: A breakthrough in vaccine design against multidrug-resistant *Pseudomonas aeruginosa* using reverse vaccinology. *PloS one*, 18(8), e0289609.